GENOMIC TARGETING AND MAPPING OF A GAMETOCIDAL GENE IN WHEAT

by

DEVEN R. SEE

B.S., Montana State University, 1998

M.S., Montana State University, 2000

AN ABSTRACT OF A DISSERTATION

submitted in partial fulfillment of the requirements for the degree

DOCTOR OF PHILOSOPHY

Department of Plant Pathology

College of Agriculture

KANSAS STATE UNIVERSITY
Manhattan, Kansas

2007

Abstract

Segregation distortion describes the transmission of an allele or alleles of a heterozygous locus at a higher frequency than expected in a Mendelian ratio. From the organism's view, segregation distortion is the preferential retention of chromosomal blocks carrying genes beneficial to its fitness and reproductive viability. In wheat the best studied segregation distorters are those introduced from *Aegilops* species; these selfish genetic elements are named gametocidal (Gc) genes and the chromosomes carrying them are called Gc chromosomes. This genetic mechanism causes chromosome breakage in gametophytes lacking the Gc carrier chromosome, thus favoring its own retention in the genome. While the mode of action of the Gc genes is not yet known, they have been used extensively in wheat genetics for the development of deletion stocks, a key resource for elucidating the structure of physical regions containing important genes. The objective of this study was to develop the tools necessary to map the *Gc2* gene derived from *Ae. sharonensis* and perform map-based cloning. Extensive physical and genetic mapping located the gametocidal gene on the distal 1% of the 4BL arm present in the T4BS·4BL-4S^{sh}#1L translocation chromosome. Comparative genomics using rice provided markers distal and proximal to the *Gc2* locus; however, synteny broke down at the locus. The characterization of this chromosomal region has provided insight into its recombination frequency, synteny and composition; however, the dynamic architecture of the end of the chromosome has made comparative mapping of this region difficult.

GENOMIC TARGETING AND MAPPING OF A GAMETOCIDAL GENE IN WHEAT

by

DEVEN R. SEE

B.S., Montana State University, 1998

M.S., Montana State University, 2000

A DISSERTATION

submitted in partial fulfillment of the requirements for the degree

DOCTOR OF PHILOSOPHY

Department of Plant Pathology

College of Agriculture

KANSAS STATE UNIVERSITY
Manhattan, Kansas

2007

Approved by:

Major Professor
Bikram S. Gill

Abstract

Segregation distortion describes the transmission of an allele or alleles of a heterozygous locus at a higher frequency than expected in a Mendelian ratio. From the organism's view, segregation distortion is the preferential retention of chromosomal blocks carrying genes beneficial to its fitness and reproductive viability. In wheat the best studied segregation distorters are those introduced from *Aegilops* species; these selfish genetic elements are named gametocidal (Gc) genes and the chromosomes carrying them are called Gc chromosomes. This genetic mechanism causes chromosome breakage in gametophytes lacking the Gc carrier chromosome, thus favoring its own retention in the genome. While the mode of action of the Gc genes is not yet known, they have been used extensively in wheat genetics for the development of deletion stocks, a key resource for elucidating the structure of physical regions containing important genes. The objective of this study was to develop the tools necessary to map the *Gc2* gene derived from *Ae. sharonensis* and perform map-based cloning. Extensive physical and genetic mapping located the gametocidal gene on the distal 1% of the 4BL arm present in the T4BS·4BL-4S^{sh}#1L translocation chromosome. Comparative genomics using rice provided markers distal and proximal to the *Gc2* locus; however, synteny broke down at the locus. The characterization of this chromosomal region has provided insight into its recombination frequency, synteny and composition; however, the dynamic architecture of the end of the chromosome has made comparative mapping of this region difficult.

Table of Contents

List of Figures

List of Tables

CHAPTER 1 - Chapter 1: Literature review

Introduction

Segregation distortion, first defined by Sandler and Novitski (1957), describes the transmission of an allele or alleles of a heterozygous locus at a different frequency than expected in a Mendelian ratio. From the organism's view, segregation distortion represents the preferential retention of chromosomal blocks carrying genes beneficial to its reproductive viability. The gametocidal genes cause segregation distortion; however, they differ from normal segregation distorters in ensuring reproductive isolation. They are essentially selfish genetic elements that ensure their own transmission.

Certain *Aegilops* species harbor an evolutionarily unique mechanism for the preservation of their genetic continuity. This genetic mechanism causes chromosome breakage in gametophytes lacking the *Aegilops* chromosome, thus favoring the chromosome's own retention within the genome. These genetic elements are designated as gametocidal genes, and the chromosomes carrying them, as gametocidal chromosomes. The first evidence of this phenomenon was discovered during experiments aimed at the introduction of the cytoplasm of *Aegilops triuncialis* into common wheat. In the cytological analysis of backcrossed lines it was observed that all of the alloplasmic substitution lines contained a specific extra chromosome even after multiple rounds of backcrossing. Since the first observation of the gametocidal action, this phenomenon has been reported in several *Aegilops* species.

While the mode of action of the gametocidal genes is not yet known, they have been used extensively in wheat genetics for the development of deletion stocks. These stocks have provided a key resource for elucidating the structure of physical regions containing important genes.

Genus Triticum

Common or bread wheat, *Triticum aestivum* L. (2*n*=6*x*=42, genome formula AABBDD) is an allopolyploid species comprising three homoeologous genomes that arose through hybridization of three diploid progenitor wheats. Restriction fragment length polymorphism (RFLP) studies indicated that the A genome progenitor was *T. urartu* Tumanian ex Gandilyan (2*n*=2*x*=14, genome formula AA) (Dvorak, 1988; Dvorak et al. 1993). Analysis of chromosome pairing identified the D genome progenitor as *Aegilops tauschii* Coss. (2*n*=2*x*=14, genome formula DD) (Kihara, 1944; McFadden and Sears 1946). Sarkar and Stebbins (1956) used morphological evidence to indicate that *Ae. speltoides* Tausch (2*n*=2*x*=14, genome formula SS) is the closest living relative of the B genome of common wheat. This was later supported by Tsunewaki and Ogihara (1983).

Analysis of chromosome pairing between interspecific hybrids shows that the species of the *Triticum*/*Aegilops* complex are closely related (Sax 1922; Kihara 1924), and in fact natural hybrids between diploids can arise in nature. The hybridization of *T. urartu* and *Ae. speltoides* gave rise to the tetraploid wheat, *T. turgidum* L. (2*n*=4*x*=28, genome formula AABB) and *T. urartu* also contributed the A genome to *T. timopheevii* Zhuk (2*n*=4*x*=28, genome formula A^tA^tGG) (Maan and Lucken 1968; Tsunewaki and Ogihara 1983; Gill and Chen 1987; Ogihara and Tsunewaki 1988; Jiang and Gill 1994). The hybridization events that gave rise to common wheat occurred at two distinct times. The first hybridization occurred approximately half a million years ago between *T. urartu* and a relative of *Ae. speltoides* (Huang et al. 2002a). The product of this hybridization, *T. turgidum*, more recently hybridized with *Ae. tauschii* to gave rise to *T. aestivum* approximately 8,000 years ago (Nesbit and Samuel 1996). Two of the three genomes that make up common wheat are derived from the *Aegilops* complex. The *Aegilops* species range over three ploidy levels and comprise ten diploid species, eleven tetraploid species

and four hexaploid species (Van Slageren 1994; Badaeva et al. 2002; Badaeva et al. 2004). It is in these *Aegilops* species that the gametocidal genes were first discovered.

Gametocidal gene discovery

The gametocidal genes were first noticed in investigations of effects of cytoplasmic interactions from polyploids and donor species. In 1975, two scientists independently observed that the critical alien chromosome in the sporophyte enforced the exclusive transmission of male and female gametes carrying that chromosome. Endo and Tsunewaki (1975) were investigating the cytoplasmic relationship between *Aegilops triuncialis* L. ($2n = 28$, genome formula $C^tC^tU^tU^t$) and possible donor species *Ae. caudata* L. ($2n = 14$, genome formula CC) and *Ae. umbellulata* Zhuk ($2n = 14$, genome formula UU). They found that all of the alloplasmic substitution lines carried an extra chromosome originating from cytoplasm donors. This study also indicated that *Ae. caudata* , but not *Ae. umbellulata* carried a gametocidal element. In 1978 Endo further characterized the *Ae. triuncialis* gametocidal-carrying chromosome and found that it was homoeologous to wheat group-3 chromosomes. At the same time, Maan was introgressing *Ae. longissima* Schweinf & Muschl. and *Ae. sharonensis* Eig. chromosomes into hexaploid wheat. He noticed that after backcrossing and selfing, only plants containing a specific *Aegilops* chromosome were functional, and concluded that there must be an apparent gametocidal action of sporophytes carrying *Aegilops* chromosomes on gametes lacking this chromosome (Maan 1975).

To date five gametocidal genes have been identified in *Aegilops* species. In the *sitopsis* group, they have been discovered in *Ae. speltoides* on chromosome 2S (Tsujimoto and Tsunewaki 1983, 1984), in *Ae. longissima* Schweinf. & Muschl. on chromosomes $2S^l$ and $4S^l$ (Endo 1982, 1985; Friebe et al. 1993), and in *Ae. sharonensis* on chromosomes $2S^{sh}$ (Endo 1982,

1985) and $4S^{sh}$ (Maan 1975; Miller et al. 1982), available in the form of a translocation stock T4B-$4S^{sh}$ in Chinese Spring (Endo, Pers. comm.). In the C genome, gametocidal genes have been discovered in *Ae. cylindrica* on chromosome $2C^c$ (Endo 1979, 1988a), in *Ae. caudata* on chromosome 3C (Endo and Katayama 1978) and in *Ae. triuncialis* on chromosome $3C^t$ (Endo 1978; Tsujimoto and Noda 1988). More recently a gametocidal gene has been reported on chromosome $4M^g$ of *Ae. geniculata* (Kynast et al. 2000).

Interrelationship of gametocidal genes in Aegilops species

While the origin of the gametocidal genes is not yet known, it has been proposed that the gametocidal genes in different *Aegilops* species are interrelated. In analyzing the gametocidal gene in *Ae. triuncialis* Endo (1978) concluded that the gametocidal gene in *Ae. triuncialis* is similar to the one in *Ae. caudata*. Because *Ae. caudata* contributed the C genome to *Ae. cylindrica* it could be postulated that the gametocidal genes in these two species are similar as well. The relationship based upon chromosome position was inferred in *Ae. triuncialis*/*Ae. caudata* and other species (Endo 1978, 1982, 1985; Tsujimoto 1995). Both Endo (1990) and Tsujimoto (1995) discussed classifying the different gametocidal genes into groups based upon gametocidal action and severity, such as belonging to chromosomes of group-2 (2S *Ae. longissima*, 2S *Ae. sharonensis*, 2S *Ae. speltoides*), group-4 (4S *Ae. longissima*, 4S *Ae. sharonensis*) and group-3 (3C *Ae. caudata*, 3C *Ae. triuncialis*, synthetic *Ae. triuncialis*).

Some evidence indicates that the interrelated gametocidal genes have diverged. In the comparison of *Ae. longissima* and *Ae. sharonensis*, both have gametocidal genes located on chromosomes 2 and 4; however, in the case of chromosome 4S there is a cytological difference between the two species. *Ae. sharonensis* chromosome $4S^{sh}$ is homoeologous with group 4 in wheat and compensates well for 4B in wheat. *Ae. longissima* chromosome 4; however, shows a

translocation, with about half of the long arm of $4S^l$ having been replaced with chromosome 7 (Chen and Gill 1983; Friebe et al. 1993; Zhang et al. 2001). Other evidence of nonhomoeology between gametocidal chromosomes can be seen in *Ae. cylindrica*, genome $C^cC^cD^cD^c$, which has a functional gametocidal gene within the CC genome derived from *Ae. caudata*. The *Ae. caudata* also donated gametocidal gene to *Ae. triuncialis*. While both *Ae. triuncialis* and *Ae. cylindrica* have gametocidal genes derived from *Ae. caudata* (Endo 1990, 1996), in *Ae. triuncialis* the gametocidal gene is on the chromosome 3C, while in *Ae. cylindrica* it is located on 2C, indicating rearrangement of chromosomal segments carrying the gametocidal gene.

Not all gametocidal genes have the same strength. Gametocidal genes from *Ae. longissima*, *Ae. sharonensis* and *Ae. speltoides* have strong gametocidal action. Endo (1990) showed that *Ae. triuncialis* and *Ae. cylindrica* contain weak gametocidal genes at least in some cultivars. This is contradicted by evidence that in some species the gametocidal action is dependent on the choice of accessions used in the analysis. In screening accessions from *Ae. longissima*, Friebe et al. (1993) observed that not all accessions show gametocidal action. In *Ae. speltoides* Tsujimoto and Tsunewaki (1984) reported gametocidal action in *Ae. speltoides* aucheri lines; however, Friebe et al. (2000a) developed a complete set of *T. aestivum–Ae. speltoides* addition lines showing no gametocidal action. In the case of *Ae. triuncialis*, it appears that specific Japanese cultivars containing the Norin 26 background contain a suppressor, *Igc1*, of gametocidal action located on chromosome 3B (Tsujimoto and Tsunewaki 1985a, 1985b; Endo 1978; Tsujimoto and Noda 1988). Preliminary evidence indicates another unique phenomenon in Norin 26, where the presence of 3C from *Ae. caudata* appears to cause nondisjunction of chromosome 3B (Tsujimoto 2005). For the *Ae. cylindrica,* Gc genes, Endo (1988a, 1988b) observed suppressed or weak gametocidal action in Chinese Spring wheat

background. This is in contrast to the strong *Ae. cylindrica* gametocidal action in the cultivar 'Jones Fife' (Endo 1979). The cause of this conflicting interaction is not known. This background effect may be similar to that observed in Norin 26 and its interaction with *Ae. triuncialis*. Chinese Spring has some ability to protect against certain gametocidal elements; however, this protecting ability is not as strong as seen in Norin 26. It is this relationship between specific gametocidal elements and cultivars for example, *Ae. cylindrica* and Chinese Spring that can be used as a tool in wheat enhancement. These weak interactions have been exploited by scientists in the development of additional aneuploids and deletion stocks in wheat and wheat relatives.

Deletion lines

The tolerance of aneuploidy conferred by polyploidy in common wheat has permitted the development of many useful genetic stocks. Sears first developed and described aneuploids in the form of monosomics, nullisomic-tetrasomics, and telocentric chromosomes (Sears 1954, 1966; Sears and Sears 1978). These aneuploids permitted gene mapping on individual chromosomes and chromosome arms, though subchromosomal mapping awaited the discovery of the gametocidal genes. Chromosome deletions in common wheat developed using gametocidal genes were first observed by Tsujimoto and Tsunewaki in 1985. A number of chromosome deletion lines have been developed by Tsujimoto (1987a). More than 400 chromosome deletion lines for all 21 chromosomes of wheat were reported by Endo and Gill (1996). Their utility as a tool in wheat improvement was discussed by Endo (1988a, 1988b) and by Tsujimoto and Noda (1988).

Deletion lines have been used extensively in mapping and gene discovery. In a study of speltoid suppression of α and β-amylase genes on chromosome 5 in *Ae. speltoides*, Tsujimoto

and Noda (1988, 1990) used deletion lines to mark their physical boundaries. Deletion lines have been used in the development of cytologically-based physical maps of the 21 chromosomes of wheat (Werner et al. 1992a; Gill et al. 1993, 1996a 1996b; Hohmann et al. 1994; Delaney et al. 1995a, 1995b; Mickelson-Young et al. 1995). Deletion lines have also been developed in barley (Schubert et al. 1998; Shi and Endo 1999), and rye (Endo et al. 1994; Friebe et al. 2000b). A subset of 109 deletion lines described by Endo and Gill (1996) was used to develop the most comprehensive physical map of wheat to date, containing 16,099 mapped expressed sequence tags (EST); for an overview of this project see Qi et al. (2003, 2004; http://wheat.pw.usda.gov/NSF/data). In gene cloning efforts, determining the physical location of a target gene is an initial important step towards map-based cloning and comparative analysis, and deletion lines have been used for this purpose for agronomic and disease resistance genes (Faris and Gill 2002; Dieguez et al. 2006; Lu et al. 2006; Mateos-Hernandez et al. 2006).

