Influence of surrogate L chain on D_HJ_Hreading frame 2 suppression in mouse precursor B cells

Dirk Haasner, Antonius Rolink, and Fritz Melchers

Basel Institute for Immunology, Grenzacherstrasse 487, 4005 Basel, Switzerland

Key words: D_HJ_H rearrangement, reading frame, surrogate L chain

Abstract

 $D_{\mu}J_{\mu}$ rearrangements start in progenitor and precursor B cells and occur in three reading frames (rf). A strong bias for rf I has been noticed in murine and chicken antibodies, while the representation of rf II has been found suppressed both in peripheral as well as in precursor B cells. H chain gene loci D_HJ_H rearranged in rf II are potentially capable of expressing a truncated D_HJ_HC, protein on the cell surface. Mice incapable of expressing this protein on the surface have previously been shown to have all reading frames represented in near equal frequency, suggesting that membrane-bound D_HJ_HC_z protein is involved in the suppression of rf II. In this paper we show that suppression of rf II is not yet established in c-k/t+ CD43+ IL-7/stromal cell-reactive pre-B I cells of fetal liver at day 15 of gestation, but becomes established when such precursor cell populations are expanded in vitro on stromal cells in the presence of IL-7. H chain gene loci using the D₀₅₂ segment for rearrangements (which contains a stop codon in rf II, thus being unable to make D_HJ_HC_a protein) do not show rf II suppression under these conditions. The same type of fetal liver-derived pre B-I cells from λ 5 deficient mice also do not show rf II suppression after in vitro expansion. Bone marrow-derived pre B-I cells from normal mice assayed ex vivo and expanded in vivo show rf II suppression, while the corresponding pre-B I cells from λ 5T mice do not. Collectively these experiments suggest that surrogate L chain is involved in rf II suppression. This may happen by inhibition of proliferation of pre-B cells expressing a complex of D_HJ_HC₂ protein and surrogate L chain.

Introduction

The Ig heavy (H) chain gene locus on chromosome 12 of the mouse consists of probably >100 V_H gene segments, 15 D_H gene segments, and four J_H gene segments (1-3). Of the 15 D_H segments, two are D_{FL} segments (D_{FL161} and D_{FL162}), 12 are D_{SP} segments (D_{SP21} - DSP_{SP211} plus D_{SP2X}), and one is a D_{OS2} segment.

During differentiation of progenitors (pro-B cells) to precursors of the B lineage pathway (pre-B I cells; for nomenclature see 4), D_H segments are first rearranged to J_H segments (5). The intervening sequences between the rearranged D_H and J_H are frequently deleted as circular DNA. As long as D_H segments at the 5' side and J_H segements at the 3' side remain in the rearranged H chain gene locus, secondary rearrangements are possible. Such secondary $D_H J_H$ rearrangements were shown by studies of circular excision products in which pre-existing $D_H J_H$ joints were found (6). Secondary $D_H J_H$ rearrangements have also been implicated from analyses of $D_H J_H$ joints in clones of pro- and pre-B I cells of fetal liver and bone marrow early in development (7). D_HJ_H rearrangements can occur in three reading frames (rf) (8,9). The D_H segments carry promoter-like elements upstream of the coding sequences and an ATG start codon (at position – 63 for all D_{SP} segments, – 108 for D_{RL} segments, and – 120 for the D_{OS2} segment) which is 'in frame' with J_H when the D_HJ_H rearragement occurred in rf II. The protein product of such a rf II rearranged locus, a truncated H chain consisting of $D_{H_{\star}}J_{H_{\star}}$ and C_{μ} , has been detected in one cell line (10). Since the D_{OS2} segment carries a stop codon 48 nucleotides after the start, only D_{SP} and $D_{R_{\star}}$, but not D_{OS2} -containing D_HJ_H rearranged H chain loci can express the rf II rearranged locus as a truncated μ H chain.

Pre-B cells express the proteins $\lambda 5$ and V_{pre-B} , which can be found on the surface as a surrogate light (L) chain (11,12), reviewed in (13). One Abelson virus-transformed cell line has been found to express the truncated $D_{H}J_{H}C_{\mu}$ protein together with surrogate L chain on the surface (14).

 $D_H J_H$ joints in rf I are over-represented. Short stretches of sequence homology in the D_H and J_H segments might help to

Correspondence to: D Haasner

Transmitting editor: O Mäkelä

align the recombining DNA strands and this is likely to contribute to the rf I over-representation (3,8,9,15-17). When D-J recombination reactions are measured with extrachromosomal substrates transfected into murine pre-B cell lines *in vitro*, i.e. when D_HJ_H rearrangements can occur without cellular selection, a rearrangement using a four nucleotide overlap (as in D_HJ_H rf I) occurs at 55% (18). A similar preference for rf I rearrangements is observed in pre-B cells from fetal liver which do not express high levels of the enzyme terminal deoxynucleotidyl transferase (TdT) (19,20), and, therefore, do most often not insert non-templated (N) nucleotides into the D_HJ_H joints (7,9,15,16,21,22). The insertion of N nucleotides appears to correlate with the level of TdT expression (23,24) which is high in bone marrow-derived pre-B cells. N-region insertion reduces the preference for overlap-mediated joints (18). A preference for rf I has also been found in chicken (25).

A different mechanism, apparently independent of TdT expression, is the insertion of so called P nucleotides, which consist of short palindromic (P) sequences specific to the joining ends of the gene segments (26). P nucleotides are present at the coding joint when exonuclease activity is low (16) and have been frequently observed in sequences derived from fetal liver (9,15,16,22).

While the preference for $D_{H}J_{H}$ joints in rf I appears to be the consequence of a molecular selection of DNA strands during rearrangement, the suppression of rf II is thought to arise through cellular counterselection against those pre-B cells which expess the truncated $D_{H}J_{H}C_{\mu}$ protein on their surface (4,27,28). Further evidence comes from μ MT mice which can neither express $D_{H}J_{H}C_{\mu}$ protein nor μ H chains on their surface due to disruption of the transmembrane portion-encoding exon. In the non-functional, targeted alleles of splenic B cells of heterozygous μ MT mice, rf II $D_{H}J_{H}$ joints are normally represented and not suppressed (27).

The surrogate L chain can form a disulfide-bonded complex with $D_{H}J_{H}C_{\mu}$ protein as well as with μ H chains (14, 29). Membrane deposition on pre-B cells of $D_{H}J_{H}C_{\mu}$ protein and μ H chains may well be dependent on this association with surrogate L chain, just as membrane deposition of IgM on mature B cells is dependent on the association of μ H chains with normal L chains. If this were so, then pre-B cells of mice with a defective λ 5 gene (λ 5T mice; (30)) should be unable to deposit $D_{H}J_{H}C_{\mu}$ proteins in membranes, which would also abolish the suppression of pre-B cells with H chain loci $D_{H}J_{H}$ rearranged in rf II.

In this paper we analyze the structures of D_HJ_H joints in pre-B cells obtained from fetal liver and bone marrow of normal as well as λ5T mice to determine their rf distribution. B220- c-kitow pro-B cells and B220+ c-kit+ CD43+ pre-B I cells are clonable ex vivo with high efficiency and proliferate for long periods of time in vitro on stromal cells in the presence of IL-7 (7,31). Although a defective λ5 gene leads to the depletion of later stages of B cell development (pre-B II cells, immature B cells) and to a delayed appearance of slg⁺ cells in the periphery (30), the defect does not impair the generation of normal numbers of pro-B and pre-B I cells (32). In this paper we, therefore, also analyze the structures of D_HJ_H joints of pre-B I cell lines and clones obtained from fetal liver and bone marrow of normal and λ5T mice. All Dsp segments and one of the two D_{B_1} segments (i.e. $D_{B_16_1}$), but not $D_{B_16_2}$ and D_{052} are detected by a polymerase chain reaction (PCR) with an oligonucleotide primer which hybridizes in the 5' regions of all these D segments. A second oligonucleotide primer is employed to detect D₀₅₂₋J_H joints.

Collectively our results present evidence for the involvement of

surrogate L chain in the selection of rfs of $D_H J_H$ joints in pre-B cells, which appears to function by a suppression of proliferation of pre-B I cells with rf II $D_H J_H$ rearranged H chain gene loci.

Methods

Mice

(C57BL/6 (×) DBA/2)F₁ (BDF₁) mice were obtained from Institut für Biologisch-Medizinische Forschung AG (Füllinsdorf, Switzerland). Homozygous λ 5T mice (30) were bred at the Institute's animal facilities. Cells for FACS sorting and pre-B cell culture were prepared from different lymphopoietic organs at different developmental stages (fetal liver, newborn and adult liver, spleen, and bone marrow) as described (7).

FACS staining and sort

Cell staining procedures and antibodies employed in the staining reaction have been described previously (7,31). Cells expressing B220, c-kit, S7(CD43), BP1, or combinations thereof were sorted using the FACS-Star Plus (Beckton-Dickinson, Mountain View, CA).

Cell culture

Cell suspensions were plated under limiting dilution conditions on a feeder layer of 3300 rad irradiated stromal cells (PA-6 cells, (37)) in serum free medium containing murine rIL-7 at a concentration of 100 – 200 U/ml. The culture conditions for the growth of these non-transformed pre-B cells have been described previously (31). Pre-B cell clones were expanded to ~ 5×10^6 cells before they were harvested for the preparation of DNA.

DNA Preparation

Cells (5×10^5) were harvested, washed in PBS, and lysed by boiling for 5' in 500 μ l PBS. Proteinase K (Boehringer, Mannheim, Germany; 20 μ g/ml final) was added, the lysate digested at 55°C for 3 h and boiled again to destroy Proteinase K activity.

The solution was extracted once with phenol:chloroform:isoamylalcohol (25:24:1) and once with chloroform:isoamylalcohol (24:1). DNA was precipitated with 1 volume isopropanol/0.1 volume NaAcetate, pH 5.2, centrifuged, the pellet washed with 1 volume 70% Ethanol, and air dried. The DNA pellet was dissolved in 500 μ l 10 mM Tris, pH 8.3. Aliquots of 5 μ l of this preparation (containing the DNA of 5000 cells) were subsequently used for PCR amplification.

PCR Amplification and Cloning

The PCR conditions and oligonucleotide primers to amplify $D_H - J_H$ rearrangements have been previously described by Gu *et al.* (27). The upstream primer binds 5' of all D_{SP} segments and $D_{R_{-16.1}}$. The downstream primer binds 3' of J_H4 , thereby generating PCR products of different lengths according to the J_H segment used for rearrangement (7). A Perkin-Elmer Cetus DNA Thermal Cycler and Cetus Taq Polymerase (Perkin-Elmer Cetus, Norwalk, CT) were used for PCR amplification. $D_H - J_H1$ rearrangements generate products of 1700 bp, $D_H - J_H2$ 1450 bp, $D_H - J_H3$ 1100 bp, and $D_H - J_H4$ 600 bp respectively.

A different 5' primer was used to amplify D_{OS2} rearrangements in conjunction with the 3' J_H primer. The primer sequence is 5'-GCC TCA GAA TTC CTG TGG TCT CTG ACT GGT-3'; it contains an *Eco*RI cloning site. PCR product lengths are 2200 bp for germline, 1500 bp for $D_Q - J_H 1$, 1170 bp for $D_Q - J_H 2$, 790 bp for $D_Q - J_H 3$, and 230 bp for $D_Q - J_H 4$ respectively.

The PCR products and the M13mp19 vector (New England Biolabs, Beverly, MA) were digested with two different restriction enzymes (New England Biolabs) according to the enzyme manufacturer's conditions (forced cloning), and size fractionated on a low melting point agarose gel (Ultra Pure LMP Agarose; BRL, Bethesda, MD). Bands of interest and the linearized vector were cut out under UV illumination, the agarose remelted, ligation reagents and T4 DNA Ligase (Pharmacia, Uppsala, Sweden) mixed into the agarose, and ligation carried out directly (39). Ligated vector was heat shock transfected into competent Escherichia coli JM 105 bacteria and plated out on YT plates. Recombinant plaques were identified by plaque hybridization with a radioactive J_H4 oligonucleotide probe (AGGAACCTCAGTCACCGGATCCGT) (all procedures according to (39)). Single-stranded M13 DNA was sequenced using a Sequenase 2.0 sequencing kit (United States Biochemicals, Cleveland, OH) and an IBI sequencing gel apparatus (Eastman Kodak, Rochester, NY).

Results

Structures of $D_{\mu}J_{\mu}$ joints in FACS-sorted pre-B cells from fetal liver and bone marrow of normal and λ 5T mice

Cell suspensions from fetal liver or bone marrow of normal BDF₁ and surrogate L chain deficient λ 5T mice were sorted for B220⁺ c-*kit*⁺ or B220⁺ CD43⁺ pre-B cells as described (7), and DNA was prepared from these cells for D_HJ_H joint sequencing. Table 1 shows 36 sequences of normal fetal liver cells (day 15, B220⁺ c*kit*⁺), 25 sequences of λ 5T fetal liver cells (day 13, B220⁺ c-*kit*⁺), 58 sequences of normal bone marrow cells (3 weeks of age, B220⁺ c-*kit*⁺ or S7⁺ BP1⁺) and 31 sequences of λ 5T bone marrow (14 weeks of age, B220⁺ c-*kit*⁺). Pre-B cells from fetal liver of normal (day 15) as well as λ 5T (day 13) mice only rarely displayed N or P nucleotides (Table 1a and b), whereas bone marrow-derived pre-B cells (normal: w3, λ 5T w14) displayed high junctional diversity due to added nucleotides (Table 1c and d). Table 3 summarizes the sequencing data and was used to generate Fig. 1(a and b).

In the fetal liver of both normal and λ 5T mice, most D_HJ_H joints were in rf I (60 – 67%) (Fig. 1a, 1 + 2). This is presumed to be the consequence of a preferred alignment of short stretches of sequence homology in the D_H and J_H segments. In these cells, D_HJ_H joints in rf II and rf III were present in approximately equal amounts (18 – 23%). This distribution of frequencies of rf I versus rf II versus rf III D_HJ_H joints closely resembles the distribution found in a system where recombinants of the D_HJ_H type were generated on extrachromosomal substrates transfected into murine pre-B cells of fetal liver origin *in vitro*, i.e. without selection *in vivo* (18). In addition, the results in Fig. 1(a) also show that rf II is not suppressed in fetal liver pre-B cells *ex vivo*. It suggests that no selection of H chain alleles and/or cells carrying those alleles has taken place at that early stage of B cell development.

In bone marrow of normal and of λ 5T mice, rf I and rf III D_HJ_H joints are present at similar frequencies, i.e. rf I is not overrepresented, and most of these joints carry N region sequences inserted by TdT. Hence this result agrees with Gerstein and Lieber's findings (18) with extrachromosomal rearrangement substrates that the constraint to align short homologous sequences of D_H and J_H is diminished by TdT and N-region insertion. Although D_{OS2} – J_H

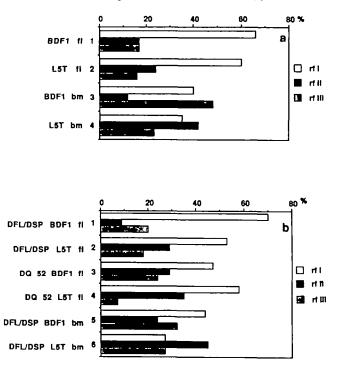


Fig. 1. Presence or absence of rf II suppression in different populations of pre-B cells from normal and λ 5T mice. The figure shows the rf usage in FACS-sorted pre-B cells (a) and cultured pre-B cells (b). Values are given as percent of total sequences analyzed. The numbers of total sequences are given in Table 2 Panel (a) includes D_HJ_Hrearrangements using D_{FL16.1} or all D_{SP} segments in cells of BDF1 fetal liver (1), λ 5T fetal liver (2), BDF₁ bone marrow (3), and λ 5T bone marrow (4). Panel (b) includes D_HJ_H rearrangements using D_{FL16.1} or all D_{SP} segments in cultured cells obtained from BDF₁ fetal liver (1), λ 5T fetal liver (2), BDF₁ bone marrow (5), and λ 5T bone marrow (6), and D_HJ_H rearrangements using the DQ52 segment in cultured cells obtained from BDF₁ fetal liver (3) and λ 5T fetal liver (4). Details for sequencing of D_HJ_H joints are given in Methods.

joints are not analyzed here, we expect that they show a similar pattern of rf usage (see Note added in proof).

Most important for the possible role of surrogate L chain in the rf selection process is the finding that rf II is represented in bone marrow cells of λ 5T mice in frequencies nearly equal to those for rf I and rf III, while it is suppressed in bone marrow cells of normal mice (*P*=0.003) (Fig. 1a, 3 + 4). These results indicate that the inability of pre B cells to express the surrogate L chain V_{pre-P}/ λ 5 abolishes the mechanism(s) which suppresses rf II representation in D_{I-J-H} joints.

Structures of $D_{\mu}J_{\mu}$ joints in pre-B cell lines and clones proliferating in vitro

Pre-B cells from fetal liver and bone marrow of normal and λ 5T mice were cloned by limiting dilution and expanded by proliferation on stromal cells in the presence of IL-7 to ~10⁶ cells (i.e. for at least 20 divisions) as described (31). DNA was prepared and D_HJ_H joints sequenced. Again, D_HJ_H joints of fetal liver-derived lines and clones only rarely contained P or N nucleotides while those of bone marrow frequently did (Table 2a – d). The rf 1 D_HJ_H joints were found to be strongly over-represented in all lines and clones except in D_{FL}/D_{SP} – J_H joints of bone marrow from normal and λ 5T mice (Fig. 1b, 5 + 6). While D_{Q52} – J_H joints in rf III were unexpectedly

24 Surrogate L chain in DJ rf 2 suppression

Table1 a-b: D-J sequences (DFL/DSP) of BDF1 and L5T/L5T sorted fetal liver preB cells

