DEVELOPING A STRATEGY FOR RED CELL ANTIGEN TYPING AND MATCHING OF BLOOD FOR CHRONIC TRANSFUSION

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A thesis submitted in partial fulfilment of the requirements of
the Faculty of Health and Life Sciences
University of the West of England, Bristol for the degree of
Professional Doctorate in Biomedical Science

This research program was carried out in collaboration with the
School of Biomedical and Healthcare Sciences
Plymouth University Peninsula Schools of Medicine and
Dentistry, Plymouth
and
The Royal Devon and Exeter NHS Foundation Trust, Exeter

Submission date: July 2018

ABSTRACT

Red cell allo and autoantibodies have the potential to cause haemolytic transfusion reactions and can also create challenges with subsequent compatibility testing, sourcing compatible blood, delays in the provision of blood and cost implications. This is particularly relevant in patients who are dependent on chronic transfusion support; such as those with sickle cell disease, thalassaemia, haematological malignancies and renal disease. A retrospective review of chronically transfused patients with haematological malignancies and renal disease, treated at the Royal Devon and Exeter NHS Foundation Trust (RD&E), revealed considerably higher costs associated with provision of blood for patients with red cell allo/autoantibodies than for non-immunised patients, providing new evidence to support the cost effectiveness of extended antigen matching for these groups of patients.

The risk of development of red cell allo/autoantibodies could be reduced by a type and match strategy for, at least, Rh (CcEe) and K antigens as well as the standard ABO and RhD match. To support this strategy a novel technique was validated for high throughput extended automated red cell antigen serological phenotyping suitable for use in the hospital transfusion setting.

Red cell genotyping assays can also support a type and match strategy; however, these assays have not been evaluated for use in the hospital transfusion service setting in the United Kingdom (UK). A platform for this

technique was evaluated; the results compared well to the serological assay, and the assay showed some potential for routine use.

A large scale randomised controlled trial to investigate the benefit and cost effectiveness of a type and match strategy has not been attempted in the UK, therefore a pilot study was performed in which patients were randomly assigned to a standard care or intervention (type and match) group. The pilot study demonstrated the feasibility of a larger scale trial and provided new evidence supporting the potential to implement a type and match strategy within the hospital transfusion service, using routine blood stocks.

Implementation of an extended type and match strategy, utilising the new assay for extended serological phenotyping and the lessons learned from the pilot study, has been implemented for patients with haematological malignancies and renal disease at the RD&E. Patients identified as potential recipients of chronic transfusion support are serologically phenotyped for Rh (CcEe) and K antigens prior to transfusion. Changes have been made to the red cell stock storage area and the laboratory information management system to support provision of matched blood for transfusion. The program is being monitored for its effectiveness in reducing both allo/autoimmunisation rate and the cost of provision of blood.

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PUBLICATIONS

Typing and matching blood for chronically transfused patients – a pilot study. Davies, J. Transfusion Medicine (2016), 26 (Suppl.2): 35.

Blood Group Genotyping Using the BloodChip ID Core XT: Potential for Use in the Hospital Transfusion Setting. Davies, J. Transfusion Medicine (2014), 24 (Suppl. 2), 39.

Developing a strategy for red cell antigen typing and matching of blood for chronic transfusion. Davies, J. Transfusion Medicine (2013), 23, (Suppl. 2): 43.

ABBREVIATIONS

AHG	Anti-human globulin
ALL	Acute lymphocytic leukaemia
AML	Acute myeloid leukaemia
ANCOVA	Analysis of covariance
APML	Acute pro-myelocytic leukaemia
BCSH	British Committee for Standards in Haematology
BMT	Bone marrow transplant
C3d	Complement component 3
CAT	Column agglutination test
CD	Cluster of differentiation
CI	Confidence interval
CLL	Chronic lymphocytic leukaemia
CMML	Chronic myeloid/monocytic leukaemia
DAT	Direct antiglobulin test
DARC	Duffy antigen chemokine receptor
DNA	Deoxyribonucleic acid
DSTR	Delayed serological transfusion reaction
EDTA	Ethylenediamine tetraacetic acid
EPO	Erythropoietin
ESRD	End stage renal disease

FAB French-American-British

HEA Human erythrocyte antigens

HLA Human leukocyte antigens

hrEPO Human recombinant Erythropoietin

HUGO Human Genome Organisation

IAT Indirect antiglobulin test

IgG Immunoglobulin G

IgM Immunoglobulin M

IPS Integrated Pathology System

ISBT International Society of Blood Transfusion

ITP Idiopathic thrombocytopaenic purpura

JPAC Joint United Kingdom Blood Transfusion and Tissue Transplantation Services Professional Advisory Committee

LISS Low ionic strength saline

MALDI-TOF MS Matrix Assisted Laser Desorption/ionisation Time of Flight Mass Spectrometry

MDS Myelodysplastic syndrome

MPD Myeloproliferative disorder

MPN Myeloproliferative neoplasm

MPS Massively parallel sequencing

NCABT	National Comparative Audit of Blood Transfusion
NEP	Nonexofacial polymorphism
NGS	Next Generation Sequencing
NHL	Non-Hodgkin's lymphoma
NHS	National Health Service
NHSBT	National Health Service Blood and Transplant
NICE	National Institute for Health and Care Excellence
NIHR	National Institute for Health Research
NRES	National Research Ethics Service
NTD	Not determined
PBS	Phosphate buffered saline
PCR	Polymerase chain reaction
PRV	Polycythaemia rubra vera
QC	Quality control
RCT	Randomised controlled trial
SAPE	Streptavidin R-phycoerythrin
SCD	Sickle cell disease
SD	Standard deviation
SNP	Single nucleotide polymorphism
SSP-PCR	Sequence specific primer – polymerase chain reaction

UK United Kingdom

VAT Value Added Tax

VWD Von Willebrand's disease

WW1 World War 1

ACKNOWLEDGEMENTS

I would like to express my gratitude to the following people who have supported me in the completion of this project:

Dr Ruth Morse and Dr Paul White at the University of the West of England. Dr Morse for her help and support as my supervisor and Dr White for his assistance with the statistical elements of the work.

Dr Neil Avent and Dr Tracey Madgett at the University of Plymouth for their support with the blood group genotyping testing.

Dr Paul Kerr at the Royal Devon and Exeter NHS Foundation Trust for his support and assistance with the pilot study.

Stacey Flay at the Royal Devon and Exeter NHS Foundation Trust for recruiting the patients to the pilot study.

The Exeter Leukaemia Fund at the Royal Devon and Exeter NHS Foundation Trust for donating funding to support the purchase of the blood group genotyping assay kit.

The Molecular Genetics Department at the Royal Devon and Exeter NHS Foundation Trust for DNA extraction work.

John Herbert for creating the diagrams of the red cell antigen structures in section 1.3.2.

1 INTRODUCTION

1.1 Blood and blood components for transfusion

The collection and storage of blood for transfusion was introduced during the First World War (WW1) in 1917 (Robertson, 1918; Makins, 1922). Blood was collected from “lightly wounded” soldiers and mixed with a preservative/anticoagulant solution of sodium citrate with glucose, allowing storage for up to 14 days. This process became known as blood banking and it gave the army the ability to transfuse close to the front line with lifesaving effects (Makins, 1922). The birth of the modern blood bank, with blood collected from volunteer donors from the general population is attributed to Percy Lane Oliver, who, in 1921, received a request for an emergency donor and within five years had recruited 400 volunteers to a donor panel (Starr, 1999).

In the interval between the First and Second World Wars, methods for the separation of whole blood into its component parts (red cells and plasma), led to the clinical use of plasma for treating severe infections by Strumia and his group in 1927 (Strumia and McGraw, 1941). The introduction of plastic bags for the storage of blood in 1950 (Walter and Murphy, 1952), rather than the glass bottles as originally used, facilitated further separation of the donated blood. This enabled the separation of whole blood into the blood components (including fresh frozen plasma, platelet concentrates, and cryoprecipitate) available today. The availability of these blood components enables targeted therapy for

specific deficiencies of blood constituents in patients, caused by inherited or acquired conditions.

Blood and blood components are used in a wide variety of medical and surgical conditions and their life saving qualities are without question. In the United Kingdom (UK) more than 50% of the red cell components collected, processed and distributed by the National Health Service Blood and Transplant (NHSBT) are transfused for non-surgical conditions (JPAC, 2014). A national audit of blood use in medical patients conducted in 2011 in the UK (NCABT, 2011) revealed that the majority of red cells were transfused to patients with haematological diagnoses (28%), despite the audit restricting the number of patients with those conditions that were included within the review. Other recipients of red cells were patients with acute or chronic gastrointestinal haemorrhage (17%), non-haematological cancer (15%), patients in intensive care units (7%) and patients with renal failure (4%). A later audit in 2014 (NCABT, 2014) revealed that medical usage accounted for 67.4% of all red cell units used in the UK, with haematological and non-haematological (including renal failure) anaemia being the largest user (54.5%) Other blood usage was seen in gastrointestinal bleeding (12%), obstetrics and gynaecology (6%), cardiothoracic surgery (6%), gastrointestinal surgery (4%), trauma (4%) and orthopaedics (4%). Thus, a large proportion of the approximately two million red cell components collected annually in the UK are given to patients requiring chronic transfusion support, namely those with

haematological malignancies, non-haematological cancers and renal failure.

At the Royal Devon and Exeter NHS Foundation Trust (RD&E) the red cell usage is broken down as follows; medical conditions (78%), surgery (21%) and obstetrics/gynaecology (1%). The majority of red cell usage is for patients with haematological (41%) and non-haematological anaemia (27%), followed by gastrointestinal bleed (8%) and trauma (8%). The RD&E clinical haematology department has an inpatient and outpatient service providing care for patients with haematological conditions, and also performs autologous peripheral blood stem cell transplants for patients with conditions such as myeloma and lymphoma. A comprehensive day case, inpatient and outpatient renal service is provided at the main hospital site and in five satellite hospital units. The service provides treatment for patients with acute (usually reversible) and chronic (usually irreversible) kidney failure, and those with kidney transplant. The fact that the majority of red cells are transfused to patients with haematological or renal anaemia provided the rationale for the focus on these cohorts within the research work. The non-emergency nature of blood transfusion in chronic anaemia, compared to that in gastrointestinal haemorrhage and trauma, would, in theory, allow for antigen typing and extended matching of blood for these patients.

1.2 Blood component support in chronic transfusion

Cancer is the one of the most common causes of mortality in the developed world (Cartwright *et al.,* 1999; Ferlay *et al.,* 2007; Office for National Statistics, 2012). In 2012 lymphoid cancer, a haematological malignancy, accounted for 2.6% of the death rate in males (Office for National Statistics, 2012). In addition to the substantial mortality rate for this type of cancer, and other haematological malignancies, treatment costs can also be high, including prolonged hospitalisation, chemotherapy, drugs and other specialised support such as blood component therapy (Yu *et al.,* 2007).

The haematological malignancies are a diverse group which were originally divided into the leukaemias/myelodysplasias, coded by the French-American-British (FAB) classification (Bennet *et al*., 1976) and the Morphology Immunology Cytogenetic classification (Van den Berghe, 1988), and the lymphomas, which historically were subjected to a multitude of classifications (Gerrard-Marchant *et al.,* 1974; Lukes and Butler, 1986; Harris *et al.,* 1994; Chan *et al.,* 1994; Chan *et al*., 1995). They were classified according to lineage by the World Health Organization Clinical Advisory Committee (Swerdlow *et al*., 2008) in an attempt to present a classification system that is recognised worldwide. The classifications have been more recently revised in 2016 for lymphoid neoplasms (Swerdlow *et al.,* 2016*)* and myeloid neoplasms and acute leukaemia *(*Arber *et al.,* 2016*).* A simplified version of the World Health

Organisation (WHO) classification of lymphoid neoplasms, myeloid neoplasms and acute leukaemias is shown in table 1.1.

Table 1.1: World Health Organisation (WHO) classification of lymphoid neoplasms, myeloid neoplasms and acute leukaemia

The table shows a simplified version of the WHO classification of lymphoid neoplasms (Swerdlow et al., 2016) myeloid neoplasms and acute leukaemia (Arber et al., 2016). For the purposes of this study the table only includes the major subtypes (in bold type) and categories seen in the patients included within the retrospective review (chapter 3) and the pilot study (chapter 6). The full classifications can be found using the hyperlinks for lymphoid neoplasms and myeloid neoplasms and acute leukaemia.

Lymphoid neoplasms	***Myeloid neoplasms***	***Acute leukaemia***
Chronic lymphocytic leukaemia (CLL)	*Myelodysplastic/myeloproliferative neoplasms (MDS/MPS)*	*Acute myeloid leukaemia (AML)*
Hairy cell leukaemia (HCL)	*Chronic myelomonocytic leukaemia (CMML)*	*Acute lymphoblastic leukaemia (ALL) (B-cell or T-cell)*
Waldenström macroglobulinemia	*Chronic myeloid leukaemia (CML)*	
Mantle cell lymphoma (MCL)		
Diffuse large B-cell lymphoma (DLBCL)		
Hodgkin lymphoma		
Plasma cell myeloma		

Morbidity and mortality rates have historically been high in patients with haematological malignancies, with mortality rates reaching 75.6% in certain countries (Grais, 1962). In England and Wales during the years 1945 to 1957, mortality rates were found to range between 19.8% for chronic myeloid leukaemia to 59% for acute leukaemia (Court-Brown and Doll, 1959). Recent advances in the treatment of patients with haematological malignancies, using chemotherapy or high dose chemotherapy combined with bone marrow or stem cell transplantation, have increased the survival rate in this group of patients (Champlin and Gale, 1987), with complete remission rates of more than 80% seen in young adult patients with acute lymphocytic leukaemia (Dombret and Gardin, 2016). However, the intense treatment regimens directed at the progenitor cells within the bone marrow result in anaemia and thrombocytopenia, which, if untreated, are also life threatening conditions, consequently the patient's survival becomes dependent on blood component support (NICE 2003).

Patients with acute or chronic kidney disease may also suffer from anaemia caused by the disease (Brugnara and Eckardt, 2011) and be dependent on blood transfusion for periods of time. Anaemia is common in patients with kidney disease, which is caused by decreased synthesis of erythropoietin, a hormone produced by the kidneys that stimulates the bone marrow to make red blood cells (Erslev, 1953; Jacobson *et al.,* 1957). The identification and treatment of anaemia in this group of patients is important because anaemia has the potential to cause adverse

effects including reduced oxygen utilisation, increased cardiac output and left ventricular hypertrophy, increase in the progression of the disease and reduction in immune responsiveness (NICE 2011). A study in diabetic nephropathy, the leading cause of end stage renal disease (ESRD), found that even mild anaemia increased the risk of progression to ESRD and that anaemia was an independent risk factor for disease progression (Mohanram *et al.,* 2004). For patients with ESRD a common treatment option is haemodialysis, however, this process can cause blood loss during the processing stage within the haemodialysis machine, exacerbating the extent of anaemia (NIH, 2016). The prevalence of anaemia in chronic kidney disease in the UK is approximately 12% (NICE 2011). A review in the United States estimated that anaemia in patients with kidney disease ranged from 2% in the early stages to over 70% in ESRD (Astor *et al.,* 2002).

The Canadian Hemodialysis Morbidity Study found that for patients with ESRD on haemodialysis the probability of surviving 12 months without receiving a blood transfusion was 47.2% for males and 27.5% for females (Churchill *et al.,* 1992). Although blood transfusion therapy in patients with renal disease has dramatically reduced over the last 20 years since the introduction of human recombinant erythropoietin (hrEPO) therapy, blood transfusion is still a treatment option if clinically indicated (NICE 2011; Mikhail *et al.,* 2010) especially during haemodialysis. In addition approximately 10% of patients become resistant to the effects of hrEPO (Van der Putten *et al.,* 2008) for various reasons including iron deficiency,

infection/inflammation, severe hyperparathyroidism and inadequate dialysis (Drüeke, 2001; Priyadarshi and Shapiro, 2006; Ribeiro *et al.*, 2013).

1.3 Blood group systems and red cell antigens

1.3.1 Blood group systems

The term blood group refers to variations and polymorphisms in the blood, related to red cell surface antigens (Daniels, 2013). The most well-known system is the ABO system and the most well-known antigen is the RhD, due to their use in the blood donor setting. Variations in the antigens on the red cell surface can only be called a blood group if they are defined by an antibody.

The ABO blood group system and corresponding antibodies were first discovered by Landsteiner in 1900 using direct agglutination techniques (Landsteiner, 1900 cited in Daniels 2013). However, not all blood group antibodies are able to directly agglutinate red cells, and it was not until the development of the indirect antiglobulin test (IAT) in 1945 (Coombs *et al.*, 1945a; Coombs *et al.*, 1945b) that other, so-called “incomplete” red cell antibodies could be identified, and their corresponding blood group systems and antigens named. New DNA based technologies have facilitated the identification of new blood group systems and allowed mapping of the genes controlling the expression of the antigens within the system to the chromosomal location. As such, the number of recognised

blood group systems is ever increasing. A standard nomenclature for these blood groups and their antigens was first developed by the International Society of Blood Transfusion (ISBT) Working Party on Red Cell Immunogenetics and Blood Group Terminology in 1980. Each blood group system is assigned a number, the system name which, for the well-known systems may be the historically assigned name, the system symbol and the symbol for each gene within the system (table 1-2). To facilitate international standardisation of gene symbols, each gene symbol for the blood group families are recognised and approved by the Human Genome Organisation (HUGO). Application of this nomenclature on an international scale ensures that publications including information on blood group systems have standardised terminology, facilitating literature searches for researchers. In order for a red cell antigen to be named as a blood group system it is required to fulfil the criteria set out by the ISBT; it must be defined by a corresponding human alloantibody, it must be an inherited character, the gene encoding the antigen must have been identified and sequenced and its chromosomal location must be known (Daniels *et al.,* 2004).

An explanation of the structure, molecular basis and function of blood group systems relevant to this study are given in section 1.3.2. This includes blood group antigens detected using the serological phenotyping assay (chapter 4) and/or the genotyping assay (chapter 5) described in this study. As such, the section will focus on the following blood group systems; ABO, Rh, Kell, Kidd, Duffy, MNS, Diego, Dombrock, Colton, Yt and Lutheran.

Table 1.2: The blood group systems with the gene symbols as recognised by the HUGO (Human Genome Organisation) Gene Nomenclature Committee and the ISBT (International Society of Blood Transfusion)

Table of the blood group systems with the gene symbols as recognised by the HUGO Gene Nomenclature Committee (www.genenames.org updated October 2012) and the ISBT. Approval by the HUGO Gene Nomenclature Committee ensures that each gene symbol is unique thus facilitating electronic data retrieval from publications and databases. The nature of the encoded protein is included; if unknown this is denoted in the table. Key:N/A = not applicable

No.	System name	System symbol	No. of antigens	Gene symbol(s)	Chromosomal location	CD number	Nature of the encoded protein
001	ABO	ABO	*4*	*ABO*	9q34.2	N/A	Galactosyltransferase and N-acetylgalactoseaminyltransferase
002	MNS	MNS	*48*	*GYPA, GYPB, GYPE*	4q31.21	CD235	Unknown
003	P1PK	P1PK	*3*	*A4GALT*	22q13.2	N/A	Galactosyltransferase
004	Rh	RH	*55*	*RHD, RHCE*	1p36.11	CD240	Unknown
005	Lutheran	LU	*22*	*LU*	19q13.32	CD239	Adhesion molecule
006	Kell	KEL	*36*	*KEL*	7q34	CD238	Metalloendopeptidase?

No. (continued)	System name (continued)	System symbol (continued)	No. of antigens (continued)	Gene symbol(s) (continued)	Chromosomal location (continued)	CD number (continued)	Nature of the encoded protein (continued)
007	Lewis	LE	*6*	*GUT3*	19q13.3	N/A	Fucosyltransferase
008	Duffy	FY	*5*	*DARC*	1q23.2	CD234	Chemokine receptor
009	Kidd	JK	*3*	*SLC14A1*	18q12.3	N/A	Urea transporter
010	Diego	DI	*22*	*SLC4A1*	17q21.31	CD233	Anion exchanger
011	Yt	YT	*3*	*ACHE*	7q22.1	N/A	Acetylcholinesterase
012	Xg	XG	*2*	*XG, MIC2*	Xp22.33	CD99 (MIC2 product)	Adhesion molecule
013	Scianna	SC	*7*	*ERMAP*	1p34.2	N/A	Adhesion molecule?
014	Dombrock	DO	*7*	*ART4*	12p12.3	CD297	ADP ribosyltransferase
015	Colton	CO	*4*	*AQP1*	7p14.3	N/A	Water channel
016	Landsteiner-Wiener	LW	*3*	*ICAM4*	19p13.2	CD242	Adhesion molecule
017	Chido/Rodgers	CH/RG	*9*	*C4A, C4B*	6p21.3	N/A	Complement factor
018	H	H	*1*	*FUT1*	19q13.33	CD173	Fucosyltransferase
019	Kx	XK	*1*	*XK*	Xp21.1	N/A	Membrane transport protein?

No. (continued)	System name (continued)	System symbol (continued)	No. of antigens (continued)	Gene symbol(s) (continued)	Chromosomal location (continued)	CD number (continued)	Nature of the encoded protein (continued)
020	Gerbich	GE	*11*	*GYPC*	2q14.3	CD236	Cytoskeletal element
021	Cromer	CROM	*19*	*CD55*	1q32.2	CD55	Complement cascade regulator
022	Knops	KN	*9*	*CR1*	1q32.2	CD35	Cell surface receptor
023	Indian	IN	*5*	*CD44*	11p13	CD44	Adhesion molecule
024	Ok	OK	*3*	*BSG*	19p13.3	CD147	Plasma membrane protein
025	Raph	RAPH	*1*	*CD151*	11p15.5	CD151	Adhesion molecule
026	John Milton Hagen	JMH	*6*	*SEMA7A*	15q24.1	CD108	Adhesion and signalling molecule?
027	I	I	*1*	*GCNT2*	6p24.2	N/A	N-acetylglucosaminyltransferase
028	Globoside	GLOB	*1*	*B3GALT3*	3q26.1	N/A	N-acetyl galactosaminyltransferase
029	Gill	GIL	*1*	*AQP3*	9p13.3	N/A	Water channel
030	Rh-associated glycoprotein	RHAG	*4*	*RHAG*	6p21-qter	CD241	Ammonium and carbon dioxide transporter
031	FORS	FORS	*1*	*GBGT1*	9q34.13	N/A	Unknown

No. (continued)	**System name (continued)**	**System symbol (continued)**	**No. of antigens (continued)**	**Gene symbol(s) (continued)**	**Chromosomal location (continued)**	**CD number (continued)**	Nature of the encoded protein (continued)
032	JR	JR	*1*	*ABCG2*	4q22	N/A	Unknown
033	LAN	LAN	*1*	*ABCB6*	2q36	N/A	Unknown
034	Vel	VEL	*1*	*SMIM1*	1p36.32	N/A	Unknown
035	CD59	CD59	*2*	*CD59*	11p14-p13	CD59	Unknown
036	Augustine	AUG	*2*	*SCL29A1*	6p21.1	N/A	Unknown

1.3.2 Biochemistry, genetic basis and function of blood groups systems

Blood group antigens are either protein determinants, which represent the primary products of blood group system genes, or carbohydrate determinants on glycoproteins or glycolipids, in which the products of the genes controlling antigen expression are glycosyltransferase enzymes (Daniels, 2013). The following subsections explain the biochemistry, molecular basis and function of the blood group systems and antigens important to this study. Unless otherwise referenced, the information in sections 1.3.2.1 to 1.3.2.11 is taken from the Human Blood Groups reference book by Daniels (2013).

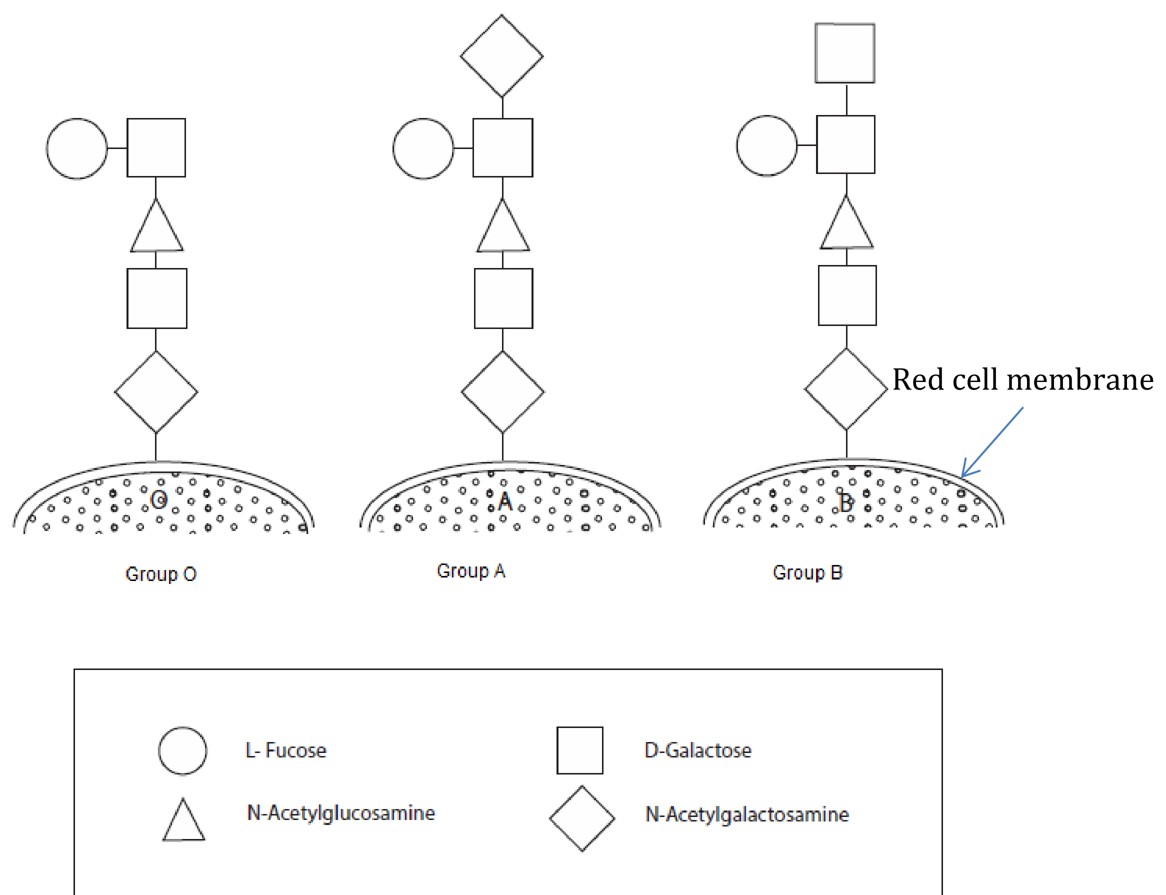
1.3.2.1 ABO system

The ABO blood group system comprises of four antigens, the H antigen encoded by the *FUT1* locus on chromosome 19 and the ABO antigens encoded by the *ABO* gene on chromosome 9. The *H* allele produces α1,2-L fucosyltransferase at the *FUT1* locus, this enzyme catalyses the transfer of L-fucose to its acceptor substrate, D-Galactose, resulting in the H determinant. The ABO blood group type is determined by alleles at the *ABO* locus. The product of the *A* allele is α1,3-N-acetyl-D-galactosaminyltransferase, which attaches N-acetylgalactosamine to the H determinant and the *B* allele produces α1,5-D-galactosyltransferase, which attaches D-Galactose to the H determinant. The third allele at the locus, *O*, does not produce an active enzyme and so the H determinant

remains unchanged. ABO antigens are expressed on carbohydrate chains on glycoproteins, mainly the poly-N-acetyllactosaminyl N-glycans of the band 3 or band 4.5 proteins. Expression of the antigens is dependent on the presence of specific monosaccharides attached to a precursor disaccharide at the non-reducing end of a carbohydrate chain, shown in simple diagrammatic form in figure 1.1. The carbohydrate chains are built up by the sequential addition of monosaccharides catalysed by a specific glycoslytransferase. It is these glycoslytransferases that represent the primary products of the ABO genes.

The function of the ABO antigens is unknown; however, the carbohydrate structures which carry the ABO red cell antigens form part of the glycocalyx, an extra-cellular matrix acting to protect the cell from damage or invasion by pathogenic micro-organisms (Viitala and Järnefelt, 1985; Kościelak, 2012). The ABH determinants on the red cells are carried, mainly, on the anion exchange protein, band 3, and band 4.5 which is a glucose transporter.

Figure 1.1 Structure of the ABO antigens



The diagram shows the immunodominant sugars in the ABO blood group system. The L-Fucose sugar denoting the blood group O is, more correctly, known as the H determinant, if this sugar is not present then A or B antigens cannot be expressed, even if the genes are present. This results in the rare H-deficient (Bombay) phenotype. Expression of A and B antigens is determined by enzymes produced by alleles at the ABO locus which catalyse the attachment of the relevant sugar determinants to the H structure. (Adapted from Diamed, cited in Immunobase 1, http://www.bio-rad.com/en-uk/product/immunobase?ID=LO52IK5Y7).

1.3.2.2 Rh system

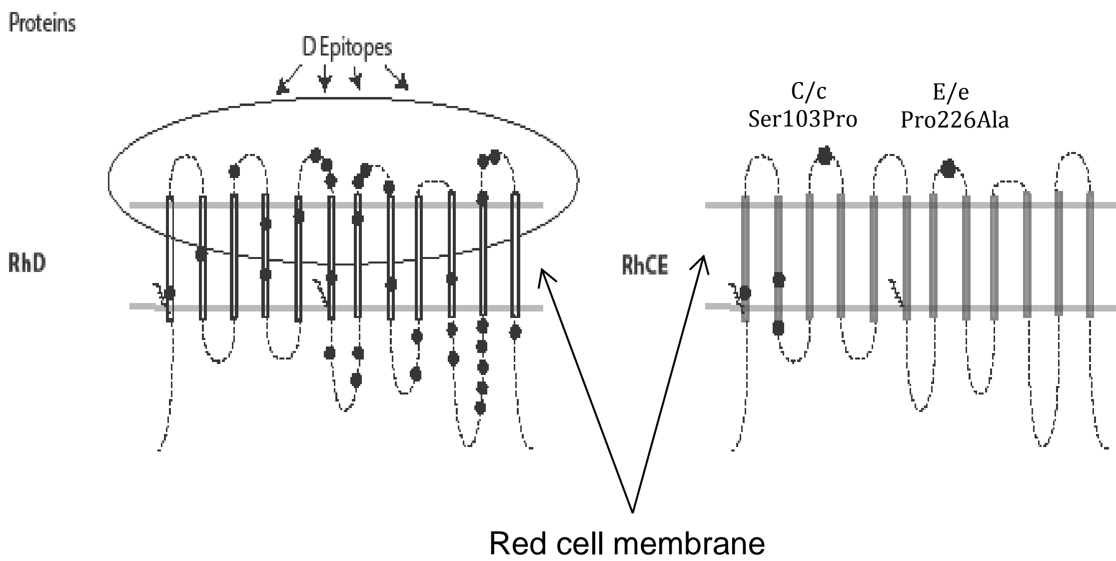
The Rh blood group system is a highly complex system, with 55 antigens encoded by two homologous, closely linked genes on chromosome 1 (ISBT 004 RHCE alleles v4.0_20180208). The *RHD* gene produces the RhD antigen, and the *RHCE* gene produces the Cc and Ee antigens. C and c, E and e represent two pairs of antithetical antigens, with polymorphisms controlled by *RHCE.* The C/c and E/e phenotypes arise as a result of a single amino acid substitution; serine to proline at position 103 for C/c and proline to alanine at position 226 for E/e.

Each antigen has been allocated a number, for example, RH1 (D), RH2 (C), RH3 (E), RH4 (c), RH5 (e) and RH8 (C^w). The alleles are inherited as haplotypes, often referred to using the Fisher-Race or Wiener terminology. The Fisher-Race terminology was based on the premise that the Rh phenotype was controlled by three closely linked loci on each chromosome of a homologous pair, each of which has its own set of alleles; Dd, Cc and Ee (the d antigen does not exist but is used in this terminology to denote the absence of the D antigen). They postulated that the loci were so closely linked that the three genes on chromosome were always inherited together (Fisher, cited in Race, 1944). Wiener, conversely, theorised that there was only one gene complex with eight alleles, R^o, R^1, R^2, R^z, r, r', r'', r^y, controlling the Rh phenotype (Wiener, 1943). Both theories are too simplistic to explain the Rh system antigens and resultant phenotypes but they are commonly used for the interpretation of serological reactions within hospital transfusion services.

The Rh system antigens (RhD, C, c, E and e) are carried on hydrophobic, non-glycosylated proteins which cross the red cell membrane 12 times (Daniels, 2013)(figure 1.2). An associated protein, the RhAG glycoprotein forms complexes with the Rh protein within the cell membrane. The exact functions of the Rh and RhAG proteins are not yet known, but there is some evidence to suggest that the RhAG is involved in the transport of ammonium ions and carbon dioxide (Marini *et al.,* 1997; Endeward *et al.,* 2008). The RhD negative phenotype is a result of the total absence of the RhD polypeptide from the red cell membrane, in Caucasian populations this is usually as a result of homozygosity of a deletion of *RHD*. In black Africans, however, the D negative phenotype is often caused by the presence of an inactive *RHD* called the *RHD* pseudogene, or a hybrid gene *RHD-CE-D*^{s}. The hybrid genes do not produce a D antigen, but probably produce an abnormal C antigen, and are associated with the VS+V- phenotype (Daniels, 2013). There are many variant antigens within the Rh system, as described by Daniels (2013), which create challenges for serological phenotyping and genotyping assays. The most common variants in the UK involve the D antigen, recommended practice in hospital laboratories is to test the patient cells against an IgM monoclonal anti-D reagent that does not detect the DVI variant (BCSH 2012). This practice is recommended as individuals with the DVI phenotype are likely to produce anti-D if transfused with D positive red cells, whereas other D variants are at less risk of developing anti-D. Variants to other Rh antigens are rare, particularly in Caucasian

populations, and so testing is not included in serological phenotyping assays. However, assays for some of these variants are included in genotyping assays (see chapter 5). The Rh_{null} phenotype, in which neither RhD nor CcEe antigens are expressed on the red cell surface, is extremely rare. There are two types of Rh_{null}; the amorph type, which is a result of inactivating mutations in the *RHCE* and deletion of the *RHD*, or the regulator type, in which the Rh genes are normal but there are inactivating mutations in the *RHAG* gene.

Figure 1.2 Diagrammatic representations of the RhD and RhCE antigen structures



The RhD and RhCE proteins span the red cell membrane and are similar, differing by only 32 to 35 amino acids, the sections of the protein above and below the cell membrane are denoted by dotted lines on the diagram. RhD is composed of many different epitopes (highlighted in the oval above the cell membrane). The RhD variant phenotype occurs when one or more of these epitopes are missing. The RhCE protein carries the Cc and Ee antigens, two pairs of antithetical antigens that differ by a single amino acid change. At position 103 C antigen expression is result of serine and c antigen expression by proline, and at position 226 E results from proline and e from alanine. (Diagram adapted from Westhoff, 2007)

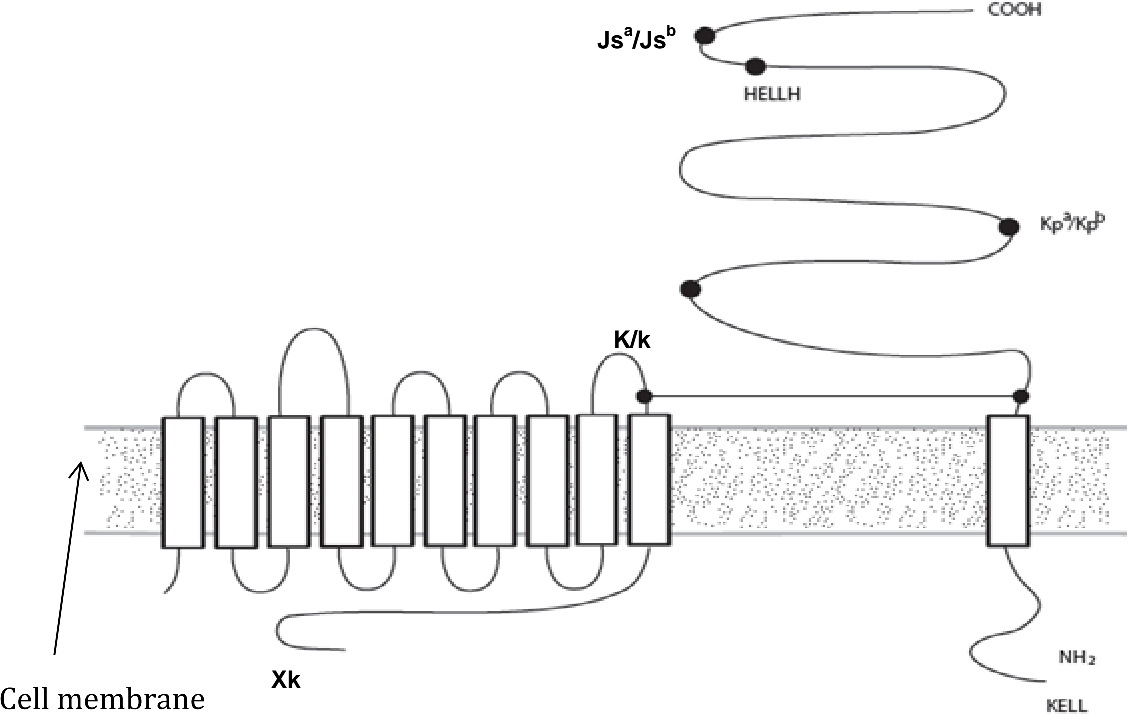
1.3.2.3 Kell system

The Kell system comprises of 36 antigens encoded by a single gene (*KEL*) on chromosome 7 ((ISBT 006) blood group alleles v4.0 160701). The system includes seven sets of antigens with allelic relationships: K and k; Kp^a, Kp^b and Kp^c; Js^a and Js^b; K11 and K17; KEL14 and KEL24; KEL25 and KEL28; KEL31 and KEL38. The antithetical antigens arise as a result of single amino acid changes at different positions on the Kell glycoprotein. The Kell antigens are located on CD238, a red cell transmembrane glycoprotein, which is closely associated with another protein, Xk (see figure 1.3). The Kell-Xk heterodimer is part of the red cell membrane complex that contains band 3, the Rh complex and glycophorin C.

The prevalence of the commonly encountered Kell antigens differs by ethnic group: for example, K positive is more common in Caucasian samples and less often seen in African-Americans; Kp(a+) phenotype is almost always found in whites; and Js(a+) is almost exclusively found in individuals of African ethnicity (Westhoff and Shaz, 2013). Similar to the RhD antigen, the K antigen is strongly immunogenic and the antibody is clinically significant, hence it is recommended in the UK to select K negative red cells for transfusion in females of child bearing potential (BCSH 2012). The Kell-null phenotype (K_0), in which none of the Kell antigens are expressed on the red cell, is a result of homozygosity for *KEL* inactivating mutations. In the K_{mod} phenotype, which also results from *KEL* mutations, the antigens are present but expressed weakly.

The function of the Kell glycoprotein is unclear, although suggestions have been made regarding possible physiological functions in heart, red cell ion transport, neovascularisation in tumours and motor function (Zhu *et al*., 2009) and a role in erythropoiesis (Belhacene *et al.,* 1998).

Figure 1.3 The Kell and Xk heterodimer



The Xk protein and the Kell glycoprotein are linked by a disulphide bond. The diagram shows the approximate locations of the antithetical antigens, K/k, Js^a/Js^b and Kp^a/Kp^b on the Kell glycoprotein. The antithetical antigens arise as a result of single amino acid changes in the glycoprotein; K/k change at position 578 (threonine to methionine), Js^a/Js^b at position 597 (leucine to proline) and Kp^b/Kp^a at position 281 (arginine to tryptophan). The Kx system consists of one antigen which is encoded by the X-linked gene, XK, and located on the Xk protein. The glycoprotein structure also carries a pentameric zinc-binding motif, HELLH. Picture adapted from Slideshare (https://image.slidesharecdn.com/kellbloodgroupsystem-150908110628-lva1-app6892/95/kell-blood-group-system-10-638.jpg?cb=1441710657).

1.3.2.4 MNS system

The MNS system is another highly complex blood group system, with 48 antigens included in the system, encoded by three genes (*GYPA, GYPB* and *GYPE)* located on chromosome 4 (MNS (ISBT 002) blood group alleles v4.1 170119). M and N determinants are carried on glycophorin A (GPA), the major red cell sialic acid-rich glycoprotein. The M and N antigen status of red cells is defined by an amino acid sequence polymorphism at positions 1 and 5 on Glycophorin A. The M antigen has serine at position 1 and glycine at position 5, whereas, the N antigen has leucine at position 1 and glycine at position 5. In addition, the first 26 amino acids of the Glycophorin B protein on the red cell surface are identical to those of the N antigen on Glycophorin A (Daniels, 2013). This gives rise to an antigen denoted "N" to distinguish it from the N antigen on Glycophorin A, this antigen is present on almost all human red cells, irrespective of their MN status.. Rarely, individuals may lack the GPA, and cannot express M and N antigens, this is known as the En(a-) phenotype.

The S and s antigens are located on Glycophorin B (GPB); the S antigen has methionine at position 29, whereas the s antigen has threonine. Individuals deficient in GPB do not express the S, s or the high frequency U antigens. The S-s- phenotype is very rare in Europeans but is noted with a higher frequency in African populations.

Mur is a low incidence antigen, part of the, now obsolete, Miltenberger series, which arises as a result of a replacement of a small section of *GYPB* with a 55 base pair section of *GYPB*. This gives rise to a hybrid glycophorin GP (B-A-B) expressing the Mur antigen. Although the Mur phenotype is rare in white populations, it is relatively common in Asia and is important in terms of clinical significance (see section 1.4.1), hence testing for the antigen is a useful addition to genotyping assays.

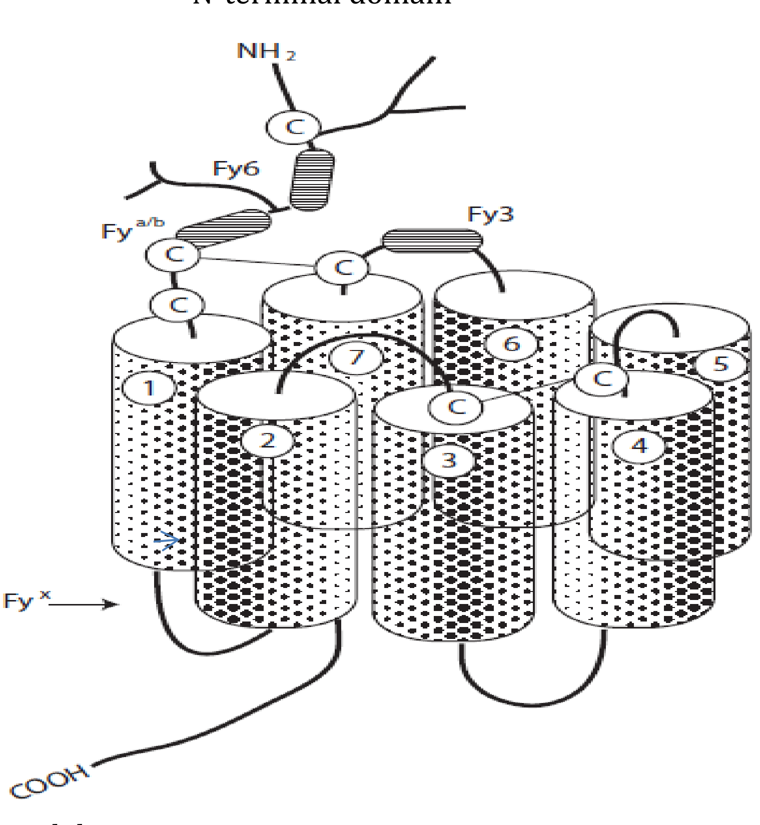
GPA and GPB cross the cell membrane once, and probably exist in their monomeric and dimeric forms. GPA is closely associated with band 3 and is part of the band 3/Rh macrocomplex. Glycophorins have a long, glycosylated extracellular domain, which carries a negative charge. It is thought that the function of the glycophorins may involve prevention of aggregation of red cells, protection against mechanical damage and microbial attack. It is known that individuals with the En(a-) phenotype and those with S-s- have red cells that are less susceptible to malarial invasion.

1.3.2.5 Duffy system

The Duffy blood group system consists of five antigens encoded by a single gene (*DARC*) located on chromosome 1 ((ISBT 008) blood group alleles v4.1 160816). The system includes the antithetical antigens Fy^a and Fy^b, which are polymorphic in both black and white populations, and the high frequency antigens Fy3, Fy5 and Fy6. The Fy(a-b-) phenotype is common in the African population as it confers resistance to the malarial

parasite, *Plasmodium vivax*. This phenotype is caused by homozygosity for a mutation within an erythroid-specific, GATA-1 transcription-factor binding site upstream of the coding region of the Duffy gene. The Duffy antigens are located on a glycoprotein which acts as a chemokine receptor (Pruenster and Rot, 2006) (see figure 1.4), hence it is often referred to as the Duffy antigen receptor for chemokines (DARC). DARC is N-glycoslyated and appears to be a member of the band 3, Rh, Kell/Xk macrocomplex. The GATA mutation prevents the expression of the Duffy glycoprotein on the red cells. The Fy^a/Fy^b polymorphism is a result of an amino acid change from glycine to aspartic acid at position 42. Fy3 and Fy6 are high frequency antigens expressed on red cells of all Duffy phenotypes and Fy5 is similar to Fy3, with the exception that it is not expressed on Fy(a-b-) and Rh_{null} cells. The Fy^x phenotype, which is encoded by the *FY*X* allele results in an amino acid substitution in the intracellular domain of the glycoprotein. This phenotype, which is relatively common in white populations, behaves as a weak expression of the Fy^b antigen. It is also associated with reduced expression of Fy3, Fy5 and Fy6, suggesting that it is a product of reduced levels of DARC in the membrane.

Figure 1.4 The Duffy glycoprotein



A diagrammatic illustration of the Duffy glycoprotein showing how the structure spans the red cell membrane seven times, the cylindrical shapes represent the area of the glycoprotein that passes through the cell membrane. The Fy^a/Fy^b polymorphism is located at position 42 near the N terminal. Fy^X is expressed in the intracellular component at position 89 and is thought to be associated with reduced levels of DARC. The approximate positions of the Fy3 and Fy6 antigens are shown on the diagram.

Adapted from Genome Research (http://genome.cshlp.org/content/17/5/577/F3.expansion).

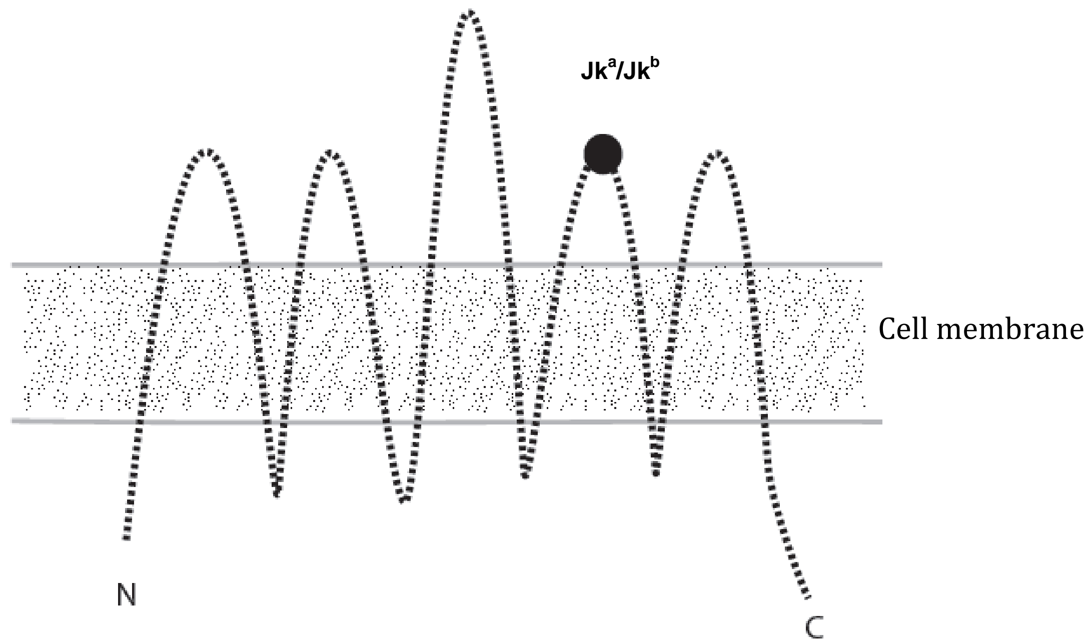
1.3.2.6 Kidd system

The Kidd blood group system comprises of three antigens encoded by the *SLC14A1* gene on chromosome 18 ((ISBT 009) blood group alleles v4.0 160705). The antigens include the antithetical pair, Jk^a and Jk^b and the high incidence antigen Jk3. The Kidd antigens are carried on a glycoprotein that spans the red cell membrane 10 times (figure 1.5). The antithetical antigens, Jk^a and Jk^b, are differentiated by a single amino acid change on the fourth extracellular loop of the glycoprotein (aspartic acid to asparagine at position 280).

The null phenotype, Jk(a-b-), is rare in most populations, with the exception of the Polynesians. It is caused by homozygosity, or compound heterozygosity for a variety of inactivating mutations in the *SLC14A1* gene. Another rare cause of the Jk null phenotype, seen in a Japanese family was considered to be the result of a dominant inhibitor gene that is not inherited at the *JK* locus.

The Kidd glycoprotein is known to be a urea transporter (Sidoux-Walter *et al.*, 1999). It is very similar to another urea transporter, UT-A (Olives *et al.*, 1996), and it is thought that compensating activity by this urea transporter is one of the reasons why the Kidd null phenotype is not associated with any clinical problems.

Figure 1.5 The Kidd glycoprotein



Diagrammatic representation of the Kidd glycoprotein which spans the red cell membrane 10 times. The Jk^a and Jk^b antigen site is located at position 280 (demonstrated by the filled circle on the diagram); the difference between the two antigens is the result of a single amino acid change (aspartic acid and asparagine). The Jk3 phenotype is expressed when either Jk^a and/or Jk^b are present.

(Adapted from: https://ars.els-cdn.com/content/image/1-s2.0-S0065242316300518-f06-04-9780128046869.jpg)

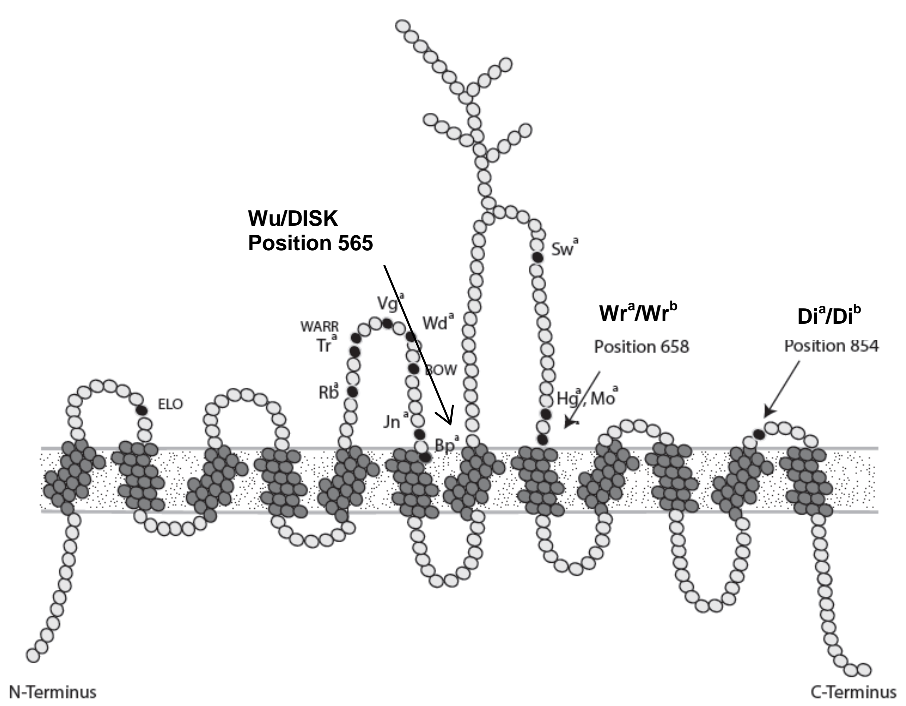
1.3.2.7 Diego system

The Diego system comprises of 22 antigens encoded by a single gene (*SLC4A1)* located on chromosome 17 ((ISBT 010) blood group alleles v3.0 160630). The system includes three pairs of antithetical antigens (Di^a and Di^b, Wr^a and Wr^b, Wu and DISK) and 16 low frequency antigens.

The Diego antigens are expressed on the red cell membrane glycoprotein band 3, Di^a and Di^b, and Wr^a and Wr^b are the result of single amino acid substitutions, leucine/proline and glutamic acid/lysine, at their respective positions 854 and 658. The Wu/DISK polymorphism is a result of a single amino acid substitution, alanine/glycine, at position 565 (see figure 1.6). The remaining low frequency antigens in the Diego system are also the result of a single amino acid substitutions.

Band 3 is an intrinsic membrane glycoprotein acting as a structural protein and also an anion exchanger (Tanner, 1993). Band 3 plays a vital role in the red cell membrane which is why the Diego null phenotype (band 3 deficiency) has not been reported.

Figure 1.6 Diego antigens located on band 3 glycoprotein



Diagrammatic representation of the band 3 glycoprotein with associated Diego antigens, including the antithetical antigens Wr^a/Wr^b, Di^a/Di^b and Wu/DISK antigens at positions 658, 854 and 565 respectively, expressed as a result of single amino acid substitutions. The approximate positions of some of the other low frequency antigens in the system are also shown on the diagram.

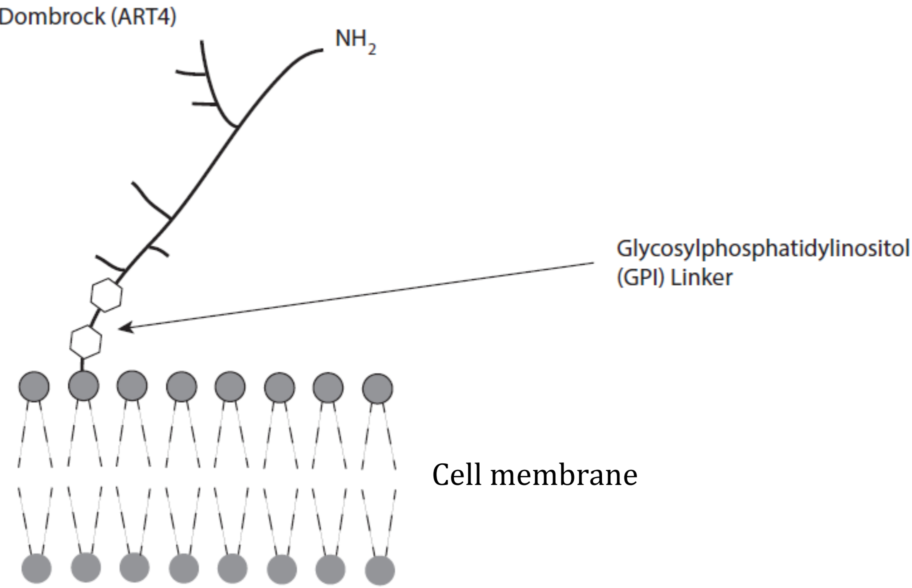
(Adapted from: http://www.bloodjournal.org/content/bloodjournal/92/12/4836/F2.large.jpg?sso-checked=true)

1.3.2.8 Dombrock system

The Dombrock system includes 7 antigens ((ISBT 014) blood group alleles v4.0 160623) encoded by a single gene (*ART4*) located on chromosome 12. The system includes the antithetical antigens Do^a and Do^b, and the high frequency antigens Gy^a, Hy, Jo^a, DOYA, DOMR and DOLG. Do^a and Do^b are expressed as a result of a single amino acid substitution (asparagine to aspartic acid) at position 265. Expression of the remaining high frequency antigens are also the result of single amino acid substitutions, with the exception of Gy^a. The Gy^a negative phenotype can result from a variety of different mutations in the gene, and includes the Do_{null} phenotype in which the red cell lacks all of the Dombrock antigens.

The Dombrock antigens are located on the ART4 glycoprotein, which is attached to the red cell membrane through glycosylphosphatidylinositol (see figure 1.7). The exact function of the ART4 glycoprotein is not known, although it does belong to a family of adenosine diphosphate (ADP)-ribosyltransferases responsible for catalysing the transfer of ADP-ribose from nicotinamide adenine to a protein substrate.

Figure 1.7 Dombrock antigens on the ART4 glycoprotein



Diagrammatic representation of the structure (shown here as a line) that expresses the antigens of the Dombrock system. The Do^a/Do^b polymorphism arises as a result of a single amino acid substitution at position 265 (asparagine to aspartic acid). The ART4 glycoprotein is attached to the red cell membrane via the GPI anchor which is inserted into the red cell membrane.

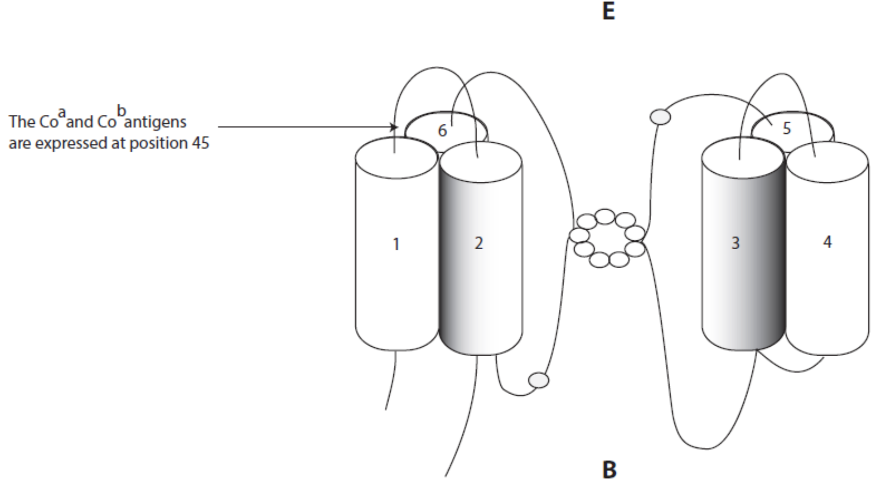
(Adapted from: https://clinicalgate.com/human-blood-group-antigens-and-antibodies/)

1.3.2.9 Colton system

The Colton blood group system includes four antigens encoded by the *AQP1* gene located on chromosome 7 ((ISBT 015) blood group alleles v3.0 160623). The system includes the antithetical antigens Co^a and Co^b, and two high frequency antigens Co3 and Co4. The Colton polymorphism is represented by a single amino acid change at position 45; alanine gives rise to Co^a and valine to Co^b. The Co3 antigen is present on all cells with the exception of the Co_{null} phenotype Co(a-b-). The Co4 antigen is represented by glutamine at position 47.

The glycoprotein structure that carries the Colton antigens acts as a water channel (King *et al.,* 2004 (a)). The structure spans the red cell membrane six times (see figure 1.8), and includes three extracellular loops and two cytoplasmic loops. One extracellular loop and one cytoplasmic loop pass into the membrane to create the channel which allows water molecules to pass.

Figure 1.8 The Colton glycoprotein structure



Model of the glycoprotein structure that carries with Colton antigens, which spans the red cell membrane six times, as represented by the cylindrical structures in the diagram. The extracellular and cytoplasmic loops that create the water channel are represented by B and E. The two antithetical antigens Co^a and Co^b, which result from a single amino acid change, are expressed at position 45, the approximate position of the antigens on the glycoprotein are demonstrated in the diagram.

(Adapted from:

https://www.sciencedirect.com/science/article/pii/S1246782001001422)

1.3.2.10 Yt system

The Yt system consists of two antigens, Yt^a and Yt^b, encoded by the *ACHE* gene located on chromosome 7 ((ISBT 011) blood group alleles v5.0 180207). The antigens Yt^a and Yt^b are antithetical, and are represented by a single amino acid change at position 353 (histidine to asparagine). A third antigen, YTEG, a high frequency antigen, was reported in 2017 (Laundy *et al*., 2017). An inherited Yt_{null} phenotype, Yt(a-b-) has not been reported.

The Yt antigens are located on acetylcholinesterase (AChE), a GPI linked glycoprotein, similar to the Dombrock antigens (see figure 1.7). The exact nature of the red cell AChE is not known, but AChE is known to play an essential role in neurotransmission. This essential role may explain why the null phenotype is not seen.

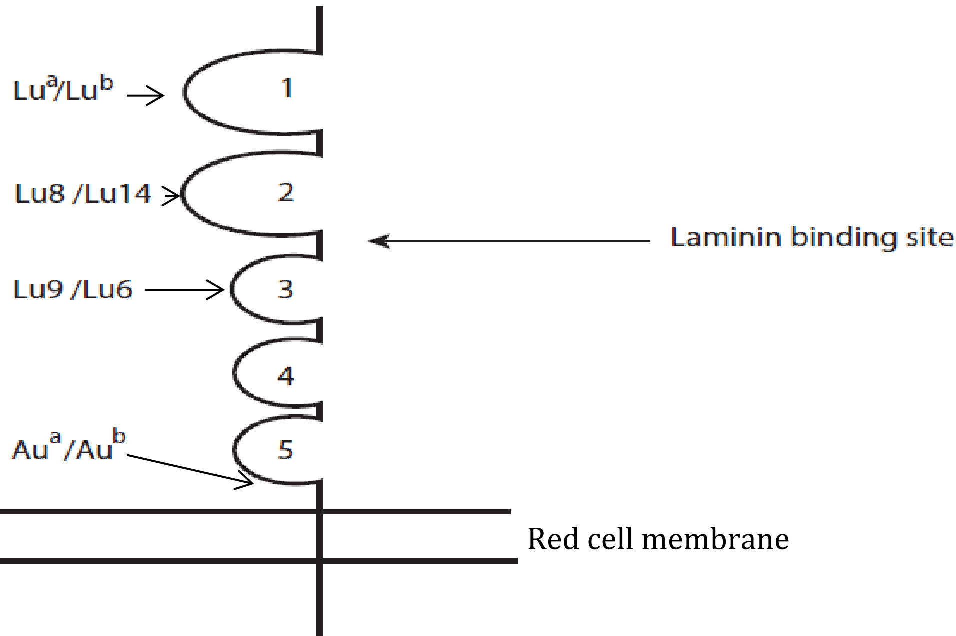
1.3.2.11 Lutheran system

The Lutheran system has 22 antigens ((ISBT 005) blood group alleles v4.1 170106) and is encoded by the *LU* gene on chromosome 19. The system includes four pairs of antithetical antigens: Lu^a and Lu^b, Lu6 and Lu9, Lu8 and Lu14 and Au^a and Au^b. These antithetical antigens are all the products of single amino acid changes; Lu^a/Lu^b (histidine to arginine at position 77), Lu6/Lu9 (phenylalanine to serine at position 275), Lu8/Lu14 (lysine to methionine at position 204) and Au^a/Au^b (alanine to threonine at position 539). The null phenotype, Lu(a-b-) exists as a result

of homozygosity for an inactivated Lutheran gene. Red cells of individuals with the null phenotype lack all Lutheran antigens.

Lutheran antigens are located on glycoprotein structures which are members of the immunoglobulin superfamily, a large family of receptors and adhesion molecules (Isacke and Horton, 2000). The Lutheran antigens are associated with two glycoproteins, which act as ligands for laminin, an extracellular matrix glycoprotein (see figure 1.9).

Figure 1.9 Structure of the Lutheran glycoprotein



Diagrammatic representation of the Lutheran glycoproteins, which consist of five extracellular domains, with a flexible linker and laminin binding site between domains 2 and 3. Each domain is composed of two β-sheets stabilised by a disulphide bond and consists of approximately 100 amino acids. The position of the laminin binding site and the approximate locations of the four antithetical pairs of antigens (which result from single amino acid substitutions) on the immunoglobulin superfamily domains are shown on the diagram.

(Adapted from: http://www.bloodjournal.org/content/89/11/4219)

1.4 Antibodies to red cell antigens and their clinical relevance

1.4.1 Clinical relevance of red cell antibodies

One of the effects of the transfusion of allogeneic blood in any group of patients and in particular with chronic blood transfusion, is the development of red cell alloantibodies, produced in response to antigenic differences between the recipient and the donor red cells. As the blood group antigens are extremely polymorphic it is almost inevitable that there will be antigenic differences between the donor (transfused) red cells and the recipient red cells. This can lead to the recognition of these foreign antigens by the recipient immune system and the production of alloantibodies.

Alloimmunisation has the potential to cause transfusion reactions in individuals if they are subsequently transfused with allogeneic red cells bearing the corresponding antigen. Immune mediated transfusion reactions can be acute or delayed. Acute reactions are defined by the Serious Hazards of Transfusion (SHOT) group as fever and other symptoms/signs of haemolysis within 24 hours of transfusion, whereas delayed reactions may be seen more than 24 hours after transfusion (SHOT 2016). Transfusion reactions can result in deleterious health effects including haemolysis, jaundice, fever, renal failure and shock, and may be fatal in some cases (Beauregard and Blajchman, 1994; SHOT 2016). Red cell antibodies most commonly implicated in transfusion reactions include; Anti-D, -C, -c, -E, -e, (Rh system) -K, -k, (Kell system) -Jk^a, -Jk^b, (Kidd system) -M, -S, -s, -U, (MNS system) -Fy^a, -Fy^b (Duffy

system) and Wr^a (Diego system) (BCSH 2013). Antibodies to antigens within the Dombrock, Colton, and Yt systems have been implicated in haemolytic transfusion reactions, and antibodies to Lutheran antigens may cause mild or delayed transfusion reaction (Daniels, 2013).

Alloimmunisation also has the potential to cause haemolytic disease of the fetus and newborn (HDFN), if there is an antigenic difference between the maternal red cells and the fetal red cells. Maternal red cell antibodies, which may have developed as a result of transfusion or via transfer of fetal cells to the maternal circulation, may cross the placenta and cause destruction of the fetal red cells. Certain antibodies, notably anti-D, anti-c and anti-K can cause severe fetal symptoms, including anaemia, jaundice, hydrops and stillbirth (RCOG, 2014).

Red cell alloantibodies are typically IgM or IgG in nature and are usually produced in response to a foreign red cell antigen stimulus. Others, such as the IgM antibodies directed against the well-known A and B antigens, are believed to be naturally occurring as there is no requirement for red cell antigen exposure. Instead they are probably made in response to bacterial antigens that are similar in structure to red cell antigens (Springer *et al.,* 1959a; Springer *et al.,* 1959b; Springer and Horton, 1969). Some red cell antibodies, such as the IgM type anti-A and anti-B, are capable of causing intravascular lysis of the red cell by their ability to activate the complement cascade through the formation of the membrane attack complex, and the subsequent release of anaphylatoxins leading to

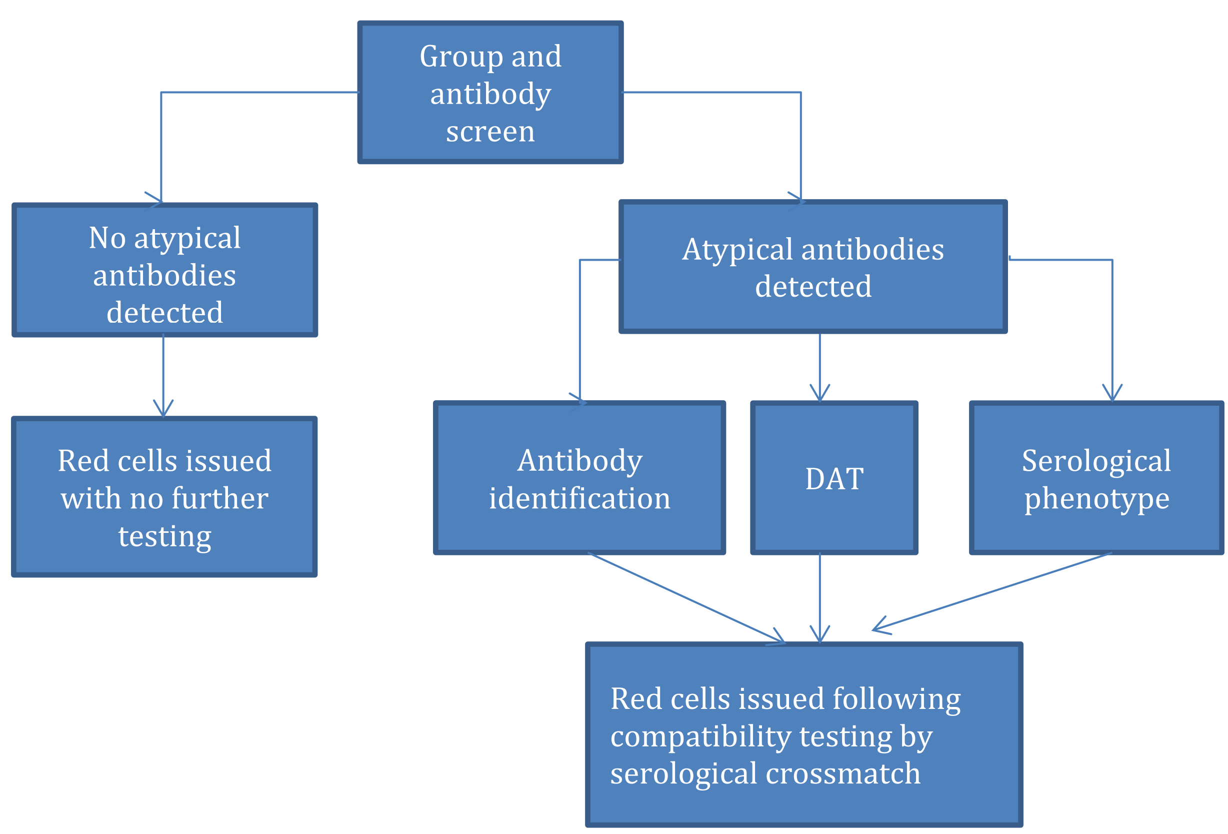
acute systemic effects (Murphy *et al.,* 2013). Other red cell alloantibodies, normally IgG type, can cause extravascular destruction of foreign red cells, in the spleen, by interacting with the Fcγ receptors on the cells of the mononuclear phagocytic system (Murphy *et al.,* 2013).

Red cell alloantibodies may be transient in nature, this is particularly well known for alloantibodies such as anti-Jk^a and anti-Jk^b. Non-persistent antibody detection has been reported in several studies (Ramsey and Larson, 1988; Rosse *et al*., 1990; Reverberi, 2008). A similar phenomenon has also been reported for autoantibodies (Young *et al*., 2004). The reasons given for this phenomenon may include; lack of antigenic stimulus resulting in decrease of antibody production over time, low levels of antibody production that are at the limit of the antibody detection assays and may only be detectable on some occasions, improvements in the sensitivity of antibody detection assays over time and inter-batch variation within the same assay technique.

1.4.2 Laboratory relevance of red cell antibodies

In addition to having the potential to cause haemolytic transfusion reactions, the presence of red cell alloantibodies in patient blood samples also brings laboratory related issues. They increase the workload and cost pressures on the hospital transfusion laboratory services by introducing requirements for specialised testing techniques and sourcing antigen matched blood for transfusion, which may cause delays in blood provision. Standard laboratory testing, within the hospital transfusion service, prior to the transfusion of red cells, includes ABO and RhD typing

of the patient red cells and a screening technique for the detection of any atypical red cell antibodies in the patient's plasma, commonly referred to as a group and antibody screen. Additional testing, if atypical red cells antibodies are detected, includes identification of the antibody specificity, serological red cell phenotyping, direct agglutination test (DAT) and serological crossmatch of donor red cells to determine compatibility. At the RD&E all of these assays are performed in the hospital transfusion laboratory. If antibody specificity or compatibility cannot be determined using the techniques available in the hospital transfusion laboratory, referral to a reference laboratory at the NHSBT may be required. A simplified flow chart for pre-transfusion testing in the hospital transfusion laboratory is shown below:



1.4.2.1 Group and antibody screen

Prior to any blood transfusion episode, a blood sample must be taken from the patient for blood grouping (ABO and RhD) and antibody screening. Blood grouping and antibody screening may be performed using manual or automated techniques. ABO and RhD typing utilises direct agglutination techniques with patient red cells using commercial anti-sera. Antibody screening is performed using indirect antiglobulin techniques using patient plasma against commercial antibody screening cells with a known antigen profile. For the purposes of detection of clinically significant red cell antibodies (that are known to be capable of causing haemolysis of transfused red cells) in patient samples presented for testing within the hospital transfusion setting the BCSH (2013) recommend that the screening cell set employed contains the following common antigens:

C, c, C^w, D, E, e, K, k, Fy^a, Fy^b, Jk^a, Jk^b, S, s, M, N, P1, Le^a and Le^b.

If no red cell alloantibodies are detected in the patient's plasma there is no requirement for further laboratory testing. Blood for transfusion is selected that is ABO and RhD compatible for the patient and may be issued electronically, with no serological compatibility testing between the donor cells and recipient plasma, in accordance with BCSH guidelines (BCSH 2013).

At the RD&E red cells are selected for transfusion dependent patients (excluding SCD) in accordance with the BCSH (2013) recommendations;

ABO/D matched. The BCSH guidance states that additional typing and matching for Rh and K should be a local decision. At the RD&E it has been recommended that red cells for these patients should be K negative, but this was not policy and there were no processes in place to ensure that this occured.

To reduce the risk of the development of red cell antibodies known to cause Haemolytic Disease of the Fetus and Newborn, in some countries, including France, red cell transfusions for females with child-bearing potential may be matched for Rh (CcEe) and K antigens (French Transfusion guidelines cited in Moncharmont *et al*., 2015). In the UK it is recommended that K negative red cell units are selected for this group of patients, but without the requirement for K typing the patient (BCSH 2013). At the RD&E it is recommended that red cell units are selected that are also negative for Rh c and E antigens wherever possible. However, phenotyping has not been advocated in our institution as transfusion is uncommon in this group of patients and suitable red cells can easily be sourced from routine stocks.

1.4.2.2 Antibody Identification

If red cell alloantibodies are detected in the antibody screening technique further laboratory assays are required in order to ascertain the specificity of the alloantibody. Antibody identification techniques employ the same principles as the antibody screening techniques but using commercial cells with an extended range of known antigen profiles. Whereas a

screening cell set is commonly composed of two or three red cell reagents, an antibody identification set may contain more than 10, the extended range enabling determination of the antibody specificity, rather than just the presence of a red cell alloantibody. As with antibody screening methodology, antibody identification may be performed manually or on an automated system, column agglutination and solid phase technology being commonly employed.

To avoid potential haemolytic transfusion reactions the BCSH (2013) recommend that, for patients whose plasma has been shown to contain clinically significant antibodies as identified in antibody screening and identification techniques, either antigen negative blood, or unselected but crossmatch compatible (by IAT) blood should be selected for transfusion. As a general rule if the patient has an antibody that has been reported to cause haemolytic transfusion reactions then antigen negative blood must be selected, whereas the presence of an antibody with no reported cases of transfusion reactions needs only to be crossmatch compatible (table 1-3) (BCSH, 2013).

1.4.2.3 Serological red cell phenotyping

Serological phenotyping is the identification of red cell antigens present on the patient red cells, other than ABO/D, using commercially available antisera. Currently available methods for serological phenotyping include direct and indirect agglutination either by tube techniques (see section 1.6.1), or column agglutination techniques based on the principles of

Lapierre (1990) (section 1.6.2). Additionally, solid phase tests, based on the principles of Plapp (1984) and Juji (1972) (section 1.6.3), in which red blood cells are bound to a solid support such as a microtitre plate well, can be used for the identification of red cell antigens. Serological red cell phenotyping is explained in more detail in section 1.5.

1.4.2.4 Direct Antiglobulin Test

Direct Antiglobulin Testing (DAT) may also be required; this test detects the presence of antibodies or complement fractions on the surface of the patient's red cells. Methodology commonly employed in hospital transfusion laboratories includes column agglutination tests or solid phase technology, which may be performed manually or on automated systems.

1.4.2.5 Serological crossmatch

If atypical red cell antibodies are present, compatibility testing, known as crossmatching, of each unit of blood must be performed. Testing must be performed by IAT, either column agglutination or solid phase may be used to ensure compatibility of the selected red cell units for transfusion (BCSH, 2013). The technique may be performed manually or by automated technology.

Table 1.3: Likely clinical significance of red cell alloantibodies

Likely clinical significance of red cell antibodies reported in this study and recommendations for the selection of blood for patients with their presence. Taken from the BCSH guidelines for pre-transfusion compatibility procedures in blood transfusion laboratories (BCSH 2013) and Daniels (2013).

System	Antibody	Likely clinical significance in transfusion	Recommendation
ABO	Anti-A_1	No	IAT crossmatch compatible
H	Anti-H (in A_1 and A_1B patients)	No	IAT crossmatch compatible
Rh	Anti-D,-C,-c,-E,-e,-f	Yes	Antigen negative
Rh	C^w	No	IAT crossmatch compatible
Kell	Anti-K,-k,	Yes	Antigen negative
Kell	Anti-Kp^a	No	IAT crossmatch compatible
Kidd	Anti-Jk^a,-Jk^b	Yes	Antigen negative
MNS	Anti-M (active at 37°C)	Yes	Antigen negative
MNS	Anti-M (not active at 37°C)	No	IAT crossmatch compatible
MNS	Anti-N, -Mur, -Hut	No	IAT crossmatch compatible
MNS	Anti-S,-s,-U	Yes	Antigen negative
Duffy	Anti-Fy^a,-Fy^b	Yes	Antigen negative
P	Anti-P_1	No	IAT crossmatch compatible
Lewis	Anti-Le^a,-Le^b,-Le^{-a+b}	No	IAT crossmatch compatible
Lutheran	Anti-Lu^a	No	IAT crossmatch compatible
Diego	Anti-Wr^a	Yes	IAT Crossmatch compatible
Yt	Anti- Yt^a, -Yt^b	Possible	IAT crossmatch, least incompatible for anti-Yt^a
Chido/Rodgers	Anti-Chido-Rodgers	No	IAT Crossmatch compatible
Knops	Anti-Knops McCoy	No	IAT Crossmatch compatible
Others	Autoantibodies	No	ABO/D Rh (CcEe) and K matched

1.5 Serological red cell phenotyping

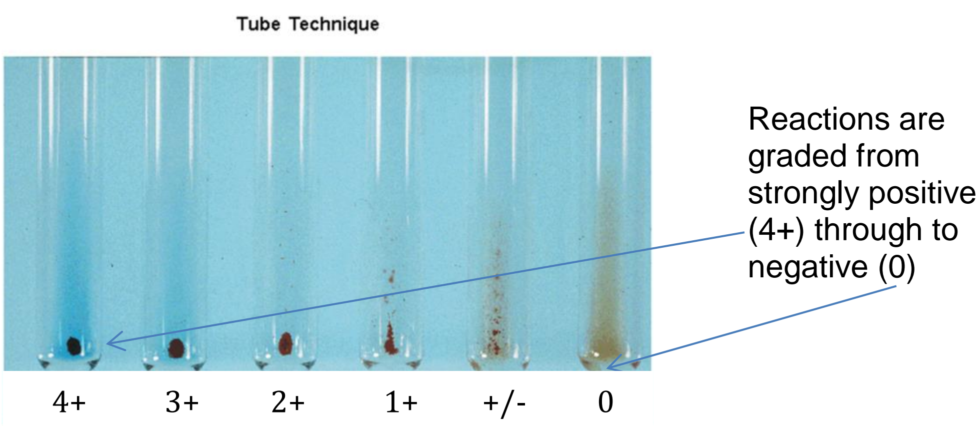
Positive identification of a red cell alloantibody in a patient's plasma also includes testing the patient's red cell antigen type. This is performed by serological phenotyping using a combination of monoclonal and polyclonal reagent antisera, utilising direct or indirect agglutination techniques. Identification of alloantibody specificity can be supported if the patient's red cells are negative for the corresponding antigen (BCSH, 2013). Methods for serological phenotyping within the hospital transfusion setting include direct agglutination in tube technology, column agglutination and microtitre plates and indirect agglutination using column agglutination and solid phase methods. However, unlike blood grouping, antibody screening and antibody identification, serological phenotyping methods are currently, generally performed manually, and may employ a combination of the available techniques. Automation of these techniques has been limited by the availability of appropriate reagents and testing profiles that could be used on the high throughput blood grouping analysers commonly used by hospital transfusion services in the UK. However, manual techniques are labour intensive and are prone to errors during sample preparation, testing, result interpretation and result reporting stages. It is for this reason that extended phenotyping, typing for the presence of more than the antigen implicated by the antibody identification, has not been common practice, even though the information gained from the extended phenotype could be used to select blood that might protect the patient from further alloimmunisation. In addition, extended serological phenotyping could be used for prophylactic

antigen matching of blood to prevent alloimmunisation for patients with conditions that might require chronic transfusion in the future.

1.5.1 Principles of direct agglutination in tube technology

Direct agglutination is a well-recognised technique (as described by Issitt and Anstee, 1998) for detecting the presence of antibodies or antigens and is used across many applications in clinical medicine. Some commercially available monoclonal antisera are capable of agglutinating red cells in test tubes to determine the presence of specific blood group antigens on red cells. In these techniques, an aliquot of a suspension of patient red cells, with unknown antigen status, is placed in a test tube along with the antisera. A short incubation period allows the antisera to combine with the red cell antigens, if present, on the patient red cells. Centrifugation of the test tube then forces the red cells together, allowing the antisera to crosslink between red cells, causing agglutinates to form. In the absence of the corresponding antigens on the patient red cells, there will be no antigen-antibody reaction and no agglutinates will form following centrifugation. The presence of agglutinates is determined macroscopically by gently shaking the test tube after the centrifugation stage, and the agglutination strength may be graded as shown in figure 1.10. This technique is performed manually and the macroscopic reading of the results is subjective and dependent on the experience of the operator. As a result of these factors the technique is labour intensive and prone to the known errors of manual testing (Stainsby *et al.*, 2006) in both preparation and the result determination.

Figure 1.10: Principles and reactions of the direct agglutination assay tube technique for the determination of red cell antigen status



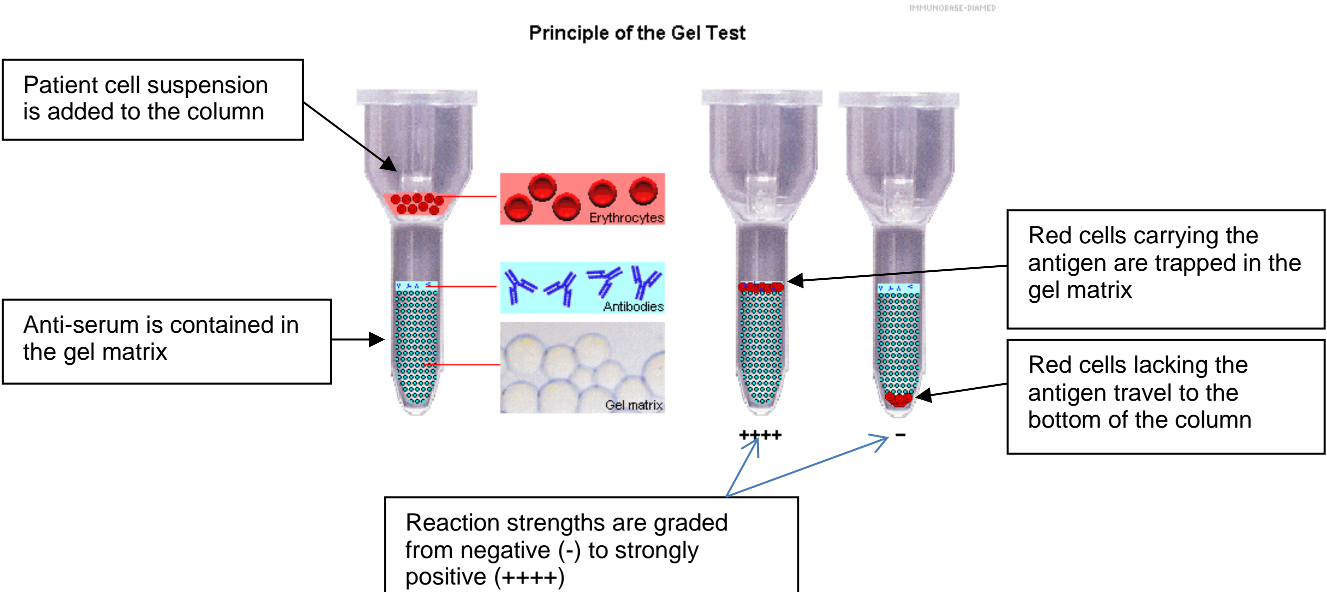
In direct agglutination assays patient red cell suspension is mixed with the relevant anti-serum and incubated within the test tube. Centrifugation forces the red cells together allowing antigen-antibody complexes to form if antigen is present on the patient red cells; reaction patterns are graded from strongly positive (4+) to weakly positive (+/)-, as indicated in the figure. A negative reaction is seen if the patient red cells do not carry the antigen and therefore do not form complexes.

(Picture courtesy of Bio-Rad, cited in Immunobase 1 – Diamed, http://www.bio-rad.com/en-uk/product/immunobase?ID=LO52IK5Y7).

1.5.2 Principles of the Column Agglutination Test (CAT)

The column agglutination test is performed in specially designed cards which employ the use of either antisera within the column designed to capture red cells with the corresponding antigen (direct agglutination), or via agglutination of red cells through indirect agglutination techniques. The techniques may be performed manually or using automated methods. At the RD&E lack of automation for these tests means that they must be performed and read manually, thus introducing the risk of error. Phenotyping using monoclonal antisera, for Rh (CcEe) and K antigens using the Diamed technique (Bio-Rad Laboratories Inc.), is performed on a single card containing six separate reaction columns. Each column contains a specific antiserum (anti-C, anti-c, anti-E, anti-e or anti-K) within a gel matrix and a negative control well is included to confirm that any positive reactions are due to the presence of the corresponding red cell antigen on the patient's cells and not false positive reactions due to auto-agglutination. A red cell suspension containing patient cells of unknown antigen status is added to the top of the column, the card is then centrifuged which forces the patient red cells through the gel matrix containing the specific antisera. If the patient red cells carry the corresponding antigen, antigen-antibody complexes form, trapping the cells in the column and demonstrating a positive result. Conversely, cells lacking the corresponding antigen will not form antigen-antibody complexes and will be forced to the bottom of the column denoting a negative reaction (see figure 1.11). Results can be read macroscopically if performed manually or this can be performed via an automated system.