Cause of segregation distortion

In monosomic addition lines involving *Aegilops* species with gametocidal genes, chromosomes with Gc genes are preferentially transmitted to the progeny. In contrast, where the gametocidal chromosome is not present in the gametophyte, chromosome aberrations occur. The usual result is gamete abortion caused by chromosome breakage due to segregation of gametocidal chromosomes (Finch et al. 1984, Nasuda et al. 1998). This is the case for most of the gametocidal genes reported. However, some gametocidal genes do not always cause gamete abortion as observed in *Ae. caudata* by Nasuda et al. (1998).

Timing and regulation of these chromosomal aberrations are unique and still not fully understood. As only gametophytes lacking the gametocidal chromosome show chromosome

breakage (Finch et al. 1984), the gene responsible for chromosome fragmentation must be expressed prior to segregation of the chromosome carrying it. While the gene must be transcribed early in meiosis, the product of expression is not observed until S-phase of first pollen mitosis, indicating that the gene is not active until this stage of development (Finch et al. 1984; Nasuda et al. 1998).

Fate of broken chromosomes

The breakage-fusion-bridge BFB cycle is initiated when broken ends of chromosomes fuse to form dicentric chromosomes that in turn initiates additional BFB cycles, causing further chromosome rearrangements (McClintock 1941, 1951). Chromosome breakage due to the gametocidal gene occurs prior to chromosome replication at S phase in the first post-meiotic mitosis (Finch et al. 1984), leading to the observation of chromosome fragments in ana/telophase of first pollen mitosis. In second pollen mitosis, fewer chromosome bridges are observed than chromosome breaks in the first pollen mitosis, indicating that BFB cycles are initiated due to chromosome breakage in first pollen mitosis. In second pollen mitosis, Nasuda et al. (1998) observed both single and double chromatid bridges indicating that both chromatid and chromosome BFB types occurred, and less chromosome damage in the second pollen mitosis also indicated that some chromosome ends were healed (Nasuda et al. 1998).

The broken ends of the chromosomes resulting from BFB cycle are healed by the addition of telomeres. Using synthetic telomeric probes and *in situ* hybridization, Werner et al. (1992b) investigated deletion stocks derived from the use of a gametocidal chromosome from *Aegilops cylindrica*, and observed the addition of telomeres to the broken ends of the chromosomes. Tsujimoto (1993) indicated that the telomere repetitive sequences were

synthesized progressively to the full length, taking more than one generation. Most likely the acquisition of telomeric sequences is achieved quickly after breakage; however, due to the low resolution of *in situ* hybridization the early telomere addition stages are not observed (Kynast et al. 2000; Friebe et al. 2001).

Dual-function model

Endo in (1990) proposed a dual-function model to explain the behavior of Gc genes that induces chromosome breakage sporophytically and suppresses it gametophytically. In this model the Gc genes produce two products. One causes chromosome damage and is expressed in the meiotic stage prior to chromosome segregation. The second protects against the gametocidal factor but is not produced until the gametophytic stage. Gametes lacking the Gc gene suffer chromosome damage because they have the first product but lack the protection product.

Evidence to support the dual-function model can be seen in a mutant gametocidal line developed by Friebe et al. (2003). The mutant was developed from a line T4B-4S^{sh}#1 containing a small terminal translocation on 4BL containing a functional *Gc2* gene derived from *Ae. sharonensis* (T. R. Endo pers. comm.). The hemizygous seeds (*Gc2*/-) were treated with a chemical mutagen to knock out the gametocidal gene. After the mutant (*Gc2*^{mut}) was developed, it was testcrossed to the functional (*Gc2*) gametocidal line. Spike fertility in the testcross progeny of *Gc2*/*Gc2*^{mut} was normal, and pollen mitosis was screened with no chromosome fragments seen (Friebe et al. 2003). This indicated that the breaking agent was no longer functional in the mutant line, whereas the protecting agent was still functioning and able to suppress the functional gametocidal gene derived from the wild-type *Gc2*. In contrast, in a single-gene model, where the gene was self-regulating, a mutant at this locus when crossed with a functional *Gc2* carrier would act as a null allele phenotypically, with fifty percent sterility.

The development of this mutant provides possible explanations for some lines that can suppress Gc action. If the breaking agent was suppressed due to mutagenesis or chromosomal loss, then stable hemizygous crosses with Gc carrying chromosomes would be possible, giving rise to plants that lacked the gametocidal drive but retained the protecting agent. Norin 26 may be one example of such an occurrence. Whether this cultivar is a result of such evolution at this locus is not known; however, a stable mutant that down regulates the gametocidal gene supports the dual-function hypothesis for the gametocidal gene.

Two-component systems are observed in other organisms. The dual-function model is similar to the restriction modification (RM) system described in bacteria (Wilson and Murray 1991). Tsujumoto and Noda (1988) pointed out the similarity between the nature of the gametocidal gene and the RM model found in many bacteria. In the RM system a type II restriction endonuclease cleaves dsDNA at specific recognition sites. The protector is a methylase that modifies the recognition site and prevents cleavage. In *Drosophila* a segregation distortion system also occurs in which the segregation distorter (SD) chromosome is transmitted from SD/SD$^+$ males in excess, causing dysfunction of the SD$^+$ spermatids (Merrill et al. 1999). The SD gene has been cloned and found to encode a gene called *RanGAP*, which is a guanosine triphosphatase (GTPase) activator for the Ras-related nuclear regulatory protein RAN. A third system in mice shows preferential transmission in heterozygous males for the *t*-chromosome (Hermann et al. 1999). This two-component system encodes a *distorter* and *responder* gene. The distorter gene impairs spermatozoa and the *responder* gene only functions in sperm carrying the *responder* locus. Cloning of the responder locus showed the presence of a sperm motility kinase gene.

Postulated molecular mechanism of gametocidal genes

Many authors have speculated about the type of gene that causes chromosomal breaks. Finch et al. (1984) commented that the breakage that occurred arose in predetermined chiasma sites and that a faulty DNA repair mechanism left them unhealed. Tsujimoto and Noda (1989) speculated that due to the similarity of the gametocidal system with the restriction modification system in bacteria, a similar restriction system might play a role in the gametocidal system. In a review, Tsujimoto (2005) took this idea further and proposed a restriction modification model to explain chromosome breakage in zygotic cells. In this model a restriction enzyme was regulated by a methylation enzyme implicating methylation as a regulation mechanism of the Gc gene. Methylation was also implicated as regulatory mechanism for gametocidal action and chromosome cleavage by De Las Heras et al. (2001). A transposon theory was mentioned by Tsujimoto and Tsunewaki (1985b). With no known function attributed to the Gc gene none of the proposed models can be rejected, and it may be that some type of restriction enzyme or faulty DNA repair mechanism is at work in the gametocidal system as several authors have proposed. Characterization of a gametocidal gene is needed before any of these proposed models can be validated.

DNA marker types

RFLP markers

Mapping, map-based cloning and marker-assisted selection in breeding populations require the ability to identify and track DNA differences between alleles. DNA-based markers are used to identify allelic differences. One of the first DNA markers and still widely used is restriction fragment length polymorphism (RFLP) (Botstein et al. 1980). RFLP rely upon digestion of genomic DNA using restriction endonucleases, immobilization on a nylon membrane (Southern 1975) and hybridization with a radioactively labeled probe (Rigby et al.

1977). The ability of the restriction enzyme to cleave DNA selectively allows the distinction of polymorphic alleles between genotypes, and makes this a codominant marker system. RFLP technology has been used extensively in wheat to develop genetic maps (Chao et al. 1989; Kam-Morgan et al. 1989; Gill et al. 1991; Devos and Gale 1993; Van Deynze et al. 1995a; Nelson et al. 1995a, 1995b, 1995c; Marino et al. 1996). RFLP markers are also uniquely suited in polyploid wheat in a dominant assay in screening for the presence or absence of aneuploids. In wheat aneuploids have been used to assign RFLP probes to specific chromosomes, chromosome arms, and deletion bins (Sharp et al. 1989; Anderson et al. 1992; Qi et al. 2004). One problem with RFLP is the polymorphism detection rate in some organisms. Kam-Morgan et al. (1989) found in screening many hexaploid wheats that only one in three loci were polymorphic. A similar ratio was reported by Chao et al. (1989).

PCR-based markers

With the invention of polymerase chain reaction PCR by Mullis and Faloona (1986), more rapid methods for sequence polymorphism detection became available. PCR permits the exponential amplification of specific DNA sequences through a cyclic thermal regime that involves denaturation of double-stranded DNA, annealing of short oligonucleotides to known priming sequences, and an extension phase where a thermostable DNA polymerase (*Thermus aquaticus* (Saiki et al. 1988)) adds new nucleic acids by base complementation. This ability to amplify short DNA sequences with high selectivity opens up new areas in both marker selection, and detection platforms, and increases efficiency.

Sequence-tagged site (STS)

Sequence-tagged site (STS) markers are among the first types of markers that capitalized upon the PCR based approach. STS markers have the potential to be codominant markers that

utilize short primers, approximately 20 base pairs (bp) in length, derived from known flanking sequence. STS markers were originally developed from sequenced RFLP probes (Olson et al. 1989; Tragoonrung et al. 1992; Talbert et al. 1994). Direct use of STS markers to identify polymorphism works in several ways. Sequence differences within the priming regions give rise to a dominant marker with amplification of one allele and lack of amplification of the other allele due to lack of priming. Insertion and deletion events between priming sites provide codominant detection of polymorphisms as a result of mobility shift. Indirect use of STS markers involves post-PCR selection of the amplicon using restriction endonuclease digestion to screen for sequence difference between priming sites. PCR restriction analysis is known as cleaved amplified polymorphic sequence CAPS (Saiki et al. 1985). A variant of CAPS used in mutant screening is the utilization of a specific endonuclease from celery CEL I. In CEL I assays amplicons from different varieties are annealed together in the presence of CEL I which nicks DNA at single stranded regions. The process works when amplicons from different varieties are annealed together and polymorphisms between amplicons act as unpaired regions. CEL I recognizes the unpaired region as single-stranded and cleaves at this site (Oleyowski et al. 1998).

Simple sequence repeats (SSRs)

Microsatellites have a high degree of variability within the repeat region, making them a good polymorphic marker (Schlötterer 2000). With a mutation rate between 10^{-6} to 10^{-2} mutants per base pair microsatellites have a higher mutation rate than random base substitutions. Microsatellite sequences, also known as simple sequence repeats (SSRs), are types of sequences that contain repeated segments of DNA. These repeats of one to multiple, usually six or fewer, short sequence motifs in tandem are ubiquitous in eukaryotic genomes (Tautz and Renz 1984; Tautz et al. 1986; Litt and Luty 1989). This high degree of variability is most likely due to

slippage during DNA replication (Tautz et al. 1986). Another advantage of microsatellites is that they occur at higher frequency in expressed sequences than in non-expressed genomic DNA (Morgante et al. 2002). For large, complex genomes these factors make microsatellites a useful marker for mapping (Röder et al. 1995; Stephenson et al. 1998; Röder et al. 1998; Korzun et al. 1999; Pestsova et al. 2000; Paillard et al. 2003; Gao et al. 2004; Song et al. 2005).

Amplified fragment length polymorphism (AFLP)

Amplified fragment length polymorphism (AFLP) is a good marker when genomic sequence is not known. For AFLP detection genomic DNA is digested with multiple restriction endonucleases to fragment the genome. Then PCR is used to amplify the restricted fragments based upon nucleotide composition. In practice, AFLP technology uses six-base and four-base restriction enzymes to digest genomic DNA. The cleaved DNA fragments are then ligated to short oligonucleotide adapters that recognize the digested overhangs providing a stable platform for the amplification of genomic DNA by PCR. Once the oligonucleotide adapters are attached, they can be used as priming sites for selective amplification based upon the nucleotide composition just inside the restriction enzyme recognition site (Vos et al. 1995).

This ability to fragment, then amplify a genome makes AFLP a versatile marker. Comparing multiple marker platforms including RFLP, SSR, RAPD, and AFLP, AFLP had a higher number of scorable genotypes per assay unit (Russell et al. 1997). AFLP does have a drawback in that it produces dominant genotypes which prevent direct analysis between alleles at a given locus. AFLP are used for three main purposes. In genetic mapping AFLP markers by themselves are not linked; however, they can be used to saturate genetic maps reducing the centiMorgan distances between known linked makers (Peng et al. 2000; See et al. 2002; Dieguez et al. 2006). AFLP are also useful in map-based cloning efforts to develop additional markers

(Faris and Gill 2002; Haen et al. 2004). In population diversity studies, AFLP are a rapid technology providing multiple data points per assay (Russell et al. 1997; Heun et al. 1997).

Random amplified polymorphic DNA (RAPD)

Random amplified polymorphic DNA (RAPD), takes advantage of one of the drawbacks of PCR based markers; this drawback in PCR is that the sequence of the locus must first be known prior to the development of primers. RAPD use random short 10 bp oligonucleotides to amplify polymorphic bands from one parent but not the other (Williams et al. 1990). While RAPD are highly polymorphic and have been used in wheat (He et al. 1992), they have several problems that make them a poor marker. The main problems with RAPDs are reproducibility and amplification of repetitive DNA (Devos and Gale 1992).

Single nucleotide polymorphisms (SNPs)

Single nucleotide polymorphisms (SNPs) are the most abundant source of polymorphisms in a genome. In common wheat it is estimated there is 1 homoeologous sequence variant (HSV) per 24 bp and 1 SNP every 540 bp (Somers et al. 2003). In comparison with other cereals Ching et al. (2002) reported 1 SNP every 60 bp in out-breeding maize, in barley Bundock et al. (2003) observed 1 SNP per 131 bp and in rice Yu et al. (2005) observed 1 SNP per 300 bp. SNPs are single base or insertion-deletion events that result in a single nucleotide change. SNPs are one of the newer marker technologies; however, the underlying premise behind this technology is not new. Several older methodologies also rely on the ability to discern single nucleotide changes like RFLP, CAPs and AFLP. There are many different SNP marker detection platforms available; the platform of choice depends on the cost, throughput and efficiency of the method.

There are four main reaction principles behind SNP detection. Oligonucleotide ligation involves pairs of oligonucleotides that anneal adjacent to the target sequence having an allele-specific 3' or 5' end. When the oligonucleotides perfectly match the template sequence the oligonucleotides can be ligated and extension occurs. In the case of a mismatch the oligonucleotide does not ligate properly and extension does not occur. (Samiotaki et al. 1994; Grossman et al. 1994; Lizardi et al. 1998). In the allele specific oligonucleotide probe method, two short allele specific oligonucleotides are used as a probe. The probes are allowed to pair with the target DNA which contains the SNP and only in conditions of a perfect match are the probes stable (Saiki et al. 1989; Livak et al. 1995; Tyagi and Kramer 1996; Hacia et al. 1998). Minisequencing, or single nucleotide primer extension, uses competing primers with a 3' determinant nucleotide. Perfect annealing of the correct primer allows for extension by DNA polymerase of a single dye-labeled dideoxynucleotide. This is a robust technology that is adaptable to many detection platforms; multiplexed sequencing (Pastinen et al. 1996), enzyme-linked immunosorbent assay (ELISA) (Nyren et al. 1993), matrix-associated laser desorption time-of-flight mass spectrometry (MALDI-TOF) (Braun et al. 1997) and microarray analysis (Lindroos et al. 2001). The last method involves allele-specific primer extension. In this method, two primers with a 3' determinant nucleotide compete to anneal adjacent to a SNP. The primer with the complimentary nucleotide at the 3' end anneals correctly and extension can occur producing an amplicon. This method is robust and adaptable to high throughput (Whitcombe et al. 1999; See et al. 2000; Pastinen et al. 2000; Hirschhorn et al. 2000; Fan et al. 2000). The allele-specific primer extension method is currently being used to develop SNP from physically mapped ESTs for the wheat genome (http://wheat.pw.usda.gov/SNP/new/index.shtml).