nte, origin	DF1 fetai fiver preB cells day 15 Desegnent	NP-seque	nce J-segment	D	reading J Irame N/P-I
1	CC TAC TAT AGT TAC TAT AGT TA CC TAC TAT AGT AAC TAC	c	GAC TAC TTT GAC TAC TG TTT GAC TAC TG		2 µ - 2 1 -
<u>N</u>	GAT GOT TAC TA		T GCT ATG GAC TAC TO	IG 5P2.9	4 1 -
11 12	TC TAC TAT OGT AAC T TC TAT GAT GGT T		TT GCT TAC TG TT GCT TAC TG	G SP2.1 G SP2.9	
	TC TAC TAT OGT AAC T		GG TTT GCT TAC TO	G 5P2.1	š i -
H 11	COT ACT ATA GTA AC CC TAC TAT AGT TAC G		C TGG TIT OCT TAC TG CT ATG GAC TAC TC TAT GCT ATG GAC TAC TG	G SP2.11	3 8 -
3	CC TAC TAT AGT TAC GAC CC TAC TAT AGT AAC TAC		TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG	G SP2.11	
1	TC TAT GAT GOT TAC		TTT GAC TAC TG	G SP2.0	2 1 -
2	CCT ACT ATA TC TAT GAT OGT TAC TAC		TOG TAC TTC GAT GTC TO TAC TAT GCT ATG GAC TAC TG	G 3P2.11/X G 3P2.9	
n i	TC TAC TAT GGT AAC TAC		10	G \$P2.5	2 .
2	TC TAC TAT GAT TAC GA CC TAC TAT AGT AAC TAC		T TAC TAT GCT ATG GAC TAC TG GCC TGG TTT GCT TAC TG	G SP2.X	3 1 -
14. 11	TC TAC TAT OGT AAC TAC TC TAC TAT GAT TAC G		TAC TIT GAC TAC TO CT TAC TO	G SP2.5	2 -
É.	TCT ATG ATG GTT ACT AC	G	TGG TTT GCT TAC TO	G 8P2.0	3 11 P+-
1 0	TC TAT GAT OGT TAC TAC T CTA CTA TGG <u>TAA</u> CTA C	G	OCC TOG TTT GCT TAC TO T TAC TAT GCT ATG GAC TAC TO		3 I - 4 11 P+
1	T CTA CTA TOG <u>TAA</u> CTA		TTT GCT TAC TG	G 8P2.5	3 11 -
2 J	T CTA <u>tiga</u> tigg tta cta c TC tac tat ggt aac ta	G	C TAC TO T GCT ATG GAC TAC TO		2 101 P+- 4 1 -
1	CC TAC TAT AGT AAC TAC		TAC TIT GAC TAC TO	G SP2.X	2 1 -
2	C CTA CTA <u>TAG TAA</u> CTA C T CTA <u>TGA</u> TGG TTA CTA C	GT AC	TT GCT TAC TG C TAC TTT GAC TAC TG		3 11 - 2 11 P+
M	TC TAC TA	01.40	C TG	G SP2.5	2 1 -
1	TCT ATG ATG GTT ACT AC TCT ACT ATG ATT ACG		C TOG TTT OCT TAC TO OCC TOG TTT OCT TAC TO	G SP2.9	
3	TCT ACT ATG GT	•	C TOG TIT GCT TAC TO	G 8P2.5	3 0 -
4	CC TAC TAT AGT AAC T TC TAC TAT GGT TAT GAC		TT GCT TAC TG GCT ATG GAC TAC TG	G 5P2X	3 1 -
2	T CTA <u>TGA</u> TGG TTA C		AT TAC TAT GCT ATG GAC TAC TO	ig sp2.0	4 m -
4	TC TAC TAT GGT AAC TAC TC TAC TAT GGT AAC TAC		TAC TAT OCT ATG GAC TAC TG TAT OCT ATG GAC TAC TG	G 5P2.5	4 1 1
	5T/L5T fetal liver pre8 cells day	13 (R220			reading
nae. origin 1	D-segment TC TAC TAT QGT AAC TAC	NP-eeouer		D 20.899 =	J trame N/P-e
1	OC TAC TAT AGT AAC TAC		TTT GAC TAC TG	KG SP2.X	2 1 -
2	T CTA CTA TOG TAA CTA C TC TAT GAT OGT TAC T		AC TAC TG TT GAC TAC TG	G 5P2.5 G 5P2.9	2 10 -
4	TCT ACT ATG ATT ACG AC	GT	TT GAC TAC TG AC TAC TTT GAC TAC TG	G 5P22	2 H P+
2	TCT ACT ATG GTA ACT TC TAC TAT GGT AAC TAC		TTT GCT TAC TO GCC TGG TTT GCT TAC TO	G 5P2.5	3 1 -
1	OC TAC TAT AGT AAC TA		T GCT ATG GAC TAC TO	ig sp2.x	4 1 -
2	TC TAC TAT GGT AAC TAC TCT ATG ATG GTT ACT AC	GA	TAT OCT ATG GAC TAC TG AC TAC TG	G SP2.0	4 I - 2 8 P+
3	TC TAC TAT GGT TAC TC TAC TAT GAT TAC		TIT GAC TAC TO TIT GAC TAC TO	G SP2.34	2 1 -
1	TC TAC TAT GAT TA		T GCT TAC TO T GCT TAC TO T GCT ATG GAC TAC TO	G 8P2.2	3 1 -
3	TC TAC TAT GGT AAC TA TC TAT GAT GGT TAC T		T OCT ATG GAC TAC TO TT OCT TAC TO	KI 5P2.1 IG 5P2.9	4 -
		-			
	TCT ACT ATG GTA ACT	т	AT TAC TAT OCT ATG GAC TAC TG	G 8P2.5	4 0 P+-
j	TC TAC TAT GAT TAC GAC	T	AT TAC TAT OCT ATG GAC TAC TG TAT OCT ATG GAC TAC TG TAC TAT OCT ATG GAC TAC TG	G SP2.2 G SP2.5	4 1 - 4 1 - 4 21 -
3 1 2	TC TAC TAT GAT TAC GAC T CTA CTA TOG TAA T CTA CTA TGA TTA OGA C	T G	AT TAC TAT OCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG T GCT ATG GAC TAC TG	IG 8P2.2 IG 8P2.5 IG 8P2.2	4 1 - 4 20 - 4 20 P+-
3 1 2 1	TC TAC TAT GAT TAC GAC T CTA CTA TGG TAA T CTA CTA TGA TTA CGA C TCT ATG ATG GTT AC T CTA CTA TGG		AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG T GCT ATB GAC TAC TG C TGG TTT GCT TAC TG TTT GAC TAC TG	IG 8P2.2 IG 8P2.5 IG 8P2.2 IG 8P2.9 IG 8P2.5	4 Î -
3 1 2 1 2 2	TC TAC TAT GAT TAC GAC T CTA CTA TGG TAA T CTA CTA TGA TTA CGA C TCT ATG ATG GTT AC T CTA CTA TGG		AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG T GCT ATB GAC TAC TG C TGG TTT GAC TAC TG TTT GAC TAC TG TAC TAC TG	IG 8P2.2 IG 8P2.5 IG 8P2.9 IG 8P2.9 IG 8P2.5 IG 8P2.5	4 1 - 4 20 - 4 10 P+- 3 11 - 2 12 - 3 1 -
3 1 2 2 2 3 2 3	TC TAC TAT GAT TAC GAC T CTA CTA TGA TAA T CTA CTA TGA TAA T CTA CTA TGA TA GAA C TCTA CTA TGA TTA CGA C TCTA CTA TGA TTAC T CTA CTA TGAT TAC TC TAC TAT GAT TAC G TCT ACT ATG GAT ACG AC TC TAC TAT GAT TAC GAC	G	AT TAC TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TGCT ATG GAC TAC TG C TGG TTT GAC TAC TG TTT GCT TAC TG C TGG TTT GCT TAC TG C TGG TTT GCT TAC TG TAT GCT ATG GAC TAC TG	ig sp2.2 (g sp2.5 (g sp2.5 (g sp2.5 (g sp2.5 (g sp2.2 (g sp2.2 (g sp2.2) (g sp2.2) (g sp2.2) (g sp2.2)	4 1 - 4 00 - 4 00 - 3 0 - 2 14 - 3 1 - 3 1 - 3 1 - 4 1 -
	TC TAC TAT GAT TAC GAC T CTA CTA TGG TAA T CTA CTA TGG TAA T CTA CTA TGA TTA CGA C TCT ATG ATG GTT AC T CTA CTA TGG T CTAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TATG GTT ACG AC	ु <u>२) of BD</u>	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TGCT ATB GAC TAC TG TGGT TT GCT TAC TG TTT GCT TAC TG TTT GCT TAC TG TAC TAC GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG	G 8922 G 8925 G 8925 G 8929 G 8929 G 8929 G 8922 G 8922 G 8922 G 8922 G 8922 G 8922	4 1 - 4 00 - 4 00 - 3 0 - 2 14 - 3 1 - 3 1 - 3 1 - 4 1 -
5 1 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	TC TAC TAT GAT TAC GAC T CTA CTAT TGG TAA T GTA CTA TGG TAA T GTA CTA TGG TTA GA TCTA TGA TGG TTA CA TCTA CTA TGG TTAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GAC TC TAC TAT GAT TAC GAC I: D-J sequences (DFL/DS D-sequences (DFL/DS D-sequences CBFL/DS D-sequences CBFL/DS D-sequences CBFL/DS D-sequences CBFL/DS D-sequences CBFL/DS TTAT ACT ACG ATG GTA GCT A	G <u>P) of BD1</u> <u>220+/c-kit+</u> NP-sequent GA	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TATB GAC TAC TG TGCT ATB GAC TAC TG C TGG TTT GAC TAC TG TTT GCT TAC TG TTT GCT TAC TG C TGG TTT GCT TAC TG C TGG TTT GCT TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG F1 and L5T/L5T sorted bo markens or S7+/BP1+ marken Jacqueri	G 872.2 G 872.5 G 872.5 G 872.5 G 872.5 G 872.2 G 872.2 G 872.2 G 872.2 He marroy He marroy L D D A R.16.1	4 1 4 10 P+ 3 1 - 2 14 - 3 1 - 3 1 - 3 1 - 4 3 - 4 1 - wpreBcells meding J trans NP-8 4 8 N+
i 2 2 2 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3	TC TAC TAT GAT TAC GAC T GTA CTAT GAT AA T GTA CTA TGA TGA CA TCT ATGA TA GTA AC TCT ATGA TGA GTA AC T CTA CTA TGA TGA TC TAC TAT GAT AC TC TAC TAT GAT ACG TC TAC TAT GAT ACG TC TAC TAT GAT ACG TC TAC TAT GAT ACG TC TAC TAT GAT ACG D-signert TTT ATT ACT ACG ATG GTA GCT A	G P) of BD1 220+/c-kit+ NP sequen	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TGC ATB GAC TAC TG C TGG TTT GCT TAC TG TTT GCT TAC TG TTT GCT TAC TG CC TGG TTT GCT TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG CAT TAC TAT GCT ATG GAC TAC TG AT TAC TAT GCT ATG GAC TAC TG	G SP2.2 G SP2.5 G SP2.5 G SP2.5 G SP2.5 G SP2.5 G SP2.5 G SP2.2 G SP2.2 G SP2.2 G SP2.2 G SP2.2 G SP2.2 D D Q R.16.1 G SP2.16 Q SP2.16	4 I - 4 II - 4 II - 3 II - 3 I - 3 I - 3 I - 3 I - 4 I - w preB cells making 1 tame NP-6 4 I N+ 4 I N+ 4 I N+ 4 I N+
s 1 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	TC TAC TAT GAT TAC GAC T CTA CTAT TGAT TAC GAA T GTA CTA TGA TGA TA GGA C TCTA GTA TGA TGA TTA CGA C TCTA GTA TGAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC G TC TAC TAT GAT TAC GAC TC TAC TAT GAT TAC GAC I: D-J SOGUENCESS (DFL/DS) D=1 bone marrow preB cells (B) D-soguent TTT ATT ACT ACG ATG GTA GCT A TC TAC TAT GGT AC TAC TC TAC TAT GGT AC TAC	G P) of BD 220+/c-kit+ NF equen GA T GA T GA T	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TGCT ATB GAC TAC TG TGCT ATB GAC TAC TG TT GCT TAC TG TT GCT TAC TG TAC TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG	G SP2.2 G SP2.5 G SP2.5 G SP2.5 G SP2.2 G SP2.2 G SP2.2 G SP2.2 G SP2.2 G SP2.2 D SP2.3 G SP2.4 G SP2.2 D G G SP2.16 G SP2.16 G SP2.19	4 11 4 12 4 12 14 15 14 15 15 15 15 15 15 15 15 15 15
s 1 2 2 2 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	TC TAC TAT GAT TAC GAC T CTA CTA TGA TAG GTA T GTA CTA TGA TGA TTA CGA C TCTA TGA TGA TGA TTA CGA TC TAC TA TGA TGGT TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GAC TC TAC TAT GAT TAC GAC I: D-J sequences (DFL/DS D-segment TTT ATT ACT ACG ATG GTA GCT A TC TAC TAT GGT AC TAC TC TAC TAT GGT AC TAC TC TAC TAT GGT AC TAC	G 201-/C-kit+ NP-sequer GGA T	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TGCT ATB GAC TAC TG TGCT ATB GAC TAC TG TT GCT TAC TG TT GCT TAC TG TT GCT TAC TG TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG CT GG TAC TTC GAT GTC TG GAT TAC TAT GCT ATG GAC TAC TG CT GG TAC TTC GAT GTC TG GAT TAC TAT GCT ATG GAC TAC TG CT GAT GAC TAC TG CT GAT GTC TTC GAT GTC TG GAC TAC TTC GAT GTC TG	G 872.2 G 872.5 G 872.5 G 872.5 G 872.5 G 872.5 G 872.5 G 872.2 G 872.2 G 872.2 G 872.1 G 872.16 G 872.1	4 I - 4 II - 4 II - 3 II - 3 I - 3 I - 3 I - 3 I - 4 I - w preB cells making 1 tame NP-6 4 I N+ 4 I N+ 4 I N+ 4 I N+
ble 1 C-C	TC TAC TAT GAT TAC GAC T CTA CTA TGA TAG GTA T GTA CTA TGA TGA TTA CGA C TCTA TGA TGA TGA C TCTA TGA TGGT AC TC TAC TAT GGT TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GAC I: D-J sequences (DFL/DS D-segment TTT ATT ACT ACG ATG GTA GCT A TC TAC TAT GGT AC TAC TC TAC TAT GGT AC TAC TC TAC TAT GGT AC TAC TC TAT GAT GGT AC CTAC TC TAC TA TGG IAA CTA C TC TAC TA TGG IAA CTA C	G P) of BDI 220+/c-kit+ NF + squar GA GA GA C C C C C C C C C	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TGGT ATB GAC TAC TG TGGT TT GCT TAC TG TTGGT TTG GAC TAC TG TAC TTG TAC TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG GAT TAC TAT GCT ATB GAC TAC TG GAC TAC TG GAC TAC TG TT GAAC TAC TG TAT GCT ATB GAC TAC TG GAC TAC TG GAC TAC TG TT GAAC TAC TG TT GAAC TAC TG	KG 872.2 KG 872.5 KG 872.5 KG 872.5 KG 872.5 KG 872.5 KG 872.5 KG 872.5 KG 872.5 KG 872.5 KG 872.1 KG 872	4 1 4 13 4 13 7 1 7 1 7 1 7 1 7 1 7 1 7 1 7 1
ble 1 c-d b sorted B(sorted B(sort	TC TAC TAT GAT TAC GAC T CTA CTA TGA TAG TAA T GTA CTA TGA TGA TTA CGA C TCTA TGA TGA TGA TTA CGA C TCTA TGA TGA TGA TAC TC TAC TA TGA TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GAC CTA CTA TGA TTAC GAC CTA CTA TGA TTAC GAC CTA CTA TGA TAC GAC CTA CTA TGA TAC GAC D-J SOCRUCCOS (DFL/DS) D-STORMENT TTT ATT ACT ACG ATG GTA GCT A TC TAC TAT GGT TAC TAC TC TAC TAT GGT TAC TAC TC TAC TAT GGT TAC TAC TC TAC TAT GG TAC CTA C TCTA CTA TGG TAA CTA C TCTA CTA TGG TGA TCA C TCTA CTA TGG TGA CTA C TCTA CTA TGG TGA CTA C TCTA CTA TGG TGA CTA C	G P) of BDJ 220-/C-kit+ NF-sequent GA GA GA GA GA GA GA GA GA GA	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TGCT ATB GAC TAC TG TGCT ATB GAC TAC TG TT GCT TAC TG TT GCT TAC TG TT GCT TAC TG TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG GAT TAC TAT GCT ATB GAC TAC TG CT GB TAC TTC GAT GTC TG GAT TAC TAT GCT ATB GAC TAC TG CT GB TAC TTC GAT GTC TG GAT TAC TAT GCT ATB GAC TAC TG CT GAT GAC TAC TG CT GAT GTC TTC GAT GTC TG GAC TAC TTC GAT GTC TG	KG 872.2 KG 872.5 KG 872	4 I 4 B 4 B 4 B 4 B 4 B 4 B 4 B 4 B
ble 1 c-ci ble 1 c-ci	TC TAC TAT GAT TAC GAC T CTA CTAT TGA TAA T GTA CTA TGA TGA TG TA TGA TGA TGA TG TAT TA TGA TGA TC TAC TA TGA TC TAC TAT GAT TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GAT GTA CTA TGA TAC GAT GTA CTA TGA CTAC TAT GAT CTAC TAT GAT CTAC TAT GAT CTAC TAT GAT TC TAC TAT GAT TC TAC TAT GAT CTAC TAT GAT TC TAC TAT GAT CTAC TAT CAT CTAC CTAC TAT CAT CTAC CTAC TAT CAT CTAC CTAC TAT CAT CTAC CT	G P) of BDJ 220+/C+kit+ NP sequent GA GAT C GAT C CA GAT C CA CA CA CA CA CA CA CA CA	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TATB GAC TAC TG TGCT ATB GAC TAC TG TGCT ATB GAC TAC TG TT GCT TAC TG TTT GCT TAC TG TTT GCT TAC TG TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG GAT TAC TAT GCT ATB GAC TAC TG GAT TAC TAT GCT ATB GAC TAC TG GAT TAC TAT GCT ATB GAC TAC TG CT ATB GAC TAC TG GAT TAC TAT GCT ATB GAC TAC TG CT ATB GAC TAC TG GAT TAC TAT GCT ATB GAC TAC TG GAT TAC TAT GCT ATB GAC TAC TG CT GG TAC TTC GAT GTC TG GAC TAC TG GAC TAC TG CT GG TAC TTC GAT GTC TG GAC TAC TG GAC TAC TG CT GG TAC TTC GAT GTC TG GAC TAC TG CT GG TAC TTC GAT GTC TG GAC TAC TG CT GG TAC TTC GAT GTC TG GAC TAC TG CT GG TAC GTT GCT TAC TG CT GCT TAC GTT GCT TAC TG CT GCT TAC GTT GCT TAC TG	KG 872.2 KG 872.5 KG 872.5 KG 872.5 KG 872.5 KG 872.5 KG 872.5 KG 872.2 KG 872.2 KG 872.3 KG 872.3 KG 872.1 G 872.2 G 872.2	4 I - 4 II - 4 II - 3 I - 3 I - 3 I - 3 I - 3 I - 4 I - 2 III - 3 I - 3 I - 3 I - 3 I - 4 I - 2 III - 3 I - 3 I - 3 I - 3 I - 4 I
ble 1 c-ci ble 1 c-ci	TC TAC TAT GAT TAC GAC T CTA CTAT TGA TAA T GTA CTA TGA TAG TG A CTA TGA TAG AT CTA CTA TGA TGA TTA CGA TC TAC TA TGA TC TAC TA TGAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC CT ACT ATTG GAT ACGA CT ACT ATG GAT ACGA CT TAC TAT GAT TAC TT ATT ACT ACGA ATG GTA GCT A TC TAC TAT GGT TAC TC TAC TAT GGT CTA C TC TAC TAT GGT C TC TAC TAT C TC	G 20) of BDJ 220+C-kit+ NF-sequent CA CA CA CA CA CA CA CA CA CA	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TATB GAC TAC TG TGCT ATB GAC TAC TG TGCT ATB GAC TAC TG TT GCT TAC TG TTT GCT TAC TG TTT GCT TAC TG TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG GAT TAC TAT GCT ATB GAC TAC TG GAC TAC GT TT GCT TAC TG GAC TAC TG TAC TG TAC TAC TG GAC TAC TG TAC TG TAC TG GAC TAC TG TT GCT TAC TG GAC TAC TG TT GCT TAC TG GAC TAC TG TAC TAC TG GAC TAC TG TT GCT TAC TG GAC TAC TAT GCT ATB GAC TAC TG GAC TAC TG TT GCT TAC TG GAC TAC TG TT GCT TAC TG GAC TAC TAC GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC GT TT GCT TAC TG GAC TAC GAC TAC TG	KG 872.2 KG 872.5 KG 872.5 KG 872.5 KG 872.5 KG 872.5 KG 872.2 KG 872.2 KG 872.2 KG 872.2 KG 872.3 KG 872.1 G 872.1 G 872.1 G 872.1 G 872.1 G 872.1 G 872.1 G 872.1 G 872.1 G 872.3 G 872.2 G 872.2	4 I
ble 1 C-C sorted B/ sorted B/ sorted S sorted sorte	TC TAC TAT GAT TAC GAC T CTA CTAT TGA TAC GAA T GTA CTA TGA TGA TA TCTA TA TGA TGA TA TCTA CTA TGA TGA TAC TC TAC TAT TGA TC TAC TAT GAT AC TC TAC TAT GAT AC TC TAC TAT GAT ACG TC TAC TAT GAT ACG TC TAC TAT GAT ACG CT ACT ATGA TAC TC TAC TAT GAT ACG D-segment TTT ATT ACT ACG ATG GTA GCT A TC TAC TAT GGT ACC TAC TC TAC TA TGG TAC TAC TC TAC TA TGG TACTAC TC TAC TA TGG TACTAC TC TAC TA TGG TACTAC TC TACTA TGG TACTAC	G P) of BDI P20+/c-kit+ MF-sequent GA GA GA CCCCC CCCCCC	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TGCT ATB GAC TAC TG TGCT ATB GAC TAC TG TGCT ATB GAC TAC TG TTGCT TAC TG TTGCT TAC TG TTGCT TAC TG TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG GAT TAC TAT GCT ATB GAC TAC TG GCT TGG TAC TTC GAT GTC TG GCT TGG TAC TTC GAT GTC TG GCT TAC TAT GCT ATG GAC TAC TG GCT TAC TAC TAC TAC TAC TAC TAC TAC TAC T	KG 872.2 KG 872.5 KG 872.5 KG 872.5 KG 872.5 KG 872.5 KG 872.5 KG 872.7 KG 872	4 1 - 4 13 - 4 13 - 4 13 - 2 13 - 2 13 - 3 1 - 3 1 - 3 1 - 4 1 - vpreBcells vpreBcells vpreBcells vpreBcells 4 1 - vpreBcells 4 1 - v 4 1
	TC TAC TAT GAT TAC GAC T CTA CTA TGA TAG AA T GTA CTA TGA TGA TGA CA T CTA TA TGA TGA TTA CGA C TC TATA TA TGG TTA CA TC TAC TAT GGA TC TAC TAT GAT AC TC TAC TAT GAT ACGAC TC TAC TAT GAT ACGAC TC TAC TAT GAT ACGAC 1: D-J sequences (DFL/DS) D-squent 1: TATT ACT ACG ATG GTA GCT A TC TAC TAT GGT AC TAC TC TAC TAT GGT AGC TA TC TAC TAT GGT AGC TAC TC TAC TAT GGT AGC TAC	G P) of BDI 220+/c-kit+ MF-sequer GA GA GA GA CCC CCC GAA CCC CCC	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TGCT ATB GAC TAC TG TGCT ATB GAC TAC TG TT GCT TAC TG TT GCT TAC TG TAC TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG GAT TAC TAT GCT TAC TG GAT TAC TAT GCT ATG GAC TAC TG GCT TGG TAC TG GAC TAC TG GCT TGG TAC TG GAC TAC TG GCT TAC TAT GCT ATG GAC TAC TG GCT TAC TAT GCT TAC TG GCT TAC TAC TAC TG GCT TAC TAC TAC TG GCT TAC TAC TG GCT TAC TAC TG	G SP2.2 G SP2.2 G SP2.5 G SP2.5 G SP2.5 G SP2.5 G SP2.2 G SP2.5 G SP2.2 G SP2.2 G SP2.2 G SP2.1 G SP2.16 G SP2.17 G SP2.2 G SP2.2 <td< td=""><td>4 1</td></td<>	4 1
	TC TAC TAT GAT TAC GAC TC TAC TAT TGA TAC TC TAC TA TGA TGA TC TAC TA TGA TGA TC TAC TA TGA TGA TC TAC TA TGA TGA TC TAC TAT GAT TC TAC TAT GAT TC TAC TAT GAT TC TAC TAT GAT TC TAC TAT GAT TAC TAC TC TAC TAT GAT TAC TAC TC TAC TAT GAT TC TAC TAT GAT TC TAC TAT GAT TC TAC TAT TGA TC TAC TAT TGA TC TAC TAT TGA TC TAC TAT GAT TC TAC TAT GAT TC TAC TAT GAT TC TAC TAT GAT TC TAC TAT TGA TC TAC TAT GAT TC TAC TAT TGAT TC TAC	G P) of BD 220+4-C+kit+ MP + sequent GA GA C C C C C C C C C C C C C	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TGCT ATG GAC TAC TG TGC TTG GAC TAC TG TTT GCT TAC TG TTT GCT TAC TG TTT GCT TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TG TG GAC TAC TG GAC TAC TG GAC TAC TG GCT GG TAC TG GAC TAC TG GCT GG TAC TAT GCT ATG GAC TAC TG GCT ATG	G SP2.2 G SP2.2 G SP2.5 G SP2.5 G SP2.5 G SP2.2 G SP2.2 G SP2.2 G SP2.2 G SP2.2 G SP2.2 G SP2.16 G SP2.16 G SP2.2 G SP2.2 G SP2.2 G SP2.16 G SP2.2 G	4 I
ble 1 C-C sorted Bi s. orbin 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	TC TAC TAT GAT TAC GAC TC TAC TAT TGA TAC ACA TC TA TAT TGA TAG TC TAC TA TGA TGA TTA CGA C TC TAT ATGA TGG TTA CC TC TAC TAT GGT TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GAC TC TAC TAT GAT TAC GAC TC TAC TAT GAT TAC GAC CT AC TAT GAT TAC GAC TC TAC TAT GAT ACT AC TC TAC TAT GGT TAC TAC TC TAC TAT GGT TAC TAC TC TAC TAT GGT ACT AC TC TAC TAT GGT ACC TAC TC TAC TAT GGT ACT AC TA	G P) of BD 220+c-kit+ MP-sequent GA GA CC CC CC CA CA CA CA CA CA C	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TGCT ATB GAC TAC TG TGCT ATB GAC TAC TG TTT GCT TAC TG TTT GCT TAC TG TTT GCT TAC TG TAC TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC TG GCT GAT GAC TAC TG GCT GAT GCT ATG GAC TAC TG GCT GAT GCT ATG GAC TAC TG GCT GAT GCT ATG GAC TAC TG GCT ATG GAC TAC TAC TG GCT ATG GAC TAC TG G	G SP2.2 G SP2.2 G SP2.5 G SP2.5 G SP2.5 G SP2.2 G SP2.1 G SP2.1 G SP2.2 G SP2.2 G SP2.1 G SP2.2 G	4 1 4 10 4 10 3 0 3 1 3 1 3 1 3 1 9 preB cells reading J tame NP-9 J tame NP-9
ble 1 C-C sontad B/ s. orbin 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	TC TAC TAT GAT TAC GAC T CTA CTA TGA TAG TAA T GTA CTA TGA TGA TGA CA T CTA TA TGA TGA TTA CGA C TC TAT ATG GTT AC TC TAC TAT GGT AC TC TAC TAT GAT ACGA TC TAC TAT GAT ACGAC TC TAC TAT GAT ACGAC I: D-J sequences (DFL/DS D-segment TTT ATT ACT ACG ATG GTA GCT A TC TAC TAT GAT ACGAC TAC TC TAC TAT GGT ACT AC TC TAC TA TGG TAC TAC TC TAC TAT GGT AGT ACT AC TC TAC TA TGG TAC TAC TC TAC TAT GGT ACT AC TC TAC TAT GGT ACC TAC TC TAC TAT GGT ACT AC TC TAC TAT GGT ACC TAC	G CA GA GA GA GA GA CA CA CA CA CA CA CA CA CA C	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TGC ATB GAC TAC TG C TGG TTT GAC TAC TG TTT GCT TAC TG TTT GCT TAC TG C TGG TTT GCT TAC TG C TGG TTT GCT TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG C TGG TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG C TGG TAC TT GCT TAC TG GAC TAC TAT GCT ATG GAC TAC TG C TGG TAC TT GCT ATG GAC TAC TG GAC TAC TAT GCT ATG GAC TAC TG GAC TAC GCT ATG GAC TAC TG GAC TAC GCT ATG GAC TAC TG GAC TAC GCT ATG GAC TAC TG GAC TAT GCT ATG GAC TAC TG GAC TAC TAT GCT ATG GAC TAC TG GAC TAC TAC GCT ATG GAC TAC TAC TG GAC TAC TAC GCT ATG GAC TAC TG GAC TAC TAC GCT ATG GAC TAC TAC TG GAC TAC TAC GCT ATG GAC TAC TAC TG GAC TAC TAC GCT ATG GAC TAC TG GAC TAC TAC GCT TAC GAC TAC TG GAC TAC TAC GCT ATG GAC TAC TG GAC TAC TAC GCT TAC TAC TAC GAC TAC TG GAC T	G SP2.2 GG SP2.2 GG SP2.2 GG SP2.2 GG SP2.4 GG SP2.5 GG SP2.2 GG SP2.1 GG SP2.1 GG SP2.2 GG SP2.2 GG SP2.1 GG SP2.2	4 1 4 10 4 10 3 0 3 0 3 1 3 1 3 1 3 1 4 1 y preB cells reacing J trans NP-6 J trans NP-6 4 1 4 1 4 5