Figure 1.11: Principles of the column agglutination assay

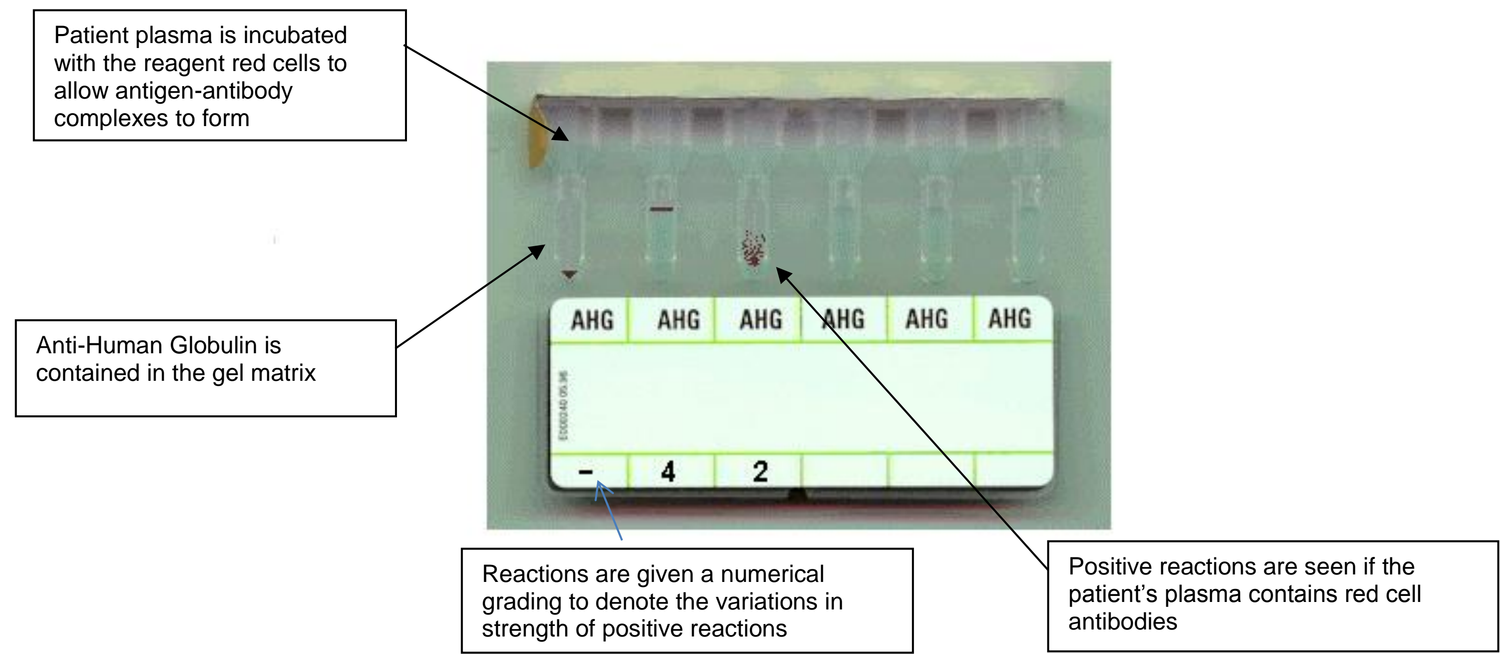


A diagrammatic representation of the principle of the column agglutination technique for the determination of red cell antigen status. The patient cell suspension is added to the column and centrifugation forces the red cells through the gel matrix containing the anti-serum. Red cells positive for the antigen form antigen-antibody complexes and are trapped in the gel matrix. Cells that do not express the antigen travel to the bottom of the column during centrifugation. See section 1.5.4 for information on grading of results.

(Picture courtesy of Bio-Rad, cited in Immunobase 1 – Diamed, http://www.bio-rad.com/en-uk/product/immunobase?ID=LO52IK5Y7).

Phenotyping techniques using column agglutination may also be performed via indirect agglutination. Generally this is required when using polyclonal antisera, which are incapable of forming antigen-antibody complexes that can bridge between red cells forming agglutinates directly. In these techniques, the use of antihuman globulin (antibodies to human antibodies, usually of goat or murine extraction) is employed to link red cells coated with the specific antiserum. An aliquot of a suspension of patient red cells of unknown antigen status is incubated with the specific antiserum in an incubation chamber at the top of the column. An incubation period performed at 37°C, simulating an *in vivo* situation, allows antigen-antibody complexes to form if the corresponding antigen is present on the patient red cells. A centrifugation stage then forces the red cells through the gel matrix containing antihuman globulin (AHG), if antigen-antibody complexes are present on the patient red cells they are trapped by the AHG within the column. In the absence of antigen-antibody complexes the red cells will travel to the bottom of the column, denoting a negative result (see figure 1.12). The results can be read macroscopically or via automated technology.

Figure 1.12: Reaction patterns of the column agglutination assay



A diagrammatic representation of the results seen with IAT column agglutination technique for the determination of red cell antigen status Patient red cells are incubated with the commercial anti-sera to allow antigen-antibody complexes to form in the incubation well. Centrifugation then forces the red cell/antiserum mix through the gel matrix containing Anti-Human Globulin (AHG). If the patient red cells do not carry the antigen being tested then the unsensitised red cells will fall to bottom of the column. Positive reactions are denoted by patient red cells trapped in the gel. Positive reactions are graded from strongly positive (4+) through to weakly positive (+/-).

(Picture courtesy of Bio-Rad, cited in Immunobase 1 – Diamed, http://www.bio-rad.com/en-uk/product/immunobase?ID=LO52IK5Y7).

1.5.3 Principles of automated phenotyping methodology on the Immucor NEO® analyser

Development of high throughput automated methods for extended red cell phenotyping would not only introduce a technique for reducing manual testing (with its inherent risks) for patients who had developed a red cell alloantibody, but also facilitate extended phenotyping for patients prior to transfusion. This has the potential to allow for more specific matching of red cell antigens on the donor blood for patients likely to require chronic transfusion support, thus potentially reducing the risk of alloimmunisation. Column agglutination technology may be automated, currently available platforms that could support this type of automated phenotyping include; the Bio-Rad IH500 and IH1000 (Bio-Rad Laboratories Ltd., Watford, UK), the Grifols Erytra and Erytra Eflexis (Grifols UK Ltd., Cambridge, UK) and the Ortho AutoVue® Innova System (Ortho Clinical Diagnostics, Buckinghamshire, UK).

The Immucor NEO Iris and ECHO Lumena automated analysers (IBG Immucor Ltd., West Midlands, UK) offer serological phenotyping using direct agglutination techniques in microtitre plates and solid phase methodology. The Immucor NEO analyser is currently utilised in the RD&E transfusion laboratory for routine ABO/D typing, antibody screening and antibody identification, but has not been developed for automated serological phenotyping. This study details the development and validation of a novel, high throughput method for extended

serological red cell phenotyping using the Immucor NEO® analyser system.

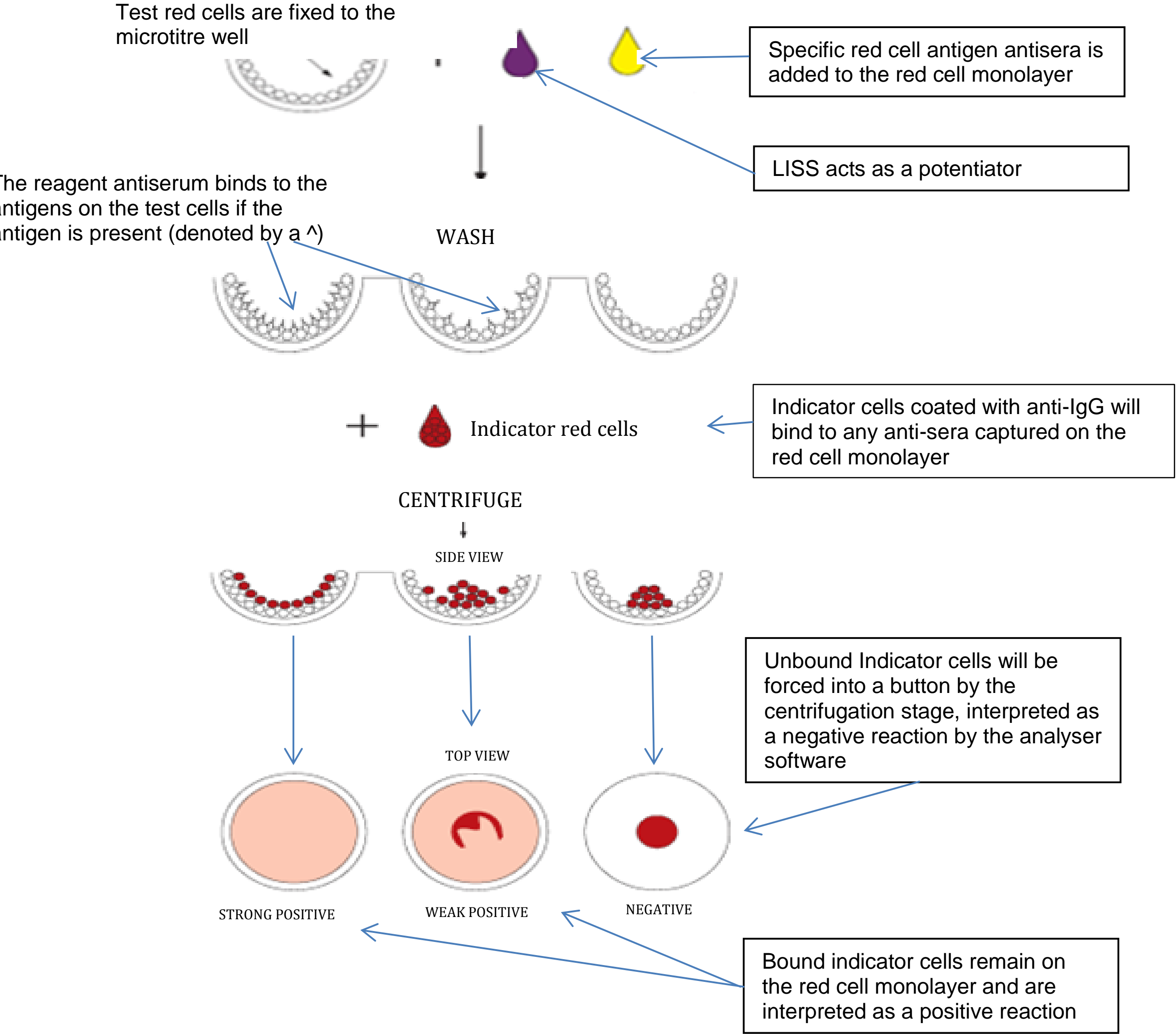
The automated technique using the Immucor NEO® analysers employs two distinct methods for the determination of the presence of red cell antigens; direct agglutination and solid phase technology. In the direct agglutination test the patient red cells are mixed with the specific antiserum in a well of the microtitre plate, an incubation phase allows the red cells to settle together permitting cross-linking of the IgM molecules in the antiserum with the corresponding antigen on the red cells. This effect is increased during a centrifugation phase enabling a quicker reaction to occur. Direct agglutination of red cells with a particular reagent indicates the presence of the corresponding antigen. The microtitre plate is then gently shaken by the analyser, during this process red cells that have not been agglutinated by the antiserum will break apart and form a loose layer of cells in suspension, and cells that have agglutinated may stay together forming a clump, reactions similar to those seen in direct agglutination in tubes. The analyser captures images of these reactions and the differing patterns are then converted into reactions grades (which vary from negative (no agglutinates), through to strongly positive (indicated by a tight button of cells at the bottom of the well) using in-built computerised algorithms.

Solid phase (Capture-R) assays are based on the procedure of Plapp (Plapp *et al.,* 1984) and Juji (Juji *et al.,* 1972) and are used in conjunction

with polyclonal antisera that are not capable of direct agglutination. The individual wells of the microwell strips are coated with an affinity isolated goat anti-murine antibody and a murine anti-RBC antibody; these are used to support the formation of a red cell monolayer, created from the patient sample by the automated analyser, to the microwell surface. Reagent antiserum is then dispensed into the well, followed by low ionic strength saline (LISS) and an incubation phase. Lowering the ionic strength acts to increase the rate of formation of antigen-antibody complexes, and can reduce the incubation time needed for the complexes to form (cited in Rolih *et al.*, 1985). During the incubation period the antigens carried on the immobilised patient red cells are bound to the specific IgG antibodies in the antiserum. Following incubation, residual unbound immunoglobulins are removed from the wells by an automated washing step and anti-human IgG coated Capture-R Ready indicator red cells are added. A centrifugation step allows the indicator red cells to come into contact with any antibodies bound onto the surface of the patient's immobilised red cells. If the patient's cells are positive for the antigen being identified then IgG-anti-IgG complexes will form between the indicator cells and the sensitised patient red cells. The indicator cells will then adhere to the surface of the immobilised patient red cells forming a second layer of cells. If the patient cells are negative for the antigen being determined then the indicator cells will not bind to the immobilised cells and, during the centrifugation phase, will form a pellet at the bottom of the well (see figure 1.13). The analyser image

capture system converts the reactions seen in the wells into reaction grades denoting the presence or absence of the specific red cell antigen.

Figure 1.13: Principles of the solid phase phenotyping assay



Diagrammatic view of the solid phase technology utilised by the IBG NEO® analyser system Red cells are bound to the microwell surface by the analyser, a potentiator LISS (low ionic strength saline) is added which increases the rate of formation of antigen-antibody complexes. Antibodies to red cell antigens are "captured" on the microwell during incubation, unbound immunoglobulins are then rinsed from the wells in a wash phase. Capture R anti-IgG Indicator red cells are added, which "sandwich" the "captured" antibodies, making them visible. A centrifugation phase then brings the indicator red cells in contact with antibodies bound to the reagent red cell membranes. (Diagram courtesy of Caryn Conway, Immucor, personal communication).

1.5.4 Grading reactions in phenotyping techniques

The reaction strengths in the different methods for serological red cell antigen phenotyping can be graded from negative (-) through to strongly positive (4+); a comparison of the grading reactions seen in Capture-R Select, tube agglutination and gel column agglutination techniques is shown in figure 1.14. The grading of the reaction strength is important as weak, or mixed field, reactions may be indicative of the presence of transfused red cells, or, in the case of polyclonal antisera, the presence of a positive DAT (BCSH, 2013). In either case the true phenotype of the patient cannot be determined until the cause of the weak or mixed field reaction has been investigated. Grading of reaction strengths for tests performed manually is subjective and dependent on the experience of the individual performing the test, thus some operators may misclassify a weak, false positive, reaction as a positive reaction and report an incorrect result without further investigation (SHOT, 2014). Automation of phenotyping methods, as for the column agglutination and solid phase assays, removes this subjectivity and allows a more standardised approach to grading, thus reducing the risk of misreading a false positive result due to the presence of transfused cells or a positive DAT (Stainsby *et al.*, 2006).

Figure 1.14: Comparison of reaction patterns in phenotyping assays

Grading	Capture R	Hemagglutination	Gel / CAT
4+			
3+			
2+			
1+			
0 negative			

A comparison of grading reaction between Capture R Select (IBG NEO analyser), haemagglutination performed in a tube (direct agglutination) and column agglutination (Gel/CAT). Grading ranges from 0 (negative), no reactions between the red cells and the plasma, through 1+ (weakly positive reactions) to 4+ (strongly positive reaction) Note: weak (+/-) reactions shown in previous figures are not demonstrated.

(Picture courtesy of Caryn Conway, Immucor – personal correspondence).

1.6 Red cell antigen genotyping

Serological red cell phenotyping in patients with a recent history of blood transfusion is complicated by the presence of donor red cells within the circulation. In these situations it is not possible to determine whether positive reactions seen in serological phenotyping tests are due to the presence of red cell antigens on the patient (recipient) cells, or on those of the transfused donor cells. In these circumstances the red cell phenotype may be predicted by genotyping the patient's DNA. Genetic testing of patient DNA to determine the red cell antigen genotype, and thus predict the phenotype, is possible post transfusion, because DNA is extracted from the patient's white blood cells, which are uncontaminated by transfused blood containing only red cells. However, this is an expensive, labour intensive, specialised test that, currently, does not lend itself to the hospital setting; the DNA based approaches that are available include the BLOODChip (Progenika Biopharma SA) (Avent *et al.,* 2007), sequence-specific primer-polymerase chain reaction (SSP-PCR) (Renoud *et al.*, 2006), BeadChip (Hashmi *et al.,* 2005; Hashmi *et al.,* 2007), PCR-restriction fragment length polymorphism GenomeLab SNPstream (Denomme and Van Oene, 2005; Montpetit *et al.,* 2006) and the matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry (MALDI-TOF MS) (Gassner *et al.*, 2013). The availability of some of these techniques on high throughput platforms, such as the BLOODChip (using the Luminex xMAP analyser) and the MALDI-TOF MS, are making these options more attractive to the hospital transfusion service.

As discussed in section 1.3, the molecular basis of most blood group antigens is now known. The majority of blood group polymorphisms are caused by single nucleotide polymorphisms (SNPs) in the genes that dictate the blood group antigen; this may be the protein itself where the gene codes for the blood protein antigen, or where gene codes for a glycosyltransferase which then catalyses the addition of monosaccharide(s) to the blood group oligosaccharide (Avent, 2009). Commercial blood group genotyping techniques use polymerase chain reaction (PCR) to amplify DNA obtained from a whole blood sample, using target specific primers. The amplified products can then be identified using probes corresponding to allelic pairs of blood group SNPs. Scanning systems are employed to detect the allele specific probes and specially designed software systems can interpret these results into genotypes and predicted phenotypes.

High throughput, automated genotyping techniques have been available now for more than a decade but have yet to be adopted into routine use in the UK, either in the NHSBT for donor typing, or in the hospital transfusion service for patient typing. One of the reasons for this slow uptake is the cost of genotyping; new equipment would be required as the assays could not be added to the current equipment performing serological testing. In addition, manual steps in the PCR processing phase remain a limiting factor in the implementation of the technique into a busy hospital transfusion laboratory setting. A common criticism of genotyping is that the genotype does not always reflect the phenotype

(Avent, 2009). This may be due to the null phenotypes seen in some blood group systems, such as, Rh, ABO, Jk and Fy, or due to a new, previously unknown allele. The length of time for genotype testing is also considered restrictive, particularly within the hospital transfusion service where provision of matched blood may be required urgently. The BLOODChip IDCOREXT assay has been demonstrated to have a processing time of less than 4 hours, which is shorter than that for other systems including PCR-SSP and BeadChip (Finning *et al.*, 2016). Wagner and co-workers (Wagner *et al.*; 2017) have attempted to address this by devising a novel method using PCR amplification without the need for DNA extraction. This group have reported that, using the new method results can be available within 40 minutes of receipt of the blood sample, which may make the technique applicable to the hospital transfusion setting.

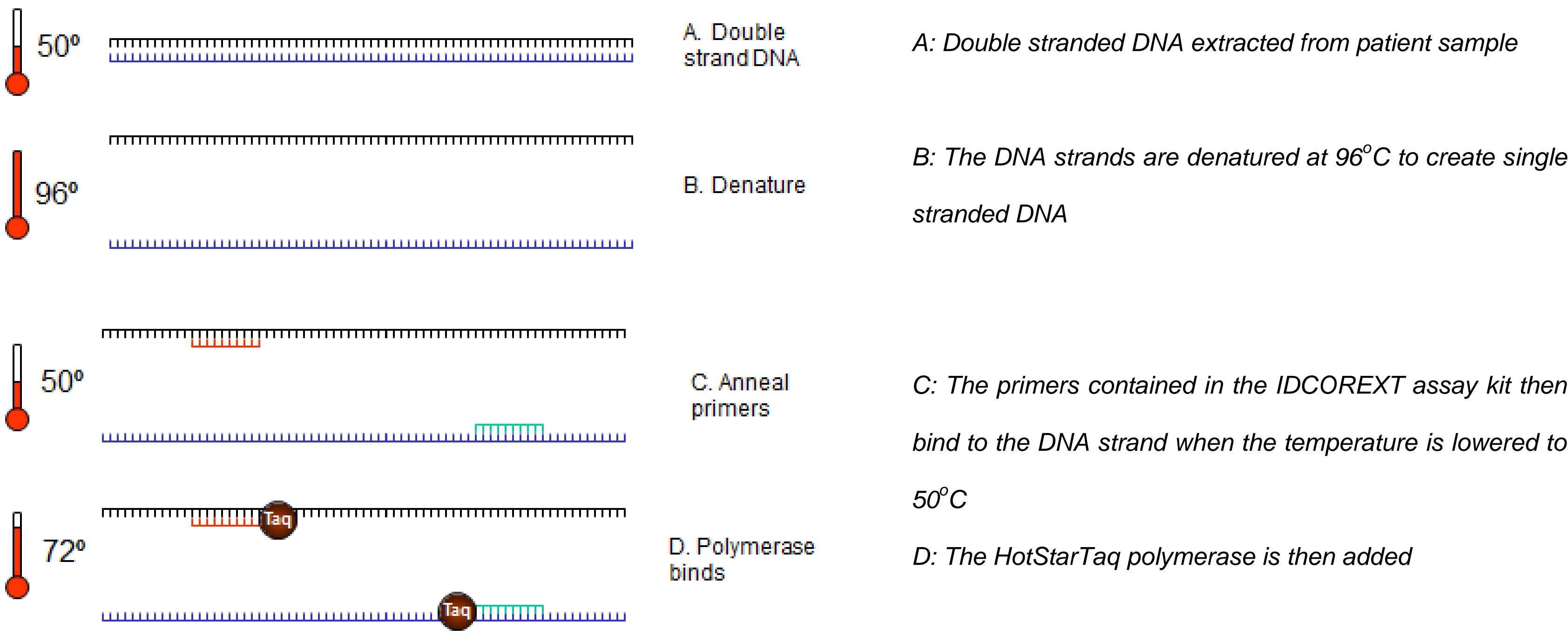
This study aimed to compare the results from blood group genotyping using one of the currently commercially available genotyping assays, BLOODChip, with those found by traditional serological methods for a variety of blood group antigens. Additionally, the study aimed to assess the feasibility of implementing such a DNA based approach in the routine hospital laboratory, including a cost comparison of the two different approaches to red cell antigen typing and their advantages and disadvantages.

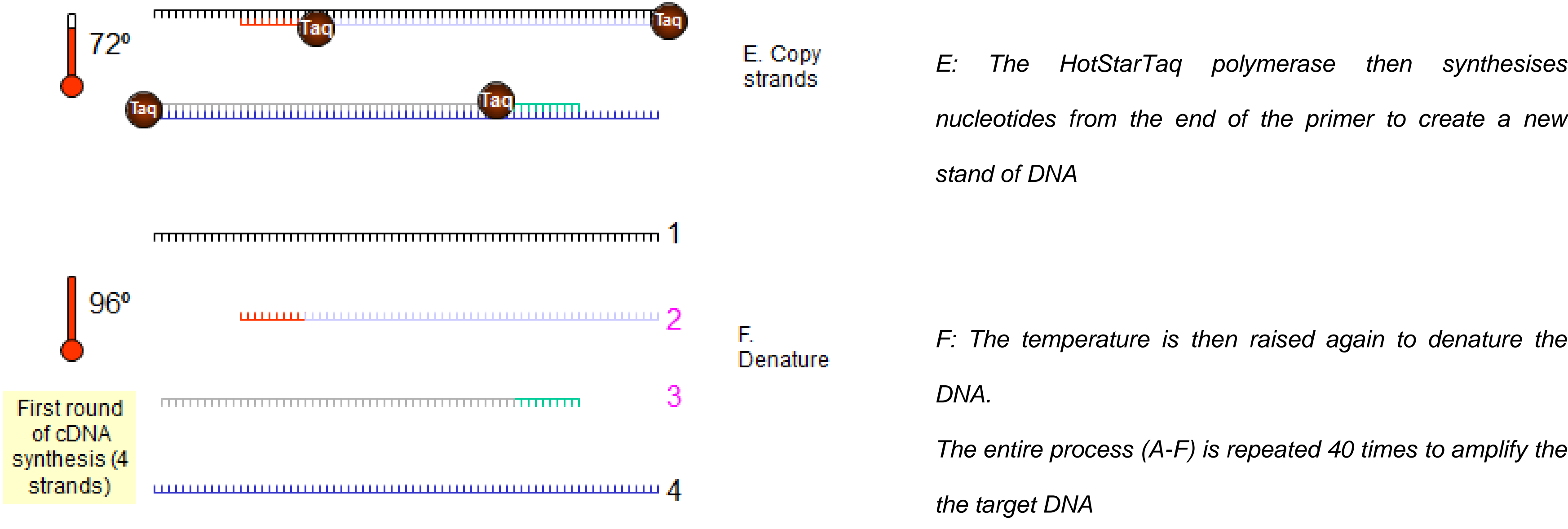
1.6.1 Principles of the BLOODChip blood group genotyping assay

The BLOODChip IDCOREXT (Progenika Biopharma, Derio, Spain) uses a microarray system for the determination of polymorphisms within the Rh, Kell, Kidd, Duffy, MNS, Diego, Dombrock, Colton, Yt (previously Cartwright) and Lutheran blood group systems (see section 5.1). Extracted DNA is amplified using a PCR mix containing HotStarTaq polymerase, primers, biotinylated nucleotides and a buffer solution. The amplification products are then hybridised to allele specific oligonucleotide probes attached to microspheres, and then labelled with fluorescence-conjugated streptavidin-phycoerythrin (SAPE) (figure 1.15). The microspheres contain two distinct dyes, red and infrared, which emit light in different regions of the spectrum. The combination of dyes in different concentrations results in 100 unique fluorescent colour tones, each correlating to a different spectral address defining a bead class (Goldman *et al*., 2015). Quantification of the amounts of labelled PCR products hybridised to the beads is then performed using the Luminex xMAP analyser system (Luminex Corporation, Austin, Texas, USA).

Figure 1.15: The principles of the IDCOREXT Assay

Diagrammatic representation of the amplification, hybridisation and labelling phases in the IDCOREXT assay,
Step 1: The amplification phase separates the DNA strands allowing the target specific primers to bind to the DNA. The addition of the HotStarTaq polymerase allows new DNA strands to be produced. The cycle is repeated 40 times to produce sufficient DNA for analysis (picture courtesy of Dr Ruth Morse, University of the West of England, personal communication).



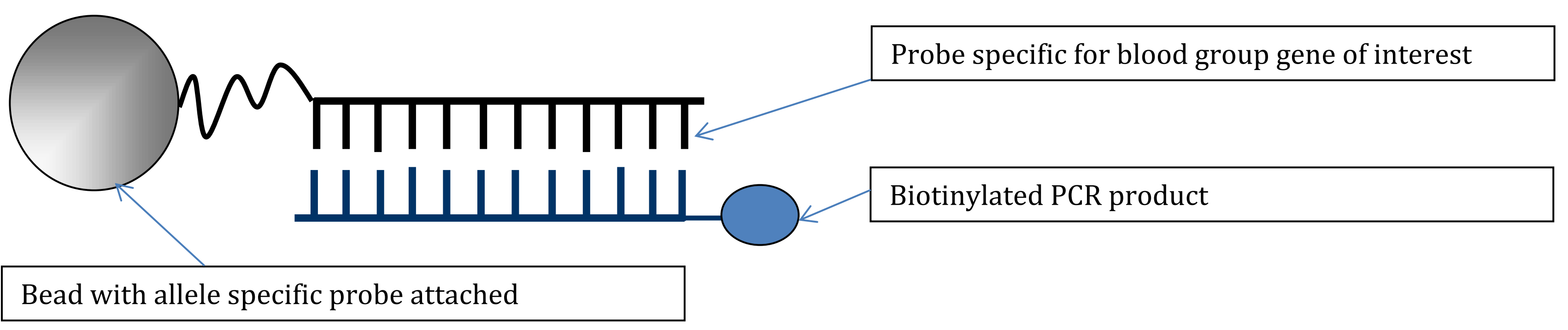


E: The HotStarTaq polymerase then synthesises nucleotides from the end of the primer to create a new stand of DNA

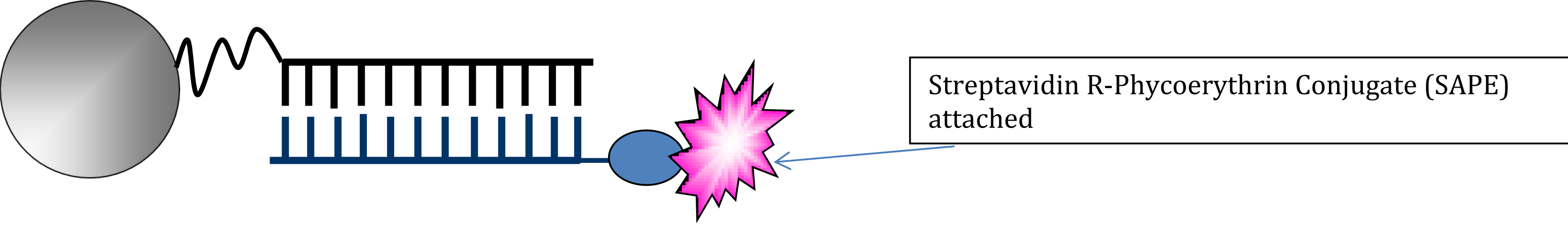
F: The temperature is then raised again to denature the DNA.

The entire process (A-F) is repeated 40 times to amplify the the target DNA

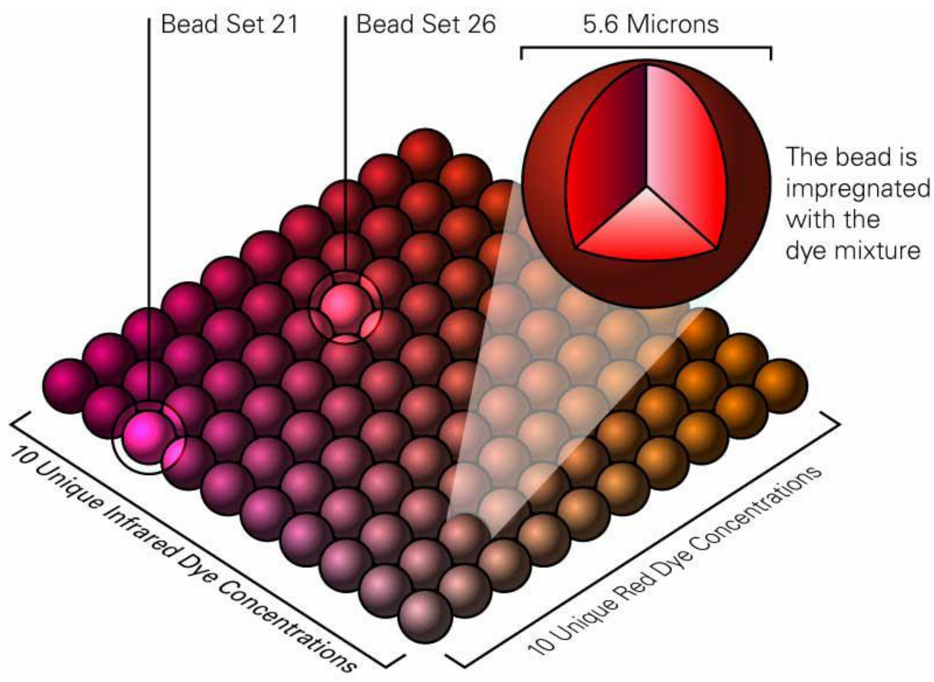
Step 2: The amplified DNA is then hybridised with allele specific probes attached to beads in suspension (picture courtesy of Louise Redfern, Grifols, personal communication).



Step 3: A fluorescent marker (SAPE) is then added to the bead suspension. This marker will then attach to the DNA if present on the allele specific probe forming a dye-DNA conjugate. Excitation of the dye-DNA conjugate by the Luminex analyser then allows the bead specific emission to be quantified by the Luminex xMAP analyser. (Picture courtesy of Louise Redfern, Grifols, personal communication).



Step 4: The sample is analysed on the Luminex xMAP analyser system. The allele specific probes are attached to beads of different combinations of red and infrared dyes which allow the Luminex xMAP analyser to distinguish one bead set from another and hence identify the presence of specific alleles (picture courtesy of Luminex (figure courtesy of Lawrence Rentoul, Merck Millipore, personal communication)).

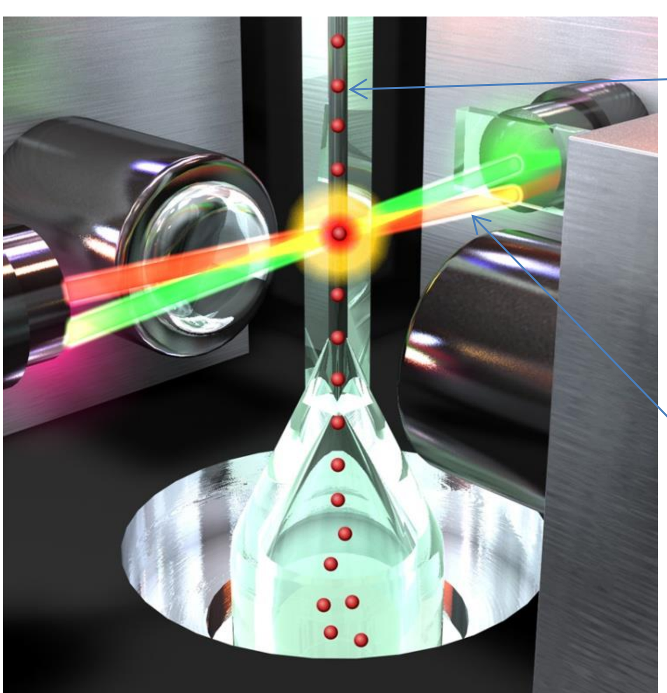


1.6.2 Principles of the Luminex xMAP analyser

The Luminex xMAP analyser system uses a multiplexing system to detect multiple nucleic acid sequences in a single reaction. In a process similar to that of a flow cytometer, the analyser directs the beads into a cuvette and past red and green lasers. The beads are sorted into their different classes, in accordance with the dye concentration, by the red laser, allowing the analyser to distinguish one bead class from another. The green laser excites the SAPE allowing the analyser to identify the presence of a specific allele hybridised to an allele specific probe. Fluorescence and side scatter are measured and the information is reported as median fluorescent intensity (MFI) (see figure 1.16). The BLOODChip analysis software extracts this information from the analyser and converts this into a report containing the genotypes and predicted phenotypes. The system can test up to 48 samples in a single batch. The manufacturer recommends that a negative and positive control is included with each batch.

Figure 1.16 Principles of the Luminex xMAP analyser

The Luminex xMAP® technology uses fluidics, optics, and digital signal processing combined with the BLOODChip IDCOREXT proprietary microsphere technology to deliver multiplexed assay capabilities. The sample is moved through the instrument and reaches the cuvette. As the beads enter the cuvette, the sheath fluid moves at 90ul/sec and forms a core around the beads which move at 1ul/sec. This is known as hydrodynamic focusing. The red laser excites the red and infrared dyes of each of the beads, the analyser collects this information to determine where the bead falls on the bead map, and side scatter is also measured to determine if the bead is 5.6µm. A Double Discriminator is gated to rid the data of any outliers such as small particulates and doublet beads. The green laser excites the reporter dye, SAPE, and the information is interpreted to determine the analyte being tested. (Picture reproduced courtesy of Louise Redfern, Grifols, personal communication).



Beads with attached allele specific probes are directed through the cuvette

The red laser excites the dye within the bead and the green laser excites the SAPE

1.7 Risk of alloimmunisation in chronic transfusion

The risk of alloimmunisation is dependent on the immunogenicity of the red cell antigen, hence it has long been advocated that all blood transfusions should be matched for the highly immunogenic RhD antigen (Woodrow and Donohoe*,* 1968) as well as the standard ABO antigens discovered by Landsteiner (1900 cited in Daniels 2013). Other red cell antigens which may evoke an immune response, and cause a transfusion reaction, in antigen negative transfusion recipients include those of the Rh (CcEe), K, Fy, Jk, MN and Ss blood group systems. However, these are only weakly immunogenic, immunising only 2-6% of transfusion recipients (Seyfried and Walewska, 1990; Heddle *et al*., 1995; Hoeltge *et al.,* 1995) compared to the RhD antigen which has an alloimmunisation rate of 30-90% (Freda *et al.,* 1967; Gunson *et al.,* 1970; Cook, 1971; Frohn *et al.,* 2003). The RhD antigen is particularly immunogenic as RhD negative individuals lack the entire RhD protein from the red cell membrane (Daniels, 2013).

Studies have suggested that alloimmunisation may also be influenced by other factors such as; underlying disease, gender, age, inflammatory status and the frequency and number of transfusions (Coles *et al.,* 1981; Blumberg *et al.,* 1983; Blumberg *et al.,* 1984; Fluit *et al.,* 1990; Hendrickson *et al.,* 2006). Alloimmunisation rates in patients with haematological malignancies vary. A retrospective study undertaken in the Netherlands (Schonewille *et al.,* 1999) found an overall alloimmunisation rate of 9% in patients with malignant myeloproliferative

and lymphoproliferative diseases whereas another study by Blumberg and co-workers (1983) showed rates of 16% in patients with myelogenous leukaemias and 11% in aplastic anaemia but no alloimmunisation in patients with lymphocytic leukaemias. Another study demonstrated a relatively high alloimmunisation rate amongst patients with myelodysplastic syndrome MDS; 36% of patients given more than 30 units of blood, and 64% given in excess of 100 units were found to have developed alloantibodies (Milic *et al.,* 2011).

More recent studies have been published regarding the alloimmunisation rates of patients with non-haematological malignancies or renal insufficiency. Alloimmunisation rates of 13.8% have been reported for patients with SCD (Master *et al.*, 2016) and 7.98% for those with thalassamia (Abdelrazik *et al.,* 2016). An interesting study by Türkmen and co-workers (2016) reported an alloimmunisation rate of 0.12% in a cohort of neonates and children up to the age of 3 years. In contrast, their control group, comprising of adult patients aged 45 years and older, had an immunisation rate of 3.55% after a median of 5 red cell transfusions, rising to 10.24% after 40 red cell units. A review of the published literature regarding alloimmunisation rates in SCD by Zheng and Maitta (2016) revealed that the United States had a higher immunisation rate (22.3%) compared to other regions (16.5%) including South America, the Caribbean, Middle East, Africa and Europe. They concluded that this was probably a result of the limited ethnicity of the donor pool, where Black donors represent a minority. In populations where donors and recipients

are ethnically similar, such as Uganda and Jamaica, the alloimmunisation rate is much lower (Olujohungbe et al., 2001). Differential expression of red cell antigens are noted between Caucasian and Black populations for many of the blood group systems, most notably for Rh (Daniels, 2013).

There is a paucity of recent publications on the alloimmunisation rates in the UK for chronically transfused patients with haematological malignancies or renal insufficiency, providing a rationale for this research.

1.8 Red cell autoantibodies

Patients with haematological malignancies may also make antibodies to red cell antigens on their own cells (Timura *et al.,* 2000; Solal-Celigny *et al.*, 1984) and this can also create challenges with the provision of blood by the hospital transfusion services. The production of red blood cell autoantibodies has been shown to be associated with blood transfusion and the subsequent production of alloantibodies by the recipient (Young *et al.,* 2004). This can sometimes cause haemolytic episodes (Young *et al.,* 2004) but probably occurs more commonly with no ill effects in the patient (Garratty, 2004). It has been suggested that the production of autoantibodies in a transfused patient may be due to the presence of donor lymphocytes in the transfused blood that produce an alloantibody to the recipient red cells, thus mimicking an autoantibody (Ishikura *et al.,* 1993). In the United Kingdom (UK) there is currently no reported data on

the occurrence of red cell autoantibodies associated with alloimmunisation following blood transfusion in patients with renal disease or haematological malignancies and whether the presence of these antibodies has an effect on the transfusion requirements of the patients remains unknown.

1.9 Extended red cell antigen matching of blood in chronic transfusion

There is no current evidence on the rates of alloimmunisation and autoimmunisation in patients with chronic transfusion requirements as a result of haematological malignancies or renal failure in the UK and whether there are risk factors within this heterogeneous group of patients that could be used to predict those at greatest risk of producing allo and/or autoantibodies during the course of their treatment.

It has been advocated by some workers (Michail-Merianou *et al.,* 1987; Rosse *et al.,* 1990) that certain groups of chronically transfused patients, for example those with sickle cell disease (SCD) and thalassaemia, should receive blood that is matched for more than the standard ABO and RhD antigens. In the UK the British Committee for Standards in Haematology (BCSH) also endorse this practice for patients with SCD and thalassaemia (BCSH, 2013) but it is not standard practice for other groups of chronically transfused patients, such as those with haematological malignancies. This has mainly been due to the cost

implications of performing the tests, the perceived difficulties in providing matched blood for large numbers of patients and the lack of evidence of the benefits of such an approach.

Blood transfusions in patients with renal disease and haematological malignancies account for a substantial proportion of the total red cells transfused within the hospital setting. At the RD&E this usage is approximately 30% of the total red cells transfused. There are some historical studies (Fluit *et al.,* 1990; Shirey *et al.,* 2002; Schonewille *et al.,* 2009; Kadar, 2010; Schonewille *et al.,* 1999; Domen and Ramirez, 1988; Blumberg *et al.,* 1984) that have investigated the occurrence of red cell antibodies in these groups of patients and the potential benefits and cost effectiveness of strategies to reduce immunisation. However, the advent of improvements in high throughput automated analysers in the hospital transfusion service, allowing rapid automated red cell phenotyping, along with novel genotyping platforms and increased red cell antigen typing of donor red cells has now made this topic relevant to review.

This research aimed to review the current extent of allo and/or autoimmunisation in chronically transfused patients attending the RD&E, and review the effect that extending matching of blood for transfusion from ABO/D to additional antigens might have on the immunisation rate. It aimed to validate a new technique for extended serological phenotyping using the IBG NEO analyser and investigate the feasibility of introducing a genotyping assay into a hospital transfusion laboratory. It aimed to

review the cost effectiveness of implementing serological phenotyping or genotyping assays to support a type and match program. In addition, ethical approval was obtained from the National Research Ethics Service (NRES) Committee South West - Cornwall & Plymouth (MREC No.12/SW/0251 R&D Study No. 13017733), to recruit patients attending the haematology clinic at the RD&E to a pilot study, a small randomised controlled trial. Patients recruited to the study were randomly assigned to one of two groups; patients assigned to group 1 received standard care with regard to blood transfusions (ABO and RhD compatible blood) and group 2 patients were to be assigned blood that was matched for Rh (C, e, E and e) and K in addition to the standard ABO and RhD. The pilot study was designed to investigate the feasibility of the provision of blood matched for Rh (CcEe) and K antigens within this cohort of patients as well as reviewing recruitment and drop-out rates. A more extensive randomised controlled trial has been performed by Sanquin in the Netherlands (Schonewille *et al*, 2016); this multicentre study aimed to review the incidence of alloimmunisation in a general transfusion population using a multi-centre, parallel group randomised trial. Randomisation of study participants into one of two study arms; ABO-D matched only, or extended match (including c, C, K, Fya, Jka and S antigens) demonstrated a 64% reduction in alloimmunisation risk in surgical patients. The pilot study undertaken in our institution was designed to investigate the feasibility of performing a larger multicentre study in the UK. The results of the pilot study could then be used to design a larger randomised control trial with the aim of investigating the

benefits and cost effectiveness of a strategy for preventive extended antigen matching for patients with haematological malignancies. Neither a pilot study, nor a randomised control trial such as this, has yet been attempted in the UK.

A type and match program for chronically transfused patients has the potential to reduce the risk of alloimmunisation, with the subsequent patient safety benefits of reduction of risk of transfusion reaction or HDFN (see section 1.4). It is this hypothesis that underpins this research project.

1.10 Aims and Hypothesis

- The hypothesis underpinning this research is that allo and autoimmunisation in chronically transfused patients can be reduced by the provision of blood subjected to extended red cell phenotyping and/or genotyping.
- The research aims to test the hypothesis are:
    - To evaluate the frequency of allo- and autoantibodies in two cohorts of patients with chronic transfusion requirements using retrospective patient data from patient cohorts transfused at the RD&E (Haematology and Renal patients)
    - To identify any risk factors for the development of allo- and autoantibodies in these two cohorts of patients with chronic transfusion requirements using the retrospective patient data
    - To evaluate the use of novel fully automated, high throughput, red cell serological phenotyping profiles on the NEO® analyser (IBG Immucor) automated analyser
    - To evaluate and compare the cost effectiveness of a strategy of red cell phenotyping and matching blood for transfusion in patients treated for haematological malignancies and those treated for renal insufficiency using information obtained from the retrospective patient data.
    - To evaluate the use of the BLOODChip IDCOREXT blood group genotyping kit and compare the predicted phenotypes obtained from genotypes with those obtained by the

automated serological phenotyping profiles on the NEO® analyser.

- To evaluate the results of a pilot study recruiting patients with haematological malignancies investigating the effects of prospectively typing and matching red cell antigens for this cohort of patients. This pilot study is designed to assist with the protocol for a larger randomised controlled trial.

2 MATERIALS AND METHODS

2.1 Overview of the project

An overview of the work undertaken for this research is show in the form of a flow chart:

Retrospective review of chronically transfused patients treated at the RD&E to establish:

- Rate of allo/autoimmunisation
- Risk factors for allo/autoimmunisation
- Costs associated with allo/autoimmunisation
- Potential benefit of a type and match strategy

Validation of a fully automated high throughput serological phenotyping assay to support a type and match strategy:

- Comparison of phenotype results with current manual methods
- Cost analysis
- Suitability for routine use to support type and match strategy

Validation of the BLOODChip IDCOREXT blood group genotyping assay:

- Comparison of IDCOREXT predicted phenotype with the serological phenotype
- Feasibility of technique for use in hospital transfusion service
- Cost analysis
- Suitability for routine use to support type and match strategy

Pilot study – randomised controlled trial:

- Feasibility of introducing a type and match stategy in a hospital transfusion service
- Identification of changes required in service provision to support the strategy

Cost analysis:

- Analysis of the costs associated with allo/autoimmunisation in chronically transfused patients and methods for high throughput phenotyping/genotyping
- Review of cost effectiveness of a type and match strategy

2.2 Retrospective review of chronically transfused patients

2.2.1 Sample size for retrospective review

Two cohorts of transfusion dependent patients were selected for inclusion in the retrospective review; patients with haematological malignancies and patients with renal insufficiency. Sample size for the retrospective review was calculated with the aim of achieving a 95% confidence level with the minimum margin of error (<5%), whilst taking into account the amount of historic information available in the computer records and the timeframe of the study. The decision was taken to include a minimum of 800 patients in each study cohort, giving a margin of error of 3.4%.

2.2.2 Patients with haematological malignancies

Data were collected for 1107 randomly selected patients admitted for red cell transfusions within the haematology ward and haematology day case unit at the RD&E between 1995 and 2012. Patients were identified using an in-house enquiry package designed to extract the hospital number and name of patients who had crossmatch tests recorded in the pathology computer system (Integrated Pathology System (IPS)) and had the location codes of YAR (haematology in-patient ward) or YARD (haematology day case). Patients who had received at least one unit of blood on one occasion were included in the database. Ethical approval was not considered appropriate for this retrospective audit as agreed at the Cornwall and Plymouth Research Ethics Committee on the 5th September 2012 (MREC No.12/SW/0251 R&D Study No. 13017733).

Blood samples from patients attending the haematology ward and day case unit at the RD&E during this time period were routinely screened for atypical red cell antibodies, using a selected set of reagent red cells for antibody detection, as part of the pre-compatibility testing. From 1995 to 2000 antibody detection was undertaken manually using the low ionic strength solution (LISS) gel cards (column agglutination technology; Diamed UK). From the years 2000 to 2008 automated antibody screening was performed by the IBG Multisampler (IBG Immucor) robotic system using low ionic strength solution gel test cards (Diamed UK). From 2008 to the present day, antibody screening has been undertaken using capture technology (solid phase technology) on the IBG Galileo/NEO and Echo fully automated analysers (IBG Immucor). Over the study period, antibody identification was performed using a variety of techniques including column agglutination (Diamed UK) and automated Capture Ready ID (IBG Immucor). Laboratory processes for antibody identification also included the DAT by column agglutination (Diamed UK) and, if appropriate, the use of column agglutination with monospecific anti-human globulin (AHG) reagents to identify the type of antibody and/or complement fraction coating the red cells.

Test costs were calculated using an in-house spreadsheet calculator (Microsoft Excel) taking into account reagent costs, equipment maintenance, consumables, quality control and staff time incurred during the financial year 2011-2012. Total test costs for the additional testing

performed on patient samples during the retrospective review period were calculated using current tests costs, although it is accepted that this is an approximation of the actual costs of the tests performed and is subject to error due to variations such as different testing techniques and inflation.

Data were collected on the gender, age at first transfusion, red cell transfusion history, platelet transfusion history, requirement for irradiated blood components, allo/autoantibody status and additional testing requirements for 1107 patients admitted for red cell transfusions within the haematology ward and day case unit at the RD&E between 1995 and 2012.

2.2.3 Patients with renal insufficiency

Data were collected for 877 randomly selected patients admitted for red cell transfusions within the renal ward and haemodialysis unit at the RD&E between 1995 and 2013. Patient data were collected as described for haematology patients in section 2.2.2, with the exception that the location codes of SID (renal in-patient ward) or CRE (haemodialysis unit) were used in the computer enquiry. Patients who had received at least one unit of blood on one occasion were included. Ethical approval was not considered appropriate for this retrospective audit as agreed at the Cornwall and Plymouth Research Ethics Committee on the 5th September 2012 (MREC No.12/SW/0251 R&D Study No. 13017733).

Screening of patients' samples for atypical red cell antibodies during this time period was as for patients admitted to the haematology wards. Data were collected on the gender, age at first transfusion, red cell transfusion history, renal transplant history, allo/autoantibody status and additional testing requirements for 877 patients admitted for red cell transfusions within the renal ward and haemodialysis unit at the RD&E between 1995 and 2013.

2.3 Comparison of manual and automated red cell phenotyping

One hundred patient samples, to be discarded, were selected for comparative extended serological red cell antigen phenotyping in the current manual systems and novel automated method. The BCSH guidelines for validation and qualification of new techniques in the laboratory setting (BCSH, 2012) recommend that a predetermined number of samples are tested in duplicate with the current system, quoting "2 weeks or 250 samples whichever occurs first" as a target value. At the time of the validation approximately 140 samples per year were phenotyped for Rh (CcEe) and K antigens, and less typed for Jk, Fy, Ss and MN antigens. It was, therefore, considered that 100 samples would be an acceptable size for comparison testing, which would test all the reagents and provide the sensitivity required to give confidence in the performance of the technique. All samples were collected into EDTA anticoagulant and stored at 2-8°C until tested. Patients who had records

on the hospital computer system, of blood transfusion in the three months prior to the collection of the sample were excluded from analysis due to the interference caused by circulating transfused red cells in these serological techniques. Ethical approval for this stage of the project was not required as it was considered to be service development. Samples had been taken for routine blood group and antibody screening and no additional samples were required.

2.3.1 Manual red cell phenotyping

Manual red cell phenotyping for Rh (CcEe) and K antigens was performed by column agglutination using DiaClon Rh-Subgroups and K (Catalogue number: 50110, Bio-Rad, Watford, UK) microgel card for 100 patient samples. The microgel card contains monoclonal antibodies (anti-C (cell line MS-24), anti-c (cell line MS-33), anti-E (cell line MS-260), anti-e (cell lines MS-16, MS-21 and MS-63) and anti-K (cell line MS-56)) within each gel matrix and also includes a negative control well.

Method:

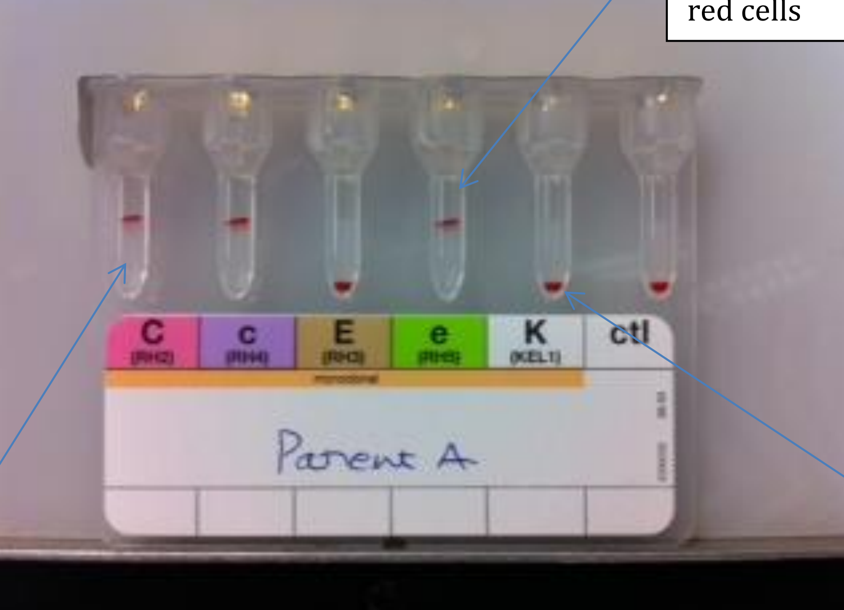
A 5% suspension of patient red cells was prepared by mixing 0.5mL of ID-Diluent 2, a modified, low ionic strength solution (catalogue number 05761, Bio-Rad) with 25 µL of packed cells, in accordance with manufacturer's instructions.

Patient red cell suspension (10 µL) was then added to each well of the microgel and the card was then centrifuged in an ID-Centrifuge 12 S II (Bio-Rad) at 85xg for 10 minutes.

The results were read macroscopically, with positive reactions denoted by red cell agglutinates visible in the gel matrix and negative reactions by a button of red cells at the bottom of the column (see figure 2.1).

Figure 2.1: Rh and K antigen phenotyping by column agglutination

Positive reactions are seen if the antigen is present on the patient red cells



Negative reactions are seen if the antigen is not present on the patient red cells

Specific antiserum is contained within the gel matrix

Example of a patient red cell phenotype performed using column agglutination methodology (Bio-Rad). Each column within the card contains a specific antiserum, a suspension of the patient red cells is added to each column, and centrifugation then forces the patient red cells through the gel matrix containing the antiserum. If the patient red cells have the corresponding antigen then the cells are trapped in the gel matrix, if the red cell antigen is absent then the patient cells will travel to the bottom of the column. The patient phenotype in the example shown here is C+, c+, E-, e+, K-; the negative reaction in the control column validates the results and confirms the absence of any false positive reactions caused by auto-agglutination.

Manual red cell phenotyping for the Fy (a and b), Jk (a and b), s and k antigens was performed using polyclonal reagents supplied by Lorne (Lorne Laboratories Limited, Early, UK) in an IAT. The following reagents were used: monoclonal anti-Fy^a (cell line DG-FYA-02 code 774002) anti-s (cell line P3YAN3 code 771002) and anti-Fy^b (code 317002), anti-Jk^a (code 323002), anti-Jk^b (code 324002), anti-k (code 320002) prepared from pooled human sera.

<u>Method:</u>

A 0.9% suspension of patient red cells was prepared by mixing 10 µL of packed red cells with 1mL of ID-Diluent 2 (Bio-Rad).

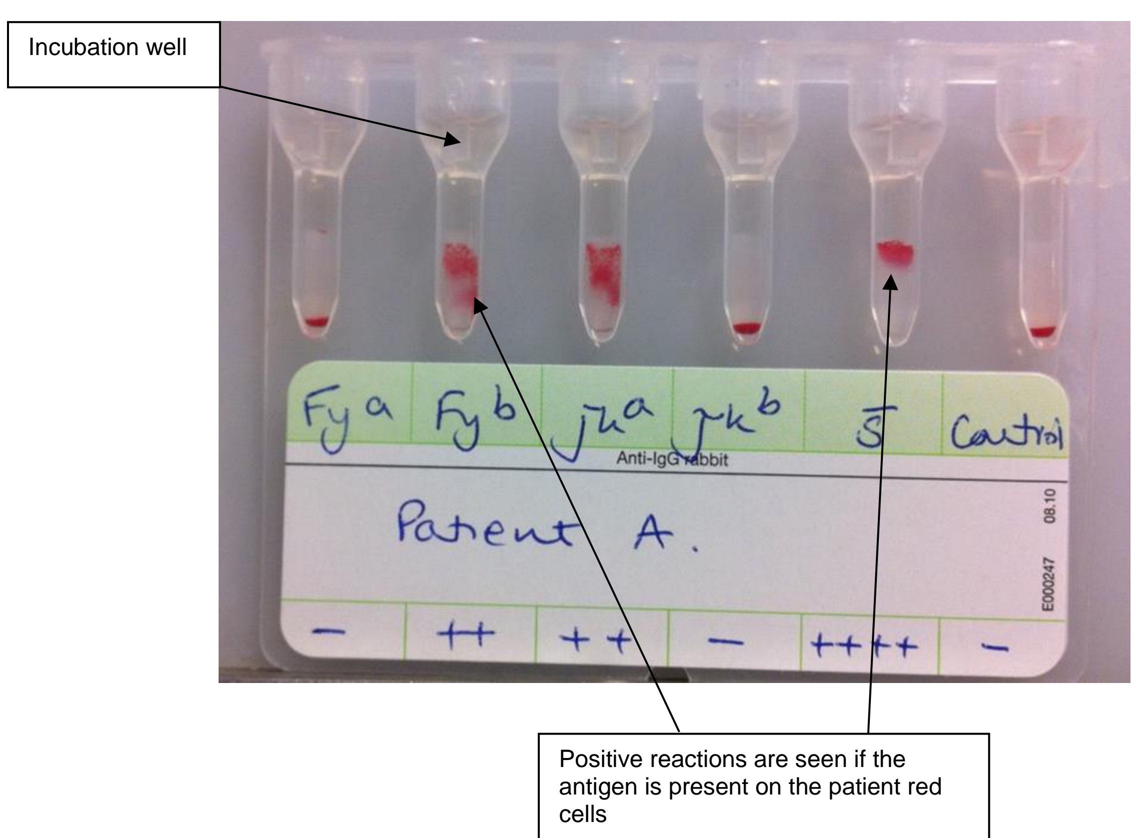
Patient red cell suspension (50 µL) was then added to each well of a LISS Coombs Anti-IgG microgel card (Catalogue number: 50540, anti-IgG, rabbit, Bio-Rad) followed by 25 µL of the appropriate anti-sera.

A control well was included on the microgel card by the addition of 50 µL of patient red cell suspension to one of the wells within the Coombs Anti-IgG microgel card.

The microgel was incubated for 15 minutes in a DiaMed-ID Incubator 37°C (Bio-Rad) and then centrifuged in an ID-Centrifuge 12 S II (Bio-Rad) at 85 x g for 10 minutes.

The results were then read macroscopically, a positive reaction in the control well invalidated the results (see figure 2.2).

Figure 2.2: Manual Serological phenotyping for Fy (a and b), Jk (a and b) and s antigens by column agglutination



In the manual column agglutination Indirect Antiglobulin Test (Bio-Rad) patient red cells in suspension are incubated with specific antisera at 37°C to allow antigen-antibody complexes to form. Centrifugation then forces the red cells through a gel containing anti-human globulin. Red cells with antibodies attached are then caught by the anti-human globulin within the gel. Negative reactions are denoted by a button of patient red cells at the bottom of the column and positive reactions by red cell agglutinates trapped within the gel matrix. The patient shown in this figure has the phenotype Fy (a-b+), Jk (a+b-) and s+, the negative reaction in the control well indicates that the reactions with the antisera are valid and not due to the presence of a positive Direct Antiglobulin Test.

Manual red cell phenotyping for the M, N, S and C^w antigens was performed using monoclonal reagents manufactured by Millipore (Millipore UK Ltd, Watford, UK). The following antisera were utilised; Anti-M (cell line LM110/140), anti-N (cell line BO3), anti-S (cell line MS-94) and anti-Cw (cell line MS-110). A 3-5% red cell suspension was prepared by mixing 0.5mL of Phosphate Buffered Saline (PBS 0.9% pH7.0, IBG Immucor) with 75 μL of the patient packed cells. The same cell suspension was used for all the tube techniques described below.

Method:

N antigen status was determined by adding 75 μL of cell suspension and 75 μL of anti-N to an appropriately labelled test tube.

The mixture was agitated gently and then centrifuged in an Immufuge II (Baxter Healthcare Ltd, Newbury, UK) for 1 minute at approximately 200-300 x g.

The results were then read by gently agitating the tube to dislodge the red cells and examining macroscopically for agglutination.

M antigen status was determined by adding 75 μL of red cell suspension and 75 μL of anti-M to an appropriately labelled test tube.

This was mixed well and incubated at room temperature for 5 minutes. The tube was then centrifuged at approximately 1000 x g for 20 seconds. The results were then read by gently agitating the tube to dislodge the red cells and examining macroscopically for agglutination.

S antigen status was determined by adding 75 µL of patient red cell suspension and 75 µL of anti-S to an appropriately labelled test tube.

This was mixed and then centrifuged at approximately 1000 x g for 20 seconds.

The results were then read by gently agitating the tube to dislodge the red cells and examining macroscopically for agglutination. C^w antigen status was determined by the same methodology as the S antigen status.

All negative and weakly positive reactions for M, N, S and C^w antigens were then incubated at room temperature for a further five minutes before being centrifuged (Immufuge II; Baxter Healthcare Ltd) for 1 minute at approximately 200-300 x g) again for repeat macroscopic reading.

2.3.2 Automated red cell phenotyping using the NEO analyser

Automated red cell phenotyping was performed using the fully automated Galileo-NEO® analyser (IBG Immucor). This analyser is used within the transfusion laboratory at the RD&E for routine ABO/D typing, antibody screening and antibody identification techniques. It also has the capacity for automated DAT testing and crossmatching, although these tests have yet to be validated on the analyser at the RD&E. Reagents for red cell antigen typing are also supplied by IBG Immucor, which are CE marked for tube, slide and automated techniques, however, these are not used for automated testing within the UK (personal communication from Berndine Kokkelink, IBG Immucor). Provision of extended, automated

serological phenotyping profiles was considered to be a novel way of introducing high throughput phenotyping technology within the hospital transfusion service, which could then be adopted by other centres using the same platforms. The assay would enable identification of a range of red cell antigens in a single, automated test profile, which is not yet available in the UK.

A profile to determine the Rh (CcEeC^{w}), K, M and N antigen status was set up on the NEO® analyser. Immuclone® IgM (IBG Immucor) monoclonal reagents suitable for use on the IBG NEO® analyser system in 96 well U-bottom microplates were utilised for this profile. The monoclonal reagents used were; anti-C (derived from cell line MS-24), anti-c (derived from cell line MS-33), anti-E (derived from cell lines MS-80 and MS-258), anti-e (derived from cell lines MS-16, MS-21 and MS-63), anti-K (derived from cell line MS-56), anti-M (clone M-11H2), anti-N (clone 1422-C7) and anti-C^{w} (derived from human cell line MS-110). The reagents were loaded into a single reagent rack, enabling a simple and fast method for reagent presentation to the analyser. The patient primary blood sample was centrifuged in a Labofuge400 centrifuge for 11 minutes at 2,250 x g prior to placing on the NEO® analyser.

Method:

The automated process enables the analyser to produce a red cell suspension from the patient primary sample tube; 10µL of red cells taken

from the primary sample are mixed with 314μL of Diluent (IBG Immucor kit, ref: 0066058).

Aliquots (40μL) of this cell suspension are then added to the first eight wells of the 96 well U-bottom microplate in a vertical pattern.

An aliquot (10μL of anti-C^w, -C, -c, -E, -e, -K or 20μL of anti-M, -N) of the monoclonal reagent is then added to the appropriate well of the microtitre plate in the order shown in figure 2.3.

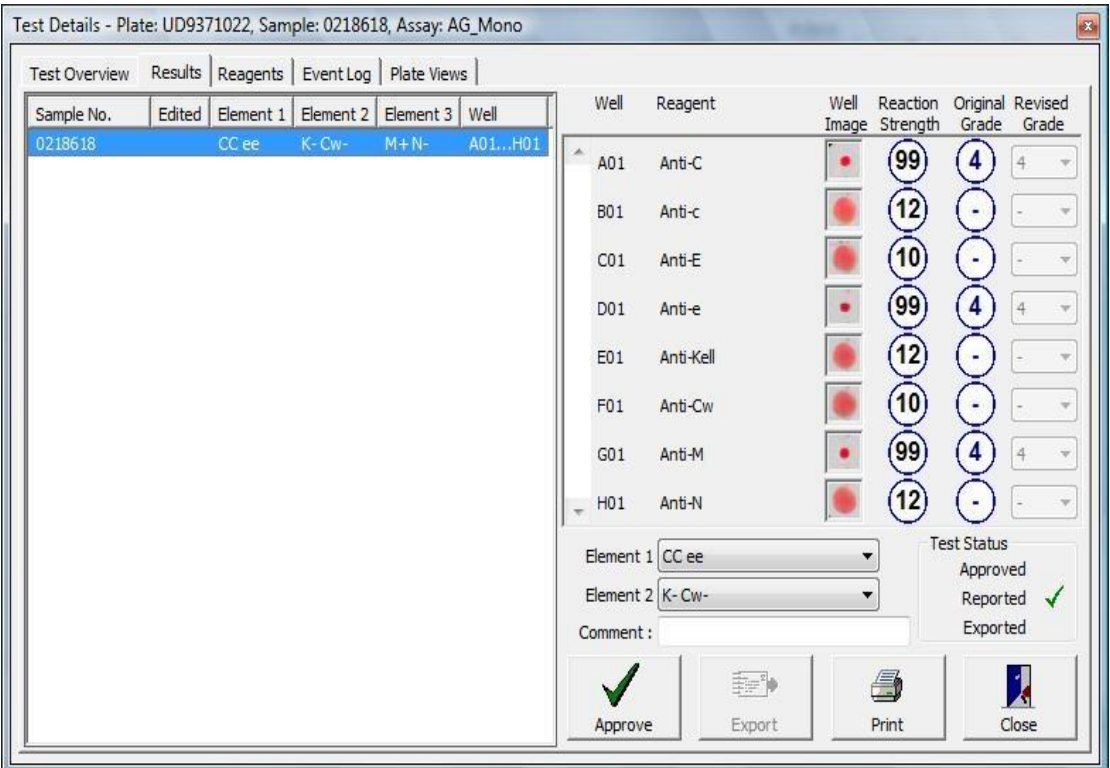
An incubation phase performed at 20°C for 10 minutes allows the antigen-antibody complexes to form, if the antigens are present. Centrifugation of the plate (30 seconds at 80 x g followed by 30 seconds at 170 x g) enhances the antigen-antibody reaction by forcing the red cells closer together allowing the antisera to bind red cells together as agglutinates.

Automated shaking of the plate for 60 seconds then disperses red cells that have not been agglutinated, leaving a loose layer of red cells within the microwell. Cells that had been agglutinated by the formation of antigen-antibody complexes remained as a tight button of cells at the bottom of the microwell.

The automated reader within the analyser is then able to interpret the reaction patterns of the red cells, recognising a positive reaction (tight button of cells at the bottom of the microwell) from a negative reaction (loose layer of cells around the microwell). The pattern of cells detected

by the automated reader is then converted into a numerical reaction strength (between 0 and 99) and a corresponding reaction grade (between 0 and 4; figure 2.3). The user is able to view both reaction strengths and grades; the availability of the reaction grade allows some comparability with manual techniques that may also be employed in the laboratory.

Figure 2.3: Reaction patterns generated by automated red cell antigen phenotyping for Rh(CC^{w}cEe), K, M and N antigens



Format of the results and reaction patterns generated by the automated monoclonal profile on the NEO®. The left hand side of the screen shows the laboratory number associated with the patient sample being tested and the antigen status of the patient red cells. The right hand side of the screen shows the image of the reaction in the well captured by the analyser camera, the reaction strength generated by the analyser and the grade of reaction. A negative reaction is equivalent to reaction strength of 23 or below, equivocal and positive reactions are variable and dependent on the antisera used. The "well image" column shows a photographic image of the agglutination of the cells (positive reaction) or the loose layer of non-agglutinated cells denoting a negative reaction. (Picture courtesy of Caryn Conway, IBG Immucor, personal communication).

Automated red cell phenotyping for Fy(a and b), Jk(a and b), S, s and k antigens was performed using commercial polyclonal antisera prepared from pools of human sera (IBG Immucor) in Capture-R Select microwell strips (IBG Immucor ref: 006446). The reagents are loaded in a single reagent rack, as for the monoclonal reagents. The patient primary blood sample was centrifuged in a Labofuge400 centrifuge for 11 minutes at 2,250 x g prior to placing on the NEO® analyser.

Method:

The automated process enables the analyser to produce a red cell suspension from the patient primary sample tube; 4µL of red cells from the sample tube are mixed with 270µL of Diluent (IBG Immucor kit). Aliquots (40µL) of this cell suspension are then added to the first eight wells of the 96 well of the Capture-R Select microwell strips in a vertical pattern. The Capture-R Select microwell is supplied as a ready to use kit and is pre-coated with an affinity isolated goat anti-murine and an anti-RBC antibody to immobilise red blood cells to the microwell surface.

The analyser performs a shake phase for 15 seconds to enable the patient red cells to bind to the Capture-R Select coated microwell.

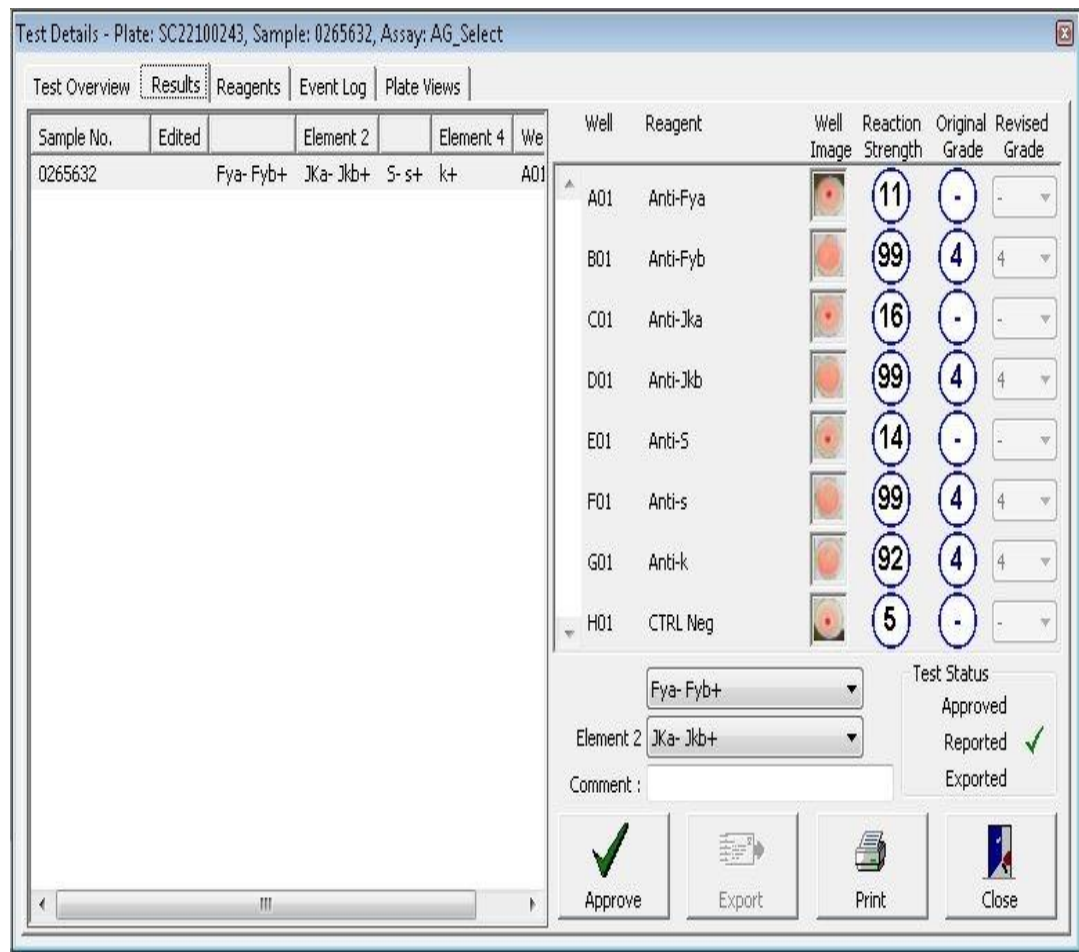
A double centrifugation stage (60 seconds at 150 x g followed by 60 seconds at 500 x g) then enables the formation of the red cell monolayer. An aliquot (25µL) of the polyclonal reagent was then added to the appropriate well of the microtitre plate along with 35µL of negative control reagent (IBG Immucor) in the order shown in figure 2.4.

An incubation phase performed at 39°C (enabling a 37°C temperature within the reaction well) for 20 minutes allows the antigen-antibody complexes to form, if the antigens are present on the patient's red cells. The analyser then completes a wash cycle to remove any unbound antibodies. Immucor Capture-R Ready Indicator Red Cells (a suspension of red blood cells coated with murine monoclonal anti-human IgG molecules, 50µL) were then added to the microwell.

These cells are captured by the antigen-antibody complexes in the presence of the antigen, but remain free in suspension in the absence of the antigen. A double centrifugation stage (30 seconds at 80 x g followed by 30 seconds at 170 x g) followed by a shake phase and further centrifugation (20 seconds at 15 x g) then forces free cells to the bottom of the microwell but bound cells remained as a monolayer of cells around the microwell.

Automated reading of the microwell plate by the analyser allowed the distinction between the monolayer of cells, indicating a positive reaction, or a button of cells in the bottom of the microwell indicating a negative reaction (figure 2.4).

Figure 2.4: Reactions patterns generated by automated red cell antigen typing for Fy^a, Fy^b, Jk^a, Jk^b, S, s and k antigens



Screenshot showing the reaction patterns generated by the NEO analyser. In the Capture R Select solid phase test positive reactions are denoted by a layer of patient red cells coating the bottom of the well and negative reactions are denoted by a tight button of cells, this is in contrast to the reaction patterns seen in the direct agglutination testing using the monoclonal reagents (as shown in figure 2.3). The serological phenotype of the patient sample is shown in the top left hand side of the screen. (Picture courtesy of Caryn Conway, Immucor, personal communication).

2.3.3 Extended phenotyping profile result interpretation on the NEO® analyser

A monoclonal antisera reagent profile (anti-C, Anti-c, Anti-E, anti-e, anti-K, anti-C^w, anti-M and anti-N) was created on the IBG Immucor Galileo-NEO® analyser (section 2.3.2, figure 2.3) along with a polyclonal antisera reagent profile (anti-Fy^a, anti-Fy^b, anti-Jk^a, anti-Jk^b, anti-S, anti-s, anti-k and auto control; all reagents from IBG Immucor, figure 2.4). The Galileo-NEO® analyser provides the test result in three different formats; a "+" or "-" result, a numerical value (0 to 99) and a reaction strength value (0, 1+, 2+, 3+ and 4+). The numerical value has programmed cut-off points for generating the reaction strength values, which vary according to the antisera (see appendix 3). These cut-off points have been validated by the supplier and cannot be influenced by the laboratory staff operating the analyser. A numerical value of 23 for the monoclonal profile and 20 for the polyclonal profile, or below generated by the analyser is set to correspond to a negative result and borderline values between negative and the set positive value (1+ reaction) are expressed as "not determined" (NTD). The analyser returns an "X" in the testing well if it detects an insufficient volume; this could be due to insufficient sample or insufficient antisera and acts as an internal quality control system to minimise the risk of false negative results.

The antisera used for the automated testing were all CE marked and validated for use in automated techniques, with the exception of the anti-N (immuClone) which was CE marked only for use in tube and slide tests.

This validation also intended to review the effectiveness of this antiserum for use in the automated technique on the Galileo-NEO®.

2.3.4 Quality control testing

The NHSBT ten cell ID panel profile (0.8% cell suspension) in Cellstab preservative (item code: PR143, NHSBT, UK) with known red cell phenotypes (figure 2.5) was used to determine the accuracy of the automated phenotyping profiles prior to commencing comparative work with patient samples. The panel was tested on four occasions over four weeks to determine any intra- and inter-test variation. The panel contained a mixture of cells with homozygous and heterozygous expression of red cell antigens. The NHSBT three cell screen profile product (3% cell suspension) in Alsevers preservative (item code: PR122, NHSBT) as shown in figure 2.6), selected to include all the relevant antigens including homozygous and heterozygous expression of red cell antigens, was tested over five separate occasions to challenge the stability and accuracy of the antisera over an extended period. The NHSBT titration cell set profile (0.8% cell suspension in Cellstab, item code: PR407), including a two cell set with homozygous and heterozygous expression of red cell antigens (figure 2.7), was tested on two separate occasions.

The purpose of quality control for red cell antigen phenotyping is to detect the weakest expression of the antigen, hence the requirement for examples of heterozygous expression of antigens. Red cells that are

heterozygous express both the antigen and its antithetical counterpart, for example Jk(a+b+). Whereas, homozygous expression is the presence of one antigen but not the antithetical antigen, for example Jk(a+b-). There are no clear recommendations from the BCSH (BCSH 2013) on the requirements for quality control for phenotyping reagents, only that suitable positive and negative controls should be included. In the absence of any commercial quality control for phenotyping reagents, with the exception of RhCcEe and K, the NHSBT cells were selected as they included heterozygous and homozygous expression of the majority of antigens and, thus, could provide both the positive and negative controls required.

Figure 2.5: NHSBT ten cell ID panel profile

FORM FRM783/2 | Effective: 20/03/13

ID Panel Profile

CE IVD | NHS Blood and Transplant

NBS REAGENTS **Panel 1**

Product	Lot No.	Product	Lot No.	Product	Lot No.
ID Panel in Alsevers	R144 3322	ID Panel Papainised in Alsevers	R154 3322	ID Panel in LISP	R146 3322
ID Panel in CellStab	R143 3322	ID Panel Papainised in CellStab	R153 3322	Expiry Date : 2015.04.30	
ID Panel in CellMedia	R163 3322	ID Panel Papainised in CellMedia	R173 3322		

Patient's Name / D.O.B.		Ref. No.	Sample No.	Conclusion / Tested by / Date

Unless otherwise indicated, all cells are positive for Kp^b and Lu^b and negative for Wr^a and Co^b.

Instructions for use can be found at http://www.blood.co.uk/reagents

	Rh	C	D	E	c	e	C^w	M	N	S	s	P1	Lu^a	K	k	Kp^a	Le^a	Le^b	Fy^a	Fy^b	Jk^a	Jk^b	Other						
1	$R_1^wR_1$	+	+	0	0	+	+	0	+	0	+	0	0	0	+	0	0	+	0	+	0	+							
2	R_1R_1	+	+	0	0	+	0	+	0	+	0	3	0	+	0	0	+	0	+	0	+	0							
3	R_2R_2	0	+	+	+	0	0	0	+	0	+	0	0	0	+	0	0	+	+	0	+	0							
4	$r'r$	+	0	0	+	+	0	+	0	0	+	0	0	0	+	0	0	+	0	+	+	0							
5	$r''r$	0	0	+	+	+	0	+	0	+	0	3	0	0	+	0	+	0	0	+	0	+							
6	rr	0	0	0	+	+	0	+	+	0	+	4	0	+	0	0	0	0	0	+	+	0							
7	rr	0	0	0	+	+	0	0	+	0	+	0	0	+	+	0	+	0	+	0	0	+							
8	rr	0	0	0	+	+	0	0	+	0	+	2	0	0	+	+	0	+	+	0	+	0							
9	rr	0	0	0	+	+	0	+	0	+	0	0	+	0	+	0	0	0	0	+	0	+							
10	rr	0	0	0	+	+	0	0	+	+	0	0	0	0	+	0	0	+	0	+	+	0							

Reagent							DAT Profile	Anti-IgG	IgA	IgM	C3c	C3d	Ctrl
Lot No.							Result						

Cross-Referenced in Primary Document: SOP883 | (Template Version 01/04) Page 1 of 1

An example of an NHSBT ten cell ID panel. Panels are available in a variety of preservative media; the ID Panel in CellStab was used for quality control of the automated extended phenotyping technique. Antigen profiles of the red cells in the panel are denoted by a positive (+) or negative (-) in the table. The panel sheet supplied by the NHSBT (shown in this example) also allows for result entry in the blank section on the right hand side and for documentation of a DAT result at the bottom of the table. This sheet can then be retained as a worksheet within the laboratory as part patient result record. (Picture reproduced courtesy of NHSBT, taken from the reagent product profiles http://hospital.blood.co.uk/diagnostic-services/reagents/product-profiles/).

Figure 2.6: NHSBT three cell screen profile product

FORM FRM833/2.1 Effective: 06/09/13

3 Cell Screen Profile Product

CE 0843

IVD

NHS Blood and Transplant

NHSBT REAGENTS

Product	Lot No	Product	Lot No.	Expiry Date
Alsevers	R121 3451	CellStab	R122 3451	2015.04.16
CellMedia	R123 3451	Papainised in Alsevers	R124 N/A	

Unless otherwise indicated, all cells are positive for Kp^b and Lu^b and negative for Wr^a, Lu^a and Co^b
Instructions for use can be found at www.blood.co.uk/reagents

	Rh	C	D	E	c	e	C^w	M	N	S	s	P1	K	k	Kp^a	Le^a	Le^b	Fy^a	Fy^b	Jk^a	Jk^b	Other
1	$R_1{}^wR_1$	+	+	0	0	+	+	+	+	+	+	+	0	+	0	+	0	+	0	+	0	Cob+
2	R_2R_2	0	+	+	+	0	0	+	0	+	0	0	+	+	0	0	0	0	+	+	0	
3	rr	0	0	0	+	+	0	0	+	0	+	+	0	+	+	0	+	0	+	0	+	

(Template Version 01/04)

Cross-Referenced in Primary Document: SOP883 Page 1 of 1

An example of an NHSBT three cell screen profile set. The product is available in different preservative media suitable for use in a variety of antibody screening techniques; the product in Alsevers (3% cell suspension) was used for quality control of the extended automated phenotyping technique. (Picture reproduced courtesy of NHSBT, taken from the reagent product profiles http://hospital.blood.co.uk/diagnostic-services/reagents/product-profiles/).

Figure 2.7: NHSBT titration cell set profile

FORM FRM843/1.2 Effective: 26/09/13

Titration Cell Set Profile

CE

IVD

NHS Blood and Transplant

NHSBT REAGENTS

Product	Lot No.	Expiry
Titration cells in CellStab	R407 3159	2015.04.16

Please note that Cell 2 is Cob+.

Cell	Rh	M	N	S	s	K	k	Fy^a	Fy^b	Jk^a	Jk^b	Other
1	R_1R_z	+	+	+	+	0	+	+	+	+	+	
2	R_1R_2	+	0	+	+	+	+	+	+	+	+	

(Template Version 01/04)

Cross-Referenced in Primary Document: SOP883 Page 1 of 1

Example of an NHSBT two cell titration set profile. This product is available for use in techniques designed to determine the strength of a red cell antibody by titration methods. It was selected for use as a quality control product in the validation of the extended automated phenotyping technique as it has a selection of red cells that are heterozygous for some of the red cell antigens which were used for determination of the performance of the automated technique with red cells of a weaker expression than homozygous cells. (Picture reproduced courtesy of NHSBT, taken from the reagent product profiles http://hospital.blood.co.uk/diagnostic-services/reagents/product-profiles/).

2.4 Blood Group genotyping

2.4.1 DNA Extraction

DNA was obtained from whole blood samples taken from 47 patients attending the haematology clinic for routine blood samples and who consented to have an additional sample taken for genetic analysis (ethical approval for this was obtained from the NRES Committee South West - Cornwall & Plymouth (MREC No. 12/SW/0251, R&D Study No. 1301733)). The BLOODChip IDCOREXT kit funded for this research included 48 tests, 47 patient assays and one negative quality control sample. The sample size for this study group was determined by the funding obtained. It was not possible within the funding of the research to include replicates to investigate the reproducibility of the results.

DNA was extracted from the whole blood samples in EDTA anticoagulant (2.7ml) using the Autopure LS (Qiagen, Hilden, Germany), a fully automated, high throughput analyser that uses PureGene chemistry (Qiagen). This method gently removes contaminants and inhibitors to enable purification of high molecular weight (100-200kb) DNA that can be stored for analysis.

The analyser uses a red cell lysis solution (Qiagen, 15ml), part of the Autopure LS whole blood extraction kit (used according to manufacturer's instructions) to remove the red cells from the whole blood sample and then uses centrifugation (3000 x g for 5 min) to produce a pellet of white

blood cells. The white cells are then dispersed and lysed using a cell lysis solution (Qiagen Autopure LS whole blood extraction kit used according to manufacturer's instructions, 5ml) and the proteins precipitated (2.2ml Autopure protein precipitation solution, Qiagen) by mixing vigorously (rapid tube inversions for 5 minutes). The supernatant containing the DNA is then dispensed into tubes containing isopropanol (Autopure 100% isopropanol 6.5ml). These tubes are rotated and centrifuged (rotated 50 times, centrifuged at 3000 x g for 5 min) to precipitate and pellet the DNA, the isopropanol (entire volume) is then discarded and the DNA treated with 70% ethanol (Autopure 70% ethanol, 6.5ml), centrifuged (3000 x g for 5 min) and drained to evaporate any remaining alcohol. A DNA hydration solution (Autopure DNA hydration solution, 300µl) is then dispensed into the tubes to hydrate the DNA. Concentration and purity were measured using the Nanodrop ND8000 spectrophotometer (measured in ng/µl and ratios to indicate the purity of the samples). The samples were then stored at -20°C until required for testing.

2.4.2 IDCOREXT test

2.4.2.1 IDCOREXT Workflow

The IDCOREXT protocol consists of four steps:

- Amplification
- Hybridisation/Labelling
- Data acquisition on Luminex
- Data analysis

2.4.2.2 DNA Amplification

DNA preparation was undertaken in a laminar flow fume hood (Astec – Bioquell UK Ltd, Andover, UK). The IDCOREXT PCR master mix, containing the allele specific primers (product ref: 1020120100, Progenika Biopharma S.A), was brought to room temperature, vortexed for 10 seconds and then spun for 10 seconds in a micro-centrifuge (13000 xg) before use. The HotStarTaq® DNA polymerase (Qiagen) was kept frozen until ready for use and then immediately prior to use the tube was flicked gently and spun down in a micro-centrifuge for 10 seconds. A PCR reaction mix was prepared using the IDCOREXT PCR master mix and the HotStarTaq® DNA polymerase in accordance with the quantities (volumes in μL) shown in table 2.1.

Table 2.1: Reagent volumes required to produce the PCR mix using the IDCOREXT

Reagent volumes required to produce the PCR mix (volumes in μL) using the IDCOREXT PCR master mix and the HotStarTaq® DNA polymerase (Qiagen). Volumes are given for sample batch sizes of 1, 8, 24 and 48.

Number of samples	1	8	24	48
IDCOREXT PCR master mix	22.5	180	540	1080
HotStarTaq DNA Polymerase (5 U/μL)	0.5	4	12	24

The 47 patient samples were run in three batches for ease of sample preparation. A 96 well reaction plate (MicroAmp® Optical 96 well reaction plate, Applied Biosystems®) (ThermoFisher Scientific, Cramlington, UK) was used for the amplification phase. The PCR reaction mix was vortexed and spun rapidly for 10 seconds in a micro-centrifuge, 20μL of this mix was then dispensed into one well of the PCR reaction plate for each sample. The frozen DNA samples were brought to room temperature, vortexed and spun rapidly. DNA sample, 5μL, (concentration >10ng/μL, A260/A280 ratio in the range 1.6-1.95, as recommended by the package insert) was then added to the corresponding wells and the resulting suspension mixed gently by pipetting up and down.

The plate was then sealed with adhesive film (Microamp® Clear adhesive film, Applied Biosystems®). The plate was then placed in the thermal cycler block (Veriti® Applied Biosystems®) with a PCR compression pad on the top. An amplification program was applied to the samples as shown in table 2.2, which resulted in the production of the biotinylated PCR product (Biotin labelled dCTP, included within the amplification kit).

Table 2.2 Amplification program details for IDCOREXT

Program details for the amplification stages; the denaturation, annealing and extension phases are linked for 40 cycles and then the plates were kept in the thermal cycler at 4°C until ready for the hybridisation phase.

	Temperature	Time	Cycles
Polymerase Activation	95°C	15 mins	1
Denaturation	95°C	30 sec	40
Annealing	60°C	30 sec	40
Extension	72°C	80 sec	40
Final extension	72°C	7 min	1
Hold	4°C	∞	1

2.4.2.3 Hybridisation of amplified DNA to allele specific probes

The ID-COREXT Beads Master Mix (product ref: 1020120200, Progenika Biopharma S.A.), a solution containing a mix of beads with allele specific probes attached, was brought to room temperature and vortexed vigorously for 30 seconds before use. The beads mix include probes specific for the following alleles:

RHCE blood group: *RHCE*ce; RHCE*Ce, RHCE*cE; RHCE*CE, RHCE*CeCW, RHCE*ceCW, RHCE*CECW, RHCE*ceAR, RHCE*CeFV, RHCE*CeVG , RHCE*cEFM, RHCE*ce[712G] , RHCE*ce[733G] , HCE*ce[733G,1006T] , RHCE*CE-D[2, 5,7]-CE, RHCE*cE[697G,712G,733G], RHD*r's-RHCE*ce[733G,1006T].*

KELL blood group*: KEL*K_KPB_JSB, KEL*k_KPB_JSB, KEL*k_KPA_JSB, KEL*k_KPB_JSA.*

Kidd blood group*: JK*A, JK*B, JK*B_null(871C), JK*B_null(IVS5-1a).*

Duffy blood group*: FY*A; FY*B, FY*B_GATA, FY*B[265T]_FY*X*

MNS blood group*: GYPA*M, GYPA*N, GYPB*s, GYPB*S, GYPB*Mur, GYPB*deletion, GYPB*S_, null(230T) , GYPB*S_null(IVS5+5t)*

Diego blood group: *DI*A, DI*B.*

Dombrock blood group*: DO*A, DO*B, DO*B_HY-, DO*A_JOA*

Colton blood group*: CO*A, CO*B*

Cartwright blood group*: YT*A, YT*B*

Lutheran blood group*: LU*A, LU*B*

This process was repeated before dispensing for each sample to ensure that the beads remained fully dispersed within the mix. ID-COREXT Beads Master Mix (46µL) was dispensed into relevant wells of a 96 well Thermowell P polycarbonate clear PCR plate (Corning, New York, USA). The PCR plate containing amplified DNA from patient samples was removed from the thermal cycler and 4µL of the PCR product was dispensed into the corresponding well containing the hybridisation mix; the resulting suspension was gently mixed by pipetting up and down.