Comparative genomics

Within the grass family, the major agronomically important species include rice, maize and wheat. Gene discovery within these species relies on genetic demarcation of the gene of interest. It is compounded by genome size, composition and chromosome location all of which determine the rate of success of positionally cloning a specific gene. The grass family contains approximately 10,000 species and arose between 50 to 80 million years ago (Kellog 1998; Huang et al. 2002b). The genomes of these important crop species range in size and complexity from 430 Mb for rice with 16% repeat elements, 2,500 Mb in maize with 50% repeats, and 16,000 Mb in wheat with 92% repeats (Feng et al. 2002; Meyers et al. 2001; Li et al. 2004). The linear correlation between genome expansion and repeat-element frequency makes direct sequencing of large complex genomes difficult. To circumvent this problem, comparative genomics was investigated and became a powerful tool in complex or large genomes which are not amenable to genomic sequencing projects.

The choice of species to use as a reference in comparative genomics was based upon size and composition of the genome. The concept of classifying the grasses as a single genetic system was first discussed by Bennetzen and Freeling (1993). This brought about several low-resolution comparative genome maps (Ahn et al. 1993; Moore et al. 1995; Van Deynze et al. 1995b; Gale and Devos 1998) that produced at least at the macro level, a consensus map of the grasses. Comparative mapping along with the small genome size and low repeat-element frequency in rice made rice a good candidate for genome sequencing as scientists viewed rice as the Rosetta Stone for the rest of the cereals. Messing and Llaca (1998) stated that sequencing the rice genome as an anchor genome of the grasses would provide instantaneous access to the same genes in the same relative physical position in other grasses.

With the sequenced genome of rice in hand a more in-depth analysis of synteny revealed a mosaic of conserved and nonconserved regions between the genomes (Sorrells et al. 2003; Guyot et al. 2004; Singh et al. 2006). At the DNA or micro level, a more complex picture emerged. In some regions microcolinearity is conserved, and comparative mapping becomes a useful tool in cloning specific genes (Dubcovsky et al. 2001; SanMiguel et al. 2002; Ramakrishna et al. 2002; Mammadov et al. 2005; Yan et al. 2004). In other instances comparative mapping indicates that at the microcolinearity level synteny is not conserved (Li and Gill 2002; Dunford et al. 2002; Spielmeyer and Richards 2004; Valárik et al. 2006).

The breakdown of colinearity at the macro or chromosome level is mainly caused by recombination, duplications, intergenic expansions, and inversions. Duplications and deletions as discussed by Akhunov et al. (2003a, 2003b) are correlated with recombination rates and are localized to the high recombination regions in the distal portions of the chromosomes. Intergenic expansion occurs primarily as a result of insertions and reshuffling of repeat elements by recombination resulting in both expansion and deletion events (Bennetzen et al. 2000; Shirasu et al. 2000; Devos et al. 2002). The end result is a complex picture where repeats, polyploidization and evolution have influenced some regions of genomes while leaving others intact, complicating the process of comparative mapping for gene discovery.

References Literature review

Akhunov ED Akhunova AR Linkiewicz AM Dubcovsky J Hummel D Lazo G Chao S Anderson OD Jacques D Qi LL Echalier B Gill BS Miftahudin J Gustafson P La Rota M Sorrells ME Zhang D Nguyen HT Kalavacharla V Hossain K Kianian SF Peng J Lapitan NLV Wennerlind EJ Nduati V Anderson JA Sidhu D Gill KS McGuire PE Qualset CO Dvorak J (2003a) Synteny perturbations between wheat homoeologous chromosomes caused by locus duplications and deletions correlate with recombination rates. Proc Natl Acad Sci USA 100:10836-10841.

Akhunov ED Goodyear AW Geng S Qi LL Echalier B Gill BS Miftahudin J Gustafson P Lazo G Chao S Anderson OD Linkiewicz AM Dubcovsky J La Rota M Sorrells ME Zhang D Nguyen HT Kalavacharla V Hossain K Kianian SF Peng, J Lapitan NLV Gonzalez-Hernandez JL Anderson JA Choi DW Close TJ Dilbirligi M Gill KS Walker-Simmons MK Steber C McGuire PE Qualset CO Dvorak J (2003b) The organization and rate of evolution of wheat genomes are correlated with recombination rates along chromosome arms. Genome Res 5:753-763.

Anderson JA Ogihara Y Sorrells ME Tanksley SD (1992) Development of a chromosomal arm map for wheat based on RFLP markers. Theor Appl Genet 83:1035-1043.

Ahn S Anderson JA Sorrells ME Tanksley SD (1993) Homoeologous relationships of rice, wheat and maize chromosomes. Mol Gen Genet 241:483-490.

Badaeva ED Amosova AV Muravenko OV Samatadze TE Chikida NN Zelenin AV Friebe B Gill BS (2002) Genome differentiation in *Aegilops*. 3. Evolution of the D-genome cluster. Plant Syst Evol 231:163-190.

Badaeva ED Amosova AV Samatadze TE Zoshchuk SA Shostak NG Chikida NN Zelenin AV Raupp WJ Friebe B Gill BS (2004) Genome differentiation in *Aegilops*. 4. Evolution of the U-genome cluster. Plant Syst Evol 246:45-76.

Bennetzen JL (2000) Comparative sequence analysis of plant nuclear genomes: Microcolinearity and its many exceptions. Plant Cell 12:1021-1029.

Bennetzen JL Freeling M (1993) Grasses as a single genetic system: Genome composition, colinearity and compatibility. Trends Genet 9:259-261.

Botstein D White RL Skolnick M Davis RW (1980) Construction of a genetic linkage map in man using restriction fragment length polymorphisms. Am J Hum Genet 32:314-331.

Braun A Little DP Koster H (1997) Detecting *CFTR* gene mutations by using primer oligo base extension and mass spectrometry. Clin Chem 43:1151-1158.

Bundock PC Christopher JT Eggler P Ablett G Henry RJ Holton TA (2003) Single nucleotide polymorphisms in cytochrome P450 genes from barley. Theor Appl Genet 106:676-682.

Chao S Sharp PJ Worland AJ Warham EJ Koebner RMD Gale MD (1989) RFLP-based genetic maps of wheat homoeologous group 7 chromosomes. Theor Appl Genet 78:495-504.

Chen PD Gill BS (1983) The origin of chromosome 4A, and genomes B and G of tetraploid wheats. Proc 6th Int Wheat Genet Symp, Kyoto, Japan 39-48.

Ching A Caldwell KS Jung M Dolan M Smith OS Tingey S Morgante M Rafalski AJ (2002) SNP frequency, haplotype structure and linkage disequilibrium in elite maize inbred lines. BMC Genet 3:19-33.

Delaney DE Nasuda S Endo TR Gill BS Hulbert SH (1995a) Cytologically based physical maps of the group-2 chromosomes of wheat. Theor Appl Genet 91:568-573.

Delaney DE Nasuda S Endo TR Gill BS Hulbert SH (1995b) Cytologically based physical maps of the group-3 chromosomes of wheat. Theor Appl Genet 91:780-782.

Dieguez MJ Altieri E Ingala LR Perera E Sacco F Naranjo T (2006) Physical and genetic mapping of amplified fragment length polymorphisms and the leaf rust resistance *Lr3* gene on chromosome 6BL of wheat. Theor Appl Genet 112:251-257.

De Las Heras JI King IP Parker JS (2001) 5-azacytidine induces chromosomal breakage in the root tips of wheat carrying the cuckoo chromosome $4S^{L}$ from *Aegilops sharonensis*. Heredity 87:474-479.

Devos KM Gale MD (1992) The use of random amplified polymorphic DNA markers in wheat. Theor Appl Genet 84:567-572.

Devos KM Gale MD (1993) The genetic maps of wheat and their potential in plant breeding. Outlook Agric 22:93-99.

Devos KM Brown JKM Bennetzen JL (2002) Genome size reduction through illegitimate recombination counteracts genome expansion in *Arabidopsis*. Genome Res 12:1075-1079.

Dubcovsky J Ramakrishna W SanMiguel P Busso CS Yan L Shiloff B Bennetzen J (2001) Comparative sequence analysis of colinear barley and rice bacterial artifical chromosomes. Plant Physiol 125:1342-1353.

Dunford RP Yano M Kurata N Sasaki T Huestis G Rocheford T Laurie DA (2002) Comparative mapping of the barley *Ppd-H1* photoperios response gene region, which lies close to a junction between two rice linkage segments. Genetics 161:825-834.

Dvorak J (1988) Cytogenetical and molecular inferences about the evolution of wheat. Proc. 7th Int. Wheat Genet. Symp., 187-192. (Institute of Plant Science Research Cambridge, UK.)

Dvorak J Terlizzi PD Zhang H Resta P (1993) The evolution of polyploid wheat: identification of the A genome donor species. Genome 33:21-31.

Endo TR (1978) On the *Aegilops* chromosomes having gametocidal action on common wheat. In: Ramanujam S (ed) Proceedings 5th Int. Wheat Genet Symp, New Delhi. 306-314.

Endo TR (1979) Selective gametocidal action of a chromosome of *Aegilops cylindrica* in a cultivar of common wheat. Wheat Inf Serv 50:24-28.

Endo TR (1982) Gametocidal chromosomes of three *Aegilops* species in wheat. Can J Genet Cytol 24:201-206.

Endo TR (1985) Two types of gametocidal chromosomes of *Aegilops sharonensis* and *Ae. longissima*. Jpn J Genet 60:125-135.

Endo TR (1988a) Induction of chromosomal changes by a chromosome of *Aegilops cylindrica* L. in common wheat. J Heredity 79:366-370.

Endo TR (1988b) Chromosome mutations induced by gametocidal chromosomes in common wheat. In: Miller, TE, Koebner RMD (eds) Proceedings of the 7th International Wheat Genetics Symposium. Institute of Plant Science Research. Cambridge laboratory, Cambridge. 259-265.

Endo TR (1990) Gametocidal chromosomes and their induction of chromosome mutations in wheat. Jpn J Genet 65:135-152.

Endo TR (1996) Allocation of a gametocidal chromosome of *Aegilops cylindrica* to wheat homoeologous group 2. Genes Genet Syst 71:243-246.

Endo TR Katayama Y (1978) Finding of a selectively retained chromosome of *Aegilops caudata* L. in common wheat. Wheat Inf Serv 47-48:32-35.

Endo TR Tsunewaki K (1975) Sterility of common wheat with *Aegilops triuncialis* cytoplasm. J Heredity 66:13-18.

Endo TR Yamamoto M Mukai Y (1994) Structural changes of rye chromosome 1R induced by a gametocidal chromosome. Jpn J Genet 69:13-19.

Endo TR Gill BS (1996) The deletion stocks of common wheat. J Heredity 87:295-307.

Fan JB Chen X Halushka MK Berno A Huang X Ryder T Lipshutz RJ Lockhart DJ Chakravarti A (2000) Parallel genotyping of human SNPs using generic high-density oligonucleotide tag arrays. Genome Res 6:853-860.

Faris JD Gill BS (2002) Genomic targeting and high-resolution mapping of the domestication gene Q in wheat. Genome 45:706-718.

Feng Q Zhang Y Hao P Wang S Fu G Huang Y Li Y Zhu J Liu Y Hu X Jia P Zhang Y Zhao Q Ying K Yu S Tang Y Weng Q Zhang L Lu Y Mu J Lu Y Zhang LS Yu Z Fan D Liu X Lu T Li C Wu Y Sun T Lei H Li T Hu H Guan J Wu M Zhang R Zhou B Chen Z Chen L Jin Z Wang R Yin H Cai Z Ren S Lv G Gu W Zhu G Tu Y Jia J Zhang Y Chen J Kang H Chen X Shao C Sun Y Hu Q Zhang X Zhang W Wang L Ding C Sheng H Gu J Chen S Ni L Zhu F Chen W Lan L Lai Y Cheng Z Gu M Jiang J Li J Hong G Xue Y Han B (2002) Sequence and analysis of rice chromosome 4. Nature 420:316-320.

Finch RA Miller TE Bennett MD (1984) "Cuckoo" *Aegilops* addition chromosome in wheat ensures its transmission by causing chromosome breaks in meiospores lacking it. Chromosoma 90:84-88.

Friebe B Tuleen N Jiang J Gill BS (1993) Standard karyotype of *Triticum longissimum* and its cytogenetic relationship with *T. aestivum*. Genome 36:731-742.

Friebe B Qi LL Nasuda S Zhang P Tuleen NA Gill BS (2000a) Development of a complete set of *Triticum aestivum-Aegilops speltoides* chromosome addition lines. Theor Appl Genet 101:51-58.

Friebe B Kynast RG Gill BS (2000b) Gametocidal factor-induced structural rearrangements in rye chromosomes added to common wheat. Chromosoma 8:501-511.

Friebe B Kynast RG Zhang P Qi L Dhar M Gill BS (2001) Chromosome healing by addition of telomeric repeats in wheat occurs during first mitotic division of the sporophyte and is a gradual process. Chromosome Res 9:137-146.

Friebe B Zhang P Nasuda S Gill BS (2003) Characterization of a knock-out mutation at the *Gc2* locus in wheat. Chromosoma 111:509-517.

Gale MD Devos KM (1998) Comparative genetics in the grasses. Proc Natl Acad Sci USA 95:1971-1974.

Gao LF Jing RL Hou NX Li Y Li XP Zhou RH Chang XP Tang JF Ma ZY Jia JZ (2004) One hundred and one new microsatellite loci derived from ESTs (EST-SSRs) in bread wheat. Theor Appl Genet 108:1392-1400.

Gill BS Chen PD (1987) Role of cytoplasm-specific introgression in the evolution of the polyploid wheats. Proc Natl Acad Sci USA 84:6800-6804.

Gill KS Lubbers EL Gill BS Raupp WJ Cox TS (1991) A genetic linkage map of *Triticum tauschii* (DD) and its relationship to the D genome of bread wheat (AABBDD) Genome 34:362-374.

Gill KS Gill BS Endo TR (1993) A chromosome region-specific mapping strategy reveals gene-rich telomeric ends in wheat. Chromosoma 102:374-381.

Gill KS Gill BS Endo TR Boyko EV (1996a) Identification and high-density mapping of gene-rich regions in chromosome group 5 of wheat. Genetics 143:1001-1012.

Gill KS Gill BS Endo TR Taylor T (1996b) Identification and high-density mapping of gene-rich regions in chromosome group 1 of wheat. Genetics 144:1883-1891.

Grossman PD Bloch W Brinson E Chang CC Eggerding FA Fung S lovannisci DA Woo S and Winn-Deen ES (1994) High-density multiplex detection of nucleic acid sequences: oligonucleotide ligation assay and sequence-coded separation. Nucl Acid Res 22:4527-4534.

Guyot R Yahiaoui N Feuillet C Keller B (2004) In silico comparative analysis reveals a mosaic conservation of genes within a novel colinear region in wheat chromosome 1AS and rice chromosome 5S. Funct Integr Genomics 4:47-58.

Hacia JG Sun B Hunt N Edgemon K Mosbrook D Robbins C Fodor SPA Tagle DA Collins FS (1998) Strategies for mutational analysis of the large multiexon ATM gene using high-density oligonucleotide arrays. Genome Res 8:1245-1258.

Haen KM Lu H-J Friesen TL Faris JD (2004) Genomic targeting and high-resolution mapping of the *Tsn1* gene in wheat. Crop Sci 44:951-962.

He S Ohm H Mackenzie S (1992) Detection of DNA sequence polymorphisms among wheat varieties. Theor Appl Genet 84:573-578.