	TC TAC TAT GAT TAC GAC TC TAC TAT TAG TAA TG TA TA TGA TAG TG A CTA TGA TGA TTA CGA C TC TATG ATG GTT AC TC TATG ATG GTT AC TC TAC TAT GGT TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GAC TC TAC TAT GAT GAT GAT GAT TC TAC TAT GAT GAT GAT TC TAC TAT GAT GAT GAT TC TAC TAT GAT GAT TAC TC TAC TAT GAT GAT CAC TC TAC TAT GAT TAC TAC TC TAC TAT GAT TAC CAC TC TAC TAT GAT TAC TAC TC TAC TAT GAT TAC TAC TAC TC TAC TAT GAT TAC TAC GAC	G P) of BDI P20+rc-kit+ MF-sequer GA GA GA GA CCC CCC CCC CCC CC	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TGCT ATB GAC TAC TG TGCT ATB GAC TAC TG TT GCT TAT GCT ATC TG TT GCT TAC TG TT GCT TAC TG TAT GCT ATG GAC TAC TG TT TAC TAT GCT ATG GAC TAC TG GAT TAC GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT TAC GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GCT GG TTT GCT TAC TG GCT GGT TT GCT TAC TG GCT GGT TAC GAC TAC TG GCT ATG GAC T	G SP2.2 GG SP2.2 GG SP2.5 GG SP2.5 GG SP2.5 GG SP2.2 GG SP2.2 GG SP2.2 GG SP2.2 GG SP2.2 GG SP2.2 GG SP2.1 GG SP2.1 GG SP2.1 GG SP2.1 GG SP2.2 GG SP2.1 GG SP2.2	4 1
	TC TAC TAT GAT TAC GAC TC TAC TAT TGAT TAG TAA TG TA TAT TGA TAG TC TA TA TGA TGA TG A CTA TGA TGA TTA CGA TC TAG TA TGAT GGT TC TAC TAT GGT TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GAC TC TAC TA GAT GAT GAT TT TATT ACT AGG ATG GTA GCT A TC TAC TAT GAT GAT GAT TC TAC TAT GAT GAT TAC TC TAC TAT GAT GAC TA TC TAC TAT GAT GAC TA TC TAC TAT GAT GAC TAC TC TAC TAT GAT GAT CAC TC TAC TAT GAT GAC TAC TC TAC TAT GAT TAC TAC CC TAC TAT GAT TAC TAC TC TAC TAT GAT TAC CAC CC TAC TAT GAT TAC CAC	G 2) of BD 220+/c-kit+ MF-sequer GA GA GA C C C C C C C C C C C C C	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TGCT ATB GAC TAC TG TGCT ATB GAC TAC TG TGCT TG GAC TAC TG TT GCT TAC TT TT GCT TAC TT TAC TAT GCT ATB GAC TAC TG TT TAC TAT GCT ATB GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GCT TGG TAC TTC GAT GTC TG GCT TGG TAC TATG GAC TAC TG GCT ATG GCT ATG GCT ATG GCC GCT ATG GCT ATG GCT ATG GC	G SP2.2 GG SP2.2 GG SP2.5 GG SP2.5 GG SP2.2 GG SP2.1 GG SP2.16 GG SP2.16 GG SP2.2 GG SP2.2 GG SP2.16 GG SP2.2 GG SP2.2 </td <td>4 1</td>	4 1
ble 1 C-C sorted B/ s. orgen s. orgen s	TC TAC TAT GAT TAC GAC TC TAC TAT TGAT TAG TAA TC TA CTA TGA TAG A TC TA TA TGA TGA TTA CGA TC TATA TGA TGG TTA CC TC TAG TAT GAT AC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GAC TC TAC TAT GAT TAC GAC 1: D-J sequences (DFL/DS DF1 bone marrow prefi cells (B: D-sequent TTT ATT ACT ACG ATG GTA GCT A TC TAC TAT GAT TAC TAC TC TAC TAT GAT TAC TAC TC TAC TAT GAT ACT AC TC TAC TAT GAT GAT ACT AC TC TAC TAT GAT GAT CT AC TC TAC TAT GAT ACT AC TC TAC TAT GAT CAC TC TAC TAT GAT ACT AC TC TAC TAT GAT TAC TAC CT ACT ATA GAT ACT AC CT ACT ATA GAT ACT AC CT ACT ATA GAT ACT AC CT ACT ATA GAT TAC TAC CT ACT ATA GAT TAC CAC CT ACT ATA GAT ACT AC CT ACT ATA GAT ACT AC CT ACT ATA GAT TAC CAC CT ACT ATA GAT ACT AC CT ACT ATA GAT ACC CT ACT ATA GAT ACT AC CT ACT ATA GAT AC CT ACT ATA CAT ACT AC C	G (P) of BDJ (C) of C) of BDJ (C) of C) of BDJ (C) of C)	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TGCT ATG GAC TAC TG TGCT ATG GAC TAC TG C TGG TTT GCT TAC TG TTT GCT TAC TG TTT GCT TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC GCT ATG GAC TAC TG GAC TAC GCT ATG GAC TAC TG GAC TAC GCT ATG GAC TAC TG GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GCT ATG GCT ATG GCT ATG TG GCT ATG GCT ATG GAC TAC TG GCT ATG GCT ATG GCT ATG TG GCT ATG GCT ATG GAC TAC TG GCT	G SP2.2 G SP2.2 G SP2.5 G SP2.2 D SP2.1 G SP2.16 G SP2.11 G SP2.12 G SP2.13 G SP2.14 G SP2.13 G SP2.2 G SP2.2 G SP2.2 G SP2.2	4 1 4 10 4 10 3 1 2 11 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 1 3 1 1 <t< td=""></t<>
	TC TAC TAT GAT TAC GAC TC TAC TAT TAG TAA TG TA TAT TA TAG TAA TG TA TA TAG TA TG A CTA TGA TG GTT AC TC TAG TA TGA TG GTT AC TC TAG TAT GAT TAC TC TAC TAT GAT AC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GAC TC TAC TAT GAT AC TAC TC TAC TAT GAT TAC TAC TC TAC TAT GAT TAC TAC TC TAC TAT GAT AC TAC TC TAC TAT GAT TAC TAC TC TAC TAT GAT GAT AC TAC TC TAC TAT GAT GAT CAC TC TAC TAT GAT TAC TAC TC TAC TAT GAT TAC TAC TAC TAC TC TAC TAT GAT TAC TAC TAC TAC TAC TC TAC TAT TAG TAC TAC TAC	G P) of BD S20+AC-kit+ GA GGAT GGAT GGAT GGAT C C C C C C C C C C C C C	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TG GTT GAC TAC TG C TGG TTT GCT TAC TG TTT GAC TAC TG TTT GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG GAT TAC TAT GCT ATB GAC TAC TG GAC TAC GCT ATB GAC TAC TG GAC TAC TAT GCT ATB GAC TAC TG GCT ATB GCT ATB GAC TAC TG GCT AT	G SP2.2 G SP2.2 G SP2.5 G SP2.2 D FL16.1 G SP2.16 G SP2.1 G SP2.2 G SP2.1 G SP2.2 G SP2.2 G SP2.2 G SP2.2 G SP2.2 G	4 1 4 10 4 10 3 1 3 1 3 1 3 1 3 1 3 1 3 1 4 1 y preB cells reading 4 1 y preB cells reading y preB cells reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading reading
	TC TAC TAT GAT TAC GAC TC TAC TAT GAT TAG TAA TG TA TAT TAG TAA TG TA TA TGA TAG TA TC TA TA TGA TG GTT AC TC TAG TA TGA TG GTT AC TC TAC TA TGG TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GA TC TAC TAT GAT TAC GAC TC TAC TAT GAT TAC GAT GAT GAT TC TAC TA GGT AA TC TAC TAT GGT AAC TAC TC TAC TAT GGT AAC TAC TC TAC TAT GGT GAA TC TAC TAT GGT GAA TC TAC TAT GGT GAC TA TC TAC TAT GGT GAC TA TC TAC TAT GGT GAC TA TC TAC TAT GGT GAC TAC TC TAC TAT GGT GAC TAC TC TAC TAT GGT AC TAC TC TAC TAT GGT TAC TAC CC TAC TAT GGT TAC TAC CC TAC TAT GGT TAC CTAC CC TAC TAT	а 2) of BDJ 220-4-С+К1: 220-4-С+К1: 220-4-С+К1: 220-4-С+К1: 220-4-С+К1: 220-4-С+К1: 220-4-С+К1: 220-4-С+К1: 220-4-С+К1: 220-4-С+К1: 220-4-С-К1: 200-4-С-К1: 200-4-С-К1: 200-4-С-К1: 200-4-С-К1: 200-4-С-К1: 200-4-С-К1: 200-4-С-К1: 200-4-С-К1: 200-4-С-К1: 200-4-С-К1: 200-4-С-К1: 200-4-С-К1: 200-4-С-К1: 200-4-С-С-С-С-С-С-С-С-С-С-С-С-С-С-С-С-С-С	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TGCT ATB GAC TAC TG TGCT ATB GAC TAC TG TT GCT TAC TG TT GCT TAC TG TT GCT TAC TG TT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG GAT TAC TAT GCT ATB GAC TAC TG GAC TAC GAT TAC GAC TAC TG GAC TAC GAC TAC TG GAC TAC GAC TAC TG GAC TAC TAT GCT ATB GAC TAC TG GAC TAC GAC TAC TG GAC TAC GAC TAC TG GAC TAC TAT GCT ATB GAC TAC TG GAT TAC CAT GCT ATB GAC TAC TG GAT TAC TAT GCT ATB GAC TAC TG GAT TAC CAT GCT ATB GAC TAC TG GAT TAC CAT GCT ATB GAC TAC TG GAT TAC CAT GCT ATB GAC TAC TG TG CAT GAT GAC TAC TAC TG CAT GAC TAC TAC TAC TAC TAC TAC TAC TG	G SP2.2 G SP2.2 G SP2.5 G SP2.1 G SP2.16 G SP2.2 G SP2.4 G SP2.4 <	4 1
	TC TAC TAT GAT TAC GAC TC TAC TAT GAT TAG TAA TG TA CTA TGA TAG ATA TG A CTA TGA TGA TTA CGA C TC TATG ATG GTT AC TC TAC TAT GGT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GAC TC TAC TAT GAT TAC TAC TC TAC TAT GAT GAT TAC TC TAC TAT GAT TAC TAC CC TAC TAT GAT TAC TAC CAC CC TAC TAT GAT TAC CAC CC TAC TAT TAG TAC TAC CAC CC TAC TAT GAT TAC TAC CAC CC TAC TAT TAG TAC TAC CAC CC TAC TAT TAG TAC TAC CAC CC TAC TAT GAT TAC CAC CC CC TAC TAT TAG TAC CAC CC CC TAC TAT TAG TAC TAC CAC	G P) of BDJ 220-4C-kti- GA GA GA GA GA GA GA GA GA GA	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TAC TAT GCT ATB GAC TAC TG TG GTT GAC TAC TG TT GCT TAC TG TT GCT TAC TG TT GCT TAC TG TT TAC TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG TAT GCT ATB GAC TAC TG GAT TAC TAT GCT ATB GAC TAC TG GAC TAC TAT GCT ATB GAC TAC TG GAT TAC TAT GCT	G SP2.2 GG SP2.2 GG SP2.5 GG SP2.5 GG SP2.5 GG SP2.2 GG SP2.1 GG SP2.16 GG SP2.16 GG SP2.2 GG SP2.2 <td>4 1 4 10 4 10 7 1 8 1 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1</td>	4 1 4 10 4 10 7 1 8 1 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	TC TAC TAT GAT TAC GAC TC TAC TAT TAG TAA TG TA TA TAG TAA TG ATA TATA T	G P) of BDI P) of BD	AT TAC TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TTG GAT TAC TAC TG C TGG TTT GCT TAC TG TTT GCT TAC TG TTT GCT TAC TT TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC TAC GAT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC TAC GAT ATG GAC TAC TG GAC TAC TAC GAT ATG GAC TAC TG GAC TAC TAC GAT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT TAC TAC TAC TAT GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT TAC TAC TAC TT GAC TAC TG GAT TAC TAC TAC TAT GAC TAC TG GAT TAC TAC TAC TT GAC TAC TG GAT TAC TAC TAC TAC TAC TAC TAC TG GAT TAC TAC TAC TAC TAC TAC TAC TAC TAC T	G SP2.2 GG SP2.2 GG SP2.5 GG SP2.5 GG SP2.5 GG SP2.5 GG SP2.2 GG SP2.2 GG SP2.2 GG SP2.1 GG SP2.2 GG SP2.1 GG SP2.1 GG SP2.1 GG SP2.2 GG SP2.1 GG SP2.2	4 1
	TC TAC TAT GAT TAC GAC TC TAC TAT TGAT TAC GAA TG TA TAT TAGA TA TC TA TAT TA TA CAA TC TA TA TATA TA	G P) of BDJ 220-4C-kti- GA GA GA GA GA GA GA GA GA GA	AT TAC TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TT GCT TAC GAC TAC TG C TGG TTT GCT TAC TG TTT GCT TAC TG TTT GCT TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC GCT ATG GAC TAC TG GAC TAC TAT GCT ATG GAC TAC TG GAC TAC TAC GCT ATG GAC TAC TG GAC TAC TAC GCT ATG GAC TAC TG GAC TAC TAC GT ATG GAC TAC TG GAC TAC TAC GCT ATG GAC TAC TG GCT ATG GAC TAC TG GCT ATG GAC TAC TG GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC TG GAT TAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TG G	G SP2.2 GG SP2.2 GG SP2.5 GG SP2.5 GG SP2.5 GG SP2.5 GG SP2.2 GG SP2.1 GG SP2.1 GG SP2.1 GG SP2.2 GG SP2.2 GG SP2.1 GG SP2.2	4 1 4 10 4 10 4 10 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	TC TAC TAT GAT TAC GAC TC TAC TAT GAT TAG TAA TG TA TAT TAG TAA TG TA TA TAG TAA TG ATA TATA T	G P) of BDJ 220-4C-ktt+ GA GGA T GGA GGA CCC CCA C GAC GGA ACC CCC CCA C GAC GGA ACC CCC CCA C CCA C C CCA C C C C C C C C C C C C C C	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TG GTT GCT TAC TG TT GCT TAC TG TT GCT TAC TG TT TAC TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC TAT GCT ATG GAC TAC TG GAT ATG CAT ATG GAC TAC TAC TG GAT ATG CAT AC TAC TAC TAC TAC TAC TAC TAC TAC	G SP2.2 G SP2.2 G SP2.5 G SP2.5 G SP2.5 G SP2.2 G SP2.5 G SP2.5 G SP2.2 G SP2.1 G SP2.2 G SP2.1 G SP2.2 G	4 1
	TC TAC TAT GAT TAC GAC TC TACTAT TGAT TAGA TC TATA TGATA TGA TC TATA TGA TAGA TC TATA TGA TG GTT AC TC TATG ATG GTT AC TC TAGT ATG GTT AC TC TACTAT GAT AC TAC TAT GAT AC TAC TAT GAT AC TAC TAT GAT AC TAC TAT GAT AC TC TACTAT GAT AC TC TACTAT GAT TC TACTAT GAT TC TACTAT GAT TC TACTAT GAT TC TACTAT GAT TC TACTAT TAC TAC TAT GAT TC TACTAT GAT TC TACTAT GAT TC TACTAT GAT TC TACTAT GAT TC TACTAT TGAT TC TACTAT TGAT TACTAC TC TACTATAT TACTAT TACTAC TC TACTAT TGAT TACTAC TC TACTAT TACTAT TACTAC TC TACTAT TGAT TACTAC TC TACTAT TACTAT TACTAC TC TACTAT TA	G CA GA GA GA GA GA GA GA GA GA G	AT TAC TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TGC TATG GAC TAC TG TGC TATG GAC TAC TG TTG GTT GCT TAC TG TTT GCT TAC TG TTT GCT TAC TG TTT GCT TAC TG TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC TAC GCT ATG GAC TAC TG GAC TAC TAC GCT ATG GAC TAC TG GAC TAC TAC GCT ATG GAC TAC TG GAC TAC TAT GCT ATG GAC TAC TG GAC TAC TAT GCT ATG GAC TAC TG GAC TAC GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TAC TG GAG G TAC TAC TAC TAC GAT GTC TG TAC TAC TAC TAC TAC TAC TAC TAC TAC TAC	G SP2.2 G SP2.2 G SP2.5 G SP2.4 G SP2.5 G SP2.1 G SP2.16 G SP2.1 G SP2.1 G SP2.1 G SP2.1 G SP2.2 G	4 1
	TC TAC TAT GAT TAC GAC TC TACTAT TGAT TAG TAA TG TA TAT TA TA GAA TG TA TA TA TGA TA TC TA TA TA TG TTA CA TC TAT TA TA TG GT TAC TC TACTA TGAT GAT TAC TC TACTAT GAT TAC TC TACTAT GAT TAC GAC TC TACTAT GAT GAT GAT GAT TT TATTACT ACG ATG GTA GCT A TC TACTA GAT GAT GAT TC TACTAT GAT GAT GAT TC TACTAT GAT GAT TAC TC TAC TAT GAT GAT TAC TC TAC TAT GAT GAT TAC TC TACTAT GAT GAT CAC TC TACTAT GAT GAT CAC TC TACTAT GAT TAC TAC TC TACTAT GAT TAC GAC TC TACTAT GAT TAC GAC CC TACTAT GAT TAC GAC CC TACTAT GAT TAC GAC CC TACTAT GAT TAC GAC CC TACTAT TAG GAT ACCTAC CC TACTAT TAG GAT ACCTAC CC TACTAT TAG GAT ACCTAC CC TACTAT GAT TAC GAC CC TACTAT GAT TAC TAC CC TACTAT TAG GAT ACCTAC CC TACTAT TAG GAT ACCC CC TACTAT TAG GAT ACC CC TACTAT TAG GAT ACC CC TACTAT TAG GAT ACC	G P) of BD P)	AT TAC TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TGCT ATG GAC TAC TG TGCT ATG GAC TAC TG TT GCT TAC TG TT GCT TAC TG TT GCT TAC TG TT TAC TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GCT TGG TAC TTC GAT GTC TG GAT TAC TAT GCT ATG GAC TAC TG GCT TGG TAC TG GAC TAC TG GCT TGG TAC TGG GAC TAC TG GCT TGG TAC TGG GAC TAC TG GCT TGG TAC TGG GAC TAC TG GCT TAG GAC TAC TG GCT TGG TAC TGG GAC TAC TG GCT TGG TAC TAC TGG GAC TAC TG GCT TGG TAC TGG TGG GCT TGG TAC TGG TG GCT TGG TAC TGG TG GG TT GCT TAC TG GG TT GC	G SP2.2 G SP2.2 G SP2.5 G SP2.1 G SP2.2 G	4 1 4 10 4 10 4 10 7 1 7 1 7 1 1 1
	TC TAC TAT GAT TAC GAC TC TAC TAT TAG TAA TG TA TAT TAG TAA TG TA TA TAG TAA TG TA TA TA TA GAA TG TA TA TA TAG TA TC TAG TA TA TAG TC TAC TA TGA TAG TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GAC TC TAC TA GAT GAT GAT GAT TT TATT ACT AGG ATG GTA GCT A TC TAC TA GGT GAC TAC TC TAC TA GGT GAT GAT GAC TC TAC TA GGT GAT GAT GAT TC TAC TA GGT GAT GAT GAC TC TAC TAT GGT GAC TAC TC TAC TAT GGT GAT GAT C TC TAC TAT GGT GAC TAC TC TAC TAT GGT GAC TAC C TAC TAT GGT GAC TAC C TAC TAT GGT GAC TAC TC TAC TAT GGT GAC TAC C TAC TAT GGT TAC CAC C C TAC TAT GGT GAC CT C C TAC TAT GGT GAC CC C C TAC C	G P) of BDJ P) of BDJ P220+/c-kit+ GA GA GA GA GA GA GA GA C CCC C CAC GA GA C CCC C CAC GA C CCC C CCC C CCC C CCC C CCC C	AT TAC TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TGCT ATG GAC TAC TG TGCT ATG GAC TAC TG C TGG TTT GCT TAC TG TTT GCT TAC TG TTT GCT TAC TG TT TAC TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GCT TG GTT ATG GAC TAC TG GCT TG GT ATG GAC TAC TG GCT TG GT ATG GAC TAC TG GCT TAT GCT ATG GAC TAC TG GCT TAT GCT TAC GAC TAC TG GCT ATG GAC TAC TG	G SP2.2 GG SP2.2 GG SP2.5 GG SP2.5 GG SP2.5 GG SP2.5 GG SP2.2 GG SP2.2 GG SP2.1 GG SP2.16 GG SP2.17 GG SP2.16 GG SP2.17 GG SP2.17 GG SP2.17 GG SP2.17 GG SP2.17 GG SP2.17 GG SP2.27 GG SP2.27 GG SP2.27 GG SP2.27 GG SP2.27 GG <	4 1
	TC TAC TAT GAT TAC GAC TC TAC TAT TAG TAA TG TA TATA TAGA TG ATA TGA TAGA TG ATA TATA T	G P) of BDJ 220+AC-kit+ GA GGAT GA GGAT GG GA GGAT C C C C C C C C C C C C C	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TG GTT GAC TAC TG TT GCT TAC TG TT GCT TAC TG TT GCT TAC TG TT TAC TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC TAC GCT ATG GAC TAC TG GAC TAC GCT ATG GAC TAC TG GAC TAC GCT ATG GAC TAC TG GAC TAC GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG TG TAC TAT GCT TAC TG TG TAC TAT GCT TAC TG TG TAC TAC TAC TAC TAC TG TG TAC	G SP2.2 GG SP2.2 GG SP2.5 GG SP2.5 GG SP2.5 GG SP2.5 GG SP2.2 GG SP2.5 GG SP2.2 GG SP2.2 GG SP2.2 GG SP2.2 GG SP2.1 GG SP2.1 GG SP2.1 GG SP2.2 GG SP2.2 GG SP2.1 GG SP2.2	4 1
	TC TAC TAT GAT TAC GAC TC TAC TAT TAG TAA TG TA TAT TA TAG TAA TG TA TAT TA TA CGA TC TATA TATA TAG TAC TC TAG TA TATA TG TAC TC TAC TAT GGT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GA TC TAC TAT GAT TAC GA TC TAC TAT GAT TAC GAC TC TAC TA GGT AA TC TAC TAT GGT AA TC TAC TAT GGT GAC TA TC TAC TAT GGT GAC TC TAC TAT GGT GAC TA TC TAC TAT GGT GAC TA TC TAC TAT GGT GAC TAC TC TAC TAT GGT GAC TAC TC TAC TAT GGT GAC TAC TC TAC TAT GGT AC TAC CC TAC TAT GGT AC CAC CC TAC TAT GGT AC CC	G P) of BDJ P) of BDJ P220+/c-kit+ GA GA GA GA GA GA GA GA C CCC C CAC GA GA C CCC C CAC GA C CCC C CCC C CCC C CCC C CCC C	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATG GAC TAC TG TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TG GTT GAC TAC TG TTG GAT TAC TAC C TGG TTT GCT TAC TG TTT GAC TAC TG TTT GAC TAC TG TAC TAT GCT ATG GAC TAC TG TAG GAC TAC TG GAC TAC TAT GAC TAC TG GAC TAC TG GAC TAC TAT GAC TAC TG GAC TAC TG GAC TAC TAT GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG TG TAC TAC TAC GAT GTT TAC TAC GAT TAC TAT GCT ATG GAC TAC TG GAT TAC TAC TAC TAC TAC TAC TAC TAC TAC T	G SP2.2 GG SP2.2 GG SP2.5 GG SP2.2 GG SP2.2 GG SP2.1 GG SP2.2 GG SP2.2	4 1
	TC TAC TAT GAT TAC GAC TC TAC TAT TAG TAA TG TA TAT TA TAG AA TG TA TA TAG TA TG A CTA TAG TA TA CGA TC TAG TA TGA TAG TA TAC TC TAC TA TGG TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GA TC TAC TAT GAT TAC GAC TC TAC TAT GGT AA TC TAC TAT GGT AA TC TAC TAT GGT GAA TC TAC TAT GGT GAC TA TC TAC TAT GGT GAC TC TAC TAT GGT GAC TC TAC TAT GGT AC TC TAC TAT GGT AC TAC TAT GGT TAC TAC TC TAC TAT GGT TAC TAC CC TAC TAT GGT TAC CAC TC TAC TAT GGT TAC CAC TC TAC TAT GGT TAC CAC CC TAC TAT GGT AC CC TAC TAT GGT ACC CC TAC TAT G	G P) of BDJ P) of BDJ P 2204-C-Hit+ GA GA GA C C C C C C C C C C C C C	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TAC TAT GAC TAC TG TGCT ATG GAC TAC TG TTGCT TAC TT TTGCT TAC TG TTTGCT TAC TG TTTGCT TAC TG TTTGCT TAC TG TTTGCT TAC TG TAC TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG C TGG TAC TTG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG C TGG TAC TTG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT ATG CAT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT TAC T	G SP2.2 GG SP2.2 GG SP2.5 GG SP2.5 GG SP2.5 GG SP2.2 GG SP2.2 GG SP2.2 GG SP2.2 GG SP2.2 GG SP2.2 GG SP2.1 GG SP2.1 GG SP2.1 GG SP2.2 GG SP2.1 GG SP2.1 GG SP2.2	4 1
	TC TAC TAT GAT TAC GAC TC TAC TAT TGAT TAC GAA TG TAT TATGATA TG TA TATA TGA TA TG A CTA TGA TGA TGA TC TAG TA TGA TGG TT AC TC TAC TAT GG TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GAC TC TAC TAT GAT TAC GAC TT TATT ACT ACG ATG GTA GCT A TC TAC TAT GGT TAC TAC TC TAC TAT GGT GAT GAT AC TC TAC TAT GGT GAT GAT AC TC TAC TAT GGT GAT GAT A TC TAC TAT GGT GAT GAT AC TC TAC TAT GGT GAT GAT TAC TC TAC TAT GGT GAT AC TC TAC TAT GGT GAT AC TC TAC TAT GGT GAT AC TC TAC TAT GGT GAT CAC TC TAC TAT GGT GAT CAC TC TAC TAT GGT GAC TAC TC TAC TAT GGT GAC TAC CC TAC TAT GGT GAC TAC CC TAC TAT GGT TAC CTAC CC TAC TAT GGT TAC CTAC CC TAC TAT GGT GAC TAC CC TAC TAT GGT GAC TAC CC TAC TAT GGT GAC TAC CC TAC TAT GGT TAC CTAC CC TAC TAT GGT GAC CTAC CC TAC TAT GGT	G P) of BDJ P) of BDJ P 2204-C-Hit+ GA GA GA C C C C C C C C C C C C C	AT TAC TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG C TGG TTT GCT TAC TG TTT GCT TAC TG TTT GCT TAC TG TTT GCT TAC TG TAC TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC GT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC GT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC GT ATG GAC TAC TG GAC TAC TAC GT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC TAC TAG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT GT TAC TAT GCT ATG GAC TAC TG GAC	G SP2.2 GG SP2.2 GG SP2.5 GG SP2.1 GG SP2.2	4 1
	TC TAC TAT GAT TAC GAC TC TAC TAT TAG TAA TG TA TAT TA TAG AA TG TA TA TAG TA TG A CTA TAG TA TA CGA TC TAG TA TGA TAG TA TAC TC TAC TA TGG TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC TC TAC TAT GAT TAC GA TC TAC TAT GAT TAC GAC TC TAC TAT GGT AA TC TAC TAT GGT AA TC TAC TAT GGT GAA TC TAC TAT GGT GAC TA TC TAC TAT GGT GAC TC TAC TAT GGT GAC TC TAC TAT GGT AC TC TAC TAT GGT AC TAC TAT GGT TAC TAC TC TAC TAT GGT TAC TAC CC TAC TAT GGT TAC CAC TC TAC TAT GGT TAC CAC TC TAC TAT GGT TAC CAC CC TAC TAT GGT AC CC TAC TAT GGT ACC CC TAC TAT G	G P) of BDJ P) of BD	AT TAC TAT GCT ATB GAC TAC TG TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TAC TAT GCT ATG GAC TAC TG TAC TAT GAC TAC TG TGCT ATG GAC TAC TG TTGCT TAC TT TTGCT TAC TG TTTGCT TAC TG TTTGCT TAC TG TTTGCT TAC TG TTTGCT TAC TG TAC TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG C TGG TAC TTG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG C TGG TAC TTG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TG GAC TAC TAT GCT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT ATG CAT ATG GAC TAC TG GAT TAC TAT GCT ATG GAC TAC TG GAT TAC T	G SP2.2 GG SP2.2 GG SP2.5 GG SP2.1 GG SP2.2	4 1