The plate was then covered with a non-adhesive sealing film (Bio-Rad MSA-5001 film) and placed in the thermal cycler with silicone pads. A program of denaturation and hybridisation was then applied to allow amplified DNA to attach to the specific alleles on the beads (table 2.3).

Table 2.3 Thermal cycler program for denaturation and hybridisation

PCR amplicons from patient samples were hybridised to beads with allele specific probes was performed by denaturation at 95°C, followed by a hybridization phase at 52°C, the samples were then held prior to fluorescent labelling.

	Temperature	Time
Denaturation	95°C	2 min
Hybridisation	52°C	30min
Hold	52°C	∞

2.4.2.4 Fluorescent labelling of hybridised DNA

The SAPE (Streptavidin R-Phycoerythrin Conjugate) mixture containing the fluorescent marker (product ref: 000020100, Progenika Biopharma S.A.) and SAPE Dilution Buffer (product ref: 000020200, Progenika Biopharma S.A.) were brought to room temperature and the SAPE vortexed and spun rapidly. A labelling mix was then prepared using the SAPE Dilution Buffer and the SAPE reagent (volumes μL) as shown in table 2.4. The labelling mix was then vortexed and protected from the light by covering with aluminium foil.

Table 2.4 Fluorescent labelling mix

The hybridised DNA attached to the allele specific beads was then labelled with a fluorescent mix for detection and quantification by the Luminex analyser. The labelling mix using the SAPE Dilution Buffer and the SAPE reagent (volumes µL) for different batch sizes of patient samples are shown in the table below.

Number of samples	1	8	24	48
SAPE Dilution Buffer	87	696	2088	4176
SAPE	4.6	36.8	110.4	220.8

At the 52°C hold step in the thermal cycler program (shown in table 2-3) the lid was opened, and the silicone pads and sealing film carefully removed. Labelling mix (80µL) was then dispensed into each well of the hybridisation plate and gently mixed by pipetting up and down. The samples were then immediately analysed on the Luminex X-Map® system. Fluorescent labelling is stated here in volumes rather than final concentrations, as stated in the IDCOREXT package insert, and in accordance with confidential, proprietary information (kit product ref: 1020120034, Progenika Biopharma S.A.).

2.4.3 Luminex xMAP Analyser

2.4.3.1 Luminex® X-Map system analysis

The Luminex Gold heater block was placed on the plate holder and the temperature was set to 52°C to correlate with the hold temperature of the thermal cycler as rapid cooling of the samples could result in non-specific hybridisation (it is a recommendation of the Luminex assay process that the temperature is maintained through the process). This was done one hour in advance of the labelling phase to enable the heater block to reach the correct temperature.

Prior to analysis, the Luminex analyser was calibrated using the following reagents (used as per manufacturer's instructions, Luminex® xPONENT® 3.1 Quick Guide, Luminex Corporation)

xMAP Classification Calibrator Microspheres (CAL 1), polystyrene microspheres internally labelled with fluorescent dyes and intended to normalise the kittings for the classification channels (CL1 and CL2).

xMAP Reporter Calibrator Microspheres (CAL 2), polystyrene microspheres internally labelled with fluorescent dyes and intended to normalise the analyser reporter channel (RP1)

xMAP Classification Control Microspheres (CON1), polystyrene microspheres internally labelled with fluorescent dyes and intended to

verify the calibration and optical integrity for the classification channels and the doublet discriminator channel.

xMAP Reporter Control Microspheres (CON2), polystyrene microspheres internally labelled with fluorescent dyes and intended to verify the calibration and optical integrity for the reporter channel.

Batches for the sample runs were created on the Luminex® xPONENT® 3.1 software (in accordance with the manufacturer's instructions) using the **Create a New Batch from an existing Protocol** option in the **batches** tab. The corresponding protocol (TLMX_ID-COREXT) was then selected. The batch run was named and the sample identification numbers were manually input into the corresponding positions on the plate layout.

A negative control was run with the sample batch, as per manufacturer's recommendation. Due to the limited funding for the research it was not possible to include a positive control as well. The negative control was performed by setting up a test reaction with molecular biology grade water known to be free of any DNA contamination.

The **Eject** icon was clicked to eject the plate holder, and the hybridisation plate was placed into the plate holder. The **Retract** icon was then selected to place the plate holder into the analyser ready for analysis. The analysis process was then started, once the batch analysis had been

completed the data was exported as a comma separated values (csv) file and saved into a folder labelled with the batch name.

The IDCOREXT analysis software was then used to convert the raw data into a report including the predicted phenotype. The analyser raw data includes internal quality control designed to identify any invalid results and prevent reporting of potentially incorrect genotypes and phenotypes. A "green" alert denotes a valid analysis for genotype and predicted phenotype. Invalid results are denoted by the following alerts:

- Indeterminate genotype – the software is not able to assign a result for one or more polymorphisms.
- Low signal intensity – the signal intensity does not fulfil the acceptable threshold for one or more polymorphisms.
- Low bead count – the bead count does not reach the acceptable threshold for one or more polymorphisms.
- Unknown genotype(s) and predicted phenotype(s) – a particular combination of SNPs is not included in the software. The genotype has not been previously described as associated to a phenotype. In this circumstance an alternative method should be used to confirm the genotype and serology used to predict the phenotype.
- Invalid test – the sample analysis result is not acceptable.
- Invalid reading – the raw data cannot be analysed by the software.

In the event of invalid results, a report will not be generated and the sample(s) must be re-tested. The raw data obtained from the analysis can be seen in appendix 4.

2.5 Randomised Controlled Trial

A total number of 60 patients were recruited to the pilot study, selected from patients attending the haematology out-patient clinic. The number of participants was calculated to provide 80% power to detect an acceptance rate of 85% or lower if the true acceptance rate in the population is 95% using a one-sided binomial test of size $\alpha = 0.05$ (as determined with Dr Paul White (University of the West of England) and in accordance with Moore *et al*., 2011).

The eligibility criteria for recruitment was that the patient was an adult capable of giving informed consent for inclusion into the trial, in accordance with the Mental Capacity Act 2005, and that there was no record of historic red cell antibodies on the patient's electronic records. The pilot study was approved by the Cornwall and Plymouth Research Ethics Committee on the 5th September 2012 (MREC No.12/SW/0251 R&D Study No. 13017733) and patient information leaflets were provided for all patients approached for recruitment into the trial. Recruitment commenced on the 9th November 2012 and the required number of recruits was reached by the 16th July 2014. Patients were randomly assigned to one of two groups; the standard care group, who had a standard blood group performed for ABO and RhD type and would receive blood matched only for ABO and RhD groups or to the intervention group, who, in addition to the standard care, also had their blood typed for Rh (CcEe) and K antigens and were flagged on the pathology computer system to receive blood matched for the additional

antigen types. Provision was made for the intervention group patients to receive standard blood for transfusion should there be an emergency situation that did not allow for additional time for the acquisition or matching of blood with the extra antigens. Laboratory staff was requested to create a comment on the pathology computer system (visible to laboratory staff only) in the event that matched blood could not be provided from the routine blood stocks in the time frame required by the clinical team attending the patient.

Patients were assigned to the standard care or intervention group using a modified block randomisation technique to ensure that the groups were comparable in size and the total number of patients recruited amounted to 60. The two groups were allocated a number (1 for the standard care and 2 for the intervention); each number was registered on 30 separate pieces of paper which were then sealed into 60 individual envelopes. Upon recruitment of each patient an envelope was selected at random by a healthcare member of staff not related to the research and the researcher was then informed of the allocated group of the patient. If the patient was allocated to the intervention group the researcher then requested that the patient blood group sample was typed for Rh (CcEe) and K antigens, in addition to the standard ABO and RhD. A clinical note was then added to the patient electronic record on the pathology computer system stating the patient Rh (CcEe) and K antigen type and the antigen requirements of blood that would be required in the event of a transfusion.

The patients remained in the trial until it was closed on the 31st July 2015, at this point data were collected for each patient which included:

- Number of patients transfused in each study group
- Recruitment rates
- Underlying disease condition of the patient
- Number of units of blood transfused during the trial period
- Number of transfusion episodes
- Provision of matched red cell units for patients in the intervention group
- Development of any red cell allo/autoantibodies
- Length of time that the patient had been included in the trial.
- Rh (CcEe) and K antigen type of the patient
- Frequencies of Rh phenotypes

This data was collated on an excel file and subjected to statistical analysis in order to investigate any significant differences between the number of units of blood transfused during the trial period, the number of transfusion episodes, development of any red cell allo/autoantibodies and the length of time that the patient had been included in the trial.

Ethnicity of the patients was not included in the data collection, primarily because this data is not recorded in the pathology computer system as part of the patient demographics. It was not felt necessary to request this information at recruitment as part of the purpose of the pilot study was to review the availability of matched blood from routine stocks held in the

transfusion laboratory. The region served by the RD&E does not have an ethnically diverse population; the Exeter census profile (2011) reported 80.49% of the population to be white British. The results of the pilot study could then be used to review the ease of providing matched blood from the current stocks, and to direct any changes that may be required to blood ordering and stock storage.

2.6 STATISTICAL ANALYSIS

2.6.1 Retrospective review of haematology and renal patients

Patient information obtained from the retrospective review of haematology and renal transfusions, excluding any personal identifiers, was input into an excel spreadsheet and analysed using SPSS version 19 (see appendices 1 and 2). Fisher's Exact Test was used to examine associations between allo/autoimmunisation and categorical factors (gender, immunosuppression) and the independent samples t-test was used to examine any associations on numeric scale variables (age at first transfusion, number of units transfused, number of transfusion episodes).

Correspondence analysis was used to investigate any associations between red cell antibody type (alloantibody only, allo- and autoantibody in combination or autoantibody only) with disease conditions within the haematology cohort. Correspondence analysis is a multivariate graphical statistical technique designed to depict associations in cross-tabulation

tables (Hirschfeld, 1935). The process is a decomposition of the classic chi-squared test of association into two orthogonal components which are plotted against one another; points which are close on the plot show positive associations. The process is a non-parametric exploratory depiction of potential associations and is not based on the ideas of statistical significance. The technique allows an exploration of relationships between multiple categorical variables at the same time, removing the need to conduct separate chi-square tests for each pair of variables (Sourial *et al*, 2010).

2.6.2 Comparison of the manual and automated red cell phenotyping results

Red cell antigen typing results obtained using serological automated testing were directly compared to those obtained by current manual techniques. Red cell antigen results obtained by serological automated testing using the NHSBT commercial red cell panels were compared to the known antigen status as recorded on the antigen profile sheets supplied with the panels (see figures 2.5 – 2.7).

2.6.3 Comparison of the serological phenotyping and genotyping results

Red cell antigen types obtained using the automated serological phenotyping techniques were directly compared to the antigen type

predicted by the genotyping technique, with result types being identified as positive or negative.

2.6.4 Review of the pilot study – randomised controlled trial

Patient information obtained from the pilot study involving haematology patients, excluding any personal identifiers, was input into an excel spreadsheet and analysed using SPSS version 19. Fisher's Exact Test was used to examine any differences in the number of patients in the standard care group that received a transfusion compared to the number in the intervention group. The t-test was used to investigate any significant differences between the two groups with regard to numeric scale variables, time spent in trial, number of units transfused and number of transfusion episodes.

3 RETROSPECTIVE REVIEW RESULTS

3.1 Introduction

This study reports on a retrospective review of over 1000 patients admitted for at least one blood transfusion into the haematology inpatient ward and outpatient day case ward, and over 800 patients transfused as a result of renal insufficiency in a National Health Service (NHS) Foundation Trust hospital. The data collected for each patient included the total number of units of blood transfused, number of transfusion episodes, age at first documented transfusion, gender, diagnosis, intensity of treatment regime and extent of immunosuppression. A tabulated summary of the raw data obtained for the retrospective review can be seen in appendix 1 (haematology cohort) and appendix 2 (renal cohort).

Concomitant platelet therapy and the requirement for irradiated blood components were used as surrogate markers for severe immunosuppression in the haematology patients, as historical studies have suggested this may result in a tolerance to alloimmunisation (Schonewille *et al.,* 1999; Holohan *et al.,* 1981; Dutcher *et al.,* 1981; Asfour *et al.,* 2004; Ramsey *et al.,* 1989). Renal transplant was used as a marker for severe immunosuppression in patients transfused on the renal wards. Renal transplant patients are treated with life-long or long-term immunosuppressive drugs aimed at reducing the risk of acute graft rejection, often using multiple immunosuppressive agents (Lee and Gabardi, 2012). Immune suppression is achieved either by depleting the

number of lymphocytes, diverting the lymphocyte traffic or by blocking the lymphocyte response pathway (Hallorhan, 2004). Patients receive induction therapy of high dose immunosuppressives at the time of the transplant to prevent acute rejection (Norman and Turka, 2001; Hallorhan, 2004; Nashan, 2005; Terasaki and Mizutani, 2006; Cornell *et al.,* 2008; Gabardi *et al.,* 2011) followed by a lower maintenance dose using a combination of drugs (Gaston, 2001; Zhang, 2013). Suppression of the immune system in renal transplant to reduce the risk of production of HLA alloantibodies could also, in theory, reduce the risk of production of red cell antibodies in transfused renal transplant patients.

The aim of this review was to identify potential risk factors and/or protective factors related to the production of allo and/or autoantibodies within these groups of chronically transfused patients. This information could then be used to identify an allo/autoantibody immunisation risk group that would benefit from extended red cell phenotyping and matching of blood for transfusion. Risk factors for alloimmunisation, such as the number of red cell transfusions (Zalpuri *et al.,* 2012) and the gender of the recipient (Hoeltge *et al.,* 1995) have already been suggested and, in addition, it is also known that patients who develop one alloantibody are more likely to produce additional antibodies following subsequent red cell transfusion (Schonewille *et al.,* 1999; Fluit *et al.,* 1990). The identification of a high risk group destined for chronic red cell transfusion therapy would help to target the implementation of a strategy for pre-transfusion extended red cell antigen phenotyping and matching

of blood for transfusion in this group of patients. Such a strategy could have the potential to reduce the risk of alloimmunisation, in turn reducing the burden of additional testing for the hospital transfusion service and the risk of transfusion reactions in the patients.

3.2 Patients with haematological malignancies

A total of 1107 records of patients admitted to the haematology wards for transfusion were reviewed, 1006 patients for anaemia secondary to haematological disorders, 54 with solid organ cancer and 47 for anaemia secondary to other conditions (see table 3-1). The 1107 patients received a total of 31,890 units of red cells during 14,013 clinical episodes, the average number of units transfused was 29 (SD 42.1). The average number of transfusion episodes was 13 (SD 17.1) and the age of the patients at first recorded transfusion ranged from 13 to 99 with an average of 72 years (SD 14.7).

Of the 1107 patients, 256 (23%) either presented with, or developed, allo and/or autoantibodies to red cell antigens. Of the original 1107 patients sixty patients (5.4%) presented with allo and/or autoantibodies at the first recorded test, of these, 21 (1.9%) presented with an identifiable red cell alloantibody only. Eleven (18.3%) of the 60 patients who presented with red cell allo and/or autoantibodies developed additional allo and/or autoantibodies following transfusion.

A total of 1086 patients presented with no detectable red cell alloantibodies, 140 (12.9%) developed one or more alloantibodies post transfusion. The average number of units given prior to the production of allo/autoantibodies was 15.46 (maximum =270, minimum = 2, average = 5.5, SD = 6.35).

3.2.1 Antibodies and disease conditions

Allo and/or autoantibodies were most commonly seen in patients with haemolytic anaemia (78%), aplastic anaemia (57%), Waldenström macroglobulinaemia (42%) and chronic lymphocytic leukaemia (39%). Within the disease groups chronic myeloid / monocytic leukaemia (CMML), myelodysplastic syndrome (MDS) and myeloproliferative disorder (MPD), 30% of patients were found to have allo/autoantibodies. In addition 30% of patients transfused for less common haematological conditions (shown as "other" in table 3-1), such as amyloidosis, sideroblastic anaemia and essential thrombocythaemia, were found to have allo/autoantibodies. Allo/autoantibodies were less commonly seen in patients with acute lymphocytic leukaemia (0%), Hodgkin's lymphoma (7%) and non-Hodgkin's Lymphoma (16%). Table 3-1 shows the number of patients with allo and/or autoantibodies in relation to disease condition. It is important to note that in some of the groups the percentages quoted may be high, or low, because the patient numbers are small.

Table 3.1: Allo/autoantibodies and disease conditions

A retrospective review of patients transfused within the haematology cohort (n=1107) was performed to investigate any associations between the risk of development of allo/autoantibodies and the disease status of the patient. This table shows the total number of patients reviewed in each disease group, along with the number of patients in that group found to have allo/autoantibodies and the relative percentage.

Disease	Total number of patients	Number of patients with allo/autoantibodies	% with allo/autoantibodies
Acute lymphocytic leukaemia	14	0	0
Acute myeloid leukaemia	145	35	24
Anaemia	26	7	27
Aplastic anaemia	14	9	57
Chronic myeloid/monocytic Leukaemia	20	6	30
Chronic lymphocytic leukaemia	57	22	39
Haemolytic anaemia	9	7	78
Hodgkin's lymphoma	29	2	7
Lymphoma	61	13	21
Myelodysplastic syndrome	151	45	30
Myeloma	187	33	18
Myeloproliferative disorders	23	7	30
Non-Hodgkin's lymphoma	258	41	16
Solid organ cancer	54	10	19
Other	47	14	30
Waldenström macroglobulinaemia	12	5	42

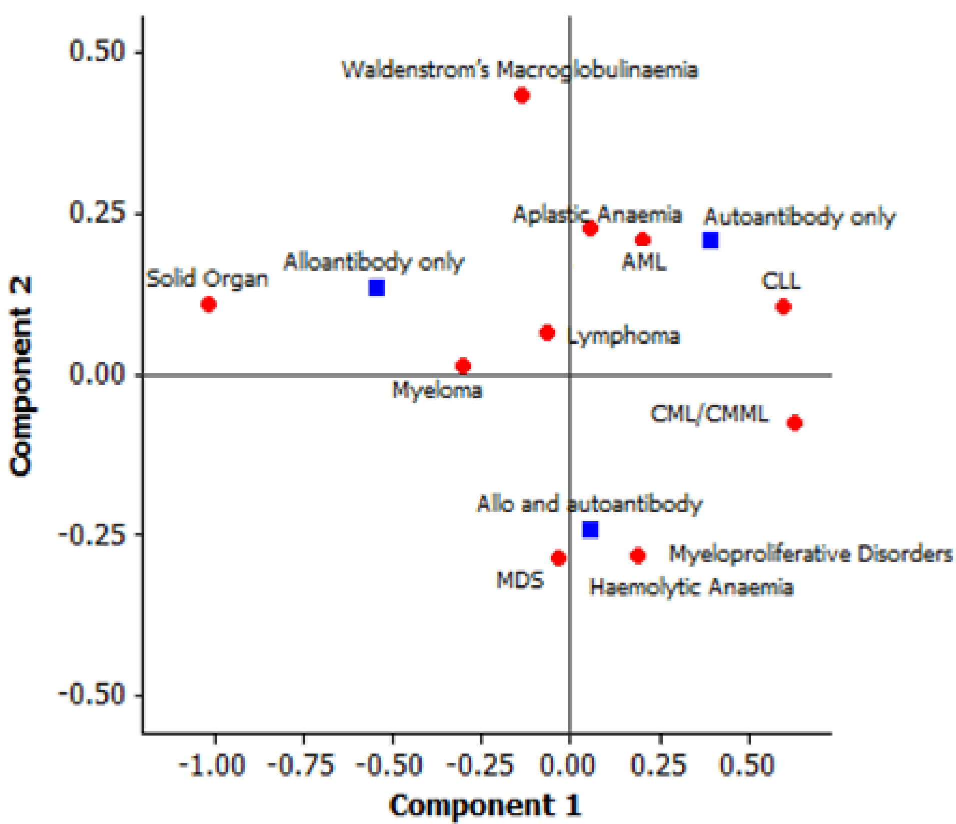
Further analysis of the incidence of alloantibodies only, alloantibodies in combination with autoantibodies, and autoantibodies only, was performed in some of the disease conditions (Table 3-2). Correspondence analysis was performed to investigate any associations between disease status and antibody type (Figure 3.1). This demonstrated that haemolytic anaemia, MDS, and MPD show an association with allo and autoantibody in combination, whereas AML, CLL and aplastic anaemia are associated with autoantibody production only. Four (57.1%) of the seven immunised patients with haemolytic anaemia had alloantibodies in combination with autoantibodies. One patient with a non-autoimmune haemolytic anaemia developed anti-Fy^a and anti-Chido-Rogers. Twelve (54.5%) of the 22 immunised patients with CLL had autoantibodies only, 9 (40.9%) developed autoantibodies in combination with alloantibodies and one patient developed an alloantibody only. Twenty six (57.8%) of the immunised patients with MDS had alloantibodies in combination with autoantibodies, 11 (24.4%) had alloantibodies only and eight (17.8%) had autoantibodies only.

Table 3.2: Red cell antibody type in relation to disease

Analysis of red cell antibody type in relation to disease within the immunised patient group (n=256) in the haematology patient cohort (n=1107) was performed for a selection of disease groups. Antibody types are grouped into alloantibody only, allo and autoantibody in combination and autoantibody only. The total number of immunised patients in each disease group is represented, along with the total numbers of patients within each disease group with certain antibody types and the representative percentages.

Disease	Total number of immunised patients	Alloantibody only	Allo and autoantibody	Autoantibody only
MDS	45	11 (24.4%)	26 (57.8%)	8 (17.8%)
AML	35	10 (28.6%)	11 (31.4%)	14 (40.0%)
Myeloma	33	13 (39.4%)	13 (39.4%)	7 (21.2%)
CLL	22	1 (4.5%)	9 (40.9%)	12 (54.5%)
Lymphoma	13	4 (30.8%)	5 (38.5%)	4 (30.8%)
Solid organ cancer	10	7 (70.0%)	3 (30.3%)	0 (0.0%)
Aplastic anaemia	9	2 (22.2%)	3 (33.3%)	4 (44.4%)
Haemolytic anaemia	7	1 (14.3%)	4 (57.1%)	2 (28.6%)
Myeloproliferative disorders	7	1 (14.3%)	4 (57.1%)	2 (28.6%)
CML/CMML	6	0 (0.0%)	3 (50.0%)	3 (50.0%)
Waldenström macroglobulinaemia	5	2 (40.0%)	1 (20.0%)	2 (40.0%)

Figure 3.1: Correspondence analysis of the association between disease types and antibody types in the Haematology cohort



Correspondence analysis showing clusters of disease types associated with antibody type in the immunised patients within the haematology cohort (n=256). The blue squares represent the antibody type (alloantibody only, autoantibody only and allo and autoantibody in combination) and the red circles represent the disease type. The components (1 and 2) and the X and Y axes are derived from a process known as eigenvalue decomposition of the chi-square test of association. The "map" produced by this process will demonstrate any relationships between the variables by the proximity of the plotted points; haemolytic anaemia, MDS, and MPD show an association with allo and autoantibody in combination, whereas AML, CLL and aplastic anaemia are associated with autoantibody production only. Analysis performed by Dr Paul White, University of the West of England.

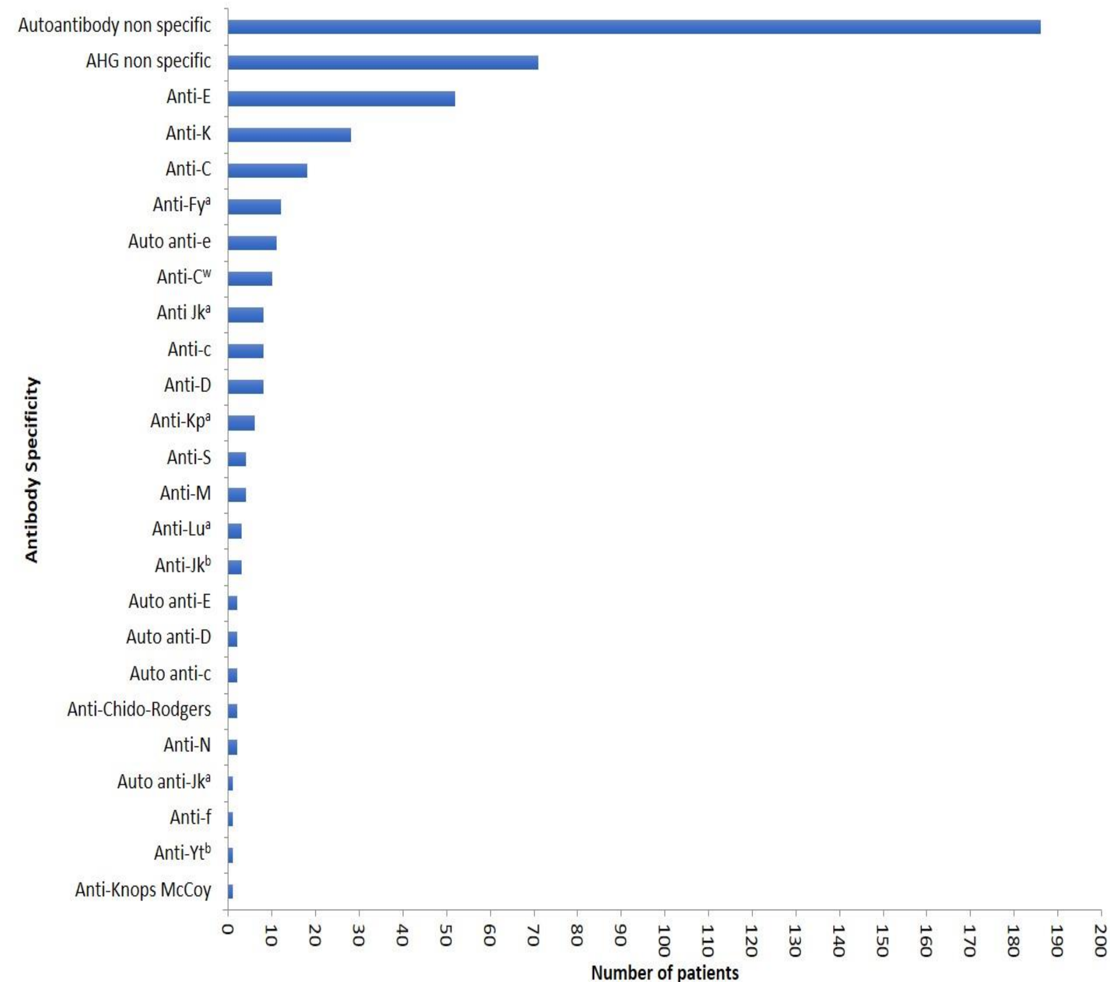
3.2.2 Antibody Specificities

Of the 256 red cell antigen immunised patients, 70 (27.3%) developed alloantibodies only, 101 (39.4%) developed alloantibodies in combination with autoantibodies and 85 (33.2%) developed autoantibodies only. The incidence of antibody specificities is presented in figure 3.2. A total of 242 alloantibodies were detected, of these 71 (29.3%) could not be identified. Of the 171 identifiable alloantibodies 114 (66.7%) were to Rh (D, C, c, E, e) or Kell antigens. The most common specificity was anti-E (21.5%), followed by anti-K (11.6%) and anti-C (7.4%). Two hundred and four autoantibodies were detected, 18 (8.8%) had definable specificities within this group auto-anti-e was the most common (61%). Autoantibody specificity was either confirmed at the reference laboratory (NHSBT) (11 patients) or assigned in the transfusion laboratory based on antibody identification and phenotype results (7 patients). Antibodies to variant antigens were not excluded for any of these patients. Of the 256 red cell antigen immunised patients, 101 (39.2%) had alloantibodies in combination with autoantibodies. Of these 101 patients, 80 (79.2%) developed the autoantibody after the alloantibody, 8 (7.9%) developed the alloantibody after the autoantibody, 9 (8.9%) presented with alloantibody and autoantibody in combination, and 4 (3.9%) developed allo and autoantibody in combination following transfusion. Analysis of the specificities of patients with identifiable alloantibodies revealed 60 patients with single specificity (61.6%), 28 with two alloantibodies (25%), 11 with three antibodies (9.8%), three with four antibody specificities

(2.7%) and one patient who developed five separate alloantibodies (0.9%).

Patients (n=186) who presented with, or developed autoantibodies had records detailing the type of antibody or complement fraction on the surface of their red cells. Within this group 140/186 (75.3%) were found to have IgG only, 17/186 (9.1%) were found to have C3d only and 29/186 (15.6%) were found to have a combination of IgG and C3d. Autoantibodies of a transient nature could be demonstrated in 117 of the 186 patients (62.9%).

Figure 3.2: Incidence of antibody specificities within the haematology cohort



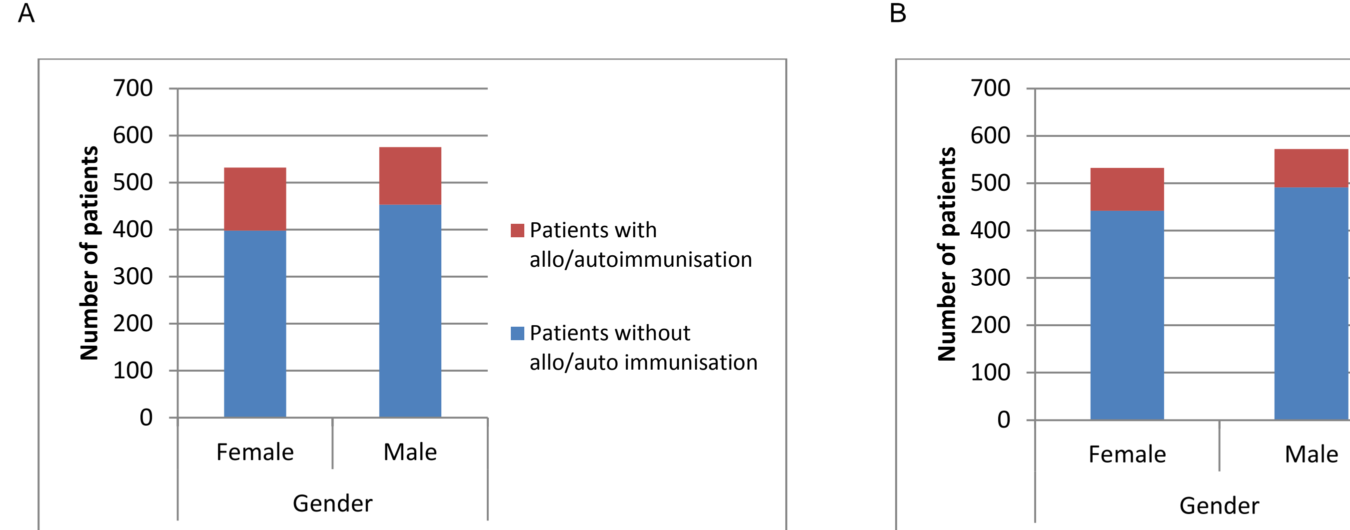
The incidence and specificity of allo- and autoantibodies within the immunised group of the haematology patient cohort (n=256). The specificity of the antibody is shown on the Y-axis, alloantibodies are denoted by the antigen specificity and autoantibodies are denoted separately. Autoantibodies showing no specificity were most commonly seen in this cohort of patients (n=186/256), within the group of autoantibodies demonstrating a red cell antigen specificity, auto anti-e was the most common (n=11/18). Alloantibodies to antigens within the Rh and Kell blood group systems were the most common (n=114/171). (AHG = Anti-human globulin).

3.2.3 Antibodies and patient factors

3.2.3.1 Gender and immunisation rates

Of the 1107 patient records reviewed in the haematology cohort, 532 were female and 575 were male. Analysis (Figure 3.3a) of the allo/autoantibody immunisation rate in males (122/575, 21.22%) and females (134/532, 25.19%) showed no statistical significant difference (Fisher's Exact Test P=0.1340). In addition, no significant difference was seen in the rates in males (81/575, 14.10%) and females (90/532, 16.92%) with alloantibodies only (Fisher's Exact Test P=0.1310) (Figure 3.3b).

Figure 3.3: Immunisation rates in males and females within the Haematology cohort



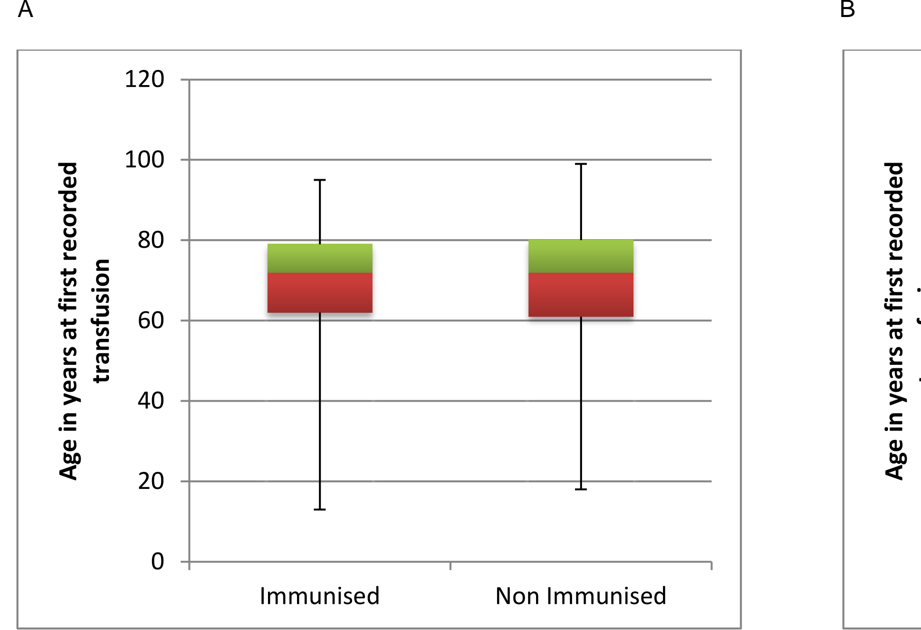
Graphs showing the allo/autoimmunisation rates in males and females in the haematology cohort (n=1107). The number of patients who did not demonstrate allo/autoimmunisation is denoted by the blue bar and the number with red cell allo/autoimmunisation is denoted by the red bar. Statistical analysis of the allo/autoantibody immunisation rate in males (122/575= 21.22%) and females (134/532 =25.19%) showed no significant difference (Fisher's Exact Test P=0.1340) Figure A. In addition there was no significant difference seen in the rates in males (81/575=14.10%) and females (90/532=16.92%) with alloantibodies only (Fisher's Exact Test P=0.1310) Figure B.

3.2.3.2 Age and immunisation rates

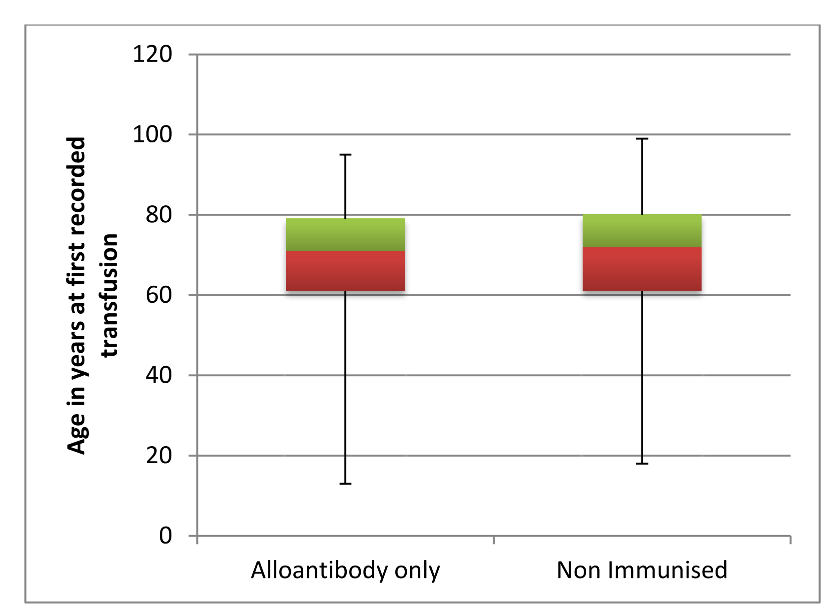
The age of patients receiving blood transfusions in the haematology cohort ranged from 13 to 99 years (n=1107). The mean age at the first recorded transfusion for patients with allo/autoimmunisation was 69.18 (range 13-95 years, standard deviation (SD) 14.62) and the mean age for those patients without allo/autoantibodies was 69 years (range 18-99, SD 14.73). There was no statistically significant difference between the mean age at first recorded transfusion and the incidence of allo/autoantibody immunisation (t-test P=0.8637). Further review of patients to investigate any relationship between age at first recorded transfusion and the development of alloantibodies only revealed a mean age at first recorded transfusion of 69.82 (SD 14.22) for those with alloimmunisation and a mean age of 69 (SD 14.73) for the non-immunised patients (Figures 3.4A and 3.4B respectively). Again, no statistical significance was demonstrated (t-test P= 0.5042)

Figure 3.4: Influence of age at first transfusion and allo/autoantibody development within the haematology cohort

A



B



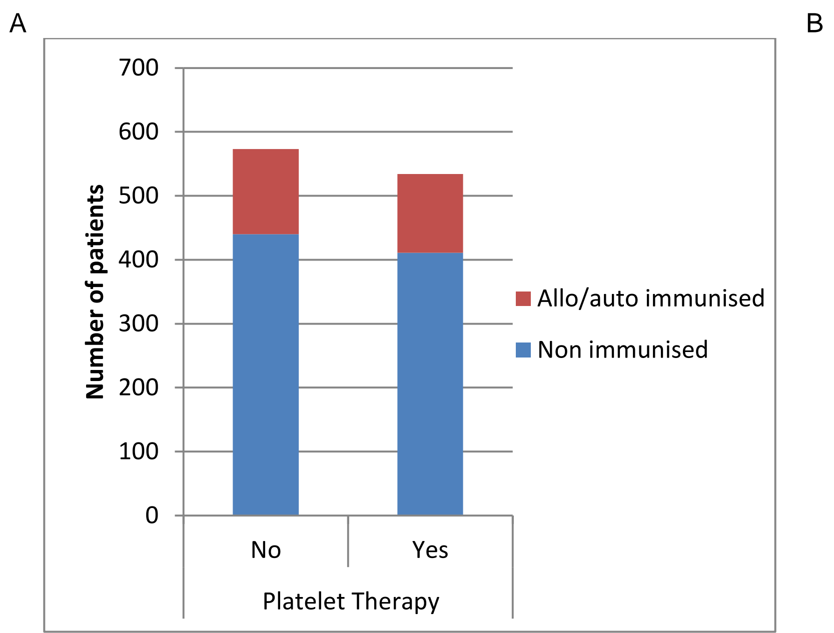
Box-and-whiskers plots showing the minimum and maximum age at first transfusion (black line), the first quartile, median (second quartile) and third quartile. This figure shows the age at first recorded transfusion in patients in the haematology cohort (n=1107) with or without allo/autoantibodies (figure A) and with or without alloantibodies only (figure B). There was no significant difference between the mean age at first recorded transfusion and the incidence of allo/autoantibody immunization (mean 69.18 years, SD14.62) compared to the non-immunised group (mean = 69 years, SD14.73) (t-test P=0.8637); Figure A. Figure B shows the mean age at first recorded transfusion in patients with alloantibodies only (mean 69.82, SD 14.22) and those non-immunised (mean = 69, SD 14.73), no significant difference was seen (t-test P= 0.5042).

3.2.3.3 Immune suppression and incidence of immunisation

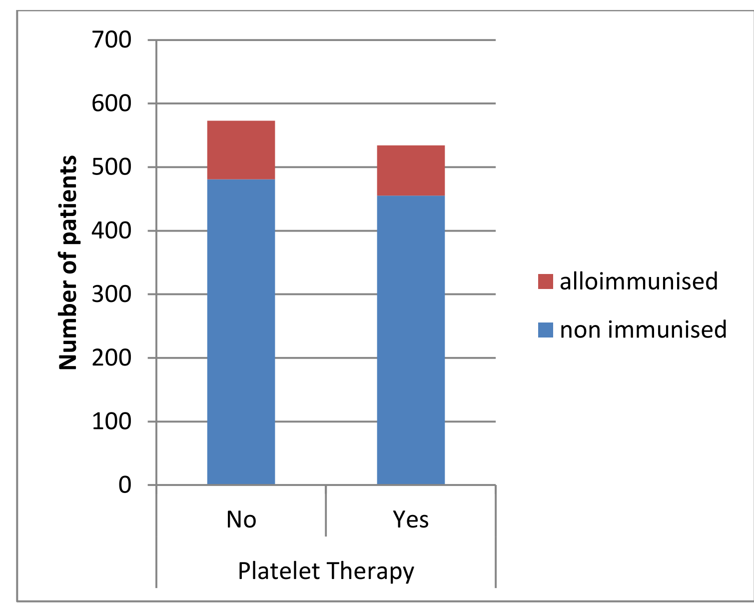
Concomitant platelet support and the requirement for irradiated blood were used as surrogate markers for immune suppression in order to investigate any relationship between immune suppression and the incidence of immunisation to red cell antigens. In the haematology cohort (n=1107) 534 patients were recorded as having received concomitant platelet therapy, of these 123 (23.0%) patients had a recorded allo/auto antibody. The incidence of allo/autoantibodies in patients not receiving any platelet support (n=573) was 23.2%. Therefore, concomitant platelet therapy appeared to have no influence on the rate of allo/autoantibody formation (Fisher's Exact Test P=1.00). Further analysis of patients with alloantibodies only revealed that 79 (14.8%) of the 534 patients receiving platelets were recorded as having alloantibodies and 92 (16.0%) had no alloantibodies, also showing no statistically significant difference (P=0.6750) (figures 3.5a and b respectively).

Figure 3.5: Influence of immune suppression (platelet requirement) on allo/autoantibody development in the haematology cohort

A



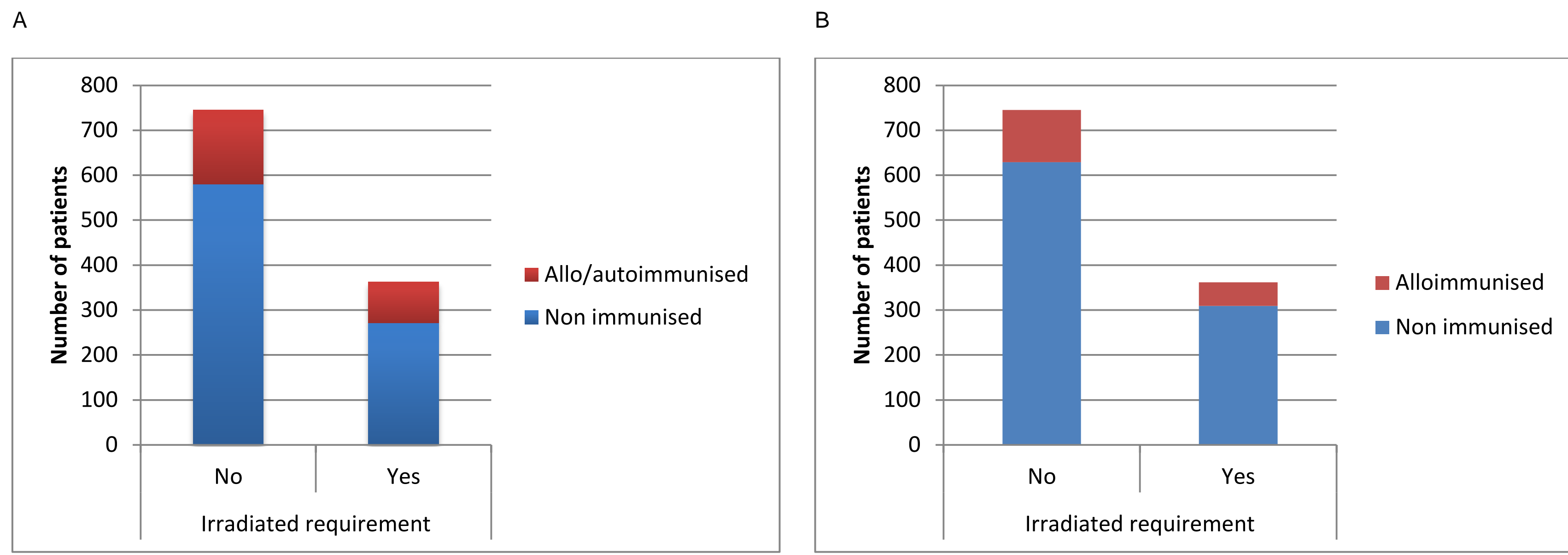
B



Concomitant platelet therapy was used as an indicator of immune suppression. In the haematology cohort (n=1107) 534 patients were recorded as having received concomitant platelet therapy, of these 123 (23.0%) patients had a recorded allo/auto antibody. The incidence of allo/autoantibodies in patients not receiving any platelet support (n=573) was 23.2%. Therefore, concomitant platelet therapy had no influence on the rate of allo/autoantibody formation (Fisher's Exact Test P=1.00) or on the rate of alloimmunisation only (P=0.6750) (Figures A and B respectively).

A total of 362 patients in the haematology cohort were given irradiated blood components, 91/362 (25.1%) of these patients developed an allo/autoantibody and 165/745 (22.2%) of patients not requiring irradiated blood components had allo/autoantibodies. Analysis of patients with alloantibodies only demonstrated an incidence 14.6% (53/362) in patients receiving irradiated components and 15.6% (116/745) in patients not receiving irradiated components. Therefore the requirement for irradiated blood components appeared to have no influence on the rate of allo/autoantibody formation (Fisher's Exact Test P=0.2876) or on the rate of alloimmunisation (P= 0.6750) (Figures 3.6a and b).

Figure 3.6: Influence of immunosuppression (irradiated requirement) on allo/autoantibody development in the haematology cohort



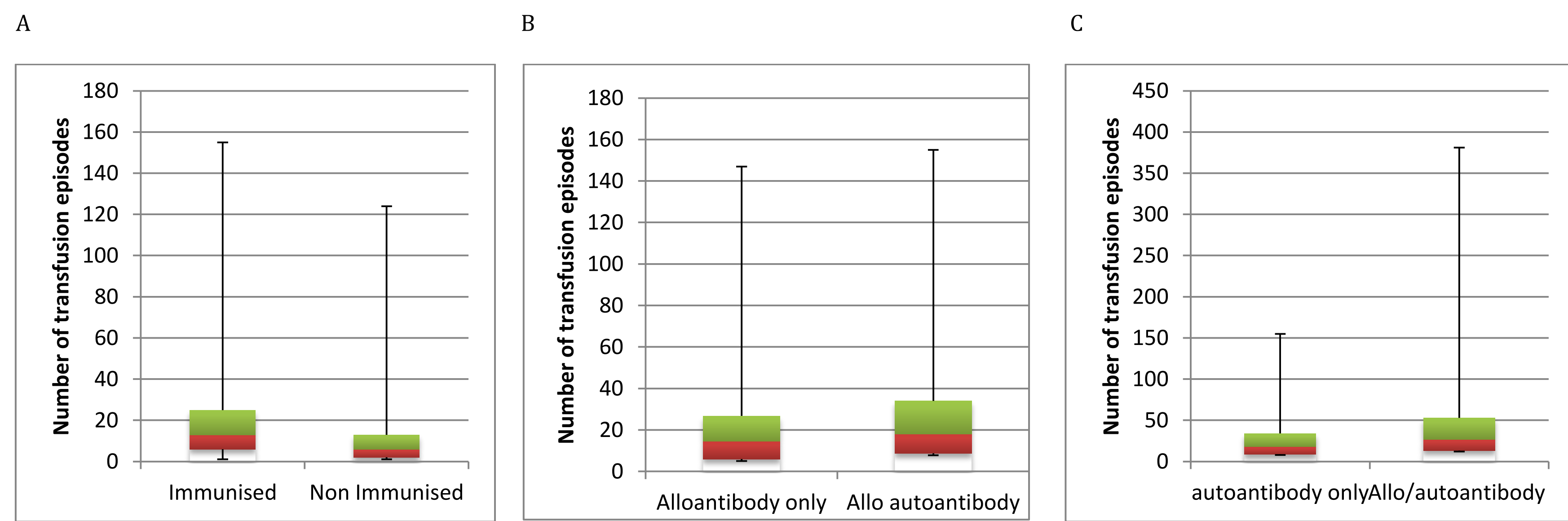
The allo/autoimmunisation rate in patients with a requirement for irradiated blood components was 25.1% (91/362) compared to 22.2% (165/745) not requiring irradiated blood components (figure A). Analysis of patients with alloantibodies only demonstrated an incidence 14.6% (53/362) of alloantibodies in patients receiving irradiated components and 15.6% (116/745) in patients not receiving irradiated components (Figures B). Therefore the requirement for irradiated blood components appeared to have no influence on the rate of allo/autoantibody formation (Fisher's Exact Test P=0.2876) or on the rate of alloimmunisation (P= 0.6750).

3.2.3.4 Number of transfusions and incidence of immunisation

In the haematology cohort (n=1107) the average number of transfusion episodes recorded over the review period for all patients was 13 (range 1-155) and the average number of units given to the patients was 29 (range 1-382).

In the immunised group (n=256) the average number of transfusion episodes was 20.3 (SD 23.68), compared to an average of 10.36 (SD 13.33) episodes in the non-immunised group (n=851), demonstrating a statistically significant difference in the number of transfusion episodes and the incidence of allo/autoimmunisation (t-test P=<0.0001) (figure 3.7a). Further analysis of immunised patients showed a significant difference in the number of transfusion episodes between patients with alloantibodies only (average 21.57, SD 24.98) and those with allo and autoantibodies (average 45.95, SD 57.45 (t-test P= 0.0007), as shown in figure 3.7b. In addition, a significant difference was also demonstrated in the number of transfusion episodes in patients with allo +/- autoantibodies (average 23.04, SD 24.93) compared to those with autoantibodies only (average 13.37, SD 16.95) (t-test P= 0.0014), as shown in figure 3.7c.

Figure 3.7: Influence of the number of transfusion episodes on the development of all/autoantibodies in the haematology cohort



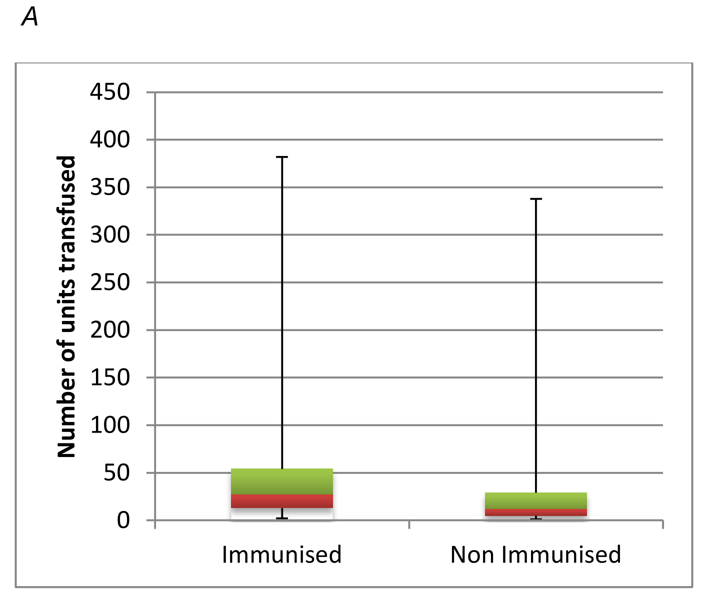
Box-and-whiskers plots showing the minimum and maximum numbers (black line) of transfusion episodes (figure A) (the first quartile, median (second quartile) and third quartile are denoted by the coloured blocks) in immunised and non-immunised patients in the haematology cohort (n=1107). There was a statistically significant difference (t-test P=<0.0001) in the number of transfusion episodes in the immunised group (n=256, average number of episodes 20.3, SD 23.68) compared to the non-immunised group (n=851 average10.36, SD 13.33) (figure A). A significant difference (t-test P= 0.0007), was also seen in the number of transfusion episodes in patients with alloantibodies only (average 21.57, SD 24.98) compared to those with allo and autoantibodies (average 45.95, SD 57.45) as shown in figure B and also between those with allo+/-autoantibody (average 23.04, SD 24.93) and those with an autoantibody only (average 13.37, SD 16.95) (t-test P= 0.0014) as shown in figure C.

Analysis of the number of red cell units transfused within the haematology cohort (n=1107) during the review period revealed that the number of units transfused ranged from 1 to 382, with an average of 29 (SD 42.1). The average number of red cell units given to patients in the immunised group (n=256) was 46.99 (SD 59.65) compared to 23.43 (SD 32.04) in the non-immunised group (n=851), demonstrating a statistically significant difference (t-test P=<0.0001), as shown in figure 3.8a. This difference was also seen in the number of units given in patients with allo +/- autoantibodies (n=171, average number of units given 54.42, SD 65.40) compared to those with autoantibodies only (n=85, average number of units given 32.72, SD 42.82) (t-test P= 0.0059), as shown in Figure 3.8b.

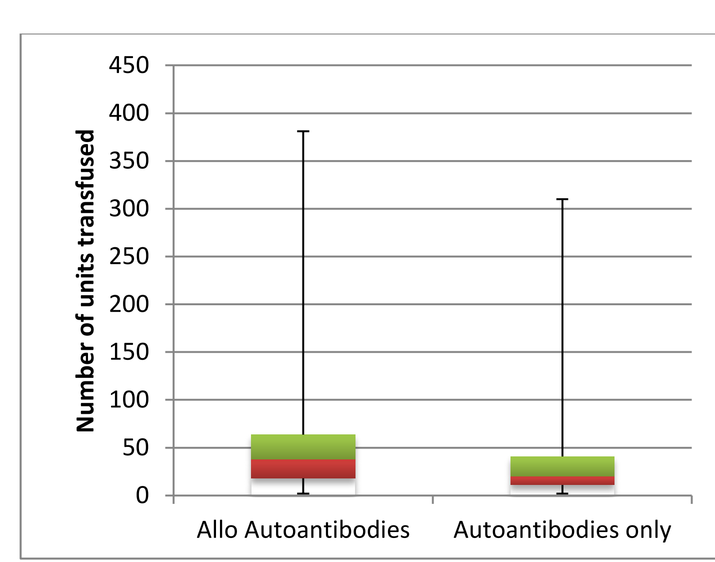
This demonstrates that the risk of developing an allo +/- autoantibody increases as the number of transfusion episodes and number of red cell units given increases. However, the incidence of autoantibodies alone does not appear to be influenced by the number of transfusion episodes or number of units given.

Figure 3.8: Influence of the number of red cell units transfused on the development of allo/autoantibodies in the haematology cohort

A



B

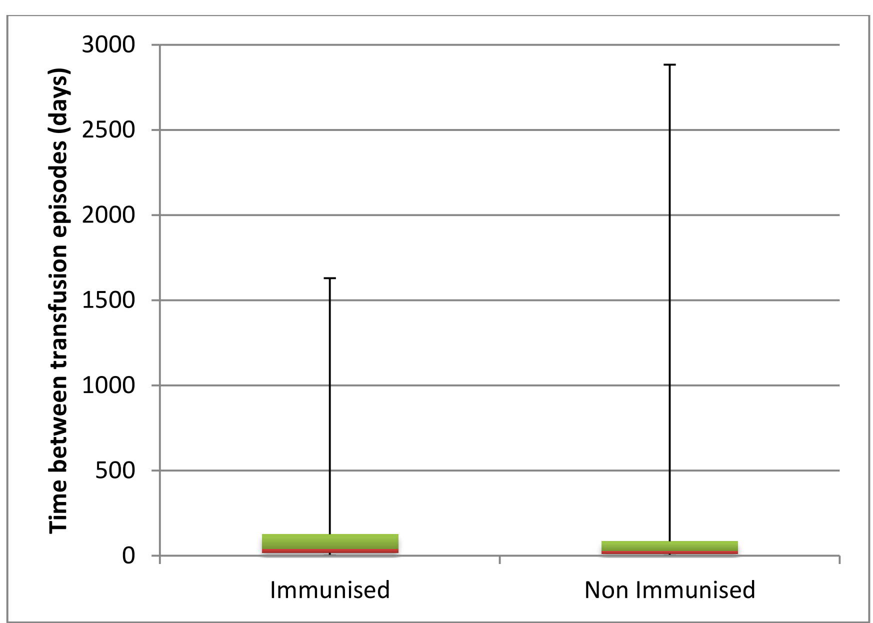


Box-and-whiskers plots showing the minimum and maximum numbers (black line) of red cell units transfused and numbers of red cell units transfused (the first quartile, median (second quartile) and third quartile are denoted by the coloured blocks) in immunised and non-immunised patients in the haematology cohort (n=1107). The average number of red cell units given to patients in the immunised group (n=256) was 46.99 (SD59.65) compared to 23.43 (SD 32.04) in the non-immunised group (n=851), demonstrating a statistically significant difference (t-test P=<0.0001) (figure A). The number of units given in patients with allo +/- autoantibodies (n=171, average number of units given 54.42, SD 65.40) compared to those with autoantibodies only (n=85, average number of units given 32.72, SD 42.82) (t-test P= 0.0059), as shown in Figure B.

3.2.3.5 Time between transfusions and the incidence of immunisation

Analysis was performed on the time (in days) between transfusion episodes for patients within the haematology cohort (n=1107). The time between transfusion episodes for all patients ranged from 0 to 2882 days, with an average time of 107.39 (SD 220.42) days. The average time between transfusion episodes for the immunised patients was 113.3 (SD 192.42) days (n=256, range 0 to 1629 days) compared to an average of 102.5 (SD 228.22) days for non-immunised patients (n=851, range 0 to 2882.5 days). There was no significant difference seen in the average time between transfusion episodes in the two groups (t-test P=0.4925), as shown in figure 3.9. This suggests that the frequency at which the recipients are exposed to foreign red cell antigens does not influence the development of allo/autoantibodies.

Figure 3.9: Influence of the frequency of transfusion episodes on the development of allo/autoantibodies in the haematology cohort



Box-and-whiskers plot showing the minimum and maximum (black line) number of days between transfusion episodes (the first quartile, median (second quartile) and third quartile are denoted by the coloured blocks) in the haematology cohort. The average time between transfusion episodes for the immunised patients was 113.3 (SD 192.42) days (n=256, range 0 to 1629 days) compared to an average of 102.5 (SD 228.22) days for non-immunised patients (n=851, range 0 to 2882.5 days). There was no significant difference seen in the average time between transfusion episodes in the two groups (t-test P=0.4925).

3.2.4 Transfusion Reactions

Of the 1107 patient records reviewed within the haematology cohort, 24 (2.17%) were investigated for a suspected transfusion reaction, giving an overall transfusion reaction incidence of 1 in 1328.75 units. In the immunised group the incidence of investigation of transfusion reactions was 11/256 (4.3%) compared to an incidence of 13/851 (1.5%) in the non-immunised group. An approximate three fold difference was seen in the rate of suspected transfusion reactions in the allo/auto immunised group compared to the non-immunised group (see table 3-3). Analysis using the Fisher's Exact Test shows that the difference between the groups is statistically significant (P=0.0128).

Patients included within the immunised group for review of suspected transfusion reactions were those with known red cell allo/autoantibodies being transfused with antigen negative and/or crossmatch compatible blood, not patients who had suffered a transfusion reaction as a result of development of antibodies subsequent to a transfusion. Therefore the difference between the immunised and the non-immunised group is suggestive that even when allo/antibodies have been detected and blood compatible by current *in vitro* methods is provided the likelihood of a transfusion reaction is higher if the patient has known allo/autoantibodies.

Table 3.3: Transfusion reactions in the haematology cohort

The number of suspected transfusion reactions reported in the haematology cohort (n=1107) for immunised (patients with allo/autoantibodies) patients was 11/256 and those reported in non-immunised patients was 13/851. Fisher's Exact Test shows that the difference between the groups is statistically significant (P=0.0128). The risk of transfusion reaction was higher in the immunised group despite the fact that this group was transfused with blood that was deemed compatible by in vitro methods.

	Total number of patients	Number of investigated transfusion reactions	%
Non-immunised	851	13	1.5
Immunised	256	11	4.3
Total	**1107**	**24**	

3.2.5 Cost of additional testing

A total of 6914 serological tests, in addition to the standard ABO and Rh D group and antibody screen, were performed for the patients in the haematology cohort (n=1107) at a total cost of £50,262.42. A total of 358 serological tests were performed for the non-immunised patients (n=851) compared to 6556 additional tests for the immunised group (n=256). A breakdown of the additional serological tests performed and the costs of the additional testing are shown in table 3-4. Test costs were calculated, using an in-house spreadsheet calculator (Microsoft Excel), taking into account reagent costs, equipment maintenance, consumables, quality control and staff time incurred during the financial year 2011-2012. Total test costs for the additional testing performed on patient samples during the retrospective review period were calculated using these current costs, although it is accepted that this is not representative of the actual costs of the tests performed due to changes in costs of staff salaries over the time period reviewed and changes in test procedures, reagents and analysers used.

Table 3.4: Cost of additional testing in the haematology cohort

The number and cost of additional serological testing performed in immunised (256/1107) and non-immunised patients (851/1107) within the haematology cohort. The total cost of additional testing for patients with allo/autoantibodies was approximately 32 fold greater than that for those without antibodies.

	Immunised group		**Non immunised group**	
Test	Number of tests	Cost	Number of tests	Additional Cost
Antibody identification panel	2694	£19,181.28	0	0
Direct Antiglobulin Test	2174	£9,152.54	355	£1,494.55
Monospecific Coombs test	1279	£7,098.54	2	£11.10
NHSBT RCI referral	249	£12,474.90	0	0
Rh CcEe type	98	£426.30	0	0
Red cell phenotype	50	£209	1	£4.18
Autoabsorption	3	£44.88	0	0
Cold agglutinin screen	9	£165.15	0	0
Total	6556	£48,752.59	358	£1,509.83

3.3 Patients with renal insufficiency

A total of 877 blood transfusion records of patients admitted to the renal wards for transfusion were reviewed. The 877 patients received a total of 11822 units of red cells during 5238 clinical episodes, the average number of units transfused was 13.5 (SD 18.36) with a range of 1 to 246. The average number of transfusion episodes was 5.98 (SD 7.37) with a range of 1 to 67. The age of the patients at first recorded transfusion ranged from 15 to 95 with an average of 68.14 years (SD 14.42).

Of the 877 patients in the renal cohort, 134 (15.3%) either presented with, or developed, allo and/or autoantibodies to red cell antigens. Of the original 877 patients, 41 patients (4.7%) presented with allo and/or autoantibodies at the first recorded test, 27 (3.1%) of these presented with a red cell alloantibody only. Five (12.2%) of the 41 patients who presented with red cell allo and/or autoantibodies developed additional allo and/or autoantibodies following transfusion.

A total of 850 patients presented with no detectable red cell alloantibodies, 33 (3.9%) of these developed one or more alloantibodies post transfusion

The average number of units given prior to the production of alloantibodies was 9.66 (range 0 - 143, SD = 16.79). The average number of units given prior to the production of autoantibodies was 11.46 (range 0 - 91, SD = 18.02).

3.3.1 Antibody Specificities

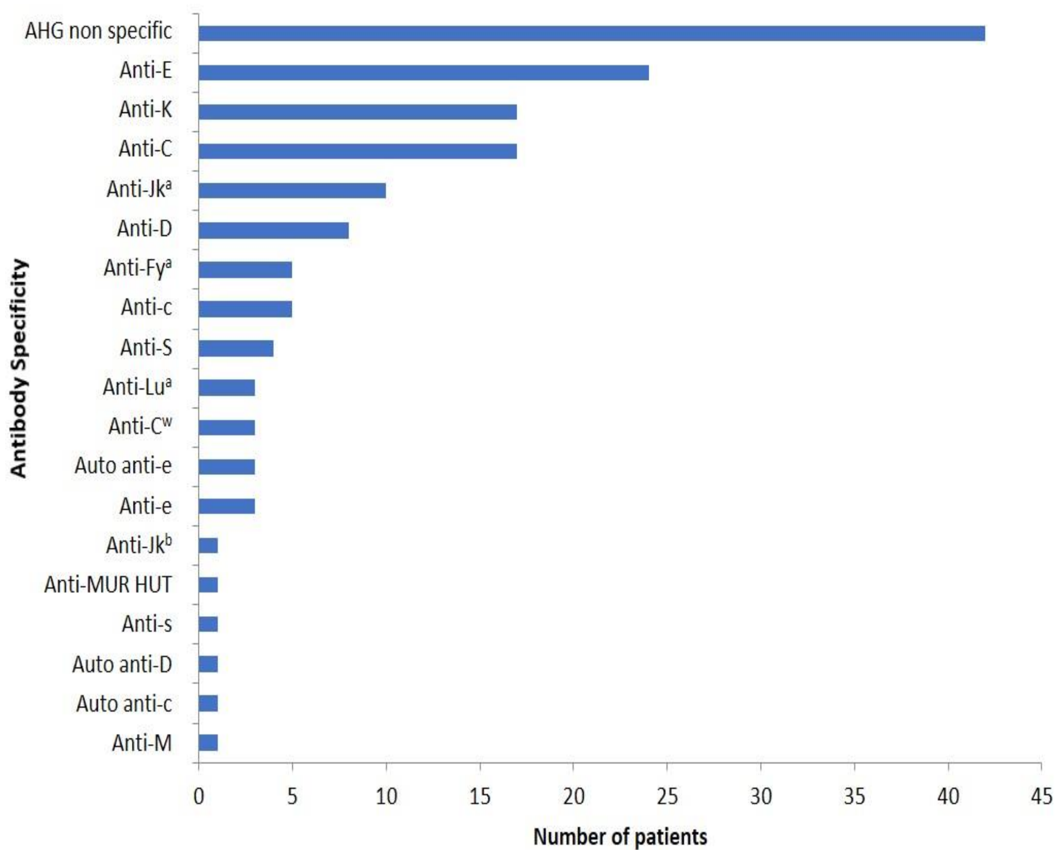
Of the 134 red cell antigen immunised patients in the renal cohort, 60 (44.78%) developed alloantibodies only, 55 (41.04%) developed alloantibodies in combination with autoantibodies and 19 (14.2%) developed autoantibodies only. The incidence of antibody specificities is presented in figure 3.10. A total of 147 alloantibodies were detected, of these 42 (28.6%) could not be identified. Of the 112 identifiable alloantibodies 75 (67.0%) were specific to Rh (D, C, c, E, e) or Kell antigens. The most common specificity was anti-E (16.3%), followed by anti-K (11.6%) and anti-C (11.6%).

A total of 66 autoantibodies were detected, 7/66 (10.6%) had definable specificities with auto-anti-e being the most common (3/7, 42.9%) (figure 3.10). A total of 34 (25.4%) of the 134 red cell antigen immunised patients had alloantibodies in combination with autoantibodies. Of these patients six (17.6%) developed the autoantibody after the alloantibody, none developed the alloantibody after the autoantibody, 26 (76.5%) developed the alloantibody and autoantibody in combination following transfusion and two presented with an allo/autoantibody combination (5.9%).

Analysis of the specificities of patients with identifiable alloantibodies revealed 38 patients with single specificity (60.3%), 18 with two alloantibodies (28.6%), 4 with three antibodies (6.34%) and three with four antibody specificities (4.76%). Sixty six patients who presented with, or developed autoantibodies had records detailing the type of antibody or

complement fraction on the surface of their red cells. Sixty one (61/66, 92.4%) were found to have IgG only, two (2/66, 3.0%) were found to have C3d only and two (2/66, 3.0%) were found to have a combination of IgG and C3d. One patient did not have a recorded autoantibody type.

Figure 3.10: Incidence and specificity of allo/autoantibodies in the renal cohort



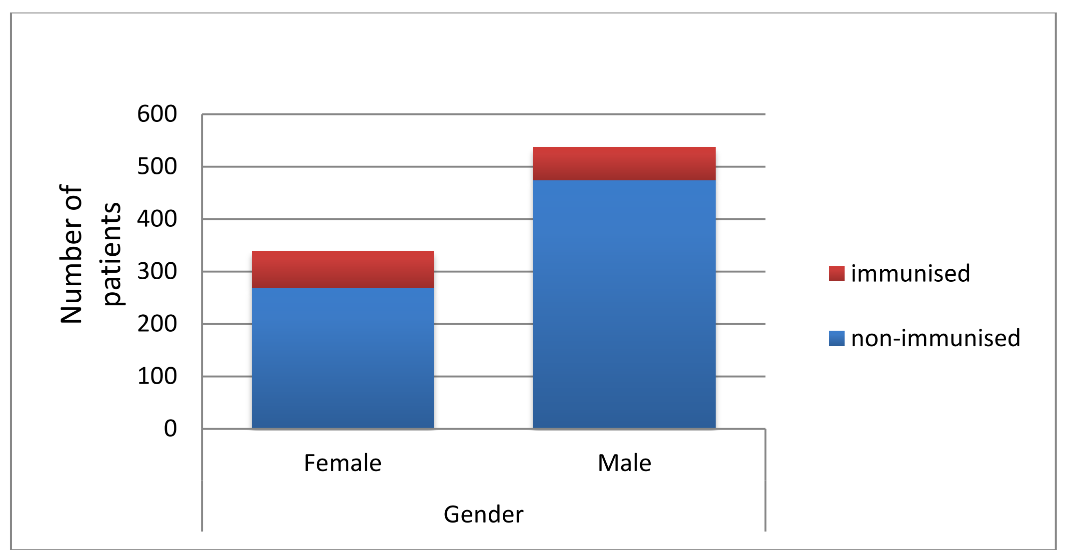
The incidence and specificity of allo- and autoantibodies within the renal patient cohort (n= 877). The specificity of the antibody is shown on the Y-axis, alloantibodies are denoted by the antigen specificity and autoantibodies are denoted separately. Autoantibodies with no definable specificity were most commonly detected (n=58), along with alloantibodies reactive in Indirect Anti Human Globulin (AHG) tests with no definable specificity (n=42). The most commonly detected alloantibody was anti-E (n= 24), followed by anti-C (n=17) and anti-K (n=17).

3.3.2 Antibodies and patient factors

3.3.2.1 Gender and immunisation rate

Of the 877 records reviewed in the renal patient cohort, 339 (38.7%) were female and 537 (61.2%) were male. The allo/autoantibody immunisation rate in males was 11.7% (63/537), compared to 20.9% in females (71/339) demonstrating a significant difference (Fisher's Exact Test P=0.0003) and indicating that females are significantly more likely to develop allo/autoantibodies than males in this group of patients (figure 3.11).

Figure 3.11: Influence of gender on the development of allo/autoantibodies in the renal cohort

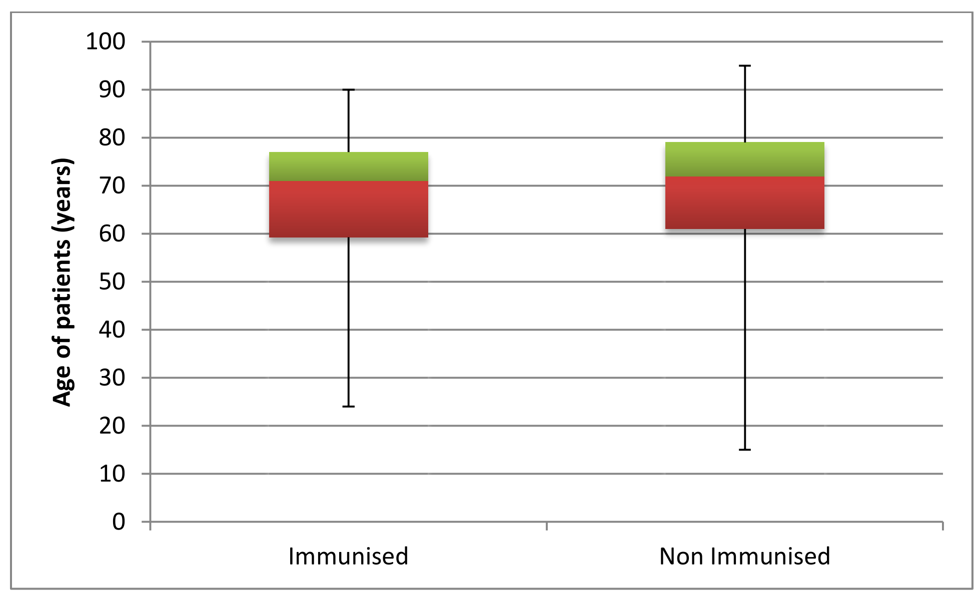


Incidence of immunisation rates in males and females in the renal cohort (n=877). The incidence of immunisation in male patients was 11.7% (63/537) compared to an incidence rate of 20.9% (71/339) in female patients. A significant difference (Fisher's Exact Test P=0.0003) was seen between allo/autoimmunisation rates in males and females in this group of patients.

3.3.2.2 Age and immunisation rate

In the renal cohort (n=877) the age of the patients at first recorded transfusion ranged from 15 to 95 years with an average of 68.14 years (SD14.42). Within the immunised group (n=134) the average age at first transfusion was 66.58 years (range 24 – 90, SD 14.70) and within the non-immunised group the average age was 68.42 years (range 15 – 95, SD 14.36). There was no significant difference between the mean age (in years) at first recorded transfusion in the patients with allo/autoantibodies and those without (t-test P=0.4599) (figure 3.12), indicating that age at first transfusion does not influence the incidence of immunisation.

Figure 3.12: Influence of age at first recorded transfusion on the development of allo/autoantibodies in the renal cohort

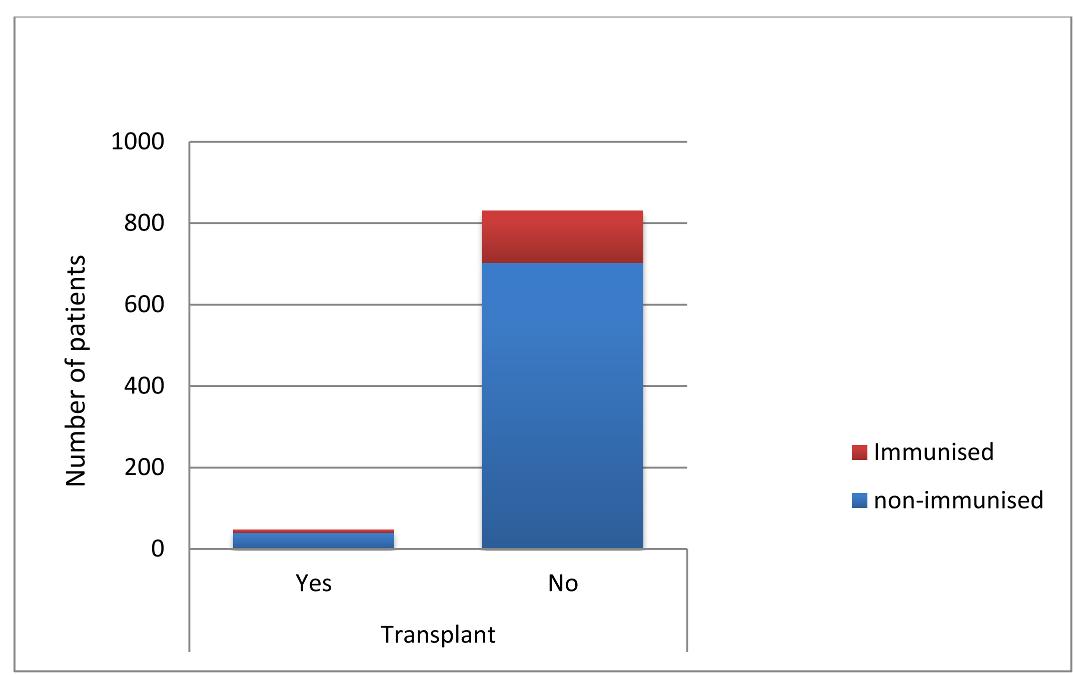


Box-and-whiskers plot showing the range of age at first transfusion (black line) in the immunised and non-immunised patients within the renal cohort (n=877). The first and third quartiles and the median (second quartile) are denoted by the red and green blocks. The average age at first transfusion in the immunised group was 66.58 years (range 24 – 90, SD 14.70) and in the non-immunised group the average age was 68.42 years (range 15 – 95, SD 14.36). No significant difference was seen between the mean age (in years) at first recorded transfusion in the patients with allo/autoantibodies and those without (t-test P=0.4599)

3.3.2.3 Immune suppression and immunisation rate

Receipt of a renal transplant was used as a surrogate marker of immune suppression, within the renal cohort, in order to investigate any relationship between immunosuppression and immunisation rate. Forty seven patients within this group (n=877) had records indicating that they had received a renal transplant. An immunisation rate of 2.1% (7/47) was seen in the patients with a record of renal transplant compared to an immunisation rate of 15.3% (127/830) in the non-transplanted patients. Statistical analysis of the groups showed that there is a statistical significance between these rates indicating that immune suppression in this group of patients may have a protective effect against immunisation to red cell antigens (Fisher's Exact Test P=0.0029) as shown in figure 3.13.

Figure 3.13: Influence of immunosuppression on the development of allo/autoantibodies in the renal cohort



Comparison of the incidence of immunisation in renal patients (n=877) with and without recorded renal transplant, used as a surrogate marker of immune suppression. An immunisation rate of 2.1% (7/47) was seen in the patients with a record of renal transplant compared to an immunisation rate of 15.3% (127/830) in the non-transplanted patients. The difference in these rates is statistically significant (Fisher's Exact Test P=0.0029)

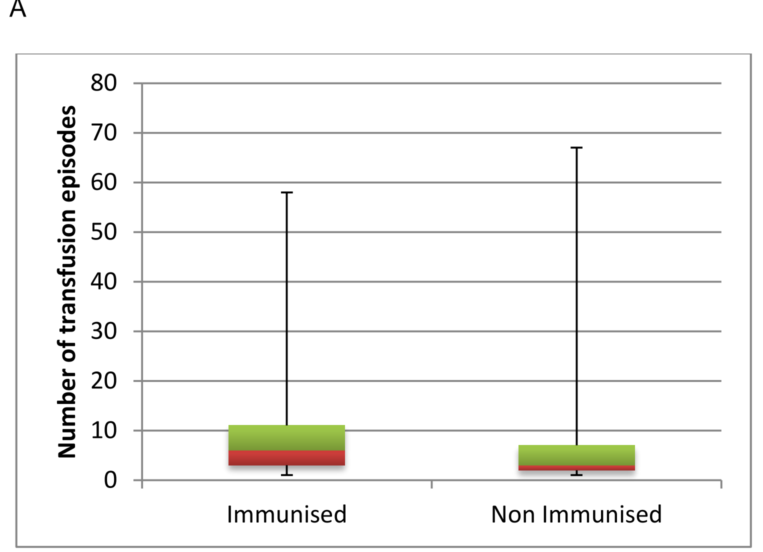
3.3.2.4 Number of transfusion episodes and incidence of immunisation

The number of transfusion episodes and the number of red cell units transfused was reviewed for the immunised and the non-immunised patients in the renal cohort of patients. The average number of transfusion episodes across the patients in this group (n=877) was 5.98 (range 1-67, SD 7.38). Within the immunised group (n=134), the average number of transfusion episodes was 9.69 (range 1-58, SD 11.53), compared to an average of 5.30 (range 1-67, SD 6.12) for the non-immunised group, demonstrating a significant difference in the number of transfusion episodes and incidence of allo/autoimmunisation (t-test P= <0.0001) (figure 3.14a).

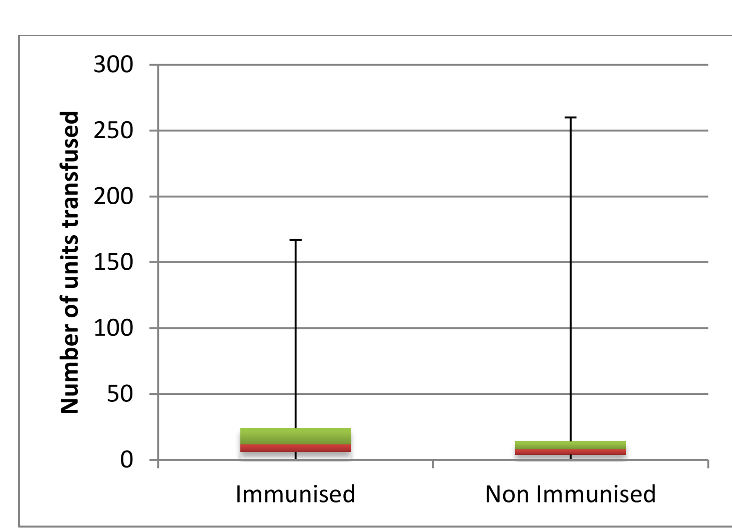
The average number of red cell units transfused to all patients in the renal cohort (n=877) was 13.50 (range 1-246, SD 18.36). Within the immunised group (n=134), the average number of units was 21.85 (range 2-143, SD 25.72), compared to an average of 11.97 (range 1-246, SD 16.26) in the non-immunised group (n=743), again demonstrating a significant difference (t-test P= <0.0001) (figure 3.14b)

Figure 3.14: Influence of the number of transfusion episodes and number of units transfused on the development of allo/autoantibodies in the renal cohort

A



B

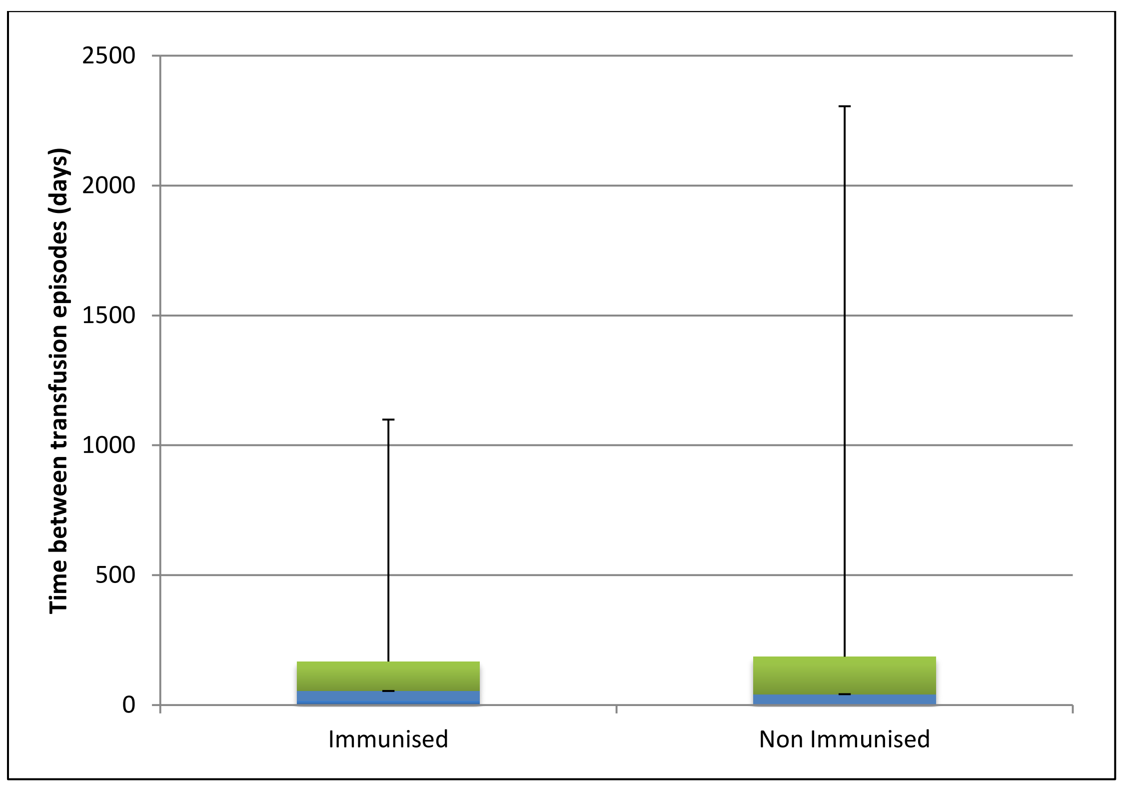


Box-and-whiskers plot showing the range (black line) of transfusion episodes and number of units given in the immunised and non-immunised patients within the renal cohort (n=877). The first and third quartiles and the median (second quartile) are denoted by the red and green blocks. The average number of transfusion episodes in the immunised group (n=134, average=9.69, SD 11.53) was significantly different to that seen in the non-immunised group (n=743, average=5.3, SD6.12) (figure A). Similarly, the average number of units transfused in the immunised group (n=134, average=21.85, SD25.72) was significantly different to that seen in the non-immunised group (n=743, average=11.97, SD 16.26) (figure B)

3.3.2.5 Time between transfusion and the incidence of immunisation

Time between transfusions, in days, was reviewed for the patients within the renal cohort (n=877) to investigate any relationship between the incidence of immunisation and the time frames for transfusion of blood units. For all patients in this group (n=877), the time (days) between transfusion ranged from 0 to 2120.5 days, with an average of 136.64 (SD 218.09). Within the immunised group (n=134) the average time between transfusions was 118.6 days (range 0-931.9, SD 157.65) and within the non-immunised group (n=743) the average was 139.5 days (range 0-2120.5, SD 227.30), demonstrating no significant difference between the two groups (t-test P=0.3076) (figure 3.15). This would suggest that the frequency (time between transfusion) of exposure to foreign red cell antigens does not influence the incidence of immunisation in this group of patients.

Figure 3.15: Influence of the frequency of transfusion episodes on the development of allo/autoantibodies in the renal cohort



Box-and-whiskers plot showing the range of time in days (black line) between transfusion episodes in the immunised and non-immunised patients within the renal cohort (n=877). The first and third quartiles and median (second quartile) are denoted by the red and green blocks. The average time between transfusion for the immunised group (118.6 days, range 0-931.9, SD 157.65) was not significantly different to that seen in the non-immunised group (139.5 days, range 0-2120.5, SD 227.30) (t-test P=0.3076)

3.3.3 Transfusion Reactions

Of the 877 patient records reviewed within the renal cohort, 5 patients (0.6%) were investigated for a suspected transfusion reaction, giving an overall transfusion reaction incidence of 1 in 2364.4 units. An incidence of 2.2% of patients were investigated for a suspected transfusion reaction in the immunised group (n=134, 3/134), compared to an incidence of 0.3% (n=743, 2/743) in the non-immunised group. An approximate eight fold difference was seen in the rate of suspected transfusion reactions in the allo/auto immunised group compared to the non-immunised group (see table 3-5). The difference between the suspected transfusion reaction rates between the two groups showed a significant difference (t-test P=0.0276), although it should be noted that the number of patients in the group that experienced reactions was very small. Patients included within the immunised group for review of suspected transfusion reactions were those with known red cell allo/autoantibodies being transfused with antigen negative and/or crossmatch compatible blood, not patients who had suffered a transfusion reaction as a result of development of antibodies subsequent to a transfusion, therefore the difference between the immunised and the non-immunised group is suggestive that even when allo/antibodies have been detected and blood compatible by current *in vitro* methods is provided the likelihood of a transfusion reaction is higher if the patient has known allo/autoantibodies.

Table 3.5: Transfusion reactions in the renal cohort

Within the renal cohort (n=877), immunised patients (n=134) showed an incidence of 2.24% suspected transfusion reaction compared to just 0.3% in the non-immunised cohort (n=743). An approximate eight fold difference was seen in the rate of suspected transfusion reactions in the allo/auto immunised group compared to the non-immunised group. The risk of transfusion reaction was higher in the immunised group despite the fact that this group was transfused with blood that was deemed compatible by in vitro methods.