Hermann BG Koschorz B Wertz K McLaughlin J Kispert A (1999) A protein Kinase encoded by the *t* complex *responder* gene causes non-Mendelian inheritance. Nature 402:141-146.

Heun M Schäfer-Pregl R Klawan D Castagna R Accerbi M Borghi B Salamini F (1997) Site of Einkorn wheat domestication identified by DNA fingerprinting. Science 278:1312-1314.

Hirschhorn JN Sklar P Lindblad-Toh K Lim YM Ruiz-Gutierrez M Bolk S Langhorst B Schaffner S Winchester E Lander ES (2000) An array-based method for efficient single-nucleotide polymorphism genotyping. Proc Natl Acad Sci USA 97:12164-12169.

Hohmann U Endo TR Gill KS Gill BS (1994) Comparison of genetic and physical maps of group 7 chromosomes from *Triticum aestivum* L. Mol Gen Genet 245:644-653.

Huang S Sirikhachornkit A Su X Faris J Gill B Haselkorn R Gornicki P (2002a) Genes encoding plastid acetyl-CoA carboxylase and 3-phosphoglycerate kinase of the *Triticum* / *Aegilops*

complex and the evolutionary history of polyploid wheat. Proc Natl Acad Sci USA 99:8133-8138.

Huang S Sirikhachornkit A Faris JD Su X Gill B Haselkorn R Gornicki P (2002b) Phylogenetic analysis of the acetyl-CoA carboxylase and 3-phosphoglycerate kinase loci in wheat and other grasses. Plant Mol Biol 48:805-820.

Jiang J and Gill BS (1994) Different species-specific chromosome translocations in *Triticum timopheevii* and *T. turgidum* support the diphyletic origin of polyploid wheats. Chromosome Res 2:59-64.

Kam-Morgan LNW Gill BS Muthukrishnan S (1989) DNA restriction fragment length polymorphisms: a strategy for mapping of D genome of wheat. Genome 32:724-732.

Kellog EA (1998) Relationships of cereal crops and other grasses. Proc Natl Acad Sci USA 95:2005-2010.

Kihara H (1924) Cytologische und genetische Studien bei wichtigen Getreidearten mit besonderer Rücksicht auf das Verhalten der Chromosomen und die Sterilität in den Bastarden. Men Coll Sci Kyoto Imp. Univ. Ser. B:1-200

Kihara H (1944) Discovery of the DD-analyser, one of the ancestors of *Triticum vulgare*. (in Japanese) Agric Hortic 19:13-14.

Korzun V Röder MS Wendehake K Pasqualone A Lotti C Ganal MW Blanco A (1999) Integration of dinucleotide microsatellites from hexaploid bread wheat into a genetic linkage map of durum wheat. Theor Appl Genet 98:1202-1207.

Kynast RG Friebe B Gill BS (2000) Fate of multicentric and ring chromosomes induced by a new gametocidal factor located on chromosome $4M^g$ of *Aegilops geniculata*. Chromosome Res 8:133-139.

Li W Gill BS (2002) The colinearity of the *Sh2/A1* orthologous region in rice, sorghum and maize is interrupted and accompanied by genome expansion in the Triticeae. Genetics 160:1153-1162.

Li W Zhang P Fellers JP Friebe B Gill BS (2004) Sequence composition, organization, and evolution of the core Triticeae genome. Plant J. 40:500-511.

Lindroos K Liljedahl U Raitio M Syvanen AC (2001) Minisequencing on oligonucleotide microarrays: comparison of immobilization chemistries. Nucl Acid Res 29:E69-9.

Livak KJ Flood SJ Mamaro J Guisti W Deetz K (1995) Oligonucleotides with fluorescent dyes at opposite ends provide a quenching probe system useful for detecting PCR product and nucleic acid hybridization. PCR Methods Appl 4:357-362.

Litt M Luty JA (1989) A hypervariable microsatellite revealed by in vitro amplification of a dinucleotide repeat within the cardiac muscle actin gene. Am J Hum Genet 44:397-401.

Lizardi PM Huang X Zhu Z Bray-Ward P Thomas DC Ward DC (1998) Mutation detection and single-molecule counting using isothermal rolling-circle amplification. Nat Genetics 19:225-232.

Lu H-J Fellers JP Friesen TL Meinhardt SW Faris JD (2006) Genomic analysis and marker development for the *Tsn1* locus in wheat using bin-mapped ESTs and flanking BAC contigs. Theor Appl Genet 112:1132-1142.

Maan SS (1975) Exclusive preferential transmission of an alien chromosome in common wheat. Crop Sci 15:287-292.

Maan SS and Lucken KA (1968) Male-sterility durum: Interaction of *Triticum boeoticum* and *T. monococcum* cytoplasms with *T. durum* nucleus. Wheat Inform Serv 26:5-18.

Mammadov JA Steffenson BJ Saghai Maroof MA (2005) High-resolution mapping of the barley leaf rust resistance gene *Rph5* using barley expressed sequence tags (ESTs) and synteny with rice. Theor Appl Genet 111:1651-1660.

Marino CL Nelson JC Lu TH Sorrells ME Leroy P Tuleen NA Lopes CR Hart GE (1996) Molecular genetic maps of the group 6 chromosomes of hexaploid wheat (*Triticum aestivum* L. em. Thell.) Genome 39:359-366.

Mateos-Hernandez M Singh RP Hulbert SH Bowden RL Huerta-Espino J Gill BS Brown-Guedira G (2006) Targeted mapping of ESTs linked to the adult plant resistance gene *Lr46* in wheat using synteny with rice. Funct Integr Genomics 6:122-131

McClintock B (1941) The stability of broken ends of chromosomes in *Zea mays*. Genetics 26:234-282.

McClintock B (1951) Chromosome organization and genic expression. Cold Spring Harbor Symp. Quant Biol 14:13-47.

McFadden ES Sears ER (1946) The artificial synthesis of *Triticum spelta*. Rec. Genet. Soc. Amer. 13:6-27.

Merrill C Bayraktaroglu L Kusano A Ganetzky B (1999) Truncated RanGAP encoded by the segregation distorter locus of *Drosophila*. Science 283:1742-1745.

Messing J Llaca V (1998) Importance of anchor genomes for any plant genome project. Proc Natl Acad Sci USA 95:2017-2020.

Meyers BC Tingey SV Morgante M (2001) Abundance, distribution, and transcriptional activity of repetitive elements in the maize genome. Genome Res 11:1660-1676.

Mickelson-Young L Endo TR Gill BS (1995) A cytogenetic ladder map of the wheat homoeologous group-4 chromosomes. Theor Appl Genet 61:27-33.

Miller TE Hutchinson J Chapman V (1982) Investigation of a preferentially transmitted *Aegilops sharonensis* chromosome in wheat. Theor Appl Genet 61:27-33.

Moore G Devos KM Wang Z Gale MD (1995) Grasses, line up and form a circle. Curr Biol 5:737.

Morgante M Hanafey M Powell W (2002) Microsatellites are preferentially associated with nonrepetitive DNA in plant genomes. Nat Genetics 30:194-200.

Mullis K Faloona F Scharf S Saiki R Horn G Erlich H (1986) Specific enzymatic amplification of DNA in vitro: The polymerase chain reaction. Cold Spring Harbor Symp Quant Biol 51:263.

Nasuda S Friebe B Gill BS (1998) Gametocidal genes induce chromosome breakage in the interphase prior to the first mitotic cell division of the male gametophyte in wheat. Genetics 149:1115-1124.

Nelson JC Van Deynze AE Autrique E Sorrells ME Lu YH Merlino M Atkinson M Leroy P (1995a) Molecular mapping of wheat. Homoeologous group 2. Genome 38:516-524.

Nelson JC Van Deynze AE Autrique E Sorrells ME Lu YH Negre S Bernard M Leroy P (1995b) Molecular mapping of wheat. Homoeologous group 3. Genome 38:525-533.

Nelson JC Sorrells ME Van Deynze AE Lu YH Atkinson M Bernard M Leroy P Faris JD Anderson JA (1995c) Molecular mapping of wheat: Major genes and rearrangements in homoeologous groups 4, 5, and 7. Genetics 141:721-731.

Nesbitt M, Samuel D (1996) From staple crop to extinction? The archaeology and history of hulled wheats. In : Padulosi S, Hammer K, Heller J, Pacoli C (eds) Hulled wheats. Promoting the conservation and use of underutilized and neglected crops. Proc 1st Int Workshop Hulled Wheats. International Plant Genetic Resources Institute, Rome, Italy, pp 41-100.

Nyren P Pettersson B Uhlen M (1993) Solid phase DNA minisequencing by an enzymatic luminometric inorganic pyrophosphate detection assay. Anal Biochem 208:171-175.

Ogihara Y and Tsunewaki K (1988) Diversity and evolution of chloroplast DNA in *Triticum* and *Aegilops* as revealed by restriction fragment analysis. Theor Appl Genet 76:321-332.

Oleykowski CA Bronson Mullins CR Godwin AK Yeung AT (1998) Mutation detection using a novel plant endonuclease. Nucl Acid Res 26:4597-4602.

Olson M Hood L Cantor C Botstein D (1989) A common language for physical mapping of the human genome. Science 245:1434-1435.

Paillard S Schnurbusch T Winzeler M Messmer M Sourdille P Abderhalden O Keller B Schachermayr G (2003) An integrative genetic linkage map of winter wheat (*Triticum aestivum* L.) Theor Appl Genet 107:1235-1242.

Pastinen T Partanen J Syvanen AS (1996) Fluorescent, solid-phase minisequencing for efficient screening of DNA sequence variation. Clin Chem 42:1391-1397.

Pastinen T Raitio M Lindroos K Tainola P Peltonen L Syvänen AC (2000) A system for specific, high-throughput genotyping by allele-specific primer extension on microarrays. Genome Res 10:1031-1042.

Peng J Korol AB Fahima T Roder MS Ronin YI Li YC Nevo E (2000) Molecular genetic maps in wild emmer wheat, *Triticum dicoccoides*: genome-wide coverage, massive negative interference, and putative quasi-linkage. Genome Res 10:1509-1531.

Pestova E Ganal MW Röder MS (2000) Isolation and mapping of microsatellite markers specific for the D genome of bread wheat. Genome 43:689-697.

Qi L Echalier B Friebe B Gill BS (2003) Molecular characterization of a set of wheat deletion stocks for use in chromosome bin mapping of ESTs. Funct Integr Genomics 3:39-55.

Qi LL Echalier B Chao S Lazo GR Bulter GE Anderson OD Akhunov ED Dvorak J Linkiewicz AM Ratnasiri A Dubcovsky J Bermudez-Kandianis CE Greene RA Kantety R La Rota CM Munkvold JD Sorrells SF Sorrells ME Dilbirligi M Sidhu D Erayman M Randhawa HS Sandhu D Bondareva SN Gill KS Mahmoud AA Ma XF Miftahudin Gustafson JP Conley EJ Nduati V Gonzales-Hernandez JP Anderson JA Peng JH Lapitan NLV Hossain KG Kalavacharla V Kianian SF Pathan MS Zhang DS Nguyen HT Choi DW Fenton RD Close TJ McGuire PE Qualset CO Gill BS (2004) A chromosome bin map of 16,000 expressed sequence tag loci and distribution of genes among the three genomes of polyploid wheat. Genetics 168:701-712.

Ramakrishna W Dubcovsky J Park YJ Busso CS Emberton J SanMiguel P Bennetzen JL (2002) Different types and rates of genome evolution detected by comparative sequence analysis of orthologous segments from four cereal genomes. Genetics 162:1389-1400.

Rigby PWJ Dieckmann M Rhodes C Berg P (1977) Labeling deoxyribonucleic acid to high specific activity *in vitro* by nick translation with DNA polymerase I. J Mol Biol 113:237.

Röder MS Plaschke J König SU Börner A Sorrells ME Tanksley SD Ganal MW (1995) Abundance, variability and chromosomal location of microsatellites in wheat. Mol Gen Genet 246:327-333.

Röder MS Korzun V Wendehake K Plaschke J Tixier MH Leroy P Ganal MW (1988) A microsatellite map of wheat. Genetics 149:2007-2023.

Russell JR Fuller JD Macaulay M Hatz BG Jahoor A Powell W Waugh R (1997) Direct comparison of levels of genetic variation among barley accessions detected by RFLPs, AFLPs, SSRs and RAPDs Theor Appl Genet 95:714-722.

Saiki RK Arnheim N Erlich HA (1985) A novel method for the detection of polymorphic restriction sites by cleavage of oligonucleotide probes: Application to sickle-cell anemia Bio/Technology 3:1008-1012.

Saiki RK Gelfand DH Stoffel S Scharf SJ Kiguchi R Horm GT Mullis KB Erilich HA (1988) Primer-directed enzymatic amplification of DNA with a thermostable DNA polymerase. Science 239:487.

Saiki RK Walsh PS Levenson CH Erlich HA (1989) Genetic analysis of amplified DNA with immobilized sequence-specific oligonucleotide probes. Proc Natl Acad Sci USA 86:6230-6234.

Sandler L Novitski E (1957) Meiotic drive as an evolutionary force. Am Nat 91:105-110.

Samiotaki M Kwiatkoswki M Parik J Landegren U (1994) Dual-color detection of DNA sequence variants by ligase-mediated analysis. Genomics 20:238-242.

SanMiguel P Ramakrishna W Bennetzen JL Busso CS Dubcovsky J (2002) Transposable elements, genes and recombination in a 215-kb contig from wheat chromosome 5A(m). Funct Integr Genomics 2:70-80.

Sarkar P Stebbins GL (1956) Morphological evidence concerning the origin of the B genome in wheat. Amer J Bot 43:297-304.

Sax K (1922) Sterility in wheat hybrids. II. Chromosome behavior in partially sterile hybrids. Genetics 7:513-552.

Sears ER (1954) The aneuploids of common wheat. Mo Agr Exp Sta Res Bull. 572:1-58.

Sears ER (1966) Nullisomic-tetrasomic combinations in hexaploid wheat. In: Chromosome Manipulations and Plant Genetics (Riley, R., Lewis, K. R. eds) Oliver and Boyd. 29-45.

Sears ER Sears LMS (1978) The telocentric chromosomes of common wheat. Proc 5th Intl Wheat Genet Symp (Ramanujam S, ed) New Delhi, India. 389-407.

See DR Kanazin V Talbert H Blake T (2000) Electrophoretic detection of single-nucleotide polymorphisms. BioTechniques 28:710-176.

See DR Kanazin V Kephart K and Blake T (2002) Mapping genes controlling variation in barley grain protein concentration. Crop Sci 42:680-685.

Sharp PJ Chao S Desai S Gale MD (1989) The isolation, characterization and application in the *Triticeae* of a set of wheat RFLP probes identifying each homoeologous chromosome arm. Theor Appl Genet 78:342-348.

Schlötterer C (2000) Evolutionary dynamics of microsatellite DNA. Chromosoma 109:365-371.

Schubert I Shi F Fuchs J Endo TR (1998) An efficient screening for terminal deletions and translocations of barley chromosomes added to common wheat. Plant Journal 14:489-495.

Shi F Endo TR (1999) Genetic induction of structural changes in barley chromosomes added to common wheat by a gametocidal chromosome derived from *Aegilops cylindrica*. Genes Genet Syst 74:49-54.

Singh NK Dalal V Batra K Singh BK Chitra G Singh A Ghazi IA Yadav M Pandit A Dixit R Singh PK Singh H Koundal KR Gaikwad K Mohapatra T Sharma TR (2006) Single-copy genes define a conserved order between rice and wheat for understanding differences caused by duplication, deletion, and transposition of genes. Funct Integr Genomics DOI: 10.1007/s10142-006-0033-4.

Shirasu K Schulman AH Lahaye T Schulze-Lefert P (2000) A contiguous 66-kb barley sequence provides evidence for reversible genome expansion. Genome Res 7:908-915.

Somers DJ Kirkpatrick R Moniwa M Walsh A (2003) Mining single-nucleotide polymorphisms from hexaploid wheat ESTs Genome 49:431-437.