Table 1 (cont.)

63	w3	TO TAC TAT OGT AAC TAC	CTC TIT G	GG		3 1	N+
84 11	¥3 ¥3	TCT ATG ATG GTT ACT AC T CTA TGA TGG TTA CTA C	CTC C	G TTT GCT TAC TGG C TAT GCT ATG GAC TAC TGG			Р+ Р+
12	*3	TC TAC TAT GAT TAC	TC	C TAT GCT ATG GAC TAC TGG	8P2.2	4 Î	P+
13 14	¥3 ¥3	T CTA CTA TOG TAA CTA C	GC CC C117	T TAC TAT GCT ATG GAC TAC TGG TAT GCT ATG GAC TAC TGG		4 M 4 D	N+ P+
	#32	T CTA CTA T <u>IGA</u> T CTA C	CC TTT G	AT GCT ATG GAC TAC TGG	SP2.2/34	4 1144	N+
u1 54	w32 w32	TC TAC TAT QQT AAC T TC TAC TAT QQT	CCC G	AT TAC TAT GCT ATG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG		4	N+ N+7
w1	*12	C CTA CTA <u>TAG</u> T		AT GCT ATG GAC TAC TGG	8P2_X	4 m	
w0	w32	CC TAC TAT AGT AAC	CACC	CT ATG GAC TAC TGG	SP2.X	4	N+
		/_ST bone marrow preB cells w			D	reading	
neme,	ongen	D-segment	N/P-sequence G GGG		•	J trame	N/P-eeq
G11 G12		TCT ACT ATG ATT ACG AC T CTA TGA TGG TTA	TC	GCT ATG GAC TAC TGG C GAT GTC TGG	SP2.9	4 11 1 12	* *
G13 G14		TC TAC GAT GGT TAC TCT ACT ATG ATT ACG AC	TOG G GAG	GCT ATG GAC TAC TGG	8P2.1 SP2 2	4 3 11	+
G21		TCT ACT ATG GTT ACG AC	GGTGA	TTT GCT TAC TGG AC TTT GAC TAC TGG	5P2.344	2 8	÷
624 631		TCT ACT ATG ATT AOG AC TC TAC TAT GGT AAC TAC	G GOG ACC	GCT ATG GAC TAC TGG TTT GCT TAC TGG	5P2.5	4 13 3 I	*
G32 G33		TCT ATG ATG GTT ACT AC TCT ACT ATG ATT AC	G TCG C CCT	OCT TAC TOG TTT OCT TAC TOG	8P2.9	3 8	•
G41		TC TAC TAT GAT TAC GAC	AAG	GCT ATG GAC TAC TOG	8P2_2	4 <u>î</u>	:
G42 G43		CC TAC TAT AGT AAC TAC TC TAT GAT GGT TAC	000 000 CTT 1T	T GCT ATG GAC TAC TOG T TAC TAT GCT ATG GAC TAC TOG		4	:
G44		TC TAT GAT GOT TAC TAC	GG GG	TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG	SP2.0	4 1	-
H11 H12		TCT ACT ATG GTA A TCT ACT ATG GTA ACT AC	GICG	GCC TGG TTT GCT TAC TGG	SP2.5	S H	÷
H21 H31		T CTA <u>IGA</u> TGG I T CTA <u>IGA</u> TGG TTA C	AG G CA AGC CTA	GG TTT GCT TAC TOG CGA GCT TAC TGG		3 K 10 L	+
H32		C CTA CTA <u>TAG TAA</u> CT	T CCG A	TT OCT TAC TOG	8P2.X	i ii	÷
H34 H42		CCT ACT ATA GTA AC T CTA CTA TGG TT	C CCT G GOOG	THT CCT TAC TGG GCT ATG GAC TAC TGG	SP2.X SP2.34	3 14	:
HAS		TCT ACT ATG G CCT ACT ATA GTA ACT AC	GG GG	C TAT GCT ATG GAC TAC TOG	5P2.5	4 0	•
J11		TCT ATG ATG GTT ACT AC	G	AT GCT ATG GAC TAC TOG TAC TAT GCT ATG GAC TAC TOG	SP2.9	4 II.	• ₽+-
J13 J21		TC TAT GAT OGT TAC TCT ACT ATG GTA ACT	CCT TCT	TIT GCT TAC TGG TAT GCT ATG GAC TAC TGG		3 I 4 H	:
J22		TC TAC TAT GAT TAC GAC	CCC TIT T CG CCT	AC TAC TTT GAC TAC TOG	SP2.2	2 Î	+
J31 J41		CC TAC TAT AGT A TC TAC TAT OGT IA	GAGA	TIT OCT TAC TOG TAC TAT GCT ATG GAC TAC TOG	8P2.34	4	÷.
J42 J43		T CTA <u>tiga</u> tigg tita CC tac	AAG GG C	T GCT ATG GAC TAC TGG CT ATG GAC TAC TGG		4 11	+ P+-
,44,		T CTA IGA TOG TTA CTA C	AGTITT	CT ATG GAC TAC TGG		4 W	+
			~	· · · · · · · · · · · · · · · · · · ·			
Tab) <u>le 2 a-b;</u>	D-J sequences (DFL/DS	P) of BDF	1 and L51/L5T fetal liver	preB cell	culture	5
		BDF1 fetal liver preB cells	-			reading	
A3	, origin clone 1	D-segment	NP-sequence		D		N/P-eeq
81	clone 5	TC TAC TAT OUT TAC GAC TT TAT TAC TAC OUT AGT AGC TAC		TGG TAC TTC GAT GTC TGG TAC TTT GAC TAC TGG		1 1 2 1	:
842 C1	cione 5 cione 8	TTT ATT ACT GCG GTA GTA GCT TT TAT TAC TAC GGT AGT AGC T		GAC TAC TOG TT GAC TAC TGG		2 I 2 I	-
E1	cione 18	T TTA TTA CTA COO <u>TAG</u> TA		C TIT GAC TAC TOG	FL 16.1	2 1	
=2,1 b2,1	PAL1 #d12	TAT TAC TAC OGT AGT AGC TAC CC TAC TAT OGT AAC TAC		TAC TTT GAC TAC TGG TAC TTT GAC TAC TGG	FL 14.1 8P 2.7	2 2	:
62.3	8 d 12 8 d 12	TCT ACT ATG GTA ACT AC TC TAC TAT GGT AAC		T GCT ATG GAC TAC TGG TAC TGG	8P 2.1.6	4 U	-
c1	11 d 12	TC TAC TAT OGT TAC GAC		GCT ATG GAC TAC TGG	SP 2.34	2 I 4 I	:
62.1	5 d 12 5 d 12	TC TAC TAT GGT AAC TA CC TAC TA		T TAC TAT GCT ATG GAC TAC TGG C TTT GAC TAC TGG	84P 2, 1/5 84P 2, 6/7	4 I 2 I	:
പ്പോ	5 d 12 5 d 12	TC TAC TAT GGT AAC TAC T CTA CTA TGG		TIT GAC TAC TGG TAT GCT ATG GAC TAC TGG		2 1	•
d1	6 d 12	TC TAT TAT OGT TAC		TAC TAT OCT ATG GAC TAC TOG	SP 2,34	4 1	:
d2 d2.1	1 d 12 1 d 12	T CTA TCA TOO TTA C TC TAC TAT	^	T TAC AGT OCT ATG GAC TAC TGG - GGC CAA GGC	5P 2.34 SP 2.34	4 DI 2 I	:
62.2 62.3	8 d 12 8 d 12	CC TAC TAT AGT TAC GAC T CTA CTA TGG		TAC TOIG GAC TAC TOG TIT GAC TAC TOG		2 1	2.DJ
63 H1	6 d 12	TC TAC TAT GGT A		AC TAT OCT ATG GAC TAC TOG	8P 2.34	4 i	:
H3	5 d 13 8 d 13	CC TAC TAT AGT AAC TA CC TAC TAT AGT AAC TA		T TAC TAT GCT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG	5P2X 5P2X	4	:
m1 [1]1	F13L7.4 (d1: 8 d 14	3)T CTA CTA TOG TC TAC TAT GGT AAC TAC		GCT TOG TIT GCT TAC TOG TOG TAC TIC GAT GTC TOG		3 in 1 i	-
7.1	5 d 14	TC TAC TAT OGT AAC TAC		GCT ATG GAC TAC TGG	SP 2.1/5	4	:
7 <u>.2</u> •1	11 14 11 15	CC TAC TAT OGT AAC TA T CTA CTA TOG <u>TAA</u> CTA		T TAC TAT GCT ATG GAC TAC TGG TAC TAT GCT ATG GAC TAC TGG	8P 2.7 8P 2.1/6	4 I 4 B	:
11 91	8 d 15 8 d 15	CC TAC TAT OGT AAC TAC TCT ACT ATG GTA ACT AC		TAT GCT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG	5P 2.7 8P 2.1/5	4 I 4 U	•
62	5 d 15	T CTA CTA TOG TTA		TAC TAT OCT ATG GAC TAC TOG	SP 2.34	4 III (+	, . , .
92.2 J1	5 d 15 5 d 15	CC TAC TAT COT A C CTA CTA <u>TAG</u> TA		AC TAC TOG T GCT ATG GAC TAC TOG		2 1 4 DD	:
5	1d 15	TC TAC TAT AGT AAC		GCT ATG GAC TAC TGG	SP 2,1/5	4	•
h2.2 #1	11 d 15 11 d 15	CC TAC TAT AGT AAC C CTA CTA TOG		GAC TAC TGG TAT GCT ATG GAC TAC TGG		2 I 4 11	:
11	8 d 18 8 d 18	TT TAT TAC TAC OGT AGT AGC TA C CTA CTA TOG		T GAC TAC TOG TAC TOG	FL 16.1	2 2	•
B1	18L1	TC TAT GAT GGT TAC		TGG TTT GCT TAC TGG	SP2.	5 i	:
82 84	18L2 18L2	CC TAC TAT AGT AAC TA TCT ACT ATG GTA ACT AC		T TAC TAT GCT ATG GAC TAC TOG G TIT OCT TAC TGG	SP2.X SP2.1/5	4	:
C1 D1	181.5.2 19.1	TC TAC TAT GGT AAC TAC TC TAC TAT GGT AAC T		TAT GCT ATG GAC TAC TGG TT GAC TAC TGG	SP2.1/5	4 Ï	•
Ēi	19.2	TC TAC TAT GGT AAC TAC	GTG GG	C TAC TOG	8P2.1/5	2 1 2 1	PAN+
52 53	19.2 19.2	CCT ACT ATA GT T ACT ATA GTT AC TC TAC TAT GG	GAC G <u>TAG</u> / CG	ACC TAC TGG AC TTT GAC TAC TGG	SP2,X+2,11 SP2,344	2 1	P+,D-C P+
E4 F1	19.2 F19L2	CC TAC TAT AGT AAC TAC		GAC TAC TOG	SP2.X	2 i	
G1	19.3	TC TAC TAT GAT TAC G TC TAC TAT GOT AAC TAC	GTG G	CT TAC TGG GG	SP2.1/5	3 2	Р+
H1 H2	F19L4 F19L4	TO TAC TAT GGT AAC TAC	AC CO TTT	G TIT OCT TAC TGG TIT OCT TAC TGG		т с 1	P+ P+
J1 J2	F19L5 F19L5	T CTA CTA TOG TT CC TAC TAT AGT AAC TAC		T GCT TAC TGG TAC TTT GAC TAC TGG	8P2.34	3 İB(+)	•
JA Ki	F19L5 F19L6	TC TAC TAT GGT TAC GAC		TOG TAC TTC GAT GTC TOG	8P2.34	2	:
NI I	FINE	TT TAT TAC TAC OGT AGT AG		G TAC TTC GAT GTC TGG	FL16.1	1 1	•
		5T/L5T fetal liver preB cells	N/D ages	Lassa	n.	reading	NO
A1	. origin 1.5.12.1	D-segment TCT ATG ATG GTT ACT AC	N/P-sequence	J-segment C TOO TITL OCT TAC TOO	D .		N/P-seq
AZ	15.12.1	TC TAC TAT TOG T	TA CTG ACT	TGG TTT GCT TAC TGG	8P2.10 1	i ï	•
A3 #1	L5.12.1 L5.12.1	TCT ACT ATG GTA ACT AC T CTA CTA TGG TT	GT A	T TAC TAT GCT ATG GAC TAC TOG T GCT TAC TOG	SP2.1/5 4 SP2.3/4 5		•
2	L5.12.1 L5.12.1	CC TAC TAT ADT AAC TAC TC TAC TAT QGT AAC TAC		GCT ATG GAC TAC TOG	8P2.X 4	1 1	•
84	L5.12.1	TCT ATG ATG GTT ACG		TIT GAC TAC TGG TAT GCT ATG GAC TAC TGG	8P2.1/5 2 8P2.3/4	i 11	:
Bi	15.12.2	OC TAC TAT AGT AAC T		GG TTT GCT TAC TGG	8P2.X 1		•
82	15.12.2	TC TAC TAT GGT AAC TA		T GCT ATG GAC TAC TGG	SP2.1/5 4	1 1	-

Table 2 (cont.)