	Total number of patients	**Number of investigated transfusion reactions**	**%**
Non-immunised	743	2	0.27
Immunised	134	3	2.24
Total	877	5	

3.3.4 Cost of additional testing

A review was performed of the additional laboratory testing undertaken for the patients within the renal cohort (n=877). A total of 1919 serological tests, in addition to the standard ABO and Rh D group and antibody screen were performed for the 877 patients at a total cost of £14,604.59. A total of 25 additional tests costing £155.53 were performed for the non-immunised patients (n=743) compared to 1894 additional tests and a cost of £13,094.76 for the immunised group (n=134). A breakdown of the additional serological tests performed and the costs of the additional testing are shown in table 3-6. The cost of testing for patients with allo/autoantibodies was approximately nine times greater than that for the non-immunised group, compared to the 32 fold difference seen within the haematology immunised and non-immunised cohort. Test costs were calculated, using an in-house spreadsheet calculator (Microsoft Excel), taking into account reagent costs, equipment maintenance, consumables, quality control and staff time incurred during the financial year 2011-2012. Total test costs for the additional testing performed on patient samples during the retrospective review period were calculated using these current tests costs, although it is accepted that, as discussed previously (section 3.2.5), there is a lack of accuracy due to estimates based on current costings.

Table 3.6: Cost of additional testing in the renal cohort

The table shows the additional laboratory tests performed for patients within the renal cohort (n=877), the test type, number of tests performed and cost of testing is shown for the immunised and non-immunised groups. The costs for the additional laboratory tests required for the patients within the renal cohort were substantially higher for the immunised group (n=134) than those for the non-immunised group (n=743).

	Immunised group		**Non-immunised group**	
Test	Number of tests	Cost	Number of tests	Additional Cost
Antibody identification panel	962	£6,849.44	1	£7.12
Direct Antiglobulin Test	588	£2,475.48	21	£88.41
Monospecific Coombs test	221	£1,226.55	1	£5.55
NHSBT RCI referral	44	£2,204.40	1	£50.10
Rh CcEe type	51	£221.85	1	£4.35
Red cell phenotype	28	£117.04	0	0
Total	1894	£13,094.76	25	£155.53

3.4 Comparison of renal patients and haematology patients

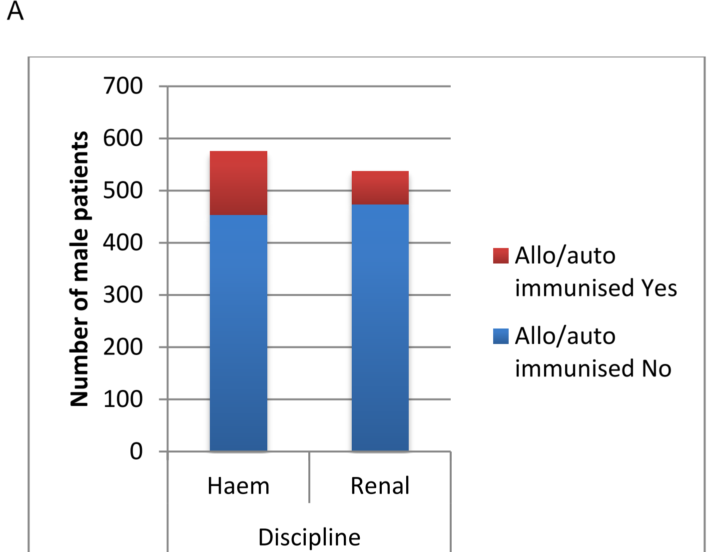
3.4.1 Gender and the incidence of immunisation

Statistical analysis of the numbers of male and female patients with and without allo/autoantibodies treated on the haematology wards showed no significant differences, indicating that the sex of the patient had no influence on the development of allo/autoantibodies. This difference, however, was not replicated in the patients transfused on the renal wards. In order to further investigate this anomaly the rates of allo/autoantibody production in each of the sexes across the two disciplines were subjected to statistical analysis using the Fisher's Exact Test.

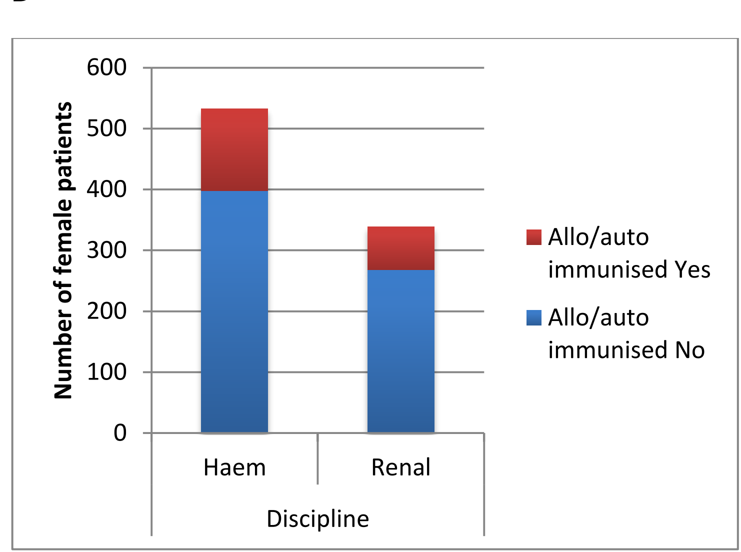
An immunisation rate of 21.2% was seen in the male haematology cohort (n=575) compared to a rate of 11.7% in the male renal cohort (n=537). Female patients showed an immunisation rate of 25.2% in the haematology cohort (n=532) and a rate of 20.9% in the renal cohort (n=340). A statistically significant difference was seen in the rates of allo/autoantibody production for males (Figure 3.16a) in the two cohorts (Fisher's Exact Test, P=<0.0001), but this was not seen for females (Fisher's Exact Test, P=0.1640) (Figure 3.16b). This suggests that females are equally likely to develop red cell all/autoantibodies whether they are transfused for haematological malignancies or renal insufficiency whereas males are less likely to produce red cell allo/autoantibodies if they are transfused for renal insufficiency than they are if transfused for haematological malignancies.

Figure 3.16: Comparison of the influence of gender on the development of allo/autoantibodies in the haematology cohort versus the renal cohort

A



B



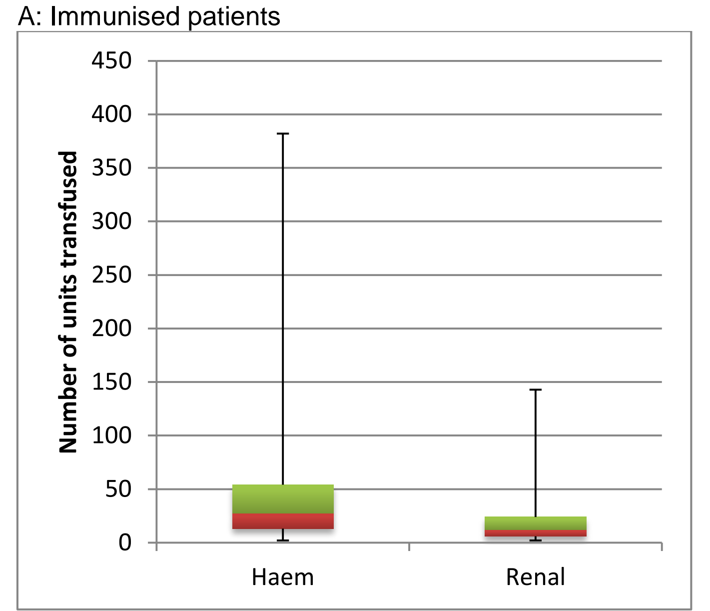
The rates of red cell allo/autoantibody production in male patients transfused on the haematology wards (haem) (n= 575, incidence of immunisation 21.2%) and the renal wards (n=537, incidence of immunisation 11.7%) are shown in figure 3.16a. There is a statistically significant difference in allo/autoantibody development between the two groups (Fisher's Exact Test, P=<0.0001). The immunisation rates in females within the haematology cohort (n=532, incidence 25.2%) compared to the rate in the renal cohort (n=339, incidence 20.9%) is shown in figure 3.16b. No significant difference in immunisation rates was seen in these groups.

3.4.2 Number of units transfused and immunisation rate

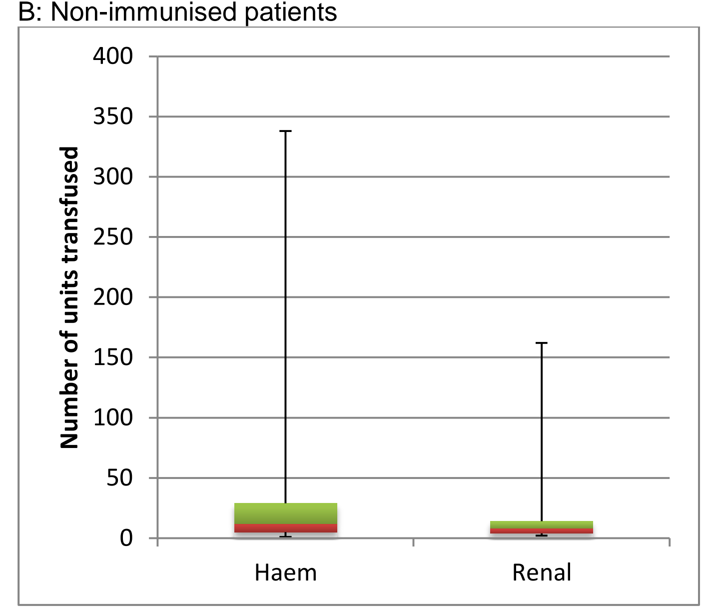
Patients within the haematology cohort (n=1107) were transfused with an average of 28.8 units (SD 42.10) over the review period, compared to an average of 13.5 (SD 18.36) for the renal patients (n=877). The average number of red cell units transfused to immunised haematology patients (n=256) was 46.99 (SD 59.65), compared to an average of 21.85 (SD 25.72) units transfused to immunised renal patients (n=134). Non-immunised patients in the haematology cohort (n=851) received an average of 23.43 (SD 32.01) units of red cells compared to an average of 11.97 (SD 16.26) transfused to the non-immunised renal patients (n=743). Analysis of the number of units transfused to patients on the haematology wards compared to those on the renal wards demonstrated that patients transfused for haematological malignancies received significantly more units of blood than those transfused for renal insufficiency irrespective of whether they had red cell allo/autoantibodies (figure 3.17a, t-test P value P=<0.0001) or not (figure 3.17b, t-test P value P=<0.0001).

Figure 3.17: Comparison of the number of red cell transfusions given in the haematology and renal cohorts

A: Immunised patients



B: Non-immunised patients



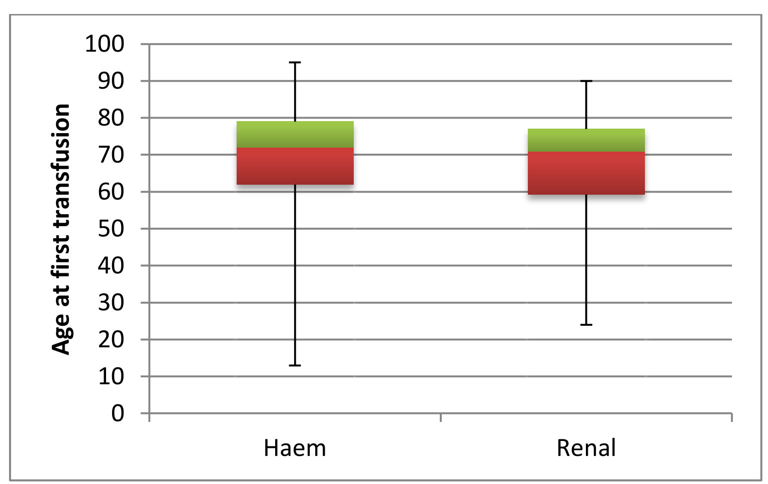
Box-and-whiskers plots showing the range of number of transfusions given (black line) in the immunised and non-immunised patients within the haematology cohort (n=1107) and renal cohort (n=877). The first and third quartiles and the median (second quartile) are denoted by the red and green blocks. Immunised haematology patients received an average of 46.99 units of red cells (SD 59.65) compared to an average of 21.85 (SD 25.72) in the immunised renal patients (figure 3.17a). In comparison, non-immunised haematology patients received an average of 23.43 units (SD 32.01) compared to an average of 11.97 units (SD 16.26) in the renal patients (figure 3.17b). Patients transfused for haematological malignancies received significantly more units of blood than those transfused for renal insufficiency irrespective of whether they had red cell allo/autoantibodies (Figure 3.17a, t-test P value P=<0.0001) or not (Figure 3.17b, t-test P value P=<0.0001).

3.4.3 Age at first transfusion and incidence of immunisation

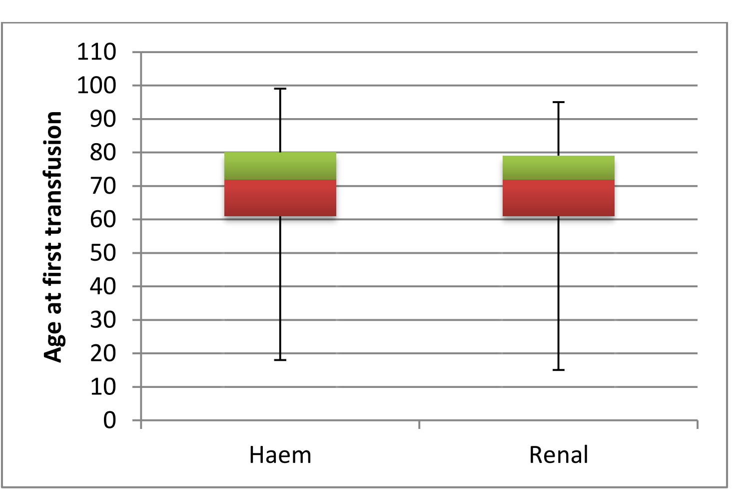
The average age of patients at first transfusion in the haematology cohort (n=1107) was compared to that of patients within the renal cohort (n=877) for immunised and non-immunised patients. Non-immunised patients within the haematology cohort (n=851) were transfused at an average age of 69.18 (SD 14.7) years compared to an average of 68 years (SD 14.4) in the renal cohort (n=743). For immunised patients the average age at first transfusion was 69 (SD 14.7) years for haematology patients (n=256) and 67 (SD 14.7) for renal patients (n=134). No statistically significant difference was seen in age at first transfusion within the immunised patients (figure 3.18a t-test P value = 0.2007) or the non-immunised patients (figure 3.18b t-test P value = 0.1067).

Figure 3.18: Comparison of age at first transfusion and incidence of immunisation in the haematology and renal cohorts

A Immunised patients



B Non-immunised patients



Box-and-whiskers plots showing the range (black line) of number of transfusions given in the immunised and non-immunised patients within the haematology (haem) cohort (n=1107) and renal cohort (n=877). The first and third quartiles and the median (second quartile) are denoted by the red and green blocks. Immunised haematology patients received the first transfusion at an average age of 69 years (SD 14.7) compared to an average age of 67 (SD 14.7) in the immunised renal patients (figure A). In comparison, non-immunised haematology patients received the first transfusion at an average age of 69.18 (SD 14.7) compared to an average age of 68 years (SD 14.4) in the renal patients (figure B). No statistically significant differences were seen in the age at first transfusion for either the immunised (Figure A, t-test P value P=0.207) or the non-immunised patients (Figure B, t-test P value P=0.1067).

3.5 Discussion

It is well accepted in the UK that patients with SCD and thalassaemia should have extended red cell antigen typing prior to transfusion, and should receive blood that is matched for at least Rh (CcEe) and Kell antigens (BCSH, 2013). This strategy has been implemented in response to the wealth of evidence that this group of patients have a relatively high alloimmunisation rate (Coles *et al.,* 1981; Davies *et al.,* 1986; Michail-Merianou *et al.,* 1987; Rosse *et al.,* 1990; Spanos *et al.,* 1990; Hmida *et al.,* 1994; Tahhan *et al.,* 1994; Moreira *et al.,* 1996). Patients with SCD and thalassaemia require frequent transfusion support over a long period of time; the frequency of transfusion makes red cell antigen phenotyping difficult if left until after the production of a red cell alloantibody when transfused cells are present in the circulation. The majority of alloantibodies produced by these patients were found to be Rh or Kell system related (Davies *et al.,* 1986; Rosse *et al.,* 1990), hence the recommendation to match for these antigens prophylactically. More recent studies have noted that patients with SCD have high rates of alloimmunisation despite strategies to match for Rh and Kell antigens (Chou *et al*., 2013; Woldie *et al*., 2015). This may be related to ethnic differences between donor and recipient populations, altered *RH* alleles when the donor and recipient populations are matched, or patients receiving transfusions in other centres where matching does not occur. This information has reignited the debate regarding the benefits and cost effectiveness of a prophylactic matching strategy for these chronically

transfused patients. It has also questioned whether the introduction of genotyping, particularly for *RH,* would improve matching and reduce the alloimmunisation rate.

Patients with haematological malignancies or renal failure are also likely to require frequent blood transfusion support over an extended period, often several years, and so it is reasonable to consider the implementation of such a strategy for typing and matching blood for transfusion in these groups of patients as well. There has been some debate in the literature regarding typing and matching of blood in chronically transfused patient groups, other than those with SCD and thalassaemia. Initially publications reported that prophylactic matching was either unnecessary or not cost effective (Blumberg *et al.,* 1984; Domen and Ramirez, 1988; Schonewille *et al.,* 1999). However, later studies supported this strategy in certain selected groups (Fluit *et al.,* 1990; Shirey *et al.,* 2002; Schonewille *et al.,* 2009; Kadar, 2010). A study by Alves and co-workers (2012) found a relatively high rate of alloimmunisation in patients transfused for surgical or clinical emergencies. Their results suggest that a type and match strategy could also be beneficial for non-chronically transfused patients.

To continue the debate, this retrospective study of patients who received blood transfusions in a UK haematology ward and a renal ward setting, collected and analysed data on the allo and auto-immunisation rates, potential risk factors and cost of additional testing, providing new

evidence to support a type and match strategy. The retrospective review found an overall alloimmunisation rate in patients transfused on the haematology wards of 12.9%, which is not dissimilar to the 9% found by Schonewille *et al.,* (1999) and 11.8% by Fluit *et al.,* (1990) in similar groups of patients. In this study alloantibodies were most commonly seen in patients with aplastic anaemia (35.7%), MDS (24.5%), solid organ cancers (18.5%), CLL (17.5%), AML (14.5%) and myeloma (13.9%). Other workers have found lower rates, 11% in aplastic anaemia (Blumberg *et al.,* 1983) and 15% (Sanz *et al.,* 2013) in MDS/CMML. Higher rates were seen in MDS by Milic and co-workers (2011), who found 36% alloimmunisation rate in patients who received more than 30 units of blood and 64% in those who received more than 100 units. These differences may be explained by factors such as, the number of patients studied, the sensitivity of the antibody screening techniques and the transfusion policies in place. Some studies have indicated that patients with lymphocytic leukaemias do not develop alloantibodies (Blumberg *et al.,* 1983; Blumberg *et al.,* 1984; Fluit *et al.,* 1990; Seyfried and Waleska, 1990), however, both this study and that of Schonewille *et al*., (1999) have found alloimmune responses in these patients. Correspondence analysis of the data found in this study revealed that haemolytic anaemia, MDS and MPD showed an association with the development of allo and autoantibody, whereas CLL, AML and aplastic anaemia appeared to be associated with the development of autoantibodies only.

In the cohort of 877 patients transfused due to renal failure, 15.3% were found to have allo and/or autoantibodies, with 13% having red cell alloantibodies. This is slightly higher than the rates seen in a similar study by da Silva and co-workers (2013) who reported 7.4% of 393 patients with chronic kidney disease on a transplant waiting list having red cell alloantibodies. Sangole and Chaudhari (2013) found red cell alloantibodies in 25% of patients with chronic renal failure who had experienced transfusion reactions; however, this study involved a very small number of chronically transfused patients.

Age appeared to have no influence on the alloimmunisation rate in either the haematology patients or the renal patients, a fact supported by Schonewille *et al.,* (1999) and Sanz and co-workers (2013), but not by Seyfried and Waleska (1990) who reported that the probability of alloimmunisation is a quadratic function of age. A large study of patients and donors in the Unites States of America found the alloimmunisation increased with age for certain antibodies (anti-K, -Kp^a, -Fy^a, -D, -C and –E) and decreased with age for others (anti-Le^a, -Le^b, -M and -P1) presumably due to the inclusion of increasing numbers of women immunised through pregnancy and both sexes immunised through transfusion (Winters *et al.*, 2001).

This retrospective review reported only on adult patients, the youngest patients included were 13 years for the haematological cohort and 15 years for the renal cohort. Other studies have reported much lower rates

of alloimmunisation in paediatric patients transfused as a result of SCD or thalassaemia (Spanos *et al.,* 1990; Aygun *et al.,* 2002), with statistically significant differences seen in the rate of alloimmunisation in patients transfused before the age of three, compared to those transfused after three years of age (Spanos *et al.,* 1990). In a study of transfused patients awaiting kidney transplantation, which included a patient population with an age range of 4 to 77 years, no differences were seen in the mean age of the immunised group compared to the non-immunised group (da Silva *et al.,* 2013). It would seem reasonable to assume that in a non-selective population the incidence of red cell alloantibodies increases with age but in transfused population this finding is not apparent after three years of age.

In the haematological cohort, gender appeared to have no influence on the alloimmunisation rate, a fact supported by other studies in similar groups of patients (Blumberg *et al.,* 1983; Redman *et al.,* 1996 Schonewille *et al.,* 1999; Sanz *et al*., 2013). Within the renal cohort gender did appear to have an influence on the alloimmunisation rate, with females being more likely to produce alloantibodies. This association has also been reported by other groups in less selective cohorts of patients and/or blood donors (Hoeltge *et al.,* 1995; Winters *et al.,* 2001; Bauer *et al.,* 2007), and is generally believed that the greater frequency of red cell antibodies seen in females is due to pregnancy related alloimmunisation. The study of renal patients by da Silva and co-workers (2013) suggested that the determining factor for the differences in alloimmunisation rates in

males and females was not only the gestations, but also due to greater numbers of transfusions given to females (average 7 +/- 3) compared to males (average 3 +/- 2.6). However, in this study of renal patients, no statistically significant difference was seen between the number of red cells transfused between males and females (average 13.51 and 13.43 respectively t-test P value 0.9499) or the number of transfusion episodes (average 5.90 and 6.01 respectively, t-test P value 0.8296). Further analysis of the red cell immunisation rates in males and females between the haematological cohort and the renal cohort in this study found that that there was no significant difference in the rates for females (t-test P value 0.1640) but that there was a highly significant difference in the red cell immunisation rate for males (t-test P value 0.0001). This shows that male patients transfused for renal failure are much less likely to produce red cell antibodies than males transfused for haematological malignancies, suggesting that the disease status itself may put male haematology patients on an equal footing to females with regard to the development of red cell allo and/or autoantibodies. This apparent equality in red cell allo/autoimmunisation could be related to the immune dysregulation found in certain haematological malignancies (Barrett *et al.,* 2000; Maciejewski *et al.,* 2007; Alfinito *et al.,* 2010). Alternatively, it could be related purely to the fact that patients with haematological malignancies received, on average in this study, significantly more red cell transfusions over the course of their treatment than the renal patients (46.99 units vs 12.0 units t-test P value 0.0001 for immunised patients

respectively and 23.43 units vs 8.0 units t-test P value 0.0001 for non-immunised patients).

The current study found that the requirement for concomitant platelet therapy and irradiated blood components, used here as surrogate markers for intensive chemotherapy and immune suppression, did not influence alloimmunisation rates, while other workers have reported that immunosuppressed patients are less likely to produce antibodies (Ramsey *et al.,* 1989; Schonewille *et al.,* 1999; Asfour *et al.*, 2004; Zalpuri *et al.,* 2014). It is possible that the surrogate markers used in this study did not identify patients whose immune suppression was of a similar state to those reported in the other studies. Schonewille and co-workers (1999) reported occurrence of antibodies in patients receiving intensive chemotherapy, whereas the patients studied by Asfour and co-workers (2004) had received bone marrow and/or peripheral blood stem cell transplant, and Ramsey and co-workers (1989) studied patients who received liver and heart transplants. The comprehensive two-centre case-reference study by Zalpuri *et al.* (2014) demonstrated that exposure to immunosuppressives was associated with a considerably lower risk of alloimmunisation. Using a case controlled study they demonstrated that, patients taking only corticosteroids, patients taking only other immunosuppressants, and those taking both, had a lower alloimmunisation risk (adjusted Risk Ratios of 0.70 (95% CI, 0.42-1.16); 0.51 (95% CI, 0.04-7.10) and 0.19 (95% CI, 0.07-0.53) respectively) than that of patients not taking any immunosuppressants (Zalpuri *et al.,* 2014).

The surrogate markers used in this study were chosen because they were believed to be adequate markers for patients undergoing the type of intensive chemotherapy which would substantially suppress the immune system. The difference seen in this study and that of Zalpuri and co-workers (2014) may be due to the fact that in this study it was not known if the immunosuppressive therapy was given before or after the alloimmunisation, which may have influenced the results. In addition, there is evidence to suggest that the transfusion of platelets can, in fact, increase the risk of red cell alloantibody development by inducing an inflammatory response in the recipient from infused cytokines (Yazer *et al.,* 2009).

Review of the transfused renal patients showed an apparent relationship between immune suppression as a result of renal transplantation and allo/autoimmunisation, suggesting that immune suppression may have a protective effect against immunisation to red cell antigens in this group of patients. However, the number of patients identified as having received renal transplants in this study was small and it was not possible to ascertain whether the patients had produced allo/autoantibodies prior to or subsequent to the transplant.

The current data supports that of other studies (Sarnaik *et al.,* 1986; Fluit *et al.,* 1990; Hoeltge *et al*., 1995; Zalpuri *et al.,* 2012), that the development of alloantibodies is related to the number of red cell

transfusions given; in this study both the total number of units and the number of transfusion episodes were related to the risk of antibody formation in both cohorts of patients. Antibodies were formed after an average of 15.46 units had been transfused in the haematology cohort, a figure similar to that found by Schonewille *et al.,* (1999) and after an average of 9.66 units in the renal cohort.

In this study a substantial proportion of alloantibodies could not be identified; 29.3% in the haematology cohort and 28.6% in the renal cohort. This is similar to the figures found by Schonewille *et al.,* (1999), Redman *et al.,* (1996) and da Silva *et al.,* (2013) who found 22.5%, 17.6% and 34.5%, respectively. The majority of patients formed a single antibody specificity (61.6% in the haematology cohort and 60.3% in the renal cohort) with 43 haematology patients and 25 renal patients forming multiple specificities, although no patients formed more than five antibody specificities, comparable with results found by Winters *et al.,* (2001) in an American population.

As in other studies (Fluit *et al*., 1990; Hmida *et al*., 1994; Redman *et al.,* 1996; Schonewille *et al.,* 1999; Sanz *et al*., 2013; da Silva *et al.,* 2013) the majority of antibodies identified were Rh and Kell related, with anti-E being the most common in both patients transfused for haematological malignancies and those transfused for renal insufficiency. Almost all red cell units received from the NHSBT in our institution have their Rh (CcEe) and K antigen status documented on the unit, making these antigens the

easiest to match with phenotyped patients. A strategy to type and match Rh (CcEe) and K antigens in chronically transfused patients with haematological malignancies and renal insufficiency has the potential to eliminate alloantibodies to these antigens and reduce the additional cost burdens currently seen with alloimmunised patients.

The analysis of additional testing and the associated costs for the patients included in our retrospective review showed that immunised patients in the haematology cohort, in general, required approximately 19 times the number of additional serological tests than the non-immunised patients, and that the increase in costs required were 32 fold. In the renal cohort, the additional testing for the immunised group was approximately 75 times more than that for the non-immunised group, and the increase in cost was approximately nine fold. The differences in the costs between the groups is, in part, due to the higher number of some additional tests (in particular the DAT) being performed for haematology patients as part of routine screening for certain diseases, and regardless of immunisation to red cell antigens. It is likely that these figures would lead to an underestimation of projected figures, of both test numbers and costs, if used to predict cost effectiveness of a type and match program. This is because changes in transfusion policy throughout the study period meant that, in contrast to current pre-transfusion compatibility guidelines (BCSH, 2013), tests for antibody identification, confirmatory antigen status and the use of elution techniques for patients with autoantibodies were regularly omitted from the screening process and so have not been

included in the costs. The costs of crossmatching red cell units for the immunised and non-immunised group were not included in this study, but would, obviously, impact on the financial burden to the hospital service as well. Non-immunised patients may have red cells issued for transfusion by electronic issue, whereas immunised patients always require serological crossmatching (BCSH, 2013) with the ensuing cost implication.

A less well documented, and not completely understood, complication of blood transfusion is the development of red cell autoantibodies, which are often found in combination with alloantibodies (Shirey *et al.,* 2002; Young *et al.,* 2004; Ahrens *et al.,* 2007) in transfused patients. The frequency of auto and alloimmunisation in combination varied in these studies from 28% to 40%, not dissimilar to the figure found in this study for haematology patients (39.4% of immunised patients) and renal patients in this study (41.0% of immunised patients). In the majority of cases, in this study, production of the autoantibody was subsequent to production of the alloantibody, in accordance with results found by Sanz and co-workers (2013), and also, in this study the autoantibodies appeared to be clinically insignificant. Unfortunately, throughout the study period, the transfusion policy within our institution did not require the use of an eluate kit to determine the specificity of an autoantibody appearing post transfusion, and so no records were available to confirm that it was not indicative of a delayed or acute transfusion reaction. A substantial proportion (75.3% of haematology patients and 92.4% of renal patients)

of the patients with a positive DAT had IgG demonstrable on the surface of their red cells; elution of these antibodies would be a useful piece of further work to investigate any potential specificities. However, the presence of the autoantibodies did not appear to increase the transfusion requirements of the patients, suggesting that they were not of clinical significance. In this study, 158 patients treated on the haematology wards with autoantibodies had follow up testing and, of these, 123 (77.9%) of the autoantibodies were transient, a phenomenon also described by Young and co-workers (2004). This would seem to support the theory of Ahrens and co-workers (2007) that the alloantibody is initially of low affinity (compared to the matured antibody) and so it cross reacts with other structures on the red cell membrane as well as the alloantigen. A similar phenomenon has been demonstrated in an animal model by Weigle (1965), who demonstrated that autoimmunity could be induced in rabbits by the injection of heterologous or chemically altered homologous thyroglobulin. Another theory that has been put forward to explain transfusion-induced autoantibodies is the nonexofacial polymorphism (NEP) hypothesis. This hypothesis is based on the theory that differences in red cell antigenic structures are present both on the surface of the red cell and within the cytoplasmic or transmembrane domains of the blood group molecule (Zimring *et al.,* 2007). NEPs have been shown to exist for some blood group systems including Duffy (Neote *et al*., 1994; Mallinson *et al.,* 1995; Olsson *et al*., 1998; Parasol *et al.,* 1998), Kidd and Kell (Zimring *et al.,* 2007). It has been demonstrated that autoreactive B cells specific for red cell antigens exist naturally even in the presence of a

functional tolerance mechanism (Murakami and Honjo 1996), and that they are prevented from maturing by the thymic deletion of autoreactive CD4+ T helper cells. Zimring and co-workers (2007) postulated that transfusion of red cells that have the same external red cell antigens, but different NEPs, could lead to non-deletion of the autoreactive T helper cells, leaving them available to assist the autoreactive B cells, ultimately leading to red cell autoantibody production. Another suggestion that has been put forward is that the appearance of red cell autoantibodies is due to the presence of lymphocytes from previous transfusions which have survived and produce alloantibodies that attach to the recipient red cell, thus mimicking an autoantibody (Petz and Garratty, 1980; Garratty, 1996; Petz and Garratty, 2004).

The relatively high level of autoantibodies seen in the haematology cohort of this study, with or without associated alloantibodies, is further complicated by the original pathology of the patients within the study group. Patients with lymphoproliferative disorders are prone to the production of red cell autoantibodies (Kipps and Carson, 1993; Timura *et al.,* 2000) due to immune dysregulation resulting from the underlying disease. Similarly, patients with MDS have also been shown to produce autoantibodies to red cell antigens (Sokol *et al.,* 1989; Novaretti *et al.,* 2001) as do patients with CML (Steegmann *et al.*, 2003). In this study the highest proportion of autoantibodies were found, not unexpectedly, in patients with haemolytic anaemia (85.7%), followed by aplastic anaemia (50.0%), CLL (36.8%), CML/CMML (30%), MDS (21.9%), AML (17.2%)

and myeloma (10.6%), compared to only 5.5% of patients with solid organ cancer. The levels of autoantibodies present in patients with MDS in this study is higher than that found by others; Sokol and co-workers found just 7% (Sokol *et al.,* 1989) with other groups finding 3.7% (Martin-Vega *et al.,* 1988) and 8.2% (Mufti *et al.,* 1986), however the current data is similar to the 21.6% found by Seitanides and co-workers (Seitanides *et al.,* 1988). The higher levels in this study may be due to differences in sensitivity of screening techniques and/or the smaller number of patients included. Red cell autoantibodies in patients with renal disease are not so well documented. They may be related to the immune dysregulation seen in ESRD, which is exacerbated by dialysis, and can result in inflammation caused by immunoactivation (Deschamps-Latscha and Chatenoud 1996; Kato *et al.,* 2008). The relatively high rates of autoantibodies and alloantibodies in combination, in both the haematology and renal cohorts in this study, is in contrast to the rate (3.8%) seen in a non-selected population of red cell immunised patients and blood donors (Winters *et al.,* 2001), which supports the theories that non-clinically significant red cell autoantibodies in combination with alloantibodies may be related to the disease condition.

Throughout the study period, no patients in either cohort were documented as having suffered haemolytic transfusion reactions, either acute or delayed. A small percentage (2.17% of haematology patients and 0.57% of renal patients) of patients were investigated for suspected transfusion reactions, slightly higher than that found in cancer patients

(0.3%) by other workers (Huh and Lichtiger, 1987). This difference may be explained by improvements, since 1987, in the clinical observations of transfused patients and changes in the laboratory investigations of transfusion reactions. A large proportion of the reactions seen by Huh and Lichtiger (1987) were febrile non-haemolytic reactions, presumably caused by transfused white blood cells. Since November 1999, all allogeneic red cell units in the UK have been leucocyte depleted, the UK specification requires that more than 90% of manufactured leucocyte depleted blood components should have less than 1×10^6 leucocytes and more than 99% should have less than 5×10^6 leucocytes (JPAC, 2013). Leucocyte depletion of red cells has been demonstrated to reduce the incidence of febrile non-haemolytic transfusion reactions (King *et al,* 2004 (b)) hence, relatively small numbers of this type of reaction would have been seen in this study. Review of the 11 haematology patients with allo and/or autoantibodies, investigated for suspected transfusion reactions in this study, revealed that none of these patients had developed a newly positive DAT or newly developed alloantibody after the transfusion, although no eluates were performed to confirm this. Delayed Serological Transfusion Reactions (DSTR), defined by the detection of a positive DAT and a new alloantibody specificity post transfusion, were reported as being a frequent finding in multiply transfused patients (Ness *et al.,* 1990), although generally benign in nature and not causing clinical haemolysis, however, this was not seen in our patients. Introduction of the use of eluate testing as part of the laboratory investigation of positive DATs post transfusion, as recommended in the BCSH guidelines (BCSH, 2013),

may increase the number of regularly transfused patients diagnosed with DSTR in our patient population.

In conclusion, this study found that patients chronically transfused for haematological or renal indications are at risk of alloimmunisation. The antibodies developed by the patients are mainly to the Rh and Kell antigens, which could, potentially, be reduced by a type and match strategy. There are considerable costs associated with the provision of blood in the presence of alloantibodies, and an increased risk of transfusion reaction for the patients. Blood units supplied by the NHSBT are typed for Rh and Kell antigens, and the information is visible on the component label, facilitating blood selection in a type and match strategy. However, implementation of a strategy for type and match would need a suitable method, within the hospital transfusion laboratory, to type patient samples for the corresponding antigens. The method would need to support a high throughput, and have a high level of automation to reduce the risk of error. Hospital transfusion laboratories currently use high throughput automation for routine blood group and antibody screening, a novel method for serological phenotyping on one of these platforms is explored in chapter 4. Alternatively, commercial assays are available for blood group genotyping, which could also be suitable for a hospital transfusion laboratory. The suitability of one of these assays is explored in chapter 5. Although red cell units for transfusion supplied by NHSBT are typed for Rh and Kell antigens, provision of matched units from the stocks held in a hospital transfusion laboratory could be challenging. The

challenges for the laboratory provision of blood are explored in the pilot study, detailed in chapter 6. The high throughput assay selected to support a type and match strategy would also need to be cost effective. The costs for serological phenotyping and genotyping assays are explored in the relevant sections and compared in chapter 7.

4 AUTOMATED RED CELL PHENOTYPING

4.1 Introduction

Recent developments in the use of automated serological phenotyping techniques in the NHSBT facilities in the UK have meant that the majority of red cell units supplied to hospital transfusion services are now typed and labelled not only for ABO and RhD, but also for Rh (CcEe) and Kell antigens. The BCSH, however, do not recommend that hospital transfusion services in the UK routinely type patients for antigens other than ABO and RhD prior to transfusion (BCSH 2013). This is mainly due to the lack of automated techniques available for performing these tests within the hospital transfusion service setting and the risks associated with performing these tests manually on a large scale. Development of a system to perform automated red cell antigen phenotyping profiles for pre-transfusion patients would enable hospital transfusion services to prophylactically select and match blood for, at least, Rh (CcEe) and Kell antigens and possibly other antigens from routine blood stocks.

The NEO® blood grouping analyser system (IBG Immucor) was implemented in the RD&E in 2011 for blood grouping, antibody screening and identification. The analyser also has the potential to perform rapid automated extended red cell phenotyping profiles including Rh (CcEeC^{w}), K, Fy (a and b), Jk (a and b), M, N, S, s and k antigens. Although this technology has been in widespread use throughout the UK for many years for blood grouping, antibody screening and antibody identification, profiles for automated serological phenotyping have not been developed

or implemented for routine use. Introducing serological phenotyping to the system offers an opportunity for hospital transfusion services to access large scale, cost effective extended red cell serological phenotyping. As part of this study, development work was undertaken with the supplier to create the assay profiles on the automated system. This involved determination of the antisera to be used, setting the assay protocols on the analyser software and creating a report format. The study aimed to validate the antisera for automated use using commercially available red cells with known antigen types. In addition, comparability of manual red cell phenotyping, using a combination of techniques, and automated red cell phenotyping using the NEO® blood grouping analyser (IBG Immucor) for patient samples, was performed in accordance with BCSH guidelines for validation (BCSH, 2012).

The study also reviewed the comparability of cost between manual and automated red cell phenotyping, with the aim of providing a projected cost for the implementation of a strategy for targeted extended red cell phenotyping and matching of blood for transfusion in patients with haematological malignancies or renal insufficiency.

4.2 Results of the automated phenotyping validation

Automated extended red cell antigen testing on the IBG NEO® using the monoclonal reagents (anti-C, anti-c, anti-E, anti-e, anti-K, anti-M and anti-N) with the commercial NHSBT ten cell profile (0.8% cell suspension in Cellstab), three cell profile (3% cell suspension in Alsevers) and two cell titration profile (0.8% cell suspension in Cellstab) over multiple occasions (ten cell profile n=4, three cell profile n=5 and two cell profile n=2) showed no failures and no discrepancies with the known red cell antigen types reported in the product insert. Reaction values on the IBG NEO® were consistently strongly positive (4+) with both homozygous and heterozygous expression of red cell antigens.

Automated extended red cell antigen testing on the IBG NEO® with the polyclonal reagents (anti-Fy^a, anti-Fy^b, anti-Jk^a, anti-Jk^b, anti-S, anti-s and anti-k) with NHSBT ten cell profiles, three cell profile and two cell titration profile over multiple occasions (ten cell profile n=4, three cell profile n=5 and two cell profile n=2) showed one invalidated result with the anti-k reagent and one weak and undefinable (NTD) result during Jk^a testing. Following repeat testing, the invalidated result was positive and the weak positive result was negative, giving expected results. There were no discrepancies found with the known red cell antigen types reported in the product insert. Reaction values on the IBG NEO® were consistently strongly positive (4+) with homozygous and heterozygous expression of red cell antigens. One cell, on one occasion, produced a 3+ result with the anti-k reagent. The consistency of the reactions with homozygous and

heterozygous expression of red cell antigens is shown in table 4-1 using the NHSBT titration two cell profile as an example.

Table 4.1: Consistency of automated screening reactions with homozygous and heterozygous expression of red cell antigens

The automated profiles were tested on two occasions using the NHSBT titration two cell profile to review the consistency of the reaction grades. The titration panel includes red cells demonstrating both homozygous (shown in green) and heterozygous (shown in red) expressions of red cell antigens. The antigen profiles of the cells are shown in bold type and the reaction grades are shown as negative (-) or the numerical value (graded 1- 4 by the analyser). On both testing occasions results for homozygous and heterozygous antigen expression were strongly positive (3 or 4 strength reactions).

	C	**c**	**E**	**e**	**C^w**	**K**	**M**	**N**	**S**	**s**	**Fy^a**	**Fy^b**	**Jk^a**	**Jk^b**	**k**
Cell 1 antigen profile	**+**	**-**	**+**	**+**	**-**	**-**	**-**	**+**	**-**	**+**	**-**	**+**	**+**	**+**	**+**
Cell1 – test 1	4	-	4	4	-	-	-	4	-	4	-	4	3	4	4
Cell 1 – test 2	4	-	4	4	-	-	-	4	-	4	-	4	3	4	4
Cell 2 antigen profile	**+**	**+**	**+**	**+**	**-**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**
Cell2 – test 1	4	4	4	4	-	3	4	4	4	4	4	4	4	4	4
Cell2 – test 2	4	4	4	4	-	3	4	4	4	4	4	4	4	4	4

One hundred patient samples were selected for automated extended red cell antigen serological phenotyping on the IBG NEO® and comparative testing in the manual system. A mixed field reaction, demonstrating the presence of a dual population of cells with, and without, the E antigen, was seen with the anti-E reagent for one patient in both the automated and the manual testing. This type of reaction suggests interference from red cells from a recent blood transfusion. Following discussion with the patient it was confirmed that a transfusion has been performed at another hospital.

A weak reaction was seen with the anti-Fy^a reagent in both the automated (1+ reaction strength) and the manual technique for one patient. This sample also produced a weakly positive (2+) result with the anti-S reagent in the automated profile; manual testing with anti-S produced a negative result. Weakly positive results are suggestive of interference by red cell autoantibodies, which should be identified by the inclusion of a control test using patient cells analysed against the patient plasma or a commercial neutral reagent. A DAT on the patient sample confirmed the presence of a weak autoantibody.

A weak reaction (2+) was seen with the anti-Fy^b reagent in automated testing in one sample, repeat testing of this sample showed a negative result, in accordance with the manual testing results (table 4.2). This was considered to be a false positive reaction generated by the analyser system. The cut off values for the anti-Fy^b assay between the top end of

the “not determined” result (40.998) and the lower end of the 2+ positive result (50.999) are relatively tight (see appendix 3). There are a number of sample and/or analytical factors that may affect the value of a reaction within the system, these include; insufficient centrifugation of the sample, reagent deterioration and particles of dirt on the imaging system. These weak reactions seen in the initial testing with commercial cells, and again during patient testing were important in terms of recognition of false positives. In the hospital transfusion setting it is extremely important to reduce the risk of false positive results as these could lead to transfusion of incorrectly matched red cell units. The information obtained from the validation was used to determine the cut off values for reporting serological phenotyping results. It was concluded that only strongly positive values of 3+ and 4+ could be confidently reported as positive, and any results between “not determined” and 2+ would be considered invalid results requiring further investigation.

Table 4.2: Phenotyping anomalies in automated and manual assays

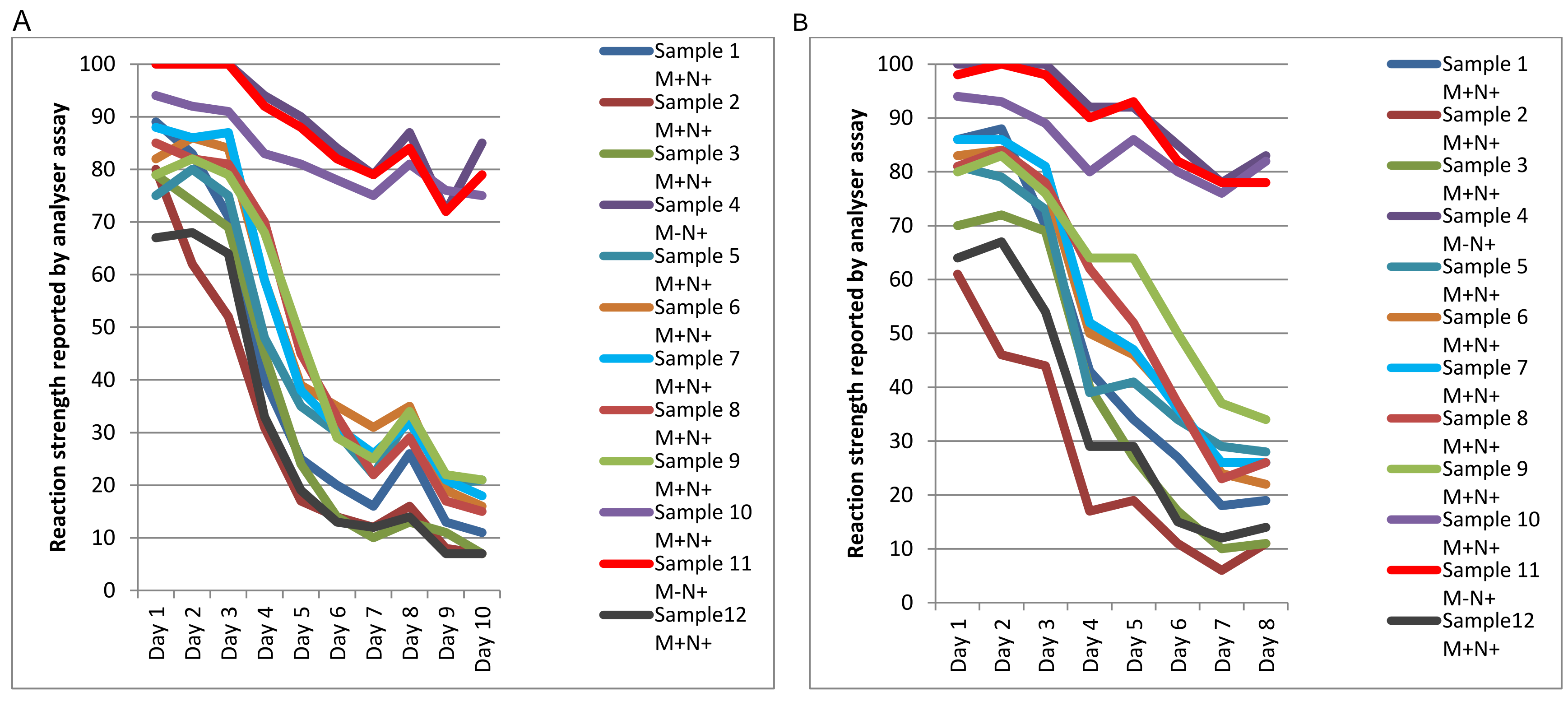
Anomalous results in serological phenotyping assays were seen for three patients; patient 1 demonstrated a mixed field reaction (MF) (shown in green) with the anti-E reagent in manual testing and weak positive in the automated assay, patient 2 reacted weakly positive with the anti-Fy^a reagent in both the automated and manual assays, this patient also produced a weakly positive reaction with the anti-S reagent in the automated profile (shown in red). Patient 3 reacted weakly with the anti-Fy^b reagent in the automated assay (shown in blue). The validation determined that reaction strengths between 1 and 2 are suggestive of false positive results and should be invalidated.

	Red cell antigen							
	E	***Fy^a***	***Fy^b***	***Jk^a***	**Jk^b**	**S**	***s***	***k***
Patient 1 manual assay	*MF*	+	+	+	+	+	+	+
Patient 1 automated assay	*NTD*	*4*	*4*	*4*	*4*	*4*	*4*	*4*
Patient 2 manual assay	+	*Weak positive*	+	+	+	-	+	+
Patient 2 automated assay	*4*	*1*	*4*	*4*	*4*	*2*	*4*	*4*
Patient 3 manual assay	-	+	-	+	+	+	-	+
Patient 3 automated assay (primary test)	-	*4*	*2*	*4*	*4*	*4*	-	*4*
Patient 3 automated assay (repeat test)	*N/A*	*4*	-	*4*	*4*	*4*	-	*3*

One discrepancy was seen with N typing for one patient, this sample repeatedly produced a negative result in automated testing using the immuClone anti-N and a positive result in manual testing using the Millipore anti-N. Confirmatory testing at the Red Cell Immunohaematology Laboratory at Filton NHSBT supported the positive result seen in the manual testing assay, and testing of the patient sample using the immuClone anti-N in a manual tube technique also gave a positive result. The discrepancy was thought possibly to be due to stability issues relating to sample storage time prior to testing. In addition, the temperature of the reagents at testing was also considered as a potential source of the weakened reactions (personal communication from Berndine Kokkelink, IBG Immucor). The performance of certain Immucor reagents, in particular LISS, are affected by temperature, and it is noted in the manufacturer's instructions that they should be allowed to come to 18-20°C before use. This was not noted in the instructions for the phenotyping antisera. However, the anti-N reagent had not been validated by the supplier for automated use, and so it was reasonable to exclude temperature as a cause of the discrepancy. A further 12 N positive samples (10 M+N+ and two M-N+) were selected for stability testing and reagent temperature testing. These samples were repeatedly tested over a 10 day period; each day the samples were tested with reagents taken straight from refrigerated storage and again after the reagents had been allowed to stand at room temperature for at least 4 hours. With the exception of one N heterozygote all other M+N+ samples tested gave negative results with the anti-N reagent at day 7 (figures 4.1a

and b). Using the manual technique, all nine of these samples were still strongly positive with anti-N (Millipore) at day 8. The reaction strength with anti-N (immuClone) in the automated technique for the nine samples clearly demonstrated a reduction in strength over the testing period with reagents taken directly from refrigerated storage and those held at room temperature prior to testing (figure 4.2). However, investigation of the potential effect of temperature of the reagents on the reaction strength showed no significant difference (figure 4.2) on each day of testing and testing was discontinued on day 8.

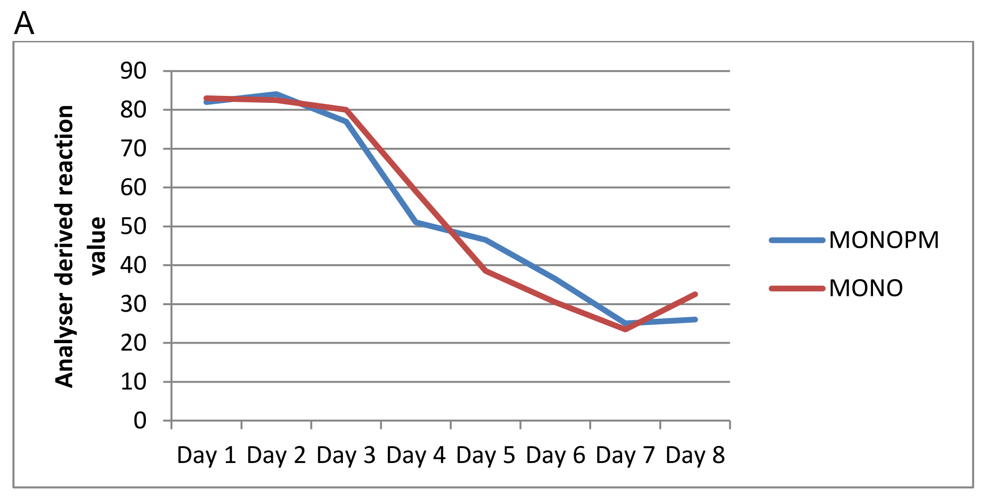
Figure 4.1: The influence of reagent temperature on the reaction strength of automated serological phenotyping testing



Reaction strengths of the automated serological phenotyping assay using monoclonal reagents over time with M+N+ and M-N+ cells using reagents taken from refrigerated storage (A) or used at room temperature (B). The numerical value calculated by the automated analyser is shown on the Y axis and the day of testing on the X axis. The majority of M+N+ cells reach the negative cut off value of 23 by day 7 regardless of the temperature of the reagents.

Figure 4.2: Influence of age of sample and temperature of reagent on the reactions strength of automated serological phenotyping

A



B

	Day 1	Day 2	Day 3	Day 4	Day 5	Day 6	Day 7	Day 8
MONOPM	82	84	77	51	46.5	36.5	25	26
MONO	83	82.5	80	59	38.5	30.5	23.5	32.5
P value	0.8287	0.785	0.6345	0.3974	0.4607	0.5867	0.8932	0.5711

This figure (A) shows the comparison between the average numerical value for each of the nine M+N+ samples over time for serological phenotyping using reagents directly from refrigerated storage (MONO) and those held at room temperature prior to testing (MONOPM). The numerical value calculated by the automated analyser is shown on the Y axis and the day of testing on the X axis. T-test values for each paired results shown in the table (B) did not demonstrate any statistically significant difference, suggesting that the temperature of the reagent during use doe not influence the reaction strength of the result.

Manual testing for Rh (CcEe) and K, C^w, M, N took approximately 25 minutes per patient, which included 10 minutes of staff time preparing the tests and reading the results. Manual testing for Fy^a, Fy^b, Jk^a, Jk^b, S, s and k required approximately 35 minutes per patient which included 10 minutes of staff time preparing the tests and reading the results. To reduce the risk of error, best practice is to test one patient at a time and include positive and negative reagent cell controls for each anti-serum used (BCSH, 2013).

Automated testing incurred approximately 2 minutes of staff time to load the reagents onto the analyser; this is independent of the number of patient samples tested. Preparation of samples for testing took approximately 2 minutes for 12 samples. The analyser is capable of processing three patient samples for monoclonal profiles in 28 minutes and three patient samples for polyclonal profiles in 50 minutes. The analyser is capable of processing single samples and samples in batches of various sizes.

Overall, the repeat rate for automated extended red cell antigen phenotyping was 1/100 for monoclonal antibodies (anti-C, Anti-c, Anti-E, anti-e, anti-K, anti-M and anti-N) and 3/100 for polyclonal antibodies (anti-Fy^a, anti-Fy^b, anti-Jk^a, anti-Jk^b, anti-S, anti-s and anti-k). The repeat rate for manual testing was 1/100 for polyclonal antisera (anti-Fy^a, anti-Fy^b, anti-Jk^a, anti-Jk^b, anti-s and anti-k). No repeat testing was required for manual tests performed using monoclonal antisera.

The frequency of red cell antigens in the tested patient samples (table 4-3) showed percentages comparable with that reported in the literature for Caucasian populations (Issit and Anstee, 1998; Dean 2005; Daniels and Bromilow, 2010) demonstrating that the selection of samples for testing was representative of the mainly Caucasian population tested in our institution.

Table 4.3: The frequency of antigens found in samples selected for validation of the automated serological phenotyping assays

The frequency of antigens present in the sample population selected for validation of the automated serological phenotyping assay was representative of a mainly Caucasian population when compared to others studies performed in similar populations (Issitt and Anstee, 1998; Dean, 2005; Daniels and Bromilow, 2010;). Antigenic frequencies not stated by the reporters are denoted by NS in the table.

Antigen	**C**	**c**	**E**	**e**	**K**	**C^{w}**	**Fy^{a}**	**Fy^{b}**	**Jk^{a}**	**Jk^{b}**	**S**	**s**	**M**	**N**	**k**
% positive in this study	68.7	80.8	37.4	94.9	15.2	2.02	65.7	81.8	81.8	70.7	53.5	86.7	81.9	77.8	99
Dean, 2005	68	80	29	98	10	NS	66	83	77	74	55	89	78	72	99
Daniels and Bromilow, 2010	68	81	29	98	9	NS	NS	NS	76	72	NS	NS	NS	NS	NS
Issitt and Anstee, 1998	70	80	30	98	9	1	66	83	76.9	72.5	57	88	78	72	99.8

4.3 Comparison of test costs for manual and automated serological phenotyping

Test costs were calculated for the manual and automated serological phenotyping assays. Staff costs were calculated at Band 5 (Agenda for Change, NHS pay scale 2015) pay point 20 and reagent costs were calculated at supplier cost 2014-2015 (excluding VAT). Costs for the relevant equipment maintenance were included, based on the proportion of tests processed on the equipment per year, and internal quality control costs were also included. Manual serological phenotyping assays performed in column agglutination tests and tube tests required approximately five minutes of staff time to prepare patient sample solutions, set up the test and quality control, and approximately five minutes for result interpretation and recording (table 4-4). Automated phenotyping took approximately 2 minutes for sample preparation and reagent preparation, with no time required for result interpretation and recording (table 4-5). Quality control costs for the manual phenotyping assays were based on the use of NHSBT two cell titration profile cells used with each assay; quality control for the automated phenotyping assay was based on the use of the NHSBT three cell profile in Alsevers, used on a monthly basis. Test costs for automated red cell antigen profiles processed on the NEO® analyser were considerably less than those for manual typing, mainly due to the reduction of staff time required for the process.

Table 4.4: Breakdown of test costs for the manual serological phenotyping assay.

Cost per test was calculated for extended phenotyping performed in manual assays, for the antigens shown in the first column. The table shows the breakdown of the cost per test of the anti-serum, quality control (QC), consumables, diluent, equipment and staff time. The cost for equipment is allocated as a proportion of the total tests performed on the system. The total cost for an extended phenotype performed using manual assays was £50.46.

Antigen	**Anti-serum cost per test (£)**	**QC cost (£)**	**Consumables (£)**	**Diluent 2 (£)**	**Equipment (£)**	**Staff time (£)**	**Total (£)**
Fya	0.28	0.043	1.49	0.11	0.22	2.35	**4.50**
Fyb	0.19	0.043	1.49	0.11	0.22	2.35	**4.40**
s	0.31	0.043	1.49	0.11	0.22	2.35	**4.53**
S	1.81	0.043	0.46	NA	0.22	2.35	**4.88**
Jka	0.73	0.043	1.49	0.11	0.22	2.35	**4.94**
Jkb	0.37	0.043	1.49	0.11	0.22	2.35	**4.59**
k	0.24	0.043	1.49	0.11	0.22	2.35	**4.45**
M	0.76	0.043	0.46	NA	0.22	2.35	**3.84**
N	0.76	0.043	0.46	NA	0.22	2.35	**3.84**
Cw	0.94	0.043	0.46	NA	0.22	2.35	**4.01**
Rh (CcEe) and K	NA	0.033	3.78	0.11	0.22	2.35	**6.49**
Total							**50.46**

Table 4.5: Breakdown of the test costs for the automated serological phenotyping assay

Cost per test was calculated for extended phenotyping performed in manual assays, for the antigens shown in the first column. The table shows the breakdown of the cost per test of the anti-serum, quality control (QC), consumables, diluent, equipment and staff time. The cost for equipment is allocated as a proportion of the total tests performed on the system. The total cost for an extended phenotype performed by the automated method was £19.55.

Antigen	QC cost (£)	Consumables (£)	Liss and Indicator cells	Equipment (£)	Staff time (£)	Total (£)
Fya	0.05	0.24	0.028	0.66	0.07	**1.40**
Fyb	0.05	0.24	0.028	0.66	0.07	**1.55**
s	0.05	0.24	0.028	0.66	0.07	**1.42**
S	0.05	0.24	0.028	0.66	0.07	**1.42**
Jka	0.05	0.24	0.028	0.66	0.07	**1.42**
Jkb	0.05	0.24	0.028	0.66	0.07	**1.42**
k	0.05	0.24	0.028	0.66	0.07	**1.51**
M	0.05	0.07	0.028	0.66	0.07	**1.18**
N	0.05	0.01	0.028	0.66	0.07	**1.09**
Cw	0.05	0.01	0	0.66	0.07	**1.19**
C	0.05	0.01	0	0.66	0.07	**0.97**
c	0.05	0.01	0	0.66	0.07	**0.89**
E	0.05	0.01	0	0.66	0.07	**0.89**
e	0.05	0.01	0	0.66	0.07	**0.98**
K	0.05	0.01	0	0.66	0.07	**1.15**
Neg control	0.05	0.24	0.028	0.66	0.07	**1.09**
Total						**19.55**

4.4 Discussion

The automated phenotyping profiles were demonstrated to be simple, robust and rapid assays for the serological testing of Rh (CcEe), K, C^w, M, N, Fy^a, Fy^b, Jk^a, Jk^b, S, s and k antigens, suitable for use in routine hospital transfusion service laboratories. Weakly positive reactions in the automated assay (reactions strengths between 1+ and 2+) were suggestive of false positive results and so the assay was amended to exclude these reactions strengths from being reported as positive.

Only one discrepancy was identified during comparative testing of patient samples; N antigen testing of one patient sample gave repeatedly positive results in the manual test and negative results in the automated test. It was initially thought that this may have been caused by the automated reagent having cross reactivity with the "N" antigen. The anti-N reagent used in manual typing for the comparative study was a murine monoclonal IgG reagent (Millipore (UK) Ltd), which is stated not to react with the "N" antigen, when used by the recommended tube technique. The anti-N used in the automated typing was also a murine monoclonal reagent (immuClone), licensed for use in tube and slide techniques and was also stated not to have "N" reactivity. Consequently, the discrepancy between the Millipore and immuClone anti-N reagent reactivity with this one patient sample was discounted as being the result of cross reactivity with the "N" antigen in the manual tube technique, since both suppliers clearly state that there is no "N" reactivity with their reagents. Anecdotal

evidence suggested that the strength of reactivity of the anti-N reagent in the automated profile (verbal correspondence) may be dependent on the age of the sample at testing and/or the temperature of the reagents. The manufacturer of the immuClone anti-N used in the automated technique (Immucor Gamma) stated in the product insert that Ethylenediamine Tetraacetic Acid (EDTA) samples may be tested up to 14 days from collection, or until the expiry of the anticoagulant, if stored at 2 – 8°C. This particular sample was first tested at day 11, then at days 18 and 43. Review of the reaction strengths with the anti-N reagent revealed that the reactivity reduced from a score of 22 at day 11, 17 at day 18 and 14 at day 43, all giving negative qualitative results but noticeably reducing with age of sample. A stability study was then initiated to investigate this theory. It was felt that if stability of sample was an issue with anti-N testing, then this was most likely to affect heterozygous expression of the N antigen (M+N+ patients). Consequently, the stability study included 10 samples showing heterozygous expression (M+N+) and two samples showing homozygous expression (M+N-). These samples were tested daily for up to 10 days to determine a cut-off point for sample testing. The stability study demonstrated that, as a general rule, the reaction strength with N heterozygous cells would reduce to a negative value by day 7, and that to achieve the acceptable 3+ or 4+ reaction strength samples should be tested within three days of collection. In addition, it was also suggested (verbal correspondence) that the temperature of the reagents during testing may affect the reaction strengths. To test this effect, the stability study was also designed to compare the reaction strengths of the

anti-N using reagents taken directly from refrigerated storage 2 – 8°C, with the reaction strengths using reagents that had reached room temperature. The comparison of the reaction strength between the two groups showed no significant difference, indicating that temperature of the reagents does not affect the strength of the reaction.

The reason for the reduction in reaction strength of the anti-N (immuClone) is not clear, and would appear not to affect all N heterozygous cells, since one M+N+ cell remained strongly positive at day 10. The fact that the nine M+N+ cells, that gave negative results in the automated testing at day 10, still remained strongly N positive when tested with the anti-N (Millipore) reagent in manual testing, suggests that the N antigen itself is not affected by storage. Both the ImmuClone and the Millipore reagents are murine monoclonal reagents, and are from different clone lines. However, this difference was not thought to affect the reaction strength, since the ImmuClone reagent was found to give a strong positive reaction in the tube technique with the original discrepant sample. The reduction in reaction strength, seen with the automated technique over time, is possibly due to the centrifugal forces applied by the automated analyser, or the forces applied during the shaking step prior to result analysis. Although this validation demonstrated that the immuClone anti-N reagent is suitable for use in automated techniques, samples must be tested within 3 days of collection to minimise the risk of false negative results.

Automated assays are considerably cheaper than manual assays, mainly due to the reduction in staff time required for preparing and reading the assays. In addition, reactions in the automated assay are graded by the analyser in accordance with a computer generated algorithm, in contrast to the macroscopic, human eye, reading of reactions strengths in the manual assay which may be subject to discrepancies between individual staff. Thus, the automated assay has the potential to standardise results and reduce the risk of mis-interpretation.

This validation confirmed the fact that serological phenotyping assays are prone to false positive results in the presence of transfused cells and positive DAT. As reported here, measures can be implemented to reduce the risk of reporting false negative results in the presence of a positive DAT, but challenges will inevitably remain in the presence of circulating, transfused red cells. Genotyping assays overcome the limitations of the serological assays by testing genetic material extracted from white blood cells in the patient sample. The red cell phenotype is then predicted from the genotype. Thus, genotyping assays are useful when attempting to antigen type regularly transfused patients and those with positive DAT. The following chapter aims to assess the feasibility of DNA based assays for use in a hospital transfusion service setting, and to compare phenotypes predicted by genotyping with those found in the automated serological assay.

5 BLOOD GROUP GENOTYPING

5.1 Introduction

For patients undergoing multiple transfusions, serological phenotyping can be complicated by the presence of transfused cells within the circulation (BCSH, 2013). A definitive determination of the red cell phenotype of the patient is not possible whilst donor cells are still present in the circulation, and this makes it difficult to determine whether any antibodies detected are alloantibodies (reacting against the donor cells) or autoantibodies (reacting against the patient's own cells). This, in turn, leads to difficulties with selection of appropriate antigen matched blood for subsequent transfusions. Serological phenotyping can also be further complicated by the presence of antibodies bound to antigens on the surface of the red cells, which can lead to false positive results, if using polyclonal antisera. The benefits of genotyping techniques have already been shown in the determination of blood groups in multiply-transfused patients (Guelsin *et al.,* 2010), as red cells (transfused or recipient) do not carry DNA, only the DNA from recipient white cells is analysed. Blood components in the UK are leucocyte depleted, the small amounts of white cell DNA transferred to the recipient during transfusion does not interfere with the genotyping results, and even if transfusions of non-white cell depleted units are given this does not appear to interfere (Rozman *et al.,* 2000).

Advances in gene cloning and sequencing of blood group genes have determined the molecular basis for almost all of the clinically significant blood group polymorphisms (Daniels, 2013). The majority of genetically defined blood group antigens are the result of single-nucleotide polymorphism (SNP) (Castilho and Junior, 2004) which give rise to the amino acid changes described in section 1.3.2, and determine the antigenic phenotype. It is this knowledge that enables the use of DNA based assays, which detect these SNPs, to ascertain the allelic variations and predict the blood group antigens expressed on the surface of the red cells. Information regarding the blood group systems, genotype and allelic variations that make up the antigens of the various blood group systems can be found in the ISBT blood group alleles database and the Erythrogene database (Möller *et al.*, 2016).

DNA techniques have also been shown to have a high concordance rate with serological phenotyping techniques in blood donor and patient samples (Karpasitou *et al.,* 2008), although limitations are seen with null and/or weak phenotypes, which may be detected only by serological techniques (Drago *et al.,* 2010). Knowledge of the molecular basis of null phenotypes and weakened expression of antigens on the red cells allows the inclusion of assays into the red cell antigen genotyping profiles designed to detect the mutations silencing the expression of the antigen. This allows the genotyping results to predict the red cell antigen phenotype with a greater level of accuracy, as the presence of the gene does not always lead to the presence of the antigen on the surface of the

red cell. The IDCOREXT assay, evaluated in this study, includes probes designed to detect the SNPs responsible for null phenotypes in the Kidd, Duffy and MNS blood group systems, thus reducing the potential for incorrect prediction of the presence of the red cell antigens. This study aimed to evaluate the applicability of this assay in a routine hospital transfusion service setting, as yet untested in the UK.

The following subsections will focus on the genetic basis of the blood group antigens predicted by the BLOODChip IDCOREXT assay, table 5.1 contains a summary of the blood group systems, genes, alleles, nucleotide changes associated with the allelic variations and the predicted amino acid changes included in the assay. The antigenic phenotypes predicted by the alleles assayed by the IDCOREXT test are shown in table 5-2. The IDCOREXT test (Progenika Biopharma S.A.) can be used to type allelic variants which determine the blood group antigens tested in the serological phenotyping section of this study (Rh (CcEe), C^w, Kell (K and k), Kidd (Jk^a and Jk^b), Duffy (Fy^a and Fy^b), M, N, S and s), and also includes those of other blood group systems (Diego, Dombrock, Colton, Yt and Lutheran systems). Information regarding the biochemistry, genetic basis and function of the blood group systems are detailed in section 1.3.2.

Table 5.1: Blood group system alleles detected by the BLOODChip ID CORE^{XT} assay

Blood group systems in the Erythrogene database and ISBT Blood Group Alleles showing the system name, gene, allele, nucleotide change and predicted amino acid change for the blood group antigen phenotypes predicted by the BLOODChip IDCOREXT assay Key: NA = not available in ISBT database

System name	Gene	Allele (ISBT)	Nucleotide change	Predicted amino acid change
Rh	*RHCE*	*RHCE*01 (RHCE*ce)*	Wild type reference	*Wild type reference*
		*RHCE*02 (RHCE*Ce)*	*48G>C 178C>T 203A>G 307C>T*	*Trp16Cys Leu60Ile Asn68ser Pro103Ser*
		*RHCE*03 (RHCE*cE)*	*676G>C*	*Ala226Pro*
		*RHCE*04 (RHCE*CE)*	*48G>C 150C>T 178C>A 201A>G 203A>G 307C>T 676G>C*	*Trp16Cys Leu60Ile Asn68ser Pro103Ser Ala226Pro*
		*RHCE*CeCW*	*122A>G*	*Gln41Arg*
		*RHCE*ceCW*	NA	*NA*
		*RHCE*CECW*	*NA*	*NA*
		*RHCE*ceAR*	*48G>C 712A>G 733C>G 787A>G 800T>A 916A>G*	*Trp16Cys Met238Val Leu245Val Arg263Gly Met267Lys Ile306Val*
		*RHCE*CeFV*	*667G>T 697C>G 712A>G*	*Val223Phe Gil233Glu Met238Val*
		*RHCE*CeVG*	*712A>G 733C>G 787A >G*	*Met238Val Leu245Val Arg263Gly*

System name (cont.)	Gene (cont.)	Allele (ISBT) (cont.)	Nucleotide change (cont.)	Predicted amino acid change (cont.)
Rh		*RHCE*cEFM*	*697C>G 712A>G*	*Gln233Glu Met238Val*
		*RHCE*ce[712G]*	*712A>G*	*Met238Val*
		*RHCE*ce[733G]*	*733C>G*	*Leu245Val*
		*RHCE*ce[733G,1006T]*	*733C>G 1006G>T*	*Leu245Val Gly336Cys*
		*RHCE*CE-D[2, 5, 7]-CE*	*307 676 712 733 1006†*	*NA*
		*RHCE*cE[697G,712G,733G]*	*697C>G 712A>G 733C>G*	*Gln233Glu Met238Val Leu245Val*
		*RHD*r's-RHCE*ce[733G,1006T]*	*IVS3+3100G 733C>G 1006G>T*	*Leu245Val Gly336Cys*
Kell	*KEL*	*KEL*k_KPB_JSB*	578C>T	Thr193Met
		*KEL*K_KPB_JSB*	Wild type reference	Wild type reference
		*KEL*k_KPA_JSB*	841C>T	Arg281Trp
		*KEL*k_KPB_JSA*	1790T>C	Leu597Pro

System name (cont.)	Gene (cont.)	Allele (ISBT) (cont.)	Nucleotide change (cont.)	Predicted amino acid change (cont.)
Kidd	*SLC14A1*	*JK*02 (JK*B)* *JK*01(JK*A)* *JK*B_null(871C)* *JK*B_null(IVS5-1a)*	Wild type reference 838A>G 871T>C 1G>A in intron 5	Wild type reference Asn280Asp Ser291Pro NA
Duffy	*DARC*	*FY*A;* *FY*B* *FY*B_GATA* *FY*B[265T]_FY*X*	125A>G Wild type reference -67T>C 265C>T	Asp42Gly Wild type reference NA Arg89Cys

System name (cont.)	Gene (cont.)	Allele (ISBT) (cont.)	Nucleotide change (cont.)	Predicted amino acid change (cont.)
MNS	*GYPA*	*GYPA*M*	Wild type reference	Wild type reference
	GYPB	*GYPA*N*	59C>T 71G>A 72T>G	Ser20Leu Gly24Glu
	GYPE			
		*GYPB*s*	Wild type reference	Wild type reference
		*GYPB*S*	143C>T	Thr48Met
		*GYPB*Mur*	*GYP(B1-136-Bψ137-204-A205-229-B230-366).*	NA
		*GYPB*deletion*	Deletion of whole gene	NA
		*GYPB*S_null(230T)*	230C>T	Thr77Met
		*GYPB*S_null(IVS5+5t)*	270+5G>T	Alternative splicing

System name (cont.)	Gene (cont.)	Allele (ISBT) (cont.)	Nucleotide change (cont.)	Predicted amino acid change (cont.)
Diego	*SLC4A1*	*DI*A* *DI*B*	2561C>T Wildtype reference	Pro854Leu Wild type reference
Dombrock	*ART4*	*DO*A* *DO*B* *DO*B_HY* *DO*A_JO*	Wild type reference 793A>G 232G>T 350C>Y	Wild type reference Asn265Asp Gly108Val Thr117Ile
Colton	*AQP1*	*CO*A* *CO*B*	Wild type reference 134C>T	Wild type reference Ala45Val
Yt (Cartwright)	*ACHE*	*YT*A* *YT*B*	Wild type reference 1057C>A	Wild type reference His353Asn
Lutheran	*LU*	*LU*A* *LU*B*	230G>A Wildtype reference	Arg77His Wild type reference

5.1.1 Rh system CcEe

RHCE encoding the various Rh (CcEe) polymorphisms is located on the short arm of chromosome 1 (Avent *et al.,* 1990; Cherif-Zahar *et al.,* 1990). The IDCOREXT assay includes probes for the common alleles encoding the C, c, E, e and C^{w} antigens. The alleles at the locus include *RHCE*01* (*RHCE*ce*), in which "c" is represented by 307C in exon 2 and "e" which is associated with 676G in exon 5. *RHCE*C* is represented by 307T in exon 2 and *RHCE*E* by 676C in exon 5. All the *RHCE* amplicons included within the IDCOREXT kit are gene-specific and so no amplification of *RHD* is expected. The C^{W} antigen is produced as a result of a single nucleotide change in exon 1 (122A>G) and is usually associated with *RHCE*Ce* (Mouro *et al*., 1995). Rarely, C^{w} is associated with *RHCE*ce* and *RHCE*CE,* the IDCOREXT assays includes probes designed to detect the nucleotide change associated with all of these alleles. Rh_{null} phenotypes are identified as a result of no amplifications of exons 5 and 7 of *RHCE*.

Additional alleles assayed within the IDCOREXT test in the Rh system include those that code for the rare V and VS antigens. VS is associated with a single nucleotide change 733C>G in exon 5 of *RHCE*ce* (Daniels, 2013). The IDCOREXT assay includes probes designed to detect the VS+V+ phenotype and the VS+V- phenotype (733C>G and 1006G>T).

The hrS and hrB antigens are associated with partial e (Shapiro, 1960; Shapiro *et al.*, 1972). These antigens are important as they may be lacking in some black populations, individuals may type serologically as e+ but make apparent anti-e. Accurate identification of individuals with these variant antigens is of relevance in the transfusion of patients with SCD (Chou and Westhoff, 2009). Allelic probes designed to detect the presence of these SNPs representing these phenotypes are also included in the IDCOREXT.

5.1.2 Kell system

KEL encoding the Kell antigens is located on chromosome 7 (7q33) (Zelinski *et al.,* 1991; Purohit *et al.,* 1992; Lee *et al.,* 1993; Murphy *et al.,* 1993). The K/k polymorphism arises as a result of a nucleotide change, 578C>T, within exon 10 of the *KEL* gene, resulting in the *KEL*K* (ISBT *K*01.01)* and *KEL*k* (ISBT *K*02*) alleles. Additional alleles within the Kell system include those that code for the antithetical antigens Kp^a and Kp^b and Js^a and Js^b. Kp^a/Kp^b arises as a result of 841C>T substitution in exon 8 and Js^a/Js^b from a 1790T>C change in exon 17.

The Kell null phenotype can result from a variety of different genetic events (Reid, 2009) and so it is not feasible within the IDCOREXT assay to include probes designed to detect the phenotype.

5.1.3 Kidd system

The gene encoding the antigens of the Kidd system (*SLC14A1*) is located on chromosome 18 (18q11-q12) (Olives *et al.,* 1996). The Jk^a/Jk^b phenotype arises as a result of a nucleotide change 838G>A in exon 9, resulting in the *JK*A* (ISBT *JK*01*) and *JK*B* (ISBT *JK*02*) alleles.

The rare Jk null phenotype, Jk (a-b-), can be caused as a result of one of two silencing mutations; a splice mutation causing skipping of exon 6, *SLC14A1*:c.471-1G>A (Lucien *et al.,* 1998) or a T871C substitution predicted to disrupt a potential N-glycosylation motif (NSS→NSP), *SLC14A1*:c.871T>C (Sidoux-Walter *et al.,* 2000). The IDCOREXT assay contains a probes designed to detect both of these mutations.

5.1.4 Duffy system

DARC (ISBT nomenclature or HUGO gene name *ACKR1)* encoding the Duffy system antigens is located on chromosome 1 (1q21-q22) (Mathew *et al.,* 1994). The Fy^b/Fy^a polymorphism arises as a result of a nucleotide change, 125A>G, in exon 2.

Tournamille and co-workers (1995) have demonstrated that the Fy_{null} phenotype, Fy(a-b-), commonly seen in African populations, is a result of disruption of a *GATA* motif in the Fy gene promoter (*DARC*:c.-67T>C). In addition, a weakened expression of Fy^b phenotype, also known to cause discrepancies between genotyping and phenotyping results, (Murphy *et al.,* 1997) was later found to be caused by an Arg89Cys substitution

(Tournamille *et al.,* 1998), the result of a nucleotide change 265C>T in exon 2. The IDCOREXT assay includes probes designed to detect both of these changes.

5.1.5 MNS system

The genes encoding the MNS polymorphisms, *GYPA* and *GYPB*, are located on chromosome 4 (4q31.21) (Kudo and Fukuda, 1990). The third gene in the family, *GYPE*, does not encode detectable protein on the red cell surface, but has been shown to be involved in some gene rearrangements that do encode hybrid proteins (ISBT, 2017). The M/N polymorphism arises as a result of nucleotide changes, 59C>T, 71G>A and 72T>G in exon 2. The S/s polymorphism arises as a result of a single change, 143T>C in exon 4.

Within the MNS system the alleles assayed include the U antigen, an antigen associated with the S-s- phenotype (Wiener *et al*., 1954) and Mi^{a}, a low frequency antigen (Levine *et al*., 1951). Mur and Mi^{a} antigens arise as a result of hybrid glycophorins (B-A-B). The *GYPB*Mur* allele detected by the IDCOREXT assay is a novel sequence derived from the composite exon; *GYPB* 5' pseudoexon 3 and *GYPA* 3' exon 3. The nucleotide change associated with this phenotype is *GYP(B1-136-Bψ137-204-A205-229-B230-366).*

The S-s-U- phenotype occurs as a result of Glycophorin B deficiency (Huang *et al.,* 1987; Rahuel *et al.,* 1991), the IDCOREXT assay includes

detection of the *GYPB*deletion* which gives rise to the S-s-U- phenotype. The S-s-Uvar (weakened expression of the U antigen) is associated with a variant Glycophorin B protein that expresses a red cell antigen known as the He antigen (Huang *et al.,* 1994; Huang *et al.,* 1995; Reid *et al.,* 1996; Huang *et al.,* 1997; Storry *et al.,* 2003). The S-s- phenotype can also rise as a result of mutations within *GYPB*, commonly within intron 5 or caused by a nucleotide change 230C>T substitution. Probes designed to identify both of these are included in the IDCOREXT assay; GYPB:c. 230C>T and GYPB:c. 270+5G>T.

5.1.6 Diego system

The Diego system antigens include three pairs of antithetical antigens; Di^a and Di^b, Wr^a and Wr^b, Wu and DISK and encoded by the gene *SLC4A1* on chromosome 7 (7q12-q21) (Schofield *et al.,* 1994). The Di^a/Di^b polymorphism arises as a result of a nucleotide change 2561T>C in exon 19. The IDCOREXT test includes an assay for the alleles that encode the Di^a and Di^b antigens, *DI*A* (ISBT *DI*01*) and *DI*B* (ISBT *DI*02)*.

5.1.7 Dombrock system

The Dombrock system antigens are encoded by the gene *ART4* gene located on chromosome 12 (12p13.2-12.3) (Eiberg and Mohr, 1996; Mauthe *et al.,* 2000); the assay tests for alleles that encode four of these antigens (Do^a, Do^b, Hy and Jo^a). The Do^a/Do^b polymorphism arises from a single nucleotide change, 793A>G in exon 2, resulting in the *DO*A*

(ISBT *DO*01*) and *DO*B* (ISBT *DO*02*) alleles. Hy is represented by 323G in exon 2 of *DO*B* and Jo^a by 350C in exon 2 of *DO*A*.

5.1.8 Colton system

The Colton blood group system consists of four antigens (Co^a, Co^b, Co3 and Co4), the gene encoding these antigens, *AQP1*, is located on chromosome 7 (7p14) (Moon *et al.,* 1993).. The Co^a/Co^b polymorphism arise from a single nucleotide change 134C>T in exon 1. The IDCOREXT assay includes probes designed to identify the alleles, *CO*A* and C*O*B*, responsible for the expression of the Co^a and Co^b phenotypes.

Although Co_{null} phenotypes exist, and some are represented by single nucleotide changes, they are rare and are not included in the IDCOREXT assay.

5.1.9 Yt system

The antigens of the Yt (previously known as Cartwright) system are encoded by the gene, *ACHE*, located on chromosome 7 (7q22) (Getman *et al.,* 1992; Ehrlich *et al.,* 1992). The Yt^a/Yt^b polymorphism results from the nucleotide change, 1057C>A, in exon 2, giving rise to the *YT*A* (ISBT *YT*01*) and *YT*B* (ISBT *YT*03)* alleles. The allele responsible for the high frequency YTEG antigen, *YT*03*, is the result of a nucleotide changes, 266G>A in exon 2.

5.1.10 Lutheran system

The Lutheran blood group system includes 22 antigens; however the IDCOREXT assay includes allelic tests for just two of these antigens (Lu^a and Lu^b). The gene that encodes the antigens of the Lutheran blood group, *LU*, system is located on chromosome 19 (19q12-q13) (Parsons *et al.,* 1997; El Nemer *et al.,* 1997). The Lu^a/Lu^b polymorphism results from a single nucleotide change, 230A>G, in exon 3, resulting in the alleles, *LU*A* (ISBT *LU*01*) and *LU*B* (ISBT *LU*02)*. The Lu_{null} phenotype is extremely rare and, as such, identification is not included in the IDCOREXT assay.

Table 5.2: The red cell antigen types determined by the IDCOREXT assay.

The IDCOREXT assay uses PCR amplification to obtain target sequences for alleles encoding red cell antigens from human blood samples. The human blood group systems and the alleles assayed by the test are shown in the table below, also shown are the red cell antigen types as denoted by their International Society of Blood Transfusion (ISBT) phenotype name.

Blood Group System	**Alleles Assayed**	**Antigens (ISBT Phenotype)**
Rh	*RHCE*ce;* *RHCE*Ce* *RHCE*cE;* *RHCE*CE* *RHCE*CeCW* *RHCE*ceCW* *RHCE*CECW* *RHCE*ceAR* *RHCE*CeFV* *RHCE*CeVG* *RHCE*cEFM* *RHCE*ce[712G]* *RHCE*ce[733G]* *RHCE*ce[733G,1006T]* *RHCE*CE-D[2, 5, 7]-CE* *RHCE*cE[697G,712G,733G]* *RHD*r's-RHCE*ce[733G,1006T]*	C (RH:2) E (RH:3) c (RH:4) e (RH:5) CW (RH:8) V (RH:10) hrS (RH:19) VS (RH:20) hrB (RH:31)
Kell	*KEL*K_KPB_JSB* *KEL*k_KPB_JSB* *KEL*k_KPA_JSB* *KEL*k_KPB_JSA*	K (KEL:1) k (KEL:2) Kpa (KEL:3) Kpb (KEL:4) Jsa (KEL:6) Jsb (KEL:7)

Blood Group System	Alleles Assayed	Antigens (continued) (ISBT Phenotype)
Kidd	*JK*A* *JK*B* *JK*B_null(871C)* *JK*B_null(IVS5-1a)*	Jka (JK:1) Jkb (JK:2)
Duffy	*FY*A;* *FY*B* *FY*B_GATA* *FY*B[265T]_FY*X*	Fya (FY:1) Fyb (FY:2)
MNS	*GYPA*M* *GYPA*N* *GYPB*s* *GYPB*S* *GYPB*Mur* *GYPB*deletion* *GYPB*S_null(230T)* *GYPB*S_null(IVS5+5t)*	S (MNS:3) s (MNS:4) U (MNS:5) Mia (MNS:7) M (MNS:1) N (MNS:2)
Diego	*DI*A* *DI*B*	Dia (DI:1) Dib (DI:2)
Dombrock	*DO*A* *DO*B* *DO*B_HY* *DO*A_JO*	Doa (DO:1) Dob (DO:2) Hy (DO:4) Joa (DO:5)
Colton	*CO*A* *CO*B*	Coa (CO:1) Cob (CO:2)
Cartwright	*YT*A* *YT*B*	Yta (YT:1) Ytb (YT:2)
Lutheran	LU*A LU*B	Lua (LU:1) Lua (LU:2)

5.2 Study design

The IDCOREXT test allows a simultaneous multiplex reaction in a single well avoiding the need for running multiple separate methods in parallel. The results obtained from the Luminex xMAP technology are then processed using the IDCOREXT analysis software, converting the alleles detected into a genotype result which is then, in turn, used to predict the phenotype for each of the allelic variants interrogated by the test (see section 1.7).

This study aimed to evaluate the IDCOREXT test for potential use as a high throughput genotyping method suitable for the hospital transfusion setting. In addition, this study aimed to compare the red cell phenotyping results obtained from blood samples taken from a selection of the patients consented from the Haematology Clinic and tested on the automated phenotyping platform, with the genotyping results obtained by the IDCOREXT test using DNA extracted from the same patient samples.

5.3 Results

5.3.1 DNA extraction

The concentration of DNA extracted from the whole blood samples (n=47) ranged from 6.03ng/µL to 812 ng/µL, the average concentration was 184.75 ng/µL (SD 180.63) (table 5-3). The DNA concentration recommended for use in the IDCOREXT assay was between 10 ng/µL and 80 ng/µL, hence, one sample was below the recommended level.

Table 5.3: Concentration and quantity of DNA extracted from whole blood samples

DNA was extracted from whole blood samples taken from 47 patients for genotyping using the IDCOREXT assay. The concentration of DNA ranged from 6.03ng/μL to 812 ng/μL.

Patient number	DNA concentration (ng/μL)	DNA quantity
1	45.74	100
2	26.17	100
3	104.8	300
4	25.58	300
5	195.1	300
6	175	300
7	300.4	300
8	6.03	300
9	271.7	300
10	812	300
11	266.1	300
12	137.7	300
13	797	300
14	45.97	300
15	80.03	100
16	64.55	300
17	28.13	100
18	397	300
19	82.78	300
20	28.78	300
21	437.6	300
22	411	300
23	182.7	300
24	25.12	300
25	130.7	300
26	96.24	300
27	215.6	300
28	95.69	300
29	24.3	300
30	185.9	300
31	111.2	300
32	71.69	300
33	300.1	300
34	121.3	300
35	129.9	300
36	297.2	300
37	349.4	300
38	516.2	300
39	168.7	300
40	47.32	300
41	108.4	300
42	134.8	300
43	43.33	300
44	124.3	300
45	258.1	300
46	76.06	300
47	130	300

5.3.2 Cost of testing

Test costs were calculated for the red cell antigen genotyping system. Staff costs were calculated at Band 5 (Agenda for Change, NHS pay scale 2015) pay point 20 and reagent costs were calculated at supplier cost 2014-2015 (excluding VAT). Costs for the relevant equipment maintenance cost per patient test were estimated, based on the number of patients registered as attending the Haematology or Renal wards for transfusion at the RD&E per year, and assuming that every patient would require a blood group genotype. True cost per test for the analyser maintenance could not be calculated as the system is not in use in our institution; however, estimated costs were calculated based on the supplier quotation. However, this may lead to over representation of the cost as the analyser system can also be used by other specialities, such as microbiology and immunology, therefore not restricted to blood group genotyping and, thus increasing the total throughput per year. Internal quality control costs were also included in the cost of the consumables. The total cost per patient test was estimated to be £73.66 (table 5-4).