Song QJ Shi JR Singh S Fickus EW Costa JM Lewis J Gill BS Ward R Cregan PB (2005) Development and mapping of microsatellite (SSR) markers in wheat. Theor Appl Genet 110:550-560.

Sorrells ME La Rota M Bermudez-Kandianis CE Greene RA Kantety R Munkvold JD Miftahudin Mahmoud A Ma X Gustafson PJ Qi LL Echalier B Gill BS Matthews DE Lazo GR Chao S Anderson OD Edwards H Linkiewicz AM Dubcovsky J Akhunov ED Dvorak J Zhang D Nguyen HT Peng J Lapitan NLV Gonzalez-Hernandez JL Anderson JA Hossain K Kalavacharla V Kianian SF Choi DW Close TJ Dilbirligi M Gill KS Steber C Walker-Simmons MK McGuire PE Qualset CO (2003) Comparative DNA sequence analysis of wheat and rice genomes. Genome Res 13:1818-1827.

Spielmeyer W Richards RA (2004) Comparative mapping of wheat chromosome 1AS which contains the tiller inhibition gene (*tin*) with rice chromosome 5S. Theor Appl Genet 109:1303-1310.

Stephenson P Bryan G Kirby J Collins A Devos K Busso C Gale M (1998) Fifty new microsatellite loci for the wheat genetic map. Theor Appl Genet 97:946-949.

Southern EM (1975) Detection of specific sequences among DNA fragments separated by gel electrophoresis. J Mol Biol 98:503-517.

Talbert LE Blake NK Chee PW Blake TK Magyar GM (1994) Evaluation of "sequence-tagged-site" PCR products as molecular markers in wheat. Theor Appl Genet 87:789-794.

Tautz D Renz D (1984) Simple sequences are ubiquitous repetitive components of eukaryotic genomes. Nucl Acid Res 12:4127-4138.

Tautz D Trick M Dover GA (1986) Cryptic simplicity in DNA is a major source of genetic variation. Nature 322:652-656.

Tragoonrung S Kanazin V Hayes PM Blake TK (1992) Sequence-tagged-site facilitated PCR for barley genome mapping. Theor Appl Genet 84:1002-1008.

Tsujimoto H (2005) Gametocidal genes in wheat as the inducer of chromosome breakage. Wheat Inf Ser 100:33-48.

Tsujimoto H Tsunewaki K (1983) Genetic analyses on a gametocidal gene originated from *Aegilops Aucheri*. In: Sakamoto S (ed) Proc 6th Int Wheat Genet Symp, Plant Germplasm Institute, Kyoto Univ, Kyoto, Japan. 1077-1081.

Tsujimoto H Tsunewaki K (1984) Gametocidal genes in wheat and its relatives. I. Genetic analyses in common wheat of a gametocidal gene derived from *Aegilops speltoides*. Can J Genet Cytol 26:78-84.

Tsujimoto H Tsunewaki K (1985a) Gametocidal genes in wheat and its relatives. II. Suppressor of the chromosome 3C gametocidal gene of *Aegilops triuncialis*. Can J Genet Cytol 27:178-185.

Tsujimoto H Tsunewaki K (1985b) Hybrid dysgenesis in common wheat caused by gametocidal genes. Jpn J Genet 60:565-578.

Tsujimoto H (1987) Chromosome structure of speltoid mutants induced by gametocidal genes of common wheat, *Gc1* (in Japanese) Japan Journal of Breeding 37:Supl 1:382-383.

Tsujimoto H (1993) Molecular cytological evidence for gradual telomere synthesis at the broken ends in wheat. J Plant Res 106:239-244.

Tsujimoto H (1995) Gametocidal genes in wheat and its relatives. IV. Functional relationships between six gametocidal genes. Genome 38:283-289.

Tsujimoto H (2005) Gametocidal genes in wheat as the inducer of chromosome breakage. Wheat Inf Ser 100:33-48.

Tsujimoto H Noda K (1988) Chromosome breakage in wheat induced by the gametocidal gene of *Aegilops triuncialis* L.: Its utilization for wheat genetics and breeding. Proc. 7th Int. Wheat Genet Symp, Cambridge, 455-460.

Tsujimoto H Noda K (1990) Deletion mapping by gametocidal genes in common wheat: position of speltoid suppression (*Q*) and *β*-amylase (*β-Amy-A2*) genes on chromosome 5A. Genome 31:850-853.

Tsunewaki K, Ogihara Y (1983) The molecular basis of genetic diversity among cytoplasms of *Triticum* and *Aegilops species*. II. On the origin of polyploid wheat cytoplasms as suggested by chloroplast DNA restriction fragment patterns. Genetics 104:155-171.

Tyagi S Kramer FR (1996) Molecular beacons: probes that fluoresce upon hybridization. Nat Biotechnol 16:49-53.

Valárik M Linkiewicz AM Dubcovsky J (2006) A microcolinearity study at the earliness *per se* gene *Eps-A^{m}1* region reveals an ancient duplication that preceded the wheat-rice divergence. Theor Appl Genet 112:945-957.

Van Deynze AE Dubcovsky J Gill KS Nelson JC Sorrells ME Dvořák J Gill BS Lagudah ES McCouch SR Appels R (1995a) Molecular-genetic maps for group 1 chromosomes of Triticeae species and their relation to chromosomes in rice and oat. Genome 38:45-59

Van Deynze AE Nelson JC Yglesias ES Harrington SE Braga DP McCouch SR Sorrells ME (1995b) Comparative mapping in grasses. Wheat relationships. Mol Gen Genet 248:744-754.

Van Slageren MW (1994) Wild wheats: A monograph of *Aegilops* L. and *Amblyopyrum* (Jaub. & Spach) Eig (Poaceae). Wageningen Agricultural University papers 94-97.

Vos P Hogers R Bleeker M Reijans M Van De Lee T Hornes M Frijters A Pot J Peleman J Kuiper M Zabeau M (1995) AFLP: A new technique for DNA fingerprinting. Nucl Acid Res 23:4407-4414.

Werner JE Endo TR Gill BS (1992a) Toward a cytogenetically based physical map of the wheat genome. Proc Natl Acad Sci USA 89:11307-11311.

Werner JE Kota RS Gill BS Endo TR (1992b) Distribution of telomeric repeats and their role in the healing of broken chromosome ends in wheat. Genome 35:844-848.

Williams JGK Kubelik AR Livak KJ Rafalski JA Tingey SV (1990) DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. Nucl Acid Res 18:6531-6535.

Wilson GG Murray NE (1991) Restriction and modification systems. Annual Review Genetics 25: 585-627

Whitcombe D Theaker J Guy SP Brown T Little S (1999) Detection of PCR products using self-probing amplicons and fluorescence. Nat Biotechnol 17:804-807.

Yan L Loukoianov A Blechl A Tranquilli G Ramakrishna W SanMiguel P Bennetzen JL Echenique V Dubcovsky J (2004) The wheat *VRN2* gene is a flowering repressor down-regulated by vernalization. Science 203:1640-1644.

Yu J Wang J Lin W Li S Li H Shou J Ni P Dong W Hu S Zheng C Zhang J Zhang Y Li R Xu Z Li S Li X Zheng H Cong L Lin L Yin J Geng J Li G Shi J Liu J Lv H Li J Wang J Deng Y Ran L Shi X Wang X Wu Q Li C Ren X Wang J Wang X Li D Liu D Zhang X Ji Z Zhao W Sun Y Zhang Z Bao J Han Y Dong L Ji J Chen P Wu S Liu J Xiao Y Bu D Tan J Yang L Ye C Zhang J Xu J Zhou Y Yu Y Zhang B Zhuang S Wei H Liu B Lei M Yu H Li Y Xu H Wei S He X Fang L Zhang Z Zhang Y Huang X Su Z Tong W Li J Tong Z Li S Ye J Wang L Fang L Lei T Chen C Chen H Xu Z Li H Huang H Zhang F Xu H Li NZhao C Li S Dong L Huang Y Li L Xi Y Qi Q Li W Zhang B Hu W Zhang Y Tian X Jiao Y Liang X Jin J Gao L Zheng W Hao B Liu S Wang W Yuan L Cao M Mcdermott J Samudrala R Wang J Wong GK Yang H (2005) The genomes of *Oryza sativa*: a history of duplications. PloS Biol

3:e38.Zhang H Reader SM Liu X Jia JZ Gale MD Devos KM (2001) Comparative genetic analysis of the *Aegilops longissima* and *Ae. sharonensis* genomes with common wheat. Theor Appl Genet 103:518-525.

CHAPTER 2 - Genomic targeting and mapping of a gametocidal gene in wheat

Introduction

Segregation distortion, first described by Sandler and Novitski (1957), is the transmission of an allele or alleles at a heterozygous locus at a different frequency than the expected Mendelian ratio. Segregation distortion is observed in many eukaryotic organisms including fungi, plants, and animals (Burt and Trivers 2006). The segregation distorters in the model organisms of *Drosophila* (Temin et al. 1991) and mouse (Silver 1993) are the best studied.

In discussing the model systems specifically in *Drosophila* and mice some information can be gained into how segregation distortion works. The *Drosophila*, segregation distorter (SD) chromosome is transmitted from SD/SD$^+$ only in males, and it involves the induced dysfunction of sperm that receive the SD$^+$ homologue (Hartl et al. 1967). The main gene required for distortion is *Sd*, which interacts with an array of repeated satellite DNA sequences known as the *Responder* (*Rsp*) locus. The copy number of the repeats is correlated to the sensitivity of the *Rsp* locus (Hartl 1974; Pimpinelli and Dimitri 1989). This sensitivity at the *Rsp* locus is the result of an imperfect tandem 204-bp repeat where insensitive chromosomes have 100-200 repeats while the wild-type sensitive chromosomes have up to 2400 copies of the repeat (Houtchens and Lyttle 2003). Spermatids receiving a copy of the *SD* chromosome with a sensitive *Rsp* locus fail to reach maturity. The *Sd* gene has been cloned and found to encode gene *Sd-RanGAP*, a guanosine triphosphatase (GTPase) activator for the Ras-related nuclear regulatory protein RAN (Merrill et al. 1999). The *Sd-RanGAP* responsible for distortion is a truncated version of the wild-type

RanGAP. Normal *RanGAP* is localized in the cytoplasm associated with the outer periphery of the nuclear envelope. The *Sd-RanGAP* missing 234 amino acids from the C terminus is no longer transported to the cytoplasm instead it is localized in the nuclei (Kusano et al. 2001). Additional work by Kusano et al. (2002) showed that it is not specifically the action of the *Sd-RanGAP* that causes segregation distortion instead, localization to the nuclei of either normal *RanGAP* or mutant both cause segregation distortion. While the exact mechanism for sperm dysfunction is unclear, it was postulated that the *RanGAP* localized in the nuclei interferes with nuclear transport in spermatids carrying the sensitive *Rsp* locus.

In mice, segregation distortion occurs in heterozygous males at the *t*-haplotype complex (*t*/+) causing dysfunctional sperm. A 12-cM (30–40 Mb) region in the proximal part of chromosome 17 controls the transmission of the *t*-haplotype chromosome to 99% of progeny (Silver 1993). The *t* locus accounts for one-third of chromosome 17 and recombination between the *t*-haplotype DNA and wild-type is suppressed in this region by four non-overlapping inversions, which ensure that the *t* locus is inherited as a single unit (Hammer et al. 1989). This two component system encodes *distorters* (*Tcd1* to *Tcd3*) which act in all sperm cells and *responder* (*Tcr*) gene which acts only in sperm carrying the *Tcr* locus. The working model is that heterozygosity at the *distorter* loci causes a strong harmful effect on the wild-type form of the *responder*; however, its effect on the *t-responder* (*Tcr*) is weak, leading to distortion in favor of *Tcr*. Homozygosity at the *distorter* loci has a strong harmful effect on both the wild type *responder* and *Tcr*, causing sterility (Lyon 1986). Cloning of the *responder* locus showed the presence of a ”sperm motility kinase” *Smok* gene that may control axonemal components essential for flagellar movement (Hermann et al. 1999). While the responder locus has been characterized, none of the distorters have been cloned. Deletion screening by Lyon et al. (2000);

and Planchart et al. (2000) have narrowed down the physical region of *Tcd1* but have yet to clone this gene. Genes including the dynein gene *Dnahc8*, which affect both flagellar formation and movement have been suggested as likely candidates for the distorter (Fossella et al. 2000), other possible candidates have been described as well, for review see (Lyon 2003). In these systems, the segregation distorters either destroy gametes that carry the alternative allele (*Drosophila*) or render them dysfunctional in heterozygous males (mice).

Similar segregation distorters have been found in plants: tobacco (Cameron and Moav 1957), wheat (Loegering and Sears 1963), and tomato (Rick 1966). The best understood segregation distortion system in plants is found in rice. The rice segregation distortion results from hybrid sterility usually between japonica and indica varieties. Chromosomal regions containing loci that cause segregation distortion have been reported on all rice chromosomes. Segregation distorter loci affecting spikelet sterility have been reported on chromosomes 2, 5, 6, 7, 8, and 11 (Li et al. 1997; Wang et al. 2005). Gamete eliminators, or pollen killer loci, have been reported on chromosomes 1, 3, 4, 6, 7, and 11 (Xu et al. 1997). Sano (1990) mapped the gamete eliminator *S1* to chromosome 6, tightly linked to the waxy locus. More recently Hu et al. (2006) have mapped the pollen killer *S29*(*t*) to the short arm of chromosome 2. However to date, no pollen killer genes have been cloned.

The best studied segregation distorters in wheat are those introduced from *Aegilops* species; these selfish genetic elements are named gametocidal (Gc) genes and the chromosomes encoding them are called Gc chromosomes (Endo 1978). In wheat, the gametocidal genes function irrespective of the sex of the carrier individual. In Gc/- individuals, gametophytes lacking the Gc gene show extensive chromosome breakage (King and Laurie 1993; Nasuda et al. 1998). The first evidence of this preferential transmission was identified from the introduction of

the cytoplasm of *Aegilops triuncialis* L. into common wheat by Endo and Tsunewaki (1975). At the same time, Maan (1975) was introgressing *Ae. longissima* Schweinf. & Muschl. and *Ae. sharonensis* Eig. chromosomes into hexaploid wheat. The cytological analysis of fertile lines revealed that all of the alloplasmic lines contained an identical extra chromosome even after several rounds of backcrossing. Preferential transmission of Gc gene occurred in progeny of Gc/- euplasmic individuals as well. Since the first observation of the gametocidal action, this phenomenon has been reported in several *Aegilops* species. Gametocidal genes are known to be on chromosomes $3C^t$ of *Ae. triuncialis* (Endo and Tsunewaki 1975), 3C of *Ae. caudata* L. (Endo and Katayama 1978), $2C^c$ of *Ae. cylindrica* Host (Endo 1979, 1988a, 1996), 2S and 6S in *Ae. speltoides* Tausch (Tsujimoto and Tsunewaki 1983, 1985b; Kota and Dvorak 1988), $2S^{sh}$ and $4S^{sh}$ in *Ae. sharonensis* (Maan 1975; Endo 1982; Miller et al. 1982), $2S^l$ and $4S^l$ of *Ae. longissima* (Endo 1985; Friebe et al. 1993; Tsujimoto 1994, 1995), and $4M^g$ of *Ae. geniculata* Roth (Friebe et al. 1999).

The action of the different Gc genes ranges from strong to weak. Chromosome breakage in lines containing *Ae. speltoides* and *Ae. sharonensis* Gc genes is severe, and only gametophytes with the Gc gene are functional. Background also has an affect on different Gc genes; the Gc gene from *Ae. cylindrica* in a common wheat background when backcrossed with wheat cultivar 'Jones Fife' is transmitted exclusively to progeny (Endo 1979). However, in the cultivar Chinese Spring, the Gc gene does not cause extensive gamete abortion instead most gametes are viable but with chromosome aberrations (Endo 1988b). In the case of the *Ae. triuncialis* Gc gene, specific Japanese cultivars carrying the Norin 26 background carry a inhibitor of gametocidal action, *Igc*1 located on chromosome 3B (Tsujimoto and Tsunewaki 1985a, 1985b; Endo 1978; Tsujimoto and Noda 1988).