83							
	15.12.2	TO TAC TAT GAT TAC GAC	т	AC TAC TTT GAC TAC TOG	8P2.2	2	
84 51	15.12.2	T GTA CTA TOO TA CC TAC T		C TTC GAT GTC TGG TT GAC TAC TGG	SP2.1/5 SP2.6/7	1 2	III(+)
2	L5.12.2	TCT ACT ATG ATT TOG		GCC TOG TTT GCT TAC TOG	SP2_2	5	i i
C1 C2	LE.12.3 LE.12.3	TC TAT GAT GGT TAC TAC TC TAC TAT GGT AAC TAC		TAC TIT GAC TAC TOG TOG TAC TIC GAT GTC TOG	5P2.9	2	1 .
ä	15.12.3	TC TAC TAT GAT TA		T GCT ATG GAC TAC TGG	SP2.1/5 SP2.2	1	1 :
C4	15.12.3	TCT ACT ATG ATT ACG		TTT OCT TAC TOG	8P2.2	3	
1 1	L5.12.3 L5.12.3	TCT C CTA CTA <u>TAG TAA</u> CTA C	GT	TGG GAC TAC TGG	5P2.1/5 5P2.X	2	н. н Р
22	15.12.4	T CTA CTA TOG TAA CT		T GAC TAC TOG	SP2.1/5	ž	i i
	L5.12.4	TT TAT TAC TAC GGT AGT AGC TAC		TGG TAC TTC GAT GTC TGG	FL18.1	1	· -
11 -1	LS.12.4 LS.12.5	TC TAC TAT GGT AAC TAC TC TAT GAT GGT TAC TAC		TAT GCT ATG GAC TAC TGG TAC TTT GAC TAC TGG	SP2.1/5 SP2.3/4	4	1 :
a i	15,12.5	OC TAC TAT AGT AAC TAC		TTT GAC TAC TOG	SP2.X	ž	1 1
MA F1	L5,12.5 L5,12.7	TC TAC TAT OUT AAC TAC		TAT OCT ATG GAC TAC TOG T OCT TAC TOG	SP2.1/5	4	L -
2	15,127	T CTA <u>IGA</u> TOG TTA CT CC TAC TAT AGT AAC TAC		TAC TTT GAC TAC TGG	8P2.0 SP2.X	3	19 ·
F4 -	15.12.7	CC TAC TAT AGT AAC T	C	C TAT OCT ATG GAC TAC TOG	SP2X	4	1 7
2	L5.12.7	TCT ACT ATG GTA ACT		GCT TAC TOG	8P2.1/5	3	
31	L5.12.7 L5.12.8	TCT ACT ATG ATT ACG A TC TAC TAT GAT TAC GAC	GC .	GCT ATG GAC TAC TGG TAT GCT ATG GAC TAC TGG	8P2.2 8P2.2	4	■ P.
1	15.12.0	C CTA CTA TAG TAA CTA C	GT	TAC TAT GCT ATG GAC TAC TGG	SP2.X	4	B P
2	L5.12.8	TCT ACT ATG ATT ACG AC	G IGA T	AT TAC TAT GCT ATG GAC TAC TOG	SP2.2	4	Weep P
3 1	L5.12.8 L5.12.9	T TTA TTA CTA COO TAO TAO CTA C TC TAC TAT OAT TAC GAO	GG	GCT ATG GAC TAC TOG GCT ATG GAC TAC TOG	FL16.1 SP2.2	4	DI Pe
	12.12.9	TCT ATG ATG GTT AC		C TOR TTT OCT TAC TOG	SP2.9	3	1 1
1	L12.5.9	TCT ATG ATG GTT ACT AC		C TGG TTT GCT TAC TGG	SP2.3	3	¥ -
2	15.12.9	TC TAC TAT GAT TAC	CCT C	TTT GAC TAC TOG TT GAC TAC TGG	SP2.2 SP2.2	2	I Pa
	15.12.9	TC TAC TAT GAT TAC GAC	-			2	
a	le 2 c-d:	D-J sequences (DFL/DS	P) of BDF	1 and L5T/L5T bone man	<u>ow preB</u>	ce	il cultu
c)	cultured BI	0F1 newborn blood, liver, spice	n. bone ma	urrow and "adult" bone marrow o	reB cells	n	ending
	origin	D-segment	NP-sequence		D		trame NP
.1	blood d 7	TT TAT TAC TAC OGT AGT AGC TAC	000 000	T TAC TAT GCT ATG GAC TAC TOG	FL 16.1	4	<u> </u>
21	Brend 7 Brend 21	TTT ATT ACT ACG G	ç	C TAT GCT ATG GAC TAC TGG CT ATG GAC TAC TGG	FL 16.1 SP 2.344	4	1 :
7.1	Sher d 21	TC TAT GAT GGT TAC TCT ACT ATG GTT	ÉCC TC	T TAC TAT GCT ATG GAC TAC TOG	SP 2.34	2	
7.4	Brer d 21	TC TAC TAT GAT	CCA CTC C	AT TAC TAT GCT ATG GAC TAC TOG	SP 2.2	4	÷Ľ, ÷
L1 L2	liver d 28 liver d 29	TCT ATG ATG GTT AC T CTA	TACG TGA	GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG	SP 2.34 SP 2.2	4	
.1	apleas d 7	C CTA CTA TAG TAA	AGG GG	C TAT GCT ATG GAC TAC TGG	FL 16.1	4	- III +
L1	apieen d 21	T CTA C	CC TIT G	AT GCT ATG GAC TAC TOG	SP 2.2	4	11 (+) +
2	aplean d 21 Bm2L1 (w2)	TCT ACT ATG ATT ACG TC TAT GAT GGT TAC		TAT GCT ATG GAC TAC TGG TAC TAT GCT ATG GAC TAC TGG	SP 2.2 SP 2.34	4	1 :
	Bin21,4 (w2)	C CTA CTA TAG TAA CTA C	TAGG	CTACTEG	SP 2.X	2	in i
1	Ben2LA (w2)	CC TAC TAT OG		IGC CAG AGC CTA A TT GCT TAC TG	8P 2.7	3	l +
1	Bm21.5 (m2) Bm21.10 Am21	TCT ACT ATG ATT ACG AC TC TAC TAT GGT AAC T	G GAC GAC	GGA C AC TAC TOG TTT OCT TAC TOG	SP 2.2 SP 2.1/6	2	1 1
	Bm21.12 (w2)	CC TAC TAT AGT AAC TAC	õ	GG TTT GCT TAC TOG	SP 2X	5	-i -I
.1	bm w 3	OCT ACT ATC GTA ACT AC	TOGA	TTT GAC TẠC TGG	SP 2.7	2	H +
A .1	ba w 3 ba w 3	T TTA TTA CTA COG <u>TAG TAG</u> CT CC TAC TAT COT	C COT TO OTO O	T GŤC TGG AC TIT GAC TAC ŤGG	FL 16.1 SP 2.7	1	· · · ·
D.1	basw 3	TCT ACT ATQ GTT AC	TCT	C TAT GCT ATG GAC TAC TGG	SP 2.34	4	u I
23	ba w 3	TCT ACT ATG ATT A	0	C TAT GCT ATG GAC TAC TGG	8P 2.2	4	<u> </u>
0.4 2	bm w 3 bm w 4	A TOG TTA C CC TAC TAT AGT TAC TAT AGT GAC (C TAT GCT ATG GCC TAC TGG TGG TTT GCT TAC TGG	SP 2.34 SP 2.6	4	₩ + I D-
1	baw4	TC TAC TAT GAT TAC GAC	GTG GGG	GCT ATG GAC TAC TGG	SP 22	4	1 4
1	8x:5L2 (w6)	CC TAC TAT AGT AAC TAC		TGG TTT GCT TAC TGG	SP 2.X	3	1 .
3	BraSL2 (wS) BraSL4 (wS)	TTT ATT ACT ACG GTA T CTA CTA TGG <u>TAA</u> CTA C	CCCG AGA G	GG TTT GCT TAC TGG GCC TGG TTT GCT TAC TGG	FL18.1 8P 2.5	3	
	Ban5L6 (w5)	C CTA CTA TAG TTA CGA	11110	TGG TTT GCT TAC TGG	SP 2.6	•	
						3	- H.
1	Bestus (w5)	TC TAC TAT GGT AAC T	т	C TAT GCT ATG GAC TAC TGG	SP 2.1/5	3	ш. - +
1	BeeSLS (wS) BeeSLS (wS)	TC TAC TAT GOT AAC T TC TAC TAT COT AAC TAC	AAT TTC	C TAT GCT ATG GAC TAC TGG GCC TGG TTT GCT TAC TGG	SP 2.1/5 SP 2.1/5	4	+ +
	Bestus (w5)	TC TAC TAT GGT AAC T	AAT TTC BAC GTA C	C TAT GCT ATG GAC TAC TOG GCC TGG TTT GCT TAC TGG GGA G AT TAC TAT GCT ATG GAC SA G TTT GCT TAC TGG	SP 2.1/5 SP 2.1/5 SP 2.6 SP 2.6	4	
1 2 1.1 1	BacSL# (wS) BacSL# (wS) BOB14.2 bas w 15 bm w 15	TC TAC TAT GGT AAC T TC TAC TAT COT AAC TAC CC TAC TAT COT AAC TAC CC TAC TAT AGT TAC TAT AGT TAC C CC TAC TAT AGT TAC TAT AGT TAC C CC TAC TAT AGT AAC TA	AAT TTC AAC GTA (AAC CTT (C TAT GCT ATG GAC TAC TGG GCC TGG TTT GCT TAC TGG GGA G AT TAC TAT GCT ATG GAC A G TTT GCT TAC TGG TTAC TAT GCT ATG GAC TAC TGG	SP 2.1/5 SP 2.1/5 SP 2.8 SP 2.8 SP 2.8	43434	
1 2 1.1 1	BmSL# (w5) BmSL# (w6) BDB14.2 bm w 15 bm w 15 bm w 15	TC TAC TAT GGT AAC T TC TAC TAT CGT AAC TAC CC TAC TAT CGT TAC TAC CC TAC TAT AGT TAC TAT AGT TAC C CC TAC TAT AGT TAC TAT AGT TAC C CC TAC TAT AGT AAC TA CTA CTA TGG <u>IAA</u> CTA C	AAT TTC AAC GTA (AAC CTT (TC OLG	C TAT GCT ATG GAC TAC TGG GCC TGG TTT GCT TAC TGG GGA G AT TAC TAT GCT ATG GAC 3A G ATT GCT ATG GAC 3A G TTT GCT ATG TGG T TAC TAT GCT ATG GAC TAC TGG C TTT GAC TAC TGG	SP 2.16 SP 2.16 SP 2.8 SP 2.8 SP 2.8 SP 2.X SP 2.15	434342	
1 2 1.1 1 2	ButSL& (wS) ButSL® (wS) BOB14.2 bas w 15 bas w 15 bas w 15 bas w 15 bas w 15	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC TAC OC TAC TAT GOT AAC TAC OC TAC TAT AGT TAC TAT AGT TAC C CC TAC TAT AGT TAC TAT AGT TAC C CC TAC TAT AGT ACT A T CTA CTA TOG IAA CTA C C CTA CTA TOG IAA	AAT TTC AAC GTA (AAC CTT (C TAT GCT ATG GAC TAC TGG GCC TGG TTT GCT TAC TGG GGA G AT TAC TAT GCT ATG GAC A G TTT GCT TAC TGG TTAC TAT GCT ATG GAC TAC TGG	SP 2.1/5 SP 2.1/5 SP 2.8 SP 2.8 SP 2.8	4343422	
1 2 1 1 1 2 1 1 2 0	ButSL& (wS) ButSL® (wS) BOB14.2 bas w 15 bas w 15 bas w 15 bas w 15 bas w 15	TC TAC TAT GGT AAC T TC TAC TAT CGT AAC TAC CC TAC TAT CGT TAC TAC CC TAC TAT AGT TAC TAT AGT TAC C CC TAC TAT AGT TAC TAT AGT TAC C CC TAC TAT AGT AAC TA CTA CTA TGG <u>IAA</u> CTA C	AAT TTC AAC GTA (AAC CTT (TC OLG	C TAT GET ATG GAC TAC TOG GCC TOG TTT GCT TAC TOG SGA G AT TAC TAT GCT TAC GG A G TT AC TAT GCT TAC GGA TTAC TAT GCT ATG GAC TAC TOG C TTT GAC TAC TOG TTT GAC TAC TOG	SP 2.16 SP 2.16 SP 2.8 SP 2.8 SP 2.8 SP 2.X SP 2.15	4343422	+ + + - - + + +
1 2 1.1 1 1 1 2 1 2 1 1 2 1 1 1 2 1 1 1 1	BasSL8 (wS) BasSL9 (wS) BOB14.2 bas w 15 bas w 15	TO TAK TAT GOT AAC T TO TAK TAT GOT AAC TAK TO TAK TAT AGT TAK TAT AGT TAK COTAK TAT AGT TAK TAT AGT TAK COTAK TAT AGT TAK TA COTAK TAT AGT TAK TAK TAT AGT TAK COTAK TAT TAG TAK COTAK TAT TAG TAK TAT AT A TAK TAT A TAK TAT A TAK TAK TAT A TAK TAK TAK TAK TAK TAK TAK TAK TAK TAK	AAT TTC BAC GTA (BAC CTT (BAC CTT (TC OLG OLG GGA	C TAT GCT ATG GAC TAC TOG GCC TGA TTI GCT TAC TOG SGA G AT TAC TAT GCT TAC GG A G TTI AC TAT GCT ATG GAC A G TTI GCT TAC TGG TTAC TAT GCT ATG GAC TAC TOO C TTT GAC TAC TGG TTT GAC TAC TGG	SP 2.1.6 SP 2.1.6 SP 2.8 SP 2.8 SP 2.X SP 2.1.5 SP 2.7 D	4343422	+ + + - - + + +
1 2 1.1 1 1 2 1 1 2 1 1 4	BmSL& (vd) BmSL# (vd) 80814.2; bm v 15 bm v 15	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC TAC TC TAC TAT GOT AC TAC COT AC TAT AGT TAC TAC COT AC TAT AGT TAC TAC COT AC TAT AGT AAC TA T CTA CTA TOG IAA CTA CTA TOG IAA CTA CTA TOG IAA CTA CTA TOG IAA Designent CC TAC TAT AGT AAC TAC TTATT ACT ACT ACT ACT TAC TACT ACT ACT ACT CTA CTA TACT ACT ACT CTA CTA TACT ACT ACT CTACT ACT ACT ACT ACT	AAT TTC SAC GTA (SAC CTT (TC GG GGG GGA NP-sequence	C TAT GET ATG GAC TAC TOG GCC TGA TTI GET TAC TOG SGA G AT TAC TAT GCT ATG GAC A TTI GET TAC TGG T TAC TAT GCT ATG GAC TAC TGG C TTI GAC TAC TGG TTI GAC TAT GCA TAC TGG J-segment GCT ATG GAC TAC TGG T TAC TAT GET ATG GAC TAC TGG	SP 2.18 SP 2.18 SP 2.8 SP 2.8 SP 2.18 SP 2.18 SP 2.18 SP 2.7 D SP2.X FL18.1	4343422 J 44	I + I + I + II + II + II + II + II + II
1 2 1.1 1 1 2 1 1 2 1 1 4 1	BacSLS (vc3) BacSLS (vc3) 80814.2 bm v 15 bm v 15 bm v 15 bm v 15 bm v 15 cultured 15 critic PLS-3 PLS-20	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC T TC TAC TAT AGT TAC TAT AGT TAC CC TAC TAT AGT TAC TAT AGT TAC CC TAC TAT AGT TAC TA CC TAC TAT AGT AAC TA CC TAC TAT GG IAG CT AC TAT CG IAG CT TAC TAT AGT AAC TAC TTT ATT ACT AGG GT TCT ACT ATG GTA ACT AC	AAT TTC BAC GTA (BAC CTT (BAC CTT (TC OLG OLG GGA	C TAT GCT ATG GAC TAC TOG GCC TGG TTT GCT TAC TOG SGA G AT TAC TAT GCT TAC GGA G TT GCT TAC TAG G TT GCT TAC TAG C TTT GAC TAC TGG C TTT GAC TAC TGG J-segment GCT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG GCT TAC GCT ATG GAC TAC TGG GCT TAC GCT ATG GAC TAC TGG	SP 2.16 SP 2.6 SP 2.6 SP 2.8 SP 2.15 SP 2.7 D SP2.X FL16.1 SP2.15	4343422 J 443	+ + + + - - - - + + + + + + + + + +
1 2 1.1 1 2 1 1 2 1 1 4 1 2	BmSL& (vd) BmSL# (vd) 80814.2; bm v 15 bm v 15	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC TAC TC TAC TAT GOT AC TAC COT AC TAT AGT TAC TAC COT AC TAT AGT TAC TAC COT AC TAT AGT AAC TA T CTA CTA TOG IAA CTA C CTA CTA TOG IAA CTAC TAC TAT AGT AAC TAC TTAT TACT ACG GT TCT ACT ATG GTA ACT AC TTAT TACT ACG GT	AAT TTC SAC GTA (SAC CTT (TC GG GGG GGA NP-sequence	C TAT GET ATG GAC TAC TOG GEC TOG TT GET TAC TOG SOA G AT TAC TAT OCT ATG GAC 3 G TT GET TAC TAG T TAC TAT GET ATG GAC TAC TOG T TAC TAT GET ATG GAC TAC TOG TTT GAC TAC TAG GET ATG GAC TAC TGG GET TAC TOG GET TAC TOG GET TAC TOG C TOG GT TAC TGG GET TAC TGG	SP 2.16 SP 2.6 SP 2.6 SP 2.6 SP 2.X SP 2.X SP 2.7 D SP 2.7 D SP 2.X FL 16.1 SP 2.15 FL 16.1	4343422 J 44	I + I + I + II + II + II + II + II + II
1 2 1.1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 1 2 2 1.1 1 1 2 2 1.1 1 1 2 2 1.1 1 1 2 2 1.1 1 1 2 2 1.1 1 1 2 2 1.1 1 1 1	BasSLS (w5) BasSLS (w5) BasSLS (w5) BOB142 bas w 15 bas w	ΤC ΤΑΤ COT ΛΑC Τ TC ΤΑC ΤΑΤ COT ΛΑC ΤΑC CC ΤΑC ΤΑΤ AGT ΤΑC ΤΑC CT ΑC ΤΑΤ AGT ΤΑC ΤΑC CC ΤΑC ΤΑΤ AGT ΤΑC ΤΑC CT ΑC ΤΑΤ AGT ΛΑC ΤΑC CT ΑC ΤΑΤ TAG ΤΑC CT ΑC ΤΑΤ AGT ΛΑC ΤΑC CT ΤΑC ΤΑΤ AGT ΛΑC ΤΑC TT ΑT ΤΑC ΤΑC GT CT ΤΑC ΤΑΤ AGT ΛΑC ΤΑC TT ΑT ΤΑCT AGG GT TC ΤΑCT AT GT ΛΑCT AC TT ΑT ΤΑCT AGG GT CT ΤΑCT ΤΑG GTA CCAC CT ΤΑC ΤΑ TAGT AGT ACT AC TT ΑT TACT AGG GT CT ΤΑC ΤΑG GTA CCAC CT ΤΑC ΤΑG GTA CCAC CT ΤΑC ΤΑG GTA CCAC CT ΤΑC ΤΑG	AAT TTC BAC GTA (BAC CTT (TC GG GGG GGA NP-equeno G IAG AAG T AGG	C TAT GET ATG GAC TAC TOG GEC TOG TT GET TAC TOG SGA G AT TAC TAT GET TAC TOG A G TT GET TAC TGG T TAC TAT GET ATG GAC TAC TOG C TTT GAC TAC TOG TTT GAC TAC TOG C TATG GAC TAC TOG GET ATG GAC TAC TOG GET TAC TAG GAC TAC TOG GET TAC TOG T GEC TOG TTT GET TAC TOG GET TAC TOG T GEC TOG TTT GET TAC TOG GET TAC TOG	SP 2.16 SP 2.6 SP 2.6 SP 2.6 SP 2.15 SP 2.7 D SP2.X R16.1 SP2.15 R18.1 SP2.15 R18.1 SP2.15 R18.1 SP2.11	4343422 J 4433	I + I + I + I - II + II + II + II + II +
1 2 1.1 1 1 2 2 1 1 4 1 2 3 1 1 4 1 2 3 1 1 1	BasSLS (w5) BasSLS	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC TAC TC TAC TAT AGT TAC TAT AGT TAC TAC CC TAC TAT AGT TAC TAT AGT TAC C CC TAC TAT AGT TAC TA CC TAC TAT TAG TAC TA CC TA CTA TAG TAG TAC TAC CC TA CTA TAG TAG TAC TAC CC TA CTA TAG TAC TAC TAC TAT AGT AAC TAC TTA TTACT AGT AGT ACT AC TTA ATTACT AGT GTA ACT AC TTA ATTACT AGT GTA ACT AC TTA ATTACT AGT GTA CTAC CC TAC TA TAG CC TAC TATA	AAT TTC BAC GTA (DAC CTT (TC GG GGG GGA NH ^P esquenc G IAG AAG T	C TAT GET ATG GAC TAC TOG GEC TOG TTG GET TAC TOG SGA G AT TAC TAG GAC A G AT TAC TAT GET ATG GAC A G AT TAC TAT GAC TAC TOG T TAC TAT GCT ATG GAC TAC TOG C TTT GAC TAC TOG TTT GAC TAC TOG TTT GAC TAC TOG C TAG GAC TAC TOG C TOG TTT GCT TAC TOG C TOG TTT GCT TAC TOG GCT TAC TOG C TOG TTT GCT TAC TOG C TOG TAC TOG C TOG TAC TOG	9P 2.16 8P 2.16 8P 2.6 8P 2.8 8P 2.1 9P 2.15 8P 2.7 D 8P2.X FL16.1 8P2.11 8P2.11 8P2.11 8P2.11	4343422 J 4453351	+ + + + - + - + - + - - - - - - - -
11 2 1.1 1 1 2 2 1 1 4 1 2 1 1 2 1 1 5	BasSLS (w5) BasSLS (w5) BasSLS (w5) BOB142 bas w 15 bas w	ΤC ΤΑΤ COT ΛΑC Τ TC ΤΑC ΤΑΤ COT ΛΑC ΤΑC CC ΤΑC ΤΑΤ AGT ΤΑC ΤΑC CT ΑC ΤΑΤ AGT ΤΑC ΤΑC CC ΤΑC ΤΑΤ AGT ΤΑC ΤΑC CT ΑC ΤΑΤ AGT ΛΑC ΤΑC CT ΑC ΤΑΤ TAG ΤΑC CT ΑC ΤΑΤ AGT ΛΑC ΤΑC CT ΤΑC ΤΑΤ AGT ΛΑC ΤΑC TT ΑT ΤΑC ΤΑC GT CT ΤΑC ΤΑΤ AGT ΛΑC ΤΑC TT ΑT ΤΑCT AGG GT TC ΤΑCT AT GT ΛΑCT AC TT ΑT ΤΑCT AGG GT CT ΤΑCT ΤΑG GTA CCAC CT ΤΑC ΤΑ TAGT AGT ACT AC TT ΑT TACT AGG GT CT ΤΑC ΤΑG GTA CCAC CT ΤΑC ΤΑG GTA CCAC CT ΤΑC ΤΑG GTA CCAC CT ΤΑC ΤΑG	AAT TTC BAC GTA C AC CTT C TC OG OGG OGA NP-sequence G IAG AAG T AGG AAC GTC CC	C TAT GET ATG GAC TAC TOG GCC TOG TT GCT TAC TOG SGA G AT TAC TAG TAG TAC TOG TH GCT ATG GAC TAC TOG T TAC TAT GCT ATG GAC TAC TOG C TTT GAC TAT GAC TAC TOG C TTT GAC TAC TOG TTT GAC TAT GAC TAC TOG C TAG GAC TAC TGG C TOG TAT GAC TAC TGG C TOG TAT GCT ATG GAC TAC TGG C TOG TAC TGC GAC TAC TGG C TOG TAC TGC GAC TAC TGG C TGG TAC TGC GAC TAC TGG	99 2.16 89 2.16 87 2.8 89 2.8 89 2.15 89 2.7 D 89 2.15 89 2.15 89 2.15 89 2.15 89 2.15 89 2.15 89 2.15 89 2.15 89 2.15 89 2.16 89 2.11 89 2.16 89 2.16 89 2.16 89 2.16 89 2.16 80 2.16	4343422 J J 44333	I + I + I + I - II + II + II + II + II + II + II - II - II - II - II - II - II - II - II + II - II + II - II -
1 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 1 2 2 1 1 1 2 2 1 1 1 2 2 1 1 1 2 2 1 1 1 2 2 1 1 1 2 2 1 1 1 1 2 2 1 1 1 1 2 2 1 1 1 1 2 2 1 1 1 1 2 2 1 1 1 1 2 2 1 1 1 1 2 2 1 1 1 1 1 2 2 1 1 1 1 1 2 1	BandSLS (wd) BandSLS (wd) BandS	TC TAC TAT GOT AAC T TC TAC TAT GOT ACT TAC CC TAC TAT AGT TAC TAC TAC CC TAC TAT AGT TAC TAC TAC CC TAC TAT AGT TAC TA GOT TAC CC TAC TAT AGT AAC TA C TA CTA TOG IAG TAC TAT TOG IAG TAC TAT TAGT AAC TAC TTATT ACT AGT GTA ACT AC TTATT ACT AGT GTA ACT AC TTATT ACT AGT GTA ACT AC TTATT ACT AGT GTA ACT AC CT ACT A TAG CT ACT A TAG CT ACT A TAG CT ACT ATAG CT ACT ATAG TAC TACT TAT ACT ACT ACT TTATT ACT ACT ACT AC CT ACT ATAG CT ACT ATAG TAC TAC TTATT ACT ACT ACT ACT CT ACT ATAG TAC CT ACT ATAG TAC CT ACT ATAG TAC TAC TTATT ACT ACT ACT ACT TTATT ACT ACT AGT ACT ACT CT ACT ATAG TAC	AAT TTC BAC GTA (C AC CTT (C TC GG GGG GGA GGG GGA MP-sequence G IAG AAG T AGG AAC GTC CC G GGG GT	C TAT GET ATG GAC TAC TOG GEC TOG TT GET TAC TOG SGA G AT TAC TAT GET TAC TOG G TT GET TAC TAG TAC TAT GET ATG GAC TAC TOG T TAC TAT GET ATG GAC TAC TOG TT GAC TAC TOG TT GAC TAC TOG GET ATG GAC TAC TOG GET ATG GAC TAC TOG T GEC TOG TTT GAC TAC TOG GET TAC TOG T GEC TOG TAT GAC TAC TOG C TOG TAC TOG C TOG TAC TTC GAT GET TAC T TAC TAT GET ATG GAC TAC TOG GAT TAC TAT GET ATG GAC TAC TOG C TTAC TAT GET ATG GAC TAC TOG C TAC TAT GET ATG GAC TAC TOG C TAC TAT GET ATG GAC TAC TOG C ATT AC TAT GET ATG GAC TAC TOG C TAC TAT GET ATG GAC TAC TOG C ATT AC TAT GET ATG GAC TAC TOG C ATT AC TAT GET ATG GAC TAC TOG C TTAC TAT GET ATG GAC TAC TOG	97 216 57 2.6 57 2.6 57 2.6 57 2.6 57 2.15 57 2.15 57 2.15 57 2.15 57 2.15 57 2.11 57 2.11 57 2.11 57 2.11 57 2.11 57 2.11 57 2.15 57 2.15	4343422 J 4433331442	I + I + I + I + I + I + I + I - II + II + I - II + II +
11 2 1,1 11 11 12 11 12 11 12 11 15 11 15 11	BasSLS (w5) BasSLS	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC T TC TAC TAT GOT AAC TAC COT AC TAT AGT TAC TAT AGT TAC C CC TAC TAT AGT TAC TA GOT TAC CC TAC TAT AGT TAC TA CC TAC TAT TGG TAG TAC CC TAC TAT TGG TAG TAC CC TAC TAT TGG TAG TAC TAC TAT AGT AAC TAC TTA TTACT AGT GTA ACT AC TTA ATTACT AGG GTA CC TAC TAT AGT AAC TA CC TAC TAT AGT AAC TA CT TACT AGT AGT AGT AGT AGC TAC	AAT TTC BAC GTA C TC GG GGG GGA NP-equano G IAG AAG T AGG AAC GTC CC	C TAT GET ATG GAC TAC TOG GCC TOG TT GCT TAC TOG SGA G AT TAC TAG TAG TAC TOG TH GCT ATG GAC TAC TOG T TAC TAT GCT ATG GAC TAC TOG C TTT GAC TAT GAC TAC TOG C TTT GAC TAC TOG TTT GAC TAT GAC TAC TOG C TAG GAC TAC TGG C TOG TAT GAC TAC TGG C TOG TAT GCT ATG GAC TAC TGG C TOG TAT GCT TAC TOG C TTG TAT GCT TAC TGG T TAC TAT GCT ATG GAC TAC TGG GCT TAC TGG C TGG TAC TGG GAC TAC TGG C TGG TAC TGC GAC TAC TGG C TGG TAC TGG GAC TAC TGG C TGG TAC TGC GAC TAC TGG C TGG TAC TGC GAC TAC TGG	97 216 57 2.6 57 2.6 57 2.6 57 2.6 57 2.15 57 2.15 57 2.15 57 2.15 57 2.15 57 2.11 57 2.11 57 2.11 57 2.11 57 2.11 57 2.11 57 2.15 57 2.15	4343422 J 445355144	+ + + + + - - - - - - - - - -
11 2 1.1 11 11 2 2 11 11 11 11 11 11 11 11 11 1	BacLis (not) BacCis (not) BOB14.2 bas w 15 bas w	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC TAC TC TAC TAT AGT TAC TAT AGT TAC COT AC TAT AGT TAC TAT AGT TAC COT TAC TAT AGT TAC TA COT AC TAT AGT TAC TA COT AC TAT TAG TAG TAG TAT AGT AAC TA TACTAT TAG TAG TAC TAT AGT AAC TAC TTA TTACT AGT AGT ACT AC TTA T AGT AGT ACT AC TTACT AGT AGT ACT AC TTACT AT AGT AAC TAC	AAT TTC DAG GTAC TC OLG GOOG GCA GOOG GCA G JAQ AAG T AGG AAC GTC CC G GOOG GT CAG AGG T	C TAT GET ATG GAC TAC TOG GCC TOG TT GCT TAC TOG SGA G AT TAC TAT GCT TAC GGG TAC TAT GCT ATG GAC TAC GGG TTAC TAT GCT ATG GAC TAC TOG C TTT GAC TAC TGG TTT GAC TAT GCT ATG GAC TAC TGG TTT GAC TATG GAC TAC TGG T AC TAT GCT ATG GAC TAC TGG C TGG TTG GAC TAC TGG T GCC TGG TTT GCT TAC TGG T GCC TGG TTT GCT TAC TGG C C TGG TAT GCT ATG GAC TAC TGG GAT TAC GAT GCT ATG GAC TAC TGG C TGG TAG GCT ATG GAC TAC TGG GAT TAC CAT GCT ATG GAC TAC TGG C TTG GAT ATG GAC TAC TGG C TTT GAC TATG TGG C TTT GAC TAT TGG	SP 21.6 SP 2.4 SP 2.4 SP 2.4 SP 2.1 SP 2.1 SP 2.7 D SP 2.7 F 1.6 SP 2.1 SP 2.1	4343422 J 44333314422	I + I + I + I + I + I + I + I + I + I +
	Bancis (noi) Bancis (noi) BOB144 ban v 13 ban v 14 ban v 13 ban v 14 ban v	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC TAC TC TAC TAT AGT TAC TAC TAC COT AC TAT AGT TAC TAC TAC COT AC TAT AGT TAC TAC COT AC TAT AGT TAC TAC COT AC TAT TAG TAC TAC COT AC TAT TAG TAC TAC COT AC TAT TAG TAC TAC TAT TAG TAC TAC TAT AGT AAC TAC TTAT TAC TAC AGG GT COT AC TAT AGT AAC TAC TTAT TAC TAC TAG TAC TAC TCT ACT ATAG COT AC TAT AGT AAC TA COT AC TAT AGT AAC TAC TTAT TAC TAC GAG TAC TAC TCT ACT ATAG COT AC TAT AGT AAC TAC TTAT TAC TAC GAG TAC TAC TCT ACT ATG GTA AC C CTAC TAT AGT AAC TAC TTAT TAC TAC TAC GGT ACT ACC C TAC TAT AGT AAC TAC TTAT TAC TAC GGT ACT ACC C TAC TAT TAG C TAC TAT AGT AAC TAC TTACT ATG GTA ACC C CTAC TAT TAG C TAC TAT TAG C TAC TAT TAG C TAC TAT TAG C TAC TAT AGT ACC TAC TTAC TAC TAG GGA CC C CTAC TAT TAG C TAC TAT TAG C TAC TAT TAG C TAC TAT AGT ACC TAC TTAC TAC TAC TAC C TAC TAT TAG C TAC TAT TAG C TAC TAT AGT ACC TAC TTAC TAC TAC TAC C TAC TAT TAG C TAC TAT TAG C TAC TAT AGT ACC TAC TTAC TAC TAC TAC C TAC TAT TAG C TAC TAT TAG C TAC TAT AGT ACC TAC TTAC TAC TAC TAC TAC C TAC TAT TAG C TAC TAT TAG C TAC TAC TAC TAC TAC C TAC TAC TAC TAC C TAC TAC TAC TAC TAC TAC TAC TAC TAC TA	ANT TTC ANC GTAN TC GG GGG GGA GGG GGA G TAG ANG T AGG ANC GTC CC G GGG GTC CC G GGG GTC CAG AGG T	C TAT GET ATG GAC TAC TOG GEC TOG TT GET TAC TOG SGA G AT TAC TAT GET TAC TOG G TT GET TAC TAG TAC TAT GET ATG GAC TAC TOG T TAC TAT GET ATG GAC TAC TOG TT GAC TAC TOG C TTT GAC TAC TOG GET ATG GAC TAC TOG G C TAG GAC TAC TOG G C TAG TAG GAC TAC TOG G C TAG TAG GAC TAC TOG G C TOG TTT GET TAC TOG G C TOG TAC TTC GAT GET TAC T TAC TAT GET ATG GAC TAC TOG G C TAC TOG C TOG TAC TTC GAT GET TAC TOG GAT TAC TAT GET ATG GAC TAC TOG GAT TAC TAT GCT ATG GAC TAC TOG C TTT GAT TAC TAT GCT ATG GAC TAC TOG	SP 21.6 SP 2.4 SP 2.4 SP 2.4 SP 2.1 SP 2.1 SP 2.7 D SP 2.7 F 1.6 SP 2.1 SP 2.1	4 3 4 2 2 1 4 4 3 3 3 1 4 4 2 2 1 4 4 2 2 1 4 4 2 2 1 4 4 2 2 1 4 1 4	+ + + + + + + + + +
	BacLis (noi) BacCis (noi) BOBLIA BacCis (noi) BOBLIA Bac II ban w 15 ban w	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC T CC TAC TAT GOT ACT TAC TAC CC TAC TAT GOT ACT TAC TAC CC TAC TAT GOT ACT TACT TAC CC TAC TAT GOT AAC TA CC TAC TAT TOG LAG TAC TAT TOG LAG CC TAC TAT GOT AAC TAC CC TAC TAT GOT AAC TAC TTT ATT ACT ACG GOT CC TAC TAT GOT ACT AC CT TAC TAT CT AC GOT ACT AC CT TAC TAT GOT ACT AC CT TAC TAT GOT ACT AC CT TAC TAT CT AC GOT ACT AC CT TAC TAT ACT AC GOT ACT AC CT TAC TAT ACT AC GOT ACT AC CT TAC TAT ACT AC GOT ACT ACT AC CT TAC TAT ACT AC GOT ACT ACT AC CT TAC TAT ACT AC GOT ACT ACT ACT ACT ACT ACT ACT ACT ACT AC	ANT TTC ANC GTA AND CTTC TC GG GGG GGA AND G TAG ANG T AGG ANC GTC CC G GGG GTC CC G GGG GTC CAG AGG T CAG AGG T CAG AGG T	C TAT GET ATG GAC TAC TOG GEC TOG TT GET TAC TOG GAT GET TAC TAG GAC A G TTT GET TAC TAG GAC TAC TAT GET ATG GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG GET ATG GAC TAC TOG GAT ATG GAC TAC TOG C TOG TTT GET TAC TOG C TOG TTT GET TAC TOG C TOG TTT GET TAC TOG C TOG TTT GAT TAC TOG C TTG TAT GAC TAC TOG C TAC TAT GAC TAC TOG C TAC TAT GAC TAC TOG C TAC TAT GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG C TAT GAT ATT GAC TAC TOG C TTT GAT ATG GAC TAC TOG C TTT GAT ATG GAC TAC TOG C TAT GAT ATG GAC TAC TOG C TTT GAT GAC TAC TOG C TAT GAT ATG GAC TAC TOG C TAC TAT GAC TAC TOG C TAC TAC TAC TAC TAC TAC TAC TAC TOG C C TAC TAC TAC TAC TAC TOG C C TAC TAC TAC TAC TAC TOG C C TAC TAC TAC TAC TOG C C TAC TAC TAC TAC TOG C C TAC TAC TAC TAC TAC TOG C C TAC TAC TAC TAC TAC TAC TOG C C TAC TAC TAC TAC TOG C C TAC TAC TAC TAC TOG C C TAC TAC TAC TAC TAC TOG C C TAC TAC TAC TAC TAC TOG C C TAC TAC TAC TAC TOG	SP 21.6 SP 21.6 SP 2.8 SP 2.8 SP 2.7 D SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.15 SP 2.11 SP 2.15 SP 2.16 SP 2.57 M	4 3 4 2 2 1 4 4 3 3 3 1 4 4 2 2 1 1 4 4 2 2 1 1 4 4 2 2 1 1 1 4 4 2 2 1 1 1 1	I + + + + + + + + + + + + + + + + + + +
	Bucks (wd) Bucks (wd)	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC T CC TAC TAT AGT TAC TAC COT AC TAT AGT TAC TAC CC TAC TAT AGT TAC TAC CC TAC TAT AGT AAC TA CC TAC TAT AGT AAC TAC CC TAC TAT TGG IAA CTAC C CTA CTAT TGG IAA CTAC C TAC TAT AGT AAC TAC TTATTACT AGT GTA ACT AC TTATTACT AGT GTA ACT AC TTATTACT AGT GTA ACT AC C TAC TAT AGT AAC TAC TTATTACT AGT GTA ACT AC C TAC TAT AGT AACT AC C TAC TATA C TACT ATAG C TAC TATAG C TAC TAC TAC C TAC TATAG C TAC TAC TAC C TAC TATAG C TAC TAC TAC C TAC TAC TAC TAC C TAC TAC TAC C TAC TAC TAC C TAC TAC TAC TAC C TAC TAC TAC TAC C TAC TAC TAC C TAC TAC TAC TAC C TAC TAC TAC TAC C TAC TAC TAC TAC TAC C TAC TAC TAC TAC TAC TAC C TAC TAC TAC TAC TAC TAC TAC TAC TAC C TAC TAC TAC TAC TAC TAC TAC TAC TAC TA	ANT TTC ANC GTAN TC GG GGG GGA GGG GGA G TAG ANG T AGG ANC GTC CC G GGG GTC CC G GGG GTC CAG AGG T	C TAT GET ATO GAC TAC TOG GEC TOG TIT GET TAC TOG A G AT TAC TAT GET TAC TOG TAC TAT GET ATO GAC TAC TOG C TH GAC TAC TOG C TH GAC TAC TOG C TH GAC TAC TOG C TH GAC TAC TOG C TAG TAG GAC TAC TOG C TAG TAG GAC TAC TOG C TAG TAG GAC TAC TOG C TOG TH GET TAC TOG C TAG TAC TAG GAC TAC TOG C TAG TAC TAG GAC TAC TOG C AT GCT ATO GAC TAC TOG C TAG TAC TAG TAC TAC TOG C TAG TAC TAG CAC TAC TOG C AT GET ATO GAC TAC TOG C AT GET ATO GAC TAC TOG C AT GET ATO GAC TAC TOG C AT TAC TAT GET ATO GAC TAC TOG AC TAC TAT GAC TAC TOG AC TAC TAT GAC TAC TOG AC TAC TAT GAC TAC TOG C AT TAC TAC TAC TAC TOG C AT TAC TAC TAC TAC TOG C AT TAC TAT GAC TAC TOG C AT TAC TAC TAC TAC TOG C AT TAC TAC TAC TAC TOG C AT TAC TAC TAC TAC TOG C AT TAC TAT GAC TAC TOG C AT TAC TAC TAC TOG C AT TAC TOG C AT TAC TAC TAC TAC TOG C AT TAC TAC TOG C AT TAC TAC TAC TAC TOG C AT TAC TAC TOG C AT TAC TAC TAC TAC TOG C AT TAC TAC TOG C AT TAC TAC TOG C AT TAC TAC TAC TOG C AT TAC TAC TAC TAC TAC TAC TAC TOG C AT TAC TAC TAC TAC TAC TAC TAC TAC TA	SP 21.6 SP 21.6 SP 2.8 SP 2.8 SP 2.4 SP 2.1 SP 2.1	4 3 4 4 2 2 1 4 4 3 3 3 1 4 4 2 2 1 4 4 2 2 1 4 4 2 2 1 1 4 4 5 3 3 1 1 4 4 2 2 1 1 1 4 1 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1	I + + + + + + + + + + + + + + + + + + +
1 2 1.1 1 2 2 1.1 1 2 2 1.1 1 2 2 1.1 1 2 2 1.1 1 2 2 2 1.1 1 2 2 2 1 1 1 1 2 2 2 1 1 1 1 2 2 2 1 1 1 1 2 2 2 1 1 1 1 2 2 2 1 1 1 1 2 2 2 1 1 1 1 1 1 1 2 2 2 1	Band Si (no) Band Si (no) PLS-30 PLS-	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC TAC TC TAC TAT GOT ACTAC COT AAC TAT GOT ACTAC COT ACTA TAGT TAC TAC COT ACTA TAGT TAC TAC TAC TAC TAGT AAC TA CTA CTA TAGT AAC TAC TACTAT TAGT AAC TAC TTA ST TACT ACT ACTAC TTA ST ACT ACTAC TTA ST ACT ACTAC TTA ST ACT ACTAC TTA ST ACT ACTAC TC ACTA TAG ST ACTAC TTACT ACTAC CT ACTA TAG ST ACTAC TC ACTAC TAG ST ACTAC CT ACTA TAG ST ACTAC CT ACTA TAG ST ACTAC CT ACTAC TAG ACTAC	An TTC ANC GTAN ANC GTTC TC GG GGG GGA G TAG ANG T AGG ANC GTC CC G GGG GGT C GDG GT C GDG GT C GDG GT C GDG GT C GDG GT C GAG AGG C GAG C	C TAT GET ATG GAC TAC TOG GCC TGG TT GCT TAC TGG GAT GG AT TAC TAT GCT ATG GAC G TT GCT TAT GCT TAT GG TAC TAT GCT ATG GAC TAC TGG TTAC TAT GCT ATG GAC TAC TGG C TTT GAC TAC TGG GCT TAT GCT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG GCT TAC TGG GCT TAC TGG C TGG TAC TGG GAC TAC TGG C TTAC TAT GAC TAC TGG C TGG TAC TGG C TGG TAC TGG GAC TAC TGG C TAC TAT GAC TAC TGG C TGG TAC TGG GAC TAC TGG C TTAC TAT GAC TAC TGG C TAC TAT GAC TAC TGG C TTG CAC TAC TGG C TAC TGG C TAC TGG C CAC TGC TGG C TAC TGG C CAC TGG C TAC TGG C CAC TGG C TAC TGG C CAC TGC TGG C TAC TGG C CAC TGG C TGG C CGG C CAC TGG C CCCCCCCCCCCCCCCC	SP 21.6 SP 2.6 SP 2.6 SP 2.6 SP 2.7 SP 2.	4 3 4 2 2 1 4 4 3 3 3 1 4 4 2 2 1 1 4 4 2 2 1 1 4 4 2 2 1 1 1 4 4 2 2 1 1 1 1	I + + + + + + + + + + + + + + + + + + +