Table 5.4: Cost of Blood Group genotyping

The cost per test was estimated for blood group genotyping using the IDCOREXT test. All costs shown in this table are cost per patient sample tested. Staff time costs were estimated assuming that the testing and reporting of results would be performed by a band 5 Biomedical Scientist. Equipment maintenance costs were based on an assumption that all patients admitted for transfusion on the haematology and renal wards would require a blood group genotype test (n=1674 for the financial year 2014-2015).

DNA extraction (£)	IDCOREXT + kit (£)	Consumables (£)	Equipment (£)	Staff time (£)	Total cost per patient sample (£)
8.95	45.00	1.50	0.87	17.34	**73.66**

5.3.3 Comparison of phenotyping and genotyping results

DNA extracted from 47 patients was analysed for the presence of known blood group SNPs on the Luminex XMAP analyser using the IDCOREXT kit. Whole blood samples from each of these 47 patients had previously been analysed for serological phenotype using the automated phenotyping method (IBG Immucor) to allow comparison of the phenotyping result with the predicted phenotype generated by the genotyping result. The IDCOREXT contains assays for 49 different alleles that are used by the software to predict 37 red cell phenotypes. The report produced by the software details the blood group system, the alleles assayed within that system, along with the genotype result, the corresponding red cell antigen with their ISBT phenotype notation and the predicted phenotype (figure 5.2). The predicted phenotype, as interpreted by the software, was then used for direct comparison with the phenotypes reported by the automated serological phenotyping assay. The raw data obtained from the IDCOREXT assay are detailed in Appendix 4.

Figure 5.1: DNA analysis report generated by the Luminex XMAP analyser

An example of the report generated by the Luminex XMAP analyser for each sample of DNA processed. The alleles assayed for each blood group system are shown, along with the genotype result, the corresponding red cell antigen (ISBT Phenotype) and the predicted phenotype.

Kit lot number: 0201040015 **CSV file:** New Batch 6_20140515_111617.csv
Enzyme lot number: 123456789 **Plate location:** 1(1,A1)
Date: 5/15/2014 **Sample ID:** EX1311988
Software version: ID-CORE XT ANALYSIS SOFTWARE v1.4.1

Blood Group System	Alleles Assayed	Genotype Result	Antigens (ISBT Phenotype)	Predicted Phenotype Result
Rh	RHCE*ce RHCE*Ce RHCE*cE RHCE*CE RHCE*CeCW RHCE*ceCW RHCE*CECW RHCE*ceAR RHCE*CeFV RHCE*CeVG RHCE*cEFM RHCE*ce[712G] RHCE*ce[733G] RHCE*ce[733G,1006T] RHCE*CE-D[2, 5, 7]-CE RHCE*cE[697G,712G,733G] RHD*r's-RHCE*ce[733G,1006T]	RHCE*ce, RHCE*Ce	C (RH:2) E (RH:3) c (RH:4) e (RH:5) CW (RH:8) V (RH:10) hrS (RH:19) VS (RH:20) hrB (RH:31)	+ 0 + + 0 0 + 0 +
Kell	KEL*K_KPB_JSB KEL*k_KPB_JSB KEL*k_KPA_JSB KEL*k_KPB_JSA	KEL*K_KPB_JSB, KEL*k_KPB_JSB	K (KEL:1) k (KEL:2) Kpa (KEL:3) Kpb (KEL:4) Jsa (KEL:6) Jsb (KEL:7)	+ + 0 + 0 +
Kidd	JK*A JK*B JK*B_null(IVS5-1a) JK*B_null(871C)	JK*A, JK*B	Jka (JK:1) Jkb (JK:2)	+ +
Duffy	FY*A FY*B FY*B_GATA FY*B[265T]_FY*X	FY*B	Fya (FY:1) Fyb (FY:2)	0 +
MNS	GYPA*M GYPA*N	GYPA*M, GYPA*N	M (MNS:1) N (MNS:2)	+ +
	GYPB*S GYPB*s GYPB*S_null(IVS5+5t) GYPB*S_null(230T) GYPB*deletion GYPB*Mur	GYPB*S, GYPB*s	S (MNS:3) s (MNS:4) U (MNS:5) Mia (MNS:7)	+ + + 0
Diego	DI*A DI*B	DI*B	Dia (DI:1) Dib (DI:2)	0 +
Dombrock	DO*A DO*B DO*B_HY- DO*A_JOA-	DO*B	Doa (DO:1) Dob (DO:2) Hy (DO:4) Joa (DO:5)	0 + + +
Colton	CO*A CO*B	CO*A	Coa (CO:1) Cob (CO:2)	+ 0
Cartwright	YT*A YT*B	YT*A	Yta (YT:1) Ytb (YT:2)	+ 0
Lutheran	LU*A LU*B	LU*B	Lua (LU:1) Lub (LU:2)	0 +

No failures of testing were encountered and there were no discrepancies seen in the serological phenotyping and genotyping for Rh (CcEeCw), K, k, N, Fy (a and b), Jk (a and b), S and s. One discrepancy was seen in the M antigen status for one patient (EX1300853), this patient typed as M+ in serological phenotyping assays but produced an M- genotype (discussed further in section 5.4). One patient (EX1312673) returned a “not determined” result for the S antigen in the automated serological assay. A repeat sample could not be obtained from the patient within the time frame of the study, due to the death of the patient, but further review of the serological assay reaction value (21) showed the result to be just above a negative value (20.998 value for the cut off high) (see result interpretation cut off values in appendix 3). Therefore, the serological phenotyping result was suggestive of a negative result, in agreement with the genotyping predicted phenotype result. Full results of the comparison of the genotyping assay and the automated phenotyping assay can be seen in Table 5-5.

Comparison of serological phenotype and genotype for some antigens predicted by the IDCOREXT assay could not be performed as there were no serological phenotypes performed, these include the antigens V, hrS, Vs and hrB of the Rh system, Kp^a, Kp^b, Js^a and Js^b of the Kell system, U and Mia of the MNS system, and antigens of the Diego, Dombrock, Colton, Cartwright and Lutheran system.

Table 5.5: Antigen phenotypes by serological analysis and genotyping

Results obtained by serological phenotyping for the 47 selected patient samples are shown in black type and those predicted by genotyping are shown in red type.

A single discrepancy was seen for the M antigen type for patient EX1300853 which is highlighted in yellow.

S antigen status for patient EX1312673 was not determined by serological phenotyping methods due to undetermined consistently weak positive reactions (highlighted in yellow)

Key: P = positive result
N = negative result
ND = not determined

	Red cell antigens assayed														
Sample No	**C**	**c**	**E**	**e**	**Cw**	**K**	**Fya**	**Fyb**	**Jka**	**Jkb**	**S**	**s**	**M**	**N**	**k**
EX1305814	P	P	N	P	N	P	P	P	P	N	N	P	P	N	P
	P	P	N	P	N	P	P	P	P	N	N	P	P	N	P
EX1305816	N	P	P	P	N	N	N	P	N	P	P	P	P	N	P
	N	P	P	P	N	N	N	P	N	P	P	P	P	N	P
EX1305815	N	P	P	N	N	N	P	N	P	N	N	P	N	P	P
	N	P	P	N	N	N	P	N	P	N	N	P	N	P	P
EX1305817	N	P	P	P	N	N	P	N	P	P	P	P	P	P	P
	N	P	P	P	N	N	P	N	P	P	P	P	P	P	P
EX1300853	N	P	P	N	N	N	P	P	P	P	N	P	P	P	P
	N	P	P	N	N	N	P	P	P	P	N	P	N	P	P

	Red cell antigens assayed (continued)													
Sample No	**C**	**c**	**E**	**e**	**Cw**	**K**	**Fya**	**Fyb**	**Jka**	**Jkb**	**S**	**s**	**M**	**N**	**k**
EX1300854	N	P	P	P	N	N	P	P	P	P	P	P	P	N	P
	N	P	P	P	N	N	P	P	P	P	P	P	P	N	P
EX1303174	N	P	P	N	N	N	P	P	N	P	N	P	P	P	P
	N	P	P	N	N	N	P	P	N	P	N	P	P	P	P
EX1306850	P	N	N	P	N	N	P	N	P	P	P	P	P	P	P
	P	N	N	P	N	N	P	N	P	P	P	P	P	P	P
EX1307336	P	P	P	P	N	N	N	P	P	N	P	N	P	P	P
	P	P	P	P	N	N	N	P	P	N	P	N	P	P	P
EX1307335	P	N	N	P	N	N	N	P	P	P	P	P	P	P	P
	P	N	N	P	N	N	N	P	P	P	P	P	P	P	P
EX1307657	P	N	N	P	N	N	P	P	P	P	N	P	P	N	P
	P	N	N	P	N	N	P	P	P	P	N	P	P	N	P
EX1307898	N	P	N	P	N	N	N	P	P	N	N	P	P	P	P
	N	P	N	P	N	N	N	P	P	N	N	P	P	P	P
EX1307899	N	P	P	P	N	P	P	P	P	P	P	P	P	P	P
	N	P	P	P	N	P	P	P	P	P	P	P	P	P	P
EX1308240	N	P	N	P	N	N	P	P	P	N	N	P	N	P	P
	N	P	N	P	N	N	P	P	P	N	N	P	N	P	P
EX1308368	P	P	N	P	N	N	P	N	P	P	N	P	P	N	P
	P	P	N	P	N	N	P	N	P	P	N	P	P	N	P
EX1308578	N	P	P	P	N	N	P	P	P	P	N	P	P	P	P
	N	P	P	P	N	N	P	P	P	P	N	P	P	P	P
EX1308762	P	N	N	P	N	N	N	P	P	N	P	P	P	N	P
	P	N	N	P	N	N	N	P	P	N	P	P	P	N	P

	Red cell antigens assayed (continued)													
Sample No	**C**	**c**	**E**	**e**	**Cw**	**K**	**Fya**	**Fyb**	**Jka**	**Jkb**	**S**	**s**	**M**	**N**	**k**
EX1308909	P	P	P	P	N	N	P	P	P	N	N	P	P	P	P
	P	P	P	P	N	N	P	P	P	N	N	P	P	P	P
EX1308908	N	P	N	P	N	N	P	N	P	N	P	P	P	P	P
	N	P	N	P	N	N	P	N	P	N	P	P	P	P	P
EX1308959	P	P	N	P	N	N	N	P	N	P	N	P	P	P	P
	P	P	N	P	N	N	N	P	N	P	N	P	P	P	P
EX1311437	P	N	N	P	P	N	N	P	N	P	N	P	P	N	P
	P	N	N	P	P	N	N	P	N	P	N	P	P	N	P
EX1311438	N	P	P	P	N	N	P	P	P	P	P	N	P	N	P
	N	P	P	P	N	N	P	P	P	P	P	N	P	N	P
EX1311988	P	P	N	P	N	P	N	P	P	P	P	P	P	P	P
	P	P	N	P	N	P	N	P	P	P	P	P	P	P	P
EX1311987	P	P	P	P	N	N	N	P	P	P	P	P	P	P	P
	P	P	P	P	N	N	N	P	P	P	P	P	P	P	P
EX1311986	P	P	P	P	N	N	P	P	P	N	P	P	P	P	P
	P	P	P	P	N	N	P	P	P	N	P	P	P	P	P
EX1311989	P	P	N	P	N	N	P	P	P	P	P	P	P	N	P
	P	P	N	P	N	N	P	P	P	P	P	P	P	N	P
EX1312296	P	P	N	P	N	N	P	N	P	N	N	P	P	N	P
	P	P	N	P	N	N	P	N	P	N	N	P	P	N	P
EX1312295	P	P	N	P	N	N	N	P	N	P	P	P	P	N	P
	P	P	N	P	N	N	N	P	N	P	P	P	P	N	P
EX1312294	N	P	N	P	N	N	P	P	P	P	N	P	P	N	P
	N	P	N	P	N	N	P	P	P	P	N	P	P	N	P

	Red cell antigens assayed (continued)														
Sample No	**C**	**c**	**E**	**e**	**Cw**	**K**	**Fya**	**Fyb**	**Jka**	**Jkb**	**S**	**s**	**M**	**N**	**k**
EX1312297	P	P	N	P	N	P	N	P	P	N	N	P	P	P	P
	P	P	N	P	N	P	N	P	P	N	N	P	P	P	P
EX1312311	P	P	N	P	N	N	N	P	N	P	N	P	N	P	P
	P	P	N	P	N	N	N	P	N	P	N	P	N	P	P
EX1312312	P	N	N	P	N	N	N	P	P	P	N	P	P	P	P
	P	N	N	P	N	N	N	P	P	P	N	P	P	P	P
EX1312453	N	P	P	P	N	N	N	P	P	P	P	N	P	N	P
	N	P	P	P	N	N	N	P	P	P	P	N	P	N	P
EX1312674	P	N	N	P	N	N	P	N	P	P	N	P	P	P	P
	P	N	N	P	N	N	P	N	P	P	N	P	P	P	P
EX1312673	P	P	N	P	N	N	N	P	P	P	ND	P	P	P	P
	P	P	N	P	N	N	N	P	P	P	N	P	P	P	P
EX1312675	P	N	N	P	P	N	N	P	N	P	N	P	N	P	P
	P	N	N	P	P	N	N	P	N	P	N	P	N	P	P
EX1312967	N	P	P	P	N	N	N	P	N	P	P	P	P	P	P
	N	P	P	P	N	N	N	P	N	P	P	P	P	P	P
EX1313154	P	P	N	P	N	N	P	P	N	P	P	N	P	N	P
	P	P	N	P	N	N	P	P	N	P	P	N	P	N	P
EX1313155	N	P	P	P	N	N	P	N	N	P	N	P	N	P	P
	N	P	P	P	N	N	P	N	N	P	N	P	N	P	P
EX1313515	N	P	P	N	N	N	N	P	P	N	P	P	N	P	P
	N	P	P	N	N	N	N	P	P	N	P	P	N	P	P
EX1313516	P	P	N	P	P	N	P	P	P	N	N	P	P	N	P
	P	P	N	P	P	N	P	P	P	N	N	P	P	N	P

	Red cell antigens assayed (continued)													
Sample No	**C**	**c**	**E**	**e**	**Cw**	**K**	**Fya**	**Fyb**	**Jka**	**Jkb**	**S**	**s**	**M**	**N**	**k**
EX1313820	P	P	N	P	N	N	N	P	N	P	N	P	P	P	P
	P	P	N	P	N	N	N	P	N	P	N	P	P	P	P
EX1400171	P	P	N	P	N	N	N	P	P	P	N	P	P	P	P
	P	P	N	P	N	N	N	P	P	P	N	P	P	P	P
EX1400887	P	P	N	P	N	N	N	P	N	P	N	P	N	P	P
	P	P	N	P	N	N	N	P	N	P	N	P	N	P	P
EX1401612	P	P	P	P	N	N	N	P	P	P	P	N	P	N	P
	P	P	P	P	N	N	N	P	P	P	P	N	P	N	P
EX1401613	P	P	N	P	N	P	P	P	P	N	P	P	P	N	P
	P	P	N	P	N	N	P	P	P	N	P	P	P	N	P
EX1401737	P	P	P	P	N	N	P	P	N	P	P	P	P	P	P
	P	P	P	P	N	N	P	P	N	P	P	P	P	P	P

5.4 Discussion

The IDCOREXT assay was demonstrated to be a robust assay showing good comparison with the automated serological phenotyping assay and a low failure rate. A discrepancy in testing was seen with the M antigen type in one patient, unfortunately it was not possible within the time scale and funding of this project to ascertain the cause of this discrepancy. In addition, repeat serological testing was not possible due to the death of the patient. It is unlikely that the discrepancy was caused by human and/or methodological error, as this would have resulted in discrepancies involving multiple antigens. The serological M type for this patient was confirmed as positive by a reference centre (NHSBT, Filton), in accordance with the serological phenotype determined by automated testing at the RD&E. Therefore the discrepancy was unlikely to be due to any issues affecting the performance of the anti-M used in the automated phenotyping assay. It is possible that the allele coding for the M antigen, in this particular patient, may have an alteration such that it is not detected by the BLOODChip IDCOREXT assay. Sequencing of the DNA could potentially have revealed if this was the case, however, this was not possible within the funding of the project. This type of discrepancy could result in a false negative result being reported. This would not cause clinically significant issues for patients within a type and match strategy as they would be transfused with antigen negative red cells. However, within the blood donor service this would have implications as the donor units would be erroneously reported as antigen negative and could elicit an immune response in a patient.

In a study by McBean and co-workers (2014b) it was noted that, although the microarray techniques are a useful tool for the determination of blood group genotypes, difficulties can arise as a result of a new or rare allele not incorporated in the assay, or a complex genetic variant. In these cases further analysis by sequence-based typing in specialist reference laboratories may elucidate the molecular basis of the unusual blood group phenotype (Seltsam and Doescher, 2009). McBean's laboratory experience suggests that up to 5-10% of complex serological cases cannot be resolved by microarray genotyping, and of these, 1-2% cannot be resolved by sequencing (McBean *et al.,* 2014b).

Genotyping assays can also generate false positive results, where there is an apparently normal allele but no corresponding antigen on the red cells. This can be caused by silencing genes outside of the assay target area, as seen in "null phenotypes". The BLOODChip IDCOREXT assay contains makers for well-known silencing genes, but hitherto unknown ones may be missed. False positive results in genotyping assays cause clinical issues within the transfusion service rather than the blood donor service, in contrast to the false negative results. A false positive result for a transfusion recipient in a type and match program would lead to selection of inappropriate red cells. Discrepancies between genotyping and phenotyping results may also arise if not all the alleles are known, and many molecular events can give rise to discrepancies. The current, commercially available, genotyping assays are restricted to testing for known SNPs, meaning that new variants will not be recognised.

Other studies have seen higher genotype-phenotype discrepancy rates than seen in this study, McBean and co-workers (2014a) found a discrepancy rate of 10.4% when comparing phenotyping with genotyping using three different genotyping platforms, the BLOODChip (Progenika), BeadChip (BioArray Solutions Ltd) and the HemoCarta Blood Group Typing Panel (Sequenom Inc.). However, it should be noted that the discrepancies between genotyping and phenotyping results seen in the McBean study and also in other studies (Drago *et al.*, 2009; Drago *et al.*, 2010) were due to mutations causing weakened antigen expression or null phenotypes. The inclusion of markers for identification of null phenotypes and silencing genes within the commercial genotyping kits will reduce the risk of incorrect prediction of antigen phenotypes.

A further limitation of the commercially available blood group genotyping assays is that they may be designed for a specific population (McBean *et al.*, 2014b). McBean and co-workers report that the BLOODChip assay was designed for a European population and the BeadChip assay was designed for the African/America population. Neither of these assays, they report, are designed for the large proportion of Asian ancestry seen in the Australian population.

The development of massively parallel sequencing (MPS) as an alternative approach to blood group genotyping has overcome some of the limitations of the commercially available microarray kits. MPS is not

restricted to the identification of blood group systems with known SNPs and, thus, allows new variant blood group antigens to be identified. MPS, or Next Generation Sequencing, can be used to obtain information on the whole genome, or restricted to whole exome or targeted gene sequencing. This technique is not currently commonly used for blood group genotyping but has been applied to resolve the genetic basis of the Vel antigen (Cvejic *et al.,* 2013) and that of the low frequency orphan antigen SARA (McBean *et al.,* 2014c). When looking to implement MPS, ethical issues should also be considered as non-blood group genetic information is also obtained. Methods for managing this information would need to be in place to ensure donor and/or patient confidentiality.

One of the advantages commonly quoted for commercially available blood group genotyping assays is their ability to provide information on multiple blood group antigens for multiple patients on an automated platform. In addition, the automated data analysis by the system software removes the risk of subjective interpretation of the traditional manual serological assays. The validation of the automated serological assay on the IBG Immucor NEO® analyser system in this study demonstrates that serological assays can also be fully automated and provide standardised, non-subjective, information on a large number of blood group antigens for multiple patients with minimal manual input. The real advantage of the genotyping assays is that they can be used to obtain a predicted phenotype in patients who have been recently transfused and in those

who have a positive DAT, areas where serological assays may give inconsistent or incorrect results.

Although DNA extraction for this study was performed by an automated system, the genotyping assay required substantial manual input for the PCR and hybridisation phases. Not only are these manual phases expensive in terms of labour, they also require specialist skills not currently used by hospital transfusion scientific staff, and they are at risk of errors in sample transposition and pipetting which may lead to incorrect results. Automation of these phases for blood group genotyping assays is not currently available, and it is this limitation which will hinder the introduction of the assays into the routine hospital laboratory setting.

The evaluation of the serological and genotyping assays, as described in this study, have demonstrated robust, accurate systems for high throughput testing that have potential for use in a hospital transfusion setting. In particular, the automated serological assay (IBG Immucor) would appear to be a cost effective method that could be easily incorporated into a type and match program. To reduce the risk of inaccurate serological phenotyping results, patient samples would need to be tested prior to initial transfusion, or in the absence of blood transfusion in the previous four months. The results of the phenotyping assay could then be used to provide blood for transfusion that was matched for Rh (CcEe) and K in addition to the standard ABO/D matching. The introduction of a “type and match” program would have the

potential to reduce the risk of alloimmunisation in chronically transfused patients. The benefits of a type and match program have not been evaluated in the UK, and would require a large number of participants enrolled into a randomised controlled trial (RCT) to adequately address the research question, given the incidence of alloimmunisation in chronically transfused patients noted in this study. Prior to initiation of such an RCT, there are other important questions that need to be addressed. These include recruitment rates, dropout rates and, more importantly, the ability of the hospital transfusion laboratories to provide matched blood from routine stocks. A useful precursor to an RCT is a pilot study, which can provide answers to some of these questions and identify any unforeseen issues. A pilot study was initiated at the RD&E, as part of this research project, designed to provide information that could be used to lead into a larger RCT, and this is described in chapter 6.

6 PILOT STUDY-RANDOMISED CONTROLLED TRIAL

6.1 Introduction

To truly assess whether typing and matching of blood for chronically transfused patients would reduce the risk of the development of allo/autoantibodies and realise the estimated cost benefits, a randomised controlled trial (RCT) is required. Patients would be recruited to either a standard care group, receiving standard ABO and RhD matched blood or to an intervention group destined to receive blood additionally matched for Rh (CcEe) and K antigens. This study has already demonstrated that the development of allo/autoantibodies occurs in around 15-25% of chronically transfused patients and that a relatively large number of transfusions are required before this effect is seen. Therefore any RCT designed to investigate the potential benefits of typing and matching blood would need large numbers of patients and would take considerable time to achieve. Given the number of patients with haematological and/or renal conditions that would be required for recruitment it is unlikely that this sort of RCT could be undertaken in one hospital site, but would more likely require a coordinated multicentre trial.

A feasibility, or pilot, study is a commonly used forerunner to a large RCT, and is described by the National Institute for Health Research (NIHR) as a piece of research done before a main study to answer the question "can this study be done?" In this way they can be used to estimate important parameters that are needed to design the main study, such as standard

deviation of the outcome measure, which is needed in some cases to estimate sample size required to gain statistical power; number of eligible patients, willingness of participants to be randomised; willingness of clinicians to recruit participants; carers or other appropriate participants; characteristics of the proposed outcome measure. In some cases feasibility studies might involve designing suitable outcome measures; follow-up rates, response rates to questionnaires, adherence/compliance rates; availability of data needed or the usefulness and limitations of a particular database; time needed to collect and analyse data (NIHR guidance). Pilot studies do not necessarily need to be RCTs but the inclusion of a control group and randomisation allows the review of willingness of the subjects to be randomised which can then inform on the recruitment requirements of the larger trial.

Pilot studies, because of their limited size, cannot provide any definite support for any specific therapeutic claims (Loscalzo, 2009), they cannot be used to evaluate safety, efficacy and effectiveness and neither do they provide meaningful effect size estimate for planning subsequent studies due to the imprecision inherent in data from small samples (Leon *et al.,* (2011); Friedman *et al.,* 1998; Kraemer *et al.,* 2006), however, the data obtained can be used to design a larger RCT and they can be useful in identifying any unexpected harm of the intervention early on in the course of its development. The ultimate aim of the larger trial should be used to guide the design of the pilot study and the participants or patients should be recruited from the same study population (Hinds and Gattuso, 1991),

this will enable the researchers to test those aspects of the intended larger trial and make any amendments in advance of embarking on any larger RCTs. Recruitment of trial subjects can be slower and more difficult than researchers imagine and many trials fail to achieve their intended sample size within the planned time frame (McDonald *et al.,* 2006; Sully *et al.,* 2013). Assessment of this within the pilot study may prevent issues developing within the larger RCT. A review of pilot studies published in seven major medical journals from 2000 to 2001 (Lancaster *et al.,* 2004) recommended that statistical analysis of pilot studies should be either mainly descriptive or focus on the estimation of the sample size and that any results from hypothesis testing should be treated with caution. Arain and coworkers (2010) revisited this review between the years 2007 and 2008 to assess whether the recommendations made by Lancaster and his team had produced a change in the practice of reporting pilot studies but found that pilot studies were still poorly reported with inappropriate emphasis on hypothesis testing. The review by Arain and coworkers found that 81% of pilot studies published reported statistics on hypothesis testing, they also found that only 69% of the studies included a control group, and although randomisation was noted in 62% of the trials, only 20% of those were blinded randomisation. Teare and coworkers (2014) recommended that pilot studies include at least 35 participants per group (total of 70) to allow estimation of the standard deviation for a continuous outcome and a total of 60 to 100 recruits for trials investigating event rates. It is recommended that any estimation using confidence intervals (CI) in pilot studies should use 85% or 75% CI rather than the commonly

used 95% CI (Lee *et al.,* 2014). There is no set sample size for a pilot study. The review by Arain and coworkers (2010) found a median number of 76 participants, with an interquartile range of 42-216. Generally, sample sizes of 30, 50 and 70 will provide 48%, 78% and 84% power to detect an acceptance rate of 85% or lower if the acceptance rate in the population is 95%, however it has been noted that the sample size is often related to the funding level rather than the likelihood of achieving the specific aims (Moore *et al.,* 2011).

With all the benefits and caveats of pilot studies in mind, a small RCT was designed and performed using participants from the haematology clinics at the RD&E. It was accepted that, given the time frame in which the pilot study was required to be completed, and to enable the participants' sufficient time to be given blood transfusions, that only 60 patients would be recruited to the trial. The 60 patients were randomised to the standard care group or to the intervention group using a modified block randomisation to ensure that there were equal numbers of patients in each group. Patients approached for recruitment into the trial were given information leaflets detailing the tests to be performed and the randomised aspect to the treatment arms (appendix 5). Patients were given time to read the information and encouraged to ask any questions regarding the trial. Specific consent forms were signed by each patient recruited and patients were given the option to drop out of the trial at any time, should they wish to do so (appendix 6). The pilot study was given ethical approval from the NRES Committee South West - Cornwall &

Plymouth (MREC No. 12/SW/0251, R&D Study No. 1301733). This is the first time that such a trial has been attempted in the UK.

The aim of the pilot study was to review recruitment rates and dropout rates for the patients and also to assess the ability to supply matched blood for transfusion in the intervention group from routine blood stocks held in a hospital transfusion laboratory. The pilot study was not powered to investigate any differences in the rates of development of allo/autoantibodies between the standard care group and the intervention group. Nor was it powered to provide an estimate of the sample size required for a larger multicentre randomised controlled trial designed to investigate any benefits of typing and matching of blood for chronic transfusion.

The blood stocks held at the RD&E during the time of the pilot study are shown in table 6.1. The red cell units were held in ABO/D specific trays within a walk-in cold room. There was no subdivision of ABO/D types for Rh or Kell antigens. Orders were made to the NHSBT for red cell stocks on a daily basis, no changes were made to the ordering procedure with respect to particular Rh antigen types. In order to locate a matching unit for a pilot study patient, the laboratory staff had to search the physical stock, there is no search function for this in the laboratory computer system. Alternatively, appropriate antigen negative blood could be ordered from the NHSBT. As such, the results of the pilot study could

also be used to design effective changes to the way that the stocks are arranged and ordered to support a type and match program.

Table 6.1 Optimum stock of red cell units held in RD&E stock

The optimum number of red cells and their ABO/D type are shown in the table below. A small stock of group O and A, K negative, irradiated units are held for patients with this special requirement. The red cell units are stored in labelled trays in accordance with their ABO/D type. (Table taken from the RD&E laboratory standard operating procedure for red cell ordering and stock control).

Blood group	Optimum Red Cell Stock	Paediatric Red Cells
O RhD Pos	30	0
O RhD Neg	10	1
A RhD Pos	30	0
A RhD Neg	12	0
B RhD Pos	6	0
B RhD Neg	4	0
AB RhD Pos	4	0
AB RhD Neg	4	0
O RhD Pos Irradiated K-	4	
O RhD Neg Irradiated K-	2	
A RhD Pos Irradiated K-	4	

6.2 Results of the randomised controlled pilot study

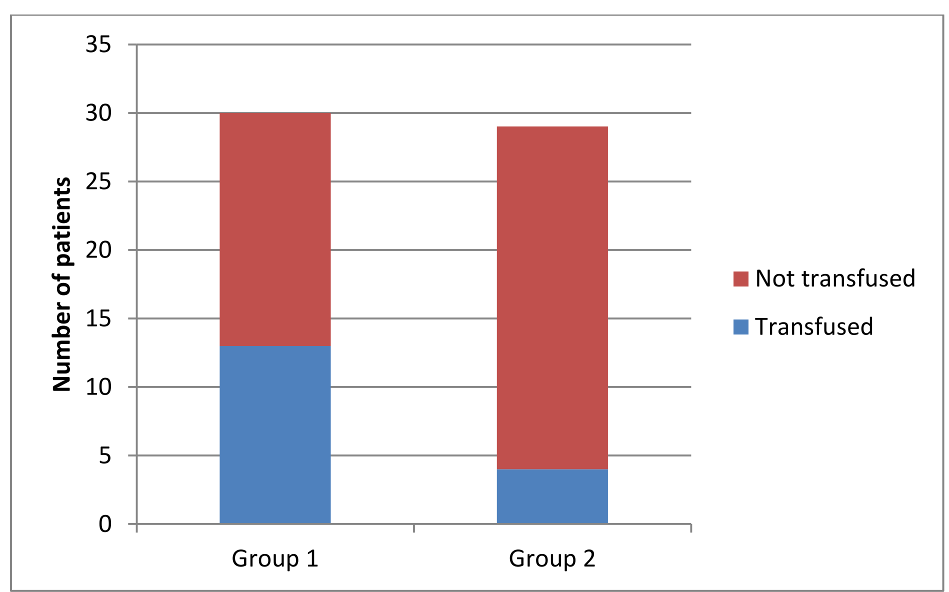
A total of 60 patients were recruited to the trial between the 8th November 2012 and the 16th July 2014. Patients were recruited from the haematology clinic with the only exclusions being individuals under the age of 18, those not capable of giving informed consent and those with a positive antibody screen recorded in the pathology computer system. Initially, recruitment was restricted to patients with haematological conditions considered likely to require blood transfusion, such as myeloma, acute and chronic leukaemias, Hodgkin's and non-Hodgkin's lymphoma, myelodysplastic and myeloproliferative disorders. However, using these criteria only eight patients were recruited over a seven month period. In order to recruit a sufficient number of patients in the time scale relevant to the study, the entry criteria were widened to include any patient attending the clinic with a confirmed haematological condition. Only one patient approached declined to enter the trial on the basis that they were alarmed by the thought of potential blood transfusions. All other patients approached were satisfied with the information that they were given regarding the trial and happy to be included.

Initially 30 patients were randomised to Group 1, the standard treatment group, and 30 to Group 2, the intervention group. One patient in Group 2 was found to have a positive antibody screen on initial testing and so was excluded from the trial.

6.2.1 Number of patients transfused in each study group

A total of 59 patients were included in the trial, of these 19 (32.2%) were transfused during the trial period. A total of 13 patients received transfusions in the standard care group, group 1 (n=30), and four patients were transfused in the intervention group, group 2 (n=29). This demonstrates that significantly more patients in group 1 received transfusions than in group 2 (Fisher's exact test p value = 0.0204) (figure 6.1).

Figure 6.1: Comparison of number of patients transfused in the pilot study groups



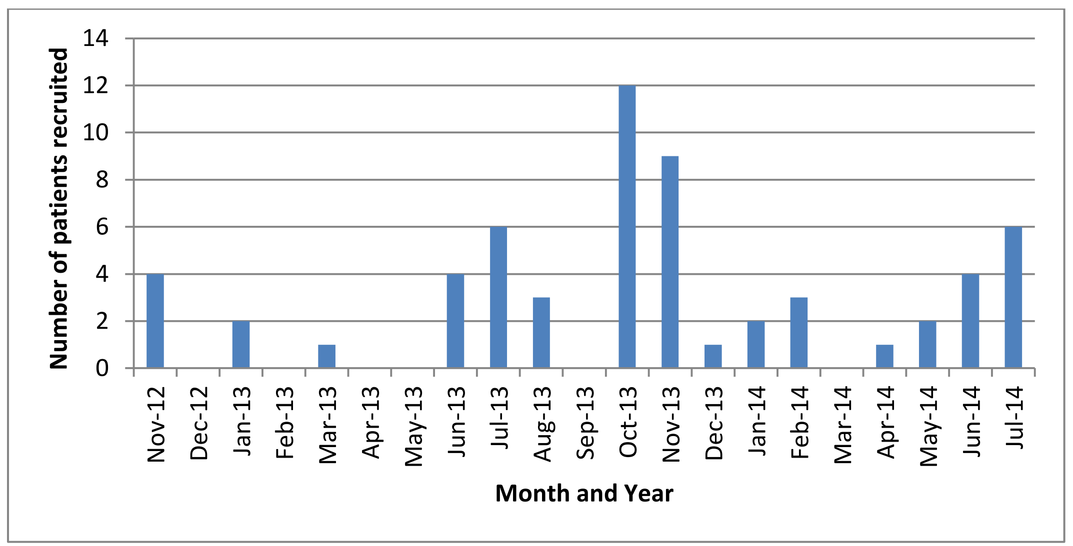
Within the standard care group (group 1, n=30) 13 (43.3%) patients were transfused, compared to 4 (13.8%) patients in the intervention group (group 2, n=29). Significantly more patients in group 1 were transfused compared to group 1 (Fisher's exact test p value = 0.0204).

6.2.2 Time spent in trial for patients in each study group

Patients were recruited to the trial between the 8th November 2012 and the 16th July 2014, the trial was closed and data collected on the 31st July 2015, consequently, in total, the trial ran over 995 days. The recruitment process lasted 615 days, longer than anticipated due to initial difficulties with the selection criteria. Over the 21 month recruitment process patients were accepted onto the trial at an average rate of 2.86 per month, however, over the first six months of the trial only seven patients were recruited (average 1.17 per month). At this point it was realised that insufficient patients would be recruited in the allocated time using the stringent criteria and so the criteria were relaxed, as a result of this, from June 2013 to November 2013 a total of 34 patients were recruited (average 5.67 per month) (figure 6.2).

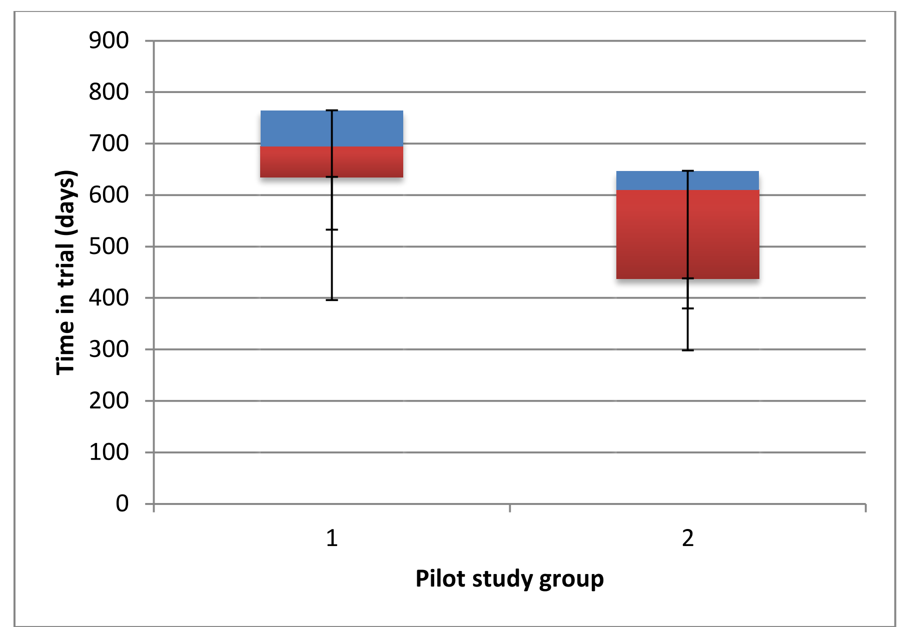
Patients in group 1 spent an average of 697.6 days (range 396 to 995 days, SD 154.8, n=30) on the trial compared to an average of 583.7 days (range 380 to 994 days, SD 165.9, n=29) for patients in group 2 (figure 6.3). Of the first 30 patients to be recruited to the trial, 21 (70%) were randomly assigned to group 1, this unexpectedly high number would account for the significant difference in length of time in the trial for patients in each of the groups (t-test p value = 0.0085).

Figure 6.2: Recruitment rates for pilot study patients



Patients were recruited to the pilot study over a 21 month period (n=60). Slow recruitment rates in the initial six month period were thought to be due to strict selection criteria focussed on patients with disease conditions considered to be at high risk of transfusion dependence. Relaxation of the selection criteria and an increase in recruitment rate was seen from June 2013 onwards, which enabled the recruitment target to be achieved within the time scale of the project.

Figure 6.3: Comparison of the length of time spent on the trial for patients in the pilot study groups



Box-and-whiskers plots showing the minimum and maximum numbers (black line) of time spent in the trial (the first quartile, mean and third quartile are denoted by the coloured blocks). Patients in group 1 (standard care group, n=30, range 396 to 995 days, SD 154.8) spent significantly longer on the pilot study trial than patients in group 2 (intervention group, n=29, range 380 to 994 days, SD 165.9). T-test p value = 0.0085.

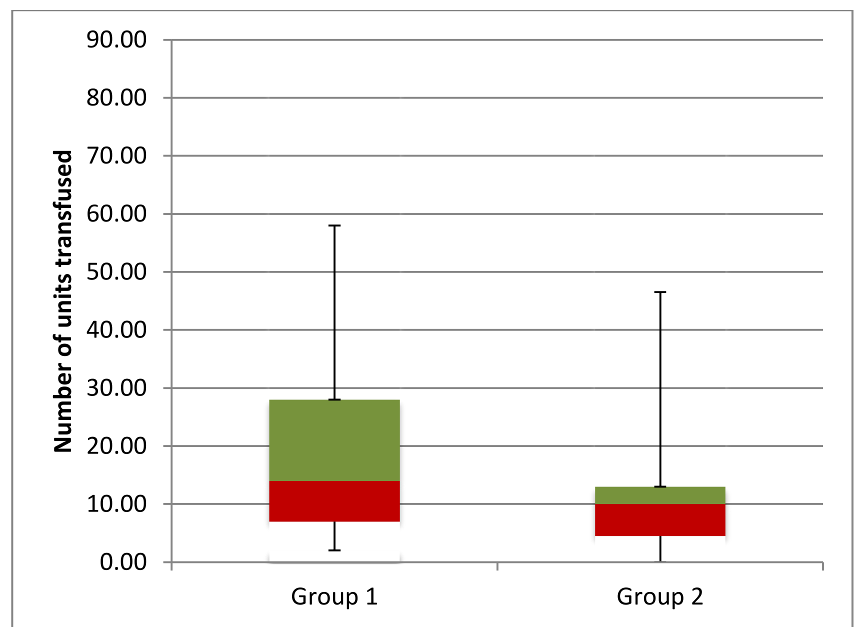
6.2.3 Comparison of the number of transfusion episodes and units given for patients in each study group

Within the standard care group (group 1 n=30) 13 patients received blood transfusions and within the intervention group (group 2, n=29) four patients received transfusions. The average number of red cell units given to transfused patients in group 1 over the study period was 27.46 (range 2 to 76, SD 26.99, n=13) and the average number of red cell units given the transfused patients in group 2 was 22.25 (range 1 to 71, SD 32.71, n=4). There was no statistically significant difference seen in the number of red cell transfusions given to patients in each study group (t-test p value = 0.7513) (figure 6.4).

The average number of transfusion episodes within the standard care group (group 1) was 11.62 (range 1 to 30, SD 10.32, n=13) compared to an average of 10.75 (range 1 to 34, SD 15.59, n=4) in the intervention group (group 2), again this demonstrated no statistically significant difference between the two groups (t-test p value = 0.8971) (figure 6.5).

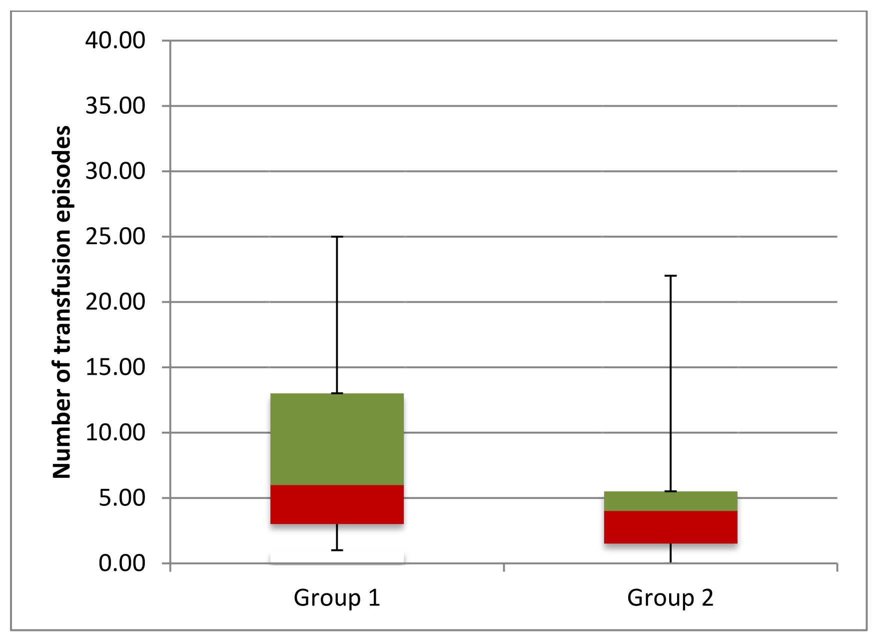
Statistical analysis of the number of red cell units transfused and the number of transfusion episodes for the transfused patients in each of the study groups demonstrated that the patients in each group were well matched despite the majority of patients recruited during the initial recruitment phase, when selection for patients likely to require transfusion was attempted, being allocated to group 1, the standard care group.

Figure 6.3: Number of red cell units transfused to patients in pilot study



Box-and-whiskers plots showing the minimum and maximum numbers (black line) of red cell units transfused (the first quartile, mean and third quartile are denoted by the coloured blocks) to patients in the pilot study. Comparison of the number of red cell units given to patients in the standard care group (group 1, average 27.46, range 2 to 76, SD 26.99, n=13) and the number given to patients in the intervention group (group 2, average 22.25, range 1 to 71, SD 32.71, n=4) showed no significant difference (t-test p value = 0.7513).

Figure 6.4: Number of transfusion episodes for patients in the pilot study

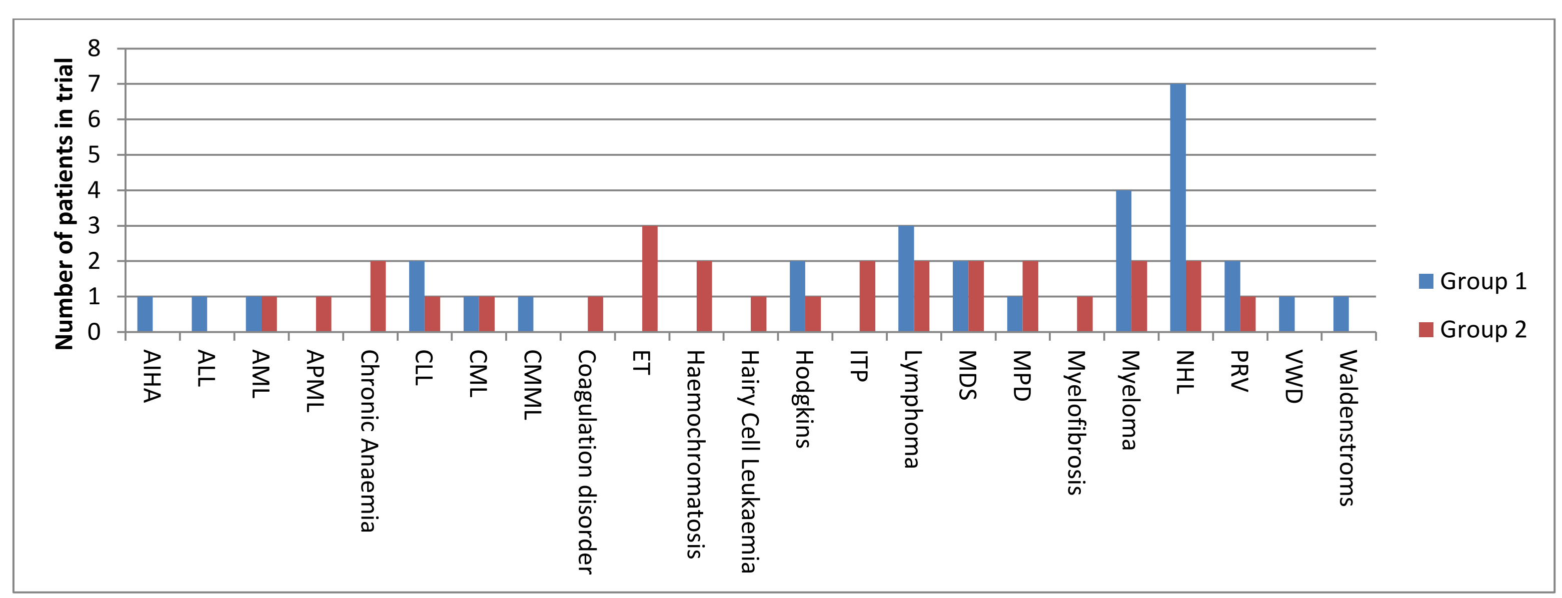


Box-and-whiskers plots showing the minimum and maximum numbers (black line) of transfusion episodes (the first quartile, mean and third quartile are denoted by the coloured blocks) experience by patients in the pilot study. Comparison of the number of transfusion episodes for patients in the standard care group (group 1, average 11.62, range 1 to 30, SD 10.32, n=13) and those for patients in the intervention group (group 2, average 10.75, range 1 to 34, SD 15.59, n=4) did not demonstrate any statistically significant difference (t-test p value = 0.8971).

6.2.4 Disease conditions in the pilot study patients

Patients recruited to the pilot study were suffering from a wide variety of haematological disease conditions (figure 6.6). The standard care group (group 1) included a larger number of myeloma and non-Hodgkin's lymphoma (NHL) patients compared to the intervention group (group 2). These disease conditions are considered high risk for requiring transfusion through the course of treatment and so, as the majority of patients in this phase were randomly assigned to group 1, this may have introduced an element of selection bias. This would explain the larger numbers of patients requiring transfusion within the standard care group. Other disease conditions expected to require blood transfusions, such as acute lymphocytic leukaemia (ALL), acute myeloid leukaemia (AML), acute pro-myelocytic leukaemia (APML), chronic lymphocytic leukaemia (CLL), chronic myelo-monocytic leukaemia (CMML), Hodgkin's lymphoma, lymphoma, myelodysplastic syndrome (MDS) and myeloproliferative disease (MPD) demonstrated a relatively more even spread across the two study groups. Relaxation of the selection criteria meant that conditions unlikely to require transfusion during the course of the disease, such as idiopathic thrombocytopaenic purpura (ITP), coagulation disorders, Von Willebrand's disease (VWD) and polycythaemia rubra vera (PRV) were also included in the trial groups.

Figure 6.5: Disease conditions in the pilot study patients



A wide variety of haematological disease conditions were seen in the pilot study patients. The number of patients recruited to the standard care group (group 1) for each disease condition is shown on the graph as blue columns and the number of patients recruited to the intervention group (group 2) is shown by the red column. Key:

AIHA = autoimmune haemolytic anaemia

ALL = acute lymphocytic leukaemia

AML = acute myeloid leukaemia

APML = acute pro-myelocytic leukaemia

CLL = chronic lymphocytic leukaemia

CML = chronic myeloid leukaemia

CMML = chronic myelo-monocytic leukaemia

ET = essential thrombocythaemia

ITP = Idiopathic thrombocytopaenia purpura

MDS = myelodysplastic syndrome

MPD = myeloproliferative disorder

NHL = non-Hodgkin's lymphoma

PRV = polycythaemia rubra vera

VWD = Von-Willebrand's disease

6.2.5 Matching red cell antigens for transfused patients in the intervention group

Patients allocated to the intervention group had Rh (CcEe) and K antigen types performed using the automated serological method (Immuncor) and by the manual laboratory method (Bio-Rad). For each of these patients a note was added to the laboratory computer record stating the Rh (CcEe) and K antigen type and the corresponding antigen negative requirements of red cell units for transfusion. Laboratory staff was requested to record, on the laboratory computer system, a reason if they were unable to provide matched red cells for the patient for any of the transfusion episodes.

A total of 89 red cell units were provided for the four transfused patients in the intervention group. Patient 1 received a total of 10 units over five transfusion episodes, patient 2 received 71 units over 34 episodes, patient 3 received seven units over three episodes and patient 4 received one unit on one occasion (table 6-1).

Table 6.2: Provision of Rh (CcEe) and K matched blood for transfused patients in the intervention group

Four patients in the intervention group (patients allocated to receive red cells for transfusion matched with their own Rh (CcEe) and K types) received transfusions during the trial period. Three patients received red cell units that were matched with their own Rh (CcEe) and K antigen type (patient numbers 1, 3 and 4). One patient received a total of 71 units of red cells, of which just 20 (28.2%) were typed and matched to their Rh (CcEe) and K antigen type.

Patient No	Rh (CcEe) and K type	Number of red cell units transfused	Number of transfusion episodes	% of units matched with Rh (CcEe) and K type
1	R^2r (cDE/cde) K neg	10	5	100%
2	R^2R^2 (cDE/cDE) K neg	71	34	28.2%
3	R^1r (CDe/cde) K neg	7	3	100%
4	R^1r (CDe/cde) K neg	1	1	100%

All four of the transfused patients were found to be negative for the K antigen, a phenotype shared by over 90% of the Caucasian population (Daniels, 2013), and as such expected to be seen in around 90% of donated red cells stored in a hospital blood bank stock. None of the red cell units transfused to any of the four patients were K positive, giving a matching rate of 100%.

Two of the four transfused patients (patients 3 and 4) were found to be positive for the C, c and e antigens and negative for the E antigen, giving them the mostly likely Rh type R^1r (CDe/cde), a phenotype shared by 32.68% of the English population (Daniels, 2013). Patient 3 was provided with seven units of blood over three transfusion episodes, and patient 4 was provided with a single unit of blood on one occasion, the Rh (CcEe) type of all of the units matched with the patients Rh (CcEe) phenotype.

Patient 1 was found to be positive for the c, E and e Rh antigens and negative for the C antigen, giving a most likely Rh type R^2r (cDE/cde), a phenotype shared by 10.97% of the English population (Daniels, 2013). This patient was provided with 10 units of blood over five transfusion episodes, all of the units provided carried the same Rh antigens as the patient.

Patient 2 was found positive for the c and E antigens and negative for the C and e antigens, giving a most likely Rh type of R^2R^2 (cDE/cDE), a phenotype shared with just 1.99% of the English population (Daniels,

2013). This patient required a total of 71 units of blood over 34 transfusion episodes during the trial period, the laboratory were only able to provide 20 units of blood that matched this patient's Rh (CcEe) phenotype. On four occasions a reason was given to explain the lack of matched blood; it was noted that there were no units in stock that matched. No reason was noted for the remainder of the transfusion episodes.

The Rh (CcEe) and K types of all the patients recruited to the trial were elucidated using the automated extended serological assay (table 6-2). The most likely phenotypes of the patients are shown in both Fisher-Race (CDE) terminology (Fisher, cited in Race, 1944) and Wiener's Rh-Hr (Wiener, 1943). The D antigen status of the patients was determined using two commercial reagents; NOVACLONE™ anti-D blend (IgM D175-2 and IgG D145, IE4) and ImmuClone® IgM (derived from cell line RUM 1). The assays were performed using the standard D typing assay on the NEO® analyser (Immucor).

The R^1r (CDe/cde) phenotype was the most common Rh type seen in the patients recruited to the pilot study (21/59, 35.6%), R^2r was seen in nine patients (15.2%), R1R1 in nine patients (15.2%), R^1R^2 in eight patients (13.6%), rr in 7 patients (11.9%) and R^2R^2 in five patients (8.5%) (Figure 6.7). The R^1R^1 phenotype is shared by 17.68% of the English population, R1R2 by 11.87%, and rr by 15.10% (Daniels, 2013), should the pilot study patients sharing these phenotypes have required a transfusion the

provision of blood should not have proved difficult from routine stocks given the frequency of phenotypes.

Table 6.3: Rh and K types of patients recruited to the pilot study

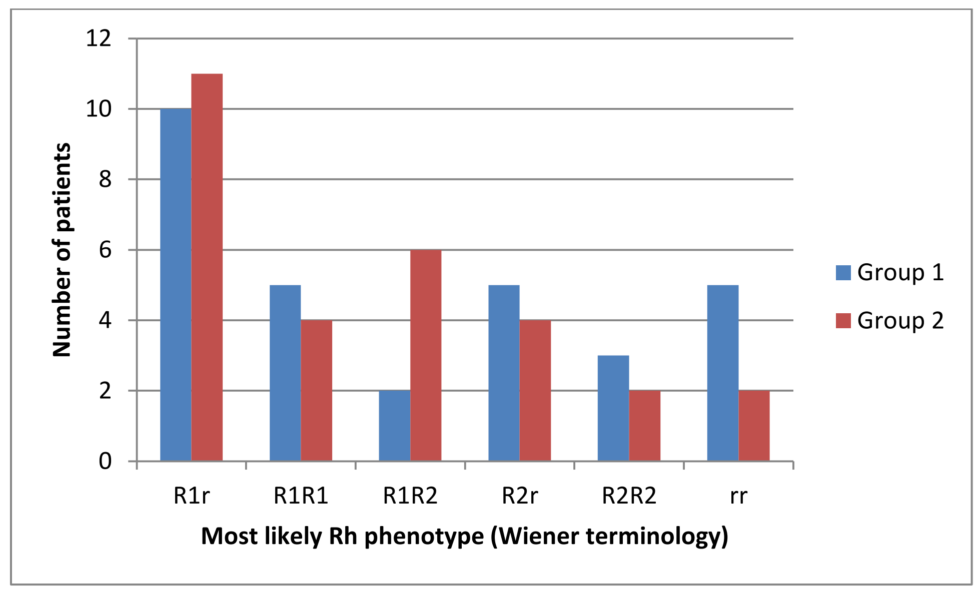
Rh and K antigen status was determined using the automated extended serological assay for all the patients recruited to the pilot study. In the table below antigen status is denoted as positive (P) or negative (N) for the antigens C, c, E, e and K, assayed using the extended automated serological phenotyping assay, the D antigen status was determined using two anti-D clones via the standard automated assay (NEO®analyser, Immucor). The most likely Rh phenotype is shown in both Fisher-Race and Wiener's terminologies.

Patient number	Trial Group	Antigens					Probable phenotype	
		C	**c**	**E**	**e**	**K**	**Fisher-Race**	**Wiener**
1	1	P	P	N	P	P	CDe/cde	R^1r
2	1	N	P	P	P	N	cDE/cde	R^2r
3	1	N	P	P	N	N	cDE/cDE	R^2R^2
4	1	N	P	P	N	N	cDE/cDE	R^2R^2
5	1	P	N	N	P	N	CDe/CDe	R^1R^1
6	1	P	P	P	P	N	CDe/cDE	R^1R^2
7	1	P	N	N	P	N	CDe/CDe	R^1R^1
8	1	P	N	N	P	N	CDe/CDe	R^1R^1
9	1	N	P	N	P	N	cde/cde	rr
10	1	N	P	P	P	P	cDE/cde	R^2r
11	1	N	P	N	P	N	cde/cde	rr
12	1	N	P	P	P	N	cDE/cde	R^2r
13	1	P	N	N	P	N	CDe/CDe	R^1R^1
14	1	N	P	N	P	N	cde/cde	rr
15	1	P	P	N	P	N	CDe/cde	R^1r
16	1	N	P	P	P	N	cDE/cde	R^2r
17	1	P	P	P	P	N	CDe/cDE	R^1R^2

Patient number	Trial Group	Antigens					Probable phenotype (continued)	
		C	c	E	e	K	Fisher-Race	Wiener
18	1	P	P	N	P	N	CDe/cde	R^1r
19	1	P	P	N	P	N	CDe/cde	R^1r
20	1	P	P	N	P	N	CDe/cde	R^1r
21	1	N	P	N	P	N	cde/cde	rr
22	1	P	P	N	P	N	CDe/cde	R^1r
23	1	N	P	P	P	N	cDE/cde	R^2r
24	1	P	N	N	P	N	CDe/CDe	R^1R^1
25	1	P	P	N	P	N	CDe/cde	R^1r
26	1	P	P	N	P	N	CDe/cde	R^1r
27	1	P	P	N	P	P	CDe/cde	R^1r
28	1	P	P	N	P	N	CDe/cde	R^1r
29	1	N	P	N	P	N	cde/cde	rr
30	1	N	P	P	N	N	cDE/cDE	R^2R^2
31	2	N	P	P	P	N	cDE/cde	R^2r
32	2	N	P	P	P	N	cDE/cde	R^2r
33	2	N	P	P	N	N	cDE/cDE	R^2R^2
34	2	P	P	N	P	N	CDe/cde	R^1r
35	2	P	P	P	P	N	CDe/cDE	R^1R^2
36	2	P	N	N	P	N	CDe/CDe	R^1R^1
37	2	P	P	N	P	P	CDe/cde	R^1r
38	2	P	P	P	P	N	CDe/cDE	R^1R^2
39	2	P	P	N	P	P	CDe/cde	R^1r
40	2	P	N	N	P	N	CDe/CDe	R^1R^1
41	2	N	P	P	P	N	cDE/cde	R^2r
42	2	P	P	N	P	N	CDe/cde	R^1r
43	2	N	P	P	P	N	cDE/cde	R^2r

Patient number	Trial Group	Antigens					Probable phenotype (continued)	
		C	c	E	e	K	Fisher-Race	Wiener
44	2	N	P	P	N	N	cDE/cDE	R^2R^2
45	2	P	P	N	P	N	CDe/cde	R^1r
46	2	P	P	N	P	N	CDe/cde	R^1r
47	2	P	P	N	P	N	CDe/cde	R^1r
48	2	P	P	P	P	N	CDe/cDE	R^1R^2
49	2	P	P	P	P	N	CDe/cDE	R^1R^2
50	2	P	N	N	P	N	CDe/CDe	R^1R^1
51	2	P	N	N	P	N	CDe/CDe	R^1R^1
52	2	P	P	N	P	N	CDe/cde	R^1r
53	2	P	P	P	P	N	CDe/cDE	R^1R^2
54	2	P	P	N	P	N	CDe/cde	R^1r
55	2	P	P	P	P	N	CDe/cDE	R^1R^2
56	2	N	P	N	P	N	cde/cde	rr
57	2	N	P	N	P	N	cde/cde	rr
58	2	P	P	N	P	N	CDe/cde	R^1r
59	2	P	P	N	P	P	CDe/cde	R^1r

Figure 6.6: Frequencies of Rh phenotypes in patients recruited to the pilot study



The graph shows the frequencies of the Rh phenotypes of the patients recruited to the pilot study (group 1, the standard care group (n=30) and group 2, the intervention group (n=29)) denoted using the Wiener terminology. The most common phenotype seen was the R^1r (35.6%), other phenotypes were seen with the following frequencies; R2r (15.2%), R^1R^1 (15.2%), R^1R^2 (13.6%), rr (11.9%) with R^2R^2 (8.5%) being the least common.

6.3 Discussion

The pilot study demonstrated that patients responded well to the recruitment process and the information that was provided regarding the trial, with only one patient declining to participate. The recruitment process itself, however, was slow, particularly when selection was limited to patients with diagnoses anticipated to require transfusion support. Recruitment increased when the selection criteria were relaxed to include patients with any disease condition. However, the number of patients in each group that actually received a transfusion was low, particularly in the intervention group where only 13.8% (4/29) of the patients received a transfusion. Comparison of the number of red cell units transfused and the number of transfusion episodes for the transfused patients in the standard care group and the intervention group demonstrated that patients were well matched in each group. The pilot study was not powered to investigate any differences in the rate of antibody development in the groups and it was noted that no patients in either group developed an allo- or autoantibody as a result of the red cell transfusions given.

No patients requested to drop out of the trial, suggesting that recruitment to a larger multi-centre trial would not pose significant issues, however, two patients died during the course of the trial. When estimating participant numbers for a multi-centre randomised controlled trial to

investigate the benefit of a typing and matching strategy for patients with haematological conditions or renal insufficient, it should be remembered that these patients have serious conditions and that the death rate in the study groups may be high. In addition, the pilot study showed low rates of transfusion in patients recruited to the trial. This was mainly attributed to a relaxation of the selection criteria in order to recruit sufficient patients in a relatively short space of time. In order to undertake a larger RCT, powered to detect any significant differences in antibody development rates in patients given standard care compared to those given antigen matched units, it would be preferable to maintain a stricter selection criteria based on haematological disease conditions considered most likely to require transfusion support.

Randomisation is a technique well known and extensively used in clinical trials to prevent selection bias during the recruitment of subjects to the trial and also reduce the risk of accidental bias during the data analysis (Rosenberger and Lachin, 2015). It also allows the use of probability theory to investigate the likelihood of chance as a source for any differences seen in the end outcome of the trial. Randomisation is particularly useful for the investigation of different treatment or intervention regimes; whether one particular treatment is better than another, no worse than another or equivalent. Randomisation has the benefit of ensuring that subjects have an equal chance of being allocated to one group or another and that the groups are balanced with respect to known, and unknown, confounding or prognostic variables and are an

essential tool for testing the efficacy of a treatment (Suresh, 2011). If randomisation is not used at the start of a clinical trial then the influence of imbalance that is introduced needs to be controlled for in the analysis of the results in order to produce an unbiased result (Kalish and Begg, 1985; Fleiss *et al.,* 2003), using techniques such as analysis of covariance (ANCOVA) or multivariate ANCOVA. Randomisation is essential to ensure that the treatment effects are reviewed appropriately. Clinical trials that been set up with unclear or inadequate randomisation have been reported to over-estimate the treatment effects by up to 40% (Schulz and Grimes, 2002a). In order to further reduce the potential for selection bias during the randomisation process, allocation concealment can be used, a technique which shields the researcher from the knowledge of the group to which subject will be allocated.

There are different types of randomisation that can be used for clinical trials; simple randomisation, block randomisation, stratified randomisation and covariate adaptive randomisation. Simple randomisation involves a single sequence of random assignments, which can be achieved by a process as simple as flipping a coin or rolling a dice. This technique is useful in clinical trials involving large numbers of subjects (200 or more) but can result in unequal numbers between the groups in trials involving smaller numbers of subjects (Altman and Bland, 1999a). In order to attempt to equalise the number of subjects being allocated to each group, block randomisation can be used, the total number of subjects required for the trial is broken down into smaller blocks with pre-determined group

assignments which has the effect of keeping the subject numbers similar at all times (Frane, 1998; Altman and Bland, 1999b). The downside to block randomisation is that it can introduce some bias as the groups could then have imbalances as the subjects are recruited, such as gender or disease type inequalities (Pocock and Simon, 1975) and it can harm the unpredictability of treatment assignments (Schulz and Grimes, 2002b). Reduction of the bias effects that simple or block randomisation may introduce within trial groups can be achieved by using stratified randomisation. This technique requires that any covariates that need to be controlled within the trial are identified prior to the selection process and can then be applied to each participant. This approach to randomisation can prove difficult in clinical trials where subjects are recruited on an individual basis or if there are numerous covariates that need to be controlled (Weir and Lees, 2003). In clinical trials involving small to moderate numbers of subjects, covariate adaptive randomisation can be used, where recruits are assigned to one of the treatment groups with reference to any covariates and also assignments of previous recruits allowing balance of a large number of covariates (Kalish and Begg, 1985; Hu *et al.,* 2014).

The randomisation technique used to allocate patients to the standard care or the intervention group in this pilot study resulted in an unexpected bias towards the standard care group for the first 30 patients recruited. This meant that patients in the standard care group spent significantly longer on the trial than patients in the intervention group. To reduce the

risk of this occurring in a larger RCT, a block or stratified randomisation approach should be utilised. Stratified randomisation would allow control of the important variables, gender and disease condition, whilst ensuring that patients in each study group have equality in the length of time on the trial.

This pilot study demonstrated issues with provision of antigen matched blood from routine stocks held in a hospital transfusion laboratory for patients with rarer Rh (CcEe) phenotypes. NHSBT blood centres test and distribute blood donated from a very wide geographical area, as such the blood stocks held within a hospital transfusion laboratory should represent the distribution of phenotypes in that general population. Thus, provision of matched blood for patients with common phenotypes such as K negative and the Rh type R^1r should be relatively easy, whereas provision of matched blood for the less common Rh phenotype, R^2R^2, is more difficult. This is supported by a study by Klapper and coworkers (2010) using a virtual type and match strategy which demonstrated that blood units could be provided from routine stocks for over 90% of requests if providing K and Rh matches. ABO blood group type will also impact on the provision of matched blood from routine stock; patients with blood type O will only be able to received matched blood from the stock of group O, whereas patients of blood type A are able to receive matched blood of type A or O, increasing the probability of finding matching blood within the stocks held, and patients of blood type AB can receive donor blood of type O, A, B or AB, further increasing the likelihood of finding a

match in the stock fridge. Patient 2 in this pilot study was of group O type, as well as being a less common R^2R^2 Rh type; this meant that selection of matched blood was restricted to the stocks of group O RhD positive. Patients with haematological diseases or renal insufficiency rarely present with emergency requirement for blood transfusion and so this should allow laboratory staff time to order blood of the appropriate Rh (CcEe) and K antigen type for specific patients from the NHSBT. A good communication system between the haematology/renal clinics and the laboratory, with regard to patients with transfusion requirement, adherence to protocols ensuring that transfusion samples are sent to the laboratory two working days in advance of transfusion, would help laboratories ensure that they have appropriately matched units of blood in the stock fridge ready for the patients. Ethnic disparity between the donor pool and patient population would need to be taken into account when making changes to the blood stock inventory control and ordering system to support a type and match strategy. Some Rh types show disparity, such as R^1 which is more common in White than Black populations, and R^0 which is more common in Blacks than Whites (Daniels, 2013). Ethnic disparity was not considered to impact on the provision of blood in this pilot study, and no issues were noted with provision of blood, by the NHSBT, of any particular Rh phenotype. Improvements in provision of matched blood by the laboratory could be achieved simply by rearranging the way that the units are stocked and setting optimum numbers of each phenotype for blood ordering.

The results of the retrospective review noted an alloimmunisation rate of approximately 67% for Rh and Kell alloantibodies for both the renal and the haematology cohort. The pilot study demonstrates that a type and match strategy for Rh and Kell antigens could be implemented to reduce the alloimmunisation rate. Changes would be needed to the blood stock arrangement and the ordering procedure to ensure that sufficient numbers of each phenotype were available. There would be no cost implications for phenotyping the red cell unit, for Rh and Kell, as this is performed at the NHSBT; however, there are cost implications for typing the patients which need to be explored (see chapter 7).

7 COST ANALYSIS

7.1 Introduction

This study has shown that the implementation of extended automated serological phenotyping, or genotyping, assays prior to transfusion in patients with disease conditions likely to require chronic transfusion support, followed by matching of blood for, at least, Rh (CcEe) and K antigens, has the potential to reduce the risk of development of red cell antibodies. However, the cost of implementation of these assays needs to be assessed and balanced against the potential savings that could be realised if the development of red cell antibodies were to be prevented. This study has also shown that both the extended automated serological phenotyping assay (NEO® analyser Immucor) and the BLOODChip IDCOREXT genotyping assay are robust and reliable techniques for the identification of red cell antigens within the hospital transfusion service setting. The cost effectiveness of both of these assays was assessed using the data regarding additional laboratory testing collected as part of the retrospective review. This is the first time that a cost analysis for a prospective type and match program has been performed in the UK.

7.2 Automated extended serological phenotyping

The total cost of additional laboratory testing incurred by the immunised patients in the haematology cohort (n=256/1107) was £48,752.59 (see section 3.2.5). In addition to this cost, each unit of blood for transfusion in this group of patients required compatibility testing by IAT assay, a test

calculated to cost £3.81/unit (RD&E 2014 cost) based on compatibility testing (crossmatching) by IAT in Column Agglutination (Bio-Rad) by a Band 5 Biomedical Scientist at pay point 20 (Agenda for Change, NHS 2015). During the retrospective review of the transfusion needs of the haematology patients, data was not collected on the type of crossmatch assay performed for each unit transfused for patients with red cell antibodies and so it is not possible to give accurate costs for compatibility testing for the immunised group in this patient cohort. However, using the average number of units transfused to the immunised group (n=256), 46.99 units, and the 2014 cost for compatibility testing (£3.81), a total cost of £45,711.87 can be estimated for this group for compatibility testing. This figure is likely to be an overestimate as the majority of patients in the immunised group developed red cell antibodies following transfusion and so, initially, provision of blood would not have required serological crossmatch by IAT. Additional laboratory testing performed for the immunised patients in the retrospective review amounted to £48,752.59, this figure, plus the estimated cost of compatibility testing, gives a total cost of £94,464.46 for laboratory tests performed over the review period. This gives a cost per head for the immunised haematology patients (n=256) of approximately £369.00. Additional testing for the non-immunised patients in the haematology cohort (n= 851) amounted to a total of £1,509.83. Again, using a cost for compatibility testing based on the average number of units given to patients in this group (23.43 units) and the 2014 cost for provision of blood without serological compatibility testing by IAT (electronic issue, £0.47/unit), it can be estimated that this

group incurred a total cost of £9,371.30 for compatibility testing. This figure, together with the additional testing figure, gives a total of £10,881.13 for the non-immunised patients, equating to a cost per head of £12.79/patient. Overall, the cost of provision of blood (additional testing plus compatibility testing) for the entire haematology cohort (n=1107) can be estimated at £105,345.59, giving a cost per head of £95.16 per patient.

Within the renal cohort (n=877) the immunised group (n=134) incurred additional testing costs of £13,094.76 and the non-immunised group (n=743) incurred a cost of £155.53. Using the average number of units transfused to patients in each group (21.85 and 11.97 respectively) and the cost of provision of blood by IAT crossmatch for the immunised patients (£3.81/unit) and electronic issue (£0.47/unit) the total cost for provision of blood for the immunised patients amounted to approximately £24,250.06 and £4,180.04 for the non-immunised patients. The cost per head for immunised renal patients can be estimated at £180.97 and for non-immunised patients at £5.62, the overall cost per head for the entire renal cohort (n=877) is estimated at £32.41 per patient.

Automated extended serological phenotyping for Rh (CcEe), K, M, N and C^w antigens cost £9.43 per patient and for Jk^a, Jk^b, Fy^a, Fy^b, S, s and k antigens the cost amounted to £10.14 per patient, giving a cost per head of £19.57 per patient. Both figures are considerably less than the current £95.16 per head for the haematology cohort and £32.41 per head for the

renal cohort for blood provision. This suggests that extended automated serological phenotyping for all haematology or renal patients could be justified if the patient phenotype could then be used to match blood for transfusion and reduce the risk of allo and/or auto-immunisation to red cell antigens. This is particularly relevant for the typing and matching of Rh (CcEe) and K antigens, for which donor blood is automatically typed. Automated serological phenotyping for Rh (CcEe) and K antigens only would amount to £5.97 per patient, this is significantly less than the cost per head estimated for the immunised haematology and renal patients (£369.0 and £180.97 respectively) and, furthermore, less than the estimated cost per head for the non-immunised patients in the haematology cohort (£12.79) and similar to the cost per head for the non-immunised renal patients (£5.62).

Manual extended serological phenotyping, at a total cost of £50.46 per head, could be justified on a cost basis for haematology patients (cost per head for immunised and non-immunised estimated at £95.16), but not for renal patients (cost per head for immunised and non-immunised estimated at £32.41). As for automated serological phenotyping, test cost for manual Rh (CcEe) and K antigen testing (estimated at £6.49 per patient) would appear to be a cost effective option if it could be demonstrated that matching blood for transfusion for these antigens prevents antibody production. However, the risks of manual testing on this scale would need to be carefully considered if this approach was used.

7.1 Genotyping Assay

The cost per patient test for the IDCOREXT test was estimated at £73.66. On a cost basis alone, this technique could be justified for all patients with haematological conditions prior to initial transfusion, but not for renal patients. This technique, however, required equipment that is not currently used in hospital transfusion services, such as extraction hoods, thermocyclers and the Luminex XMap analyser. The initial set up costs of introducing these systems into a routine hospital transfusion laboratory and the staff training required would also need to be taken into account. Costs for equipment may be kept to a minimum if other disciplines within the hospital, such as microbiology or immunology, were to share the equipment, but this may mean that the different aspects of sample preparation and analysis may take place in geographically separate areas of the hospital.

7.2 Cost comparison of serological phenotyping and genotyping techniques

Pre-transfusion phenotyping, in conjunction with a strategy for matching for the Rh (CcEe) and K antigens, appears to be a cost effective option when comparing the estimated cost per head for provision of blood for immunised patients (£369 for haematology patients and £180.97 for renal patients) with the cost per test for serological phenotyping for the Rh (CcEe) and K antigens (£5.97 for automated technique) (Table 7-1). The assumption being that serological phenotype prior to transfusion combined with a type and match strategy would reduce risk of

alloantibody development and associated costs with subsequent transfusions. Pre-transfusion genotyping appears to be cost effective but is less easy to justify in clinical practice as described in section 7.1.

Table 7.1: Cost effectiveness of serological phenotyping and genotyping techniques

The estimated current costs for the provision of blood for immunised haematology and renal patients per head (standard practice column), which includes the additional testing required once the patient has developed a red cell allo/autoantibody is considerably higher than that for pre-transfusion phenotyping or genotyping. Pre-transfusion phenotyping, or genotyping, combined with a strategy for matching for the Rh (CcEe) and K antigens, both appear to be a cost effective options with the assumption that such a strategy would prevent the development of antibodies against these antigens.

Standard practice				Phenotype for Rh (CcEe) and K antigens		Extended genotype
Haematology cohort		Renal cohort		Automated serological phenotyping	Manual serological phenotyping	Genotyping
Immunised	Non-immunised	Immunised	Non-immunised			
£369.00	£12.79	£180.97	£5.62	£5.97	£6.49	£73.66

7.3 Discussion

The additional costs incurred for the provision of blood for patients who have developed atypical red cell allo/auto-antibodies are considerably higher than the cost for provision of blood for patients without antibodies, in both the haematology cohort and the renal cohort. There is potential to reduce this financial burden by the introduction of high throughput methods of red cell antigen testing and then matching of blood for transfusion in these chronically transfused patients. Manual and automated serological red cell antigen phenotyping techniques are useful methods which can be easily incorporated into routine hospital transfusion laboratories. Manual techniques have disadvantages in that they are labour intensive, making them expensive and also introducing human error risks in the sample preparation, testing, interpretation and reporting stages. Automated readers, interfacing to laboratory computer systems and automated interpretation could eliminate some of these risks but would incur costs for computer upgrades and equipment, if not already used within the laboratory. Automated serological testing, as validated in this study, has been shown to be a robust and cost effective alternative to current manual systems. Interfacing to laboratory computer systems may incur additional one-off costs, but this would facilitate the high throughput testing required to antigen type large numbers of patients by eliminating the need for manual transcription of results.

The main disadvantage of serological testing, manual or automated, is that it cannot be used for recently transfused patients due to circulating donor cells. This would not be an issue if the hospital transfusion service chose to adopt the approach of automated serological red cell antigen typing for all haematology and renal patients prior to initial transfusion, but would restrict the use of the technique if used only for patients post development of red cell antibodies. In addition, serological techniques, manual and automated, using polyclonal anti-sera, such as those used in the detection of antigens in the Kidd, Duffy, and Ss systems cannot be used for patients with red cell autoantibodies due to the risk of false positive results (BCSH, 2013). Again, if used prior to the initial transfusion for haematology and renal patients this would not pose a significant issue, but the considerable numbers of patients with autoantibodies seen in both patient cohorts (186/1107 (16.8%) for haematology patients and 74/877 (8.4%) for renal patients) would restrict the use of the technique if only implemented post development of antibodies. Genotyping techniques, however, offer a flexible solution to red cell antigen typing that can be used for red cell antigen typing using samples from patients post-transfusion and from those with red cell autoantibodies (Guelsin *et al.,* 2010).

The potential reduction of costs for additional antibody identification tests and serological crossmatching could not be realised unless red cell antigen typing, serological phenotyping or genotyping, was implemented prior to initial transfusion and the blood provided for transfusion was

matched for, at least, the Rh (CcEe) and K antigens. Such a strategy could significantly reduce the current costs for provision of blood for patients within the haematology and renal cohorts, if the development of red cell antibodies to these antigens was prevented. The inclusion of extended phenotyping techniques, to include red cell antigens within the Jk, Fy, and Ss systems, would increase the initial costs for phenotyping. Matching of blood for these antigens is more complex, primarily because donor blood units are not automatically typed for these antigens but also because attempting to match at this secondary level reduces the likelihood of finding matched units within the routine blood stocks held by the hospital transfusion laboratory.

In addition, other benefits to patients could be realised, such as reduction in delays in provision of blood and a reduced risk of transfusion reactions. Individualising patient care in this way also has the potential to improve the patient journey, particularly for patients with haematological and renal diseases whose care and treatment can be prolonged and emotionally challenging.

8 FINAL DISCUSSION AND CONCLUSIONS

In order to implement a strategy of red cell antigen typing and matching of blood for transfusion the hospital transfusion service requires a cost-effective, robust, high throughput method for extended red cell phenotyping, or genotyping, of patient samples prior to transfusion. Current methods in hospital transfusion services for red cell antigen testing are serological, mainly manual, or, at least, require a selection of techniques for determination of individual antigen status. This results in a cumbersome, costly system with all the inherent risks of manual testing and manual input of results, which is then reserved for patient groups where there is a national requirement for pre-transfusion testing, namely the sickle cell disease and thalassaemia groups (BCSH, 2013).

Red cell antigen typing of patients red cells following production of an alloantibody is generally limited to testing only for the implicated red cell antigen, requiring a local decision regarding typing and matching for further antigens (BCSH, 2013). Decisions need to be made in conjunction with risk assessment, taking into account the limitations with the manual testing system, costs, and the amount of staff time required to perform extended typing. This study demonstrated that automated extended serological red cell antigen typing using the IBG Immucor NEO® analyser is a robust, cost effective method suitable for high throughput activity within a hospital transfusion service setting, giving the laboratory access to a robust assay for extended antigen typing. The method also lends itself to the addition of an electronic interface from the analyser to the

hospital LIM system, removing the requirement for manual input of results and reducing the risk of error. The automated system has built in quality control to ensure that sufficient antisera and patient red cells are added to the reaction mixture, a feature that is difficult to control using a manual system where such judgments are made by macroscopic reading. Testing of the automated system demonstrated that strongly positive reactions are produced for heterozygous and homozygous antigen expression in both commercial control cells (NHSBT red cell antigen cells) and patient red cells. Red cell antigen typing using polyclonal antisera in the gel column agglutination manual techniques employed in this study did not demonstrate comparable differences in heterozygous and homozygous antigen expression reaction strengths. It is possible to automate gel column agglutination tests for red cell antigen typing and it would be interesting to perform a further comparative study between the IBG Immucor extended red cell antigen profiles and similar profiles created on an automated column agglutination analyser. Weakly positive results demonstrated in this study in the automated system were shown to be false positives; although the numbers involved were small the specificity of the automated system could be further improved by instructing the analyser to invalidate any weak reaction (1+ or 2+ reaction strengths).

The automated system created for testing in this study included an auto control (patient red cells tested against a non-reactive reagent, designed to identify non-specific agglutination) as part of the polyclonal antisera testing profile to minimise the risk of false positive results due to a

positive DAT. Only one patient in the study group proved to have a positive DAT, which was identified due to weakly positive reactions in both the automated and manual systems, not by the auto control included in the automated profile. Further testing of a larger number of DAT positive patients in the automated system is necessary to demonstrate that inclusion of the auto control will identify DAT positive patients effectively. In addition, invalidation of weakly positive results will also reduce the risk of reporting false positive results. The monoclonal reagent testing profile (anti-C, anti-c, anti-E, anti-e, anti-K, anti-C^w, anti-M and anti-N) created on the IBG Immucor analyser did not include an auto control, this was not felt to be a necessary addition as, if this profile was included as part of pre-transfusion testing, the sample would also be ABO and D typed by the same analyser, a test profile that already includes an auto control.

There are currently no commercial quality control samples available specifically for extended red cell antigen typing profiles in automated systems. Whole blood quality control cells are available for use in the IBG Immucor automated systems (WBCorQC), although these were tested and found to be useful for internal quality control of the automated Rh (CcEe) and K antisera, they are pooled cells and, as such, cannot be used for internal quality control of the remaining antisera. The NHSBT 2 cell profile (3% suspension in Alsevers) is marketed for alloantibody detection but was found to be suitable as an internal quality control system for the extended red cell antigen typing profiles in this study.

However, these cells are not supplied in tubes compatible with use on the analyser and therefore had to be transferred into suitable tubes, introducing a potential source of error and removing the potential for any audit trail and reagent expiry date control on the analyser. To further improve the use and marketability of the IBG Immucor extended red cell antigen typing profiles the production of red cell controls, containing cells with negative red cell antigen expression and, preferably, cells expressing heterozygous red cell antigens should be explored. Another improvement to the automated extended red cell antigen phenotyping profiles would be the replacement of the current polyclonal reagents (anti-Fy^a, -Fy^b, -Jk^a, -Jk^b, -S, -s and –k) with monoclonal reagents. Not only would this reduce the cost of testing but it would also allow the use of the reagents on samples from patients with a positive DAT, currently one of the major limitations of this assay.

Test costs for automated red cell antigen typing profiles were found to be considerably cheaper than those for performing the same tests by manual methods in our institution. In addition, the reduction in staff time required for performing the automated profiles make this an attractive method for extended red cell antigen typing in a hospital transfusion service setting. However, the inclusion of internal quality control material for the automated system also needs to be taken into account; decisions would need to be made at a local level as to the frequency of reagent quality control and the source of the material until such time as commercial cells become available.

If one makes the assumption that typing and matching of blood for transfusion for Rh (CcEe) and K antigens would eliminate alloantibodies to Rh C, c, E, e and K, using patient numbers from the retrospective study patient group (haematology patients), use of such a strategy would have eliminated the production of Rh and Kell antibodies in 78 of the 1107 patients. Using the average number of antibody identification panels performed for the retrospective review patients with red cell alloantibodies (14.25), the total cost of antibody identification panels performed for the 78 patients was £7,913.88. If all 1107 patients included in the retrospective review of haematology patients had been tested using the monoclonal reagent testing profile the total cost would have amounted to £9,232.38. Inclusion of costs for crossmatching (£3.81 per unit) for each unit transfused for the 78 patients with Rh related or K antibodies, based on an average of 46.99 units given to immunised patients in this cohort, gives a total of £13,964.49. The total cost of antibody identification panels and crossmatching for the 78 patients in the haematology cohort with Rh related or K antibodies is estimated at £21,878.37, compared to a cost of £9,232.38 for performing an automated extended phenotyping profile including Rh (CcEe), K, M, N and Cw antigens for all the haematology patients in the cohort. Making the assumption that pre-transfusion phenotyping and matching of blood for Rh (CcEe) and K could prevent the production of antibodies against these antigens, makes, in theory, pre-transfusion phenotyping using an automated assay, a cost effective system for patients with haematological conditions.

To realise the cost benefits of introducing a pre-transfusion phenotyping strategy, particularly tying for Rh (CcEe) and K antigens, for patients with haematological conditions at most risk of developing an allo/autoantibody is recommended, this would include patients with haemolytic anaemia, aplastic anaemia, Waldenström macroglobulinaemia, chronic lymphocytic leukaemia, chronic myelo-monocytic leukaemia, acute myeloid leukaemia, myelodysplastic syndrome and myeloproliferative disease, shown to be high risk for antibody development in this study. The high proportion of antibodies to Rh and Kell antigens seen in patients in both the haematology cohort (66.7% of alloantibodies) and in the renal cohort (67.0%) would support the implementation of a typing and matching of blood for transfusion strategy for these antigens. Restriction of this strategy to female patients within the renal cohort could further improve the cost effectiveness of pre-transfusion antigen typing and matching of blood, as females in this cohort were seen to have a greater risk of antibody development than males.

Implementation of pre-transfusion testing for all patients, prior to the primary transfusion, using the polyclonal reagent testing profile (Jk^a, Jk^b, Fy^a, Fy^b, S, s, k antigens) is less easy to justify on a cost basis alone, even if restricted to the patients at most risk of development of allo/autoantibodies. However, it could be considered a useful addition to the hospital transfusion service repertoire of tests for patients following the production of a red cell alloantibody for those patients not on a regular transfusion regime. It could also be useful, and possibly cost effective, for

those hospital transfusion services dealing with more substantial numbers of sickle cell disease and Thalassaemia patients than those seen in our institution.

The use of serological phenotyping methods is limited in the presence of autoantibodies and not recommended if the patient has been recently transfused due to interference by transfused red cells (BCSH, 2013). In these cases the phenotype may be predicted using genotyping methods (BCSH, 2013). In this study red cell antigen status predicted by the BLOODChip IDCOREXT blood group genotyping technique showed a high correlation with the serological antigen status in the 47 patients tested. In addition, the IDCOREXT included assays covering a wider range of red cell antigens than that covered by the automated serological assay. Although typing and matching of blood for all antigens detected by the genotyping system is not currently possible, the additional information provided is useful in the event of the patient developing alloantibodies post transfusion.

The IDCOREXT technique was simple to use, with a low failure rate and high concordance with phenotyping results. However, the DNA preparation phases are manual and labour intensive, and, as such, do not currently lend them to the hospital transfusion setting where staff may not be specialised in genetic techniques and the risk of error makes manual testing undesirable. The advent of platforms with integrated DNA extraction and real-time PCR, such as those used for microbiological

assays (Riedlinger *et al.,* 2010; Le Guern *et al.,* 2012; Dalpke *et al.,* 2012), may mean that these types of specialised tests can be transferred into the routine service setting of the hospital transfusion laboratory. The cost of blood group genotyping is also currently prohibitive for routine use, the cost per test of the IDCOREXT assay alone is approximately £47 with the additional costs for DNA extraction, amplification, staff time and analyser costs pushing the total cost to around £73 per patient. Consequently, this type of assay is currently reserved for chronically transfused patients with multiple antibodies. As DNA testing in general becomes more mainstream and automated, it is likely that the costs will reduce and, in the future, this may succeed serological phenotyping as the routine test for pre-transfusion typing and matching strategies and confirmatory testing for patients with red cell antibodies.