The mode of action for the Gc gene is not known; however, it is hypothesized that the gametocidal gene is transcribed during the last pre-meiotic S phase and the gene product is carried through in the dyad and tetrad sporophytic stages. Before or at the first post-meiotic S phase the gametocidal gene induces chromosome breakage. Endo (1990) proposed a dual function model, which states that one gene induces chromosome breakage in the gametophytes lacking the Gc-carrier chromosome and a second gene encoding for a protecting agent suppresses it and acts in gametophytes having the Gc-carrier chromosome. One gene is expressed in the meiotic stage prior to chromosome segregation. The second gene protects against the gametocidal factor but it is not expressed until the gametophytic stage. Thus, gametophytes lacking the Gc-carrier chromosome suffer from chromosome breakage because they do not have the Gc-carrier chromosome that encodes for the protecting agent.

The gametocidal genes have an impact in plant breeding. The gametocidal genes in the *Aegilops* species are a bottleneck to introgression of useful genes to wheat from alien species. They were invaluable in the development of genetic stocks in wheat; a weak allele of Gc genes was used to isolate 436 deletion chromosome lines in common wheat by Endo and Gill (1996). The utility of the deletion lines in wheat has been demonstrated, both in gene discovery (Faris and Gill 2002) and in the development of a high-resolution physical map of wheat (Qi et al. 2003, 2004; http://wheat.pw.usda.gov/NSF/data). Because Gc genes are unique segregation distorters that may have played an important role in speciation and have been exploited in plant breeding, their molecular analysis is important.

The aim of this project was to develop the genetic stocks needed to map a gametocidal gene. The Gc genes are located on alien chromosomes that do not pair and recombine with wheat chromosomes and yet their phenotype is only observed in the wheat background. The molecular

analysis of the Gc gene presents a challenge to target the region of the genome containing the Gc gene, and develop the markers needed to map the gametocidal gene. The gametocidal gene from *Ae. sharonensis* was chosen for genetic mapping because it has a strong gametocidal action that provides a clear phenotype. In addition, multiple genetic stocks were available that provide an opportunity for mapping the Gc locus. The genetic stocks include the original *Ae. sharonensis* "Cuckoo" disomic addition line DA4S^{sh}#1 developed by Miller et al. (1982) and a translocation stock developed from the 4S^{sh}#1 addition in the form of a spontaneous wheat *Ae. sharonensis* translocation line (T4BS·4BL-4S^{sh}#1L) identified by Endo (personal comm). Additional stocks include eight 4S^{sh} disomic addition lines (Tuleen, unpublished) from different accessions of *Ae. sharonensis*, all with functional Gc genes that can be used as a source of polymorphisms for the mapping population.

Recent scientific developments in the cereals as well as the location of the *Ae. sharonensis* translocation containing the *Gc2* gene in the distal 5% of the long arm of chromosome 4B pave the way for map-based cloning. Previous publications have indicated that the subtelomeric regions of wheat chromosome arms, although constituting only a small fraction of their physical length, are gene-rich and account for most of their recombination (Werner et al. 1992; Gill et al. 1993; Akhunov et al. 2003a). The recent sequencing of the complete rice genome (Yu et al. 2002) and the development of an extensive physical map of the wheat genome (Qi et al. 2004), both have potential to provide critical genetic information.

Initially the sequencing of the rice genome was anticipated to be an anchor genome for the grasses. Specifically, sequencing of the rice genome was supposed to make available instantaneous access to the same genes in the same relative physical position in other grasses (Messing and Llaca 1998). Comparative genomics utilizing the rice genome has provided a more

complex picture; in some instances gene colinearity was instrumental in identifying genes in orthologous regions in other grasses (Yan et al. 2003, 2004; Chantret et al. 2004). In other instances colinearity with rice was disrupted (Li and Gill 2002; Spielmeyer and Richards 2004; Valárik et al. 2006). Often this disruption of colinearity is localized in the distal regions of the chromosomes (Akhunov et al. 2003b; Spielmeyer and Richards 2004; Valárik et al. 2006; See et al. 2006).

With the location of the *Gc2* gene in a high-recombination region, the level of recombination should not be a problem; however, due to the nature of the gametocidal gene Mendelian segregation and a segregating phenotype were not initially available. To overcome these problems, additional genetic stocks were produced. Specifically an EMS induced mutant at the *Gc2* locus was developed (Friebe et al. 2003). The development of this *Gc2* mutant designated $Gc2^{mut}$*#1* both restored Mendelian segregation and allowed for a distinct segregating phenotype. In addition to this, the mutant also salvages the phenotype in the heterozygous state due to a still-functional protecting agent, thus allowing recombination to occur around the *Gc2* locus.

This manuscript represents the short term objective of population development, identification and development of markers linked to the gametocidal gene, the production of a genetic map and the development of a second *Gc2* mutant. The long term goal is the molecular cloning of the *Gc2* locus to determine its mode of action.

Materials and methods

Mutant development

Gc2 hemizygous (*Gc2*/-) plants are semisterile and therefore provide a convenient target for mutagenesis for fertile spikes. Homozygous T4BS·4BL-4S^{sh}#1L(*Gc2*/*Gc2*) was crossed with Chinese Spring(-/-) to produce 3276 hemizygous (*Gc2*/-) seeds, which were treated with 0.4% ethyl methane sulfonate (EMS) for 24 hr in a 0.05 M phosphate buffer (pH 8) with gentle agitation (Williams et al. 1992). Seeds were rinsed with water, planted in 90.1 cm^3 root-trainers (Spencer Lemaire Industries, Canada) and grown in the greenhouse (22°C day, 20°C night; 16 hr daylight). Germination frequency was determined at 3 weeks after planting, and selfed-seed set was determined at 4 weeks after anthesis. A mutation at the *Gc2* locus that inhibits *Gc2* function will produce functional gametes independent of the *Gc2* carrier chromosome presence, resulting in fertile spikes. Fertile M_2 families were screened cytologically to determine the transmission of the *Gc2* chromosome T4BS·4BL-4S^{sh}#1L.

C-banding and chromosome identification and chromosome structure was identified according to Gill et al. (1991). C-banding and FISH patterns of the *Gc2* carrier chromosome T4BS·4BL-4S^{sh}#1L have been reported previously by Friebe et al. (2003). Fluorescence *in situ* hybridization (FISH) followed the protocols of Zhang et al. (2001). The 258 bp tandem repeat clone pGc1R-1 was used to identify the *Ae. sharonensis* segment in wheat (Nasuda 1999). The tandem repeat clone pGc1R-1 localizes to the subtelomere region and has 98% sequence identity to the S-genome specific repeat pAESKb52 identified by Anamthawat-Jonsson and Heslop-Harrison (1993). The telomeric repeat pAtT4, was derived from *Arabidopsis* (Richards and Ausubel 1988). Fiber FISH was done according to Jackson et al. (2001).

Mapping population development

The material utilized in this study consists of eight wheat–*Ae. sharonensis* disomic chromosome addition lines DA4S^{sh}#1 to DA4S^{sh}#9, and the Gc parental accession of *Ae. sharonensis* TA10434 (Miller et al. 1982), a derived wheat–*Ae. sharonensis* translocation line T4BS·4BL-4S^{sh}#1L, and its knockout mutant T4BS·4BL-4S^{sh}#1L(*Gc2^{mut}#1*), described as *Gc2^{mut}#1* (Friebe et al. 2003). The last genetic stocks essential for this mapping study are the disomic addition lines that are the source of the functional polymorphic parental line. Disomic 4S^{sh} addition lines cannot be used directly to produce mapping populations because chromosomes 4B, 4S^{sh}, and T4BS·4BL-4S^{sh}#1L can form trivalents and lead to distorted segregation and chromosome instability. To prevent this, the disomic addition lines were converted to disomic substitution lines. Disomic 4S^{sh} addition lines were crossed as males with the Chinese Spring (CS) monosomic 4B and selfed to produce disomic substitution (DS) lines. Disomic substitution lines were recovered for chromosomes 4S^{sh}#5 and 4S^{sh}#7 called DS4S^{sh}#5(4B), and DS4S^{sh}#7(4B). In using the derived disomic substitution lines, meiotic metaphase I pairing can only occur in the *Ae. sharonensis* segments in chromosomes 4S^{sh} and T4BS·4BL-4S^{sh}#1L, resulting in normal bivalent pairing and Mendelian segregation.

The mapping population was developed in two stages and the complete cross can be written as (DS4S^{sh}#7(*Gc2*) / T4BS·4BL-4S^{sh}#1L(*Gc2^{mut}#1*)) // CS. The first cross between homozygous T4BS·4BL-4S^{sh}#1L(*Gc2^{mut}#1*) and the wild-type disomic substitution line DS4S^{sh}#7(*Gc2*) provides the meiotic event resulting in recombination around the *Gc2* locus. This F_1 was then crossed to CS (-/-). The second cross does not contribute to further recombination since neither chromosome 4S^{sh}#7 or the *Ae. sharonensis* segment in T4B-4S^{sh}#1 can pair with 4BL. However, the second cross segregates the *Gc2* and *Gc2^{mut}*#1 encoding chromosome segment, resulting in a clear phenotype of semi-sterility or fertility. The (DS4S^{sh}#7(*Gc2*) /

T4BS·4BL-4S^{sh}#1L (*Gc2*^{mut}#1)) // CS cross produced 1288 hemizygous-testcross seeds. 1036 seeds were germinated, of these, 947 (91.4%) plants survived to maturity. Spike fertility was scored as a discrete trait, either semi-sterile (*Gc2*) or fertile (*Gc2*^{mut}*#1*).

Physical mapping and RFLP screening

Leaf tissue was collected from four-week-old plants following the protocol of Faris et al. (2000), frozen in liquid nitrogen, then ground with a mortar and pestle. DNA was isolated in 50 ml polypropylene tubes by adding 10–15 ml 65°C extraction buffer (pH 8.0) [0.5 M NaCl, 0.1 M Tris-HCl (pH 8.0), 50 mM EDTA, 0.84% (w/v) SDS and 3.8 g/l sodium bisulfite]. Extraction buffer and leaf tissue was mixed then incubated in a water bath at 65°C for 30-45 min. After incubation, an equal volume of chloroform:isoamyl alcohol (24:1) was added, the solution was mixed vigorously and centrifuged at 8000 / g for 15 min. The upper phase was removed and added to 1.5 vol. chilled 95% ethanol and incubated at -20°C for 1 hr. The precipitated DNA was further rinsed in 1.5 vol. 70% ethanol overnight at -20°C. The DNA was then dried and re-suspended in 1X TE buffer.

Restriction fragment analysis followed the protocol of Southern (1975). The specifics of the protocol are as follows; 20 µg of DNA was digested with 40 units of (*Bam*HI, *Dra*I, *Eco*RI, *Hin*dIII, *Sca*I, and *Xba*I) in the appropriate buffer for 15 hr at 37°C. After incubation 10 µl of loading dye [30% v/v glycerol, 0.25% w/v bromophenol blue, 0.25% w/v xylene cyanol FF] was added and the digested products were electrophoresed in a 0.8 (w/v), 1X TBE agarose gel at 22 V for 24 hours. The gel was stained (30 min 0.05% w/v EtBr) and visualized. After staining the DNA was depurinated for 30 min with 0.25 N HCl then denatured for 30 min. with 0.4 N NaOH. Following depurination and denaturing the DNA was transferred from gel to nylon membrane (Hybond N$^+$ Amersham, Arlington Heights, IL) (Sambrook et al. 1989). Following the protocol

of Botstein et al. (1980), prehybridization of membranes was done in 50 ml of 5X Denhardt's solution [0.1% Ficoll, 1 mg/ml BSA, 1 mg/ml polyvinylpyrrolidone (PVP)], 6X SSPE (0.9 M NaCl, 0.6 M Na_2PO_4), 0.05 mg/ml denatured salmon sperm DNA, and 0.5% sodium dodecyl sulfate (SDS). After incubation at 65°C for 16 hr, prehybridization solution was replaced with 4 ml hybridization solution consisting of 5X Denhardt's, 6X SSPE, 0.5% SDS, 0.05 mg/ml denatured salmon sperm, and 20% dextran sulfate. Probes were amplified from plasmids using M13 forward and reverse primers. The labeling protocol consisted of a 15 µl reaction containing 59.6 ng oligo (random hexamer), 25-50 ng probe, 7.5 mM nonlabeled nucleotides (dATP, dTTP, dGTP), 3 µl labeled ^{32}P-dCTP, 1X DNA polymerase buffer, 0.2 units Klenow DNA polymerase, (Promega Madison, WI), the reaction was incubated at room temperature for 16 hr. After labeling, probes were purified in 185 µl TE using centrifugation through Sephadex G50 columns (Sigma-Aldrich, St Louis, MI), denatured for 2 min, added to the membranes and allowed to hybridize for 18 hr. After hybridization membranes were washed 3 times at 65°C with 0.5% w/v SDS and decreasing concentrations of SSPE (2X, 1X, 0.5X). Membranes were placed in plastic sheets and exposed to X-ray film for 1–7 days depending on signal strength.

Physical mapping in 4BL was done for two purposes; first to identify potential markers for mapping and to identify the wheat–*Ae. sharonensis* translocation containing the *Gc2* gene. The NSF wheat physical mapping project assigned 7104 expressed sequence tag (EST) on a chromosome bin map using wheat aneuploids and deletion stocks (Qi et al. 2003). Chromosome arm 4BL was represented by three deletion bins, C-4BL1-0.71, 4BL1-0.71-0.86, and 4BL5-0.86-1.00, which accounted for 348 physically mapped loci. The ESTs in the distal 4BL-5 deletion bin (http://wheat.pw.usda.gov/NSF/data) were selected for additional screening against new deletion lines 4BL-10-0.95, 4BL-8-0.78, 4BL-7-0.70, 4BL-3-0.68, and 4BL-11-0.58 (Endo and Gill

1996). The presence / absence pattern of DNA hybridization signals among the stocks (Figure 1) allows assignment of EST loci to one or more specific deletion bins, providing the physical coverage and determining the physical region containing the *Ae*. *sharonensis* translocation.

Cosmid library construction

Since no bacterial artificial chromosome (BAC) libraries are available for *Ae*. *sharonensis*, a cosmid library was developed for chromosome walking and mutant validation. Forty µg of genomic DNA from *Ae. sharonensis* was partially digested using 0.5 units of *Sau3A* I incubated at 37°C for 2 min. The digestion gave products ranging in size from 30 to 40 kb. The fractionated DNA was cloned into a *Bam*H I cleaved pHC79 vector. Ligation conditions consisted of 1:1.5 insert / vector, 1X ligase buffer and 1 µl T4 ligase (Invitrogen); reaction was incubated at 16°C for 8 hr followed by deactivation at 65°C for 15 min. Ligated cosmids were packaged using MaxPlax Lambda packaging extract (Epicentre, Madison, WI) following manufacturer's recommendations. Bacteria containing cosmids were plated into 384-well plates at a density of ~100 cosmids per well. The library consisted of 3.3 X 10^5 cosmids, giving ~ 3X coverage. The 384-well plates were arrayed onto 22 X 22 cm nitrocellulose membranes (Amersham Biosciences). Colonies were allowed to grow at 37°C overnight, then denatured and neutralized (Sambrook et al. 1989). Colony-containing membranes were screened with flanking markers by Southern analysis. Positive wells were streaked out on media, grown overnight, transferred onto nylon membranes and re-screened by Southern analysis to identify individual positive cosmid clones. For subcloning of cosmids, purified cosmid DNA was mechanically sheared in 750 µl of 20% glycerol at 14 psi under argon gas for 1 min. This produced an average sheared DNA size of 1.5 kb. After precipitation the sheared DNA was blunt-end repaired and

dephosphorylated. The blunt DNA was cloned into the pCR®4Blunt-TOPO® vector (Invitrogen Life Technologies), then transformed into competent *E. coli* cells.