	Bacts (no) Bacts (no) Bacts (no) Bacts (no) Bacts (no) Bacts (no) bar w 15 bar w 15 bar w 15 bar w 15 bar w 15 bar w 15 cright PLS-3 PLS-30 PL	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC TAC TC TAC TAT GOT ACT TAC TAC COT AC TAT AGT TAC TAC COT AC TAT AGT TAC TAC TAC TAT AGT AAC TA AGT TAC C COT ACT A TOG IAA CTA C CTA CTA TOG IAA CTA C CTA CTA TOG IAA CTA C TTA ST ACT AT AGT AAC TAC TTA ST ACT AGT AAC TAC TTA ST ACT AGT AGT ACT TAC TTA ST ACT AGT GTA ACT AC TTA ST ACT AGT GTA ACT AC CTA CTA IAG CTA CTA IAG CTA CTA IAG CTA CTA TAG GTA ACT AC TTA ST ACT AGT AGT ACT AC CTA CTA IAG CTA CTA IAG CTA CTA TAG GTA ACT AC CTA CTA IAG CTA CTA TAG TAC TAC CTA CTA TAG TAC TAC CTA CTA TAG TAC C CTA CTA TAG TAC C CTA CTA TAG TAC C CTA CTA TAG TAC C CTA CTA TAG ACT AC C CTA CTA GG A C CTA CTA GG GA C CTA CTA GG GA	ANT TTC ANC GTA AND CTTC TC GG GGG GGA AND G TAG ANG T AGG ANC GTC CC G GGG GTC CC G GGG GTC CAG AGG T CAG AGG T CAG AGG T	C TAT GET ATG GAC TAC TOG GCC TOG TT GCT TAC TOG GAG G AT TAC TAT GCT TAT GG G TT GCT TAT GCT TAT GG G TT GCT TAT GAC TAC TOG T TAC TAT GCT ATG GAC TAC TOG C TTT GAC TAC TOG GCT ATG GAC TAC TOG GCT ATG GAC TAC TOG GCT TAC TAT GCT ATG GAC TAC TOG G C TOG TTT GAC TAC TOG G C TAC TAT GCT ATG GAC TAC TOG G C TAC TAT GCT ATG GAC TAC TOG GAT TAC TAT GCT ATG GAC TAC TOG G TAC TAT GCT ATG GAC TAC TOG G C TGG TAC TAG TGAC TAC TOG GAT TAC TAT GCT ATG GAC TAC TOG AC TAC TAT GCT ATG GAC TAC TOG AC TAC TAT GCT ATG GAC TAC TOG G TAC TAT GCT ATG GAC TAC TOG C TTG GAC TAC TGG TAC TAC TGG C TAC TAT GCT ATG GAC TAC TOG GCT TAC TAT GCT ATG GAC TAC TOG C TAC GTAT GCT ATG GAC TAC TOG	SP 21.6 SP 21.6 SP 2.8 SP 2.8 SP 2.4 SP 2.1 SP 2.15 SP 2.16 SP 2.16 SP 2.16 SP 2.15 SP 2.16 SP 2.16 SP 2.16 SP 2.15 SP 2.15	4 3 4 3 4 2 2 1 4 4 3 3 3 1 4 4 2 2 4 1 2 2 4	I + i + i + i + i + i + i + i + i
	Bucks (no) Bucks (no)	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC T CC TAC TAT GOT ACT TAC TAC CC TAC TAT AGT TAC TAC TAC CC TAC TAT AGT TAC TAC CC TAC TAT AGT AAC TA CC TAC TAT AGT AAC TAC C TAC TAT TGG IAA CTAC C TAC TAT AGT AAC TAC TTAT ACT AGT AAC TAC TTAT ACT AGG GAT CC CC TAC TAT AGT AAC TAC TTAT ACT AGG GAT AGT AGC TAC C TAC TAT AGT ACT AC C TAC TAG GAC C TAC ACT AGG AC C TAC ACT AGG AC C TAC ACT AGG AC	An TTC ANC GTAN ANC GTTC TC GG GGG GGA G TAG ANG T AGG ANC GTC CC G GGG GGT C GDG GT C GDG GT C GDG GT C GDG GT C GDG GT C GAG AGG C GAG C	C TAT GET ATG GAC TAC TOG GEC TOG TT GET TAC TOG A G TT GET TAT GET TAC TOG G TT G CT TAC TOG T TAC TAT GCT ATG GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG TTT GAC TAC TOG C TATG GAC TAC TOG C TAG TATG GAC TAC TOG C TOG TTT GCT TAC TOG C TAG TAC TTG GAC TAC TOG C TTT GAC TATG GAC TAC TOG C TTT GAC TATG GAC TAC TOG C TAT GCT ATG GAC TAC TOG C TAC GCT ATG GAC TAC TOG	SP 21.6 SP 21.6 SP 2.8 SP 2.8 SP 2.7 SP 2.7	4 3 4 3 4 2 2 1 1 4 4 3 3 3 3 1 4 4 2 2 1 1 1 4 4 2 2 1 1 1 2 2 4 4	I + I + I + I + I + I - II + I - I - I - I - I - I - I - I + I - I + I - I + I - I - I - I - I - I - I - I -
	Bacts (no) Bacts (no) Bacts (no) Bacts (no) Bacts (no) Bacts (no) bar w 15 bar w 15 bar w 15 bar w 15 bar w 15 bar w 15 cright PLS-3 PLS-30 PL	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC T CC TAC TAT GOT ACT TAC TAC CC TAC TAT AGT TAC TAC TAC CC TAC TAT AGT TAC TAC CC TAC TAT AGT AAC TAC TAC TAT TAG IAAC TAC C TAC TAT TAG IAAC TAC C TAC TAT AGT AAC TAC TTATTACT AGT AAC TAC TTATTACT AGT GAAC TAC TTATTACT AGT GAAC TAC TTATTACT AGT GAAC TAC TTATTACT AGT GAAC TAC C TAC TATAG TAC TAC C TAC TATAG TAC TAC TTATTACT AGT GAC TAC C TAC TATAG TAC TAC TTATTACT AGT GAC TAC C TAC TATAG TAC TAC C TAC TA TAG TAC TAC C TAC TA G GAC C TAC ACT GG GAC C TAC TAG GG C TAC TAG GG GC C TAC TAG GG GAC	An TTC ANC GTAN ANC GTTC TC GG GGG GGA G TAG ANG T AGG ANC GTC CC G GGG GGT C GDG GT C GDG GT C GDG GT C GDG GT C GDG GT C GAG AGG C GAG C	C TAT GET ATG GAC TAC TOG GEC TOG TT GET TAC TOG GAT GET TAC TAG GAC A G TTT GET TAC TAG G TT GET TAC TAG G TTT GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG G T TAC TAT GET ATG GAC TAC TOG G T AG TAG GAC TAC TOG C TOG TTT GCT TAC TOG G T TAC TAT GCT ATG GAC TAC TOG G TAT GCT ATG GAC TAC TOG C TTT GCT ATG GAC TAC TOG C TAT GCT ATG GAC TAC TOG C TAC CTAC TOG C TAC TOG C TAC CTAC TOG C TAC TOG C TAT GCT ATG GAC TAC TOG C TAT GCT TATG GAC TAC TOG C TAT GCT TATG CAC TAC TOG C TAT GCT TATG GAC TAC TOG	SP 21.6 SP 21.6 SP 2.8 SP 2.8 SP 2.4 SP 2.1 SP 2.1	4 3 4 3 4 2 2 1 4 4 3 3 3 1 4 4 2 2 4 1 2 2 4	I + + + + + + + + + + + + + + + + + + +
	Bacts (no) Bacts (no) Bacts (no) Bacts (no) Bacts (no) Bacts (no) bar w 15 bar w 15	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC TAC TC TAC TAT GOT ACTAC COT AC TAT AGT TAC TAC COT ACTA TAGT TAC TAC COT ACTA TAGT AAC TA AGT TAC C COT ACTA TAGT AAC TAC TCTA CTA TAGT AAC TAC TTATTACT ACTA TAGT AAC TAC TTA TTACT ACTA AGT AAC TAC TTT ATTACT ACTA GOT ACTAC TTT ATTACT ACTA GOT ACTAC TTT ATTACT ACTA GOT ACTAC TTT ATTACT ACTAC TTA TACT ACTAC CTA CTA TAGT ACTAC TTA TACT ACTAC CTA CTA TAGT ACTAC TTA TACT ACTAC TTATTACT ACTAC TTATTACT ACTAC TTATTACT ACTAC CTA CTA TAGT ACTAC TTATTACT ACTAC CTA CTA TAGT ACTAC TTATTACT ACTAC CTA CTA TAGT ACTAC CTA CTA TAGT ACTAC CTA CTA TAGT ACTAC CTA CTA TAGT ACTAC CTA CTA GOT ACC CTA CTA CTA GOT ACC CTA CTA CTA GOT ACC CTA CTA CTA GOT ACC CTA CTA CTA CTAC	ANT THE SAC STANDES CITIC TE GAG GGG GGA GGA G IAG AAG T AGG AAC GTE CC C G GGG GT C GAG AGG T C BDF1 BI NP sequence CA	C TAT GET ATG GAC TAC TOG GEC TOG TT GET TAC TOG GAG G AT TAC TAT GET TAC TOG G TT GET TAC TAG G TT GET TAC TAG T TAC TAT GET ATG GAC TAC TOG C TT GAC TAC TOG C TT GAC TAC TOG GET TAC TAT GET ATG GAC TAC TOG G CT ATG GAC TAC TOG G CT TAC TAT GET ATG GAC TAC TOG G C TAG TAG GAC TAC TOG G C TAG GAC TAC TOG G C TAG TAG GAC TAC TOG G C TAG TAG GAC TAC TOG AC TAC TAT GCT ATG GAC TAC TOG AC TAC TAT GCT ATG GAC TAC TOG C TAT GCT TATG GAC TAC TOG	SP 21.6 SP 2.1.6 SP 2.8 SP 2.8 SP 2.8 SP 2.1 SP 2.1 SP 2.15 SP 2.15	4343422 r J 44333314422 <u>J</u> 2244443	I + + + + + + + + + + + + + + + + + + +
	Bucks (no) Bucks (no)	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC T CC TAC TAT GOT ACT TAC TAC CC TAC TAT AGT TAC TAC TAC CC TAC TAT AGT TAC TACT TAC CC TAC TAT AGT AAC TAC TAC TAT TAGT AAC TAC C TAC TAT TAGT AAC TAC C TAC TAT AGT AAC TAC TT ATT ACT AGT AAC TAC TT ATT ACT AGT GAT AGT AC C TAC TAT AGT AAC TAC TT ATT ACT AGT GAT AGT AC C TAC TAT AGT ACT A C TAC TAT AGT ACT A C TAC TAG GAC C TAC TA GAG C TAC TAG GAC C TAC TAG GAC	An TTC ALC GTAL ALC GTAL TC GG GGG GGA G TAG ALG ALC GTC CC G GGG GGT CAG AGG T C BDF1 ar NP-sequence	C TAT GET ATG GAC TAC TOG GEC TOG TT GET TAC TOG A G TT GET TAT GET TAT GEG T TAC TAT GET ATG GAC TAC TOG C TTG GAC TAC TOG C TTG GAC TAC TOG C TTG GAC TAC TOG C TAG GAC TAC TOG C TAG GAC TAC TOG C TOG TTG GAC TAC TOG C TAG GAC TAC TOG C TAG GAC TAC TOG C TAT GAC TAC TOG C TAC TOG C TAC TOG C TAC TOG C TAC TOG C TAC TOG C TAC TAC TOG C TAC TOG C TAC C TAC TOG C TAC TOG C TAC TOG C TAC TOG C TAC TOG C TAC C TAC TOG C C C C TAC TOG C C C C	SP 21.6 SP 2.6 SP 2.6 SP 2.6 SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.1 SP 2.1 S	4343422 J 44333314422 III J 22444432	I + I + I + I + I + I + I + I +
	Buckle (nois) Buckle (nois) Bu	TC TAC TAT GGT AAC T TC TAC TAT GGT AAC T TC TAC TAT GGT AAC TAC CC TAC TAT AGT TAC TAC TAC CC TAC TAT AGT TAC TACT TAC CC TAC TAT AGT AAC TAC CC TAC TAT TGG IAA CTAC C TAC TAT TGG IAA CTAC C TAC TAT AGT AAC TAC TT ATT ACT AGG GGT CT AC TAT AGT AAC TAC TT ATT ACT AGG GAT AGC TAC C TAC TAT AGT AAC TAC TT ATT ACT AGG GAT AGC TAC C TAC TAT AGT ACT AC C TAC TAG GAT AGT AGC TAC C TAC TA GGA AC C TAC TAG GAC C TAC TAG AGC C TAC C TAG ACC C TAC C TAG AGC C TAC C TAG C TAG C C C TAC C TAG C C C TAC C C C C C C C C TAC C C C C C C C C TAC C C C C C C C C C TAC C C C C C C C C C C TAC C C C C C C C C C TAC C C C C C C C C C C TAC C C C C C C C C C TAC C C C C C C C C C C TAC C C C C C C C C C C C TAC C C C C C C C C C C C C C C C C C	ANT TTC AAC GTA AAC CTTC TC GG GGG GGA GGG GGA G IAG AAG T AGG AAC GTC CC G GGG GTC CC G GGG GTC CC G GGG GTC CC G GG G G G G	C TAT GET ATG GAC TAC TOG GEC TOG TT GET TAC TOG A G TTT GET TAT GET TAC TOG G TT GET TAC TOG G TT GET TAC TOG T TAC TAT GCT ATG GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG G T TAC TAT GCT ATG GAC TAC TOG C TOG TTT GCT TAC TOG C TAT GCT ATG GAC TAC TOG C TTG C TAT GCT AC TOG C TTG C TAT GCT TAC TOG C TTG C TAT GCT ATG GAC TAC TOG C TTG C TAT GCT ATG GAC TAC TOG C TTT GCT ATG GAC TAC TOG C TAT GCT TAC TOG C C TAC C C C C C C C C C C C C C C C	SP 21.6 SP 2.16 SP 2.8 SP 2.8 SP 2.8 SP 2.7 D SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.15 SP 2.11 SP 2.	4343422 r J 44333314422 r <u>I</u> 2244443233	I + + + + + + + + + + + + + + + + + + +
	Buckle (nois) Buckle (nois) Bu	TC TAC TAT GGT AAC T TC TAC TAT GGT AAC T TC TAC TAT GGT AAC TAC CC TAC TAT AGT TAC TAC TAC CC TAC TAT AGT TAC TA GGT TAC C CC TAC TAT AGT AAC TAC CC TAC TAT TGG IAA CTA C CTAC TAT TGG IAG TTA STT ACT AGT AAC TAC TTA STT ACT AGT AAC TAC TTA STT ACT AGT AAC TAC TTA STT ACT AGT ACT AC CT TAC TAT AGT AAC TAC TTA STT ACT AGG GT CT AC TAT AGT ACT AC CT AC TAG GT ACT AC CT AC TAG GT ACT AC CT AC TAG GCA CT AC TAG GCA CT AC TAG GCA CT AC TGG GCA	ANT TTC JAC OTAL AC OTAL TC ORG GGG GGA G IAG AAG T AC GTC CC G GACA G GACA G G GG GG GG GG	C TAT GET ATG GAC TAC TOG GEC TOG TT GET TAC TOG A G TT GET ATG CT TAC TOG TAC TAT GET ATG GAC TAC TOG TAC TAT GET ATG GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG C TAT GET ATG GAC TAC TOG GET TAC TAT GET ATG GAC TAC TOG C TAC TAT GET ATG GAC TAC TOG GET TAC TAT G CT ATG GAC TAC TOG C TOG TTT GET TAC TOG C TOG TAC TOG C TOG TAC TOG C TAC TAT GET ATG GAC TAC TOG C TAT GET TATG GAC TAC TOG	SP 21.65 SP 2.16 SP 2.8 SP 2.8 SP 2.8 SP 2.15 SP 2.5 SP 2.5 S	4343422 J J 44333314422 UUC 1 J 22444432334	I + I + I + I + II + II + II + II + II + II + II - II + II - II + II +
	Buckla (nois) Buckla (nois) Buckla (nois) Buckla (nois) bus w 15 bus w 15 b	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC T TC TAC TAT GOT ACT TAC TAC CC TAC TAT AGT TAC TAC TAC CC TAC TAT AGT TAC TACT TACC CC TAC TAT AGT AAC TAC CC TAC TAT TOG LAG TTA CTT TOG LAG CC TAC TAT AGT AAC TAC TTA CTT TAGT AGT AAC TAC TTA CTT AGT AGT AAC TAC TTA TAT TAC TAGG GAT CAC CC TAC TAT AGT AAC TAC TTA TAT TACT AGG GAT CAC CC TAC TAT AGT AGT AAC TAC CT TAC TAT AGT AGT AAC TAC CT TAC TAT AGT AGT ACT AC CT TAC TAT AGT AGT AAC TAC CT TAC TAT AGT AGT AAC TAC CT TAC TAT AGT AGT AAC TAC CT TAC TAT AGT ACT AC CT TAC TA GG GAT CAC CT AC TAG GAC CT AC TAG GG AC CT AC TGG GAC CT ACT GGG CAC CT ACT CT GGG CAC CT ACT GGG CAC	ANT TTC AAC GTA AAC CTTC TC GG GGG GGA GGG GGA G IAG AAG T AGG AAC GTC CC G GGG GTC CC G GGG GTC CC G GGG GTC CC G GG G G G G	C TAT GET ATG GAC TAC TGG GEC TGG TT GET TAC TGG G TT GET ATG GTAT G GAC A G TTT GET TAC TGG T TAC TAT GCT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG C TTT GAC TAC TGG G T TG GAC TAC TGG G T TAC TAT G GAC TAC TGG G T TAC TAT G GAC TAC TGG G T TAC TAT G GAC TAC TGG C TGG TTT GCT TAC TGG C TGG TTT GAC TAC TGG G TAC TGG GAC TAC TGG G TAC TGG GAC TAC TGG C TGG TTT GCT TAC TGG C TGG TTT GAC TAC TGG C TGG TTG GAC TAC TGG C TGG TTG GAC TAC TGG C TGG TTG GAC TAC TGG C TTG GTA TG GAC TAC TGG AC TAC TTT GAC TAC TGG C TAT GCT ATG GAC TAC TGG	SP 21.6 SP 2.16 SP 2.8 SP 2.8 SP 2.8 SP 2.7 D SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.15 SP 2.11 SP 2.1	4343422 J 44333314422 Ung 1 J 224444323344	I + I + I + I + I + I + I + I +
	Bucks (no) Bucks (no)	TC TAC TAT GOT AAC T TC TAC TAT GOT AAC T CC TAC TAT GOT ACTAC COT AC TAT AGT TAC TAC COT AC TAT AGT TAC TAC CC TAC TAT AGT ACTAC TAC TAT TGO IAA CTAC CC TAC TAT TGO IAA CTAC CTAC TAT TGO IAA CTAC TTATTACT ACT ACTAC TTATTACT ACT ACTAC TTATTACT ACT GOT ACTAC TTATTACT ACT GOT ACTAC CTAC TAT AGT ACTAC TTATTACT ACT GOT ACTAC CTAC TAT AGT ACTAC CTAC TATAGT ACTAC TTATTACT ACTAC CTAC TATAGT ACTAC CTAC TAG GOT ACTAC CTAC TAG GOT ACTAC CTAC TAG GOT CTAC TAG GOT CTAC TGO GAC CTAC TAG GOT ACTAC CTAC TAG GOT ACC CTAC TAG G	ANT TTC JAC OTAL AC OTAL TC ORG GGG GGA G IAG AAG T AC GTC CC G GACA G GACA G G GG GG GG GG	C TAT GET ATG GAC TAC TOG GEC TOG TT GET TAC TOG A GET TAG TAT OCT TAC TOG TAC TAT GET ATG GAC TAC TOG TAC TAT GET ATG GAC TAC TOG TAC TAT GET ATG GAC TAC TOG TT GAC TAT GET ATG GAC TAC TOG C TTT GAC TAC TOG C TAT GET ATG GAC TAC TOG GET TAC TAT GET ATG GAC TAC TOG C TOG TTT GET TAC TOG C TOG TTT GET TAC TOG GAT TAC TAT GET ATG GAC TAC TOG C TOG TTT GET TAC TOG C TOG TTT GET TAC TOG GAT TAC TAT GET ATG GAC TAC TOG C TAC TOG TAT GET ATG GAC TAC TOG C TAC TOG TAT GET ATG GAC TAC TOG C TAC TAC TOG C TAC TAT GET ATG GAC TAC TOG C TAG GAT TAC TAT GAC TAC TOG C TAT GET ATG GAC TAC TOG C TAG GET ATG GAC TAC TOG	SP 21.65 SP 2.16 SP 2.8 SP 2.8 SP 2.8 SP 2.15 SP 2.5 SP 2.5 S	4343422 J J 44333314422 UUC 1 J 22444432334	I + I + I + I + I + II + II + II + II + II - II + II - II + II +
	Buckla (nois) Buckla (nois) Buckla (nois) Buckla (nois) bus w 15 bus w 15 b	TC TAC TAT GGT AAC T TC TAC TAT GGT AAC T TC TAC TAT GGT AAC TAC CC TAC TAT AGT TAC TAC TACT TAC CC TAC TAT AGT TAC TA CAT TAC CC TAC TAT AGT AAC TAC CC TAC TAT AGT AAC TAC TC TA CTA TAGT AAC TAC TT ATT AGT AGT ACT AC TT ATT AGT AGT ACT AC TT ATT AGT AGT ACT AC TT ATT AGT AGT ACT AC CT A CT AGT AGT ACT AC CT A CT AGT AGT ACT AC CT A CT AG GTA CGA C C TAC TA TAG TAC TAC TT ATT AGT AGT ACT AC TT ATT AGT AGT ACT AC CT A CT AG GTA CGA C C TAC TA GGT AGT AGT AGC TAC CT ACT AGT AGT ACT A C TAC TAG GGA C CT AC TAG GGA C CT AC TAG GGA C CT ACT GGG GAC CT ACT GGG GAC CT ACT GGG GAC CT ACT GG GAC C TAC TGG GGA C C TAC TGG GGA C	ANT TTC ANC GTAC TC OLG GGG GGA G IAG AAG G IAG AAG T AC GTC CC G COC CT G G G G G G G G G G G G G	C TAT GET ATG GAC TAC TOG GEC TOG TTT GET TAC TOG GAT GET TAC TAG A TTAC TAT GET TAT GET A G TTT GET TAC TOG C TTAC TAT GET ATG GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG C TAG TAT GAC TAC TOG C TAG TAT GET ATG GAC TAC TOG C TOG TTT GET TAC TOG C TOG TTT GET TAC TOG C TOG TTT GET TAC TOG C TOG TAT GET ATG GAC TAC TOG GAT TAC TAT GET ATG GAC TAC TOG C TOG TTT GET TAC TOG C TOG TTT GET TAC TOG C TOG TAT GET ATG GAC TAC TOG C TAG TAG CAT ATG GAC TAC TOG C TAG TAG TAG TAG TAC TOG C TAG TAG TAG TAG TAC TOG C TTAC TAT GET ATG GAC TAC TOG C TAT GET ATG GAC TAC TOG AT TAC TAT GCT ATG GAC TAC TOG C TAT GET ATG GAC TAC TOG C TAT GCT ATG GAC TAC TOG	SP 21.6 SP 21.6 SP 2.8 SP 2.8 SP 2.8 SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.15 SP 2.16 SP 2.16	4343422 J 443333314422 Unt	I + I + I + I + I + I + I + I + I - I -
	Bactis (noi) Bactis (noi) Bacti	TC TAC TAT GGT AAC T TC TAC TAT GGT AAC T TC TAC TAT GGT AAC TAC CC TAC TAT AGT TAC TAC TAC CC TAC TAT AGT TAC TACT TAC CC TAC TAT AGT AAC TA CC TAC TAT AGT AAC TAC CC TAC TAT TGG IAA TTA CTT AGT AAC TAC TTA CTT AGT AGT AAC TAC TTA TAT TACT AGG GAT CC TAC TAT AGT AAC TAC TTA TAT ACT AGG GAT CC TAC TAT AGT AAC TAC TTA TAT ACT AGG GAT CC TAC TAT AGT AAC TAC TTA TAT ACT AGG GAT CC TAC TAT AGT AAC TAC TTA TAT ACT AGG GAT CC TAC TAT AGT AAC TAC CT AC TAT AGT ACT AC CC TAC TAT AGT ACC CC TAC CC TAT AGT CC TAC TAT AGT ACC CC TAC TAC TAT AGT ACC CC TAC TAT AGT ACC CC TAC TAC TAT AGT ACC CC TAC TAC TAT AGT ACC CC TAC TAT ACC ACC CC TAC TAC TACC ACC CC TAC TAC TACC ACC CC TACC TACC ACC C	ANT TTC MC GTALA MP GROWN G LAG ANG T AG ANC GTC CC G GAG AGG T CA G G GG GG T CT CT	C TAT GET ATG GAC TAC TGG GEC TGG TT GET TAC TGG GAT GA AT TAC TAT GET TAT GEG A G TT GET TAT GET TAC TAT GET ATG GAC TAC TGG T TAC TAT GET ATG GAC TAC TGG TTAC TAT GET ATG GAC TAC TGG TTT GAC TAC TGG GET ATG GAC TAC TGG C TGG TTT GAC TAC TGG C TGG TTT GAC TAC TGG C TGG TTT GET TAC TGG C TGG TAT GGC TAC TGG C TGG TAT GGC TAC TGG C TGG TAC TGG GAT TAC TAT GET ATG GAC TAC TGG C TGG TAC TGG C TGG TAC TGG C TGG TAC TGG C TGG TAC TGG C TTG GAC TAC TGG C TGG TAC TGG C TTG GAC TAC TGG C TTG GAC TAC TGG C TGG TAC TGG C TGG TAC TGG C TGG TAC TGG C TAC TGG C TAC TGG C TAC TGG C TAC TGG C TAC GCT ATG GAC TAC TGG C TAC GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG	SP 21.6 SP 2.16 SP 2.6 SP 2.6 SP 2.8 SP 2.7 D SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.15 SP 2.15 SP 2.15 SP 2.16 SP 2.16	4343422 J 44333314422 III J 2244443233444444	I + I + I + I + I + I + I + I +
	Bucks (no) Bucks (no)	TC TAC TAT GGT AAC T TC TAC TAT GGT AAC T TC TAC TAT GGT AAC TAC CC TAC TAT AGT TAC TAC TACT TACC CC TAC TAT AGT TAC TA CAC TAC TAT TAGT AAC TAC CC TAC TAT AGT AAC TAC CC TAC TAT TAGT AAC TAC TT ATT ACT AGT AAC TAC TT ATT ACT AGT AAC TAC TT ATT ACT AGT GTA ACT AC TT ATT ACT AGG GTA CGA C CC TAC TAT AGT AAC TAC TT ATT ACT AGG GTA CGA C CC TAC TAT AGT AAC TAC TT ATT ACT AGG GTA CGA C CC TAC TAT AGT AAC TAC TT ATT ACT AGG GTA CGA C CC TAC TAT AGT AAC TAC TT ATT ACT AGG GTA CGA C CC TAC TAT AGT AAC TAC TT ATT ACT AGG GTA CGA C CC TAC TAT AGT AAC TAC TT ATT ACT AGG GTA CGA C CC TAC TA GTA GTA ACT AC TT ATT ACT AGG GAC CC TAC TA GG GAC CT ACT GGG GAC CT ACT GGG GAC CT ACT GG GAC	ANT TTC ANC GTAC ANC GTTC TC OLG GGG GGA G IAG AAG G IAG AAG T AG AAC GTC CC G COC GT GA G G G G G G G G G G G G G	C TAT GET ATG GAC TAC TOG GEC TOG TT GET TAC TOG A G TTT GET TAT GET TAT GEG T TAC TAT GET ATG GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG C TAG TAT GET ATG GAC TAC TOG C TAG TAT GCT ATG GAC TAC TOG C TOG TTT GCT TAC TOG C TTG GAC TAC TOG C TAG TAG TAC TAC TOG C TAG TAG TAC TAC TOG C TAG TAG TAC TTG GAC TAC TOG C TAG TAT GCT ATG GAC TAC TOG C TTG GAT TC GAT GCT TAC TOG C TTG GAT TC GAT GCT TAC TOG C TTG GAT ATG GAC TAC TOG C TTG GAT CAT GCT ATG GAC TAC TOG C TTG GAT GCT ATG GAC TAC TOG C TAT GCT ATG GAC TAC TOG	SP 21.6 SP 21.6 SP 21.6 SP 24.8 SP 25.7 D D SP 21.6 SP 21.7 SP 21.7 SP 21.7 FL16.1 SP 21.15 SP 21.15 SP 21.15 SP 21.16 SP 21.17 R116.1 SP 21.16 SP 21.17 R116.1 SP 21.16 SP 21.17 Cell Cull D D D D D D D D D D D D D D SP 2.07.8 D D D D D D D D D D D </td <td>4343422 J 44333314422 III J 2244444323344444443</td> <td>I + + + + + + + + + + + + + + + + + + +</td>	4343422 J 44333314422 III J 2244444323344444443	I + + + + + + + + + + + + + + + + + + +
	Bactis (noi) Bactis (noi) Bacti	TC TAC TAT GGT AAC T TC TAC TAT GGT AAC T TC TAC TAT GGT AAC TAC CC TAC TAT AGT TAC TAC TAC CC TAC TAT AGT TAC TACT TAC CC TAC TAT AGT AAC TAC CC TAC TAT AGT AAC TAC CC TAC TAT TGG IAA CTA C C TAC TAT AGT AAC TAC TTA GTA TAT TACT AGG IAG CC TAC TAT AGT AAC TAC TTT ATT ACT AGG GGT CT AC TAT AGT AAC TAC TTT ATT ACT AGG GA CC TAC TAT AGT AAC TAC TTT ATT ACT AGG GT CC TAC TAT AGT AAC TAC TTT ATT ACT AGG GT CC TAC TAT AGT AAC TAC TTT ATT ACT AGG GT CC TAC TAT AGT AAC TAC CT AC TAT AGT ACT AC CC TAC TAG GT CC TAC TAG GAC CT AC TAG GAC	ANT TTC ALC OTAL ALC OTAL TC GG GGG GGG GGG G LAG AAG T AGG CAG AGG T CAG G GG GG TT CT ATT CT	C TAT GET ATG GAC TAC TGG GEC TGG TTT GET TAC TGG GAT GA AT TAC TAT GET TAC TGG T TAC TAT GET ATG GAC TAC TGG T TAC TAT GET ATG GAC TAC TGG T TAC TAT GET ATG GAC TAC TGG TTT GAC TAT GAC TAC TGG TTT GAC TAC TGG C TTG GAC TAC TGG C TAC TAT GET ATG GAC TAC TGG C TGG TTT GET TAC TGG C TGG TTT GET TAC TGG C TGG TTT GET TAC TGG C TGG TTT GAC TAC TGG C TGG TAT GGC ATG TAC TGG C TGG TAC TGG C TGG TAC TGG C TGG TAC TGG C TGG TAC TGG C TTG GAC TAC TGG C TTG GAC TAC TGG C TTG GAC TAC TGG C TTG GAC TAC TGG C TAC TGG TAC TGG C TAC TGG TAC TGG C TAC TGG TAC TGG C TAC TGG TAC TGG C TAC TATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG	SP 21.6 SP 2.16 SP 2.6 SP 2.6 SP 2.6 SP 2.5 SP 2.7 D SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.15 SP 2.15 SP 2.11 SP 2.15 SP 2.15 SP 2.16 SP 2.16 SP 2.4 SP	4343422 J 44333314422 III J 2244443233444444	I + + + + + + + + + + + + + + + + + + +
	Bactis (nd) Bactis (nd) Bactis (nd) Bactis (nd) Bactis (nd) Bactis (nd) bar with bar	TC TAC TAT GGT AAC T TC TAC TAT GGT AAC T TC TAC TAT GGT AAC TAC CC TAC TAT AGT TAC TAT AGT TAC TAC CC TAC TAT AGT TAC TACT TAC C CC TAC TAT AGT AAC TAC CC TAC TAT AGT AAC TAC CC TAC TAT AGT AAC TAC CC TAC TAT AGT AAC TAC TTT ATT ACT AGG GAT CC TAC TAT AGT AAC TAC TTT ATT ACT AGG GAT CC TAC TAT AGT AAC TAC TTT ATT ACT AGG GAT CC TAC TAT AGT AAC TAC TTT ATT ACT AGG GAT CC TAC TAT AGT AAC TAC TTT ATT ACT AGG GAT CC TAC TAT AGT AAC TAC TTT ATT ACT AGG GAT CC TAC TAT AGT AAC TAC CT AC TAT AGT AAC TA CC TAC TAT AGT AAC TA CC TAC TAT AGT AAC TA CC TAC TAT AGT AC TA CC TAC TAT AGT AC TA CC TAC TAT AGT AC TA CT AC TAG GA AC CT AC TAG GA AC CT AC TAG GA AC CT AC TAG GAAC CT AC TGG GAC CT AC TGG GAC CT ACC T	ANT TTC ANC GTANA CTTC TC GG GGG GGA G IAG AAG T AGG AAC GTC CC G GGG GG T T C A C G G G G G G G G G G G G G G G G G	C TAT GET ATG GAC TAC TGG GEC TGG TTT GET TAC TGG G TT GET TAT GET TAC TGG G TT G TAT GET TAC TGG G TT G CT TAC TGG T TAC TAT GCT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TTT GAC TAC TGG G T TAC TAT GCT ATG GAC TAC TGG C TGG TTT GCT TAC TGG C TGG TTT GAC TAC TGG C TGG TTT GAC TAC TGG C TGG TAC TGG GAT TAC TAT GCT ATG GAC TAC TGG C TGG TAC TGG C TGG TAC TGG C TGG TAC TGG C TTG GAC TAC TGG C TTG GAC TAC TGG C TTG GAC TAC TGG C TAC TGG TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG C TAC GTT TG GAC TAC TGG C TAC GTT GCT TGG GAC TAC TGG C TAC TTC GAT TGG GAC TAC TGG C TAC TTC GAT TGG CT TGG TAC TTC GAT TGG GAC TAC TGG C TAC TTC GAT TGG GAC TAC TGG C TAC TTC GAT TGG GAC TAC TGG C TAC TTC GAT TGG CT TGG TAC TTC GAT TGG GAC TAC TGG C TAC TTC GAT TGG GAC TAC TGG	SP 21.6 SP 2.16 SP 2.6 SP 2.6 SP 2.6 SP 2.5 SP 2.7 D SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.15 SP 2.15 SP 2.16 SP 2.16 S	4343422 J 44333314422 UJ J 22444432334444443213	I + + + + + + + + + + + + + + + + + + +
	Bucks (wc) Bucks (wc)	TC TAC TAT GGT AAC T TC TAC TAT GGT AAC T TC TAC TAT GGT AAC TAC CC TAC TAT AGT TAC TACAT AGT TACC CC TAC TAT AGT TAC TACT TACC CC TAC TAT AGT AAC TAC C TAC TAT TGG IAA CTAC C TAC TAT TGG IAA CTAC TT ATT AGT AGT AAC TAC TT ATT AGT AGT AAC TAC TT ATT AGT AGT AAC TAC TT ATT AGT AGG GAT C C TAC TAT AGT AAC TAC TT ATT AGT AGG GAT C C TAC TAT AGT ACT AC TT ATT AGT AGG GAT C C TAC TAT AGT AGT ACT AC TT ATT AGT AGG GAT C C TAC TAT AGT AGT ACT AC C TAC TAT AGT ACT A C TAC TAG GAT C C TAC TA GG AC C TAC TAG GGA C C TAC TAG GGA C C TAC TGG GAC C	ANT TTC AGE GALANG GAGA ANG G LAG ANG T AGG AAC GTC CC G AGG AGG T CAG AGG T CAG AGG T CAG AGG T CAG AGG T CAG AGG T CAG AGG C CA CG CG CG CG CG CG CG CG CG CG CG CG CG	C TAT GET ATG GAC TAC TOG GEC TOG TT GET TAC TOG A G TT AC TAT GET TAT GET A G TTT GET TAC TOG C TTAC TAT GET ATG GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG GET ATG GAC TAC TOG G T AG TAT GET ATG GAC TAC TOG C TOG TTT GCT TAC TOG C TOG TAT GCT ATG GAC TAC TOG G TAT GCT ATG GAC TAC TOG C TOG TTT GCT TAC TOG C TTG GAC TAC TOG C TAT GCT ATG GAC TAC TOG C TAC TTT GCT ATG GAC TAC TOG C TAC TTT GCT ATG GAC TAC TOG C TAT GCT ATG GAC TAC TOG C TAC TTT GCT TAC TOG C TAT G	SP 21.66 SP 21.65 SP 21.65 SP 21.65 SP 21.65 SP 21.75 FL16.1 SP 21.75 SP 21.76 SP 21.76 SP 21.76 D <td< td=""><td>4343422 J 443333914422 W J 224444323344444432134</td><td>I + + + + + + + + + + + + + + + + + + +</td></td<>	4343422 J 443333914422 W J 224444323344444432134	I + + + + + + + + + + + + + + + + + + +
	Bactis (noi) Bactis (noi) Bacti	TC TAC TAT GGT AAC T TC TAC TAT GGT AAC T TC TAC TAT GGT AAC TAC CC TAC TAT AGT TAC TACT TAC CC TAC TAT AGT TAC TACT TACC CC TAC TAT AGT AAC TAC CC TAC TAT AGT AAC TAC CC TAC TAT AGT AAC TAC CC TAC TAT AGT AAC TAC TTT ATT ACT AGG AAC TAC TTT ATT ACT AGG GAT CC TAC TAT AGT AAC TAC TTT ATT ACT AGG GAT CC TAC TAT AGT AAC TAC TTT ATT ACT AGG GAT CC TAC TAT AGT AAC TAC TTT ATT ACT AGG GAT CC TAC TAT AGT AAC TAC TTT ATT ACT AGG GAT CC TAC TAT AGT ACT AC CT AC ATA GT ACT AC CT ACT AGG GAC CT ACT AGG GAC CT ACT AGG GAC CT ACT GG GAC CT ACT G	ANT TTC ANC GTANA CTTC TC GG GGG GGA G IAG AAG T AGG AAC GTC CC G GGG GG T T C A C G G G G G G G G G G G G G G G G G	C TAT GET ATG GAC TAC TGG GEC TGG TTT GET TAC TGG G TT GET TAT GET TAC TGG G TT G TAT G CT TAT GGAC A G TTT GCT TAT G GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG TTT GAC TAT GGAC TAC TGG TTT GAC TAC TGG G T TAC TAT G CT ATG GAC TAC TGG C TGG TTT GCT TAC TGG C TGG TAT GGAC TAC TGG G T TAC TAT GCT ATG GAC TAC TGG C TGG TTT GCT TAC TGG C TGG TAC TGG GT GT GTG C TGG TAC TGG C TGG TAC TGG C TGG TAC TGG C TGG TAC TGG C TTG GT ATG GAC TAC TGG C TTG GT ATG GAC TAC TGG C TAC TAT GCT ATG GAC TAC TGG C TAC TAT GCT ATG GAC TAC TGG C TAC TATG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG AT TAC TAT GCT ATG GAC TAC TGG C TAC TTT GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT TAC TAC GCT ATG GAC TAC TGG AT CCT ATG GCT TAC TGG AT CCT TGG GAC TAC TGG AT CCT ATG GCT TGG TAC TTC GAC TAC TGG	SP 21.6 SP 2.16 SP 2.6 SP 2.6 SP 2.6 SP 2.5 SP 2.7 D SP 2.7 SP 2.7 SP 2.7 SP 2.7 SP 2.15 SP 2.15 SP 2.16 SP 2.16 S	4343422 J 44333314422 UJ J 22444432334444443213	I + + + + + + + + + + + + + + + + + + +
	Bucks (wc) Bucks (wc)	TC TAC TAT GGT AAC T TC TAC TAT GGT AAC T TC TAC TAT GGT AAC TAC CC TAC TAT AGT TAC TACAT AGT TACC CC TAC TAT AGT TAC TACT TACC CC TAC TAT AGT AAC TAC C TAC TAT TGG IAA CTAC C TAC TAT TGG IAA CTAC TT ATT AGT AGT AAC TAC TT ATT AGT AGT AAC TAC TT ATT AGT AGT AAC TAC TT ATT AGT AGG GAT C C TAC TAT AGT AAC TAC TT ATT AGT AGG GAT C C TAC TAT AGT ACT AC TT ATT AGT AGG GAT C C TAC TAT AGT AGT ACT AC TT ATT AGT AGG GAT C C TAC TAT AGT AGT ACT AC C TAC TAT AGT ACT A C TAC TAG GAT C C TAC TA GG AC C TAC TAG GGA C C TAC TAG GGA C C TAC TGG GAC C	ANT TTC AGE GALANG GAGA ANG G LAG ANG T AGG AAC GTC CC G AGG AGG T CAG AGG T CAG AGG T CAG AGG T CAG AGG T CAG AGG T CAG AGG C CA CG CG CG CG CG CG CG CG CG CG CG CG CG	C TAT GET ATG GAC TAC TOG GEC TOG TT GET TAC TOG A G TT AC TAT GET TAT GET A G TTT GET TAC TOG C TTAC TAT GET ATG GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG C TTT GAC TAC TOG GET ATG GAC TAC TOG G T AG TAT GET ATG GAC TAC TOG C TOG TTT GCT TAC TOG C TOG TAT GCT ATG GAC TAC TOG G TAT GCT ATG GAC TAC TOG C TOG TTT GCT TAC TOG C TTG GAC TAC TOG C TAT GCT ATG GAC TAC TOG C TAC TTT GCT ATG GAC TAC TOG C TAC TTT GCT ATG GAC TAC TOG C TAT GCT ATG GAC TAC TOG C TAC TTT GCT TAC TOG C TAT G	SP 21.66 SP 21.65 SP 2.8 SP 2.16 SP 2.15 SP 2.16 SP 2.11 SP 2.16 SP 2.16 SP 2.16 SP 2.11 SP 2.16 SP 2.16 SP 2.16 SP 2.11 SP 2.16 SP 2.17 D D D D SP 2.60 SP 2.60 D D D D D	4343422 J 44333314422 UU J 22444443233444444321342	I + + + + + + + + + + + + + + + + + + +