In the future, the potential for next generation sequencing (NGS), or massively parallel sequencing, is being explored as current methods detecting SNPs will only detect known blood group genotypes whereas NGS will detect unknown ones as well (Altayar *et al.,* 2013). NGS also allows for very high throughput testing making it ideal for the testing of donated blood. The use of NGS has been suggested as a potential platform to accurately characterise the blood group phenotypes in patients with sickle cell disease, particularly those in the African American population who have a high *RH* allelic diversity (Reid *et al.,* 2014).

Treatment of patients with haematological conditions using allogeneic bone marrow, or stem cell, transplants may introduce a further complication if a strategy for red cell antigen typing and matching of blood for transfusion is implemented. Allogeneic bone marrow transplant (BMT) replaces the recipient haemopoetic cells with those taken from a healthy donor. This technique has been in use for over 20 years and is mainly used as a treatment for leukaemias, lymphoproliferative disorders, solid tumours and some non-malignant disorders (EBMT, 2011). The conditioning regimes available, designed to eliminate malignant disease (Gyurkocza and Sandmaier, 2014), should also eradicate immune system cells in the bone marrow of the recipient, leaving the recipient immune suppressed and tolerant to any foreign red cell antigens introduced by the transplant. However, there are reports of recipient antibodies being detected many months, and even years after the transplant (Sparkes *et al*., 1979; Witherspoon *et al*., 1978; Korver *et al.,* 1987; Van Tol *et al.,* 1996; Ang *et al.,* 1997) suggesting that some recipient plasma cells may survive the conditioning regime and exist long term. Izumi and co-workers (2003) report an interesting case of a patient with pre-existing alloantibodies to Rh E and c antigens, the patient received a bone marrow transplant from an Rh E+ c+ donor and then suffered from chronic persistent haemolytic anaemia, with positive DAT and IAT present, for approximately 20 months after the BMT (Izumi *et al.,* 2003). Implementation of red cell antigen typing and matching of blood for transfusion for patients prior to, during and after allogeneic bone marrow transplantation would require special attention to the red cell phenotype

of the recipient, donor and that of the blood selected for transfusion at the various stages of the transplant.

The pilot study performed suggested that recruitment to a larger, multi-centre RCT would not pose any real issues, however care would need to be taken with the estimate of the number of recruits to the trial as the death rate of patients in the pilot study is suggestive of a relatively high mortality rate in this cohort. Also, the recruitment process would need to include selection for patients considered most likely to require blood transfusion in the course of their disease treatment as demonstrated in this study, such as myeloma, MDS, MPD, acute and chronic leukaemias, to ensure that sufficient blood transfusions were performed in patients within each arm of the study. Adequate numbers of patients would need to be recruited to ensure that the trial was powered to investigate differences in the rate of development of allo/autoantibodies in patients receiving standard care and those receiving antigen matched blood. An estimate of the sample size required for a two arm, binary, superiority trial designed with a 90% power, which would allow a sample size large enough to be reasonably confident of demonstrating that one of the treatment arms is superior to the other, can be achieved using a power calculator (Sealed Envelope, 2012). In such a trial the binary outcome would have two measures, chronically transfused patients develop Rh and Kell related antibodies or they do not develop antibodies. An estimate of the percentage “success” in the control group and the intervention group need to be established. In this scenario, given that approximately

25% of chronically transfused haematology patients in the retrospective review developed allo/autoantibodies and 67% of the alloantibodies were Rh or K related antibodies, an estimate of 16.75% of patients in the control arm (non matched blood) would make antibodies, compared to 0% in the intervention group (given RhCcEe and K matched blood). Using the power calculator 106 patients (53 in each arm) would be required to have a 90% chance of detecting, as significant at the 5% level, a decrease in the primary outcome measure from 16.75% in the control group to 0% in the intervention group. However, it is prudent to proceed cautiously when determining sample size to reduce the risk of under powering the trial and being unable to make conclusions from the data.

The pilot study revealed issues with availability of antigen matched blood for the less common phenotypes, these issues could be overcome by improving communication between the haematology/renal clinic and the laboratory and early pre-transfusion sample taking, giving laboratory staff sufficient time to order red cell units with appropriate antigen types. Re-design of stock holding could also facilitate supply of matched units; in this pilot study no changes were made to the way that blood units are stored in the blood stock fridge. Current local practice is to store units according to ABO and RhD group, a small stock of c, E and K negative (group O and A) are held separately, but there is no further separation of blood according to Rh and Kell antigen types. Further separation of the blood units could enable easier identification of matching units, which is currently performed by searching through the units, and provide the basis

for an optimum order level for antigen negative units to ensure there are always matching units available, even for patients with the rarer Rh types.

In conclusion, implementation of a strategy for red cell antigen typing and matching of blood for transfusion in patients with haematological conditions and renal insufficiency would appear to be an achievable and beneficial objective. This is supported by a recent study which showed a significantly lower rate of alloimmunisation of haematology patients who were phenotyped and matched for Rh/K antigens compared to a group who only received matched red cells after developing an antibody (Baia *et al*, 2015). An automated platform for rapid, cost effective high throughput extended serological red cell antigen typing, using the Immucor NEO® analyser system, has been demonstrated to be suitable for use in hospital transfusion services, with the potential for development of electronic transfer of results to the host Laboratory Information Management System (LIMS), which would allow hospital transfusion services to implement a type and match strategy encompassing large numbers of patients. The feasibility of introducing a method for blood group genotyping into a routine hospital transfusion service setting has also been assessed. Although the manual aspects of blood group genotyping would appear to preclude this assay from the majority of hospital transfusion laboratories, it remains a valuable tool for reference laboratories. Advances in automated genotyping techniques may see these assays being used in hospital transfusion laboratories in the near future. Cost analysis of the serological phenotyping assay used in this

research has demonstrated that this technique is cost effective if used within a type and match program for Rh (CcEe) and K antigens. The assay for extended serological phenotyping for other blood group systems, assessed in this research was not found to be cost effective for a type and match program. However, this assay is a valuable tool in the hospital transfusion laboratory for serological phenotyping for non-chronically transfused patients with alloantibodies, and has considerable advantages over manual techniques. The small pilot study performed demonstrated that a type and match program for Rh (CcEe) and K antigens can be achieved using the automated serological phenotyping assay for chronically transfused patients. Patients can be provided with matched blood from routine blood stocks held in the laboratory, but provision could be improved with changes to the stock ordering and holding arrangements. In addition, assurance of correct matching of blood could be improved by the addition of algorithms within the LIMS. The pilot study has also demonstrated that a large scale, multi-centre, randomised controlled trial could be conducted in the UK to investigate the potential of a typing and matching approach in reducing the risk of allo and/or autoantibody production and decreasing the cost of laboratory testing in these patient cohorts. The retrospective review of chronically transfused patients demonstrated that these cohorts of patients are at risk of development of alloantibodies, particularly to the Rh and Kell blood group systems. A prospective type and match program has the potential to reduce the transfusion complications for these patients and also reduce the cost of provision of blood for the health service.

The results of this research have been utilised to implement a type and match program and drive the changes required within the hospital transfusion service at the RD&E to ensure that the program is robust and successful. Patients have been enrolled on the program from January 2017. The automated serological phenotyping system has been introduced within the laboratory and the LIMS has been upgraded to incorporate information on the patient antigen status. All new haematology, renal, oncology and paediatric oncology patients are typed for Rh (CcEe) and K antigens prior to first transfusion, patients are identified by the laboratory staff based on the location and/or clinical details provided on the test request form. Previously transfused patients, with no red cell antibodies and with no evidence of transfusion within four months are also included on the program. The LIM system has also been upgraded to include an algorithm for cross checking the patient antigen requirements (included in the computer records as “antigen negative” and detailing the RH (CcEe) and K antigen for which the patient is negative) against the “antigen negative” status of the red cell unit selected for transfusion by the laboratory staff. The computer system allows an override if there is a mis-match in the antigen negative status of the unit and the patient, for cases of emergency transfusion when matched units cannot be supplied from the routine stock. The antigen matching algorithm is also included in the interface for red cell units dispensed from the remote allocation fridges, a system which does not include interaction from the laboratory staff. The blood stock storage arrangements have

been altered to allow red cell units to be stored in individual trays with the Rh (CcEe) and K antigen status clearly marked to enable easy and swift identification by laboratory staff. Changes have also been made to the blood stock ordering process to ensure that sufficient stock of each RhCcEe and K typed units are available.

A preliminary review of the data showed that, during the 12 month period, 273 patients were identified by the laboratory staff as being in a high risk group for chronic transfusion. None of the patients had alloantibodies and all were suitable for serological phenotype with no record of transfusion within the preceding four months. Of the 273 patients included in the type and match program, only 175 were transfused (64.1%), suggesting that identification of patients could be improved. A study by Lin and co-workers (2017) investigating the impact of prophylactic Rh and K antigen matching in patients with MDS also noted challenges in identification of patients. In their study the identification of patients was performed by the clinical staff and communicated to the transfusion laboratory, they noted that only 62% of patients that should have received matched blood were phenotyped. In contrast, in our institution, the identification of patients is performed by laboratory staff and this would appear to lead to excess of phenotyping. Further work is planned within the RD&E to address this issue. Over the study period the patients (n=175) were transfused a total of 773 (range 1 – 50, average 4.4) units of red cells. No cases were noted where matching could not be achieved. At the end of the study period (December 2017) no patients had developed antibodies to Rh or K

antigens, however, 2 patients had developed anti-Jk^a. This is a significant reduction compared to the alloimmunisation rate noted in the retrospective review of chronically transfused haematology patients (1.1% compared to 12.9%) (see chapter 3). The study by Lin and co-workers (2017) also noted no alloimmunisation to Rh and K antigens for patients receiving matched blood, but noted a 6% alloimmunisation rate for non-Rh/K alloimmunisation rate. This difference could be explained by the fact that the patients in their study were transfused over a longer time frame (3 years compared to 1 year) and received more red cell units (median 39 units) compared to the RD&E patients (median 2 units). It is accepted that a type and match strategy for Rh (CcEe) and K antigens cannot eliminate alloimmunisation to non-Rh/K antigens. However, the fact that two patients at the RD&E developed anti-Jk^a after exposure to a small number of units (one patient received 1 unit and the other received 4 units) has prompted consideration for the inclusion of typing and matching for Jk^a and Jk^b antigens into the program.

The cost of serological phenotyping for the RD&E patients amounted to £1629.81. As a crude measure of cost effectiveness, the costs for antibody identification and serological crossmatching were compared for the same time period before and after implementation of the program. The reduction in additional testing post implementation of the program resulted in savings of £1728.3, although it should be noted that this may also be affected by other factors, such as changes in the patient population and a general reduction in blood usage.

In conclusion, a type and match strategy would appear to be both achievable, in terms of service provision, and beneficial, in terms of laboratory workload, cost effectiveness and patient alloimmunisation rate for patients likely to require long-term transfusion support.

9 REFERENCES

Abdelrazik, A. M., Elshafie, S. M., El Said, M. N., Ezzat Ahmed, G. M., Al-Gamil, A.-K. A., El Nahhas, M. G. M. and Sady, A. A. B. (2016), Study of red blood cell alloimmunization risk factors in multiply transfused thalassemia patients: role in improving thalassemia transfusion practice in Fayoum, Egypt. Transfusion, 56: 2303–2307.

Agenda for Change NHS pay scale. NHS employers http://www.nhsemployers.org/case-studies-and-resources/2017/03/agenda-for-change-pay-scales-and-points-april-2017 (website accessed 20.1.2018)

Ahrens, N., Pruss, A., Kahne, A., Kieswewetter, H. and Salama, A. Coexistence of autoantibodies and alloantibodies to red blood cells due to transfusion. Transfusion 2007; 47, 813-816.

Altayar, M., Halawani, A., Kiernan, M., Reynolds, A., Kaushik, N., Madgett, T. and Avent, N. Next Generation Sequencing based genotyping of Duffy, Kidd and ABO blood group genes. Transfusion Medicine 2013; 23, 62-63.

Alfinito, F., Sica, N., Luciano, L., Della Pepa R., Palladino, C., Ferrara, I., Giani, U., Ruggiero, G. and Terrazzano, G. Immune dysregulation and

dyserythropoesis in the myelodysplastic syndromes. British Journal of Haematology 2010; 148, 90-98.

Altman, D. and Bland, J. How to randomize. British Medical Journal 1999a; 319, 703-704.

Altman, D. and Bland, J. Statistics notes. Treatment allocation in controlled trials: why randomise? British Medical Journal 1999b; 318, 1209.

Alves, V., Martins, P., Soares, S., Araújo, G., Schmidt, L., Costa, S., Langhi, D. and Moraes-Souza, H. (2012). Alloimmunization screening after transfusion of red blood cells in a prospective study. Revista Brasileira de Hematologia E Hemoterapia, *34*, 206–211.

Ang, H., Apperley, J. and Ward, K. Persistence of antibody to human parvovirus B19 after allogeneic bone marrow transplantation: role of prior recipient immunity. Blood 1997; 89, 4646-4651.

Arain, M., Campbell, M., Cooper, C. and Lancaster, G. What is a pilot or feasibility study? A review of current practice and editorial policy. BioMed Central Medical Research Methodology 2010; 10, 67.

Arber, D., Orazi, A., Hasserjian, R., Thiele, J., Borowitz, M., Le Beau, M., Bloomfield, C., Cazzola, M. and Vardiman, J. The 2016 revision to the

World Health Organization classification of myeloid neoplasms and acute leukemia. Blood 2016; 127, 2391-2405.

Asfour, M., Narvios, A. and Lichtiger B. Transfusion of RhD-Incompatible Blood Components in RhD-Negative Blood Marrow Transplant Recipients. Medscape General Medicine. 2004; 6, 22.

Astor, B., Muntner, P., Levin, A., Eustace, J. and Coresh, J. Association of kidney function with anaemia. The Third National Health and Nutrition Examination Survey (1988-1994). Archives of Internal Medicine 2002, 162, 1401-1408.

Avent, N., Ridgwell, K., Tanner, M. and Anstee, D. cDNA cloning of a 30 kDa erythrocyte membrane protein associated with Rh (Rhesus) blood-group-antigen expression. Biochemical Journal. 1990; 271, 821-815.

Avent, N., Martinez, A., Flegel, W., Olsson, M., Scott, M., Nogues, N., Pisacka, M., Daniels, G., van der Schoot, E., Muniz-Diaz, E., Madgett, T., Storrey, J., Beiboer, S., Maaskant-van Wijk, P., von Zabern, I., Jiminez, E., Tejedor, D., Lopez, M., Camacho, E., Cheroutre, G., Hacker, A., Jinoch, P., Svobodova, I. and de Haas, M. The BloodGen project: towards mass scale comprehensive genotyping of blood donors in the European Union and beyond. Transfusion 2007; 47, 405-465.

Avent, N. Large-scale blood group genotyping – clinical implications. British Journal of Haematology 2009; 144, 3-13.

Aygun, B., Padmanabhan, S., Paley, C. and Chandrasekaran, V. Clinical significance of red cell alloantibodies in sickle cell patients who received transfusions. Transfusion 2002; 42, 37-43.

Baia, F., Correia, F., Alves, B., Martinez, F., Koch, C., Carneiro, A. and Araujo. Phenotyping Rh/Kell and risk of alloimmunization in haematological patients. Transfusion Medicine 2015; 26, 34-38.

Barrett, J., Sauntharajah, Y. and Molldrem, J. Myelodysplastic syndrome and Aplastic Anaemia: distinct entities or diseases linked by a common pathophysiology? Seminars in Hematology 2000; 37, 15-29.

Bauer, M., Wiersum-Osselton, J., Schipperis, M., Vandenbroucke, J. and Briet, E. Clinical predictors of alloimmunisation after red blood cell transfusion. Transfusion 2007; 47, 2066-2071.

BCSH Working Party of the British Committee for Standards in Haematology Blood Transfusion Task Force. Guidelines for pre-transfusion compatibility procedures in blood transfusion laboratories. Transfusion Medicine 2013; 23, 3-35.

BCSH Validation and Qualification, including change control, for hospital transfusion laboratories. Transfusion Medicine 2012; 22, 5-43.

Beauregard, P and Blajchman, M. Haemolytic and pseudo-haemolytic transfusion reactions and the clinical conditions that mimic them. Transfusion Medicine Reviews 1994; 8, 184-199.

Belhacene, N., Maulon, L., Guerin, S., Ehrland, J., Colin, Y., Cartron, J. and Auberger, P. Differential expression of the Kell blood group and CD10 antigens: two related membrane metallopeptidases during differentiation of K562 cells by phorbol ester and hemin. Federation of American Societies for Experimental Biology 1998; 12, 531-539.

Bennet, J., Catovsky, D., Daniel, M., Flandrin, G., Galton, D., Gralnick, H. and Sultan, C. Proposal for the classification of the acute leukaemias. British Journal of Haematology, 1976; 33, 452-459.

Blumberg, N., Peck, K., Ross, K. and Avila, E. Immune response to chronic red blood cell transfusion. Vox Sanguinis 1983; 44, 212-217.

Blumberg, N., Ross, K., Avila, E. and Peck, K. Should chronic transfusion be matched for antigens other than ABO and Rh_0 (D)? Vox Sanguinis 1984; 47, 205-208.

Brugnara, C. and Eckardt, K. Hematologic aspects of kidney disease. In Taal MW, ed. Brenner and Rector's The Kidney. 9th ed. Philadelphia: Saunders; 2011: 2081-2120.

Cartwright, R., Gilman, E. and Gurney, K. Time trends in incidence of haematological malignancies and related conditions. British Journal of Haematology 1999; 106, 281-295.

Castilho, L. and Pellegrino Júnior, J. Blood group genotyping. Revista Brasileira de Hematologia e Hemoterapia 2004; 26, 135-140.

Champlin, R. and Gale, R. Acute myelogenous leukaemia: recent advances in therapy. Blood 1987, 69, 1551-1562.

Chan, J., Banks, P., Cleary, M., Delsol, G., De Wolf-Peeters, C., Falini, B., Gatter, K., Grogan, T., Harris, N., Isaacson, P., Jaffe, E., Knowles, D., Mason, D., Muller-Hermelink, H-K., Pileri, S., Prirs, M., Ralfkiaer, E., Stein, H. and Warnke, R. A proposal for classification of lymphoid neoplasms (by the International Lymphoma Study Group). Histopathology 1994; 25, 517-536.

Chan, J., Banks, P., Cleary, M., Delsol, G., De Wolf-Peeters, C., Falini, B., Gatter, K., Grogan, T., Harris, N., Isaacson, P., Jaffe, E., Knowles, D., Mason, D., Muller-Hermelink, H., Pileri, S., Piris, M., Ralfkiaer, E., Stein, H. and Warnke, R. A revised European-American classification of

lymphoid neoplasms proposed by the International Lymphoma Study Group. A summary version. American Journal of Clinical Pathology 1995; 103, 543-560.

Cherif-Zahar, B., Bloy, C., Le Van Kim, C., Blanchard, D., Bailly, P., Hermand, P., Salmon, C., Cartron. J. and Colin, Y. Molecular cloning of protein structure of a human blood group Rh polypeptide. Proceedings of the National Academy of Sciences 1990; 87, 6243-6247.

Chou, S. and Westhoff, C. Molecular biology of the Rh system: clinical considerations for transfusion in sickle cell disease. American Society of Hematology Education Book 2009; 1, 178-184.

Chou, S., Jackson, T., Vege, S., Smith-Whitley, K., Friedman, D. and Westhoff, C. High prevalence of red cell alloimmunization in sickle cell disease despite transfusion for Rh-matched minority donors. Blood 2013; 122, 1062-1071.

Churchill, D., Taylor, D., Cook, R., La Plante, P., Barre, P., Cartier, P., Fay, W., Goldstein, M., Jindal., K. and Mandin, H. Canadian Hemodialysis Morbidity Study. American Journal of Kidney Disease 1992; 19, 214-234.

Coles, S., Klein, H. and Holland, P. Alloimmunisation in two multitransfused patient populations. Transfusion 1981; 21, 462-466.

Cook, I. Primary rhesus immunization of male volunteers. British Journal of Haematology 1971; 20, 369-75.

Coombs, R.R.A., Mourant, A.E. and Race, R.R., 1945. Detection of Weak and “Incomplete” Rh Agglutinins: A New Test. In *Rhesus haemolytic disease* (pp. 88-88). Springer Netherlands.

Coombs, R., Mourant, A. and Race, R. A new test for detection of weak and “incomplete” Rh agglutinins. British Journal of Experimental Pathology 1945(b); 26: 255-266.

Cornell, L., Smith, R. and Colvin, R. Kidney transplantation: mechanisms of rejection and acceptance. Annual Review of Pathology 2008; 3, 189-220.

Court-Brown, W. and Doll, R. Adult Leukaemia Trends in mortality in relation to aetiology. British Journal of Medicine 1959; 1, 1063-1069.

Cvejic, A., Haer-Wigman, L., Stephens, J., Kostadima, M., Smethurst, P., Frontini, M., van den Akker, E., Bertone, P., Bielczyk-Maczyńska, E., Farrow, S., Fehrmann, R., Gray, A., de Haas, M., Haver, V., Jordan, G., Karjalainen, J., Kerstens, H., Kiddle, G., Lloyd-Jones, H., Needs, M., Poole, J., Ait Soussan, A., Rendon, A., Rieneck, K., Sambrook, J., Schepers, H., Silljé, H., Sipos, B., Swinkels, D., Tamuri, A., Verweij, N.,

Watkins, N., Westra, H-J., Stemple, D., Franke, L., Soranzo, N., Stunnenberg, H., Goldman, N., van der Harst, P., van der Schoot, C., Ouwehand, W. and Albers, C. SMIM1 underlies the Vel blood group and influences red blood cell traits. Nature Genetics 2013; 45, 542-545.

Dalpke, A., Hofko, M. and Zimmerman, S. Comparison of the BD Max Methicillin-Resistant *Staphylococcus Aureus* (MRSA) Assay and the BD GeneOhm MRSA Achromopeptidase Assay with Direct- and Enriched-Culture Techniques Using Clinical Specimens for Detection of MRSA. Journal of Clinical Microbiology 2012; 50, 3365-3367.

Daniels, G., Fletcher, A., Garratty, G., Jørgensen, J., Judd, W., Levene, C., Lomas-Francis, C., Moulds, J. J., Moulds, J.M., Overbeeke, M., Reid, M., Rouger, P., Scott, M., Sistonen, P., Smart, E., Tani, Y., Wendel, S. and Zelinski, T. Blood group terminology 2004: from the International Society of Blood Transfusion committee on terminology for red cell surface antigens. Vox Sanguinis 2004; 87, 304-316.

Daniels, G. Human Blood Groups. Third Edition 2013. Wiley-Blackwell.

Daniels, G. and Bromilow, I. Essential Guide to Blood Groups. Second Edition 2010. Wiley-Blackwell.

Da Silva, S., Ferriera, G., da Silva, S., Alves, T., Ribeiro, I., Ribeiro, T. and Cavalcante, M. Red blood cell and leukocyte alloimmunisation in

patients awaiting kidney transplantation. Revista Brasileira de Hematologia e Hemoterapia 2013; 35, 185-188.

Davies, S., McWilliam, A., Hewitt, P., Devenish, A. and Brozovic, M. Red cell alloimmunization in sickle cell disease. British Journal of Haematology 1986; 63, 241-245.

Dean, L. Blood Groups and Red Cell Antigens. Bethesda (MD): National Centre for Biotechnology Information (US); 2005. (http://www.ncbi.nlm.nih.gov/books/NBK2261/ Accessed 26.02.13).

Denomme, G. and Van Oene, M. High-throughput multiplex single-nucleotide polymorphism analysis for red cell and platelet antigen genotypes. Transfusion 2005; 45, 660-666.

Deschamps-Latscha, B. and Chatenoud, L. T cells and B cells in Chronic Renal Failure. Seminars in Nephrology 1996; 16, 183-191.

Dombret, H. and Gardin, C. An update of current treatments for adult acute myeloid leukaemia. Blood 2016; 127, 53-61.

Domen, R. and Ramirez, G. Red Cell Alloimmunization in Chronic Renal Failure Patients Undergoing Hemodialysis. Nephron 1988; 48, 284-285.

Drago, F., Karpasitou, K. and Poli, F. Microarray beads for Identifying Blood Group Single Nucleotide Polymorphisms. Transfusion Medicine and Hemotherapy 2009; 36, 157-160.

Drago, F., Karpasitou, K., Spinardi, L., Crespiatico, L., Scalamogna, M. and Poli, F. A Microsphere-Based Suspension Array for Blood Group Molecular Typing: An Update. Transfusion Medicine and Hemotherapy 2010; 37, 336-338.

Drüeke, T. Hyporesponsiveness to recombinant human erythropoietin. Nephrology Dialysis Transplantation 2001, 16, 25-28.

Dutcher, J., Schiffer, C., Aisner, J. and Wiernik, P. Long term follow up patients with leukaemia receiving platelet transfusions: identification of a large group of patients who do not become alloimmunized. Blood 1981; 58, 1007-1011.

European Group for Blood and Marrow Transplantation (EBMT). Annual report 2011: (https://www.ebmt.org/Contents/Resources/Library/Annualreport/Documents/Annual%20Report%2011%20EBMT%20vertical_Website.pdf accessed 01/06/2016).

Eiberg, H. and Mohr, J. Dombrock blood group (DO): assignment to chromosome 12p. Human Genetics 1996; 98, 518-521.

El Nemer, W., Rahuel, C., Colin, Y., Gane, P., Cartron, J. and Le Van Kim, C. Organization of the Human *LU* Gene and Molecular Basis of the Lu^a/Lu^b Blood Group Polymorphism. Blood 1997; 89, 4608-4616.

Endeward, V., Cartron, J-P. and Gros, G. RhAG protein of the Rhesus complex is a CO_2 channel in the human red cell membrane. FASEB Journal (The official journal of the Federation of American Societies for Experimental Biology) 2008; 22, 64-73.

Ehrlich, G., Viegas-Pequignot, E., Ginzberg, D., Sindel, L., Soreq, H. and Zakut, H. Mapping the Human Acetylcholinesterase Gene to Chromosome 7q22 by Fluorescent *in situ* Hybridization Coupled with Selective PCR Amplification from a Somatic Hybrid Cell Panel and Chromosome-Sorted DNA Libraries. Genomics 1992; 13, 1192-1197.

Erslev, A. Humoral regulation of red cell production. Blood 1953; 8, 349-357.

Exeter Census Profile 2011. Devon County Council http://www.devon.gov.uk/census_profile-exeter.pdf (accessed 29/01/2018).

Ferlay, J., Autier, P., Boniol, M., Haenue, M., Colombet, M. and Boyle, P. Estimates of cancer incidence and mortality in Europe 2006. Annals of Oncology 2007, 18, 581-592.

Finning, K., Bhandari, R., Sellers, F., Revelli, N., Villa, M. A., Muñiz-Díaz, E., and Nogués, N. (2016). Evaluation of red blood cell and platelet antigen genotyping platforms (ID CORE XT/ID HPA XT) in routine clinical practice. Blood Transfusion, 14, 160–167.

Fleiss, J., Levin, B. and Park, M. A statistical method for rates and proportion. How to randomize. Third edition. Hobohan NJ. John Wiley and Sons, 2003.

Fluit, C., Kunst, V. and Drenthe-Schonk, A. Incidence of red cell antibodies after multiple blood transfusion. Transfusion 1990; 30, 532-535.

Frane, J. A method of biased coin randomisation, its implementation and validation. Drug Information Journal 1998; 32, 423-432.

Freda, V, Gorman, J., Pollack, W., Robertson, J., Jennings, E. and Sullivan, J. Prevention of Rh isoimmunization: progress report of the clinical trial in mothers. Journal of the American Medical Association 1967; 199, 390-4.

Friedman, L., Furberg, C. and DeMets, D. Fundamentals of Clinical Trials 3. New York: Springer; 1998.

Frohn, C., Dumbgen, L., Brand, J., Gorg, S., Luhm, J. and Kirchner, H. Probability of anti-D development in D- patients receiving D+ RBCs. Transfusion 2003; 43, 893-8.

Gabardi, S., Martin, S., Roberts, K. and Grafais, M. Induction immunosuppressive therapies in renal transplantation. American Journal of Health System Pharmacy 2011; 68, 211-218.

Garratty, G. Novel mechanisms for immune destruction of circulating autologous cells. In: Silberstein LE, editor. Autoimmune disorders of blood. Bethesda: American Association of Blood Banks; 1996, 79-114.

Garratty, G. Autoantibodies induced by blood transfusion. Transfusion 2004; 44, 5-9.

Gassner, C., Meyer, S., Frey, B. and Vollmert, C. Matrix-assisted laser desorption/ionisation, time-of-flight mass spectrometry-based blood group genotyping – the alternative approach. Transfusion Medicine Reviews 2013; 27, 2-9.

Gaston, R. Maintenance immunosuppression in the renal transplant recipient: an overview. American Journal of Kidney Diseases. 2001; 38, S25-S35.

Gerrard-Marchant, R., Hamlin Lennart, K., Rilke, F. and Stansfield, A. Classification of NHL. Lancet 1974; ii, 406-409.

Getman, D., Eubanks, J., Camp, S., Evans, G. and Taylor, P. The Human Gene Encoding Acetylcholinesterase Is Located on the Long Arm of Chromosome 7. American Journal of Human Genetics 1992; 52, 170-177.

Goldman, M., Nogués, N. and Castilho, L. An overview of the Progenika ID CORE XT: an automated genotyping platform based on a fluidic microarray system. Immunohaematology 2015; 31, 62-68.

Grais, M. Mortality and Morbidity from Leukaemia and Aleukaemia in Specific Countries. Bulletin of the World Health Organisation 1962; 25, 683- 688.

Guelsin, G., Sell, A., Castilho, L., Masaki, V., Melo, F., Hashimotot, N., Higa, T., Hirle, L. and Visentainer, J. Benefits of Blood Group Genotyping in Multi-Transfused Patients from the South of Brazil. Journal of Clinical Laboratory Analysis 2010; 24, 311-316.

Gunson, H., Stratton, F., Cooper, D. and Rawlinson, V. Primary immunization of Rh-negative volunteers. British Medical Journal 1970; 1, 593-5.

Gyurkocza, B. and Sandmaier, B. Conditioning regimens for hematopoietic cell transplantation: one size does not fit all. Blood 2014; 124, 344-353.

Hallorhan, P. Immunosuppressive drugs for kidney transplantation. New England Journal of Medicine 2004; 351, 2715-2719.

Harris, N., Jaffe, E., Stein, H., Banks, P., Chan, J., Cleary, M., Delsol, G., De Woolf-Peeters, C., Falini, B., Gatter, K., Grogan, T., Isaacson, P., Knowles, D., Mason, D., Muller-Hermelink, H., Pileri, S., Piris, M., Ralfkiaer, E. and Warnke, R. A revised European-American classification of lymphoid neoplasms: a proposal from the International Lymphoma Study Group. Blood 1994; 84, 1361-1392.

Hashmi, G., Shariff, T., Seul, M., Vissavajjhala, P., Hue-Roye, K., Charles-Pierre, D., Lomas-Francis, C., Chaudhuri, A. and Reid, M. A flexible array format for large scale rapid blood group DNA typing. Transfusion 2005; 45, 680-688.

Hashmi, G., Shariff, T., Zhang, Y., Cristobal., J., Chau, C., Seul, M., Vissavajjhala, P., Baldwin, C., Hue-Roye, K., Charles-Pierre, D., Lomas-

Francis, C. and Reid, M. Determination of 24 minor red blood cell antigens for more than 2000 blood donors by high-throughput DNA analysis. Transfusion 2007; 47, 736-747.

Heddle, N., Soutar, R., O'Hoski, P., Singer, J., McBride, J., Ali, M. and Kelton, J. A prospective study to determine the frequency and clinical significance of alloimmunization post-transfusion. British Journal of Haematology 1995; 91, 1000-5.

Hendrickson, J., Desmarets, M., Deshpande, S., Chadwick, T., Hillyer, C., Roback, J. and Zimring, J. Recipient inflammation affects the frequency and magnitude of immunization to transfused red cells. Transfusion 2006; 46, 1526-1536.

Hinds, P. and Gattuso, J. From pilot work to a major study in cancer nursing research. Cancer Nursing 1991; 14, 132-135.

Hirschfeld, H. A connection between correlation and contingency. Proceedings of the Cambridge Philosophical Society 1935; 31, 520-524.

Hmida, S., Mojaat, N., Maamar, M., Bejaoui, M., Mediouni, M. and Boukef, K. Red cell alloantibodies in patients with haemoglobinopathies. Nouvelle Revue Francaise d'Hematologie 1994; 36, 363-366.

Hoeltge, G., Domen, R., Rybicki, L. and Schaffer, P. Multiple Red Cell Transfusions and Alloimmunization: Experience With 6996 Antibodies Detected in a Total of 159 262 patients from 1985 to 1993. Archives of Pathology and Laboratory Medicine 1995; 119, 42-5.

Holohan, T., Terasaki, P. and Deisseroth, A. Suppression of Transfusion Related Alloimmunization in Intensively Treated Cancer Patients. Blood 1981; 58, 122-128.

Huang, C-H., Johe, K., Moulds, J., Siebert, P., Fukuda, M. and Blumenfeld, O. δ glycophorin (glycophorin B) gene deletion in two individuals homozygous for the S-s-U- blood group phenotype. Blood 1987; 70, 1830-1835.

Huang, C-H., Reid, M. and Blumenfeld, O. Remodelling of the Transmembrane Segment in Human Glycophorin by Aberrant RNA Splicing. Journal of Biological Chemistry 1994; 269, 10804-18012.

Huang, C-H. and Blumenfeld, O. MNSs blood groups and major glycophorins: Molecular basis for allelic variation. In: Cartron, J-P, Rouger, P. eds. Molecular basis of human blood group antigens. New York: Plenum Press 1995, 153-188.

Huang, C-H., Blumenfeld, O., Reid, M., Chen, Y., Daniels, G. and Smart, E. Alternative Splicing of a Novel Glycophorin Allele GPHe(GL)

Generates Two Protein Isoforms in the Human Erythrocyte Membrane. Blood 1997; 90, 391-397.

Hu, F., Hu, Y., Ma, Z. and Rosenberger, W. Adaptive randomization for balancing over covariates. WIREs Computational Statistics 2014; 6, 288-303.

Huh, Y. and Lichtiger, B. Transfusion Reactions in Patients with Cancer. American Journal of Clinical Pathology 1987; 87, 253-257.

Human Genome Organisation: Gene Nomenclature Committee http://www.genenames.org/cgi-bin/genefamilies/set/454 (accessed 04/12/2015).

Isacke, C. and Horton, M. The Adhesion Molecule Facts Book, Edition 2. Academic Press. London. 2000.

Ishikura, H., Endo, J., Saito, Y., Kosaka, Y., Matsuo, S., Nagasue, N., Nakamura, T., Tsunematsu, T., Miyazaki, T. and Matsumoto, H. Graft versus host antibody reaction causing a delayed hemolytic anaemia after blood transfusion. Blood 1993; 82, 3222-3.

Issitt, P. and Anstee, D. Applied Blood Group Serology. Fourth Edition, 1998. Montgomery Scientific Publications. Durham, North Carolina, USA.

Izumi, N., Fuse, I., Furukawa, T., Uesugi, Y., Tsuchiyama, J., Toba, K., Togashi, K., Yamada, K., Ohtake, S., Saitoh, Y., Yanagisawa, N. and Aizawa, Y. Long-term production of pre-existing alloantibodies to E and c after allogeneic BMT in a patient with aplastic anemia resulting in delayed hemolytic anemia. Transfusion 2003; 43, 241-245.

Jacobson, L., Goldwasser, E., Fried, W. and Plzak, L. Role of the kidney in erythropoiesis. Nature 1957; 179, 633-634.

JPAC - Joint United Kingdom (UK) Blood Transfusion and Tissue Transplantation Services Professional Advisory Committee. transfusionguidelines.org (www.transfusionguidelines.org.uk/transfusion-handbook accessed 03.04.2015). Transfusion Handbook 5th ed. Jan 2014.

JPAC - Joint United Kingdom (UK) Blood Transfusion and Tissue Transplantation Services Professional Advisory Committee. transfusionguidelines.org. Guidelines for the Blood Transfusion Services in the United Kingdom 8th edition, 2013.

Juji, T, Kano, K. and Milgrom, F. Mixed agglutination with platelets. International Archives of Allergy. 1972; 42, 474-484.

Kadar, J. Impact of phenotype-matched red cell transfusions on the long term blood supply of patients under hematolooncologic outpatient care. Vox Sanguinis 2010, 99, 465-465.

Kalish, L. and Begg, G. Treatment allocation methods in clinical trials; a review. Statistics in Medicine 1985; 4, 129-144.

Karpasitou, K., Drago, F., Crespiatico, L., Paccapelo, C., Truglio, F., Frison, S., Scalamogna, M and Poli, F. Blood group genotyping for Jka/Jkb, Fya/Fyb, S/s, K/k, Kpa/Kpb, Jsa/Jsb, Coa/Cob and Lua/Lub with microarray beads. Transfusion 2008; 48, 505-512.

Kato, S., Chmielewski, M., Honda, H., Pecoits-Filho, R., Matsuo, S., Yazawa, Y., Tranaeus, A., Stenvinkel, P. and Lindholm, B. Aspects of immune dysfunction in end stage renal disease. Clinical Journal of the American Society of Nephrology 2008; 3, 1526-1533.

King, L., Kozono, D. and Agre, P. From structure to disease: the evolving tale of aquaporin biology. Nature Reviews Molecular Cell Biology 2004 (a); 5, 687-698.

King, K., Shirey, R., Thoman, S., Benson-Kennedy, D., Tanz, W. and Ness, P. Universal leukoreduction decreases the incidence of febrile nonhemolytic reactions to RBCs. Transfusion 2004 (b); 44, 25-29.

Kipps, T. and Carson, D. Autoantibodies in Chronic Lymphocytic Leukaemia and Related Systemic Autoimmune Diseases. Blood 1993; 81, 2475-2487.

Klapper, E., Zhang, Y., Figueroa, P., Ness, P., Stubbs, J., Abumuhor, I., Bailey, J., Epperson, L., Tauscher, C., Enriquez, E., Hashmi, G. and Seul, M. Towards extended phenotype matching: a new operational paradigm for the transfusion service. Transfusion 2010; 50, 536-546.

Korver, K., de Lange, G., van den Burgh, R., Schellekens, P. and van Loghem, E. Lymphoid chimerism after allogeneic bone marrow transplantation. Y-chromatin staining of peripheral T and B lymphocytes and allotyping of serum immunoglobulins. Transplantation 1987; 44, 643-650.

Kościelak, J. The Hypothesis on Function of Glycosphingolipids and ABO Blood Groups Revisited. Neurochemical Research 2012; 37, 1170-1184.

Kraemer, H., Mintz, J., Noda, A., Tinklenberg, J. and Yesavge, J. Caution regarding the use of pilot studies to guide power calculations for study proposals. Archives of General Psychiatry 2006; 63, 484-489.

Kudo, S. and Fukuda, M. Identification of a Novel Human Glycophorin, Glycophorin E, by Isolation of Genomic Clones and Complementary DNA

Clones Utilizing Polymerase Chain Reaction. Journal of Biological Chemistry 1990; 265, 1102-1110.

Lancaster, G., Dodd, S. and Williamson, P. Design and analysis of pilot studies: recommendations for good practice. Journal of Evaluation in Clinical Practice 2004; 10, 307-312.

Lapierre, Y., Rigal, D., Adam, J., Josef, D., Meyer, F., Greber, S. and Drot, C. The gel test: a new way to detect red cell antigen-antibody reactions. Transfusion 1990; 30, 109-113.

Laundy, R., Karamatic Crew, V., Davies, H., Harris, C., Baglow, L., Walser, P. and Thornton, N. A novel high incidence antigen in the Yt blood group system. Transfusion Medicine 2017; 27, 19-20.

Lee, E., Whitehead, A., Jacques, R. and Julious, S. The statistical interpretation of pilot trials: should significance thresholds be reconsidered? BioMed Central; Medical Research Methodology 2014; 14, 41.

Lee, R-A and Gabardi, S. Current trends in immunosuppressive therapies for renal transplant recipients. American Journal of Health-System Pharmacy 2012; 69, 1961-1975.

Lee, S., Zambas, E., Marsh, W. and Redman, C. The Human Kell Blood Group Gene Maps to Chromosome 7q33 and its Expression Is Restricted to Erythroid Cells. Blood 1993; 81, 2804- 2809.

Le Guern, R., Herwegh, S., Grandbastien, B., Courcol, R. and Wallet, F. Evaluation of a new molecular test, the BD Max Cdiff, for detection of toxigenic *Clostridium difficile* in fecal samples. Journal of Clinical Microbiology 2012; 50, 3089-3090.

Leon, A., Davis, L. and Kraemer, H. The role and interpretation of pilot studies in clinical research. Journal of Psychiatric Research 2011; 45, 626-629.

Levine, P., Stock, A., Kuhmichel, A. and Bronikovsky, N. A new human blood factor of rare incidence in the general population. Proceedings of the Society of Experimental Biology 1951; 77, 402-403.

Lin, Y., Saskin, A., Wells, R., Lenis, M., Mamedov, A., Callum, J. and Buckstein, R. Prophylactic RhCE and Kell antigen matching: impact on alloimmunization in transfusion-dependent patients with myelodysplastic syndromes. Vox Sanguinis 2017; 112, 79-86.

Loscalzo, J. Pilot trials in clinical research: of what value are they? Circulation 2009; 119, 1694-1696

Lucien, N., Sidoux-Walter, F., Olives, B., Moulds, J., Le Pennec, P-Y., Cartron, J-P. and Bailly, P. Characterization of the Gene Encoding the Human Kidd Blood Group/Urea Transporter Protein. Evidence for splice site mutations in Jk_{null} individuals. Journal of Biological Chemistry 1998; 273, 12973-12980.

Lukes, R. and Butler, J. The pathology of the nomer data of HD. Cancer Research, 1986; 26, 1077-1081.

Maciejewski, J., O'Keefe, C., Gondek, L. and Tiu, R. Immune mediated bone marrow failure syndromes of progenitor and stem cells: molecular analysis of cytotoxic T cell clones. Fiolia Histochemica et Cytochemica 2007; 45, 5-14.

Makins, G. Injuries to the Blood Vessels. In History of the Great War Medical Services. Surgery of the War London, 1922, 2, 170-296. His Majesty's Stationery Office, London.

Mallinson, G., Soo, K., Schall, T., Pisacka, M. and Anstee, D. Mutations in the erythrocyte chemokine receptor (Duffy) gene: the molecular basis of the Fy^a/Fy^b antigens and identification of a deletion in the Duffy gene of an apparently healthy individual with the Fy(a-b-) phenotype. British Journal of Haematology 1995; 90, 823-829.

Marini, A-M., Urrestarazu, A., Beauwens, R. and Andre, B. The Rh (Rhesus) blood group polypeptides are related to NH_4^+ transporters. Trends in Biochemical Sciences 1997; 22, 460-461.

Martin-Vega, C., Massuet, L., Julia, A. Autoimmune Haemolytic anaemia (AIHA) in Myelodysplastic Syndromes (MS). In: Proceedings of the XX congress of the International Society of Blood Transfusion in association with the British Blood Transfusion Society. London 1988. Manchester: British Blood Transfusion Society, 1988; 81-81.

Master, S., Ong, M. and Mansour, R. Blood Transfusion in Adult Patients with Sickle Cell Disease: Incidence of Alloimmunization. Blood 2016; 128:2459.

Mathew, S., Chaudhuri, A., Murty, V. and Pogo, A. Confirmation of Duffy blood group antigen locus (*FY*) at 1q22-q23 by fluorescence in situ hybridization. Cytogenetic and Cell Genetics 1994; 67, 68-68.

Mauthe, J., Coghlan, G. and Zelinski, T. Confirmation of the Assignment of the Dombrock Blood Group Locus (*DO*) to chromosome 12p: Narrowing the Boundaries to 12p 12.3 – p13.2). Vox Sanguinis 2000; 79, 53-56.

McBean, R., Hyland, C. and Flower, R. Molecular genotyping platforms for blood group antigen prediction. Pathology 2014a; 46, S87.

McBean, R., Hyland, C. and Flower, R. Approaches to Determination of a Full Profile of Blood Group Genotypes: Single Nucleotide Variant Mapping and Massively Parallel Sequencing. Computational and Structural Biotechnology Journal 2014b; 11, 147-151.

McBean, R., Hyland, C., Roscioli, T. and Flower, R. The low frequency SARAH blood group antigen: evidence for new MNS antigen. Vox Sanguinis. 2014c; 107, 17-17.

McDonald, A., Knight, R., Campbell, M., Entwistle, V., Grant, A., Cook, J., Elbourne, D., Francis, D., Garcia, J., Roberts, I. and Snowdon, C. What influences recruitment to randomised controlled trials? A review of trials funded by two UK funding agencies. BioMed Central; Trials 2006; 7, 9.

Mental Capacity Act 2005 (legislation.gov.uk) accessed 16/10/2015.

Michail-Merianou, V., Phamphili-Panousophoulou, L., Piperi-Lowes, L., Pelegrinis, E. and Karaklis, A. Alloimmunization to red cell antigens in Thalassaemia: comparative study of usual versus better-match transfusion programmes. Vox Sanguinis 1987; 52, 95-98.

Mikhail, A., Shrivastava, R. and Richardson, D. Anaemia of CKD. UK Renal Association, 5th edition, 2009-2012, Final Version 2010.

Milic, M., Webb, G. and Bowen, D. 344 Single centre experience of transfusion-dependent MDS demonstrates a high frequency of allo-antibody formation in heavily transfused patients. Leukemia Research 2011, 35, S138.

Mohanram, A., Zhang, Z., Shahinfar, S., Keane, W., Brenner, B. and Toto, R. Anemia and end-stage renal disease in patients with type 2 diabetes and nephropathy. Kidney International 2004; 66, 1131-1138.

Möller, M., Jöud, M., Storry, J., and Olsson, M. L. Erythrogene: a database for in-depth analysis of the extensive variation in 36 blood group systems in the 1000 Genomes Project. Blood Advances, 2016; 1:240-249. https://doi.org/10.1182/bloodadvances.2016001867 (accessed 26/01/2018).

Moncharmont, P., Barday, G. and Meyer, F. Red blood cell alloimmunisation in 18 to 50-year old transfused women: a 3-year study. Blood Transfusion 2015; 13, 345-346.

Montpetit, A., Phillips, M., Mongrain, I., Lemieux, R. and St-Louis, M. High-throughput molecular profiling of blood donors for minor red blood cell and platelet antigens. Transfusion 2006; 46, 841-848.

Moon, C., Preston, G., Griffin, C., Jabs, E. and Agre, P. The human aquaporin-CHIP gene. Structure, organization, and chromosomal localization. Journal of Biological Chemistry 1993; 268, 15772-15778.

Moore, C., Carter, R., Nietert, P. and Stewart, P. Recommendations for Planning Pilot Studies in Clinical and Translational Research. Clinical and Translational Science 2011; 4, 332-337.

Moreira, G., Bordin, J., Kuroda, A. and Kerbauy, J. Red blood cell alloimmunization in sickle cell disease: The influence of racial and antigenic pattern differences between donors and recipients in Brazil. American Journal of Hematology 1996; 52, 197-200.

Mouro, I., Colin, Y., Sistonen, P., Le Pennec, P., Cartron, J. and Le Van Kim, C. Molecular basis of the RhCW (Rh8) and RhCX (Rh9) blood group specificities. Blood 1995; 86, 1196-1201.

Mufti, G., Figes, A., Hamblin, T. Oscier, D. and Copplestone, J. Immunological abnormalities in the myelodysplastic syndromes. I. Serum immunoglobulins and autoantibodies. British Journal of Haematology 1986; 63, 143-147.

Murakami, M. and Honjo, T. Anti-red blood cell autoantibody transgenic mice: murine model of autoimmune hemolytic anemia. Seminars in Immunology 1996; 8, 3-9.

Murphy, M., Morrison, N., Miles, J., Fraser, R., Spurr, N. and Boyd, E. Regional chromosomal assignment of the Kell blood group locus (*KEL*) to chromosome 7q33-q35 by fluorescence in situ hybridization: evidence for the polypeptide nature of antigenic variation. Human Genetics 1993; 91, 585-588.

Murphy, M., Templeton, L., Fleming, J., Ferguson, M., Peterkin, M. and Fraser, R. Comparison of the Fy^b status as determined serologically and genetically. Transfusion Medicine 1997; 7, 135-141.

Murphy, M., Pamphilon, D and Heddle, N. Practical Transfusion Medicine. 4th edition 2013. Wiley-Blackwell.

Nashan, B. Antibody Induction Therapy in Renal Transplant Patients Receiving Calcineurin-Inhibitor Immunosuppressive Regimens: A Comparative Review. BioDrugs 2005; 19, 39-46.

National Comparative Audit of Blood Transfusion (NCABT). Audit of the use of blood in adult medicine – Part 1 2011. www.hospital.blood.co.uk (accessed 03.04.2015).

National Comparative Audit Reports (NCABT)– National Survey Red Cell Use – 2014 (http://hospital.blood.co.uk/audits/national-comparative-audit/national-comparative-audit-reports/) accessed 01/12/2017.

Neote, K., Mak, J., Kolakowski, L. and Schall, T. Functional and Biochemical Analysis of the Cloned Duffy Antigen: Identity With the Red Blood Cell Chemokine Receptor. Blood 1994; 84, 44-52.

Ness, P., Shirey, R., Thoman, S. and Buck, S. The differentiation of delayed serologic and hemolytic transfusion reactions: incidence, long-term serologic findings, and clinical significance. Transfusion 1990; 30, 688-693.

NICE 2003; Improving Outcomes in Haematological Cancers. The Manual. National Institute for Clinical Excellence. (https://www.nice.org.uk/guidance/ng47/evidence/improving-outcomes-in-haematological-cancers-the-manual-2487893581) accessed 18/04/2018

NICE 2011; Anaemia management in people with chronic kidney disease. www.publications.nice.org.uk/anaemia-management-in-people-with-chronic-kidney-disease-cg114 (accessed 07.03.2014).

NIH National Institute of Diabetes and Digestive and Kidney Diseases (http://www.niddk.nih.gov/health-information/health-topics/kidney-disease/anemia-in-kidney-disease-and-dialysis/Pages/facts.aspx accessed 16/04/2016).

National Institute for Health Research: Guidance Feasibility and Pilot studies (www.nets.nihr.ac.uk/glossary) accessed 17/10/2015.

Norman, D. and Turka, L. Primer on transplantation. 2nd ed. Mt Laurel NJ: American Society of Transplantation 2001; 85-102.

Novaretti, M., Sopelete, C., Velloso, E., Rosa, M., Dorlhiac-Llacer, P. and Chamone, D. Immunohematological findings in myelodysplastic syndrome. Acta Haematologica 2001; 105, 1-6.

Office for National Statistics. Cancer Statistics Registrations, England: 2012; (https://www.ons.gov.uk/peoplepopulationandcommunity/healthandsocialcare/conditionsanddiseases/bulletins/cancerregistrationstatisticsengland/2014-06-19) Accessed 25/12/2017.

Olives, B., Martial, S., Mattei, M-G., Matassi, G., Rousselet, G., Ripoche, P., Cartron, J. and Bailly, P. Molecular characterization of a new urea transporter in the human kidney. FEBS Letters 1996; 386, 156-160.

Olsson, M., Smythe, J., Hansson, C., Poole, J., Mallinson, G., Jones, J., Avent, N. and Daniels, G. The $Fy^{(x)}$ phenotype is associated with a missense mutation in the $Fy^{(b)}$ allele predicting Arg89Cys in the Duffy glycoprotein. British Journal of Haematology 1998; 103, 1184-1191.

Olujohungbe, A., Hambleton, I., Stephens, L., Serjeant, B. and Serjeant, G. Red cell antibodies in patients with homozygous sickle cell disease: a comparison of patients in Jamaica and the United Kingdom. British Journal of Haematology 2001; 113, 661-665.

Parasol, N., Reid, M., Rios, M., Castilho, L., Harari, I. and Kosower, N. A Novel Mutation in the Coding Sequence of the *FY*B* Allele of the Duffy Chemokine Receptor Gene Is Associated With an Altered Erythrocyte Phenotype. Blood 1998; 92, 2237-2243.

Parsons, S., Mallinson, G., Daniels, G., Green, C., Smythe, J. and Anstee, D. Use of Domain-Deletion Mutants to Locate Lutheran Blood Group Antigens to Each of the Five Immunoglobulin Superfamily Domains of the Lutheran Glycoprotein: Elucidation of the Molecular Basis of the Lu^a/Lu^b and the Au^a/Au^b Polymorphisms. Blood 1997; 88, 4219-4225.

Plapp, F., Sinor, L., Rachel, J., Beck, M., Coenen, W. and Bayer, W. A Solid Phase Antibody Screen. American Journal of Clinical Pathology 1984; 82, 719-721.

Petz, L. and Garratty, G. Acquired Immune Hemolytic Anemias. New York: Churchill Livingstone, 1980:331-337.

Petz, L. and Garratty, G. Immune Hemolytic Anemias. 2nd Edition. Philadelphia: Churchill Livingstone, 2004.

Pocock, S. and Simon, R. Sequential treatment assignment with balancing for prognostic factors in the controlled clinical trial. Biometrics, 1975; 31, 103-115.

Pruenster, M. and Rot, A. Throwing light on DARC. Biochemical Society Transactions 2006; 34, 1005-1008.

Priyadarshi, A. and Shapiro, J. Erythropoietin resistance in the treatment of anaemia of chronic renal failure. Seminars in Dialysis, 2006; 19, 273-278.

Purohit, K., Weber, J., Ward, L. and Keats, B. The Kell blood group locus is close to the cystic fibrosis locus on chromosome 7. Human Genetics 1992; 89, 457-458.

Race, R. An “Incomplete” Antibody in Human Serum. Nature 1944; 153, 771-772.

Rahuel, C., London, J., Vignal, A., Ballas, S. and Cartron, J-P. Erythrocyte Glycophorin B Deficiency May Occur by Two Distinct Gene Alterations. American Journal of Hematology 1991; 37, 57-58.

Ramsey, G. and Larson, P. Loss of red cell alloantibodies over time. Transfusion 1988; 28, 162-165.

Ramsey, G., Hahn, L., Cornell, F., Boczkowski, D., Staschak, S., Clark, R., Hardesty, R., Griffith, B. and Starzl, T. Low rate of Rhesus immunization from Rh-incompatible blood transfusions during liver and heart transplant surgery. Transplantation 1989; 47, 993-995

Redman, M., Regan, F. and Contreras, M. A Prospective Study of the Incidence of Red Cell Allo-Immunisation following Transfusion. Vox Sanguinis 1996; 71, 216-220.

Reid, M. Applications and Experience with PCR-Based Assays to Predict Blood Group Antigens. Transfusion Medicine and Hemotherapy 2009; 36, 168-178.

Reid, M., Storry, J., Ralph, H., Blumenfeld, O. and Huang, C-H. Expression and quantitative variation of the low-incidence blood group antigen He on some S-s- red cells. Transfusion 1996; 36, 719-724.

Reid, M., Halter-Hipsky, C., Hue-Roye, K. and Hoppe, C. Genomic analyses of *RH* alleles to improve transfusion therapy in patients with sickle cell disease. Blood Cells Molecules and Diseases 2014; 54, 195-202.

Renoud, K., Barracchini, K., Byrne, K., Adams, S., Pickett, A., Caruccio, L. and Stroncek, D. *KEL6* and *KEL7* genotyping with sequence-specific primers. Transfusion 2006; 46, 1510-1514.

Reverberi, R. The persistence of red cell alloantibodies. Blood Transfusion 2008; 4, 225-234.

Ribeiro, S., Costa, E., Belo, L., Reis, F. and Santos-Silva, A. rh EPO for the Treatment of Erythropoietin Resistant Anemia in Hemodialysis Patients – Risks and Benefits. Hemodialysis 2013; (http://www.intechopen.com/books/hemodialysis accessed 02/05/2016).

Riedlinger, J., Beqaj, S., Milish, M., Young, S., Smith, R., Dodd, M., Hankerd, R., Lebar, W. and Newton, D. Multicenter evaluation of the BD Max GBS assay for detection of group B streptococci in prenatal vaginal and rectal screening swab specimens from pregnant women. Journal of Clinical Microbiology 2010; 48, 4239-4241.

Robertson, O. Transfusion with preserved red blood cells. British Medical Journal 1918; 1, 691-695.

Rolih, S., Eisinger, R., Moheng, M., Dean, W. and Eatz, R. Solid Phase Adherence Assays: Alternatives to Conventional Blood Bank Tests. Laboratory Medicine 1985; 16, 766-770.

Rosenberger, W. and Lachin, J., 2016. Randomization in clinical trials: theory and practice. John Wiley & Sons.

Rosse, W., Gallagher, D., Kinney, T. Castro, O., Dosik, H., Moohr, J., Wang, W. and Levy, P. Transfusion and alloimmunization in sickle cell disease. Blood 1990; 76, 1431-1437.

Royal College of Obstetricians and Gynaecologists. Red Cell Antibodies during Pregnancy, the Management of Women with (Green-top Guidelines No 65) May 2014. https://www.rcog.org.uk/en/guidelines-research-services/guidelines/gtg65/ (accessed 25/01/2018).

Rozman, P., Dovc, T. and Gassner, C. Differentiation of autologous *ABO*, *RHD, RHCE, KEL, JK* and *FY* blood group genotypes by analysis of peripheral blood samples of patients who have recently received multiple transfusions. Transfusion 2000; 40, 936-942.

Sangole, V. and Chaudhury, D. Alloimmunisation of Red Blood Cells in Multitransfused Patients. International Journal of Health Sciences and Research 2013; 3, 39-41.

Sanquin Blood Supplyhttp://www.sanquin.nl/en/research/departments/transfusion-medicine/randomized-clinical-trials/ (accessed 11.2.13).

Sanz, C., Nomdedeu, M., Belkaid, M., Martinez, I., Nomdedeu, B. and Pereira, A. Red blood cell alloimmunization in transfused patients with myelodysplastic syndrome or chronic myelomonocytic leukaemia. Transfusion 2013; 53, 710-715.

Sarnaik, S., Schornack, J. and Lusher, J. The incidence of development of irregular red cell antibodies in patients with sickle cell anemia. Transfusion 1986; 26, 249-252.

Schofield, A., Martin, P., Spillett, D. and Tanner, M. The structure of the human red blood cell anion exchanger (EPB3, AE1, band 3) gene. Blood 1994; 84, 2000-2012.

Schonewille, H., Haak, H. and Van Zijl, A. Alloimmunization after blood transfusion in patients with hematologic and oncologic diseases. Transfusion 1999; 39, 763-771.

Schonewille, H., Rene, R., De Vries, P. and Brand, A. Alloimmune response after additional red blood cell antigen challenge in immunized hematooncology patients. Transfusion 2009; 49, 453-457.

Schonewille, H., Honohan, A., van der Watering, L., Hudig, F., te Boekhorst, P., Koopman-van Gemert, A. and Brand, A. Incidence of alloantibody formation after ABO-D or extended matched red blood cell

transfusions: a randomized trial (MATCH study). Transfusion 2016; 56, 311-320.

Schulz, K and Grimes, D. Allocation concealment in randomised trials: defending against deciphering. Lancet 2002a; 359, 614-618.

Schulz, K and Grimes, D. Unequal group size in randomised trials: guarding against guessing. Lancet 2002b; 359, 966-970.

Sealed Envelope Ltd. 2012. Power calculator for binary outcome superiority trial. [Online] Available from: https://www.sealedenvelope.com/power/binary-superiority/ [Accessed Nov 14 2016].

Seitanides, B., Antonopoulou, A. and Karabelis, A. Immunological abnormalities in myelodysplastic syndrome. Journal of Clinical Pathology 1988; 41, 922-923.

Seltsam, A. and Doescher, A. Sequence-Based Typing of Human Blood Groups. Transfusion Medicine and Hemotherapy 2009; 36, 204-212.

Serious Hazards of Transfusion (SHOT) annual report 2014 www.shotuk.org (accessed 21/05/2016).

Serious Hazards of Transfusion (SHOT) annual report 2016. https://www.shotuk.org/wp-content/uploads/SHOT-Report-2016_web_11th-July.pdf (accessed 25/01/2018).

Seyfried, H. and Walewska, I. Analysis of immune response to red blood cell antigens in multitransfused patients with different diseases. Materia Medica Polona 1990; 22, 21-5.

Shapiro, M. Serology and genetics of a new blood factor: hr^s. Journal of Forensic Medicine 1960; 7, 96-105.

Shapiro, M., Le Roux, M. and Brink, S. Serology and genetics of a new blood factor: hr B. Haematologia 1972; 6, 121-128.

Shirey, R., Boyd, J., Parwani, A., Tanz, W., Ness, P. and King, K. Prophylactic antigen-matched donor blood for patients with warm autoantibodies: an algorithm for transfusion management. Transfusion, 2002; *42*, 1435-1441.

Sidoux-Walter, F., Lucien, N. and Olives, B. At Physiological Expression Levels the Kidd Blood Group/Urea Transporter Protein Is Not a Water Channel. Journal of Biological Chemistry 1999; 274, 30228-30235.

Sidoux-Walter, F., Lucien, N., Nissinen, R., Sistonen, P., Henry, S., Moulds, J., Cartron, J-P. and Bailly, P. Molecular heterogeneity of the

Jk_{null} phenotype: expression analysis of the Jk (S291P) mutation found in Finns. Blood 2000; 96, 1566-1573.

Spanos, T., Karageorga, M., Ladis, V., Peristeri, J., Hatziliami, A. and Kattamis, C. Red cell alloantibodies in patients with thalassaemia. Vox Sanguinis 1990; 58, 50-55.

Sparkes, R., Sparkes, M. and Gale, R. Immunoglobulin synthesis following allogeneic bone marrow transplantation in man. Conversion to donor allotype. Transplantation 1979; 27, 212-213.

Springer, G., Horton, R. and Forbes, M. Origin of anti-human blood group B agglutinins in White Leghorn chicks. Journal of Experimental Medicine 1959a; 110, 221-244.

Springer, G., Horton, R. and Forbes, M. Origin of antihuman blood group B agglutinins in germfree chicks. Annals of the New York Academy of Sciences 1959b; 78, 272-275.

Springer, G. and Horton, R. Blood group isoantibody stimulation in man by feeding blood group-active bacteria. Journal of Clinical Investigation 1969; 48, 1280-1291.

Sokol, R., Hewitt, S. and Brooker, D. Erythrocyte autoantibodies, autoimmune haemolysis, and myelodysplastic syndrome. Journal of Clinical Pathology 1989; 42, 1088-1091.

Solal-Celigny, P., Vazeux, R., Vroclans, M., Amar, M., Herrera, A., Bernard, J. and Boivin, P. Positive Coombs tests in acute leukaemia. British Journal of Haematology 1984; 57, 563-569.

Sourial, N., Wolfson, C., Zhu, B., Quail, J., Fletcher, J., Karunananthan, S., Bandeen-Roches, K., Beland, F. and Bergman, H. Correspondence analysis is a useful tool to uncover the relationships among categorical variables. Journal of Clinical Epidemiology 2010; 63, 638-646.

Stainsby, D., Jones, H., Asher, D., Atterbury, C., Boncinelli, A., Brant, L., Chapman, C., Davison, K., Gerrard, R., Gray, A., Knowles, S., Love, E., Milkins, C., McClelland, D., Norfolk, D., Soldan, K., Taylor, C., Revill, J., Williamson, L. and Cohen, H. Serious Hazards of transfusion: a decade of hemovigilance in the UK. Transfusion Medicine Reviews 2006; 20, 273-282.

Starr, D. Blood: An epic history of medicine and commerce. 1999; Little Brown and Company, London.

Steegmann, J., Requena, M., Martin-Regueira, P., De La Cámara, R., Casado, F., Salvanés, F. and Fernández Rañada, J. High incidence of

autoimmune alterations in chronic myeloid leukemia patients treated with interferon-alpha. American Journal of Hematology 2003; 72, 170-176.

Storry, J., Reid, M., Fetics, S. and Huang, C-H. Mutations in the *GYPB* exon 5 drive the S-s-U+^{var} phenotype in persons of African descent: implications for transfusion. Transfusion 2003; 43, 1738-1747.

Strumia, M. and McGraw, J. The Development of Plasma Preparations for Transfusions. Annals of Internal Medicine 1941; 15, 80-88.

Sully, B., Julious, S. and Nicholl, J. A reinvestigation of recruitment to randomised, controlled, multicenter trials: a review of trials funded by two UK funding agencies. Trials 2013; 14, 166.

Suresh, K. An overview of randomization techniques: An unbiased assessment of outcome in clinical research. Journal of Human Reproductive Sciences 2011; 4, 8-11.

Swerdlow, S., Campo, E., Harris, N., Jaffe, E., Pileri, S., Stein, H., Thiele, J. and Vardiman, J., 2008. WHO Classification of Tumors of Hematopoietic and Lymphoid Tissues 4th Ed. (2008). IARC Publications.

Swerdlow, S., Campo, E., Pileri, S., Harris, N., Stein, H., Siebert, R., Advani, R., Ghielmini, M., Salles, G., Zelenetz, A. and Jaffe, E. The 2016

revision of the World Health Organization classification of lymphoid neoplasms. Blood 2016; 127, 2375-2390.

Tahhan, H., Holbrook, C., Braddy, L., Brewer, L. and Christie, J. Antigen-matched donor blood in the transfusion management of patients with sickle cell disease. Transfusion 1994; 34, 562-569.

Tanner, M. Molecular and cellular biology of the erythrocyte anion exchanger (AE1). Seminars in Hematology 1993; 30, 34-57.

Teare, M., Dimairo, M., Shephard, N., Hayman, A., Whitehead, A. and Walters, S. Sample size requirements to estimate key design parameters from external pilot randomised controlled trials: a simulation study. BioMed Central; Trials 2014; 15, 264.

Terasaki, P. and Mizutani, K. Antibody Mediated Rejection: Update 2006. Clinical Journal of the American Society of Nephrology 2006; 1, 400-403.

The International Society of Blood Transfusion Red Cell Immunogenetics and Blood Group Terminology Working Party. http://www.isbtweb.org/working-parties/red-cell-immunogenetics-and-terminology (accessed 03/12/2015).

Timura, G., Duman, A., Ongut, G. and Saka, O. The Significance of Autoantibodies in Non-Hodgkin's Lymphoma. Leukemia and Lymphoma. 2000; 40, 119-122.

Tournamille, C., Colin, Y., Cartron, J-P. and Le Van Kim, C. Disruption of a GATA motif in the Duffy gene promoter abolishes erythroid expression in Duffy-negative individuals. Nature Genetics 1995; 10, 224-228.

Tournamille, C., Le Van Kim, C., Gane, P., Le Pennec, P., Roubinet, F., Babinet, J., Cartron, J-P. and Colin, Y. Arg89Cys substitution results in very low membrane expression of the Duffy antigen/receptor for chemokines in Fy^x individuals. Blood 1998; 92, 2147-2156.

Türkmen, T., Qiu, D., Cooper, N., Sachs, U. J., Wößmann, W., Schranz, D., Zimmer, K.-P., Ehrhardt, H., Hackstein, H. and Bein, G. (2017), Red blood cell alloimmunization in neonates and children up to 3 years of age. Transfusion, 57: 2720–2726.

Van den Berghe, H. Morphologic, immunologic and cytogenetic (MIC) working classification of the acute myeloid leukaemias. British Journal of Haematology 1988; 68, 487-494.

Van der Putten, K., Braam, B., Jie, K. and Gaillard, C. Mechanisms of Disease: erythropoietin resistance in patients with both heart and kidney failure. Nature Clinical Practice Nephrology 2008; 4, 47-57.

van Tol, M., Gerritsen, E., de Lange, G., van Leeuwen, A., Jol-van der Zijde, C., Oudeman-Gruber, N., de Vries, E., Radl, J. and Vossen, J. The origin of IgG production and homogeneous IgG components after allogeneic bone marrow transplantation. Blood 1996; 87, 818-826.

Viitala, J. and Järnefelt, J. The red cell surface revisited. Trends in Biochemical Sciences 1985; 10, 392-395.

Wagner, F., Flegel, W., Bittner, R. and Döscher, A. Molecular typing for blood group antigens within 40 min by direct polymerase chain reaction from plasma or serum. British Journal of Haematology 2017; 176, 814-821.

Walter, C. and Murphy, W. A closed gravity technique for the preservation of whole blood in ACD solution utilizing plastic equipment. Surgery, Gynecology & Obstetrics 1952; 94, 687-692.

Weigle, W. The induction of autoimmunity in rabbits following injection of heterologous or altered homologous thyroglobulin. Journal of Experimental Medicine 1965; 121, 289-308.

Weir, C and Lees, K. Comparison of stratification and adaptive methods for treatment allocation in an acute stroke clinical trial. Statistics in Medicine 2003; 22, 705-726.

Wiener, A. Genetic Theory of the Rh Blood Types. Experimental Biology and Medicine 1943, 54, 316-319.

Wiener, A., Unger, L. and Cohen, L. Distribution and heredity of blood factor U. Science 1954; 119, 734-735.

Westhoff, C. The structure and function of the Rh antigen complex. Seminars in Hematology, 2007; 44, 42-50.

Westhoff, C. and Shaz, B. Kell and Kidd Blood Group Systems. Transfusion Medicine and Haemostasis (second edition) 2013. https://www.sciencedirect.com/topics/immunology-and-microbiology/kell-antigen-system (accessed 11/02/2018).

Winters, J., Pineda, A., Gorden, L., Bryant, S., Melton, J., Vamvakas, E. and Moore, S. RBC alloantibody specificity and antigen potency in Olmstead County, Minnesota. Transfusion 2001; 41, 1413-1420.

Witherspoon, R., Schanfield, M., Storb, R., Thomas, E. and Giblett, E. Immunoglobulin production of donor origin after bone marrow transplantation for acute leukemia or aplastic anemia. Transplantation 1978; 26, 407-408.

Woldie, I., Swerdlow, P., Bluth, M., Mohammad, U., Landolfi, E., Chaudrhy, S., Dyson, G. and O'Malley, B. Lifetime risk and characterization of red blood cell alloimmunization in chronically transfused patients with sickle cell disease. International Journal of Blood Transfusion and Immunohematology 2015; 5, 1-5.

Woodrow, J and Donohoe, W. Rh-immunization by Pregnancy: Results of a Survey and Their Relevance to Prophylactic Therapy. British Medical Journal 1968; 4, 139-144.

Yazer, M., Triulzi, D., Shaz, B., Kraus, T. and Zimring, J. Does a febrile reaction to platelets predispose recipients to red blood cell alloimmunization? Transfusion 2009; 49, 1070-1075.

Zhu, X., Rivera, A., Golub, M., Peng, J., Sha, Q., Wu, X., Song, X., Kumarathasan, P., Ho, M., Redman, C. and Lee, S. Changes in red cell ion transport, reduced intratumoral neovascularization, and some mild motor function abnormalities accompany targeted disruption of the Mouse Kell gene (*Kel*). American Journal of Hematology 2009; 84, 492-498.

Young, P., Uzielbo, A., Trulock, E., Lublin, D. and Goodnough, L. Autoantibody formation after alloimmunization: are blood transfusions a risk factor for autoimmune hemolytic anemia? Transfusion 2004; 44, 67 – 72.

Yu, Y-B., Gau, J-P., You, J-Y., Chern, H-H., Chau, W-K., Tzeng, C-H., Ho, C-H. and Hsu, H-C. Cost-effectiveness of postremission intensive therapy in patients with acute leukaemia. Annals of Oncology 2007; 18, 529-534.

Zalpuri, S., Zwaginga, J., Cessie, S. Elhuis, J., Schonewille, H. and Van der Bom, J. Red-blood-cell alloimmunization and number of red-blood-cell transfusions. Vox Sanguinis 2012; 102, 144-149.

Zalpuri, S., Evers, D., Zwaginga, J., Schonewille, H., de Vooght, K., le Cessie, S. and van der Bom, J. Immunosuppressants and alloimmunisation against red blood cell transfusions. Transfusion 2014; 54, 1981-1987.

Zelinski, T., Coghlan, G., Myal, Y., Shiu, R., Phillips, S., White, L. and Lewis, M. Genetic linkage between the Kell blood group system and prolactin –inducible protein loci: provisional assignment of *KEL* to chromosome 7. Annals of Human Genetics 1991; 55, 137-140.

Zhang, R. Modern Immunosuppressive Therapy in Kidney Transplantation. Open Journal of Organ Transplant Surgery 2013; 3, 22-31.

Zheng, Y. and Maitta, R. Alloimmunisation rates of sickle cell disease patients in the United States differ from those in other geographical regions. Transfusion Medicine 2016; 26, 225-230.

Zimring, J., Spitalnik, S., Roback, J. and Hillyer, C. Transfusion induced autoantibodies and differential immunogenicity of blood group antigens: a novel hypothesis. Transfusion 2007; 47, 2189-2196.

10 APPENDICES

10.1 Appendix 1: Raw data for retrospective review of haematology cohort

Key: N = No M=Male
Y = Yes F=Female

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Anaemia of chronic disease	53	N	N	M	24	81	N	N
AIHA	17	N	Y	F	7	27	N	N
AIHA	49	N	Y	F	23	85	N	N
AIHA	4	N	N	M	1	66	N	N
AIHA	13	Y	Y	F	4	50	N	N
AIHA	7	N	Y	F	3	70	N	Y
AIHA	35	N	Y	F	14	60	N	N
AIHA	9	Y	Y	F	4	86	N	N
AITL	6	N	Y	M	3	81	Y	Y
AITL	15	Y	Y	M	7	74	Y	Y
ALL	3	N	N	F	1	44	Y	N
ALL	8	N	N	F	3	66	Y	N
ALL	11	N	N	F	6	72	Y	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
ALL	46	N	N	F	20	54	Y	Y
ALL	38	N	N	M	12	38	Y	Y
ALL	27	N	N	F	12	75	Y	N
ALL	84	N	N	F	38	55	Y	Y
ALL	3	N	N	M	2	72	Y	N
ALL	92	N	N	M	43	41	Y	Y
ALL	35	N	N	M	17	23	Y	N
ALL	17	N	N	F	8	51	Y	N
ALL	8	N	N	M	4	84	N	N
ALL	76	N	N	M	31	66	Y	N
ALL	52	N	N	M	25	66	Y	N
AML	2	Y	Y	M	1	81	N	Y
AML	2	N	N	F	1	67	Y	N
AML	5	N	N	F	2	79	Y	N
AML	6	N	N	F	4	86	Y	N
AML	8	N	N	F	4	52	Y	Y
AML	9	N	N	M	3	80	N	N
AML	9	N	N	F	4	76	Y	N
AML	10	N	N	F	4	88	N	N
AML	11	N	N	F	4	62	Y	N
AML	11	N	N	M	5	51	Y	Y
AML	12	N	Y	F	6	71	Y	N
AML	14	N	N	M	7	60	Y	N
AML	17	N	N	M	7	55	Y	Y
AML	20	N	N	M	10	78	Y	N
AML	22	N	N	F	8	91	Y	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
AML	23	N	N	M	10	76	Y	N
AML	25	N	N	F	11	69	Y	N
AML	28	Y	Y	M	13	79	Y	Y
AML	28	N	N	M	12	51	Y	Y
AML	30	N	N	M	16	37	Y	Y
AML	30	N	N	M	14	36	Y	N
AML	32	N	N	M	15	46	Y	Y
AML	35	N	N	M	15	37	Y	Y
AML	36	N	N	M	15	57	Y	Y
AML	37	N	Y	F	18	63	Y	Y
AML	37	N	Y	M	17	32	Y	Y
AML	41	N	N	F	15	73	Y	N
AML	43	N	Y	M	20	56	Y	Y
AML	47	N	Y	F	22	39	Y	Y
AML	48	N	N	M	23	69	Y	N
AML	59	N	N	F	28	71	Y	N
AML	61	N	Y	F	26	49	Y	Y
AML	64	N	Y	M	29	54	Y	Y
AML	64	N	Y	M	32	49	Y	Y
AML	64	N	Y	M	22	68	Y	Y
AML	66	N	Y	F	33	60	Y	Y
AML	73	N	Y	F	35	82	N	N
AML	75	N	Y	M	30	19	Y	Y
AML	79	N	N	F	36	56	Y	Y
AML	85	N	N	M	43	74	N	N
AML	168	N	N	F	79	51	Y	Y

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
AML	53	N	Y	M	26	42	Y	Y
AML	51	N	Y	F	24	52	Y	Y
AML	144	N	Y	F	67	71	Y	Y
AML	14	N	N	F	7	73	N	N
AML	53	N	N	F	25	74	Y	N
AML	75	N	Y	M	34	63	Y	Y
AML	32	N	N	M	15	40	Y	Y
AML	8	N	N	F	4	89	N	N
AML	18	N	N	F	9	80	Y	N
AML	22	N	N	F	9	75	Y	N
AML	56	N	N	M	26	64	Y	Y
AML	52	N	N	F	26	50	Y	Y
AML	44	N	N	F	18	60	Y	Y
AML	13	N	N	M	6	62	Y	Y
AML	8	N	N	M	4	80	Y	N
AML	14	N	N	F	6	86	N	N
AML	80	N	N	F	35	64	Y	Y
AML	33	N	N	M	14	24	Y	Y
AML	31	N	N	F	15	57	Y	N
AML	4	N	N	F	2	55	N	N
AML	30	N	N	F	13	93	Y	N
AML	12	N	N	F	6	58	Y	Y
AML	15	N	N	M	7	82	N	N
AML	6	N	Y	F	3	74	N	N
AML	6	N	N	M	3	85	Y	N
AML	70	N	N	M	34	67	Y	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
AML	79	N	N	M	34	67	Y	N
AML	13	N	N	M	5	61	Y	N
AML	14	N	N	M	6	76	N	N
AML	25	N	N	F	13	49	Y	Y
AML	80	N	Y	F	33	67	Y	N
AML	94	N	Y	M	46	56	Y	Y
AML	53	N	Y	F	25	56	Y	Y
AML	94	N	N	M	39	81	Y	N
AML	89	N	N	F	43	63	Y	Y
AML	42	N	Y	F	18	59	Y	N
AML	33	N	N	M	16	34	Y	Y
AML	17	N	N	M	7	67	Y	N
AML	39	N	N	M	18	78	N	N
AML	44	N	N	M	19	77	Y	N
AML	30	N	Y	F	13	65	Y	N
AML	22	N	N	M	10	61	Y	Y
AML	112	N	N	F	54	52	Y	Y
AML	34	N	N	F	16	75	Y	N
AML	33	N	N	M	16	70	Y	N
AML	85	N	N	F	42	54	Y	Y
AML	42	N	N	M	21	71	Y	N
AML	39	N	N	F	18	55	Y	Y
AML	69	N	N	F	29	30	N	Y
AML	41	N	N	F	19	24	Y	Y
AML	53	N	Y	F	25	51	Y	Y
AML	28	N	N	M	10	76	Y	Y

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
AML	27	N	N	F	12	74	Y	Y
AML	31	N	N	M	17	64	Y	N
AML	18	N	N	F	9	83	Y	N
AML	10	N	N	F	4	83	Y	N
AML	33	N	N	M	15	45	Y	Y
AML	44	N	N	M	21	89	Y	N
AML	21	N	N	M	10	70	Y	N
AML	68	N	N	M	30	73	N	N
AML	10	N	N	F	5	76	Y	Y
AML	29	N	N	F	14	75	Y	N
AML	28	N	N	M	13	65	Y	N
AML	54	N	N	M	25	69	Y	N
AML	10	N	N	F	4	72	N	N
AML	35	N	N	F	17	54	Y	N
AML	52	N	N	M	25	59	Y	Y
AML	22	N	N	M	11	81	Y	N
AML	157	N	Y	M	72	58	Y	N
AML	104	Y	Y	F	53	66	Y	Y
AML	40	N	Y	M	18	66	Y	N
AML	15	N	N	F	6	84	Y	N
AML	28	N	N	M	11	74	Y	N
AML	10	N	N	F	6	63	Y	Y
AML	10	N	N	F	4	48	Y	Y
AML	42	N	N	F	21	67	Y	Y
AML	166	N	N	M	63	71	Y	N
AML	4	N	N	F	2	69	Y	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
AML	18	N	Y	F	8	60	N	N
AML	51	N	N	M	21	75	Y	N
AML	38	N	N	F	17	60	Y	Y
AML	4	N	N	F	2	70	Y	N
AML	53	N	N	F	24	54	Y	Y
AML	115	N	N	M	47	59	Y	Y
AML	26	N	N	M	9	84	Y	N
AML	23	N	N	F	12	58	Y	N
AML	27	N	Y	F	14	72	Y	N
AML	62	N	N	M	30	73	Y	Y
AML	61	N	Y	F	26	73	Y	Y
AML	88	N	N	M	39	67	Y	Y
AML	2	N	N	M	1	78	N	N
AML	18	N	N	F	9	65	Y	Y
AML	43	N	N	F	21	18	Y	N
AML	36	N	N	F	17	74	Y	N
AML	50	N	Y	M	23	61	Y	Y
AML	36	N	Y	M	17	81	Y	N
AML	31	N	N	M	13	68	Y	Y
AML	2	N	N	F	1	79	Y	N
AML	22	N	N	F	11	61	Y	N
AML	20	N	Y	F	10	75	Y	N
AML	28	N	N	F	14	76	Y	Y
AML	36	N	N	F	16	66	Y	N
AML	48	N	Y	F	23	84	Y	N
AML	65	N	N	F	29	69	Y	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
AMML	8	N	N	M	4	85	Y	N
AMYLOID	4	N	N	F	2	48	N	N
AMYLOID	47	N	N	M	10	31	Y	Y
AMYLOID	72	N	Y	F	36	55	N	N
AMYLOID	4	N	N	F	2	49	N	N
ANAEMIA	7	N	N	F	2	45	N	N
ANAEMIA	80	N	Y	M	53	42	N	N
ANAEMIA	60	N	N	M	21	71	N	N
ANAEMIA	2	N	N	F	1	62	N	N
ANAEMIA	6	N	N	F	3	41	N	N
ANAEMIA	32	N	Y	F	13	74	N	N
ANAEMIA	2	N	N	F	1	48	N	N
ANAEMIA	4	N	N	F	2	74	N	N
ANAEMIA	5	N	N	F	2	59	N	N
ANAEMIA	34	N	N	F	13	71	N	N
ANAEMIA	19	N	N	M	7	79	N	N
ANAEMIA	6	N	N	M	2	80	N	N
ANAEMIA	2	N	N	F	1	99	N	N
ANAEMIA	9	N	N	F	4	83	N	N
ANAEMIA	2	N	N	M	1	83	N	N
ANAEMIA	2	N	N	F	1	40	N	Y
ANAEMIA	6	N	N	F	3	81	N	N
ANAEMIA	16	N	N	F	8	73	N	N
APLASTIC	15	N	N	F	10	22	Y	Y
APLASTIC	19	N	Y	F	9	87	Y	N
APLASTIC	36	N	Y	M	14	26	Y	Y

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
APLASTIC	63	N	Y	F	31	86	Y	N
APLASTIC	107	N	Y	M	52	57	Y	Y
APLASTIC	26	N	N	M	13	27	Y	N
APLASTIC	10	N	N	M	3	80	N	N
APLASTIC	68	N	Y	F	30	27	Y	Y
APLASTIC	4	N	N	M	2	64	N	Y
APLASTIC	93	N	Y	F	44	58	N	N
APLASTIC	9	N	N	F	4	33	N	N
APLASTIC	88	N	Y	F	43	69	Y	N
APLASTIC	57	N	Y	F	29	79	Y	N
APLASTIC	9	Y	Y	M	4	53	N	N
APML	15	N	N	M	7	44	Y	Y
Autoimmune Neutropenia	6	N	N	F	3	80	N	N
B-Cell Lymphoma	26	N	N	M	12	67	Y	N
Cancer (solid organ)	5	N	N	M	2	71	N	N
Cancer (solid organ)	7	N	Y	F	3	60	N	N
Cancer (solid organ)	7	N	N	F	2	80	N	N
Cancer (solid organ)	7	N	N	F	4	36	N	N
Cancer (solid organ)	7	N	N	F	4	49	Y	Y
Cancer (solid organ)	8	Y	Y	M	3	53	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Cancer (solid organ)	8	N	N	F	2	54	N	N
Cancer (solid organ)	9	N	N	F	4	49	N	N
Cancer (solid organ)	11	N	Y	F	5	45	N	N
Cancer (solid organ)	12	N	Y	F	5	79	N	N
Cancer (solid organ)	23	N	N	M	10	82	N	N
Cancer (solid organ)	25	N	N	M	11	85	N	N
Cancer (solid organ)	35	N	N	F	14	46	N	N
Cancer (solid organ)	5	N	N	F	2	53	N	N
Cancer (solid organ)	5	N	N	M	2	82	N	N
Cancer (solid organ)	8	N	N	M	4	68	Y	N
Cancer (solid organ)	16	N	N	F	7	56	N	N
Cancer (solid organ)	20	N	N	F	9	35	N	N
Cancer (solid organ)	11	N	N	M	6	85	Y	N
Cancer (solid organ)	7	N	N	F	2	52	N	N
Cancer (solid organ)	14	N	N	M	6	66	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Cancer (solid organ)	3	N	N	F	2	65	N	N
Cancer (solid organ)	2	N	N	M	1	63	N	N
Cancer (solid organ)	8	N	Y	F	3	45	N	N
Cancer (solid organ)	32	Y	Y	F	12	65	N	N
Cancer (solid organ)	6	N	N	M	3	87	N	N
Cancer (solid organ)	2	N	N	F	1	59	N	N
Cancer (solid organ)	2	N	N	F	1	48	N	N
Cancer (solid organ)	2	N	N	F	1	63	N	N
Cancer (solid organ)	5	N	N	M	2	75	N	N
Cancer (solid organ)	2	N	N	F	1	75	N	N
Cancer (solid organ)	25	N	N	M	10	77	N	N
Cancer (solid organ)	3	N	N	F	1	75	N	N
Cancer (solid organ)	4	N	N	M	2	77	N	N
Cancer (solid organ)	23	N	Y	F	9	63	N	N
Cancer (solid organ)	10	N	N	F	3	31	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Cancer (solid organ)	2	N	N	F	1	61	Y	N
Cancer (solid organ)	2	N	N	F	1	51	N	N
Cancer (solid organ)	9	N	N	M	4	74	N	N
Cancer (solid organ)	6	N	N	F	3	66	Y	N
Cancer (solid organ)	2	N	N	F	1	49	N	N
Cancer (solid organ)	19	N	N	M	9	76	N	N
Cancer (solid organ)	25	N	N	M	10	74	N	N
Cancer (solid organ)	21	N	N	F	9	70	N	N
Cancer (solid organ)	17	N	N	M	8	61	N	N
Cancer (solid organ)	12	N	N	M	6	75	N	N
Cancer (solid organ)	19	N	Y	M	9	51	Y	M
Cancer (solid organ)	54	N	Y	M	20	80	N	N
Cancer (solid organ)	14	N	Y	M	7	69	Y	N
Cancer (solid organ)	13	N	N	M	6	72	Y	N
Cancer (solid organ)	6	N	N	F	3	82	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Cancer (solid organ)	23	N	N	M	8	75	N	N
Cancer (solid organ)	6	N	N	F	3	69	N	N
Cancer (solid organ)	14	N	N	M	7	89	N	N
CLL	2	N	N	M	1	78	N	Y
CLL	2	N	N	F	1	74	N	N
CLL	4	N	N	F	1	53	Y	N
CLL	6	N	Y	F	3	88	N	N
CLL	6	N	N	F	3	84	N	N
CLL	6	N	N	M	3	78	Y	N
CLL	7	N	N	M	3	91	Y	N
CLL	10	N	N	F	3	84	N	N
CLL	11	N	N	M	4	85	N	N
CLL	16	N	Y	M	6	72	N	Y
CLL	17	N	N	M	9	90	Y	N
CLL	21	N	Y	M	10	93	Y	N
CLL	65	N	N	F	27	78	Y	N
CLL	22	N	N	F	11	65	N	Y
CLL	11	N	N	M	5	93	N	N
CLL	5	N	N	M	2	84	N	Y
CLL	10	N	N	M	5	82	N	N
CLL	10	N	N	F	5	63	Y	Y
CLL	12	N	N	M	6	71	N	Y
CLL	7	N	N	F	3	86	N	N
CLL	11	Y	Y	M	4	75	Y	Y
CLL	1	N	N	F	1	91	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
CLL	8	N	Y	F	3	88	N	N
CLL	7	N	N	M	3	78	N	Y
CLL	15	Y	Y	F	7	75	N	N
CLL	36	N	Y	M	15	68	Y	Y
CLL	44	N	N	M	20	63	Y	Y
CLL	8	N	Y	F	4	67	N	N
CLL	39	N	N	M	19	71	Y	Y
CLL	212	N	Y	M	87	68	Y	Y
CLL	16	N	N	M	8	77	N	Y
CLL	18	N	Y	M	5	70	Y	Y
CLL	30	N	Y	M	15	69	Y	Y
CLL	6	N	N	M	3	86	N	N
CLL	14	Y	Y	M	6	72	N	Y
CLL	2	N	N	M	1	91	N	Y
CLL	5	Y	Y	M	2	83	N	N
CLL	6	N	N	M	3	86	N	Y
CLL	11	N	Y	M	5	73	N	Y
CLL	34	N	Y	M	17	76	Y	N
CLL	4	Y	Y	F	2	83	N	N
CLL	9	N	N	M	4	83	N	N
CLL	12	Y	Y	F	5	78	N	N
CLL	3	Y	Y	F	1	87	N	N
CLL	10	N	Y	M	4	79	N	Y
CLL	2	N	N	M	1	68	N	Y
CLL	4	Y	Y	M	2	66	N	N
CLL	10	N	N	F	5	79	N	Y