Comparative genomics, marker development

PCR-based markers in the wheat–*Ae. sharonensis* segment, were developed by BLAST of open reading frames (ORF) from rice chromosome 3 BAC to wEST (http://blast.wustl.edu/blast/). Primers were developed from wEST or the wheat tentative contig (TC) for polymerase chain reaction (PCR) (Mullis et al. 1986). Primer design used MacVectorTM 6.5.3 (Oxford Molecular Ltd., Madison, WI). For PCR, 25 ng genomic DNA was used as template in a reaction consisting of 0.4 mM dNTPs, 1X reaction buffer, 1.5 mM $MgCl_2$, 2 ng EST-specific forward and reverse primers, and 0.02 units of BIOLASE™ DNA polymerase (Bioline USA Inc., Randolph, MA). Thermocyclic conditions were: 94°C for 3 min, 35 cycles of 94°C 1 min, (variable annealing temperature) 45 sec, 72°C 1 min, followed by an end extension at 72°C for 5 min. Markers screened by single-strand conformational polymorphism (SSCP) technology followed the protocol of Hayashi and Yandell (1993). A 5.5 µl PCR sample diluted 58% in a denaturing loading buffer consisting of 95% formaldehyde, 0.02 M EDTA, 9.9 mM NaOH, 0.25% w/v bromophenol blue and 0.025% w/v xylene cyanol was loaded in a 0.4 mm thick 38 cm x 50 cm BIO *RAD* Sequi-Gen GT® Nucleic Acid Electrophoresis Cell sequencing gel with 80 ml gel solution consisting of 0.5 x MDE®, 0.6x TRIS boric EDTA, 0.0004% ammonium persulfate and 0.0004% TEMED and run at constant 3 watts for 17 hr. Staining was done using a standard silver-staining protocol (Sambrook et al. 1989). An *Ae. speltoides* subtelomeric repeat probe, pGc1R-1, which hybridizes to the sub-telomeric region of chromosome arm $4S^{sh}L$ in *Ae. sharonensis* but not *T. aestivum*, was converted to an STS marker (pAESKb52) and used as a genetic marker to define the telomeric end of the $4S^{sh}L$ arm.

AFLP analysis

Amplified fragment length polymorphism (AFLP) markers (Vos et al. 1995) were used on *DA4S^{sh}#1*, the original source of the *Gc2* gene, mutant *Gc2^{mut}#1* and seven disomic addition lines DA4S^{sh}#3 to DA4S^{sh}#9 containing the wild-type gametocidal gene *Gc2*. Fourteen primer combinations from *Eco*RI and *Mse*I-digested genomic DNA were used in a cursory screen to identify the polymorphism frequencies between DA4S^{sh}#1 and the eight disomic addition lines as the source of the wild-type parent for linkage mapping.

In bulk segregant analysis for marker enrichment, 256 primer combinations of a 6-base methylation sensitive restriction enzyme *Pst* I and a 4-base restriction enzyme *Mse*I were used on recombinant lines that had been selfed to produce bulks with five individuals in each, homozygous for the alternate allele. Bulk I consisted of five homozygous individuals with the *Gc2^{mut}#1* fertile phenotype and a recombination event distal to the gene as detected by marker BJ303051. Bulk II consisted of five homozygous individuals with the *Gc2* semisterile phenotype and a recombination event proximal to the gene as detected by BE497476. The AFLP protocol was modified from Vos et al. (1995) as follows: genomic DNA (250 ng) was mixed with 5 units of a 6-base restriction enzyme (*Eco*RI for disomic addition line screening and *Pst*I for bulk segregant analysis), 2 units *Mse*I restriction enzymes and 1X One-Phor-All Buffer Plus (Amersham Pharmacia Biotech, Inc., Piscataway, NJ). The reaction was incubated at 37°C at least 6 hr in a 25 µl reaction. Ligation was done by adding 5 pmol *Eco*RI, *Pst*I adapter, 50 pmol *Mse*I adapter, 1 µL 10 mM ATP, 1 unit T4 ligase, 0.5 µL 100X BSA, 5 µL 10X One-Phor-All Buffer Plus, and filled to a final volume of 25 µL with ddH_2O. The mixture was added to the digestion reaction and placed in the thermal cycler at 37°C for 12 hr followed by 15 min at 70°C to inactivate the enzymes. The digestion/ligation reaction mixture was then diluted 10-fold with ddH_2O. The diluted reaction mixture was used directly as template DNA for the

preamplification. To assemble the preamplification reaction (50 µL total volume), 5 µL diluted ligated DNA was used. 75 ng *Mse*I-primer (MsePre), 75 ng of the *Pst*I 1-base extension primer (PstPre), 4 µL 2.5 mM dNTPs, 1.5 ul 50 mM MgCl, 1 unit Bioline Taq (Biolase Taq polymerase from Bioline), 5 µL 10X PCR-buffer, and 32 µL water for each reaction. Thermal cycler conditions consisted of 20 cycles of 94°C for 30 s, 56°C for 60 s, and 72°C for 60 s. Three µL of the amplified DNA was added to 147 µL of ddH_2O for use as template in the selective amplifications. For each selective AFLP reaction, the following were combined: 5 ul diluted DNA from preamp, 75 ng *Mse*I-selective primer, 75 ng of the *Pst*I-selective primer, 4 µL 2.5 mM dNTPs, 1.5 ul 50 mM MgCl, 1 unit *Taq* DNA polymerase. The selective PCR amplification consisted of one cycle at 94°C for 30 s, 65°C for 30 s, and 72°C for 60 s. The annealing temperature was lowered by 0.7°C for each of 12 cycles, which produced a touchdown phase of 13 cycles followed by 23 cycles of 94°C for 30 s, 56°C for 30 s, and 72°C for 60 s. For screening the disomic addition lines, fluorescent detection was used following the protocol of See et al. (2002).

For bulk segregant analysis, polyacrylamide gels and silver staining was used. For polyacrylamide gel separation of DNA bands, a 6% polyacrylamide gel protocol was followed (Sambrook et al. 1989) using 80 ml gel solution from mixing of 37.0 ml ddH_2O, 9.6 ml Long Ranger (acrylamide), 8.0 ml 5X TBE, 33.6 ml Urea, 400 µl 10% ammonium persulfate and 40 µl of N,N,N',N'-tetramethylethylene-diamine. The gel was allowed to polymerize for approximately 1 hr then pre-run at 100 watts (180 watts for 2 gels) for 40 min in a 0.5X TBE solution to warm the gel to 51°C. Samples with loading dye (95% formaldehyde, 0.02 M EDTA, 9.9 mM NaOH, 0.25% w/v bromophenol blue and 0.025% w/v xylene cyanol) were denatured at 94°C for 10 min, then placed directly on ice. Samples of 5 µl were added to each well and the gel

was run at 70–80 watts (125–135 watts for 2 gels) for 1.5 to 2.5 hr (depending on DNA size). Staining was done using the silver staining protocol (Sambrook et al. 1989).

Bands polymorphic between bulk I and bulk II were excised from the gel. Excised products were added to 30 µl TE buffer and boiled for 15 min. Eight µl of supernatant was used as the genomic template for reamplification with the *Pst*I and *Mse*I primers. The PCR product was run on a 1% agarose gel and then excised. The excised product was eluted from the gel by immersion in liquid nitrogen for 10 min, then centrifuged at 13,000 rpm for 10 min. This product was reamplified. The second amplification product was purified using a PCR purification kit from Qiagen. The purified PCR product was used for ligation into a T/A vector (P-Gem T-easy from Promega). After cloning and electroporation, colonies were plated to LB media (Sambrook et al. 1989) with a selectable antibiotic (carbenicillin). Five white colonies were selected for each, then grown in liquid media overnight. One µl of bacterial culture was used as a template for PCR. PCR products were screened against a 4-base restriction enzyme (*Rsa*I or *Alu*I) and separated on a 1% agarose gel. Clones with single restriction patterns were further selected for sequencing. Sequenced products that did not match known repeat elements in Gramineae (http://tigrblast.tigr.org/euk) were selected for RFLP analysis.

BAC library screening

When comparative genomics analysis was no longer informative, BAC libraries from related species' genomes were screened for additional probe development. These included the *Ae. tauschii* (D-genome) BAC library developed from *Ae. tauschii* accession AS75 and the *Ae. speltoides* BAC library developed from F_4 family number 134 from the cross *Ae. speltoides* 2-12-4-8-1-1-1 / *Ae. speltoides* PI36909-12-II (Akhunov et al. 2005).

Differential display

Differential display was used to identify candidate clones for the *Gc2* gene. A cDNA library was developed to test for markers that are differentially expressed in *Gc2*/- and -/- plants. RNA was extracted from anthers at an early meiotic developmental stage of *Gc2*/-, *Gc2*^{mut}#1/- and -/- plants using the MicroPoly(A)Pure^{TM} kit (Ambion Inc., Austin, TX). RNA was converted to cDNA using the SMART^{TM} PCR cDNA synthesis kit provided by (Clonetech Laboratories, Palo Alto, CA). Prior to incorporation into a vector (pGEM® T Vector Promega Corp., Madison, WI) the cDNA was size-fractionated (cDNA size fractionation Columns GibcoBRL® Life Technologies) to remove small RNAs (<200bp) from the analysis. The *Gc2*/- cDNA library consisted of 30,000 clones with an average insert size of 1.4 kb. Colonies from *Gc2*/- cDNA were grown on nitrocellulose membranes (Hybond^{TM} N+ Amersham Pharmacia Biotech) on LB media overnight at 37°C. Inserts were lysed from bacterial colonies and adhered to membranes following the protocol of Sambrook et al. (1989). The membranes, containing 2316 ESTs each, were probed twice. Prehydridization and hybridization solutions consisted of 40 ml (0.5 M NaH_2PO4, 7% sodium dodecyl sulfate (SDS), 1% BSA, 1 mM EDTA and 400 µl 10 mg/ml salmon sperm DNA). The first hybridization involved reverse transcriptase labeling of 200 ng of RNA from -/- at the same developmental stage, 240 ng of a 6mer oligonucleotide, 0.4 mM (dATP, dGTP, DTTP) 10 µl ^{32}P-dCTP, 1X reverse transcriptase buffer, 0.8 mM dithiothreitol and 8 units of M-MLV reverse transcriptase (Invitrogen^{TM} Life Technologies). Incubation was done according to the manufacturer's recommendations. After the membrane was stripped with 0.5 M NaOH, a second hybridization was done using ^{32}P-dCTP reverse-transcriptase-labeled RNA from *Gc2/Gc2* tissue. Hybridization patterns that showed higher signal intensity from the *Gc2/Gc2* labeling were selected as potential probes. Probe screening was done by Southern analysis using the lines CS, *Gc2/Gc2* (from DS4S^{sh}#1), *Gc2*^{mut}*#1/Gc2*^{mut}*#1, Gc2*^{mut}*#1/Gc2* (*Gc2*

from DS4S^{sh}#7), and *Gc2/Gc2* (from DS4S^{sh}#7). To enrich for potential polymorphisms, five restriction enzymes were used (*Bam*HI, *Dra*I, *Eco*RI, *Hin*dIII and *Xba*I).

Microarray analysis

Microarray analysis was performed in an attempt to gain a global view of gene expression in a *Gc2* background. For microarray screening, tissue was derived from anthers collected at two developmental stages. Anthers of about 2 mm or less in length contain pollen mother cells (PMCs) at premeiotic developmental stage or are undergoing meiosis. The anthers of 3 to 6 mm in length contain PMCs at postmeiotic development stage. Anthers at both stages were collected from CS wheat, *Gc2/-, and Gc2^{mut}#1*/- plants. The GeneChip Wheat Genome Array from Affymetrix contains 61,127 probe sets representing 55,052 transcripts developed from 20,314 unigenes from diverse vegetative and reproductive tissues of the wheat plant including anthers at the meiotic stage (Chao et al. 2005).

RNA samples from anthers were labeled using Affymetrix One-Cycle target labeling and control reagents. Hybridization and wash conditions were according to the manufacturer's protocol (http://www.affymetrix.com). Data analysis used GeneChip Operating and Genespring 5.0 software to normalize the output. Genes up-or downregulated (10-fold difference) in wild type (*Gc2*) vs. mutant (*Gc2^{mut}#1*) tissue transcript profiles at premeiotic or post meiotic stages were identified.

Linkage analysis

Initially 947 plants from the cross (DS4S^{sh}#7(*Gc2*) / T4BS·4BL-4S^{sh}#1L(*Gc2^{mut}#1*)) // CS were grown and screened for phenotype. From the 947 plants, 180 individuals were used for genetic mapping. From the second mutant *Gc2^{mut}#2* 63 plants were grown, screened for phenotype and screened with flanking markers. Linkage distances were calculated with

Mapmaker 2.0 (Lander et al. 1987), using the Kosambi mapping function (Kosambi 1944). While this population underwent two rounds of recombination, only one was within the critical region. To account for one round of recombination and obtain proper linkage distances the population was labeled as a backcross in Mapmaker. All primers used in genetic mapping are listed in Table 1.

Results

Multiple genetic stocks including deletion lines, substitution lines, translocation lines, and mutagenized material were used for mapping of the segregation distorter (*Gc2*) gene in wheat. The plan for using the genetic stocks and targeting the sub-chromosomal location of both the gene and potential markers is described in Figure 2.

Identification of Gc2^{mut}#2 knockout mutant

Of the 3276 mutagenized hemizygous *Gc2*/- seeds, 2988 (91.2%) grew to maturity. Thirty plants were scored fertile and considered putative mutants for the *Gc2* locus. The fertile M_2 families were screened by FISH with the pGc1R-1 probe to determine the presence of the *Gc2* chromosome. The 29 families did not segregate for the *Gc2* chromosome and all were homozygous *Gc2/ Gc2* and hence non-mutant. One M_2 family segregated for the *Gc2* chromosome indicating a mutation, designated *Gc2^{mut}*#2, which allowed gametes lacking the *Gc2* chromosome to function. Nine M_2 plants from this line were screened, two were homozygous *Gc2^{mut}*#2/*Gc2^{mut}*#2.

FISH analysis of the *Gc2^{mut}*#2/*Gc2^{mut}*#2 plant using the pGc1R-1 probe gave a signal similar in size and location to the functional *Gc2* carrier (Figure 3), indicating that loss of function was not the result of a terminal deletion. In *Gc2* plants, the telomere of the long arm of T4BS·4BL-4S^{sh}#1L is the only region where both the telomeric repeat pAtT4 (derived from *Arabidopsis thaliana*) and the tandem subtelomeric repeat pGc1R-1 (derived from *Ae. speltoides*) co-localize. By fiber FISH, it was shown that pAtT4 is localized distally and has a size of 16.85 ± 1.6 µm on extended DNA fibers (Figure 4). Thus, the telomeric repeat of the long

arm of chromosome T4BS·4BL-4S^{sh}#1L is about 48 kb. The probe pGc1R-1 hybridized directly adjacent and proximal to pAtT4. The longest fiber that could be followed over three photographic frames had a length of 400 µm, corresponding to 1,148 kb and 1,504 copies of this repeat (repeat length is about 763 bp). The presence of the telomeric and subtelomeric repeats directly adjacent to each other indicates that the subtelomeric repeat is a good marker for screening for terminal deletions and that the *Gc2^{mut}#2* is not the result of a terminal deletion.