.

Table 2 (cont.)

E1 E2								
22	F16L1	CTA ACT GGG AC	G	GAC TAC TGG	DQ. O-	2	Ŭ	+
	FIELT	CT AAC TOG G	-	OG TAC TTC GAT OTC TOO	DO, O-	ī	ï	
Ĕ4	F16L1	CT AAC TOG GAC		TAC TGG	DQ, Q+	2	i	
			ACC	AT TAC TAT OCT ATG GAC TAC TGG	00.0			P+
n .	F16L1	CTA ACT G	AC C				ň	
2	F10L1	CTA ACT GGG A		AC TAT GCT ATG GAC TAC TGG	DO 0-	1		•
13	F16L1	CTA ACT GGG AC	T AGG AGG	GCT ATG GAC TAC TGG	00.0			+
F1	141.2	CT AAC TOG GAC		TAC TGG	DQ, Q+	2		•
F4	181.2	CT AAC TOO G	GG	TTT GAC TAC TOG	DQ, O-	2	1	+
g1	181.2	CT AAC TOG GAC		TAT GCT ATG GAC TAC TOG	DQ O+	- 4	1	•
- 20	1812	C TAA CTO G		AC TAC TGG	DQ. 0+	4		-
	181.2	CTA ACT GOG AC		T TAC TAT GCT ATG GAC TAC TOG		4	D	
94 11	1812	C TAA CTG GGA C	GT ACT G	AC TAC TIT GAC TAC TOG	00.0-	2	ũ	P+
					00.0	ž	1	P+
12	181.2	CT AAC TOG	T	AC TAC TTT GAC TAC TGG				P+
13	181.2	C TAA CTG GGA		GAC TAC TIT GAC TAC TGG	DQ, Q-	2	14	•
M	18L2	CT AAC TOG GAC		TTT GAC TAC TGG	DQ, O+	2	•	-
G1	1813	CT AAC TOG GAC		TAC TTT GAC TAC TOG	DQ, O+	2	1	-
H1	F18L4	CTA ACT GGG	G	AC TOG TAC TTC GAT GTC TOG	DQ, O-	1		+
14	F19L4	CT AAC T	Ť	C TAC TGG TAC TTC GAT GTC TGG	DQ. 0-	1	- 1	+
ji i	FIELA	CT AAC TOG GAC	ĠAA	GCT ATG GAC TAC TOG	DQ, O-	4	i i	+
js	FIELA	C TAA CTG GGA C	GG GA	G GAC TAC TOG	DO. O-	Á.	in in in its second sec	
	F19L4	CTA ACT GOG ACC	00 0	GAC TAC TOG	DQ. 0-	2		
¥1								•
¥2	F10L4	CTA ACT GGG A	AA QG	T GAC TAC TGG		2		+
h1	19.2	CTA ACT GGG AC	G GGG	GCT ATG GAC TAC TGG	DQ, Q-	- 4	8	+
h4	19.2	C TAA CTG G		AC TAC TGG	DQ, O+	- 4		•
J1	19.2	CT AAC TOG		TGG TAC TTC GAT GTC TGG	DO. 0+	1	1	•
.s	19.2	CTA ACT GGG		TOG TAC TTC GAT GTC TOG	DO, O-	1	i i	
u 1	19.2	CT AAC T		AC TAC TTT GAC TAC TGG	00.0	ż	ī	
12			GG GG	T GAC TAC TGG	200	ź	in in	
	19.2	C TAA CTG GGA C						•
بە	19,2	CTA ACT GOG		TAC TTT GAC TAC TGG	DQ, Q-	2	u .	•
- 44	19.2	CT AAC T		AC TAC TTT GAC TAC TGG	DQ, O-	2	1	•
20	cultured I	5T/L5T fetal liver ore	B cells (DQ52)				reading	
	e, origin	D-exament	N/P-sequence	e J-segment	D	J	trame	NP-seq
								her werd
P1	L5.12.1	CT AAC TOG GAC		TTT GAC TAC TOG	DO, O+	2	1	•
k1	L5.12.1	CT AAC TOG GAC		GCT ATG GAC TAC TGG		- 4	1	-
10	15.12.1	CT AAC TOG GAC		TAC TAT OCT ATG GAC TAC TOG	DQ, O-	- 4	1	-
44	15.12.1	CTA ACT GGG A	GG GG	C TAT GCT ATG GAC TAC TOG	00,0-	- 4	8	+
102	15.12.2	CTA AAC TOG G	G	C TAC TGG	DQ 0-	2	1	+
K4	15.12.2	CT AAC TGG G	ŤG	GAC TAC TOG	DO.O-	2	1	+
n	15.12.2	CT AAC TOO GA		T GCT ATG GAC TAC TOG		Ā	i	
Ë	15.12.2	CT AAC TOG	AT	C TAT OCT ATG GAC TAC TOG		, A	i	P+
H.	15.12.2	CTA ACT GGG A	î'	T TAC TAT GCT ATG GAC TAC TGG	ba õ	- 1		P.
		CT AAC TOG GAC		TOG TAC TTC GAT GTC TOG	00.0+	- 7	- 7	F+
11	L5.12.3				00,04			:
12	L5.12.3		-					P+
13		CTA ACT GGG	т	AC TAC TIT GAC TAC TOG	DQ, O-	2		
	15.12.3	CTA ACT GGG CTA ACT GGG	т	AC TAC TIT GAC TAC TOG TAC TTC GAT GTC TGG	DQ, 0- DQ, 0+	2	n	•
m1	15.12.3	CTA ACT GGG CTA ACT GGG CT AA	т	AC TAC TIT GAC TAC TOG TAC TTC GAT GTC TGG T TAC TAT GCT ATG GAC TAC TGG	D0, 0- D0, 0+ D0, 0+	1	n I	:
	15.12.3	CTA ACT GGG CTA ACT GGG	т	AC TAC TIT GAC TAC TOG TAC TITC GAT GITC TOG T TAC TAT GCT ATG GAC TAC TGG TG GAC TAC TGG	D0,040 D0,040 D0,040		n	:
m1	15.12.3	CTA ACT GGG CTA ACT GGG CT AA CTA ACT GGG A	т	AC TAC TIT GAC TAC TOG TAC TITC GAT GITC TOG T TAC TAT GCT ATG GAC TAC TGG TG GAC TAC TGG	D0,040 D0,040 D0,040	1	n I	:
na 1 na 2	L5.12.3	CTA ACT GGG CTA ACT GGG CT AA	c	AC TAC TTT GAC TAC TGG TAC TTC GAT GTC TGG T TAC TAT GCT ATG GAC TAC TGG TG GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG		1 4 4	1 	P+
m1 m2 m3 m4	15.12.3 15.12.3 15.12.3 15.12.3	CTA ACT GGG CTA ACT GGG CTAA CTAACT GGG A CTAACT GG GAC CTAACT G		AC TAC TTT GAC TAC TGG TAC TTC GAT GTC TGG T TAC TAT GCT ATG GAC TAC TGG TG GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG		1 4 4		P+
e1 62 64 w1	L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3	CTA ACT GGG CTA ACT GGG CT AA CTA ACT GGG A CTA ACT GGG A CTA ACT GG CTA ACT GGG	c	AC TAC TTT GAC TAC TGG TAC TTC GAT GTC TGG T TAC TAT GCT ATG GAC TAC TGG TG GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG		1 4 4 4 4		
81 82 83 84 92	L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3	CTA ACT GGG CTA ACT GGG CT AACT GGG A CT AACT GGG A CT AACT GG GAC CTA ACT GGG CTA ACT GGG CT AACT GGG	c	AC TAC THT GAC TAC TGG TAC TTC GAT GTC TGG T TAC TAT GCT ATG GAC TAC TGG T GAC TAC TGG GCT ATG GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TTT GAC TAC TGG		1 4 4 4 2		+
*****	L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3	CTA ACT GGG CTA ACT GGG CTA ACT GGG A CTA ACT GGG A CTA ACT GGG A CTA ACT GGG CTA ACT GGG CT AAC TGG GAC CT AAC TGG GAC	c	AC TAC THT GAC TAC TGG TAC TTC GAT ATG TGG T TAC TAT GAT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TTT GAC TAC TGG AC TGG		1 4 4 4 2 2 2		+
26652222	15.123 15.123 15.123 15.123 15.123 15.123 15.123 15.123 15.124	CTA ACT GOG CTA ACT GOG CTA ACT GOG A CTA ACT GOG A CTA ACT GOG A CTA ACT GOG CTA ACT GOG CTA ACT GOG CT ACT GOG CT ACT TGG GAC	c Gag	AC TAC TTT GAC TAC TGG TAC TTC GAT TGT GGT T TAC TT GGT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG GGT ATG GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG AC TGG TGG TAC TTC GAT GTC TGG		1 4 4 4 2 2 2 1		•
22222222	L5.123 L5.123 L5.123 L5.123 L5.123 L5.123 L5.123 L5.124 L5.124	CTA ACT GOG CTA ACT GOG CTAA CTAACT GOG A CTAACT GOG GAC CTAACT GG CTA ACT GGG CTAACT GGG CTAACT GGG CTAACT GGG CTAACT GGGG CTAACT GGGG	C GOG CCT	AC TAC TTT GAC TAC TGG TAC TTC GAT ATG CAG T TAC TAT GAC TATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TGG TAC TTC GAT GTC TGG TAC TGG TAC TTC GAT GTC TGG TAC TGG TAC TTC GAT GTC TGG		1 4 4 4 2 2 2		+
	15.123 15.123 15.123 15.123 15.123 15.123 15.123 15.124 15.124 15.124	CTA ACT GGG CTA ACT GGG CT AA CTA ACT GGG A CT ACT GGG A CT ACT GG GAC CT ACT GG CT ACT TGG GAC CT ACT TGG GAC CT ACT TGG GAC CT ACT GGG CT ACT GGG CT ACT GGG	с ССС ССС ССТ ССТ ССТ	AC TAC TTT GAC TAC TGG TAC TTC GAT TG CTGG T TAC TAT GAT ATG GAC TAC TGG T GAC TAT GAC TAT GAC TAC TGG GCT ATG GAC TAC TGG C TAT GAC TAT GAC TAC TGG TTT GAC TAC TGG TAT GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG		1 4 4 4 2 2 2 1		•
	15.123 15.123 15.123 15.123 15.123 15.123 15.123 15.124 15.124 15.124	CTA ACT GGG CTA ACT GGG CT AA CT AACT GGG A CT AACT GGG A CTA ACT GGG AC CTA ACT GGG CTA ACT GGG CTA ACT GGG CT AACT GGG GAC CTA ACT GGG AC CT AACT GGG AC	2 200 200 200 200 200 200 200 200 200 2	AC TAC TTT GAC TAC TGG TAC TTC GAC TAT GAC TAC TGG T TAC TAT GAC TAT GAC TAC TGG T GAC TAT GAC TAC TGG GCT AT GAC TAC TGG C TAT GCT AT GAC TAC TGG TTT GAC TAC TGG TTT GAC TAC TGG TGG TAC TTC GAT GTC TGG TAC TGG TAC TTC GAT GTC TGG T TAC TAT GCT AT GAC TAC TGG	00000000000000000000000000000000000000	14442221144		+ - - P+ +
19122292929292	L5.123 L5.123 L5.123 L5.123 L5.123 L5.123 L5.123 L5.124 L5.124 L5.124 L5.124	CTA ACT GGG CTA ACT GGG CTAA CTAACT GGG A CTAACT GG GAC CTAACT GG GAC CTAACT GG GAC CTAACT GG GAC CTAACT GG GAC CTAACT GGG AC CTAACT GGG AC CTAACT GG G CTAACT GG G CTAACT GG G CTAACT GG G CTAACT GG G	с ССС ССС ССТ ССТ ССС	AC TAC TTT GAC TAC TGG TAC TTC GAT TTT GAC TAT GAC TAC TG GAC TAT GAC TAT GAC TAC TG GAC TAT GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TAT GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG T GCT ATG GAC TAC TGG	00000000000000000000000000000000000000	144422211444		•
	L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 124 L5 124 L5 124 L5 124 L5 124 L5 124 L5 124	CTA ACT GGG CTA ACT GGG CTA ACT GGG A CTA ACT GGG GAC CTA ACT GGG AC CTA CTG GGA C CTA CTG GGA C CTA CTG GGA C	C GOG G G G G G G C C C C C C G T TG	AC TAC TTT GAC TAC TGG TAC TTC GAC TAT GAC TAC TGG T TAC TAT GAC TAT GAC TAC TGG TG GAC TAT GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TTT GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG TAC TGG TAC TTC GAT GTC TGG T TAC TAT GAC TAC TGG T GCT ATG GAC TAC TGG	00000000000000000000000000000000000000	14444222114442	11 	* P+ * P+
12224599999121222	L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 124 L5 124 L5 124 L5 124 L5 124 L5 124 L5 125	CTA ACT GGG CTA ACT GGG CTA ACT GGG CTA ACT GGG AC CTA ACT GG GAC CTA ACT GG CTA ACT GG CTA ACT GG GAC CTA ACT GG GAC CTA ACT GG GAC CTA ACT GGG G CTA ACT GG GAC CT AAC TGG GAC	2 200 200 200 200 200 200 200 200 200 2	AC TAC TTT GAC TAC TGG TAC TTC GAT ATG CAG T TAC TT GCT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG GCT ATG GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TAT GAC TAC TGG TAC TTT GAC TAC TGG AC TATG GAC TAC TGG AC TATG GAC TAC TGG AC TAC GAC TAC TGG	00000000000000000000000000000000000000	144442221144422		+ - - P+ +
	L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 124 L5 124 L5 124 L5 124 L5 124 L5 124 L5 124	CTA ACT GOG CTA ACT GOG CTA ACT GOG CTA ACT GOG A CTA ACT GOG GA CTA ACT GOG GA CTA ACT GOG CTA ACT GOG CTA ACT GOG CTA ACT GOG GAC CTA ACT GOG CTA ACT GOG CTA ACT GOG CTA ACT GOG CTA ACT GOG CTA CTGG GAC CTA ACT GOG GAC CTA CTGG GAC CTA CTGG GAC CTA CTGG CT CTA CTGG CT CTA CTGG CT CTA CTGG CT	C GOG G G G G G G C C C C C C G T TG	AC TAC TTT GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TG GAC TAT GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TTT GAC TAC TGG TGG TAC TGC GAT GTC TGG TAC TGG TAC TGC GAT GTC TGG T GCT ATG GAC TAC TGG T GCT ATG GAC TAC TGG AC TAC TGC GAT GTC GAC TAC TGG AC TAC TGC GAT GTC GAC TGG AC TAC TGC GAT GCT GAC TGG AC TAC GTCA TG GAC TAC TGG AC TAC GTCA TG GAC TAC TGG AC TAC GTCA TG GAC TAC TGG	\$2222222222222222222222	14444222114442	11 	* P+ * P+
12224599999121222	L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 124 L5 124 L5 124 L5 124 L5 124 L5 124 L5 125	CTA ACT GGG CTA ACT GGG CTA ACT GGG CTA ACT GGG AC CTA ACT GG GAC CTA ACT GG CTA ACT GG CTA ACT GG GAC CTA ACT GG GAC CTA ACT GG GAC CTA ACT GGG G CTA ACT GG GAC CT AAC TGG GAC	C GOG G G G G G G C C C C C C G T TG	AC TAC TTT GAC TAC TGG TAC TTC GAT ATG CAG T TAC TT GCT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG GCT ATG GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TAT GAC TAC TGG TAC TTT GAC TAC TGG AC TATG GAC TAC TGG AC TATG GAC TAC TGG AC TAC GAC TAC TGG	00000000000000000000000000000000000000	144442221144422		+ - - P+ + P+ P+
	L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 124 L5 124 L5 124 L5 124 L5 124 L5 125 L5 125 L5 125 L5 125	CTA ACT GGG CTA ACT GGG CTA ACT GGG A CTA ACT GGG A CTA ACT GG GAC CTA ACT GG CTA ACT GG GAC CTA ACT GG GAC CT ACT GG GAC CTA ACT GGG AC CTA ACT GGG GC CTAAC TGG GAC CTAAC TGG GAC CTAAC TGG GAC CTAAC TGG GAC CTAAC TGG GAC CTAACT GGG AC	C GOG G G G G G G C C C C C C G T TG	AC TAC TTT GAC TAC TGG TAC TTC GAC TATG GAC TAC TGG T TAC TAT GAC TATG GAC TAC TGG TG GAC TATG GAC TAC TGG GCT ATG GAC TAC TGG CTAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TGG TAC TTC GAT GTC TGG TAC TGG TAC TTC GAT GTC TGG T AC TGG TAC TAC GAC TAC TGG GCT ATG GAC TAC TGG T GCT ATG GAC TAC TGG AC TAC GCT ATG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG TCC TATG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG TCC TATG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG TCC TATG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG	00000000000000000000000000000000000000	14444222114444224	13 	+ - - P+ + P+ P+
1222233333321212233	L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 124 L5 124 L5 124 L5 124 L5 124 L5 124 L5 124 L5 125 L5 125 L5 125 L5 127	CTA ACT GGG CTA ACT GGG A CTA ACT GGG AC CTA ACT GGG GAC CT ACT GGG GAC CT ACT GGG GAC CT ACT GGG AC CT ACT GGG AC	C GOG GOG GOG CC CC GT TG T A	AC TAC TTT GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TG GAC TAT GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TTT GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG TAC TGG TAC TTC GAT GTC TGG TAC TGG TAC TTC GAT GTC TGG TAC TAG GAC TAC TGG TAC TAT GAC TAC TGG AC TAT GCT ATG GAC TAC TGG AC TAC GTAT TG GAC TAC TGG T GCT ATG GAC TAC TGG TT GCT ATG GAC TAC TGG T GCT ATG GAC TAC TGG	4444444444444444444444444444444444444	14444222114442244	13 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	+ - - P+ + P+ - P+ - P+ -
19255939191812293918	L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 124 L5 124 L5 124 L5 124 L5 124 L5 124 L5 124 L5 125 L5 125 L5 125 L5 127 L5 127 L5 127	CTA ACT GGG CTA ACT GGG CTA ACT GGG AC CTA ACT GGG AC CTA ACT GG CTA ACT CTA CT CTA CTA CTA CTA CTA CTA CTA CTA CTA CTA	C GOG G G G G G G C C C C C C G T TG	AC TAC TTT GAC TAC TGG TAC TTC GAC TATG GAC TAC TGG T TAC TAT GAC TATG GAC TAC TGG TG GAC TATG GAC TAC TGG GCT ATG GAC TAC TGG CTAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TGG TAC TGC GAT GTC TGG TAC TGG TAC TGC GAC TAC TGG GCT ATG GAC TAC TGG T GCT ATG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG CT TT GAC TAC TGG	62322222222222222222222222222222222222	1444422211444422442	13 	+ - - P+ + P+ P+
88988585555555555555555555585	L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 124 L5 124 L5 124 L5 124 L5 124 L5 124 L5 124 L5 124 L5 125 L5 125 L5 127 L5 127 L5 127	CTA ACT GGG CTA ACT GGG A CTA ACT GGG AC CTA ACT GGG GAC CT ACT TGG GAC CTA ACT GGG AC CT ACT TGG GAC CT ACT GGG AC CTA ACT GGG AC	C CCT G GGG CC CC GT TG T A AC AT	AC TAC TTT GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TG GAC TAT GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TTT GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG TAC TGG TAC TGG GAC TAC TGG TAC TGG TAC TGG GAC TAC TGG TAC TGG TAC TGG GAC TAC TGG TAC TAT GCT ATG GAC TAC TGG AC TAC TGG TAT TGAC TAC TGG T GCT ATG GAC TAC TGG T GCT ATG GAC TAC TGG T GCT ATG GAC TAC TGG TT GCT ATG GAC TAC TGG C TTT GAC TAC TGG C TTT GAC TAC TGG C TTT GAC TAC TGG C TAT GCT ATG GAC TAC TGG T GCT ATG GAC TAC TGG C TTT GAC TAC TGG C	\$222222222222222222222222222222222222	144442221144442244222	11 	+ - - P+ + P+ - P+ - P+ -
58858555555555555555555555555555555555	L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 123 L5 124 L5 124 L5 124 L5 124 L5 124 L5 125 L5 125 L5 125 L5 127 L5 127 L5 127 L5 127	CTA ACT GGG CTA ACT GGG CTA ACT GGG A CT AACT GGG A CT AACT GGG A CTA ACT GG GA CTA ACT GG GA CTA ACT GG GA CTA ACT GG GA CTA ACT GGG GA CTA ACT GGG AC CTA ACT GGG AC	C GOG GOG CCT GTTG T A ACAT GCT	AC TAC TTT GAC TAC TGG TAC TTC GAC TAT GAC TAC TGG TAC TTC GAC TAT GAC TAC TGG TG GAC TAT GAC TAC TGG GCT ATG GAC TAC TGG CTAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TTT GAC TAC TGG TGG TAC TTC GAT GTC TGG TAC TGG TAC TTC GAT GTC TGG TAC TGG TAC TG GAC TAC TGG AC TAT GAC TAT GAC TAC TGG AC TAT GAC TAT GG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG T GCT ATG GAC TAC TGG C TTT GAC TAC TGG C TAT GAC TAC TGG C TAT GAC TAC TGG C TAC TGG C TAC TGG C TAC TGG C TAC TGG C TAC TGG C TAC TGG C C C C C C C C C C C C C C C C C	66668888888888888888888888888888888888	1444422211444422442222		* - P+ * * P + P + P +
	L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.5 L5.12.5 L5.12.5 L5.12.5 L5.12.5 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7	CTA ACT GGG CTA ACT GGG A CTA ACT GGG AC CTA ACT GGG AC	C CCT G GGG CC CC GT TG T A AC AT	AC TAC TTT GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TG GAC TAT GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG THT GAC TAC TGG TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG T TGC TATG GAC TAC TGG T GCT ATG GAC TAC TGG C TTT GAC TAC TGG C TTT GAC TAC TGG C TAT GGC ATG GAC TAC TGG C TAT GGC ATG GAC TAC TGG C TTT GAC TAC TGG C TAT GGC ATG GAC TAC TGG C TAT GGC ATG GAC TAC TGG C TAT GGC ATG GAC TAC TGG C TAC TGG CATG GAC TAC TGG C TAC TGG GAC TGG CATG GAC TAC TGG C TAC GCT ATG GAC TAC TGG	6666668888888888888888888888888888888	1444422211444224422224	13 	+ - - P+ + P+ - P+ - P+ -
28222599292222222222828282	L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.5 L5.12.5 L5.12.7	CTA ACT GGG CTA ACT GGG A CT AACT GGG A CT AACT GGG A CT AACT GGG A CTA ACT GG GAC CTA ACT GGG GAC CTA ACT GGG GAC CT AACT GGG GAC CT AACT GGG GAC CT AACT GGG AC CT AACT GGG G CT ACT GGG G	C GOOG CCT G GOOG CC CC GT TG T A AC AT GC T	AC TAC TTT GAC TAC TGG TAC TTC GAC TAT GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TG GAC TAT GAC TAT GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TTT GAC TAC TGG TGG TAC TGC GAT GTT TGG TAC TGG TAC TGC GAT GTT TGG TAC TGG TAC TGG GAC TAC TGG C TAT GGC ATG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG C TTT GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAC TGG TAC TGG C TAC TGG TAC TGG C TAC GTG GAC TAC TGG C TAC GTA TG GAC TAC TGG	\$ \$	1444422211444422442222	1) 	* - P+ * * P + P + P +
2222599292222222328282829282	L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.5 L5.12.5 L5.12.5 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7	CTA ACT GGG CTA ACT GGG A CTA ACT GGG AC CTA ACT GGG AC	C GOOG CC CC GT TG T A AC AT GC T C	AC TAC TTT GAC TAC TGG TAC TTC GAT ATG GAC TAC TG CTAT GCT ATG GAC TAC TGG GCT ATG GAC TAC TGG GCT ATG GAC TAC TGG C TATG GAC TAC TGG C TATG GAC TAC TGG TTT GAC TAC TGG TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG T TAC TAT GCT ATG GAC TAC TGG T TGC TATG GAC TAC TGG T GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG T GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAC TGC TATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG	00000000000000000000000000000000000000	14444222114444224442222444		+ P+ + + P+ P+
282253932928222232828282	L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.5 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7	CTA ACT GGG CTA ACT GGG A CTA ACT GGG AC CTA ACT GGG GAC CT ACT GGG GAC CT ACT GGG GAC CT ACT GGG AC CT ACT GGG AC	C GOOG CCT G GOOG CC CC GT TG T A AC AT GC T	AC TAC TTT GAC TAC TGG TAC TTC GAC TATG GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TG GAC TATG GAC TATG GAC TAC TGG GCT ATG GAC TAC TGG CTAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TTT GAC TAC TGG TAC TATG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TAC TTT GAC TAC TGG C TATG GCT ATG GAC TAC TGG TGG TAC TCT GAT ATG GAC TAC TGG TGG TAC TCT GAT ATG GAC TAC TGG TAC TTT GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TATG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAC GCT C TAC GAC TAC TGG C TAC GCT ATG GAC TAC TGG C C C TAC TGG C C TAC TGG C C C C TAC TGG C C C C C C C C C C C C C C C C C	66338888888888888888888888888888888888	1444422211444224422224442	1) 	* - P+ * * P + P + P +
282259933922222233338383598352822c	L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.5 L5.12.5 L5.12.5 L5.12.5 L5.12.5 L5.12.7 L5.12.8 L5.12.8	CTA ACT GGG CTA ACT GGG CTA ACT GGG A CTA ACT GGG A CTA ACT GGG A CTA ACT GGG A CTA ACT GGG AC CTA ACT GGG CTA ACT GGG AC CTA ACT GGG AC	C GOOG CC CC GT TG T A AC AT GC T C	AC TAC TTT GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TG GAC TAT GAC TAC TGG GCT ATG GAC TAC TGG CTAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TGG TAC TGC GAC TAC TGG TAC TGC TATG GAC TAC TGG TAC TGC TATG GAC TAC TGG TAC TGC TATG GAC TAC TGG C TTT GAC TAC TGG TAC TGC TATG GAC TAC TGG T GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TAC TGC TATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AT GCT ATG GAC TAC TGG C TAT GCT TATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAT GCT C TAT GAC TAC TGG	\$	14444222114442244222244422	1) 	+ P+ + + P+ P+
2822259922222222222222222	L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.5 L5.12.5 L5.12.7 L5.12.	CTA ACT GGG CTA ACT GGG A CTA ACT GGG AC CTA ACT GGG GAC CTA ACT GGG GAC CTA ACT GGG AC CTA ACT GGG AC	C GOOG CC CC GT TG T A AC AT GC T C	AC TAC TTT GAC TAC TGG TAC TTC GAT TTT GAC TAC TGC TAC TTC GAT ATG GAC TAC TGG TG GAC TAT GAC TAT GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TGG TAC TGC GAT GTT GAC TAC TGG TGG TAC TGC GAT GTT GAC TAC TGG TAC TGG TAC TGC TAT GAC TAC TGG TAC TGG TAC TGC GAT GTT GAC TAC TGG TAC TGC GAT GTT GAC TAC TGG AC TAT GAC TAC TGG TGC TATG GAC TAC TGG TGC TATG GAC TAC TGG C TAC TGG TAC TTG GAC TAC TGG TGC TATG GAC TAC TGG TGC TATG GAC TAC TGG TGC TATG GAC TAC TGG C TTT GAC TAT GGC TAC TGG C TAC TGG GAC TAC TGG C TAC TATG GAC TAC TGG C TAC TGG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAC TGC GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAC TGC C TATG GAC TAC TGG C TAC C TAT GCT ATG GAC TAC TGG C TAC C TGG C TATG GAC TAC TGG C C TAT GCT ATG GAC TAC TGG C C TAC C TAT GC C C TAC C TGG C C TAC C TGG C C TAC C C C C C C C C C C C C C C C C	\$	14444222114442224422224442242	1) 	+ P+ + + P+ P+
282259933922222233338383598352822c	L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.5 L5.12.5 L5.12.7 L5.12.	CTA ACT GGG CTA ACT GGG CTA ACT GGG A CTA ACT GGG A CTA ACT GGG A CTA ACT GGG A CTA ACT GGG AC CTA ACT GGG CTA ACT GGG AC CTA ACT GGG AC	C GOOG CC CC GT TG T A AC AT GC T C	AC TAC TTT GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TG GAC TAT GAC TATG GAC TAC TGG GCT ATG GAC TAC TGG C TATG GCT ATG GAC TAC TGG TTT GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG OCT ATG GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG OCT ATG GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG AC TAT GCT ATG GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG AC TAT GCT ATG GAC TAC TGG TAC TGG TAC TTG GAC TAC TGG TAC TTG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG T GCT ATG GAC TAC TGG C TTT GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG AC TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TGG C TAT GCT ATG GAC TAC TGG C TGG C TAT GCT ATG GAC TAC TGG C GC C TA	\$	14444222114442224422224442242	1) 	+ P+ + + P+ P+
2822259922222222222222222	L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.5 L5.12.5 L5.12.5 L5.12.5 L5.12.5 L5.12.7 L5.12.8 L5.12.8	CTA ACT GGG CTA ACT GGG A CTA ACT GGG AC CTA ACT GGG GAC CTA ACT GGG GAC CTA ACT GGG AC CTA ACT GGG AC	C GOOG CC CC GT TG T A AC AT GC T C	AC TAC TTT GAC TAC TGG TAC TTC GAT TTT GAC TAC TGC TAC TTC GAT ATG GAC TAC TGG TG GAC TAT GAC TAT GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TGG TAC TGC GAT GTT GAC TAC TGG TGG TAC TGC GAT GTT GAC TAC TGG TAC TGG TAC TGC TAT GAC TAC TGG TAC TGG TAC TGC GAT GTT GAC TAC TGG TAC TGC GAT GTT GAC TAC TGG AC TAT GAC TAC TGG TGC TATG GAC TAC TGG TGC TATG GAC TAC TGG C TAC TGG TAC TTG GAC TAC TGG TGC TATG GAC TAC TGG TGC TATG GAC TAC TGG TGC TATG GAC TAC TGG C TTT GAC TAT GGC TAC TGG C TAC TGG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAC TGC GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAC TGC C TATG GAC TAC TGG C TAC C TAT GC C TATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAC C TGG C TATG GAC TAC TGG C C TAT GCT ATG GAC TAC TGG C C TAC C TGG C C TAC C TGC C C TGC C TAC C C C C C C C C C C C C C C C C	\$	14444222114442224422224442242	1) 	+ P+ + + P+ P+
ᇦᇣᇋᇉᇉᆙᅆᇾᅆᆴᇪᇃᇶᇉᇎᇪᅆᅇᅇᅇᅆᅆᇦᆆᄜᅇᇨᄠᄠ <u>ᇥ</u> ᇴ	L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.5 L5.12.5 L5.12.7 L5.12.	CTA ACT GGG CTA ACT GGG A CTA ACT GGG GAC CTA ACT GG GAC CTA ACT GGG GAC CTA ACT GGG AC CTA ACT GGG GAC CTA ACT GGG GAC	C GOOG CC CC GT TG T A AC AT GC T C	AC TAC TTT GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG GCT ATG GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TTT GAC TAC TGG TGG TAC TGG TAC TGG GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TGG TAC TGG GAC TAC TGG AC TAC GTAT GGAC TAC TGG AC TAC GTAT GGAC TAC TGG C TAC TGG CAT TG GAC TAC TGG C TAC TGG TAC TTG GAC TAC TGG C TAC TGG TAC TGG GAC TAC TGG C TAC TGG TAC TGG GAC TAC TGG C TAC TGG TAC TGG GAC TAC TGG C TAC TGG GAC TAC TGG C TATG GAC TAC TGG C TAC TGG GAC TAC TGG C TAT GCA TATG GAC TAC TGG C TAT GCA TATG GAC TAC TGG C TAT GCA TATG GAC TAC TGG C TAT GTA TGG GAC TAC TGG C TAC TGG C TAC TGG C TAC TGG C TAC C TGG C TAC TGG C TAC TGG C TAC C TAC TGG C TAC TGG C TAC C TAC TGG C	\$2555555555555555555555555555555555555	1444422211444222442222444221	1) 	+ P+ + + P+ P+
ᇃᅇᆑᇋᅊᆍᆙᅆᆙᅋᇔᅋᆆᇤᅆᇉᄠᅇᇾᅆᅆᅆᅆᅆᅆᇤᅇᇉᇏᅆᇥᇤ	L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.5 L5.12.5 L5.12.5 L5.12.7 L5.12.	CTA ACT GOG CTA ACT GOG CTA ACT GOG A CTA ACT GOG A CTA ACT GOG A CTA ACT GOG A CTA ACT GOG AC CTA ACT GOG CTA ACT GOG AC CTA ACT GOG GAC CTA CT GOG GAC	C GOOG CC CC GT TG T A AC AT GC T C	AC TAC TTT GAC TAC TGG TAC TTC GAC TAT GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG GCT ATG GAC TAT GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TGT GAC TAC TGG TAC TGT GAC TAC TGG TAC TGT GAC TAC TGG AC TAT GCT ATG GAC TAC TGG T GCT ATG GAC TAC TGG C TTT GAC TAC TGG C TAT GCT ATG GAC TAC TGG AC TAC TGT TG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG GCT ATG GCT ATG GAC TAC TGG GCT ATG GCT ATG GAC TAC TGG TGCT ATG GAC TAC TGG GAC TAC TGCT ATG GAC TAC TGG GAC TAC TGCT ATG GAC TAC TGG TTG GT ATG GCT ATG GAC TAC TGG TAC TAT GCT ATG GCT ATG GCT TGC TAT GCT ATG GCT TGC TGC TATG GCT TGC TAT GCT TAT GCT TAT GCT TAC TGC TAC TAT GCT TAT GCT TAC TGC TAC TAT GCT TAT GCT TAC TGC TTGCT TTG GCT TTG GCT TGC GCT TGC TTG GCT TGC TATG GCT TGC TGC TTGC T	\$222222222222222222222222222222222222	14444222114442244222244424212		+ P+ + + P+ P+
ᇦᇣᇋᇉᇉᆙᅆᇾᅆᆴᇪᇃᇶᇉᇎᇪᅆᅇᅇᅇᅆᅆᇦᆆᄜᅇᇨᄠᄠ <u>ᇥ</u> ᇾ	L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.5 L5.12.5 L5.12.5 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.7 L5.12.8 L5.12.9 L5.12.	CTA ACT GGG CTA ACT GGG A CTA ACT GGG AC CTA ACT GGG GAC CTA ACT GGG GAC CTA ACT GGG AC CTA ACT GG GAC CTA ACT GG GAC	C GOOG CC CC GT TG T A AC AT GC T C	AC TAC TTT GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG GCT ATG GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TTT GAC TAC TGG TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TGG TAC TGC GAT GTC TGG GCT ATG GAC TAC TGG TAC TGG TAC TGG GAC TAC TGG AC TAC GTAT GGAC TAC TGG AC TAC GTAT GGAC TAC TGG C TAC TGG TAC TTG GAC TAC TGG C TAC TGG TAC TTG GAC TAC TGG AC TAC TGG TAC TGG GAC TAC TGG C TAC TGG TAC TGG GAC TAC TGG C TAC TGG TAC TGG GAC TAC TGG C TAC TGG TAT GGAC TAC TGG C TAC TGG TAT GGAC TAC TGG C TAC TGG GAT TG GAC TAC TGG C TAC TGG GAC GAC TGG GAC TAC TGG C TAC TGG GAC TAC TGG C TAC TGG GAC TAC TGG GAC TAC TGG C TAC TGG GAC GAC TAC TGG C TAC TGG GAC TAC TGG GAC TAC TGG C TGG TAC TGG GAC TAC TGG GAC TAC TGG TGG TAC TGG GAC TAC TGG GAC TAC TGG TGG TAC TGG GC GAC TAC TGG TGG TAC TGG GC GAC TAC TGG TGG TAC TGG GC GAC TGG TGG TAC TGG GC TAC TGG GAC TAC TGG TGG TAC TGG GC TAC TGG GAC TAC TGG TGG TAC TGG GC TAC TGG GAC TAC TGG TGG TAC TGG GC TAC TGG GAC TAC TGG TGG TAC TGG GC TAC TGG GAC TAC TGG TGG TAC TGG GC TAC TGG GAC T	\$2222222222222222222222222222222222222	1444422211444222442222444242124		+
ᇃᅆᆑᇤᇤᆂᇥᅆᇪᆵᇔᇃᇶᇉᇎᄣᇷᅆᇲᅆᅆᅆᅆᇉᇥᄵᇤᅇᇆᇎᇥᄹᆂᇥᇥ	L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.3 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.4 L5.12.5 L5.12.5 L5.12.5 L5.12.7 L5.12.	CTA ACT GOG CTA ACT GOG CTA ACT GOG A CTA ACT GOG A CTA ACT GOG A CTA ACT GOG A CTA ACT GOG AC CTA ACT GOG CTA ACT GOG AC CTA CT GOG GAC	C GOOG CC CC GT TG T A AC AT GC T C	AC TAC TTT GAC TAC TGG TAC TTC GAC TAT GAC TAC TGG TAC TTC GAT ATG GAC TAC TGG GCT ATG GAC TAT GAC TAC TGG GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG TTT GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TGG TAC TTC GAT GTC TGG GCT ATG GAC TAC TGG TAC TGT GAC TAC TGG TAC TGT GAC TAC TGG TAC TGT GAC TAC TGG AC TAT GCT ATG GAC TAC TGG T GCT ATG GAC TAC TGG C TTT GAC TAC TGG C TAT GCT ATG GAC TAC TGG AC TAC TGT TG GAC TAC TGG C TAT GCT ATG GAC TAC TGG C TAT GCT ATG GAC TAC TGG GCT ATG GCT ATG GAC TAC TGG GCT ATG GCT ATG GAC TAC TGG TGCT ATG GAC TAC TGG GAC TAC TGCT ATG GAC TAC TGG GAC TAC TGCT ATG GAC TAC TGG TTG GT ATG GCT ATG GAC TAC TGG TAC TAT GCT ATG GCT ATG GCT TGC TAT GCT ATG GCT TGC TGC TATG GCT TGC TAT GCT TAT GCT TAT GCT TAC TGC TAC TAT GCT TAT GCT TAC TGC TAC TAT GCT TAT GCT TAC TGC TTGCT TTG GCT TTG GCT TGC GCT TGC TTG GCT TGC TATG GCT TGC TGC TTGC T	\$2222222222222222222222222222222222222	. 1 4 4 4 4 2 2 2 1 1 4 4 4 2 2 4 4 2 2 2 2		+