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
CLL	11	N	N	F	4	74	Y	Y
CLL	18	N	Y	F	9	89	N	N
CLL	19	N	N	M	7	69	Y	Y
CLL	52	N	N	M	24	75	Y	Y
CLL	46	Y	Y	F	18	62	N	Y
CLL	4	N	N	M	2	81	N	N
CLL	33	N	N	M	17	64	Y	Y
CLL	19	N	N	M	11	92	N	N
CLL	9	N	N	M	4	76	N	N
CML	24	N	N	F	11	85	N	N
CML	45	N	N	M	20	61	Y	Y
CML	22	N	Y	F	10	73	N	N
CML	7	N	N	F	3	73	N	N
CML	9	N	N	M	3	74	Y	N
CML	10	N	Y	F	4	86	N	N
CML	44	N	Y	F	19	74	N	N
CML	10	N	N	M	5	39	Y	Y
CML	2	Y	Y	M	1	62	N	N
CML	40	N	N	F	22	63	Y	Y
CML	4	N	N	F	2	73	N	N
CMML	2	N	N	F	1	66	Y	N
CMML	5	N	N	F	2	90	N	N
CMML	37	N	N	M	25	73	Y	N
CMML	37	N	N	M	16	82	Y	N
CMML	28	N	Y	M	12	70	N	N
CMML	63	N	N	M	29	76	Y	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
CMML	18	N	N	M	7	70	Y	N
CMML	11	N	Y	M	36	77	N	N
CMML	20	N	N	M	10	70	N	N
Cold Haemagglutinin Diease	12	Y	Y	F	6	73	N	N
Cold Haemagglutinin Diease	2	Y	Y	M	1	76	N	N
CRF	6	N	N	F	2	75	N	N
CRF	12	N	Y	M	6	83	N	N
CRF	32	N	Y	F	13	74	N	N
CRF	28	N	N	F	9	86	N	N
CRF	22	N	N	F	10	76	N	N
CRF	6	N	N	M	2	80	N	N
CRF	23	N	Y	F	9	81	N	N
Diamond Blackfan Anaemia	382	N	Y	F	147	13	N	N
Diffuse large B –cell lymphoma	36	N	N	M	17	59	Y	Y
Essential thrombocythaemia	4	N	N	M	2	73	N	N
Essential thrombocythaemia	8	N	N	M	4	85	N	N
Essential thrombocythaemia	6	N	N	M	2	75	Y	N
Essential thrombocythaemia	40	N	N	F	15	79	Y	N
Essential thrombocythaemia	4	N	N	M	2	68	N	N
Essential thrombocythaemia	5	N	N	F	2	74	N	N
F IX DEF	13	N	N	M	5	77	Y	N
Haemolytic anaemia	19	N	Y	F	7	76	N	N
Hairy cell leukaemia	2	N	N	M	1	60	N	Y

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Hairy cell leukaemia	14	N	N	M	7	68	N	Y
Hairy cell leukaemia	6	N	N	M	3	66	N	Y
Hairy cell leukaemia	6	N	N	M	3	79	Y	Y
Hairy cell leukaemia	2	N	Y	M	1	76	N	Y
Hodgkin's lymphoma	2	N	N	F	1	32	N	Y
Hodgkin's lymphoma	2	N	N	F	1	22	N	Y
Hodgkin's lymphoma	4	N	N	F	3	36	Y	Y
Hodgkin's lymphoma	5	N	N	F	2	76	N	Y
Hodgkin's lymphoma	6	N	N	F	3	34	N	Y
Hodgkin's lymphoma	6	N	N	M	3	21	Y	Y
Hodgkin's lymphoma	6	N	N	F	3	26	N	Y
Hodgkin's lymphoma	10	N	N	F	6	63	N	Y
Hodgkin's lymphoma	13	N	N	M	6	37	Y	Y
Hodgkin's lymphoma	2	N	N	F	1	93	N	Y
Hodgkin's lymphoma	5	N	N	F	2	31	N	Y
Hodgkin's lymphoma	13	N	N	M	6	74	N	Y
Hodgkin's lymphoma	8	N	N	M	4	54	N	Y
Hodgkin's lymphoma	8	N	N	M	4	63	N	Y
Hodgkin's lymphoma	4	N	N	M	2	63	N	Y

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Hodgkin's lymphoma	4	N	N	M	2	59	N	Y
Hodgkin's lymphoma	2	N	N	F	1	81	N	Y
Hodgkin's lymphoma	10	N	N	M	5	85	N	Y
Hodgkin's lymphoma	10	N	N	F	5	70	Y	Y
Hodgkin's lymphoma	10	N	N	M	5	77	N	Y
Hodgkin's lymphoma	6	N	N	F	3	67	N	Y
Hodgkin's lymphoma	30	Y	Y	M	15	41	Y	Y
Hodgkin's lymphoma	19	N	N	M	9	72	N	N
Hodgkin's lymphoma	6	N	N	M	3	81	N	Y
Hodgkin's lymphoma	2	N	N	F	1	52	N	Y
Hodgkin's lymphoma	2	N	N	F	1	70	N	Y
Hodgkin's lymphoma	4	N	N	F	2	68	N	N
Hodgkin's lymphoma	4	N	N	M	2	29	Y	Y
Hodgkin's lymphoma	50	N	Y	F	24	56	Y	Y
ITP	8	N	N	M	2	68	Y	N
ITP	9	Y	Y	M	4	69	Y	N
ITP	4	N	Y	F	2	82	N	N
ITP	19	N	N	M	6	84	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
ITP	4	N	N	F	2	72	Y	N
ITP	6	N	N	M	2	64	Y	N
ITP	4	N	N	M	2	82	N	N
LEA	4	N	N	F	2	97	N	N
Lymphoma	2	Y	Y	M	1	86	Y	N
Lymphoma	2	N	N	M	1	81	N	N
Lymphoma	2	N	N	F	1	87	N	N
Lymphoma	3	N	N	F	1	26	N	N
Lymphoma	5	N	N	M	3	45	Y	Y
Lymphoma	8	N	N	M	4	59	Y	Y
Lymphoma	10	N	N	M	5	75	Y	N
Lymphoma	12	N	Y	M	6	77	N	N
Lymphoma	17	N	N	M	8	68	Y	Y
Lymphoma	20	N	N	M	10	81	Y	N
Lymphoma	21	Y	Y	M	8	46	Y	Y
Lymphoma	28	N	N	M	11	63	Y	Y
Lymphoma	30	N	N	F	13	62	Y	Y
Lymphoma	20	N	N	M	10	70	Y	Y
Lymphoma	15	N	N	F	8	79	N	N
Lymphoma	6	N	N	M	3	51	Y	N
Lymphoma	5	N	N	M	2	62	N	N
Lymphoma	6	N	N	M	3	74	Y	N
Lymphoma	6	N	N	M	3	69	N	N
Lymphoma	25	N	N	M	12	61	N	Y
Lymphoma	20	Y	Y	F	8	70	N	Y
Lymphoma	12	N	N	M	5	87	Y	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Lymphoma	4	N	N	F	2	79	N	N
Lymphoma	7	N	N	F	3	87	N	N
Lymphoma	12	N	N	F	6	57	Y	N
Lymphoma	3	N	N	F	2	78	N	N
Lymphoma	11	N	N	F	7	64	Y	Y
Lymphoma	10	N	N	F	5	86	N	N
Lymphoma	3	Y	Y	M	1	82	N	N
Lymphoma	22	N	N	F	11	18	Y	Y
Lymphoma	4	Y	Y	F	2	71	N	N
Lymphoma	58	N	Y	M	24	43	Y	Y
Lymphoma	13	N	N	F	5	59	N	N
Lymphoma	4	N	N	M	2	56	Y	Y
Lymphoma	13	N	N	F	6	69	N	N
Lymphoma	2	N	N	M	1	69	Y	N
Lymphoma	51	N	Y	M	23	83	N	Y
Lymphoma	4	N	N	F	2	76	N	N
Lymphoma	4	N	N	M	2	79	N	Y
Lymphoma	4	N	N	F	2	67	Y	Y
Lymphoma	4	N	N	F	2	87	N	Y
Lymphoma	13	N	Y	M	6	82	N	N
Lymphoma	2	N	N	M	1	70	N	N
Lymphoma	4	N	N	F	2	78	N	N
Lymphoma	21	N	N	F	10	61	N	Y
Lymphoma	28	N	N	F	14	67	N	N
Lymphoma	4	N	N	F	2	85	N	N
Lymphoma	6	N	Y	F	3	70	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Lymphoma	4	N	N	F	2	87	Y	N
Lymphoma	10	Y	Y	F	5	84	N	N
Lymphoma	2	N	N	M	1	82	Y	N
Lymphoma	19	N	N	M	8	63	N	Y
Lymphoma	18	N	N	M	9	67	Y	Y
Mantle cell lymphoma	2	N	N	M	1	62	Y	Y
MDS	5	N	Y	F	2	94	N	N
MDS	5	N	N	M	2	86	N	N
MDS	8	N	N	F	3	80	N	N
MDS	8	N	N	F	3	48	N	N
MDS	8	N	N	M	2	93	N	N
MDS	8	N	N	F	4	53	Y	Y
MDS	13	N	Y	M	6	85	Y	Y
MDS	13	N	N	F	6	85	N	N
MDS	14	N	N	F	7	85	Y	N
MDS	21	N	N	M	6	80	Y	N
MDS	25	N	N	M	10	67	Y	N
MDS	30	N	Y	M	14	84	Y	N
MDS	35	N	N	F	46	90	N	N
MDS	39	N	Y	M	18	95	N	N
MDS	41	N	N	F	14	76	N	N
MDS	43	N	N	F	19	77	N	N
MDS	59	N	N	M	23	82	Y	N
MDS	67	N	N	F	32	86	N	N
MDS	70	N	N	M	27	73	Y	N
MDS	74	N	N	F	33	85	Y	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
MDS	80	N	N	F	42	89	Y	N
MDS	114	N	Y	M	48	67	Y	N
MDS	184	N	Y	F	61	88	N	N
MDS	209	N	N	F	75	72	Y	N
MDS	256	N	Y	F	94	25	N	N
MDS	310	N	Y	F	101	75	Y	N
MDS	338	N	N	M	120	69	Y	N
MDS	183	N	N	F	77	73	N	Y
MDS	7	N	N	F	3	85	N	N
MDS	8	N	N	M	4	97	Y	N
MDS	15	N	N	F	6	86	N	N
MDS	15	N	Y	F	6	73	Y	N
MDS	53	N	N	M	23	68	Y	Y
MDS	28	N	N	M	12	89	N	N
MDS	16	N	N	F	8	71	N	N
MDS	16	N	N	F	7	86	Y	N
MDS	12	N	N	M	6	71	Y	N
MDS	19	N	N	F	10	74	N	N
MDS	6	N	N	F	3	72	N	N
MDS	4	N	N	M	2	80	N	N
MDS	92	N	N	M	37	82	N	N
MDS	30	N	N	F	15	80	N	Y
MDS	109	N	N	M	51	74	Y	N
MDS	40	N	Y	M	16	76	N	N
MDS	45	N	N	M	22	85	Y	N
MDS	63	N	N	M	30	77	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
MDS	50	N	N	M	23	68	N	Y
MDS	32	N	N	F	10	59	N	N
MDS	2	N	N	F	1	88	N	N
MDS	18	Y	Y	M	9	81	Y	N
MDS	7	N	N	M	3	85	N	N
MDS	58	N	N	M	25	76	Y	N
MDS	135	N	N	F	55	80	N	N
MDS	2	N	N	F	1	71	N	Y
MDS	111	N	N	F	54	83	N	N
MDS	94	N	Y	F	36	80	N	N
MDS	61	N	N	F	21	74	N	N
MDS	38	N	N	M	19	65	Y	N
MDS	37	N	N	M	18	50	Y	Y
MDS	24	N	N	F	12	82	Y	N
MDS	32	N	N	F	15	87	N	N
MDS	224	N	N	M	87	62	Y	N
MDS	66	N	Y	M	30	79	N	N
MDS	143	N	Y	M	58	72	Y	N
MDS	119	N	N	M	40	79	N	N
MDS	10	N	N	M	5	73	N	N
MDS	15	Y	Y	F	7	82	N	Y
MDS	94	N	N	M	38	88	N	N
MDS	20	N	N	M	8	68	N	N
MDS	49	N	N	M	19	67	Y	N
MDS	332	N	Y	M	155	69	Y	Y
MDS	20	N	N	M	9	81	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
MDS	67	N	N	M	28	68	N	N
MDS	51	N	N	M	23	78	N	Y
MDS	28	N	N	F	11	80	Y	N
MDS	4	N	N	M	2	96	Y	N
MDS	32	N	N	F	14	27	Y	N
MDS	7	N	N	F	4	71	N	N
MDS	6	N	N	M	3	83	Y	Y
MDS	60	N	Y	M	27	84	N	N
MDS	287	N	N	M	124	76	Y	N
MDS	43	N	N	M	15	88	N	N
MDS	10	N	N	M	5	78	N	N
MDS	45	N	Y	M	22	83	Y	N
MDS	226	N	Y	M	81	60	Y	Y
MDS	3	N	N	M	1	81	Y	N
MDS	21	N	N	M	10	75	Y	N
MDS	35	N	N	F	14	82	N	N
MDS	6	N	N	M	2	85	N	N
MDS	33	N	Y	M	17	91	N	N
MDS	10	N	N	M	4	82	N	N
MDS	83	N	N	M	31	86	N	N
MDS	14	N	N	M	7	65	N	N
MDS	11	N	N	M	6	42	Y	N
MDS	33	N	Y	M	16	79	N	N
MDS	29	N	Y	M	13	76	Y	N
MDS	119	N	N	F	60	75	N	Y
MDS	69	N	Y	M	25	90	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
MDS	19	N	N	M	6	57	Y	N
MDS	16	N	Y	M	7	74	N	N
MDS	53	N	N	F	24	78	Y	N
MDS	52	N	Y	M	22	78	N	N
MDS	70	N	Y	F	25	84	Y	N
MDS	38	N	N	M	19	92	N	N
MDS	47	N	N	M	21	72	N	N
MDS	35	N	Y	M	16	79	Y	N
MDS	2	N	N	M	1	85	Y	N
MDS	18	N	N	M	9	81	Y	N
MDS	32	N	N	F	14	88	Y	N
MDS	14	N	N	F	6	80	N	N
MDS	61	N	Y	M	27	67	Y	N
MDS	21	N	N	F	7	77	Y	N
MDS	34	N	Y	M	17	74	Y	N
MDS	124	N	N	M	60	81	Y	N
MDS	9	N	N	M	5	87	N	N
MDS	5	N	N	F	2	82	N	N
MDS	19	N	N	M	9	89	N	N
MDS	52	N	Y	F	24	74	Y	N
MDS	24	N	Y	M	14	76	N	N
MDS	22	N	N	M	11	83	Y	N
MDS	166	N	Y	F	59	85	N	N
MDS	30	Y	Y	M	15	70	Y	N
MDS	29	N	N	M	15	74	Y	N
MDS	11	N	N	F	5	73	Y	Y

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
MDS	14	N	N	M	7	85	N	N
MDS	20	N	Y	F	7	80	N	N
MDS	140	N	Y	F	63	87	Y	N
MDS	12	N	N	M	6	85	N	N
MDS	10	N	N	F	5	75	N	N
MDS	4	N	N	F	2	66	N	N
MDS	154	Y	Y	F	62	84	N	N
MDS	14	N	Y	F	5	75	Y	N
MDS	119	N	Y	M	45	89	N	N
MDS	21	N	N	M	9	84	Y	N
MDS	69	N	Y	F	29	63	Y	Y
MDS	11	N	N	M	5	88	N	N
MDS	25	N	Y	F	11	65	N	N
MDS	16	N	Y	M	6	81	N	Y
MDS	32	N	Y	F	16	81	N	N
MDS	5	N	N	F	2	63	Y	N
MDS	6	N	N	M	3	83	N	N
MDS	8	N	N	M	3	79	N	N
MDS	179	N	Y	F	70	84	Y	N
MDS	7	N	N	F	3	78	N	N
MDS	17	N	N	F	4	77	Y	N
MDS	110	N	N	M	39	90	N	N
MDS	8	N	N	M	5	93	N	N
MDS	10	N	N	F	4	80	N	N
MDS	22	N	Y	M	10	69	Y	Y
MDS	62	N	N	M	27	90	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
MDS/AML	11	N	Y	M	5	77	Y	N
MF	14	N	N	M	5	81	N	N
MF	202	N	Y	M	83	69	Y	Y
MF	17	N	N	F	8	67	Y	N
MF	12	N	N	M	5	82	Y	N
MF	80	N	N	M	37	68	N	N
MF	33	Y	Y	F	11	80	N	N
MF	10	N	N	F	5	82	N	N
MF	17	N	N	F	11	72	Y	N
MF	34	N	N	F	17	72	N	N
MF	3	N	N	M	1	52	N	N
MF	4	N	N	M	2	83	N	N
MF	132	Y	Y	M	46	77	N	N
MF	24	Y	Y	F	12	74	N	N
MF	73	N	N	M	28	64	Y	N
MF	134	N	Y	F	61	61	Y	N
MF	26	N	N	M	10	66	Y	N
MF	18	Y	Y	F	8	61	Y	Y
MF	151	N	N	F	53	73	N	N
MF	48	N	N	F	24	59	N	N
MPD	55	Y	Y	M	22	52	Y	Y
MPD	33	N	N	F	11	64	N	N
MPD	11	N	N	M	4	84	N	N
MPD	6	N	N	F	3	74	N	N
Myeloma	2	N	Y	M	1	66	Y	Y
Myeloma	2	N	N	M	1	58	Y	Y

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Myeloma	2	N	N	M	2	76	N	N
Myeloma	2	N	N	M	1	81	N	N
Myeloma	3	N	N	F	1	80	N	N
Myeloma	3	N	N	M	1	58	Y	Y
Myeloma	4	N	N	F	2	71	N	N
Myeloma	4	N	N	M	2	88	N	N
Myeloma	4	N	N	M	2	61	N	Y
Myeloma	4	N	N	M	2	75	Y	N
Myeloma	4	N	N	M	2	89	N	N
Myeloma	4	N	N	M	2	56	N	N
Myeloma	4	N	N	F	2	82	N	N
Myeloma	4	N	N	F	2	75	N	N
Myeloma	4	N	N	F	2	54	Y	Y
Myeloma	4	N	N	M	11	64	Y	Y
Myeloma	6	N	Y	F	3	82	N	N
Myeloma	6	N	N	F	3	74	N	N
Myeloma	6	N	N	F	3	65	N	N
Myeloma	6	N	N	F	3	55	Y	Y
Myeloma	7	N	N	M	3	58	Y	Y
Myeloma	8	N	N	M	4	64	Y	Y
Myeloma	8	N	N	F	3	85	N	N
Myeloma	9	Y	Y	F	4	76	N	N
Myeloma	9	N	Y	F	3	84	N	N
Myeloma	9	N	N	F	4	83	N	N
Myeloma	10	N	Y	F	5	60	Y	Y
Myeloma	10	N	Y	M	5	61	Y	Y

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Myeloma	10	N	N	F	5	86	N	N
Myeloma	10	N	N	F	5	57	Y	Y
Myeloma	11	N	Y	F	6	75	N	N
Myeloma	12	N	N	F	6	61	Y	Y
Myeloma	12	N	N	F	6	51	Y	Y
Myeloma	12	N	N	M	7	72	Y	N
Myeloma	14	N	N	M	6	49	N	Y
Myeloma	16	N	Y	F	8	68	Y	N
Myeloma	16	N	N	M	7	78	Y	N
Myeloma	19	N	N	F	8	62	N	Y
Myeloma	20	Y	Y	M	11	56	Y	Y
Myeloma	20	N	N	F	9	75	Y	N
Myeloma	20	N	N	F	10	65	Y	N
Myeloma	21	N	Y	F	10	53	Y	Y
Myeloma	22	N	Y	M	10	71	Y	N
Myeloma	22	N	N	M	10	48	Y	N
Myeloma	23	N	N	F	10	75	N	N
Myeloma	23	N	N	M	11	68	N	N
Myeloma	24	N	N	F	10	70	Y	N
Myeloma	25	N	N	F	11	69	Y	N
Myeloma	26	N	N	F	12	89	N	N
Myeloma	26	N	N	F	14	93	N	N
Myeloma	29	N	N	M	14	62	Y	N
Myeloma	33	N	N	M	15	60	Y	Y
Myeloma	33	N	N	M	15	78	N	N
Myeloma	35	N	Y	F	20	75	Y	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Myeloma	35	N	N	F	6	61	Y	N
Myeloma	37	N	N	F	19	78	Y	N
Myeloma	37	N	N	M	16	83	Y	N
Myeloma	40	N	N	F	17	84	N	N
Myeloma	41	N	Y	M	16	71	N	N
Myeloma	47	N	N	M	22	74	Y	N
Myeloma	52	N	N	M	27	58	Y	Y
Myeloma	53	N	Y	F	35	52	Y	Y
Myeloma	55	N	N	M	21	61	Y	Y
Myeloma	56	N	N	F	26	50	Y	Y
Myeloma	57	N	N	F	24	78	N	N
Myeloma	66	N	N	F	32	49	Y	N
Myeloma	66	N	N	M	32	51	Y	Y
Myeloma	67	N	N	F	25	63	N	N
Myeloma	76	N	N	F	37	56	Y	Y
Myeloma	83	N	N	M	42	62	Y	Y
Myeloma	98	N	N	M	35	82	N	N
Myeloma	180	N	Y	M	81	48	Y	Y
Myeloma	23	N	N	F	11	70	Y	N
Myeloma	3	N	N	F	1	76	N	N
Myeloma	15	N	N	F	8	94	N	N
Myeloma	17	N	N	F	9	68	Y	Y
Myeloma	21	N	N	F	9	50	Y	Y
Myeloma	4	N	N	M	2	78	N	N
Myeloma	57	N	N	F	27	57	Y	N
Myeloma	4	N	N	F	2	63	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Myeloma	12	N	N	F	6	77	N	N
Myeloma	21	N	N	M	11	69	N	N
Myeloma	4	N	N	F	2	62	Y	Y
Myeloma	21	N	N	F	9	80	Y	N
Myeloma	4	N	N	M	2	72	N	N
Myeloma	21	N	Y	F	10	49	Y	Y
Myeloma	16	N	N	M	8	48	Y	Y
Myeloma	130	N	N	M	49	80	Y	N
Myeloma	13	N	Y	F	5	83	N	N
Myeloma	12	N	N	M	6	64	Y	Y
Myeloma	8	N	N	M	4	75	N	N
Myeloma	8	N	N	M	4	62	Y	N
Myeloma	106	N	N	F	51	70	N	N
Myeloma	3	N	N	F	1	82	N	N
Myeloma	48	N	N	F	20	72	Y	N
Myeloma	39	N	Y	M	18	76	N	N
Myeloma	26	N	N	M	12	56	Y	Y
Myeloma	51	N	N	M	21	68	Y	Y
Myeloma	14	N	N	F	7	68	Y	Y
Myeloma	11	N	N	F	6	71	N	N
Myeloma	8	N	N	F	4	79	N	N
Myeloma	124	N	Y	F	61	49	Y	Y
Myeloma	29	N	N	F	14	74	N	N
Myeloma	4	N	N	M	2	81	N	N
Myeloma	169	N	N	F	64	75	Y	N
Myeloma	27	N	N	F	14	71	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Myeloma	2	N	N	M	1	81	N	N
Myeloma	51	N	N	M	26	78	N	N
Myeloma	55	Y	Y	F	34	52	Y	Y
Myeloma	13	N	Y	F	6	84	N	N
Myeloma	4	N	N	M	2	80	N	N
Myeloma	39	N	N	F	19	78	Y	N
Myeloma	36	N	N	M	16	60	Y	Y
Myeloma	7	N	N	M	4	63	N	N
Myeloma	43	N	N	M	20	57	Y	Y
Myeloma	134	N	N	M	66	50	Y	Y
Myeloma	6	N	N	M	3	79	N	N
Myeloma	23	N	N	F	11	84	N	N
Myeloma	2	N	N	M	1	75	Y	N
Myeloma	37	N	N	M	16	70	N	N
Myeloma	8	N	N	M	4	65	N	N
Myeloma	2	N	N	F	1	66	Y	Y
Myeloma	4	N	N	F	2	83	N	N
Myeloma	13	N	N	M	6	83	N	N
Myeloma	19	N	N	M	10	82	N	N
Myeloma	23	N	N	F	11	65	N	N
Myeloma	10	N	N	F	5	87	N	N
Myeloma	19	N	Y	M	9	79	N	N
Myeloma	95	N	N	M	47	59	Y	Y
Myeloma	3	N	N	F	2	79	N	N
Myeloma	14	N	N	F	5	78	N	N
Myeloma	10	N	N	M	6	84	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Myeloma	6	N	N	M	3	82	N	N
Myeloma	4	N	N	F	2	78	N	N
Myeloma	60	N	Y	F	25	74	N	N
Myeloma	3	N	N	M	1	70	Y	N
Myeloma	73	N	N	F	37	52	Y	Y
Myeloma	11	N	N	M	5	69	N	N
Myeloma	21	N	Y	F	8	78	N	N
Myeloma	2	N	N	M	1	71	N	N
Myeloma	50	N	N	M	21	66	Y	Y
Myeloma	4	N	N	F	2	83	N	N
Myeloma	6	N	N	M	3	87	N	N
Myeloma	19	N	N	M	9	73	N	N
Myeloma	127	N	Y	M	59	78	Y	N
Myeloma	32	N	N	M	14	50	Y	Y
Myeloma	33	N	Y	M	14	51	Y	Y
Myeloma	13	N	N	M	5	88	N	N
Myeloma	2	N	N	M	1	78	N	N
Myeloma	53	N	Y	M	25	76	N	N
Myeloma	11	N	N	M	5	45	Y	Y
Myeloma	2	N	N	M	1	85	N	N
Myeloma	32	N	N	M	16	68	N	N
Myeloma	10	N	N	M	5	86	N	Y
Myeloma	19	N	N	F	5	82	Y	N
Myeloma	17	N	Y	F	8	67	N	N
Myeloma	7	N	N	F	3	83	Y	N
Myeloma	5	N	N	M	2	65	Y	Y

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Myeloma	2	N	N	M	1	72	N	N
Myeloma	37	N	N	F	18	64	N	N
Myeloma	27	N	N	M	13	74	N	N
Myeloma	8	N	N	F	4	60	N	N
Myeloma	24	N	Y	F	11	69	Y	Y
Myeloma	177	Y	Y	F	67	79	N	N
Myeloma	10	N	N	M	5	70	N	N
Myeloma	208	N	N	M	67	76	Y	N
Myeloma	4	N	N	F	2	87	N	N
Myeloma	39	N	N	M	18	71	N	N
Myeloma	8	N	N	F	3	86	N	N
Myeloma	6	N	N	F	3	80	N	N
Myeloma	10	N	N	M	6	60	N	N
Myeloma	112	N	N	M	42	84	Y	N
Myeloma	38	N	Y	M	16	69	N	N
Myeloma	2	N	N	M	1	67	Y	Y
Myeloma	40	N	N	F	16	88	N	N
Myeloma	56	N	N	M	24	54	Y	Y
Myeloma	8	N	N	M	3	68	Y	Y
Myeloma	50	N	Y	F	23	74	N	N
Myeloma	8	N	N	M	4	74	N	N
Myeloma	41	N	Y	M	21	54	Y	Y
Myeloma	10	N	N	M	6	65	Y	N
Myeloma	4	N	N	M	2	77	Y	N
Myeloma	29	N	N	F	14	57	Y	Y
Myeloma	70	N	N	M	33	62	Y	Y

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
Myeloma	2	N	N	M	1	80	N	N
Myeloma	6	N	N	M	3	81	N	N
NHL	2	N	N	M	1	69	N	N
NHL	2	N	N	M	2	62	N	N
NHL	2	N	N	M	1	41	Y	Y
NHL	2	N	N	F	1	56	N	N
NHL	3	N	N	F	1	66	N	N
NHL	4	N	Y	M	2	90	N	N
NHL	4	N	N	F	2	73	Y	N
NHL	4	N	N	M	4	74	N	N
NHL	4	N	N	F	2	83	N	N
NHL	4	N	N	F	2	45	Y	Y
NHL	4	N	N	F	2	82	N	N
NHL	4	N	N	F	2	64	N	N
NHL	4	N	N	F	2	67	N	N
NHL	4	N	N	M	2	39	N	N
NHL	5	N	N	M	2	34	Y	Y
NHL	5	N	N	F	2	68	N	N
NHL	6	N	N	M	3	72	Y	Y
NHL	6	N	N	M	2	79	Y	N
NHL	6	N	N	F	3	75	Y	N
NHL	6	N	N	F	3	56	N	Y
NHL	7	N	N	M	3	74	Y	N
NHL	8	N	Y	F	4	71	Y	N
NHL	8	N	Y	F	2	75	Y	Y
NHL	8	N	N	M	4	70	Y	Y

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
NHL	8	N	N	M	4	75	N	N
NHL	8	N	N	M	4	45	Y	Y
NHL	9	N	N	M	6	62	N	N
NHL	9	N	N	M	4	78	Y	N
NHL	10	N	Y	F	5	79	Y	Y
NHL	10	N	N	M	5	59	N	N
NHL	10	N	N	M	5	80	N	N
NHL	10	N	N	F	5	81	N	N
NHL	10	N	N	M	4	64	Y	Y
NHL	10	N	N	M	5	54	Y	Y
NHL	11	N	N	F	6	52	Y	Y
NHL	12	N	N	M	6	77	Y	Y
NHL	13	N	N	F	7	75	Y	Y
NHL	13	N	N	M	6	74	N	N
NHL	13	N	N	M	5	61	N	N
NHL	15	N	N	M	7	78	Y	Y
NHL	16	N	N	M	8	68	Y	N
NHL	16	N	N	F	7	54	Y	N
NHL	16	N	N	F	8	21	Y	Y
NHL	19	N	N	F	7	59	Y	Y
NHL	19	N	N	F	11	62	Y	N
NHL	20	N	Y	M	11	67	Y	Y
NHL	20	N	N	M	9	53	Y	Y
NHL	20	N	N	M	9	73	Y	Y
NHL	21	N	Y	M	10	80	N	Y
NHL	23	N	N	M	12	23	Y	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
NHL	24	N	Y	F	13	60	Y	Y
NHL	25	N	N	M	11	25	Y	Y
NHL	27	N	N	M	11	38	Y	Y
NHL	29	N	N	F	12	46	Y	Y
NHL	32	N	N	M	13	64	Y	N
NHL	35	N	N	F	17	67	N	Y
NHL	35	N	N	M	16	81	Y	Y
NHL	36	N	N	M	16	74	Y	Y
NHL	37	N	N	M	19	54	Y	Y
NHL	38	N	N	M	15	45	Y	Y
NHL	39	N	Y	F	19	67	Y	Y
NHL	39	N	N	M	18	63	Y	Y
NHL	40	N	N	M	19	57	Y	Y
NHL	46	N	N	M	8	47	Y	N
NHL	59	N	Y	F	31	61	Y	Y
NHL	91	N	N	M	37	84	N	N
NHL	117	N	N	F	53	58	Y	Y
NHL	31	N	N	M	16	73	Y	Y
NHL	4	N	N	M	2	72	N	N
NHL	16	N	N	F	8	70	N	Y
NHL	10	N	N	F	5	74	Y	N
NHL	6	N	N	M	3	89	N	Y
NHL	12	N	N	F	6	78	N	Y
NHL	2	N	N	F	1	93	N	N
NHL	12	N	N	M	6	73	N	Y
NHL	6	N	N	F	3	87	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
NHL	38	Y	Y	F	19	64	N	Y
NHL	2	N	N	M	1	74	N	N
NHL	61	N	Y	F	27	70	N	N
NHL	8	N	N	F	4	68	Y	N
NHL	5	N	N	F	3	84	N	N
NHL	14	N	N	M	6	61	N	N
NHL	4	N	N	M	2	76	N	Y
NHL	15	N	N	M	7	73	Y	Y
NHL	13	N	N	F	5	73	N	N
NHL	12	N	N	F	5	79	N	N
NHL	7	Y	Y	F	4	80	Y	Y
NHL	4	N	N	F	2	77	N	N
NHL	4	N	N	M	2	51	N	N
NHL	25	N	N	M	11	88	Y	N
NHL	15	N	N	F	7	61	Y	Y
NHL	3	N	N	M	2	75	N	N
NHL	4	N	N	F	2	81	N	N
NHL	29	N	N	M	15	73	Y	N
NHL	23	N	N	F	10	56	Y	Y
NHL	10	N	N	M	5	84	N	N
NHL	5	N	N	M	2	89	N	N
NHL	34	N	Y	M	16	70	Y	N
NHL	63	N	Y	M	26	68	Y	Y
NHL	37	N	N	M	14	57	Y	Y
NHL	6	N	N	M	3	68	Y	N
NHL	16	N	N	F	8	67	Y	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
NHL	17	N	N	M	8	60	Y	Y
NHL	15	N	N	M	7	71	Y	Y
NHL	5	N	N	M	2	61	Y	Y
NHL	10	N	N	M	5	58	N	N
NHL	59	N	N	M	27	56	Y	Y
NHL	26	N	N	F	13	78	N	N
NHL	24	N	N	M	11	59	Y	Y
NHL	30	N	Y	M	15	78	N	N
NHL	4	N	N	F	2	54	N	Y
NHL	6	N	N	M	3	84	N	N
NHL	3	N	N	F	1	87	Y	N
NHL	2	N	N	M	1	78	N	Y
NHL	17	Y	Y	F	7	76	N	N
NHL	8	N	N	F	4	65	N	Y
NHL	2	N	N	M	1	80	N	N
NHL	16	N	N	M	8	65	N	Y
NHL	2	N	N	F	1	71	N	Y
NHL	8	N	N	F	4	94	N	N
NHL	8	N	N	F	4	65	Y	N
NHL	6	N	N	M	3	72	N	N
NHL	5	Y	Y	F	3	74	Y	Y
NHL	10	N	N	M	5	29	Y	Y
NHL	4	N	N	F	2	71	N	N
NHL	2	N	N	F	1	80	N	N
NHL	24	N	N	F	11	89	N	N
NHL	2	N	N	M	1	78	Y	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
NHL	13	N	N	M	5	65	Y	Y
NHL	25	N	Y	M	12	60	Y	N
NHL	2	N	N	M	1	42	Y	N
NHL	17	N	N	M	9	50	Y	N
NHL	13	N	N	F	7	77	N	Y
NHL	9	N	N	F	5	61	Y	Y
NHL	14	N	N	M	6	48	Y	Y
NHL	10	N	Y	F	4	43	N	Y
NHL	49	N	N	F	21	63	Y	Y
NHL	4	N	N	M	2	59	Y	Y
NHL	7	N	N	F	4	83	N	N
NHL	7	N	N	M	3	79	N	N
NHL	17	N	N	M	6	87	N	N
NHL	18	N	Y	F	7	79	N	N
NHL	2	N	N	M	1	36	Y	Y
NHL	20	N	N	F	10	65	Y	Y
NHL	4	N	N	M	2	71	N	N
NHL	10	N	N	M	5	73	N	Y
NHL	13	N	N	F	6	63	N	N
NHL	2	N	N	F	1	81	N	N
NHL	11	N	N	M	5	66	Y	Y
NHL	26	N	N	M	11	59	Y	Y
NHL	20	N	N	M	10	63	Y	Y
NHL	8	N	N	F	4	60	Y	Y
NHL	2	N	N	F	1	78	Y	N
NHL	24	N	N	F	9	32	Y	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
NHL	15	N	Y	M	7	72	N	N
NHL	5	N	N	F	2	75	N	N
NHL	14	N	N	M	6	65	Y	Y
NHL	6	N	N	F	3	69	Y	Y
NHL	6	N	N	F	3	62	N	N
NHL	63	N	N	F	27	54	Y	Y
NHL	10	N	N	M	5	96	N	N
NHL	16	N	N	M	8	63	Y	Y
NHL	4	N	N	M	2	49	N	N
NHL	27	Y	Y	F	10	71	Y	Y
NHL	2	N	N	F	1	69	N	N
NHL	17	N	Y	F	6	83	N	N
NHL	96	N	Y	F	47	65	N	N
NHL	16	N	N	M	8	52	Y	N
NHL	63	N	Y	F	22	63	Y	Y
NHL	12	N	N	F	6	61	N	N
NHL	10	N	N	M	5	65	Y	Y
NHL	6	N	N	F	3	64	N	N
NHL	13	N	N	F	6	80	N	N
NHL	2	N	N	M	1	42	Y	Y
NHL	15	Y	Y	M	6	76	Y	N
NHL	41	Y	Y	F	8	53	Y	N
NHL	2	N	N	M	1	77	N	N
NHL	6	N	N	M	3	75	N	N
NHL	4	N	N	F	2	92	Y	N
NHL	6	N	N	M	3	91	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
NHL	46	N	Y	F	23	88	N	N
NHL	12	Y	Y	M	5	87	N	N
NHL	6	Y	Y	F	3	77	N	N
NHL	6	N	N	M	3	78	N	N
NHL	10	N	N	F	5	49	Y	Y
NHL	2	N	N	M	1	76	N	N
NHL	55	Y	Y	M	24	60	N	N
NHL	2	N	N	F	1	79	N	N
NHL	6	N	N	M	3	38	Y	Y
NHL	8	N	N	M	4	72	Y	N
NHL	8	Y	Y	M	4	65	N	N
NHL	16	N	N	F	8	76	N	N
NHL	18	N	Y	F	9	74	N	N
NHL	18	N	N	F	7	75	Y	N
NHL	70	N	N	F	27	55	Y	Y
NHL	4	N	N	F	2	46	N	N
NHL	10	Y	Y	M	5	79	N	N
NHL	7	N	N	M	3	65	Y	N
NHL	9	N	N	F	4	50	N	N
NHL	8	N	N	M	4	71	N	N
NHL	8	N	N	F	4	67	N	N
NHL	2	N	N	M	1	78	N	N
NHL	54	N	N	M	24	68	Y	Y
NHL	8	N	N	F	3	82	Y	N
NHL	4	N	N	F	2	35	N	N
NHL	2	N	N	F	1	55	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
NHL	85	N	N	M	39	61	Y	Y
NHL	8	N	N	F	4	75	N	N
NHL	33	N	N	M	12	59	Y	Y
NHL	4	N	N	F	2	77	N	N
NHL	16	N	Y	M	7	63	N	N
NHL	2	N	N	F	1	69	N	N
NHL	14	N	N	M	7	77	Y	Y
NHL	47	N	N	F	22	76	N	N
NHL	2	N	N	F	1	79	N	N
NHL	2	N	N	F	1	48	Y	Y
NHL	26	N	N	M	4	67	Y	Y
NHL	14	N	N	F	7	77	Y	Y
NHL	45	N	N	M	22	40	Y	Y
NHL	11	N	N	M	5	81	N	N
NHL	2	N	N	F	1	72	N	N
NHL	42	N	N	M	18	40	Y	Y
NHL	4	N	N	M	2	66	N	Y
NHL	4	N	N	M	2	70	N	N
NHL	4	N	N	F	2	78	N	N
NHL	13	N	N	M	6	67	Y	Y
NHL	4	N	N	F	2	67	N	Y
NHL	20	N	N	F	7	72	N	Y
NHL	13	N	N	M	6	54	Y	Y
NHL	20	N	Y	M	10	62	Y	Y
NHL	11	Y	Y	M	4	69	N	N
NHL	10	N	N	M	4	74	N	N

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
NHL	25	N	N	M	12	67	Y	N
NHL	4	N	N	M	2	89	N	N
NHL	6	N	N	M	4	86	N	N
NHL	14	N	Y	M	6	80	N	Y
NHL	67	N	N	M	33	82	Y	N
NHL	2	N	N	M	1	73	N	N
NHL	2	N	N	M	1	67	N	N
NHL	27	N	Y	M	13	81	Y	Y
NHL	14	N	N	F	7	76	Y	Y
NHL	16	N	Y	M	5	62	Y	Y
NHL	31	N	N	F	16	85	Y	N
NHL	44	N	N	M	18	77	N	Y
NHL	12	N	N	M	6	63	Y	N
NHL	33	N	N	M	15	52	Y	N
NHL	11	N	N	F	5	64	Y	N
NHL	129	N	N	F	57	27	Y	Y
NHL	4	N	N	F	2	64	N	N
NHL	6	N	N	F	3	72	N	N
NHL	2	N	N	F	1	83	N	Y
NHL	2	N	N	F	1	74	Y	N
NHL	2	N	N	M	1	69	N	N
NHL	2	N	N	F	1	79	N	N
NHL	4	N	N	M	2	80	Y	N
NHL	12	Y	Y	F	6	78	Y	Y
NHL	89	N	N	M	37	66	N	Y

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
NHL + AIHA	93	N	Y	F	34	56	Y	Y
NHL	4	Y	Y	M	2	81	N	N
Pancytopaenia	9	N	N	F	4	54	Y	N
Pancytopaenia	30	N	N	F	10	72	Y	N
Pancytopaenia	4	N	N	F	2	76	N	N
Pancytopaenia	5	N	N	M	2	36	Y	N
Pernicious anaemia	102	N	N	F	28	71	N	N
Post transplant lymphomprofilerative disease	6	N	N	F	3	24	N	N
PRV	17	N	N	F	8	74	N	N
PVR	9	N	N	F	4	70	N	N
Rheumatoid arthritis	14	Y	Y	M	4	69	N	N
Sideroblastic Anaemia	5	N	N	M	2	72	N	N
Sideroblastic Anaemia	244	N	Y	M	104	66	N	N
Sideroblastic Anaemia	76	N	N	F	28	87	N	N
Sideroblastic Anaemia	124	N	Y	F	41	77	N	N
Sideroblastic Anaemia	54	N	Y	M	26	88	N	N
Sideroblastic Anaemia	98	N	N	F	39	79	N	N
T cell prolymphocytic leukaemia	68	N	N	M	28	69	Y	Y

Diagnosis	No. units transfused	Alloimmunised at admission	Alloimmunised post transfusion	Gender	No. transfusion episodes	Age at first recorded transfusion	Platelet requirement	Irradiated requirement
T-cell leukaemia	45	N	Y	M	22	71	N	N
Thalassaemia	381	Y	Y	M	127	25	N	N
TTP	11	N	Y	F	3	30	Y	N
TTP	3	Y	Y	F	1	20	N	N
VWD	2	N	N	M	1	52	N	N
WM	32	N	Y	M	16	71	N	Y
WM	2	N	N	F	1	78	Y	N
WM	42	Y	Y	F	19	61	Y	Y
WM	20	N	N	F	12	70	Y	N
WM	23	Y	Y	F	11	75	N	Y
WM	7	N	N	F	3	65	N	N
WM	39	N	Y	F	16	77	N	N
WM	21	N	Y	F	9	73	Y	Y
WM	15	N	N	F	8	91	N	Y
WM	4	N	N	M	2	80	Y	Y
WM	16	N	N	F	8	75	Y	Y
WM	89	N	N	M	41	71	Y	Y

10.2 Appendix 2: Raw data for retrospective review of renal cohort

Key: AKI = Acute kidney injury
ARF = Acute renal failure
CKD = Chronic kidney disease
CRF = Chronic renal failure
ESRF = End stage renal failure
Y =Yes
N = No
M =Male
F = Female

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
AKI	94	N	N	N	N	M	43	87	N
AKI	7	N	N	N	N	M	3	40	N
AKI	3	N	N	N	N	F	1	65	N
AKI	2	N	N	N	N	M	1	85	N
AKI	2	N	N	N	N	F	1	66	N
AKI	2	N	N	N	N	F	1	80	N
AKI	8	N	N	N	N	M	3	79	N
ARF	30	N	N	N	N	F	14	36	Y
ARF	2	N	N	N	N	F	1	54	N
ARF	4	N	N	N	N	F	2	60	N
ARF	29	N	N	N	N	M	13	80	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ARF	6	N	N	N	N	M	3	83	N
ARF	3	N	N	N	N	F	1	71	N
ARF	6	N	N	N	N	M	3	84	N
ARF	3	N	N	N	N	F	1	76	N
ARF	4	N	N	N	N	M	1	77	N
ARF	6	N	N	N	N	M	2	75	N
ARF	4	N	N	N	N	M	2	81	N
ARF	10	N	N	N	N	M	5	77	N
ARF	4	N	N	N	N	F	2	68	N
ARF	20	N	N	N	N	F	9	53	N
ARF	2	N	N	N	N	F	1	63	N
ARF	2	N	N	N	N	F	1	41	N
ARF	14	N	N	N	N	F	6	72	N
ARF	14	N	N	N	N	M	6	61	N
ARF	1	N	N	N	N	F	1	81	N
ARF	4	N	N	N	N	M	2	78	N
ARF	5	N	N	N	N	F	2	67	N
ARF	7	N	N	N	N	F	4	66	N
ARF	15	N	N	N	N	M	6	82	N
ARF	5	N	N	N	N	F	2	74	N
ARF	2	N	N	N	N	M	1	87	N
ARF	2	N	N	N	N	M	1	76	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ARF	5	N	N	N	N	F	2	56	N
ARF	13	N	N	N	N	M	5	93	N
ARF	2	N	N	N	N	M	1	76	N
ARF	17	N	N	N	N	M	7	67	N
ARF	44	N	N	N	N	F	13	44	N
ARF	2	N	N	N	N	F	1	66	N
ARF	10	N	N	N	N	F	4	82	N
ARF	4	N	N	N	N	M	2	89	N
ARF	8	N	N	N	N	M	3	31	N
ARF	6	N	N	N	N	M	3	69	N
ARF	2	N	N	N	N	M	2	69	N
ARF	18	N	N	N	N	M	8	76	N
ARF	2	N	N	N	N	M	1	83	N
ARF	4	N	N	N	N	F	2	22	N
ARF	2	N	N	N	N	F	1	62	N
ARF	3	N	N	N	N	M	1	74	N
ARF	4	N	N	N	N	M	2	83	N
CKD	2	N	N	N	N	M	1	63	N
CKD	4	N	N	N	N	M	2	76	N
CKD	47	N	N	N	N	M	13	72	N
CKD	2	N	N	N	N	F	1	73	N
CKD	2	N	N	N	N	M	1	62	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
CKD	2	N	N	N	N	F	1	46	N
CKD	4	N	N	N	N	F	2	75	N
CKD	74	N	N	N	N	M	35	70	N
CKD	2	N	N	N	N	M	1	69	N
CKD	8	N	N	N	N	M	4	52	N
CKD	2	N	N	N	N	M	1	88	N
CKD	2	N	N	N	N	F	1	75	N
CKD	4	N	N	N	N	M	2	76	N
CKD	10	N	N	N	N	M	4	66	N
CKD	14	N	N	N	N	M	7	91	N
CKD	4	N	N	N	N	F	2	24	N
CKD	16	N	N	N	N	M	8	72	N
CKD	2	N	N	N	N	F	1	87	N
CKD	8	N	N	N	N	F	4	63	N
CKD	16	N	N	N	N	F	7	76	N
CKD	36	N	N	N	N	F	14	75	N
CKD	4	N	N	N	N	M	2	85	N
CKD	25	N	N	N	N	M	13	69	N
CKD	2	N	N	N	N	M	1	69	N
CKD	2	N	N	N	N	M	1	55	N
CKD	2	N	N	N	N	F	1	84	N
CKD	6	N	N	N	N	M	3	80	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
CKD	9	N	N	N	N	M	5	68	N
CKD	2	N	N	N	N	M	1	74	N
CKD	14	N	N	N	N	F	7	79	N
CKD	9	N	N	N	N	F	3	76	N
CKD	5	N	N	N	N	M	2	73	N
CKD	2	N	N	N	N	M	1	73	N
CKD	4	N	N	N	N	M	2	52	N
CKD	4	N	N	N	N	M	2	77	N
CKD	12	N	N	N	N	M	6	52	N
CKD	10	N	N	N	N	M	5	87	N
CKD	44	N	N	N	N	M	16	95	N
CKD	6	N	N	N	N	M	3	65	N
CKD	13	N	N	N	N	F	6	55	N
CKD	16	N	N	N	N	M	5	65	N
CKD	39	N	N	N	N	F	20	59	N
CKD	2	N	N	N	N	M	1	54	N
CKD	9	N	N	N	N	M	4	71	N
CKD	12	N	N	N	N	M	5	71	N
CKD	9	N	N	N	N	M	4	63	N
CKD	5	N	N	N	N	F	2	79	N
CKD	16	N	N	N	N	M	8	83	N
CKD	6	N	N	N	N	M	3	52	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
CKD	8	N	N	N	N	F	4	80	N
CKD	15	N	N	N	N	M	8	71	N
CKD	9	N	Y	N	Y	M	4	69	N
CKD	2	Y	Y	Y	Y	F	1	43	N
CKD	14	N	Y	N	Y	F	7	65	N
CKD	98	N	Y	N	Y	F	40	55	N
CKD	25	Y	Y	Y	Y	M	13	74	N
CRF	29	N	N	N	N	F	13	59	N
CRF	3	N	N	N	N	M	1	37	Y
CRF	3	N	N	N	N	F	1	44	Y
CRF	7	N	N	N	N	M	3	39	Y
CRF	9	N	N	N	N	M	5	43	Y
CRF	48	N	N	N	N	M	22	55	Y
CRF	26	N	N	N	N	M	13	15	Y
CRF	4	N	N	N	N	F	2	57	Y
CRF	21	N	N	N	N	M	9	57	Y
CRF	2	N	N	N	N	F	1	69	Y
CRF	12	N	N	N	N	M	5	57	Y
CRF	12	N	N	N	N	F	5	32	Y
CRF	7	N	N	N	N	M	3	39	Y
CRF	22	N	N	N	N	F	11	67	Y
CRF	8	N	N	N	N	M	4	28	Y

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
CRF	11	N	N	N	N	M	4	45	Y
CRF	2	N	N	N	N	M	1	63	Y
CRF	2	N	N	N	N	M	1	19	Y
CRF	5	N	N	N	N	M	2	41	Y
CRF	31	N	N	N	N	M	19	37	Y
CRF	12	N	N	N	N	F	6	54	Y
CRF	8	N	N	N	N	F	3	38	Y
CRF	6	N	N	N	N	M	3	51	Y
CRF	5	N	N	N	N	M	2	70	Y
CRF	5	N	N	N	N	M	3	34	Y
CRF	15	N	N	N	N	M	7	45	Y
CRF	2	N	N	N	N	F	1	70	Y
CRF	22	N	N	N	N	F	8	32	Y
CRF	5	N	N	N	N	M	3	64	Y
CRF	8	N	N	N	N	M	4	33	Y
CRF	2	N	N	N	N	F	1	49	Y
CRF	2	N	N	N	N	M	1	60	Y
CRF	22	N	Y	N	N	M	7	42	Y
CRF	143	N	Y	N	N	M	54	45	Y
CRF	4	N	Y	N	N	M	2	38	Y
CRF	4	N	Y	N	N	M	2	65	Y
CRF	8	N	Y	N	N	M	4	60	Y

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
CRF	9	N	Y	N	Y	M	4	44	Y
CRF	6	N	Y	N	N	M	3	48	Y
CRF	3	N	N	N	N	M	2	84	N
CRF	2	N	N	N	N	F	1	74	N
CRF	13	N	N	N	Y	M	6	53	N
CRF	4	N	N	N	N	M	2	71	N
CRF	4	N	N	N	N	F	2	45	N
CRF	8	N	N	N	N	F	3	39	N
CRF	5	N	N	N	N	F	3	69	N
CRF	5	N	N	N	N	F	2	82	N
CRF	3	N	N	N	N	M	2	91	N
CRF	10	N	N	N	N	F	4	63	N
CRF	4	N	N	N	N	F	2	81	N
CRF	2	N	N	N	N	F	1	68	N
CRF	7	N	N	N	N	F	3	74	N
CRF	7	N	N	N	N	M	4	53	N
CRF	12	N	N	N	N	M	5	65	N
CRF	20	N	N	N	N	F	9	77	N
CRF	2	N	N	N	N	M	1	82	N
CRF	11	N	N	N	N	M	4	80	N
CRF	5	N	N	N	N	M	2	55	N
CRF	7	N	N	N	N	M	3	73	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
CRF	21	N	N	N	N	M	9	78	N
CRF	32	N	N	N	N	F	14	58	N
CRF	11	N	N	N	N	M	5	79	N
CRF	3	N	N	N	N	M	1	81	N
CRF	3	N	N	N	N	F	2	59	N
CRF	3	N	N	N	N	M	1	84	N
CRF	6	N	N	N	N	M	3	65	N
CRF	14	N	N	N	N	M	4	65	N
CRF	4	N	N	N	N	M	1	88	N
CRF	12	N	N	N	N	M	5	68	N
CRF	4	N	N	N	N	M	2	71	N
CRF	3	N	N	N	N	M	1	66	N
CRF	7	N	N	N	N	M	3	84	N
CRF	10	N	N	N	N	F	4	80	N
CRF	2	N	N	N	N	M	1	75	N
CRF	2	N	N	N	N	M	1	82	N
CRF	6	N	N	N	N	F	2	84	N
CRF	3	N	N	N	N	M	1	72	N
CRF	6	N	N	N	N	M	2	83	N
CRF	7	N	N	N	N	M	4	76	N
CRF	11	N	N	N	N	M	5	79	N
CRF	6	N	N	N	N	F	2	32	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
CRF	17	N	N	N	N	M	6	83	N
CRF	34	N	N	N	N	F	13	46	N
CRF	4	N	N	N	N	M	1	70	N
CRF	3	N	N	N	N	F	1	61	N
CRF	5	N	N	N	N	M	3	79	N
CRF	7	N	N	N	N	M	3	78	N
CRF	4	N	N	N	N	M	2	81	N
CRF	2	N	N	N	N	M	1	77	N
CRF	8	N	N	N	N	F	2	66	N
CRF	6	N	N	N	N	M	3	80	N
CRF	6	N	N	N	N	M	3	56	N
CRF	2	N	N	N	N	M	1	54	N
CRF	6	N	N	N	N	M	3	87	N
CRF	2	N	N	N	N	M	1	42	N
CRF	8	N	N	N	N	F	4	52	N
CRF	246	N	N	N	N	M	67	75	N
CRF	2	N	N	N	N	M	1	49	N
CRF	2	N	N	N	N	M	1	75	N
CRF	2	N	N	N	N	F	1	58	N
CRF	27	N	N	N	N	M	14	42	N
CRF	22	N	N	N	N	M	8	73	N
CRF	4	N	N	N	N	M	2	66	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
CRF	6	N	N	N	N	M	2	83	N
CRF	8	N	N	N	N	M	3	59	N
CRF	10	N	N	N	N	F	4	76	N
CRF	6	N	N	N	N	M	3	89	N
CRF	3	N	N	N	N	F	2	68	N
CRF	7	N	N	N	N	M	3	76	N
CRF	10	N	N	N	N	M	4	64	N
CRF	66	N	N	N	N	F	26	47	N
CRF	2	N	N	N	N	F	1	70	N
CRF	17	N	N	Y	Y	F	8	76	N
CRF	2	N	N	N	N	M	1	81	N
CRF	31	N	N	N	N	F	15	68	N
CRF	12	N	N	N	N	F	6	71	N
CRF	21	N	N	N	N	F	9	67	N
CRF	8	N	N	N	N	M	4	60	N
CRF	9	N	N	N	N	M	4	78	N
CRF	4	N	N	N	N	M	3	82	N
CRF	13	N	N	N	N	F	6	35	N
CRF	4	N	N	N	N	F	2	68	N
CRF	7	N	N	N	N	M	4	76	N
CRF	75	N	N	N	Y	M	36	65	N
CRF	15	N	N	Y	Y	M	6	76	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
CRF	13	N	N	N	N	F	5	70	N
CRF	10	N	N	N	N	M	5	78	N
CRF	5	N	N	N	N	M	2	75	N
CRF	10	N	N	N	N	F	4	54	N
CRF	16	N	N	N	N	F	8	63	N
CRF	16	N	N	N	N	M	7	88	N
CRF	24	N	N	Y	Y	M	9	81	N
CRF	46	N	N	N	N	M	18	83	N
CRF	12	N	N	N	N	F	6	55	N
CRF	56	N	N	N	N	M	24	54	N
CRF	5	N	N	N	N	F	2	73	N
CRF	6	N	N	N	N	F	3	51	N
CRF	11	N	N	N	N	M	4	82	N
CRF	62	N	N	N	N	F	28	53	N
CRF	11	N	N	N	N	M	5	75	N
CRF	24	N	N	N	N	M	9	77	N
CRF	19	N	N	N	N	M	9	67	N
CRF	50	N	N	N	N	M	21	57	N
CRF	25	N	N	N	N	M	11	65	N
CRF	21	N	N	N	N	F	10	74	N
CRF	2	N	N	N	N	M	1	65	N
CRF	18	N	N	N	N	M	9	66	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
CRF	25	N	N	N	N	M	9	80	N
CRF	4	N	N	N	N	M	2	73	N
CRF	3	N	N	N	N	M	2	82	N
CRF	6	N	N	N	N	M	2	78	N
CRF	6	N	N	Y	Y	M	3	85	N
CRF	18	N	N	N	N	F	9	77	N
CRF	10	N	N	N	N	M	4	78	N
CRF	2	N	N	N	N	M	1	72	N
CRF	4	N	N	N	N	F	2	83	N
CRF	14	N	N	N	N	M	6	60	N
CRF	38	N	N	N	N	M	18	61	N
CRF	162	N	N	N	N	M	34	76	N
CRF	3	N	N	N	N	M	1	84	N
CRF	2	N	N	N	N	M	1	73	N
CRF	12	N	N	N	N	M	6	78	N
CRF	6	N	N	N	N	F	3	71	N
CRF	10	N	N	N	N	M	4	84	N
CRF	9	N	N	N	N	M	3	72	N
CRF	3	N	N	N	N	M	1	65	N
CRF	12	N	N	N	N	F	4	56	N
CRF	21	N	N	N	N	F	4	79	N
CRF	10	N	N	N	N	M	4	72	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
CRF	2	N	N	N	N	F	1	78	N
CRF	16	N	N	N	N	F	7	71	N
CRF	2	N	N	N	N	M	1	84	N
CRF	5	N	N	N	N	M	2	32	N
CRF	2	N	N	N	N	M	1	75	N
CRF	2	N	N	Y	Y	M	1	66	N
CRF	13	N	N	N	N	M	6	61	N
CRF	2	N	N	N	N	M	1	80	N
CRF	9	N	N	N	N	M	4	79	N
CRF	13	N	N	N	N	M	6	48	N
CRF	5	N	N	N	N	F	2	55	N
CRF	5	N	N	N	N	F	3	56	N
CRF	3	N	N	N	N	F	1	75	N
CRF	4	N	N	N	N	F	2	63	N
CRF	2	N	N	N	N	F	1	72	N
CRF	5	N	N	N	N	F	2	79	N
CRF	31	N	N	N	N	F	13	75	N
CRF	17	N	N	N	N	F	7	65	N
CRF	2	N	N	N	N	M	1	77	N
CRF	8	N	N	N	N	F	4	72	N
CRF	3	N	N	N	N	M	1	67	N
CRF	2	N	N	N	N	M	1	83	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
CRF	3	N	N	N	N	M	2	79	N
CRF	41	N	Y	N	Y	M	16	71	N
CRF	5	Y	Y	N	N	F	2	62	N
CRF	15	N	Y	N	N	F	7	74	N
CRF	21	N	Y	N	N	F	11	24	N
CRF	9	N	Y	N	N	F	5	73	N
CRF	12	Y	Y	N	Y	M	6	79	N
CRF	2	Y	Y	N	N	M	1	82	N
CRF	4	N	Y	N	N	M	2	58	N
CRF	3	N	Y	N	N	F	1	82	N
CRF	78	Y	Y	N	Y	F	37	67	N
CRF	36	N	Y	N	Y	M	11	77	N
CRF	12	N	Y	N	N	F	5	80	N
CRF	3	Y	Y	N	N	F	1	81	N
CRF	7	N	Y	N	N	F	3	84	N
CRF	6	Y	Y	Y	Y	F	3	76	N
CRF	16	N	Y	N	N	F	7	68	N
CRF	4	N	Y	N	N	F	2	90	N
CRF	22	N	Y	N	N	F	9	43	N
CRF	40	N	Y	N	N	M	18	49	N
CRF	14	N	Y	N	Y	M	6	43	N
CRF	3	N	Y	N	N	M	2	69	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
CRF	12	N	Y	N	Y	F	6	44	N
CRF	23	N	Y	N	N	F	9	81	N
CRF	5	Y	Y	N	Y	F	2	76	N
CRF	10	N	Y	N	Y	M	4	77	N
CRF	8	N	Y	N	N	M	4	73	N
CRF	8	Y	Y	N	Y	F	3	80	N
CRF	7	N	Y	N	Y	M	3	86	N
CRF	12	N	Y	N	N	M	6	76	N
CRF	103	N	Y	N	N	F	51	65	N
CRF	13	Y	Y	N	Y	M	4	73	N
CRF	107	N	Y	N	N	F	58	69	N
CRF	25	N	Y	N	Y	F	11	68	N
CRF	42	N	Y	N	Y	M	18	63	N
CRF	10	N	Y	N	Y	F	5	63	N
CRF	4	Y	Y	Y	Y	F	2	62	N
CRF	10	N	N	N	N	F	5	79	N
CRF	3	N	N	N	N	M	1	49	
ESRF	37	N	N	N	Y	F	17	34	N
ESRF	18	N	N	N	Y	M	8	68	N
ESRF	37	N	N	N	N	M	18	53	N
ESRF	5	N	N	N	N	M	2	38	Y
ESRF	14	N	N	N	N	M	6	38	Y

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	13	N	N	N	N	M	8	55	Y
ESRF	15	N	N	N	N	M	7	54	Y
ESRF	10	N	N	N	N	M	5	60	Y
ESRF	27	N	N	N	N	F	12	29	Y
ESRF	13	N	N	N	N	M	7	62	Y
ESRF	5	N	N	N	N	F	2	78	N
ESRF	8	N	N	N	N	F	4	56	N
ESRF	7	N	N	N	N	F	3	78	N
ESRF	2	N	N	N	N	M	1	91	N
ESRF	6	N	N	N	N	M	3	59	N
ESRF	7	N	N	N	N	M	3	78	N
ESRF	22	N	N	N	N	M	10	80	N
ESRF	18	N	N	N	N	M	9	76	N
ESRF	14	N	N	N	N	M	7	73	N
ESRF	12	N	N	N	N	M	5	61	N
ESRF	21	N	N	N	N	F	10	50	N
ESRF	10	N	N	N	N	M	5	72	N
ESRF	4	N	N	N	N	M	2	71	N
ESRF	4	N	N	N	N	F	2	76	N
ESRF	2	N	N	N	N	F	1	35	N
ESRF	10	N	N	N	N	F	5	69	N
ESRF	27	N	N	N	N	F	13	76	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	2	N	N	N	N	F	1	76	N
ESRF	10	N	N	N	N	F	5	67	N
ESRF	2	N	N	N	N	F	1	73	N
ESRF	13	N	N	N	N	F	6	75	N
ESRF	20	N	N	N	N	F	9	67	N
ESRF	7	N	N	N	N	F	3	64	N
ESRF	14	N	N	N	N	F	6	79	N
ESRF	18	N	N	N	N	F	8	74	N
ESRF	31	N	N	N	N	F	15	48	N
ESRF	8	N	N	N	N	F	4	81	N
ESRF	2	N	N	N	N	F	1	79	N
ESRF	16	N	N	N	N	F	8	58	N
ESRF	83	N	N	N	N	M	36	73	N
ESRF	22	N	N	N	N	F	11	58	N
ESRF	25	N	N	N	N	M	9	77	N
ESRF	7	N	N	N	N	M	4	69	N
ESRF	19	N	N	N	N	M	9	38	N
ESRF	22	N	N	N	N	M	11	60	N
ESRF	26	N	N	N	N	M	11	74	N
ESRF	19	N	N	N	N	F	7	70	N
ESRF	18	N	N	N	N	F	8	46	N
ESRF	5	N	N	N	N	F	3	62	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	73	N	N	N	N	M	27	75	N
ESRF	4	N	N	N	N	M	2	78	N
ESRF	6	N	N	N	N	M	3	81	N
ESRF	2	N	N	N	N	M	1	80	N
ESRF	9	N	N	N	N	M	4	65	N
ESRF	4	N	N	N	N	F	2	80	N
ESRF	6	N	N	N	N	F	3	81	N
ESRF	19	N	N	N	N	F	10	34	N
ESRF	19	N	N	N	Y	M	9	73	N
ESRF	6	N	N	N	N	F	3	41	N
ESRF	2	N	N	N	N	F	1	77	N
ESRF	10	N	N	N	N	M	5	52	N
ESRF	30	N	N	N	N	M	11	65	N
ESRF	7	N	N	N	N	M	4	78	N
ESRF	13	N	N	N	N	M	6	73	N
ESRF	4	N	N	N	N	M	2	84	N
ESRF	2	N	N	N	N	M	1	50	N
ESRF	2	N	N	N	N	F	1	73	N
ESRF	18	N	N	N	Y	M	8	78	N
ESRF	24	N	N	N	N	M	10	45	N
ESRF	11	N	N	N	N	M	5	37	N
ESRF	6	N	N	N	N	M	3	72	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	6	N	N	N	N	M	2	70	N
ESRF	8	N	N	N	N	M	3	71	N
ESRF	24	N	N	N	N	M	12	74	N
ESRF	8	N	N	N	N	M	4	78	N
ESRF	9	N	N	N	N	F	5	82	N
ESRF	2	N	N	N	N	M	1	68	N
ESRF	3	N	N	N	N	M	1	84	N
ESRF	5	N	N	N	N	M	2	62	N
ESRF	7	N	N	N	N	F	3	75	N
ESRF	8	N	N	N	N	M	4	52	N
ESRF	9	N	N	N	N	F	4	72	N
ESRF	4	N	N	N	N	F	2	65	N
ESRF	30	N	N	N	N	M	15	66	N
ESRF	28	N	N	N	N	M	13	67	N
ESRF	10	N	N	N	N	F	4	79	N
ESRF	2	N	N	N	N	M	2	75	N
ESRF	31	N	N	N	N	M	14	18	N
ESRF	2	N	N	N	N	F	1	76	N
ESRF	4	N	N	N	N	M	2	70	N
ESRF	14	N	N	N	N	F	5	77	N
ESRF	7	N	N	N	N	M	3	69	N
ESRF	8	N	N	N	N	M	4	72	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	3	N	N	N	N	M	1	80	N
ESRF	10	N	N	N	N	F	5	69	N
ESRF	12	N	N	N	N	M	6	53	N
ESRF	2	N	N	N	N	M	1	70	N
ESRF	12	N	N	N	N	F	6	75	N
ESRF	3	N	N	N	N	M	1	89	N
ESRF	19	N	N	N	N	M	9	69	N
ESRF	25	N	N	N	N	M	13	62	N
ESRF	15	N	N	N	N	M	7	82	N
ESRF	16	N	N	N	N	M	8	70	N
ESRF	8	N	N	N	N	M	4	85	N
ESRF	12	N	N	N	N	M	6	80	N
ESRF	5	N	N	N	N	M	2	71	N
ESRF	20	N	N	N	N	F	9	81	N
ESRF	69	N	N	N	N	M	34	60	N
ESRF	19	N	N	N	Y	F	5	79	N
ESRF	2	N	N	N	N	F	1	83	N
ESRF	3	N	N	N	N	M	1	65	N
ESRF	6	N	N	N	N	M	3	78	N
ESRF	9	N	N	N	N	M	4	61	N
ESRF	5	N	N	N	N	M	3	66	N
ESRF	12	N	N	N	N	M	6	88	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	8	N	N	N	N	M	4	82	N
ESRF	14	N	N	N	N	F	5	77	N
ESRF	4	N	N	N	N	M	2	66	N
ESRF	6	N	N	N	N	M	3	81	N
ESRF	12	N	N	N	N	F	7	79	N
ESRF	4	N	N	N	N	F	2	74	N
ESRF	4	N	N	N	N	F	2	90	N
ESRF	21	N	N	N	N	F	10	54	N
ESRF	2	N	N	N	N	M	1	81	N
ESRF	4	N	N	N	N	M	2	64	N
ESRF	2	N	N	N	N	M	1	78	N
ESRF	16	N	N	N	N	F	7	51	N
ESRF	5	N	N	N	N	F	2	81	N
ESRF	20	N	N	N	N	M	8	59	N
ESRF	2	N	N	N	N	M	1	82	N
ESRF	10	N	N	N	N	M	5	79	N
ESRF	2	N	N	N	N	M	1	84	N
ESRF	2	N	N	N	N	M	1	83	N
ESRF	21	N	N	N	N	M	11	74	N
ESRF	2	N	N	N	N	F	1	86	N
ESRF	10	N	N	N	N	M	5	74	N
ESRF	15	N	N	N	N	M	8	70	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	4	N	N	N	N	M	2	78	N
ESRF	2	N	N	N	N	M	1	63	N
ESRF	10	N	N	N	N	M	5	76	N
ESRF	2	N	N	N	N	M	1	85	N
ESRF	2	N	N	N	N	F	1	86	N
ESRF	8	N	N	N	N	M	4	72	N
ESRF	2	N	N	N	N	M	1	78	N
ESRF	23	N	N	N	N	F	10	58	N
ESRF	6	N	N	N	N	F	3	83	N
ESRF	6	N	N	N	N	F	3	76	N
ESRF	2	N	N	N	N	F	1	79	N
ESRF	6	N	N	N	N	F	3	82	N
ESRF	3	N	N	N	N	M	1	75	N
ESRF	8	N	N	N	N	M	4	46	N
ESRF	9	N	N	N	N	M	5	62	N
ESRF	4	N	N	N	N	M	2	71	N
ESRF	10	N	N	N	N	M	5	75	N
ESRF	21	N	N	N	N	M	10	42	N
ESRF	11	N	N	N	N	M	5	78	N
ESRF	14	N	N	N	N	F	7	71	N
ESRF	6	N	N	N	N	M	3	78	N
ESRF	2	N	N	N	N	M	1	87	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	11	N	N	N	N	F	6	73	N
ESRF	2	N	N	N	N	M	2	76	N
ESRF	20	N	N	N	N	F	10	75	N
ESRF	2	N	N	N	N	M	1	71	N
ESRF	12	N	N	N	N	M	6	77	N
ESRF	19	N	N	N	N	M	9	62	N
ESRF	12	N	N	N	N	M	4	84	N
ESRF	4	N	N	N	N	M	2	73	N
ESRF	11	N	N	N	N	M	4	82	N
ESRF	13	N	N	N	N	F	4	56	N
ESRF	5	N	N	N	N	M	2	86	N
ESRF	2	N	N	N	N	F	1	67	N
ESRF	8	N	N	N	N	M	5	79	N
ESRF	4	N	N	N	N	F	2	53	N
ESRF	3	N	N	N	N	M	1	87	N
ESRF	8	N	N	N	N	M	4	85	N
ESRF	10	N	N	N	N	F	5	70	N
ESRF	6	N	N	N	N	M	3	76	N
ESRF	6	N	N	N	N	M	3	74	N
ESRF	8	N	N	N	N	F	4	78	N
ESRF	12	N	N	N	N	M	6	82	N
ESRF	10	N	N	N	N	M	6	48	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	8	N	N	N	N	M	4	78	N
ESRF	9	N	N	N	N	F	4	71	N
ESRF	33	N	N	N	N	M	16	88	N
ESRF	6	N	N	N	N	F	3	73	N
ESRF	25	N	N	N	N	F	12	61	N
ESRF	8	N	N	N	N	M	4	55	N
ESRF	4	N	N	N	N	M	2	76	N
ESRF	2	N	N	N	N	F	1	75	N
ESRF	7	N	N	N	N	M	3	81	N
ESRF	36	N	N	N	N	M	17	65	N
ESRF	8	N	N	N	N	M	4	91	N
ESRF	4	N	N	N	N	M	2	84	N
ESRF	4	N	N	N	N	M	2	89	N
ESRF	23	N	N	N	N	F	11	77	N
ESRF	17	N	N	N	N	F	7	51	N
ESRF	14	N	N	N	N	F	3	65	N
ESRF	2	N	N	N	N	M	1	78	N
ESRF	2	N	N	N	N	M	1	75	N
ESRF	2	N	N	N	N	F	1	83	N
ESRF	12	N	N	N	N	M	7	75	N
ESRF	7	N	N	N	N	M	3	61	N
ESRF	4	N	N	N	N	F	2	17	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	2	N	N	N	N	F	1	86	N
ESRF	6	N	N	N	N	M	3	75	N
ESRF	8	N	N	N	N	M	4	70	N
ESRF	14	N	N	N	N	M	5	54	N
ESRF	10	N	N	N	N	M	5	72	N
ESRF	14	N	N	N	N	M	5	79	N
ESRF	6	N	N	N	N	M	3	79	N
ESRF	16	N	N	N	N	M	9	61	N
ESRF	54	N	N	N	N	M	17	49	N
ESRF	4	N	N	Y	Y	M	2	77	N
ESRF	4	N	N	N	N	F	2	64	N
ESRF	19	N	N	N	N	F	9	70	N
ESRF	2	N	N	N	N	M	1	83	N
ESRF	5	N	N	N	N	M	2	74	N
ESRF	5	N	N	N	N	M	2	65	N
ESRF	6	N	N	N	N	M	2	76	N
ESRF	6	N	N	N	N	M	3	78	N
ESRF	27	N	N	N	N	M	11	37	N
ESRF	8	N	N	N	N	F	4	80	N
ESRF	31	N	N	N	N	F	16	44	N
ESRF	6	N	N	N	N	F	3	76	N
ESRF	2	N	N	N	N	F	1	70	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	2	N	N	N	N	F	1	75	N
ESRF	4	N	N	N	N	M	2	67	N
ESRF	26	N	N	N	N	F	13	60	N
ESRF	5	N	N	N	N	F	3	64	N
ESRF	7	N	N	N	N	F	3	76	N
ESRF	2	N	N	N	N	M	1	86	N
ESRF	6	N	N	N	N	F	3	79	N
ESRF	8	N	N	N	N	F	4	75	N
ESRF	3	N	N	N	N	M	2	79	N
ESRF	13	N	N	N	N	M	6	77	N
ESRF	25	N	N	N	N	M	12	53	N
ESRF	23	N	N	N	N	F	10	65	N
ESRF	18	N	N	N	N	M	9	84	N
ESRF	5	N	N	N	N	M	2	87	N
ESRF	2	N	N	N	N	M	1	80	N
ESRF	132	N	N	N	N	F	58	70	N
ESRF	6	N	N	N	N	F	3	53	N
ESRF	6	N	N	N	N	M	3	76	N
ESRF	6	N	N	N	N	M	3	75	N
ESRF	9	N	N	N	N	M	4	81	N
ESRF	5	N	N	N	N	M	3	58	N
ESRF	22	N	N	N	N	M	11	82	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	14	N	N	N	N	F	9	85	N
ESRF	2	N	N	N	N	F	1	88	N
ESRF	8	N	N	N	N	M	4	57	N
ESRF	4	N	N	N	N	M	2	79	N
ESRF	4	N	N	N	N	F	2	73	N
ESRF	6	N	N	N	N	M	3	46	N
ESRF	6	N	N	N	N	M	3	80	N
ESRF	4	N	N	N	N	M	2	75	N
ESRF	6	N	N	N	N	M	3	78	N
ESRF	9	N	N	N	N	M	4	51	N
ESRF	2	N	N	N	N	M	1	72	N
ESRF	2	N	N	N	N	M	1	87	N
ESRF	28	N	N	N	Y	F	13	58	N
ESRF	3	N	N	N	N	F	2	60	N
ESRF	6	N	N	N	N	M	3	83	N
ESRF	4	N	N	N	N	F	2	67	N
ESRF	2	N	N	N	N	M	1	25	N
ESRF	27	N	N	N	N	M	14	72	N
ESRF	4	N	N	N	N	F	2	74	N
ESRF	17	N	N	N	N	F	9	70	N
ESRF	8	N	N	N	N	M	4	46	N
ESRF	16	N	N	N	N	M	9	62	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	7	N	N	N	N	F	4	85	N
ESRF	2	N	N	N	N	M	1	66	N
ESRF	28	N	N	N	N	M	13	52	N
ESRF	5	N	N	N	N	F	2	47	N
ESRF	54	N	N	N	N	M	24	68	N
ESRF	11	N	N	N	N	F	4	83	N
ESRF	7	N	N	N	N	M	3	61	N
ESRF	7	N	N	N	N	M	3	64	N
ESRF	2	N	N	N	N	M	1	82	N
ESRF	6	N	N	N	N	M	3	75	N
ESRF	19	N	N	N	N	M	9	55	N
ESRF	*8*	*N*	*N*	*N*	*N*	*M*	4	52	N
ESRF	7	N	N	N	N	M	3	63	N
ESRF	21	N	N	N	N	M	9	52	N
ESRF	8	N	N	N	N	F	4	75	N
ESRF	4	N	N	N	N	F	2	73	N
ESRF	27	N	N	N	N	M	4	57	N
ESRF	35	N	N	N	N	F	18	59	N
ESRF	3	N	N	N	N	F	2	50	N
ESRF	18	N	N	N	N	F	9	69	N
ESRF	3	N	N	N	N	M	1	82	N
ESRF	14	N	N	N	N	M	6	76	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	19	N	N	N	N	M	9	23	N
ESRF	12	N	N	N	N	F	7	64	N
ESRF	22	N	N	N	N	M	10	68	N
ESRF	4	N	N	N	N	M	3	65	N
ESRF	20	N	N	N	N	F	11	52	N
ESRF	20	N	N	N	N	M	9	57	N
ESRF	4	N	N	N	N	M	2	56	N
ESRF	29	N	N	N	N	M	13	67	N
ESRF	11	N	N	N	N	M	6	46	N
ESRF	31	N	N	N	N	F	12	82	N
ESRF	4	N	N	N	N	M	1	71	N
ESRF	15	N	N	N	N	M	7	71	N
ESRF	6	N	N	N	N	M	3	82	N
ESRF	5	N	N	N	N	M	2	39	N
ESRF	12	N	N	N	N	M	5	65	N
ESRF	17	N	N	N	N	M	9	66	N
ESRF	7	N	N	N	N	F	3	71	N
ESRF	16	N	N	N	N	M	6	77	N
ESRF	6	N	N	N	N	F	3	70	N
ESRF	14	N	N	N	N	M	6	41	N
ESRF	9	N	N	N	N	F	4	77	N
ESRF	2	N	N	N	N	M	1	87	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	15	N	N	N	N	M	8	81	N
ESRF	17	N	N	N	N	F	7	72	N
ESRF	21	N	N	N	N	M	10	67	N
ESRF	46	N	N	N	N	M	24	63	N
ESRF	16	N	N	N	N	F	8	66	N
ESRF	7	N	N	N	N	M	3	79	N
ESRF	17	N	N	N	N	M	8	50	N
ESRF	7	N	N	N	N	M	3	69	N
ESRF	9	N	N	N	N	M	4	82	N
ESRF	8	N	N	N	N	F	4	87	N
ESRF	7	N	N	N	N	M	3	69	N
ESRF	2	N	N	N	N	M	1	80	N
ESRF	49	N	N	N	N	M	21	72	N
ESRF	5	N	N	N	N	M	2	75	N
ESRF	9	N	N	N	N	F	4	58	N
ESRF	3	N	N	N	N	M	2	75	N
ESRF	4	N	N	N	N	M	2	49	N
ESRF	19	N	N	N	N	M	8	40	N
ESRF	16	N	N	N	N	M	8	68	N
ESRF	6	N	N	N	N	F	3	85	N
ESRF	22	N	N	N	N	F	10	71	N
ESRF	11	N	N	N	N	F	5	82	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	3	N	N	N	N	M	1	83	N
ESRF	10	N	N	N	N	F	4	77	N
ESRF	25	N	N	N	N	M	11	76	N
ESRF	16	N	N	N	N	F	7	85	N
ESRF	34	N	N	N	N	F	17	67	N
ESRF	10	N	N	N	N	M	6	65	N
ESRF	10	N	N	N	N	F	4	47	N
ESRF	37	N	N	N	N	M	18	61	N
ESRF	2	N	N	N	N	M	1	74	N
ESRF	3	N	N	N	N	M	1	63	N
ESRF	37	N	N	N	N	M	16	70	N
ESRF	51	N	N	N	N	M	19	83	N
ESRF	14	N	N	N	N	M	6	39	N
ESRF	2	N	N	N	N	M	7	69	N
ESRF	12	N	N	N	N	M	5	80	N
ESRF	29	N	N	N	N	M	10	58	N
ESRF	14	N	N	N	N	F	7	87	N
ESRF	8	N	N	N	N	M	4	84	N
ESRF	10	N	N	N	N	M	5	56	N
ESRF	15	N	N	N	N	F	6	75	N
ESRF	14	N	N	N	N	M	7	78	N
ESRF	11	N	N	N	N	M	6	84	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	34	N	N	N	N	F	10	60	N
ESRF	3	N	N	N	N	F	1	78	N
ESRF	26	N	N	N	N	F	10	79	N
ESRF	10	N	N	N	N	F	5	69	N
ESRF	27	N	N	N	N	M	10	77	N
ESRF	100	N	N	N	N	M	44	36	N
ESRF	12	N	N	N	N	F	5	35	N
ESRF	5	N	N	N	N	M	2	82	N
ESRF	10	N	N	N	N	F	5	80	N
ESRF	13	N	N	N	N	M	5	83	N
ESRF	8	N	N	N	N	F	3	77	N
ESRF	8	N	N	N	N	M	4	66	N
ESRF	28	N	N	N	N	F	11	73	N
ESRF	6	N	N	N	N	F	3	78	N
ESRF	14	N	N	N	N	M	6	84	N
ESRF	10	N	N	N	N	M	5	81	N
ESRF	27	N	N	N	N	M	12	64	N
ESRF	17	N	N	N	N	F	9	37	N
ESRF	6	N	N	N	N	F	3	26	N
ESRF	4	N	N	N	N	F	2	78	N
ESRF	4	N	N	N	Y	M	2	77	N
ESRF	18	N	N	N	N	F	9	51	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	4	N	N	N	N	M	2	70	N
ESRF	16	N	N	N	N	F	5	81	N
ESRF	15	N	N	N	N	F	7	82	N
ESRF	5	N	N	N	N	M	2	59	N
ESRF	7	N	N	N	N	M	3	79	N
ESRF	8	N	N	N	N	M	3	80	N
ESRF	2	N	N	N	N	M	1	79	N
ESRF	6	N	N	N	N	F	4	63	N
ESRF	10	N	N	N	N	M	5	69	N
ESRF	6	N	N	N	N	M	3	60	N
ESRF	12	N	N	N	N	M	6	73	N
ESRF	4	N	N	N	N	M	2	72	N
ESRF	14	N	N	N	N	M	8	69	N
ESRF	19	N	N	N	N	M	9	73	N
ESRF	28	N	N	N	N	M	13	28	N
ESRF	9	N	N	N	N	M	4	64	N
ESRF	2	N	N	N	N	M	1	86	N
ESRF	30	N	N	N	N	M	14	68	N
ESRF	14	N	N	N	N	M	6	44	N
ESRF	34	N	N	N	N	M	13	78	N
ESRF	17	N	N	N	N	F	9	56	N
ESRF	31	N	N	N	N	F	26	46	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	82	N	N	N	Y	M	35	76	N
ESRF	2	N	N	N	N	M	1	79	N
ESRF	31	N	N	N	Y	M	14	71	N
ESRF	14	N	N	N	N	M	6	72	N
ESRF	5	N	N	N	N	M	2	71	N
ESRF	15	N	N	N	N	M	6	82	N
ESRF	10	N	N	N	N	M	4	70	N
ESRF	18	N	N	N	N	F	8	61	N
ESRF	25	N	N	N	N	M	10	76	N
ESRF	2	N	N	N	N	F	1	86	N
ESRF	2	N	N	N	N	F	1	67	N
ESRF	10	N	N	N	N	F	4	67	N
ESRF	26	N	N	N	Y	F	13	73	N
ESRF	16	N	N	N	N	M	7	66	N
ESRF	18	N	N	N	N	M	9	68	N
ESRF	32	N	N	N	N	F	7	82	N
ESRF	5	N	N	N	N	M	2	44	N
ESRF	2	N	N	N	N	F	1	71	N
ESRF	11	N	N	N	N	M	5	30	N
ESRF	8	N	N	N	N	M	4	83	N
ESRF	8	N	N	N	N	M	4	77	N
ESRF	22	N	N	N	N	M	9	53	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	4	N	N	N	N	F	2	61	N
ESRF	8	N	N	N	N	M	4	80	N
ESRF	3	N	N	N	N	F	1	64	N
ESRF	2	N	N	N	N	M	1	43	N
ESRF	2	N	N	N	N	M	1	52	N
ESRF	7	N	N	N	N	M	4	77	N
ESRF	4	N	N	N	N	M	2	80	N
ESRF	9	N	N	N	N	M	4	63	N
ESRF	2	N	N	N	N	M	1	79	N
ESRF	29	N	N	N	N	F	16	77	N
ESRF	11	N	N	N	N	F	5	80	N
ESRF	5	N	N	N	N	M	2	85	N
ESRF	6	N	N	N	N	M	2	77	N
ESRF	25	N	N	N	N	M	3	65	N
ESRF	2	N	N	N	N	F	1	80	N
ESRF	38	N	N	N	N	F	18	57	N
ESRF	5	N	N	N	N	M	2	72	N
ESRF	3	N	N	N	N	M	1	87	N
ESRF	5	N	N	N	N	M	2	80	N
ESRF	22	N	N	N	Y	M	11	77	N
ESRF	35	N	N	N	N	F	17	73	N
ESRF	2	N	N	N	N	F	1	82	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	2	N	N	N	N	F	1	86	N
ESRF	2	N	N	N	N	M	1	75	N
ESRF	6	N	N	N	N	M	2	82	N
ESRF	10	N	N	N	N	M	5	76	N
ESRF	11	N	N	N	N	F	5	77	N
ESRF	2	N	N	N	N	M	1	87	N
ESRF	13	N	N	N	N	F	6	49	N
ESRF	8	N	N	N	N	F	4	80	N
ESRF	2	N	N	N	N	F	1	73	N
ESRF	6	N	N	N	N	M	3	82	N
ESRF	7	N	N	N	N	F	3	92	N
ESRF	19	N	N	N	N	M	9	75	N
ESRF	14	N	N	N	N	M	7	77	N
ESRF	14	N	N	N	N	M	7	79	N
ESRF	3	N	N	N	N	F	1	40	N
ESRF	3	N	N	N	N	M	1	73	N
ESRF	63	N	Y	N	Y	M	29	67	N
ESRF	5	N	Y	N	Y	F	2	62	N
ESRF	73	Y	Y	Y	Y	F	36	52	N
ESRF	13	N	Y	N	N	F	6	33	N
ESRF	4	Y	Y	N	N	F	2	83	N
ESRF	31	Y	Y	N	N	F	12	71	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	4	Y	Y	N	N	F	2	49	N
ESRF	11	N	Y	N	Y	F	5	49	N
ESRF	4	N	Y	N	Y	M	2	80	N
ESRF	8	N	Y	N	N	F	4	81	N
ESRF	2	Y	Y	N	N	M	1	84	N
ESRF	12	N	Y	N	Y	M	5	65	N
ESRF	6	N	Y	N	Y	M	3	61	N
ESRF	2	Y	Y	N	N	F	1	77	N
ESRF	40	N	Y	N	N	F	18	63	N
ESRF	36	N	Y	N	N	M	15	71	N
ESRF	10	N	Y	N	N	M	4	72	N
ESRF	2	N	Y	N	N	F	1	59	N
ESRF	22	N	Y	N	Y	M	10	36	N
ESRF	33	N	Y	N	Y	F	16	62	N
ESRF	16	Y	Y	N	N	M	7	79	N
ESRF	2	Y	Y	N	N	F	1	74	N
ESRF	119	N	Y	N	Y	M	53	78	N
ESRF	34	N	Y	N	N	F	17	52	N
ESRF	17	N	Y	N	N	F	7	43	N
ESRF	22	N	Y	N	N	M	9	39	N
ESRF	5	N	Y	N	N	M	2	73	N
ESRF	18	N	Y	N	N	F	8	75	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	20	N	Y	N	N	F	10	47	N
ESRF	15	N	Y	N	Y	F	7	72	N
ESRF	25	N	Y	N	Y	F	12	60	N
ESRF	12	N	Y	N	N	F	5	82	N
ESRF	6	N	Y	N	N	F	3	83	N
ESRF	6	Y	Y	N	Y	F	2	85	N
ESRF	2	N	Y	N	N	F	1	65	N
ESRF	10	N	Y	N	Y	F	5	89	N
ESRF	6	N	Y	N	Y	M	3	72	N
ESRF	11	N	Y	N	N	M	5	38	N
ESRF	101	N	Y	N	Y	M	45	77	N
ESRF	8	N	Y	N	N	F	4	76	N
ESRF	61	N	Y	N	Y	M	29	77	N
ESRF	8	N	Y	Y	Y	F	4	77	N
ESRF	12	N	Y	N	Y	F	5	77	N
ESRF	11	N	Y	N	Y	F	5	75	N
ESRF	22	N	Y	N	N	M	11	51	N
ESRF	48	N	Y	N	Y	F	19	31	N
ESRF	12	N	Y	N	N	M	4	53	N
ESRF	12	N	Y	N	Y	F	6	81	N
ESRF	50	N	Y	N	N	F	20	78	N
ESRF	10	N	Y	N	N	M	4	66	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
ESRF	37	Y	Y	N	N	F	14	86	N
ESRF	24	N	Y	N	N	F	11	69	N
ESRF	4	Y	Y	Y	Y	F	2	80	N
ESRF	13	N	Y	N	Y	F	6	63	N
ESRF	22	Y	Y	N	Y	M	11	65	N
ESRF	23	N	Y	N	N	M	10	79	N
ESRF	11	Y	Y	N	Y	M	5	61	N
ESRF	57	N	Y	N	N	F	20	80	N
ESRF	16	N	Y	N	Y	M	6	60	N
ESRF	18	N	Y	N	Y	F	6	65	N
ESRF	31	N	Y	N	Y	M	14	58	N
ESRF	9	Y	Y	Y	Y	F	4	54	N
ESRF	2	Y	Y	N	N	F	1	80	N
ESRF	12	Y	Y	Y	Y	F	4	25	N
ESRF	6	Y	Y	Y	Y	M	3	80	N
HUS	6	N	N	N	N	M	3	26	N
NHL	5	N	Y	N	Y	M	3	82	N
Pyelonephritis	5	N	N	N	N	M	2	37	N
Pyelonephritis	19	N	N	N	N	M	9	75	N
Wegener granulomatosis	5	N	N	N	N	M	3	65	N

Diagnosis	No units given	Alloimmunised at admission	Alloimmunised post transfusion	Autoimmunised at admission	Autoimmunised post transfusion	Gender	No. Episodes	Age at first transfusion	Transplant
Wegener granulomatosis	5	N	N	N	N	F	2	57	N
Wegener granulomatosis	5	N	N	N	N	M	2	46	N
Wegener granulomatosis	12	N	N	N	N	M	5	69	N
Wegener granulomatosis	39	N	N	N	N	M	12	74	N
Wegener granulomatosis	12	N	N	N	N	M	6	76	N
Wegener granulomatosis	5	N	N	N	N	M	2	57	N
Wegener granulomatosis	7	N	N	N	N	F	3	56	N
Wegener granulomatosis	4	N	N	N	N	M	2	64	N
Wegener granulomatosis	7	N	N	N	N	M	3	71	N
Wegener granulomatosis	4	N	N	N	N	F	2	82	N

10.3 Appendix 3: Programmed cut off values for the serological phenotyping profiles on the NEO analyser

Antiserum		Cut off low	Cut off high
Anti-C	Negative	0.000	23.998
	Not determined	23.999	75.998
	Positive (3+)	75.999	80.998
	Postive (4+)	80.999	99.999
Anti-c	Negative	0.000	23.998
	Not determined	23.999	75.998
	Positive (3+)	75.999	80.998
	Postive (4+)	80.999	99.999
Anti-E	Negative	0.000	23.998
	Not determined	23.999	75.998
	Positive (3+)	75.999	80.998
	Postive (4+)	80.999	99.999
Anti-e	Negative	0.000	23.998
	Not determined	23.999	75.998
	Positive (3+)	75.999	80.998
	Postive (4+)	80.999	99.999

Antiserum		Cut off low	Cut off high
Anti-K	Negative	0.000	23.998
	Not determined	23.999	27.998
	Positive (1+)	27.999	35.998
	Positive (2+)	35.999	50.998
	Positive (3+)	50.999	80.998
	Postive (4+)	80.999	99.999
Anti-C^w	Negative	0.000	23.998
	Not determined	23.999	50.998
	Positive (3+)	50.999	80.998
	Postive (4+)	80.999	99.999
Anti-M	Negative	0.000	23.000
	Not determined	23.999	75.998
	Positive (3+)	75.999	80.998
	Postive (4+)	80.999	99.999
Anti-N	Negative	0.000	23.998
	Not determined	23.999	35.998
	Positive (2+)	35.999	50.998
	Positive (3+)	50.999	80.998
	Postive (4+)	80.999	99.999

Antiserum		Cut off low	Cut off high
Anti-Fy^a	Negative	0.000	20.998
	Not determined	20.999	40.998
	Positive (1+)	40.999	50.998
	Positive (2+)	50.999	72.998
	Positive (3+)	72.999	90.998
	Postive (4+)	90.999	99.999
Anti-Fy^b	Negative	0.000	20.998
	Not determined	20.999	40.998
	Positive (1+)	40.999	50.998
	Positive (2+)	50.999	72.998
	Positive (3+)	72.999	90.998
	Postive (4+)	90.999	99.999
Anti-Jk^a	Negative	0.000	20.998
	Not determined	20.999	40.998
	Positive (1+)	40.999	50.998
	Positive (2+)	50.999	72.998
	Positive (3+)	72.999	90.998
	Postive (4+)	90.999	99.999
Anti-Jk^b	Negative	0.000	20.998
	Not determined	20.999	40.998
	Positive (1+)	40.999	50.998
	Positive (2+)	50.999	72.998
	Positive (3+)	72.999	90.998
	Postive (4+)	90.999	99.999

Antiserum		Cut off low	Cut off high
Anti-S	Negative	0.000	20.998
	Not determined	20.999	40.998
	Positive (1+)	40.999	50.998
	Positive (2+)	50.999	72.998
	Positive (3+)	72.999	90.998
	Postive (4+)	90.999	99.999
Anti-s	Negative	0.000	20.998
	Not determined	20.999	40.998
	Positive (1+)	40.999	50.998
	Positive (2+)	50.999	72.998
	Positive (3+)	72.999	90.998
	Postive (4+)	90.999	99.999
Anti-k	Negative	0.000	20.998
	Not determined	20.999	40.998
	Positive (1+)	40.999	50.998
	Positive (2+)	50.999	72.998
	Positive (3+)	72.999	90.998
	Postive (4+)	90.999	99.999
Control Negative	Negative	0.000	20.998
	Not determined	20.999	40.998
	Positive (1+)	40.999	50.998
	Positive (2+)	50.999	72.998
	Positive (3+)	72.999	90.998
	Postive (4+)	90.999	99.999

10.4 Appendix 4: Raw data for genotyping results

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown1	New Batch 4_20140514_125813.csv	Rh	RHCE*ce	RHCE*cE	C (RH:2)	0
Green	Unknown1	New Batch 4_20140514_125813.csv		RHCE*Ce		E (RH:3)	+
Green	Unknown1	New Batch 4_20140514_125813.csv		RHCE*cE		c (RH:4)	+
Green	Unknown1	New Batch 4_20140514_125813.csv		RHCE*CE		e (RH:5)	0
Green	Unknown1	New Batch 4_20140514_125813.csv		RHCE*CeCW		CW (RH:8)	0
Green	Unknown1	New Batch 4_20140514_125813.csv		RHCE*ceCW		V (RH:10)	0
Green	Unknown1	New Batch 4_20140514_125813.csv		RHCE*CECW		hrS (RH:19)	+
Green	Unknown1	New Batch 4_20140514_125813.csv		RHCE*ceAR		VS (RH:20)	0
Green	Unknown1	New Batch 4_20140514_125813.csv		RHCE*CeFV		hrB (RH:31)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown1	New Batch 4_20140514_125813.csv		RHCE*CeVG			
Green	Unknown1	New Batch 4_20140514_125813.csv		RHCE*cEFM			
Green	Unknown1	New Batch 4_20140514_125813.csv		RHCE*ce[712G]			
Green	Unknown1	New Batch 4_20140514_125813.csv		RHCE*ce[733G]			
Green	Unknown1	New Batch 4_20140514_125813.csv		RHCE*ce[733G,1006T]			
Green	Unknown1	New Batch 4_20140514_125813.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	Unknown1	New Batch 4_20140514_125813.csv		RHCE*cE[697G,712G,733G]			
Green	Unknown1	New Batch 4_20140514_125813.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	Unknown1	New Batch 4_20140514_125813.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	Unknown1	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	Unknown1	New Batch 4_20140514_125813.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	Unknown1	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown1	New Batch 4_20140514_125813.csv				Jsa (KEL:6)	0
Green	Unknown1	New Batch 4_20140514_125813.csv				Jsb (KEL:7)	+
Green	Unknown1	New Batch 4_20140514_125813.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	Unknown1	New Batch 4_20140514_125813.csv		JK*B		Jkb (JK:2)	+
Green	Unknown1	New Batch 4_20140514_125813.csv		JK*B_null(IVS5-1a)			
Green	Unknown1	New Batch 4_20140514_125813.csv		JK*B_null(871C)			
Green	Unknown1	New Batch 4_20140514_125813.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	Unknown1	New Batch 4_20140514_125813.csv		FY*B		Fyb (FY:2)	+
Green	Unknown1	New Batch 4_20140514_125813.csv		FY*B_GATA			
Green	Unknown1	New Batch 4_20140514_125813.csv		FY*B[265T]_FY*X			
Green	Unknown1	New Batch 4_20140514_125813.csv	MNS	GYPA*M	GYPA*N	M (MNS:1)	0
Green	Unknown1	New Batch 4_20140514_125813.csv		GYPA*N		N (MNS:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown1	New Batch 4_20140514_125813.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	Unknown1	New Batch 4_20140514_125813.csv		GYPB*s		s (MNS:4)	+
Green	Unknown1	New Batch 4_20140514_125813.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	Unknown1	New Batch 4_20140514_125813.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	Unknown1	New Batch 4_20140514_125813.csv		GYPB*deletion			
Green	Unknown1	New Batch 4_20140514_125813.csv		GYPB*Mur			
Green	Unknown1	New Batch 4_20140514_125813.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	Unknown1	New Batch 4_20140514_125813.csv		DI*B		Dib (DI:2)	+
Green	Unknown1	New Batch 4_20140514_125813.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+
Green	Unknown1	New Batch 4_20140514_125813.csv		DO*B		Dob (DO:2)	+
Green	Unknown1	New Batch 4_20140514_125813.csv		DO*B_HY-		Hy (DO:4)	+
Green	Unknown1	New Batch 4_20140514_125813.csv		DO*A_JOA-		Joa (DO:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown1	New Batch 4_20140514_125813.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	Unknown1	New Batch 4_20140514_125813.csv		CO*B		Cob (CO:2)	0
Green	Unknown1	New Batch 4_20140514_125813.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	Unknown1	New Batch 4_20140514_125813.csv		YT*B		Ytb (YT:2)	0
Green	Unknown1	New Batch 4_20140514_125813.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	Unknown1	New Batch 4_20140514_125813.csv		LU*B		Lub (LU:2)	+
Green	Unknown2	New Batch 4_20140514_125813.csv	Rh	RHCE*ce	RHCE*ce, RHCE*cE	C (RH:2)	0
Green	Unknown2	New Batch 4_20140514_125813.csv		RHCE*Ce		E (RH:3)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		RHCE*cE		c (RH:4)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		RHCE*CE		e (RH:5)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		RHCE*CeCW		CW (RH:8)	0
Green	Unknown2	New Batch 4_20140514_125813.csv		RHCE*ceCW		V (RH:10)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown2	New Batch 4_20140514_125813.csv		RHCE*CECW		hrS (RH:19)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		RHCE*ceAR		VS (RH:20)	0
Green	Unknown2	New Batch 4_20140514_125813.csv		RHCE*CeFV		hrB (RH:31)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		RHCE*CeVG			
Green	Unknown2	New Batch 4_20140514_125813.csv		RHCE*cEFM			
Green	Unknown2	New Batch 4_20140514_125813.csv		RHCE*ce[712G]			
Green	Unknown2	New Batch 4_20140514_125813.csv		RHCE*ce[733G]			
Green	Unknown2	New Batch 4_20140514_125813.csv		RHCE*ce[733G,1006T]			
Green	Unknown2	New Batch 4_20140514_125813.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	Unknown2	New Batch 4_20140514_125813.csv		RHCE*cE[697G,712G,733G]			
Green	Unknown2	New Batch 4_20140514_125813.csv		RHD*r’s-RHCE*ce[733G,1006T]			
Green	Unknown2	New Batch 4_20140514_125813.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown2	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	Unknown2	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	Unknown2	New Batch 4_20140514_125813.csv				Jsa (KEL:6)	0
Green	Unknown2	New Batch 4_20140514_125813.csv				Jsb (KEL:7)	+
Green	Unknown2	New Batch 4_20140514_125813.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		JK*B		Jkb (JK:2)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		JK*B_null(IVS5-1a)			
Green	Unknown2	New Batch 4_20140514_125813.csv		JK*B_null(871C)			
Green	Unknown2	New Batch 4_20140514_125813.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		FY*B		Fyb (FY:2)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		FY*B_GATA			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown2	New Batch 4_20140514_125813.csv		FY*B[265T]_FY*X			
Green	Unknown2	New Batch 4_20140514_125813.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		GYPA*N		N (MNS:2)	0
Green	Unknown2	New Batch 4_20140514_125813.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		GYPB*s		s (MNS:4)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	Unknown2	New Batch 4_20140514_125813.csv		GYPB*deletion			
Green	Unknown2	New Batch 4_20140514_125813.csv		GYPB*Mur			
Green	Unknown2	New Batch 4_20140514_125813.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	Unknown2	New Batch 4_20140514_125813.csv		DI*B		Dib (DI:2)	+
Green	Unknown2	New Batch 4_20140514_125813.csv	Dombrock	DO*A	DO*A	Doa (DO:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown2	New Batch 4_20140514_125813.csv		DO*B		Dob (DO:2)	0
Green	Unknown2	New Batch 4_20140514_125813.csv		DO*B_HY-		Hy (DO:4)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		DO*A_JOA-		Joa (DO:5)	+
Green	Unknown2	New Batch 4_20140514_125813.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		CO*B		Cob (CO:2)	0
Green	Unknown2	New Batch 4_20140514_125813.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	Unknown2	New Batch 4_20140514_125813.csv		YT*B		Ytb (YT:2)	0
Green	Unknown2	New Batch 4_20140514_125813.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	Unknown2	New Batch 4_20140514_125813.csv		LU*B		Lub (LU:2)	+
Green	Unknown3	New Batch 4_20140514_125813.csv	Rh	RHCE*ce	RHCE*cE	C (RH:2)	0
Green	Unknown3	New Batch 4_20140514_125813.csv		RHCE*Ce		E (RH:3)	+
Green	Unknown3	New Batch 4_20140514_125813.csv		RHCE*cE		c (RH:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown3	New Batch 4_20140514_125813.csv		RHCE*CE		e (RH:5)	0
Green	Unknown3	New Batch 4_20140514_125813.csv		RHCE*CeCW		CW (RH:8)	0
Green	Unknown3	New Batch 4_20140514_125813.csv		RHCE*ceCW		V (RH:10)	0
Green	Unknown3	New Batch 4_20140514_125813.csv		RHCE*CECW		hrS (RH:19)	+
Green	Unknown3	New Batch 4_20140514_125813.csv		RHCE*ceAR		VS (RH:20)	0
Green	Unknown3	New Batch 4_20140514_125813.csv		RHCE*CeFV		hrB (RH:31)	0
Green	Unknown3	New Batch 4_20140514_125813.csv		RHCE*CeVG			
Green	Unknown3	New Batch 4_20140514_125813.csv		RHCE*cEFM			
Green	Unknown3	New Batch 4_20140514_125813.csv		RHCE*ce[712G]			
Green	Unknown3	New Batch 4_20140514_125813.csv		RHCE*ce[733G]			
Green	Unknown3	New Batch 4_20140514_125813.csv		RHCE*ce[733G,1006T]			
Green	Unknown3	New Batch 4_20140514_125813.csv		RHCE*CE-D[2, 5, 7]-CE			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown3	New Batch 4_20140514_125813.csv		RHCE*cE[697G,712G,733G]			
Green	Unknown3	New Batch 4_20140514_125813.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	Unknown3	New Batch 4_20140514_125813.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	Unknown3	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	Unknown3	New Batch 4_20140514_125813.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	Unknown3	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	Unknown3	New Batch 4_20140514_125813.csv				Jsa (KEL:6)	0
Green	Unknown3	New Batch 4_20140514_125813.csv				Jsb (KEL:7)	+
Green	Unknown3	New Batch 4_20140514_125813.csv	Kidd	JK*A	JK*B	Jka (JK:1)	0
Green	Unknown3	New Batch 4_20140514_125813.csv		JK*B		Jkb (JK:2)	+
Green	Unknown3	New Batch 4_20140514_125813.csv		JK*B_null(IVS5-1a)			
Green	Unknown3	New Batch 4_20140514_125813.csv		JK*B_null(871C)			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown3	New Batch 4_20140514_125813.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	Unknown3	New Batch 4_20140514_125813.csv		FY*B		Fyb (FY:2)	+
Green	Unknown3	New Batch 4_20140514_125813.csv		FY*B_GATA			
Green	Unknown3	New Batch 4_20140514_125813.csv		FY*B[265T]_FY*X			
Green	Unknown3	New Batch 4_20140514_125813.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	Unknown3	New Batch 4_20140514_125813.csv		GYPA*N		N (MNS:2)	+
Green	Unknown3	New Batch 4_20140514_125813.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	Unknown3	New Batch 4_20140514_125813.csv		GYPB*s		s (MNS:4)	+
Green	Unknown3	New Batch 4_20140514_125813.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	Unknown3	New Batch 4_20140514_125813.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	Unknown3	New Batch 4_20140514_125813.csv		GYPB*deletion			
Green	Unknown3	New Batch 4_20140514_125813.csv		GYPB*Mur			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown3	New Batch 4_20140514_125813.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	Unknown3	New Batch 4_20140514_125813.csv		DI*B		Dib (DI:2)	+
Green	Unknown3	New Batch 4_20140514_125813.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	Unknown3	New Batch 4_20140514_125813.csv		DO*B		Dob (DO:2)	+
Green	Unknown3	New Batch 4_20140514_125813.csv		DO*B_HY-		Hy (DO:4)	+
Green	Unknown3	New Batch 4_20140514_125813.csv		DO*A_JOA-		Joa (DO:5)	+
Green	Unknown3	New Batch 4_20140514_125813.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	Unknown3	New Batch 4_20140514_125813.csv		CO*B		Cob (CO:2)	0
Green	Unknown3	New Batch 4_20140514_125813.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	Unknown3	New Batch 4_20140514_125813.csv		YT*B		Ytb (YT:2)	0
Green	Unknown3	New Batch 4_20140514_125813.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	Unknown3	New Batch 4_20140514_125813.csv		LU*B		Lub (LU:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown4	New Batch 4_20140514_125813.csv	Rh	RHCE*ce	RHCE*ce, RHCE*Ce	C (RH:2)	+
Green	Unknown4	New Batch 4_20140514_125813.csv		RHCE*Ce		E (RH:3)	0
Green	Unknown4	New Batch 4_20140514_125813.csv		RHCE*cE		c (RH:4)	+
Green	Unknown4	New Batch 4_20140514_125813.csv		RHCE*CE		e (RH:5)	+
Green	Unknown4	New Batch 4_20140514_125813.csv		RHCE*CeCW		CW (RH:8)	0
Green	Unknown4	New Batch 4_20140514_125813.csv		RHCE*ceCW		V (RH:10)	0
Green	Unknown4	New Batch 4_20140514_125813.csv		RHCE*CECW		hrS (RH:19)	+
Green	Unknown4	New Batch 4_20140514_125813.csv		RHCE*ceAR		VS (RH:20)	0
Green	Unknown4	New Batch 4_20140514_125813.csv		RHCE*CeFV		hrB (RH:31)	+
Green	Unknown4	New Batch 4_20140514_125813.csv		RHCE*CeVG			
Green	Unknown4	New Batch 4_20140514_125813.csv		RHCE*cEFM			
Green	Unknown4	New Batch 4_20140514_125813.csv		RHCE*ce[712G]			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown4	New Batch 4_20140514_125813.csv		RHCE*ce[733G]			
Green	Unknown4	New Batch 4_20140514_125813.csv		RHCE*ce[733G,1006T]			
Green	Unknown4	New Batch 4_20140514_125813.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	Unknown4	New Batch 4_20140514_125813.csv		RHCE*cE[697G,712G,733G]			
Green	Unknown4	New Batch 4_20140514_125813.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	Unknown4	New Batch 4_20140514_125813.csv	Kell	KEL*K_KPB_JSB	KEL*K_KPB_JSB, KEL*k_KPB_JSB	K (KEL:1)	+
Green	Unknown4	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	Unknown4	New Batch 4_20140514_125813.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	Unknown4	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	Unknown4	New Batch 4_20140514_125813.csv				Jsa (KEL:6)	0
Green	Unknown4	New Batch 4_20140514_125813.csv				Jsb (KEL:7)	+
Green	Unknown4	New Batch 4_20140514_125813.csv	Kidd	JK*A	JK*A	Jka (JK:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown4	New Batch 4_20140514_125813.csv		JK*B		Jkb (JK:2)	0
Green	Unknown4	New Batch 4_20140514_125813.csv		JK*B_null(IVS5-1a)			
Green	Unknown4	New Batch 4_20140514_125813.csv		JK*B_null(871C)			
Green	Unknown4	New Batch 4_20140514_125813.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	Unknown4	New Batch 4_20140514_125813.csv		FY*B		Fyb (FY:2)	+
Green	Unknown4	New Batch 4_20140514_125813.csv		FY*B_GATA			
Green	Unknown4	New Batch 4_20140514_125813.csv		FY*B[265T]_FY*X			
Green	Unknown4	New Batch 4_20140514_125813.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	Unknown4	New Batch 4_20140514_125813.csv		GYPA*N		N (MNS:2)	0
Green	Unknown4	New Batch 4_20140514_125813.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	Unknown4	New Batch 4_20140514_125813.csv		GYPB*s		s (MNS:4)	+
Green	Unknown4	New Batch 4_20140514_125813.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown4	New Batch 4_20140514_125813.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	Unknown4	New Batch 4_20140514_125813.csv		GYPB*deletion			
Green	Unknown4	New Batch 4_20140514_125813.csv		GYPB*Mur			
Green	Unknown4	New Batch 4_20140514_125813.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	Unknown4	New Batch 4_20140514_125813.csv		DI*B		Dib (DI:2)	+
Green	Unknown4	New Batch 4_20140514_125813.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+
Green	Unknown4	New Batch 4_20140514_125813.csv		DO*B		Dob (DO:2)	+
Green	Unknown4	New Batch 4_20140514_125813.csv		DO*B_HY-		Hy (DO:4)	+
Green	Unknown4	New Batch 4_20140514_125813.csv		DO*A_JOA-		Joa (DO:5)	+
Green	Unknown4	New Batch 4_20140514_125813.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	Unknown4	New Batch 4_20140514_125813.csv		CO*B		Cob (CO:2)	0
Green	Unknown4	New Batch 4_20140514_125813.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown4	New Batch 4_20140514_125813.csv		YT*B		Ytb (YT:2)	0
Green	Unknown4	New Batch 4_20140514_125813.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	Unknown4	New Batch 4_20140514_125813.csv		LU*B		Lub (LU:2)	+
Green	Unknown5	New Batch 4_20140514_125813.csv	Rh	RHCE*ce	RHCE*cE	C (RH:2)	0
Green	Unknown5	New Batch 4_20140514_125813.csv		RHCE*Ce		E (RH:3)	+
Green	Unknown5	New Batch 4_20140514_125813.csv		RHCE*cE		c (RH:4)	+
Green	Unknown5	New Batch 4_20140514_125813.csv		RHCE*CE		e (RH:5)	0
Green	Unknown5	New Batch 4_20140514_125813.csv		RHCE*CeCW		CW (RH:8)	0
Green	Unknown5	New Batch 4_20140514_125813.csv		RHCE*ceCW		V (RH:10)	0
Green	Unknown5	New Batch 4_20140514_125813.csv		RHCE*CECW		hrS (RH:19)	+
Green	Unknown5	New Batch 4_20140514_125813.csv		RHCE*ceAR		VS (RH:20)	0
Green	Unknown5	New Batch 4_20140514_125813.csv		RHCE*CeFV		hrB (RH:31)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown5	New Batch 4_20140514_125813.csv		RHCE*CeVG			
Green	Unknown5	New Batch 4_20140514_125813.csv		RHCE*cEFM			
Green	Unknown5	New Batch 4_20140514_125813.csv		RHCE*ce[712G]			
Green	Unknown5	New Batch 4_20140514_125813.csv		RHCE*ce[733G]			
Green	Unknown5	New Batch 4_20140514_125813.csv		RHCE*ce[733G,1006T]			
Green	Unknown5	New Batch 4_20140514_125813.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	Unknown5	New Batch 4_20140514_125813.csv		RHCE*cE[697G,712G,733G]			
Green	Unknown5	New Batch 4_20140514_125813.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	Unknown5	New Batch 4_20140514_125813.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	Unknown5	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	Unknown5	New Batch 4_20140514_125813.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	Unknown5	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown5	New Batch 4_20140514_125813.csv				Jsa (KEL:6)	0
Green	Unknown5	New Batch 4_20140514_125813.csv				Jsb (KEL:7)	+
Green	Unknown5	New Batch 4_20140514_125813.csv	Kidd	JK*A	JK*A	Jka (JK:1)	+
Green	Unknown5	New Batch 4_20140514_125813.csv		JK*B		Jkb (JK:2)	0
Green	Unknown5	New Batch 4_20140514_125813.csv		JK*B_null(IVS5-1a)			
Green	Unknown5	New Batch 4_20140514_125813.csv		JK*B_null(871C)			
Green	Unknown5	New Batch 4_20140514_125813.csv	Duffy	FY*A	FY*A	Fya (FY:1)	+
Green	Unknown5	New Batch 4_20140514_125813.csv		FY*B		Fyb (FY:2)	0
Green	Unknown5	New Batch 4_20140514_125813.csv		FY*B_GATA			
Green	Unknown5	New Batch 4_20140514_125813.csv		FY*B[265T]_FY*X			
Green	Unknown5	New Batch 4_20140514_125813.csv	MNS	GYPA*M	GYPA*N	M (MNS:1)	0
Green	Unknown5	New Batch 4_20140514_125813.csv		GYPA*N		N (MNS:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown5	New Batch 4_20140514_125813.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	Unknown5	New Batch 4_20140514_125813.csv		GYPB*s		s (MNS:4)	+
Green	Unknown5	New Batch 4_20140514_125813.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	Unknown5	New Batch 4_20140514_125813.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	Unknown5	New Batch 4_20140514_125813.csv		GYPB*deletion			
Green	Unknown5	New Batch 4_20140514_125813.csv		GYPB*Mur			
Green	Unknown5	New Batch 4_20140514_125813.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	Unknown5	New Batch 4_20140514_125813.csv		DI*B		Dib (DI:2)	+
Green	Unknown5	New Batch 4_20140514_125813.csv	Dombrock	DO*A	DO*A	Doa (DO:1)	+
Green	Unknown5	New Batch 4_20140514_125813.csv		DO*B		Dob (DO:2)	0
Green	Unknown5	New Batch 4_20140514_125813.csv		DO*B_HY-		Hy (DO:4)	+
Green	Unknown5	New Batch 4_20140514_125813.csv		DO*A_JOA-		Joa (DO:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown5	New Batch 4_20140514_125813.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	Unknown5	New Batch 4_20140514_125813.csv		CO*B		Cob (CO:2)	0
Green	Unknown5	New Batch 4_20140514_125813.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	Unknown5	New Batch 4_20140514_125813.csv		YT*B		Ytb (YT:2)	0
Green	Unknown5	New Batch 4_20140514_125813.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	Unknown5	New Batch 4_20140514_125813.csv		LU*B		Lub (LU:2)	+
Green	Unknown6	New Batch 4_20140514_125813.csv	Rh	RHCE*ce	RHCE*ce, RHCE*cE	C (RH:2)	0
Green	Unknown6	New Batch 4_20140514_125813.csv		RHCE*Ce		E (RH:3)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		RHCE*cE		c (RH:4)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		RHCE*CE		e (RH:5)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		RHCE*CeCW		CW (RH:8)	0
Green	Unknown6	New Batch 4_20140514_125813.csv		RHCE*ceCW		V (RH:10)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown6	New Batch 4_20140514_125813.csv		RHCE*CECW		hrS (RH:19)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		RHCE*ceAR		VS (RH:20)	0
Green	Unknown6	New Batch 4_20140514_125813.csv		RHCE*CeFV		hrB (RH:31)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		RHCE*CeVG			
Green	Unknown6	New Batch 4_20140514_125813.csv		RHCE*cEFM			
Green	Unknown6	New Batch 4_20140514_125813.csv		RHCE*ce[712G]			
Green	Unknown6	New Batch 4_20140514_125813.csv		RHCE*ce[733G]			
Green	Unknown6	New Batch 4_20140514_125813.csv		RHCE*ce[733G,1006T]			
Green	Unknown6	New Batch 4_20140514_125813.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	Unknown6	New Batch 4_20140514_125813.csv		RHCE*cE[697G,712G,733G]			
Green	Unknown6	New Batch 4_20140514_125813.csv		RHD*r’s-RHCE*ce[733G,1006T]			
Green	Unknown6	New Batch 4_20140514_125813.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown6	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	Unknown6	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	Unknown6	New Batch 4_20140514_125813.csv				Jsa (KEL:6)	0
Green	Unknown6	New Batch 4_20140514_125813.csv				Jsb (KEL:7)	+
Green	Unknown6	New Batch 4_20140514_125813.csv	Kidd	JK*A	JK*B	Jka (JK:1)	0
Green	Unknown6	New Batch 4_20140514_125813.csv		JK*B		Jkb (JK:2)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		JK*B_null(IVS5-1a)			
Green	Unknown6	New Batch 4_20140514_125813.csv		JK*B_null(871C)			
Green	Unknown6	New Batch 4_20140514_125813.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	Unknown6	New Batch 4_20140514_125813.csv		FY*B		Fyb (FY:2)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		FY*B_GATA			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown6	New Batch 4_20140514_125813.csv		FY*B[265T]_FY*X			
Green	Unknown6	New Batch 4_20140514_125813.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		GYPA*N		N (MNS:2)	0
Green	Unknown6	New Batch 4_20140514_125813.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		GYPB*s		s (MNS:4)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	Unknown6	New Batch 4_20140514_125813.csv		GYPB*deletion			
Green	Unknown6	New Batch 4_20140514_125813.csv		GYPB*Mur			
Green	Unknown6	New Batch 4_20140514_125813.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	Unknown6	New Batch 4_20140514_125813.csv		DI*B		Dib (DI:2)	+
Green	Unknown6	New Batch 4_20140514_125813.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown6	New Batch 4_20140514_125813.csv		DO*B		Dob (DO:2)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		DO*B_HY-		Hy (DO:4)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		DO*A_JOA-		Joa (DO:5)	+
Green	Unknown6	New Batch 4_20140514_125813.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		CO*B		Cob (CO:2)	0
Green	Unknown6	New Batch 4_20140514_125813.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	Unknown6	New Batch 4_20140514_125813.csv		YT*B		Ytb (YT:2)	0
Green	Unknown6	New Batch 4_20140514_125813.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	Unknown6	New Batch 4_20140514_125813.csv		LU*B		Lub (LU:2)	+
Green	Unknown7	New Batch 4_20140514_125813.csv	Rh	RHCE*ce	RHCE*ce, RHCE*cE	C (RH:2)	0
Green	Unknown7	New Batch 4_20140514_125813.csv		RHCE*Ce		E (RH:3)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		RHCE*cE		c (RH:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown7	New Batch 4_20140514_125813.csv		RHCE*CE		e (RH:5)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		RHCE*CeCW		CW (RH:8)	0
Green	Unknown7	New Batch 4_20140514_125813.csv		RHCE*ceCW		V (RH:10)	0
Green	Unknown7	New Batch 4_20140514_125813.csv		RHCE*CECW		hrS (RH:19)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		RHCE*ceAR		VS (RH:20)	0
Green	Unknown7	New Batch 4_20140514_125813.csv		RHCE*CeFV		hrB (RH:31)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		RHCE*CeVG			
Green	Unknown7	New Batch 4_20140514_125813.csv		RHCE*cEFM			
Green	Unknown7	New Batch 4_20140514_125813.csv		RHCE*ce[712G]			
Green	Unknown7	New Batch 4_20140514_125813.csv		RHCE*ce[733G]			
Green	Unknown7	New Batch 4_20140514_125813.csv		RHCE*ce[733G,1006T]			
Green	Unknown7	New Batch 4_20140514_125813.csv		RHCE*CE-D[2, 5, 7]-CE			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown7	New Batch 4_20140514_125813.csv		RHCE*cE[697G,712G,733G]			
Green	Unknown7	New Batch 4_20140514_125813.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	Unknown7	New Batch 4_20140514_125813.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	Unknown7	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	Unknown7	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	Unknown7	New Batch 4_20140514_125813.csv				Jsa (KEL:6)	0
Green	Unknown7	New Batch 4_20140514_125813.csv				Jsb (KEL:7)	+
Green	Unknown7	New Batch 4_20140514_125813.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		JK*B		Jkb (JK:2)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		JK*B_null(IVS5-1a)			
Green	Unknown7	New Batch 4_20140514_125813.csv		JK*B_null(871C)			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown7	New Batch 4_20140514_125813.csv	Duffy	FY*A	FY*A	Fya (FY:1)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		FY*B		Fyb (FY:2)	0
Green	Unknown7	New Batch 4_20140514_125813.csv		FY*B_GATA			
Green	Unknown7	New Batch 4_20140514_125813.csv		FY*B[265T]_FY*X			
Green	Unknown7	New Batch 4_20140514_125813.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		GYPA*N		N (MNS:2)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		GYPB*s		s (MNS:4)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	Unknown7	New Batch 4_20140514_125813.csv		GYPB*deletion			
Green	Unknown7	New Batch 4_20140514_125813.csv		GYPB*Mur			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown7	New Batch 4_20140514_125813.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	Unknown7	New Batch 4_20140514_125813.csv		DI*B		Dib (DI:2)	+
Green	Unknown7	New Batch 4_20140514_125813.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		DO*B		Dob (DO:2)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		DO*B_HY-		Hy (DO:4)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		DO*A_JOA-		Joa (DO:5)	+
Green	Unknown7	New Batch 4_20140514_125813.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		CO*B		Cob (CO:2)	0
Green	Unknown7	New Batch 4_20140514_125813.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	Unknown7	New Batch 4_20140514_125813.csv		YT*B		Ytb (YT:2)	0
Green	Unknown7	New Batch 4_20140514_125813.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	Unknown7	New Batch 4_20140514_125813.csv		LU*B		Lub (LU:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown8	New Batch 4_20140514_125813.csv	Rh	RHCE*ce	RHCE*Ce	C (RH:2)	+
Green	Unknown8	New Batch 4_20140514_125813.csv		RHCE*Ce		E (RH:3)	0
Green	Unknown8	New Batch 4_20140514_125813.csv		RHCE*cE		c (RH:4)	0
Green	Unknown8	New Batch 4_20140514_125813.csv		RHCE*CE		e (RH:5)	+
Green	Unknown8	New Batch 4_20140514_125813.csv		RHCE*CeCW		CW (RH:8)	0
Green	Unknown8	New Batch 4_20140514_125813.csv		RHCE*ceCW		V (RH:10)	0
Green	Unknown8	New Batch 4_20140514_125813.csv		RHCE*CECW		hrS (RH:19)	+
Green	Unknown8	New Batch 4_20140514_125813.csv		RHCE*ceAR		VS (RH:20)	0
Green	Unknown8	New Batch 4_20140514_125813.csv		RHCE*CeFV		hrB (RH:31)	+
Green	Unknown8	New Batch 4_20140514_125813.csv		RHCE*CeVG			
Green	Unknown8	New Batch 4_20140514_125813.csv		RHCE*cEFM			
Green	Unknown8	New Batch 4_20140514_125813.csv		RHCE*ce[712G]			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown8	New Batch 4_20140514_125813.csv		RHCE*ce[733G]			
Green	Unknown8	New Batch 4_20140514_125813.csv		RHCE*ce[733G,1006T]			
Green	Unknown8	New Batch 4_20140514_125813.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	Unknown8	New Batch 4_20140514_125813.csv		RHCE*cE[697G,712G,733G]			
Green	Unknown8	New Batch 4_20140514_125813.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	Unknown8	New Batch 4_20140514_125813.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	Unknown8	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	Unknown8	New Batch 4_20140514_125813.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	Unknown8	New Batch 4_20140514_125813.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	Unknown8	New Batch 4_20140514_125813.csv				Jsa (KEL:6)	0
Green	Unknown8	New Batch 4_20140514_125813.csv				Jsb (KEL:7)	+
Green	Unknown8	New Batch 4_20140514_125813.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown8	New Batch 4_20140514_125813.csv		JK*B		Jkb (JK:2)	+
Green	Unknown8	New Batch 4_20140514_125813.csv		JK*B_null(IVS5-1a)			
Green	Unknown8	New Batch 4_20140514_125813.csv		JK*B_null(871C)			
Green	Unknown8	New Batch 4_20140514_125813.csv	Duffy	FY*A	FY*A	Fya (FY:1)	+
Green	Unknown8	New Batch 4_20140514_125813.csv		FY*B		Fyb (FY:2)	0
Green	Unknown8	New Batch 4_20140514_125813.csv		FY*B_GATA			
Green	Unknown8	New Batch 4_20140514_125813.csv		FY*B[265T]_FY*X			
Green	Unknown8	New Batch 4_20140514_125813.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	Unknown8	New Batch 4_20140514_125813.csv		GYPA*N		N (MNS:2)	+
Green	Unknown8	New Batch 4_20140514_125813.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	Unknown8	New Batch 4_20140514_125813.csv		GYPB*s		s (MNS:4)	+
Green	Unknown8	New Batch 4_20140514_125813.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown8	New Batch 4_20140514_125813.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	Unknown8	New Batch 4_20140514_125813.csv		GYPB*deletion			
Green	Unknown8	New Batch 4_20140514_125813.csv		GYPB*Mur			
Green	Unknown8	New Batch 4_20140514_125813.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	Unknown8	New Batch 4_20140514_125813.csv		DI*B		Dib (DI:2)	+
Green	Unknown8	New Batch 4_20140514_125813.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	Unknown8	New Batch 4_20140514_125813.csv		DO*B		Dob (DO:2)	+
Green	Unknown8	New Batch 4_20140514_125813.csv		DO*B_HY-		Hy (DO:4)	+
Green	Unknown8	New Batch 4_20140514_125813.csv		DO*A_JOA-		Joa (DO:5)	+
Green	Unknown8	New Batch 4_20140514_125813.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	Unknown8	New Batch 4_20140514_125813.csv		CO*B		Cob (CO:2)	0
Green	Unknown8	New Batch 4_20140514_125813.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	Unknown8	New Batch 4_20140514_125813.csv		YT*B		Ytb (YT:2)	0
Green	Unknown8	New Batch 4_20140514_125813.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	Unknown8	New Batch 4_20140514_125813.csv		LU*B		Lub (LU:2)	+
Green	EX1307335	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*Ce	C (RH:2)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	0
Green	EX1307335	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	0
Green	EX1307335	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1307335	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1307335	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1307335	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307335	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1307335	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1307335	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			
Green	EX1307335	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1307335	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1307335	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1307335	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1307335	New Batch 5_20140514_171740.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1307335	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1307335	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1307335	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307335	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1307335	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1307335	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1307335	New Batch 5_20140514_171740.csv		JK*B_null(871C)			
Green	EX1307335	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1307335	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		FY*B_GATA			
Green	EX1307335	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1307335	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307335	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1307335	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1307335	New Batch 5_20140514_171740.csv		GYPB*Mur			
Green	EX1307335	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1307335	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1307335	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307335	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	0
Green	EX1307335	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1307335	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	0
Green	EX1307335	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1307335	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+
Green	EX1307336	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*Ce, RHCE*cE(10)	C (RH:2)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1307336	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307336	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1307336	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1307336	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1307336	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			
Green	EX1307336	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1307336	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1307336	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1307336	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1307336	New Batch 5_20140514_171740.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1307336	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307336	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1307336	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1307336	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1307336	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1307336	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*A	Jka (JK:1)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	0
Green	EX1307336	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1307336	New Batch 5_20140514_171740.csv		JK*B_null(871C)			
Green	EX1307336	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*B, FY*B[265T]_FY*X	Fya (FY:1)	0
Green	EX1307336	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		FY*B_GATA			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307336	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1307336	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*S	S (MNS:3)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	0
Green	EX1307336	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1307336	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1307336	New Batch 5_20140514_171740.csv		GYPB*Mur			
Green	EX1307336	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1307336	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1307336	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307336	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1307336	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	0
Green	EX1307336	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1307336	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	0
Green	EX1307336	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1307336	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+
Green	EX1307657	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*Ce	C (RH:2)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	0
Green	EX1307657	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307657	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1307657	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1307657	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1307657	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1307657	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1307657	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			
Green	EX1307657	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1307657	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1307657	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307657	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1307657	New Batch 5_20140514_171740.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1307657	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1307657	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1307657	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1307657	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1307657	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1307657	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1307657	New Batch 5_20140514_171740.csv		JK*B_null(871C)			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307657	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		FY*B_GATA			
Green	EX1307657	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1307657	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	0
Green	EX1307657	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1307657	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1307657	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1307657	New Batch 5_20140514_171740.csv		GYPB*Mur			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307657	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1307657	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1307657	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1307657	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1307657	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A, CO*B	Coa (CO:1)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	+
Green	EX1307657	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1307657	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	0
Green	EX1307657	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1307657	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307898	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*ce	C (RH:2)	0
Green	EX1307898	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	0
Green	EX1307898	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	+
Green	EX1307898	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1307898	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1307898	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1307898	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1307898	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1307898	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1307898	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1307898	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1307898	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307898	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1307898	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1307898	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1307898	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1307898	New Batch 5_20140514_171740.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1307898	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1307898	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1307898	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1307898	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1307898	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1307898	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1307898	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*A	Jka (JK:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307898	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	0
Green	EX1307898	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1307898	New Batch 5_20140514_171740.csv		JK*B_null(871C)			
Green	EX1307898	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1307898	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	+
Green	EX1307898	New Batch 5_20140514_171740.csv		FY*B_GATA			
Green	EX1307898	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1307898	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1307898	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	+
Green	EX1307898	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1307898	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	+
Green	EX1307898	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307898	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1307898	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1307898	New Batch 5_20140514_171740.csv		GYPB*Mur			
Green	EX1307898	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1307898	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1307898	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+
Green	EX1307898	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1307898	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1307898	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1307898	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1307898	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	0
Green	EX1307898	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307898	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	0
Green	EX1307898	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1307898	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+
Green	EX1307899	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*ce, RHCE*cE	C (RH:2)	0
Green	EX1307899	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1307899	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1307899	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1307899	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307899	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1307899	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1307899	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			
Green	EX1307899	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1307899	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1307899	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1307899	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1307899	New Batch 5_20140514_171740.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1307899	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*K_KPB_JSB, KEL*k_KPB_JSB	K (KEL:1)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1307899	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307899	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1307899	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1307899	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1307899	New Batch 5_20140514_171740.csv		JK*B_null(871C)			
Green	EX1307899	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		FY*B_GATA			
Green	EX1307899	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1307899	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307899	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1307899	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1307899	New Batch 5_20140514_171740.csv		GYPB*Mur			
Green	EX1307899	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1307899	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1307899	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1307899	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1307899	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	0
Green	EX1307899	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1307899	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	0
Green	EX1307899	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1307899	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+
Green	EX1308240	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*ce	C (RH:2)	0
Green	EX1308240	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	0
Green	EX1308240	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	+
Green	EX1308240	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1308240	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1308240	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308240	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1308240	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1308240	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1308240	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1308240	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1308240	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			
Green	EX1308240	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1308240	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1308240	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1308240	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1308240	New Batch 5_20140514_171740.csv		RHD*r’s-RHCE*ce[733G,1006T]			
Green	EX1308240	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308240	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1308240	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1308240	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1308240	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1308240	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1308240	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*A	Jka (JK:1)	+
Green	EX1308240	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	0
Green	EX1308240	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1308240	New Batch 5_20140514_171740.csv		JK*B_null(871C)			
Green	EX1308240	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	EX1308240	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	+
Green	EX1308240	New Batch 5_20140514_171740.csv		FY*B_GATA			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308240	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1308240	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*N	M (MNS:1)	0
Green	EX1308240	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	+
Green	EX1308240	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1308240	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	+
Green	EX1308240	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1308240	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1308240	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1308240	New Batch 5_20140514_171740.csv		GYPB*Mur			
Green	EX1308240	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1308240	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1308240	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308240	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1308240	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1308240	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1308240	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1308240	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	0
Green	EX1308240	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1308240	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	0
Green	EX1308240	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1308240	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+
Green	EX1308368	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*ce, RHCE*Ce	C (RH:2)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	0
Green	EX1308368	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308368	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1308368	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1308368	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1308368	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1308368	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1308368	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			
Green	EX1308368	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1308368	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1308368	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308368	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1308368	New Batch 5_20140514_171740.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1308368	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1308368	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1308368	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1308368	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1308368	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1308368	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1308368	New Batch 5_20140514_171740.csv		JK*B_null(871C)			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308368	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*A	Fya (FY:1)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	0
Green	EX1308368	New Batch 5_20140514_171740.csv		FY*B_GATA			
Green	EX1308368	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1308368	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	0
Green	EX1308368	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1308368	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1308368	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1308368	New Batch 5_20140514_171740.csv		GYPB*Mur			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308368	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1308368	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1308368	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1308368	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	0
Green	EX1308368	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1308368	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	0
Green	EX1308368	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1308368	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308578	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*ce, RHCE*cE	C (RH:2)	
Green	EX1308578	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1308578	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1308578	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1308578	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1308578	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1308578	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308578	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1308578	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1308578	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1308578	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1308578	New Batch 5_20140514_171740.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1308578	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1308578	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1308578	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1308578	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1308578	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1308578	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308578	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1308578	New Batch 5_20140514_171740.csv		JK*B_null(871C)			
Green	EX1308578	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		FY*B_GATA			
Green	EX1308578	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1308578	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1308578	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308578	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1308578	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1308578	New Batch 5_20140514_171740.csv		GYPB*Mur			
Green	EX1308578	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1308578	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1308578	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1308578	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1308578	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	0
Green	EX1308578	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A, YT*B	Yta (YT:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308578	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	+
Green	EX1308578	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1308578	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+
Green	EX1308762	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*Ce	C (RH:2)	+
Green	EX1308762	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	0
Green	EX1308762	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	0
Green	EX1308762	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1308762	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1308762	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1308762	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1308762	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1308762	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308762	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1308762	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1308762	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			
Green	EX1308762	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1308762	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1308762	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1308762	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1308762	New Batch 5_20140514_171740.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1308762	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1308762	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1308762	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1308762	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308762	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1308762	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1308762	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*A	Jka (JK:1)	+
Green	EX1308762	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	0
Green	EX1308762	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1308762	New Batch 5_20140514_171740.csv		JK*B_null(871C)			
Green	EX1308762	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1308762	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	+
Green	EX1308762	New Batch 5_20140514_171740.csv		FY*B_GATA			
Green	EX1308762	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1308762	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	EX1308762	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308762	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	EX1308762	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	+
Green	EX1308762	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1308762	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1308762	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1308762	New Batch 5_20140514_171740.csv		GYPB*Mur			
Green	EX1308762	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1308762	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1308762	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+
Green	EX1308762	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1308762	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1308762	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308762	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1308762	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	0
Green	EX1308762	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1308762	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	0
Green	EX1308762	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1308762	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+
Green	EX1308908	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*ce	C (RH:2)	0
Green	EX1308908	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	0
Green	EX1308908	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1308908	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308908	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1308908	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1308908	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1308908	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			
Green	EX1308908	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1308908	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1308908	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1308908	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1308908	New Batch 5_20140514_171740.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1308908	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308908	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1308908	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1308908	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1308908	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1308908	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*A	Jka (JK:1)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	0
Green	EX1308908	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1308908	New Batch 5_20140514_171740.csv		JK*B_null(871C)			
Green	EX1308908	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*A	Fya (FY:1)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	0
Green	EX1308908	New Batch 5_20140514_171740.csv		FY*B_GATA			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308908	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1308908	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1308908	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1308908	New Batch 5_20140514_171740.csv		GYPB*Mur			
Green	EX1308908	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1308908	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1308908	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308908	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1308908	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	0
Green	EX1308908	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1308908	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	0
Green	EX1308908	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1308908	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+
Green	EX1308909	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*Ce, RHCE*cE(10)	C (RH:2)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308909	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1308909	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1308909	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1308909	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1308909	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1308909	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			
Green	EX1308909	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1308909	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1308909	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308909	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1308909	New Batch 5_20140514_171740.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1308909	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1308909	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1308909	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1308909	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1308909	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1308909	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*A	Jka (JK:1)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	0
Green	EX1308909	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1308909	New Batch 5_20140514_171740.csv		JK*B_null(871C)			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308909	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		FY*B_GATA			
Green	EX1308909	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1308909	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1308909	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1308909	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1308909	New Batch 5_20140514_171740.csv		GYPB*Mur			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308909	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1308909	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1308909	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1308909	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	0
Green	EX1308909	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1308909	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	0
Green	EX1308909	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1308909	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308959	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*ce, RHCE*Ce	C (RH:2)	+
Green	EX1308959	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	0
Green	EX1308959	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	+
Green	EX1308959	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1308959	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1308959	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1308959	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1308959	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1308959	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1308959	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1308959	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1308959	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308959	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1308959	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1308959	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1308959	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1308959	New Batch 5_20140514_171740.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1308959	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1308959	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1308959	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1308959	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1308959	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1308959	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1308959	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*B	Jka (JK:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308959	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	+
Green	EX1308959	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1308959	New Batch 5_20140514_171740.csv		JK*B_null(871C)			
Green	EX1308959	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1308959	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	+
Green	EX1308959	New Batch 5_20140514_171740.csv		FY*B_GATA			
Green	EX1308959	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1308959	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1308959	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	+
Green	EX1308959	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1308959	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	+
Green	EX1308959	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308959	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1308959	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1308959	New Batch 5_20140514_171740.csv		GYPB*Mur			
Green	EX1308959	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1308959	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1308959	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1308959	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1308959	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1308959	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1308959	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A, CO*B	Coa (CO:1)	+
Green	EX1308959	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	+
Green	EX1308959	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1308959	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	0
Green	EX1308959	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1308959	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+
Green	EX1311437	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*Ce, RHCE*CeCW	C (RH:2)	+
Green	EX1311437	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	0
Green	EX1311437	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	0
Green	EX1311437	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1311437	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	+
Green	EX1311437	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1311437	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1311437	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1311437	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311437	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1311437	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1311437	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			
Green	EX1311437	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1311437	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1311437	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1311437	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1311437	New Batch 5_20140514_171740.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1311437	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1311437	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1311437	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1311437	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311437	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1311437	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1311437	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*B	Jka (JK:1)	0
Green	EX1311437	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	+
Green	EX1311437	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1311437	New Batch 5_20140514_171740.csv		JK*B_null(871C)			
Green	EX1311437	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1311437	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	+
Green	EX1311437	New Batch 5_20140514_171740.csv		FY*B_GATA			
Green	EX1311437	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1311437	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	EX1311437	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311437	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1311437	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	+
Green	EX1311437	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1311437	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1311437	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1311437	New Batch 5_20140514_171740.csv		GYPB*Mur			
Green	EX1311437	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1311437	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1311437	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1311437	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1311437	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1311437	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311437	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1311437	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	0
Green	EX1311437	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1311437	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	0
Green	EX1311437	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1311437	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+
Green	EX1311438	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*ce, RHCE*cE	C (RH:2)	0
Green	EX1311438	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1311438	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311438	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1311438	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1311438	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1311438	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			
Green	EX1311438	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1311438	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1311438	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1311438	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1311438	New Batch 5_20140514_171740.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1311438	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311438	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1311438	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1311438	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1311438	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1311438	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1311438	New Batch 5_20140514_171740.csv		JK*B_null(871C)			
Green	EX1311438	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		FY*B_GATA			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311438	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1311438	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	0
Green	EX1311438	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*S	S (MNS:3)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	0
Green	EX1311438	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1311438	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1311438	New Batch 5_20140514_171740.csv		GYPB*Mur			
Green	EX1311438	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1311438	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1311438	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311438	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1311438	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	0
Green	EX1311438	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1311438	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	0
Green	EX1311438	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1311438	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+
Green	EX1311986	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*Ce, RHCE*cE(10)	C (RH:2)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311986	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1311986	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1311986	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1311986	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1311986	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1311986	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			
Green	EX1311986	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1311986	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1311986	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311986	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1311986	New Batch 5_20140514_171740.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1311986	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1311986	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1311986	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1311986	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1311986	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1311986	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*A	Jka (JK:1)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	0
Green	EX1311986	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1311986	New Batch 5_20140514_171740.csv		JK*B_null(871C)			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311986	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		FY*B_GATA			
Green	EX1311986	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1311986	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1311986	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1311986	New Batch 5_20140514_171740.csv		GYPB*Mur			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311986	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1311986	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1311986	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1311986	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1311986	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	0
Green	EX1311986	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1311986	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	0
Green	EX1311986	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1311986	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311987	New Batch 5_20140514_171740.csv	Rh	RHCE*ce	RHCE*Ce, RHCE*cE(10)	C (RH:2)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		RHCE*Ce		E (RH:3)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		RHCE*cE		c (RH:4)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		RHCE*CE		e (RH:5)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1311987	New Batch 5_20140514_171740.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1311987	New Batch 5_20140514_171740.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1311987	New Batch 5_20140514_171740.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		RHCE*CeVG			
Green	EX1311987	New Batch 5_20140514_171740.csv		RHCE*cEFM			
Green	EX1311987	New Batch 5_20140514_171740.csv		RHCE*ce[712G]			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311987	New Batch 5_20140514_171740.csv		RHCE*ce[733G]			
Green	EX1311987	New Batch 5_20140514_171740.csv		RHCE*ce[733G,1006T]			
Green	EX1311987	New Batch 5_20140514_171740.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1311987	New Batch 5_20140514_171740.csv		RHCE*cE[697G,712G,733G]			
Green	EX1311987	New Batch 5_20140514_171740.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1311987	New Batch 5_20140514_171740.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1311987	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1311987	New Batch 5_20140514_171740.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1311987	New Batch 5_20140514_171740.csv				Jsa (KEL:6)	0
Green	EX1311987	New Batch 5_20140514_171740.csv				Jsb (KEL:7)	+
Green	EX1311987	New Batch 5_20140514_171740.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311987	New Batch 5_20140514_171740.csv		JK*B		Jkb (JK:2)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		JK*B_null(IVS5-1a)			
Green	EX1311987	New Batch 5_20140514_171740.csv		JK*B_null(871C)			
Green	EX1311987	New Batch 5_20140514_171740.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1311987	New Batch 5_20140514_171740.csv		FY*B		Fyb (FY:2)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		FY*B_GATA			
Green	EX1311987	New Batch 5_20140514_171740.csv		FY*B[265T]_FY*X			
Green	EX1311987	New Batch 5_20140514_171740.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		GYPA*N		N (MNS:2)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		GYPB*s		s (MNS:4)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311987	New Batch 5_20140514_171740.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1311987	New Batch 5_20140514_171740.csv		GYPB*deletion			
Green	EX1311987	New Batch 5_20140514_171740.csv		GYPB*Mur			
Green	EX1311987	New Batch 5_20140514_171740.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1311987	New Batch 5_20140514_171740.csv		DI*B		Dib (DI:2)	+
Green	EX1311987	New Batch 5_20140514_171740.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1311987	New Batch 5_20140514_171740.csv		DO*B		Dob (DO:2)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1311987	New Batch 5_20140514_171740.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1311987	New Batch 5_20140514_171740.csv		CO*B		Cob (CO:2)	0
Green	EX1311987	New Batch 5_20140514_171740.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311987	New Batch 5_20140514_171740.csv		YT*B		Ytb (YT:2)	0
Green	EX1311987	New Batch 5_20140514_171740.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1311987	New Batch 5_20140514_171740.csv		LU*B		Lub (LU:2)	+
Green	EX1311988	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*Ce	C (RH:2)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1311988	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1311988	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1311988	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1311988	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311988	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1311988	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1311988	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1311988	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1311988	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1311988	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1311988	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1311988	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1311988	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*K_KPB_JSB, KEL*k_KPB_JSB	K (KEL:1)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1311988	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311988	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1311988	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1311988	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1311988	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1311988	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1311988	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1311988	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1311988	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311988	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1311988	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1311988	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1311988	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1311988	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1311988	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1311988	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311988	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1311988	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1311988	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1311988	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1311988	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1311989	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*Ce	C (RH:2)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1311989	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1311989	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311989	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1311989	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1311989	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1311989	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1311989	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1311989	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1311989	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1311989	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1311989	New Batch 6_20140515_111617.csv		RHD*r’s-RHCE*ce[733G,1006T]			
Green	EX1311989	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311989	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1311989	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1311989	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1311989	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1311989	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1311989	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1311989	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		FY*B_GATA			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311989	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1311989	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	0
Green	EX1311989	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1311989	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1311989	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1311989	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1311989	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1311989	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*A	Doa (DO:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1311989	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	0
Green	EX1311989	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1311989	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1311989	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1311989	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*A, LU*B	Lua (LU:1)	+
Green	EX1311989	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1312294	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce	C (RH:2)	0
Green	EX1312294	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1312294	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312294	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1312294	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1312294	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1312294	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1312294	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1312294	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1312294	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1312294	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1312294	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312294	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1312294	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1312294	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1312294	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1312294	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1312294	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1312294	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1312294	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1312294	New Batch 6_20140515_111617.csv		JK*B_null(871C)			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312294	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1312294	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1312294	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	0
Green	EX1312294	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1312294	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1312294	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1312294	New Batch 6_20140515_111617.csv		GYPB*Mur			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312294	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1312294	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1312294	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*A	Doa (DO:1)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	0
Green	EX1312294	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1312294	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1312294	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1312294	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*A, LU*B	Lua (LU:1)	+
Green	EX1312294	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312295	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*Ce	C (RH:2)	+
Green	EX1312295	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1312295	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+
Green	EX1312295	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1312295	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1312295	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1312295	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1312295	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1312295	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1312295	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1312295	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1312295	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312295	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1312295	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1312295	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1312295	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1312295	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1312295	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1312295	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1312295	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1312295	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1312295	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1312295	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1312295	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*B	Jka (JK:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312295	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1312295	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1312295	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1312295	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1312295	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1312295	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1312295	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1312295	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	EX1312295	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	0
Green	EX1312295	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	EX1312295	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1312295	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312295	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1312295	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1312295	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1312295	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1312295	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1312295	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1312295	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1312295	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1312295	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1312295	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1312295	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1312295	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312295	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1312295	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1312295	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1312296	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*Ce	C (RH:2)	+
Green	EX1312296	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1312296	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+
Green	EX1312296	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1312296	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1312296	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1312296	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1312296	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1312296	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312296	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1312296	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1312296	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1312296	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1312296	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1312296	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1312296	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1312296	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1312296	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1312296	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1312296	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1312296	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312296	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1312296	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1312296	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*A	Jka (JK:1)	+
Green	EX1312296	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	0
Green	EX1312296	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1312296	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1312296	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*A	Fya (FY:1)	+
Green	EX1312296	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	0
Green	EX1312296	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1312296	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1312296	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	EX1312296	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312296	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1312296	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1312296	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1312296	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1312296	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1312296	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1312296	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1312296	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1312296	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+
Green	EX1312296	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1312296	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1312296	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312296	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1312296	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1312296	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1312296	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1312296	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1312296	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1312297	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*Ce	C (RH:2)	+
Green	EX1312297	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1312297	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+
Green	EX1312297	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1312297	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1312297	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312297	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1312297	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1312297	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1312297	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1312297	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1312297	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1312297	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1312297	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1312297	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1312297	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1312297	New Batch 6_20140515_111617.csv		RHD*r’s-RHCE*ce[733G,1006T]			
Green	EX1312297	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*K_KPB_JSB, KEL*k_KPB_JSB	K (KEL:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312297	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1312297	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1312297	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1312297	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1312297	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1312297	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*A	Jka (JK:1)	+
Green	EX1312297	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	0
Green	EX1312297	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1312297	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1312297	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1312297	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1312297	New Batch 6_20140515_111617.csv		FY*B_GATA			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312297	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1312297	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1312297	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	+
Green	EX1312297	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1312297	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1312297	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1312297	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1312297	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1312297	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1312297	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1312297	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1312297	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*A	Doa (DO:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312297	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	0
Green	EX1312297	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1312297	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1312297	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1312297	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1312297	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1312297	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1312297	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1312297	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1312311	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*Ce	C (RH:2)	+
Green	EX1312311	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1312311	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312311	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1312311	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1312311	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1312311	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1312311	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1312311	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1312311	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1312311	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1312311	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1312311	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1312311	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1312311	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312311	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1312311	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1312311	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1312311	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1312311	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1312311	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1312311	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1312311	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1312311	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*B	Jka (JK:1)	0
Green	EX1312311	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1312311	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1312311	New Batch 6_20140515_111617.csv		JK*B_null(871C)			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312311	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1312311	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1312311	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1312311	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1312311	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*N	M (MNS:1)	0
Green	EX1312311	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	+
Green	EX1312311	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1312311	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1312311	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1312311	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1312311	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1312311	New Batch 6_20140515_111617.csv		GYPB*Mur			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312311	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1312311	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1312311	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1312311	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1312311	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1312311	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1312311	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1312311	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1312311	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1312311	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1312311	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1312311	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1322312	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*Ce	C (RH:2)	+
Green	EX1322312	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1322312	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	0
Green	EX1322312	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1322312	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1322312	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1322312	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1322312	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1322312	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1322312	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1322312	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1322312	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1322312	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1322312	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1322312	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1322312	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1322312	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1322312	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1322312	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1322312	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1322312	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1322312	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1322312	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1322312	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1322312	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1322312	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1322312	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1322312	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1322312	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1322312	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1322312	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1322312	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1322312	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	+
Green	EX1322312	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1322312	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1322312	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1322312	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1322312	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1322312	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1322312	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1322312	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1322312	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1322312	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1322312	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1322312	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1322312	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1322312	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1322312	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1322312	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1322312	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1322312	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1312453	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*cE	C (RH:2)	0
Green	EX1312453	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	+
Green	EX1312453	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+
Green	EX1312453	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1312453	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1312453	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1312453	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1312453	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1312453	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312453	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1312453	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1312453	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1312453	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1312453	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1312453	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1312453	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1312453	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1312453	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1312453	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1312453	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1312453	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312453	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1312453	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1312453	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	EX1312453	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1312453	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1312453	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1312453	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1312453	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1312453	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1312453	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1312453	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	EX1312453	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312453	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*S	S (MNS:3)	+
Green	EX1312453	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	0
Green	EX1312453	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1312453	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1312453	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1312453	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1312453	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1312453	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1312453	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1312453	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1312453	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1312453	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312453	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1312453	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1312453	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1312453	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1312453	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1312453	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1312673	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*Ce	C (RH:2)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1312673	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1312673	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312673	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1312673	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1312673	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1312673	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1312673	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1312673	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1312673	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1312673	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1312673	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1312673	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312673	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1312673	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1312673	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1312673	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1312673	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1312673	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1312673	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1312673	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		FY*B_GATA			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312673	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1312673	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1312673	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1312673	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1312673	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1312673	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1312673	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1312673	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312673	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1312673	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1312673	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1312673	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1312673	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1312673	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1312674	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*Ce	C (RH:2)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1312674	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312674	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1312674	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1312674	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1312674	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1312674	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1312674	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1312674	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1312674	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1312674	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312674	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1312674	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1312674	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1312674	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1312674	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1312674	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1312674	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1312674	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1312674	New Batch 6_20140515_111617.csv		JK*B_null(871C)			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312674	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*A	Fya (FY:1)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	0
Green	EX1312674	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1312674	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1312674	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1312674	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1312674	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1312674	New Batch 6_20140515_111617.csv		GYPB*Mur			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312674	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1312674	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1312674	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1312674	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1312674	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1312674	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1312674	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1312674	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1312674	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312675	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*Ce, RHCE*CeCW	C (RH:2)	+
Green	EX1312675	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1312675	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	0
Green	EX1312675	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1312675	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	+
Green	EX1312675	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1312675	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1312675	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1312675	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1312675	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1312675	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1312675	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312675	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1312675	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1312675	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1312675	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1312675	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1312675	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1312675	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1312675	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1312675	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1312675	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1312675	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1312675	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*B	Jka (JK:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312675	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1312675	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1312675	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1312675	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1312675	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1312675	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1312675	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1312675	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*N	M (MNS:1)	0
Green	EX1312675	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	+
Green	EX1312675	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1312675	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1312675	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312675	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1312675	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1312675	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1312675	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1312675	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1312675	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+
Green	EX1312675	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1312675	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1312675	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1312675	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1312675	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1312675	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312675	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1312675	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1312675	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1312967	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*cE	C (RH:2)	0
Green	EX1312967	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	+
Green	EX1312967	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+
Green	EX1312967	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1312967	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1312967	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1312967	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1312967	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1312967	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312967	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1312967	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1312967	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1312967	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1312967	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1312967	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1312967	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1312967	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1312967	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1312967	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1312967	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1312967	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312967	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1312967	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1312967	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*B	Jka (JK:1)	0
Green	EX1312967	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1312967	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1312967	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1312967	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1312967	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1312967	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1312967	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1312967	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1312967	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312967	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	EX1312967	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1312967	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1312967	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1312967	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1312967	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1312967	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1312967	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1312967	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1312967	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1312967	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1312967	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1312967	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1312967	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1312967	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1312967	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1312967	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1312967	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1313154	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*Ce	C (RH:2)	+
Green	EX1313154	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1313154	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+
Green	EX1313154	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1313154	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1313154	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313154	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1313154	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1313154	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1313154	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1313154	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1313154	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1313154	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1313154	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1313154	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1313154	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1313154	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1313154	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313154	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1313154	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1313154	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1313154	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1313154	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1313154	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*B	Jka (JK:1)	0
Green	EX1313154	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1313154	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1313154	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1313154	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	EX1313154	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1313154	New Batch 6_20140515_111617.csv		FY*B_GATA			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313154	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1313154	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	EX1313154	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	0
Green	EX1313154	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*S	S (MNS:3)	+
Green	EX1313154	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	0
Green	EX1313154	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1313154	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1313154	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1313154	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1313154	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1313154	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1313154	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*A	Doa (DO:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313154	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	0
Green	EX1313154	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1313154	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1313154	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1313154	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1313154	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A, YT*B	Yta (YT:1)	+
Green	EX1313154	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	+
Green	EX1313154	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1313154	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1313155	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*cE	C (RH:2)	0
Green	EX1313155	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	+
Green	EX1313155	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313155	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1313155	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1313155	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1313155	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1313155	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1313155	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1313155	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1313155	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1313155	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1313155	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1313155	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1313155	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313155	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1313155	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1313155	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1313155	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1313155	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1313155	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1313155	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1313155	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1313155	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*B	Jka (JK:1)	0
Green	EX1313155	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1313155	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1313155	New Batch 6_20140515_111617.csv		JK*B_null(871C)			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313155	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*A	Fya (FY:1)	+
Green	EX1313155	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	0
Green	EX1313155	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1313155	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1313155	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*N	M (MNS:1)	0
Green	EX1313155	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	+
Green	EX1313155	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1313155	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1313155	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1313155	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1313155	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1313155	New Batch 6_20140515_111617.csv		GYPB*Mur			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313155	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1313155	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1313155	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+
Green	EX1313155	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1313155	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1313155	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1313155	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1313155	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1313155	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1313155	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1313155	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1313155	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313515	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*cE	C (RH:2)	0
Green	EX1313515	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	+
Green	EX1313515	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+
Green	EX1313515	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	0
Green	EX1313515	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1313515	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1313515	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1313515	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1313515	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	0
Green	EX1313515	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1313515	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1313515	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313515	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1313515	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1313515	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1313515	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1313515	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1313515	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1313515	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1313515	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1313515	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1313515	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1313515	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1313515	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*A	Jka (JK:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313515	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	0
Green	EX1313515	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1313515	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1313515	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1313515	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1313515	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1313515	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1313515	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*N	M (MNS:1)	0
Green	EX1313515	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	+
Green	EX1313515	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	EX1313515	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1313515	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313515	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1313515	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1313515	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1313515	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1313515	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1313515	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+
Green	EX1313515	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1313515	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1313515	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1313515	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1313515	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1313515	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313515	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1313515	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1313515	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1313516	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*CeCW(12)	C (RH:2)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1313516	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1313516	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1313516	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313516	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1313516	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1313516	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1313516	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1313516	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1313516	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1313516	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1313516	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1313516	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1313516	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1313516	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313516	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1313516	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1313516	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*A	Jka (JK:1)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	0
Green	EX1313516	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1313516	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1313516	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1313516	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1313516	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313516	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1313516	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1313516	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1313516	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1313516	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1313516	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1313516	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313516	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1313516	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1313516	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1313516	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1313516	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1313820	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*Ce	C (RH:2)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1313820	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1313820	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313820	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1313820	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1313820	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1313820	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1313820	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1313820	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1313820	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1313820	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1313820	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1313820	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313820	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1313820	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1313820	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1313820	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1313820	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*B	Jka (JK:1)	0
Green	EX1313820	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1313820	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1313820	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1313820	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		FY*B_GATA			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313820	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1313820	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1313820	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1313820	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1313820	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1313820	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1313820	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1313820	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1313820	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1313820	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A, CO*B	Coa (CO:1)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	+
Green	EX1313820	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1313820	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1313820	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1313820	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1400171	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*Ce	C (RH:2)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1400171	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1400171	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1400171	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1400171	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1400171	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1400171	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1400171	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1400171	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1400171	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1400171	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1400171	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1400171	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1400171	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1400171	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1400171	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1400171	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1400171	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1400171	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1400171	New Batch 6_20140515_111617.csv		JK*B_null(871C)			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1400171	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1400171	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1400171	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1400171	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1400171	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1400171	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1400171	New Batch 6_20140515_111617.csv		GYPB*Mur			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1400171	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1400171	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1400171	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1400171	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1400171	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1400171	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1400171	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1400171	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1400171	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1400887	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*Ce	C (RH:2)	+
Green	EX1400887	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1400887	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+
Green	EX1400887	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1400887	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1400887	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1400887	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1400887	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1400887	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1400887	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1400887	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1400887	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1400887	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1400887	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1400887	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1400887	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1400887	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1400887	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1400887	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1400887	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1400887	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1400887	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1400887	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1400887	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*B	Jka (JK:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1400887	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1400887	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1400887	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1400887	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1400887	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1400887	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1400887	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1400887	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*N	M (MNS:1)	0
Green	EX1400887	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	+
Green	EX1400887	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*s	S (MNS:3)	0
Green	EX1400887	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1400887	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1400887	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1400887	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1400887	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1400887	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1400887	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1400887	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1400887	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1400887	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1400887	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1400887	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1400887	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1400887	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1400887	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1400887	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1400887	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1401612	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*Ce, RHCE*cE(10)	C (RH:2)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1401612	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1401612	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1401612	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1401612	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1401612	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1401612	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1401612	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1401612	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1401612	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1401612	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1401612	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1401612	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1401612	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1401612	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1401612	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1401612	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1401612	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*A, JK*B	Jka (JK:1)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1401612	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1401612	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*B	Fya (FY:1)	0
Green	EX1401612	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1401612	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1401612	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1401612	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*S	S (MNS:3)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	0
Green	EX1401612	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1401612	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1401612	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1401612	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1401612	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1401612	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1401612	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1401612	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1401612	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1401612	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1401612	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1401613	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*ce, RHCE*Ce	C (RH:2)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	0
Green	EX1401613	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1401613	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1401613	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1401613	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1401613	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1401613	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1401613	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1401613	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1401613	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			
Green	EX1401613	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1401613	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1401613	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1401613	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1401613	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1401613	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1401613	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1401613	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*A	Jka (JK:1)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	0
Green	EX1401613	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1401613	New Batch 6_20140515_111617.csv		JK*B_null(871C)			
Green	EX1401613	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		FY*B_GATA			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1401613	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1401613	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M	M (MNS:1)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	0
Green	EX1401613	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1401613	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1401613	New Batch 6_20140515_111617.csv		GYPB*Mur			
Green	EX1401613	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1401613	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1401613	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*A, DO*B	Doa (DO:1)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1401613	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1401613	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A	Coa (CO:1)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	0
Green	EX1401613	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1401613	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1401613	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1401613	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+
Green	EX1401737	New Batch 6_20140515_111617.csv	Rh	RHCE*ce	RHCE*Ce, RHCE*cE(10)	C (RH:2)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		RHCE*Ce		E (RH:3)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		RHCE*cE		c (RH:4)	+

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1401737	New Batch 6_20140515_111617.csv		RHCE*CE		e (RH:5)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		RHCE*CeCW		CW (RH:8)	0
Green	EX1401737	New Batch 6_20140515_111617.csv		RHCE*ceCW		V (RH:10)	0
Green	EX1401737	New Batch 6_20140515_111617.csv		RHCE*CECW		hrS (RH:19)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		RHCE*ceAR		VS (RH:20)	0
Green	EX1401737	New Batch 6_20140515_111617.csv		RHCE*CeFV		hrB (RH:31)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		RHCE*CeVG			
Green	EX1401737	New Batch 6_20140515_111617.csv		RHCE*cEFM			
Green	EX1401737	New Batch 6_20140515_111617.csv		RHCE*ce[712G]			
Green	EX1401737	New Batch 6_20140515_111617.csv		RHCE*ce[733G]			
Green	EX1401737	New Batch 6_20140515_111617.csv		RHCE*ce[733G,1006T]			
Green	EX1401737	New Batch 6_20140515_111617.csv		RHCE*CE-D[2, 5, 7]-CE			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1401737	New Batch 6_20140515_111617.csv		RHCE*cE[697G,712G,733G]			
Green	EX1401737	New Batch 6_20140515_111617.csv		RHD*r's-RHCE*ce[733G,1006T]			
Green	EX1401737	New Batch 6_20140515_111617.csv	Kell	KEL*K_KPB_JSB	KEL*k_KPB_JSB	K (KEL:1)	0
Green	EX1401737	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSB		k (KEL:2)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		KEL*k_KPA_JSB		Kpa (KEL:3)	0
Green	EX1401737	New Batch 6_20140515_111617.csv		KEL*k_KPB_JSA		Kpb (KEL:4)	+
Green	EX1401737	New Batch 6_20140515_111617.csv				Jsa (KEL:6)	0
Green	EX1401737	New Batch 6_20140515_111617.csv				Jsb (KEL:7)	+
Green	EX1401737	New Batch 6_20140515_111617.csv	Kidd	JK*A	JK*B	Jka (JK:1)	0
Green	EX1401737	New Batch 6_20140515_111617.csv		JK*B		Jkb (JK:2)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		JK*B_null(IVS5-1a)			
Green	EX1401737	New Batch 6_20140515_111617.csv		JK*B_null(871C)			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1401737	New Batch 6_20140515_111617.csv	Duffy	FY*A	FY*A, FY*B	Fya (FY:1)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		FY*B		Fyb (FY:2)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		FY*B_GATA			
Green	EX1401737	New Batch 6_20140515_111617.csv		FY*B[265T]_FY*X			
Green	EX1401737	New Batch 6_20140515_111617.csv	MNS	GYPA*M	GYPA*M, GYPA*N	M (MNS:1)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		GYPA*N		N (MNS:2)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		GYPB*S	GYPB*S, GYPB*s	S (MNS:3)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		GYPB*s		s (MNS:4)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		GYPB*S_null(IVS5+5t)		U (MNS:5)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		GYPB*S_null(230T)		Mia (MNS:7)	0
Green	EX1401737	New Batch 6_20140515_111617.csv		GYPB*deletion			
Green	EX1401737	New Batch 6_20140515_111617.csv		GYPB*Mur			

Symbol	Sample	CSV	Blood Group System	Alleles Assayed	Genotype Result	Interrogated Antigens (ISBT Phenotype)	Predicted Phenotype Result
Green	EX1401737	New Batch 6_20140515_111617.csv	Diego	DI*A	DI*B	Dia (DI:1)	0
Green	EX1401737	New Batch 6_20140515_111617.csv		DI*B		Dib (DI:2)	+
Green	EX1401737	New Batch 6_20140515_111617.csv	Dombrock	DO*A	DO*B	Doa (DO:1)	0
Green	EX1401737	New Batch 6_20140515_111617.csv		DO*B		Dob (DO:2)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		DO*B_HY-		Hy (DO:4)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		DO*A_JOA-		Joa (DO:5)	+
Green	EX1401737	New Batch 6_20140515_111617.csv	Colton	CO*A	CO*A, CO*B	Coa (CO:1)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		CO*B		Cob (CO:2)	+
Green	EX1401737	New Batch 6_20140515_111617.csv	Cartwright	YT*A	YT*A	Yta (YT:1)	+
Green	EX1401737	New Batch 6_20140515_111617.csv		YT*B		Ytb (YT:2)	0
Green	EX1401737	New Batch 6_20140515_111617.csv	Lutheran	LU*A	LU*B	Lua (LU:1)	0
Green	EX1401737	New Batch 6_20140515_111617.csv		LU*B		Lub (LU:2)	+

10.5 Appendix 5: Patient information leaflet given to the participants in the pilot study

PATIENT INFORMATION SHEET

BLOOD GROUP TYPING AND MATCHING OF BLOOD FOR

TRANSFUSION IN CHRONICALLY TRANSFUSED PATIENTS

Part 1 of the Information Sheet

1. Invitation

You are being invited to take part in a research study. Before you decide whether or not to take part, it is important for you to understand why the research is being done and what it will involve. Please take time to read the following information carefully, and discuss it with others if you wish. One of our team will go through the information with you and answer any questions you have.

Ask us if there is anything that is not clear, or if you would like more information. Take time to decide whether or not you wish to take part.

Normally blood for transfusion is matched for major blood groups only. The purpose of this study is to see if it is feasible to provide blood that is more fully matched with your blood type.

2. What is the purpose of the study?

The study will give us information on whether it is possible to provide blood that is more fully matched with your blood type. This information can then be used for a larger study that will look at whether giving blood that is a closer match to your own can reduce the amount of transfusions needed for your disease type.

3. Why have I been invited?

You have been chosen because your condition means that you will need regular blood transfusions.

4. Do I have to take part?

No. It is up to you to decide whether or not to take part. If you decide to take part you will be given this information sheet to keep and be asked to sign a consent form to confirm that you understand what is involved when

taking part in this study. If you decide to take part you are free to leave the study at any time and without giving a reason. If you withdraw, unless you object, we will still keep records relating to the treatment given to you, as this is valuable to the study. A decision to withdraw at any time, or a decision not to take part, will not affect the quality of care you receive

5. What will happen to me if I take part?

- You will have the normal blood samples taken as part of the pre-transfusion testing protocol.
- You will only need to attend as usual for your normal blood tests and blood transfusions as required by your doctor.
- Your blood will be tested for blood type using your blood cells and your DNA.
- This study will last for up to 3 years.
- This study is a Randomised Trial. Sometimes we don't know which way of treating patients is best. To find out, we need to compare different treatments. We put people into groups and give each group a different treatment. The results are compared to see if one is better. To try to make sure the groups are the same to start with, each patient is put into a group by chance (randomly). This study involves two groups; one group will be given blood matched to current level and the other group will be given the blood that is a closer match. You have a 50% chance of being in the group being given blood of a closer match to your own type.

6. Expenses and Payment

There are no expenses or payments associated with this trial.

7. What will I need to do?

You will only need to attend as usual for your normal blood tests and blood transfusions as required by your doctor.

8. What are the alternatives for diagnosis or treatment?

The alternative is the current practice, providing blood that is matched only for the major blood types.

9. What are the possible disadvantages and risks when taking part?

No side effects are expected as a result of participation in this trial. However, if you do decide to take part in the study, you must report any problems you have to your study nurse or doctor. There is also a contact number given at the end of this information sheet for you to phone if you become worried at any time. In the unlikely event of an emergency occurring during the conduct of the study, we may contact your nominated next of kin.

10. What are the possible benefits of taking part?

We cannot promise the study will help you but the information we get might help improve the future treatment of people with chronic transfusion requirements.

11. What happens when the research study stops?

You will continue to receive your blood transfusion as required and discussed with your doctor.

12. What if there is a problem?

If you have a concern about any aspect of this study, you should ask to speak with the researchers who will do their best to answer your question. The researchers contact details can be found at the end of this information sheet. If you remain unhappy and wish to complain formally, you can do this through the NHS Complaints Procedure. Details can be obtained from the hospital.

In the event that something does go wrong and you are harmed during the research study there are no special compensation arrangements. If you are harmed and this is due to someone's negligence then you may have grounds for a legal action for compensation but you may have to pay your legal costs. The normal National Health Service complaints mechanisms will still be available to you.

13. Will my part in this study be kept confidential?

Yes. We will follow ethical and legal practice and all information about you will be handled in confidence. Any information about you which leaves the hospital will have your name and address removed so that you cannot be recognised.

This completes part 1 of the information sheet.

If the information in part 1 has interested you and you are considering participation, please read the information in part 2 before making any decisions.

Part 2 of the information sheet

14. What if new information becomes available?

Sometimes during the course of a clinical trial, new information becomes available on the procedures that are being studied. If this happens, we will tell you about it and discuss with you whether you want to or should continue in the study. If you decide to withdraw, we will make arrangements for your care to continue. If you decide to continue in the study you will be asked to sign an updated consent form.

On receiving new information, we might consider it to be in your best interests to withdraw you from the study. If so, we will explain the reasons and arrange for your care to continue.

If the study is stopped for any other reason, you will be told why and your continuing care will be arranged.

15. What will happen if I don't want to carry on with the study?
You can withdraw from the study at any time, this will not affect your care.

16. Informing your General Practitioner (GP)
Your GP will be made aware that you are involved in this trial.

17. What will happen to any samples I give?
Your samples will be tested as described in this information sheet. They will not be used for any other research purposes and they will be disposed of in accordance with Trust guidelines.

18. Will any Genetic testing be done?
Your DNA will be used to do blood group typing but no other genetic analysis will be performed on your DNA and your DNA will not be used for any other research.

19. What will happen to the results of this clinical trial?

The results of the study will be available after it finishes and will usually be published in a medical journal or be presented at a scientific conference. The data will be anonymous and none of the patients involved in the trial will be identified in any report or publication.

Should you wish to see the results, or the publication, please ask your study doctor.

20. Who is organising and funding this clinical trial?
This study is being organised by a member of staff in the Haematology Department at the RD&E who is undertaking a Professional Doctorate at the University of the West of England. It is being funded by the RD&E.

21. Who has reviewed the study?
All research in the NHS is looked at by independent group of people, called a Research Ethics Committee, to protect your interests. This study has been reviewed and given favourable opinion by ______________Research Ethics Committee.

22. Contact for further information

You are encouraged to ask any questions you wish, before, during or after your treatment.

General information on research can be found on the Health Research Authority website the web address is given below:
http://www.hra.nhs.uk/hra/patients-and-the-public/

If you have any questions about this study, please speak to your research specialist/coordinator or your haematology doctor, who will be able to provide you with up to date information about the treatment involved. If you wish to read the research on which this study is based, please ask your research specialist/coordinator.

If you would like advice as to whether you should participate please contact your research specialist/coordinator or your haematology doctor.

If you have any concerns during the study then you can contact the research specialist/coordinator on the details given in this leaflet, or you can contact the Haematology ward on 01392 402882.

If you decide you would like to take part then please read and sign the consent form. You will be given a copy of this information sheet and the consent form to keep. A copy of the consent form will be filed in your patient notes, one will be filed with the study records and one may be sent to the Research Sponsor.

You can have more time to think this over if you are at all unsure.

Thank you for taking the time to read this information sheet and to consider this study.

Contact Details

Your Research/Specialist Coordinator

Name Jennifer Davies Tel. Number: 01392 402959

If you have any further questions or require clarification please feel free to contact:
Jennifer Davies
Haematology Department
Royal Devon and Exeter NHS Foundation Trust
Barrack Road
Exeter
EX2 5DW
01392 402959
Jeni.davies@rdeft.nhs.uk

Chairman: James Brent **Chief Executive:** Angela Pedder

10.2 Appendix 6: Consent form signed by participants in the pilot study

Certificate of Consent

Title of study:	Antigen typing and matching of blood for chronically transfused patients
Name of Principal Investigator:	Jennifer Davies
Centre/Site number:	Royal Devon & Exeter NHS Foundation Trust
Study number:	
REC approval number:	
Participant ID:	

PLEASE INITIAL THE BOXES IF YOU AGREE WITH EACH SECTION:

1. I have read the information sheet dated………………. for the above study and have been given a copy to keep. I have had the opportunity to consider the information, ask questions and have had these answered satisfactorily. ☐
2. I understand that my participation is voluntary and that I am free to withdraw at any time without giving any reason, without my medical care or legal rights being affected. ☐
3. I understand that relevant sections of my medical notes and data collected during the study may be looked at by individuals from the Research Team only, from regulatory authorities or from the NHS Trust, where it is relevant to my taking part in this research. I give permission for these individuals to have access to my records. I understand that the information will be kept confidential. ☐
4. I understand that an extra blood sample will be taken in addition to those required for my standard care. ☐
5. I understand that my Doctor may be informed of my participation and also if any of the results of tests done as part of the research are important for my health. ☐
6. I understand that I will not benefit financially if this research leads to the development of a new treatment or test. ☐
7. I know how to contact the research team if I need to. ☐
8. I agree to participate in this study ☐

________________	________________	________________
Name of Patient	Date	Signature
________________	________________	________________
Name of Person	Date	Signature taking consent

When completed: 1 for participant; 1 for researcher site file; 1 (original) to be kept in medical notes.

09.05.12 Version 1