Tables 1 and 2

DJ sequences are shown as follows. **name, origin** indicates the name and cellular origin of the sequence **D-segment** shows the nucleotides assigned to D_H . In case of overlaps, nucleotides that could be encoded by either D_H or J_H segment are added to the D-segment. Stop codons are underlined. **N/P sequence** shows added N or P nucleotides, **J-segment** the nucleotides assigned to J_H . **D** and **J** are the names of the segments used for rearrangement. **O** + indicates overlaps between D and J. When a rearrangement in rf III is functional (+), i.e. contains no stop codon, or a rearrangement in rf I or II contains a **stop** codon, this is indicated together with the rf **I**+**I**, **D**-**D**, or **2**. **DJ** indicate D_H to D_H fusion; **N**+, **P**+, **N/P**+, or - indicate the presence or absence of added nucleotides at the junction.

infrequent in fetal liver-derived pre B cells of λ 5T mice, rf III joints were present in expected frequencies (~20 – 35%) in all other joints of all other cell populations (Fig. 1). We conclude from these findings that the proliferative expansion of pre-B cells in tssue culture does not alter the frequencies of representation of rf I and rf III within the H chain gene loci of these cells (compare Fig. 1a and b).

Similarly, the representation of rf II did not change significantly upon *in vitro* expansion of pre-B cells from fetal liver of λ 5T or from bone marrow of normal and λ 5T mice, although rf II suppression appeared less pronounced in D_{FL}/D_{SP} – J_H joints of normal pre-B cell lines from bone marrow (Fig. 1b, 5 + 6)

Most important for the possible role of the surrogate L chain in

the rf selection process are the following findings: (i) rf II is suppressed in fetal liver $D_{FL}/D_{SP} - J_H$ joints of pre-B cell clones and lines from normal, but not from λ 5T mice upon proliferative expansion *in vitro* (P=0.038) (Fig.1b, 1 + 2) and (ii) rf II is *not* suppressed in $D_{OS2} - J_H$ joints of the same lines from the same mice (Fig. 1b, 3 + 4). Therefore, we conclude that proliferative expansion *in vitro* can establish suppression of rf II in cell populations which do not show such rf II suppression when they are isolated *ex vivo*. The findings also indicate that the usage of D_{OS2} (containing a stop codon) does not allow this establishment of rf II suppression *in vitro* and suggest that a $D_H J_H C_\mu$ protein might be operative in the rf II suppression.

28 Surrogate L chain in DJ rf 2 suppression

Table 3. D_H rf distribution in preB cells

1. FACS-sorted cells DSP/DFL normal fetal liver day 15 (36 sequences) rf I 24 (67%) rf II 6 (17%) 6 (17%) rf III DSP/DFL λ5T fetal liver day 13 (25 sequences) rf I 15 (60%) rf II 6 (24%) of III 4 (16%) DSP/DFL normal bone marrow cells 3 weeks (58 sequences) rf I 23 (40%) 7 (12%) rf II rf III 28 (48%) DSP/DFL λ 5T bone marrow 14 weeks (31 sequences) rf I 11 (35%) rf 11 13 (42%) rf Ill 7 (23%) 2. Cells from pre-B cell cultures DSP/DFL normal fetal liver (54 sequences) rf I 38 (70%) rf II 5 (9%) rf III 11 (20%) DSP/DFL \lambda 5T fetal liver (38 sequences) 20 (53%) rf I rf II 11 (29%) rf III 7 (18%) DSP/DFL normal bone marrow etc. (34 sequences) rf I 15 (44%) rf II 8 (24%) rf III 11 (32%) DSP/DFL X5T bone marrow (11 sequences) rf I 3 (27%) rf II 5 (45%) rf III 3 (27%) DQ52 normal fetal liver (55 sequences) 26 (47%) rf I 16 (29%) rf II rf II 13 (24%) DQ52 λ 5T fetal liver (43 sequences) 25 (58%) rf I 15 (35%) rf II rf III 3 (7%)

All results taken together imply that a membrane-bound Ig-like complex of truncated $D_H J_H C_\mu$ protein and surrogate L chain suppresses the representation of H chain gene loci which are $D_H J_H$ rearranged in rf II.

Discussion

We found that N sequences in $D_{H}J_{H}$ joints are very frequent within precursor B cells from bone marrow, but very infrequent within similar cells from fetal liver. This confirms findings of other laboratories (9,15,16,21,22). Furthermore, it was found that H chain gene loci which are $D_{H}J_{H}$ rearranged in rf II (8) are suppressed in pre-B cells of normal mice (3,27) We have concentrated our analyses on pre-B cells which are in the process of, or have completed D_{H} to J_{H} rearrangements but which have not yet begun V_{H} to $D_{H}J_{H}$ rearrangements. These cells, which we call pre-B I cells (4), express CD45R, CD43, and c-*kit*, are clonable and will proliferate for long periods of time *in vitro* on stromal cells in the presence of IL-7 (31). When transplanted into SCID hosts, they repopulate B lineage compartments for long periods of time (31). Our results suggest, as do also the results of others (3,6,22,27,33), that at least part of the suppression of rf II is established at the early pre-B I stage of B cell development, i.e. during and directly after D_HJ_H rearrangement. It does not rule out that later stages of B cell development continue to favor rf I-rearranged H chain loci over those rearranged in rf II or III.

The two different oligonucleotide primers (D_{FL}/D_{SP} and D_{Q52}) used in the PCR reaction bind upstream of 14 out of 15 functional D segments. The frequencies of representation of D_H and J_H segments in the analyzed sequences do not necessarily reflect their representation in the pre-B cells which we have analyzed, since different primers were used in the PCR reactions for D_{O52} and D_{FL}/D_{SP} , since it is unknown whether the 5' regions of all D_{FL} and D_{SP} segments act with equal efficiency as acceptor sites for the primer used, and since the different lengths of $D-J_1$, $D-J_2$, $D-J_3$, and $D-J_4$ joints are likely to influence the efficiency of both PCR and cloning. In summary, however, rf II suppression is observed in D_{FL} - and D_{SP} -containing H chain gene loci joined to either J_H 1, 2, 3, or 4.

The situations in which suppression of fl is *not* observed shed light on the mechanism by which this suppression is mediated in pre-B cells.

(i) $D_{Q52} - J_H$ joints in normal mice. Since $D_{Q52} - J_H$ joints cannot be translated into a $D_H J_H C_{\mu}$ protein due to a stop codon, this result suggests that the $D_H J_H C_{\mu}$ protein is involved in suppression.

(ii) The non-functional $D_H J_H$ rearranged alleles of splenic B cells from μ MT mice (27). This suggests that the $D_H J_H C_{\mu}$ protein has to be inserted into (surface) membranes.

(ii) Pre-B cells from fetal liver of normal mice *ex vivo*. This suggests that early fetal liver cells have not had sufficient time to proliferate as $D_H J_H$ rearranged cells, and that they rearrange D_H to J_H preferentially in rf I due to short sequence homologies in D and J segments (9). The frequencies of rf I versus rf II versus rf III in early fetal liver cells resemble those of similar joints generated in fetal liver-derived pre-B cells with an extrachromosomal substrate for such rearrangements (18).

By contrast, pre-B cell clones from early fetal liver of normal mice, expanded in vitro by proliferation for ~ 20 divisions, show rf II suppression. This suggests that pre-B cells establish rf II suppression by proliferation and that fetal liver derived cells can do so in vitro.

(iv) Pre-B cells from λ 5T mice. This suggests that the surrogate L chain V_{pre-B}/λ 5 may form a disulfide-bonded, lg-like complex with $D_H J_H C_{\mu}$ protein and insert this complex into the (surface) membranes in normal mice.

Ligands fitting the complementarity-determining regions (CDR)like structures (CDRs of variable regions of Ig H and L chains) of this complex (13), possibly provided by stromal cells, may signal these pre-B cells to stop proliferation while pre-B cells not expressing this complex on the surface (i.e. with H chain gene loci $D_H J_H$ rearranged in rf I or III or pre-B cells of μ MT or λ 5T mice) continue to expand and thus overgrow those with rf II.

(v) Pre-B cells from bone marrow of normal mice, expanded by proliferation *in vitro*. These cells show some, but much less pronounced suppression of rf II, especially when compared with pre-B cells from bone marrow of normal mice analyzed *ex vivo* and when compared with pre-B cells from fetal liver of normal mice expanded *in vitro*. This result needs to be analyzed in greater detail

with many more sequences to see how N-region insertion could influence the structures of $D_H J_H$ joints. It might be that this N-region insertion leads to insertion of amino acids in the D_H to J_H joining site, i.e. within CDR3 which might interfere with the signalizing function of the $D_H J_H C_\mu$ -surrogate L chain complex leading to rf II suppression in pre-B cells.

In principle our results, as well as those of other investigations (3,9,15), cannot formally rule out the alternative possibility that pre-B cells with rf I and III rearranged H chain loci are selectively expanded while those with rf II are not, but are also not inhibited or deleted. While the suppression of rf II can be explained by the expression and suppressive function of a membrane-bound $D_H J_H C_{\mu}$ – surrogate L chain complex on pre-B cells we have at present no good mechanistic explanation for a possible expansion of pre-B cells with rfI and rfIII $D_H J_H$ rearranged H chain loci.

If $D_H J_H C_{\mu}$ protein is indeed involved in suppression of pre-B I cells with ff II $D_H J_H$ rearranged H chain loci, then at least 15 – 20% of all pre-B I cells in fetal liver and bone marrow of λ 5T mice should express $D_H J_H C_{\mu}$ protein. We have begun to analyze these pre-B cells for $D_H J_H C_{\mu}$ protein expression, but the levels of expression appear to be so low that immunofluorescence analyses and western blotting of protein have not yet detected $D_H J_H C_{\mu}$ protein with certainty.

Although rearrangement in three rfs can in principle lead to a more diverse repertoire of antigen-binding variable regions, it is surprising that the repertoire of B cells appears to be biased towards only one of these three rfs, i.e. rf I. First, sequence homologies in D and J favor rearrangements in rf I at the molecular level, stop codons in 50% of the D segments disfavor expression of H chains in rf III. Furthermore, the results of this paper extend previous findings. that rf II is suppressed and that this may be achieved by a D_HJ_HC_a - surrogate L chain complex. In fetal repertoires the lack of N region insertion further restricts the variability in CDR III. It remains to be a matter of debate (34) why the immune system would in such a way suppress its potential for generating variable regions of antibody molecules. It has been proposed that these invariant receptors could recognize self antigens in their environment and that this recognition may be important for the original expansion of precursor B and B cells to fill up the B cell compartment (35,36), reviewed and discussed in (28).

Acknowledgements

The able technical assistance of Andrea Groenewegen and Marc Dessing is gratefully acknowledged. We thank Drs Jan Andersson, Klaus Karjalainen, and Jim Kaufman for critical reading of the manuscript. The Basel Institute for Immunology was founded and is supported by F. Hoffmann-LaRoche Ltd, Basel, Switzerland.

Abbreviations

CDR	complementarity determining region
Н	heavy
L	light
λ5T mice	homozygous λ5 knockout mice
μMT mice	µH membrane exon knockout mice
N	non-templated
Р	palindrome
PCR	polymerase chain reaction
rf	reading frame
TdT	terminal deoxynucleotidyl transferase

References

- Kurosawa, Y. and Tonegawa, S. (1982) Organization, structure and assembly of immunoglobulin heavy chain diversity DNA segments. J. Exp. Med. 155:201.
- 2 Ichihara, Y., Hayashida, H., Miyazawa, S., and Kurosawa, Y. (1989) Only DFL16, DSP2 and DQ52 gene families exist in mouse immunoglobulin heavy chain diversity gene loci, of which DFL16 and DSP2 originate from the same primordial DH gene. *Eur. J. Immunol.* 19:1849.
- 3 Chang, Y., Paige, C. J., and Wu, G. E. (1982) Enumeration and characterization of DJH structures in mouse fetal liver. *EMBO J*. 11.1891.
- 4 Rolink, A. and Melchers, F (1993) Generation and regeneration of cells of the B-tymphocyte lineage. *Curr. Opin. Immunol.* 5:207.
- 5 Tonegawa, S. (1983) Somatic generation of antibody diversity. Nature 302:575.
- 6 Shimizu, T. and Yamagishi, H. (1992) Biased reading frames of preexisting DH – JH coding joints and preferential nucleotide insertions at VH – DJH signal joints of excision products of immunoglobulin heavy chain gene rearrangements. *EMBO J.* 11:4869.
- 7 Rolink, A., Haasner, D., Nishikawa, S. I., and Melchers, F. (1993) Changes in frequencies of clonable pre-B cells during life in different lymphoid organs of mice. *Blood* 81:2290.
- 8 Kaartinen, M. and Måkela, O (1985) Reading of D genes in variable frames as a source of antibody diversity. *Immunol. Today* 6:324.
- 9 Gu, H., Förster, I., and Rajewsky, K., Sequence homologies, Nsequence insertion and JH gene utilization in VHDJH joining: implications for the joining mechanism and the ontogenetic timing of Ly1 B-cell and B-CLL progenitor generation. *EMBO J.* 9:2133.
- Reth, M. G. and Alt, F. W. (1984) Novel immunoglobulin heavy chains are produced from DJH gene segment rearrangements in lymphoid cells. *Nature* 312 418.
- Sakaguchi, N. and Melchers, F. (1986) λ5, a new light chain-related locus selectively expressed in pre-B lymphocytes. *Nature* 324:579.
- 12 Kudo, A. and Mekchers, F. (1987) A second gene, Vpre-B in the λ5 locus of the mouse which appears to be selectively expressed in pre-B lymphocytes. *EMBO J.* 6:2267.
- 13 Melchers, F., Karasuyama, H., Haasner, D., Bauer, S., Kudo, A., Sakaguchi, N., Jameson, B., and Rolink, A. (1993) The surrogate light chain in B-cell development. *Immunol. Today* 14:60.
- 14 Tsubata, T., Tsubata, R., and Reth, M. (1991) Cell surface expression of the short immunoglobulin μ chain (Dμ-protein) in murine pre-B cells is differently regulated from that of the intact μ chain. Eur. J. Immunol. 21:1359.
- 15 Feeney, A. (1990) Lack of N regions in fetal and neonatal mouse immunoglobulin V – D – J junctional sequences. J. Exp. Med. 172:1377.
- 16 Bangs, L. A., Sanz, I. E., and Teale, J. M. (1991) Comparison of D, JH and junctional diversity in the fetal, adult, and aged B cell repertoires. *J. Immunol.* 146.1996.
- 17 Decker, D. J., Boyle, N. E., Koziol, J. A., and Klinman, N. R. (1991) The expression of the Ig H chain repertoire in developing bone marrow B lineage cells. J. Immunol. 146:350.
- 18 Gerstein, R. M and Lieber, M. R. (1993) Extent to which homology can constrain junctional diversity in V(D)J recombination. *Nature* 363:625.
- 19 Gregoire, K. E., Goldschneider, I., Barton, R. W., and Bollum, F. J. (1989) Ontogeny of terminal deoxynucleotidyl-transferase positive cells in lymphohemopoietic tissues of rat and mouse. J. Immunol. 123:1347.
- 20 Opsteiten, G., Deenen, G. J., Rozing, J., and Hunt, S. V. (1986) Blymphocyte associated antigens on terminal deoxynucleotidyl transferase-positive cells and pre-B cells in bone marrow of the rat. *J. Immunol.* 137-76.
- 21 Holmberg, D., Anderson, A., Carlsson, L., and Forsgren, S. (1989) Establishment and functional implications of B cell connectivity. *Immunol. Rev.* 110:89
- 22 Meek, K. (1990) Analysis of junctional diversity during B lymphocyte development. *Science* 250:820.
- 23 Desiderio, S. V., Yancopoulos, G. D., Paskind, M., Thomas, E., Boss, M. A., Landau, N., Alt, F. W., and Baltimore, D. (1984) Insertion of N regions into heavy chain genes is correlated with expression of terminal deoxynucleotidyl transferase in B cells. *Nature* 311:752.
- 24 Landau, N. R., Schatz, D. G., Rosa, M., and Baltimore, D. (1987)

30 Surrogate L chain in DJ rf 2 suppression

Increased frequency of N region insertion in a murine pre-B cell line infected with a terminal deoxynucleotidyl transferase retroviral expression vector. *Mol. Cell. Biol.* 7:3237.

- 25 Reynaud, C. A., Dahan, A., Anquez, V., and Weill, J. -C. (1989) Somatic hyperconversion diversifies the single VH gene of the chicken with a high incidence in the D region. *Cell* 59:171.
- 26 Lafaille, J. J., DeCloux, A., Bonneville, M., Takagake, Y., and Tonegawa, S. (1990) Junctional sequences of T cell receptor γd genes: implications for γδ T cell lineages and for a novel intermediate of V(D)J joining. *Cell* 59:859.
- 27 Gu, H., Kitamura, D., and Rajewsky, K. (1991) B cell development regulated by gene rearrangement: arrest of maturation by membranebound Dµ protein and selection of DH element reading frames. *Cell* 65:47.
- 28 Rolink, A. and Melchers, F. (1992) Molecular and cellular origins of B lymphocyte diversity. *Cell* 66:1081.
- 29 Karasuyama, H., Kudo, A., and Melchers, F. (1990) The proteins encoded by the Vpre-B and λ 5 pre-B cell-specific genes can associate with each other and with μ heavy chains. *J. Exp. Med.* 172:969.
- 30 Kitamura, D., Kudo, A., Schaal, S., Müller, W., Melchers, F., and Rajewsky, K. (1992) A critical role of λ5 protein in B cell development. *Cell* 69:823.
- 31 Rolink, A., Kudo, A., Karasuyama, H., Kikuchi, Y., and Melchers, F. (1991) Long term proliferating early pre-B cell lines and clones with the potential to develop to surface Ig-positive, mitogen reactive B cells in vitro and in vivo. EMBO J. 10:327.

- 32 Rolink, A., Karasuyama, H., Grawunder, U., Haasner, D., Kudo, A., and Melchers, F. (1993) B cell development in mice with a defective λ5 gene. *Eur. J. Immunol.* 23:1284.
- 33 Feeney, A. J., Comparison of junctional diversity in the neonatal and adult immunoglobulin repertoires. Int. Rev. Immunol. 8:113.
- 34 Cohn, M. and Langman, R. E. (1990) The protecton: The unit of humoral immunity selected by evolution. *Immunol. Rev.* 115:7.
- 35 Vakil, M. and Kearney, J. F. (1986) Functional characterization of monoclonal auto-anti-idiotype antibodies isolated from the early B cell repertoire of Balb/c mice. *Eur. J. Immunol.* 16:1151.
- 36 Vakil, M., Sauter, H., Paige, C., and Kearney, J. F. (1986) *In vivo* suppression of perinatal multispecific B cells results in a distortion of the adult B cell repertoire. *Eur. J. Immunol.* 16:1159.
- 37 Kodama, H., Amagai, Y., Koyama, H., and Kasai, S. (1982) Hormonal responsiveness of a preadipose cell line derived from newborn mouse calvaria. J. Cell. Physiol. 112:83.
- 38 Sambrook, J., Fritsch, E. F., and Maniatis, T. (1989) Molecular Cloning: A Laboratory Manual, 2 edn. Cold Spring Habor Laboratory Press, Cold Spring Harbor, NY.

Note added in proof

We have recently sequenced $D_{Q52} - J_H$ joints of sorted cells from bone marrow of normal and λ 5T mice. They show the expected rf distribution normal mice (28 sequences): rf I, 12 (43%); rf II, 7 (25%); rf III, 9 (32%); λ 5T mice (31 sequences): rf I, 11 (35%); rf II, 11 (35%); rf II, 9 (25%).