To verify that the *Gc2* locus is responsible for the knockout phenotype, *Gc2^{mut}*#2/- progeny were screened. If the *Gc2* locus is responsible for the knockout phenotype, the M_1 plant can produce two types of gametes, *Gc2^{mut}* and -. This will give rise to three types of M_2 plants in a frequency of *Gc2^{mut}*#2/*Gc2^{mut}*#2 (25%), *Gc2^{mut}*#2/CS (50%), and CS/CS (25%). In this test all plants were fertile, and no breakage was observed in ana/telophase of first pollen mitosis (Table 2) indicating that the mutation is in fact at the *Gc2* locus. Alternatively, if a locus in CS is responsible for inhibiting (I) the *Gc2* phenotype in the M_1 plants, then four gamete types are expected, I/*Gc2*, I/-, *i*/*Gc2*, and *i*/-. In a cross of *Gc2^{mut}*#2/- // -/- some of the progeny are expected to be semisterile; however, all progeny were fertile (Table 3).

The mutant *Gc2^{mut}*#2/ *Gc2^{mut}*#2 when crossed with the parental disomic substitution line DS4S^{sh}#1(4B) showed normal 1st pollen mitosis and fertile spikes. However, when *Gc2^{mut}*#2/*Gc2^{mut}*#2 was crossed with the disomic substitution DS4S^{sh}#7(4B) incomplete penetrance of the mutant was observed, 27.8% of the first pollen mitosis cells contained chromosome fragments. This result indicated that the mutation observed in *Gc2^{mut}*#2 gene is not a complete knock out, unlike the fully penetrant *Gc2^{mut}#1* reported earlier (Friebe et al. 2003).

Mapping populations

AFLP screen of DA4S^{sh}#1, (the original source of T4BS·4BL-4S^{sh}#1L and the two EMS-

induced mutants) and eight $4S^{sh}$ addition lines $DA4S^{sh}$#3 to $DA4S^{sh}$#9 indicated a polymorphism rate of 34% to 65% between the eight addition lines and $DA4S^{sh}$#1 (Figure 4). Three disomic addition lines $4S^{sh}$#3, $4S^{sh}$#5, and $4S^{sh}$#7 showed good levels of polymorphism (56%, 63%, and 56%). Lines $4S^{sh}$#3, $4S^{sh}$#5, and $4S^{sh}$#7 also showed high pairing frequencies (56%, 79%, and 69%) in their long arms with the long arm of $4S^{sh}$#1 (Figure 5). Disomic substitution line 4Ssh#7(4B), the first substitution line developed with good polymorphism (56%) and good pairing (69%) was selected as the wild-type *Gc2* donor parent. In screening progeny from the (DS$4S^{sh}$#7(*Gc2*) / T4BS·4BL-$4S^{sh}$#1L(*$Gc2^{mut}$#1*)) // CS cross, spike fertility/semi-sterility segregated in a 1:1 Mendelian ratio; 472 plants were semi-sterile and 475 fertile. 180 plants from this population were used for genetic mapping. A second population was developed from the mutant *$Gc2^{mut}$#2* using the same crossing scheme (DS$4S^{sh}$#7(*Gc2*) / T4BS·4BL-$4S^{sh}$#1L(*$Gc2^{mut}$#2*)) // CS. Spike fertility/semi-sterility segregated in a near 1:1 Mendelian ratio; 26 plants were semi-sterile and 37 fertile.

Fine physical mapping

Nasuda (1999) used 16 RFLP probes for loci known to lie in the distal 4BL region and 32 AFLP primer combinations between CS and T4BS·4BL-$4S^{sh}$#1L for assigning markers to the *Ae. sharonensis* translocation. The resulting 475 RFLP and 1180 AFLP fragments produced 1 AFLP-derived clone associated with this region (pGc1R-1) indicating that published genetic markers would not work for mapping within the *Ae. sharonensis* translocation. The recent development of the NSF physical map of wheat provided a new source of potential markers (Qi et al. 2004). In the NSF physical mapping project two deletion lines 4BL-1-0.71-1.00 and 4BL-5-0.86-1.00 were used to allocate ESTs to deletion bins. The 147 ESTs allocated to the 4BL-5 deletion bin were used for fine physical mapping using a panel of additional deletion lines 4BL-

11, 4BL-3, 4BL-7, 4BL-8, and 4BL-10. Also in the NSF mapping project only one restriction enzyme (*Eco*RI) was used; we chose to use *Eco*RI and an additional enzyme *Hind*III to increase our detection threshold. Of the 147 EST assigned to 4BL-5, 116 EST were physically mapped, 13 EST were removed because they could not be checked against the NSF mapping information, and 18 additional EST were not scorable. Eighty-two EST were assigned to 5 deletion bins spanning the distal 42% of 4BL.

Gene redundancy was estimated, based upon the hypothesis that each restriction fragment maps to one discrete location in each of the three genomes of wheat. The total number of restriction fragments observed in the 5 deletion bins was 906, on average each EST detected 5.3 restriction fragments (Table 4), which is more than the 4.8 restriction fragments observed for the whole genome in the NSF deletion mapping project. Within-deletion-bin values ranged from 7.0 fragments per locus (*Hind*III 4BL-10) to 3.3 (*Hind*III 4BL-3). The number of physically mapped fragments detected was highest in 4BL-10 and lowest in 4BL-3 and 4BL-7 (1.4, 1.0, 1.0) respectively, signifying more paralogous duplications in the distal region of the chromosome. Overall 19 EST had more than one physically mapped fragment (Table 5), 12 within deletion bins and 7 across deletion bins. Eight of the duplicated fragments were observed with both restriction enzymes, signifying that they were not the result of a restriction site within the probe sequence.

The markers within deletion bins were presumptively ordered based on BLAST similarity with the sequenced rice genome (Figure 6). The homoeologous locations of the 4BL ESTs were compared against 4A, 4D, and 5A; the latter has a homoeologous segment from 4AL due to a translocation. For the most part, homoeologous loci were detected; 54.8% of the EST had two homoeologous loci, 28.1% identified one homoeologous loci and 17.1% did not indicate any

homoeologous loci (Table 6). Within deletion bins, 4BL-10 showed the lowest detection of two homoeologous loci with 42.8%, 4BL-8 was next with 48.3%, 4BL-3, 4BL-7 showed the highest with 91.7% and 4BL-11 had 55.0%.

Characterization of homoeologous regions detected by 4BL EST showed regions of homoeology, inversions and translocations. ESTs in 4BL-10 and the distal part of 4BL-8 up to BE518255 indicate the boundary of the 4AL-5AL translocation. A portion of ESTs in deletion bin 4BL-10 and 4BL-8 indicate a rearrangement event between 4BL and 4DL as indicated by ESTs present in both the distal 4DL-12 and proximal 4DL-13 deletion bins. Deletion bins 4BL-7 and 4BL-3 were the most conserved regions on 4BL with discrete locations in 4DL-12 and 4AS-3 with the exception of BE404717 with an EST in 4AS-4. The homoeologous region defined by 4DL-13 is seen at the start of the 4BL-11 deletion bin.

In the presumptive ordering of EST within deletion bins based on rice, a large inversion of marker genetic order was seen in the 4BL region. Three ESTs with paralogous duplications BG 605572 (4BL-8, 4BL-11), BE442995 (4BL-8, 4BL-11, 4BL-11), and BF473779 (4BL-8, 4BL-11, 4BL-11) indicate the boundaries of the observed inversion. This inversion encompasses part of 4BL-11, all of 4BL-7 and 4BL-3, and part of 4BL-8 (Figure 7). From the inversion diagrammed in Figure 7 it can be hypothesized that these three ESTs duplicated first. After the duplication event an inversion and rearrangement event occurred in which half of the duplicated ESTs were involved in the rearrangement and the other half remained in their original location. After the rearrangement event two of the ESTs BE442995, and BF473779 had an additional local duplication in 4BL-11.

The physical size of the deletions characterized from 4BL-11 to the end of the chromosome is 179 Mb (based on relative chromosome size and total genome size as given in

(Gill et al. 1991)). The corresponding homoeologous region in rice identified by BLAST search spans 29 cM and 5.9 Mb of the distal end of chromosome 3 short arm. These homoeologous regions were collinear, except the previously described inversion of a region defined by rice chromosome 3 between 14.8 cM and 17.9 cM relative to a wheat region encompassing the 4BL-3 deletion bin along with parts of flanking bins 4BL-11 and 4BL-8. With selected probes from each new bin on CS and the T4BS·4BL-4S^{sh}#1L translocation, the *Gc2* gene was located within the distal 4BL-10 bin (distal 5% of the arm).

Comparative genomics and marker development

A rice contig of 14 BACs to which wheat ESTs were positioned *in silico* aligns with ESTs in the 4BL-10 bin. Initial screening identified the proximal boundary of the CS–*Ae. sharonensis* translocation within the 900-kb terminal region of the short arm of rice chromosome 3, spanning six BACs and 0.0 to 2.5 cM of the rice genetic map. Extensive screening of rice ORFs within this region produced proximal and distal markers. For the majority of the markers developed ORF sequences from rice were used to identify corresponding orthologous EST from wheat. Primers were designed from the wheat tentative contig (TC) or EST if no TC was available. Successful amplification with this approach was 86.0%.

Almost 400 markers were developed and screened for their utility as genetic markers for the *Gc2* gene. These markers included 53 RFLP, 34 cDNA-derived probes, 127 AFLP fragments, and 182 EST-derived PCR markers. Several approaches were used for mapping, including RFLP analysis, sequence tagged site (STS), CAPS, and SSCP. Observable direct PCR polymorphism detection of STS was low (2.7%). Application of restriction enzymes to STS increased the detectable polymorphism level to 17.8%. Using RFLP technology, (9.1%) were polymorphic within the region of interest. Polymorphism detection level using SSCP was higher

than other methods (22.6%) and was used for most of the genetic screening. Table 5 indicates the markers that were genetically mapped and the technology used to identify them.

To enrich for markers within the region surrounding the *Gc2* gene that could not be found using comparative genomics, a bulked AFLP strategy was used. In screening 256 primer combinations, 127 potential polymorphic bands were excised and analyzed. Sequence analysis of the 55 amplicons produced 27 (49.0%) low copy sequences. The other 28 (51.0%) were similar to known repeat elements present in Gramineae. Hybridization results indicated that 16 (59.2%) of the putative low-copy probes hybridized to repeat elements within wheat. Five probes with repeat elements derived from the proximal AFLP bulks showed distinct ladder-like banding patterns, three probes with *Dra*I bands, and one with *Hind*III, one additional probe had the same sequence as a *Dra*I repeat and was not hybridized. The high-copy discrete banding patterns indicate the presence of conserved long tandem repeats within this region. Two additional probes were similar to known subtelomeric repeats and were monomorphic by Southern. One subtelomeric repeat showed a discrete banding pattern in *Eco*RI. The second probe (Pagt/Mcga1-6) with homology to a subtelomeric repeat was converted to a STS marker Ksuds1-6 and mapped by SSCP. Of the 127 clones initially selected, 3 (2.3%) mapped within the region of interest, two by Southern analysis (Paga/Mcgc2-14, Paga/Mcgc2-14) and one by STS (Ksuds1-6). With 20,000 fragments characterized by AFLP, the overall efficiency of this approach was 0.015%.

Cosmid and BAC screening

Because no large-insert library was available for *Ae. sharonensis*, a cosmid library was developed with the intent of using the library for chromosome walking and validation of the *Gc2* mutants. The cosmid library was screened at different stages during this project against markers flanking the *Gc2* locus. Cosmids that were positive by hybridization were validated by PCR. The

PCR positive cosmids were then end-sequenced and low-copy probes were genetically screened. The distal marker BJ303051 hybridized to one cosmid 7E15 that had low-copy end-sequence; however, it was monomorphic (SSCP). TC167916 hybridized to cosmid 3B15; however, PCR validation indicated that this cosmid did not have the proper insert. BE497476 in the proximal region hybridized to two cosmids 4A14 and 7E11. End sequencing of 7E11 produced one genetically mapped probe Ksuds7E11, 1.7 cM distal to BE497476, indicating that at least for short distances chromosome walking is feasible with cosmids.

BAC screening was attempted with the intent of finding homoeologous markers useful in chromosome walking. Screening the D-genome BAC libraries was intentionally done in the hope that the preliminary work of developing a BAC contig of the D-genome might provide contigs in the D-genome that contain flanking markers from the genetic map. Distal markers BJ303051, BQ168434, and TC167916 did not produce any hits on contigs that overlapped. End-sequencing of specific BACs from BJ303051 resulted in only repetitive sequences that could not be used as probes. More success resulted from the S-genome BAC screening efforts. TC167916 hybridized to five BACs, four were positive for inserts by PCR (464M12, 417C15, 557L24, and 69P13), and one end-sequence of BAC 557L24 was low-copy but was monomorphic across six restriction enzymes and SSCP. BQ168434 hybridized to 14 BACs, four were positive for inserts (96H11, 363O2, 441J9 and 138P4). BAC 138P4 produced low-copy sequence from both ends of which one probe was monomorphic. The other probe was codominant for *Gc2*^{mut} and *DS4S*^{sh}#7, physically mapped in 4BL-10 and genetically co-segregated with BQ168434.

Genetic mapping

To observe the semisterile phenotype the *Gc2* gene needs to be in a hemizygous state but in this background some genetic markers were obscured due to CS amplification or background

interference. To eliminate this background interference, 10 seed from each of the 35 recombinants between BE497476 and BJ303051 were grown and screened with distal (BJ303051) and proximal (BJ497476) codominant markers to select homozygous lines lacking the corresponding CS 4B chromosome. All recombinants with the $Gc2^{mut}$#1 phenotype (fertile) when selfed were expected to segregate for CS. Recombinants with the *Gc2* phenotype (semi-sterile) should be homozygous *Gc2* with no CS present. In the screen of 17 lines with the $Gc2^{mut}$*#1* phenotype, 2 (11.7%) did not segregate for CS. Of the 18 lines with the *Gc2* phenotype, 4 (22.2%) segregated for CS markers. These four lines were removed from additional mapping analysis.

The comparative map of rice chromosome 3 short, and genetic maps of *Gc2* and ITMI 4B long indicate marker placement and recombination in the region around the *Gc2* locus (Figure 8). The *Gc2* map comprises 42 genetic markers, accounting for 65.4 cM of total genetic distance. The genetic marker CA497473 (Figure 9 inset C) defines the upper limit of the $4S^{sh}$#1L segment and all markers proximal to this position are dominant for the $4S^{sh}$#7 chromosome (Table 7). The genetic distance from the 4BL-10 breakpoint to CA497476 accounts for 24.9 cM, this region of the map has suppressed recombination due to homoeologous recombination between CS and $4S^{sh}$#7. The presence of the codominant marker BE497476 (Figure 9 inset E) distal to CA497473 defines the wheat–*Ae. sharonensis* translocation boundary. Recombination within the *Ae. sharonensis* translocation close to the breakpoint is also suppressed indicating that the breakpoint spanning homologous ($Gc2^{mut}$#1 / $4S^{sh}$#7) and homoeologous ($4S^{sh}$#7 / CS) segments suppresses recombination.

No suppression of recombination distal to AFLP marker, Paga/Mcgc2-14 towards the *Gc2* locus was observed. Distal to the *Gc2* locus 5 genetic markers account for 10 cM and no

suppression of recombination was observed in this region. Recombination was screened in the second mapping population *Gc2*^{mut}#2. Flanking co-dominant markers BE497476 and BJ303051 were used to check for phenotype, genetic location and recombination. The *Gc2*^{mut}#2 phenotype was genetically mapped in the same region between markers BJ303051 (11.5 cM distal) and BE497476 (14.9 cM proximal).

The presence of multiple different classes of markers within the *Ae. sharonensis* segment indicated that not all markers are homoeologous between *Ae. sharonensis* and CS in the 4BL-10 deletion bin. Distal to the translocation breakpoint 10 of 22 markers in the *Gc2* map were codominant, or as in the case of Ksuds1-6 and Ksuds7E11 dominant for *Gc2*^{mut}#1. Figure 9 insets A, B, C, and D show other marker types observed in this study; inset A is a low-copy RFLP probe physically mapped in 4BL-10, with a compensating 4BL-*Ae. sharonensis* fragment, but with no evident polymorphism across 6 restriction enzymes or by SSCP. Inset B is a codominant AFLP probe that maps proximal to the *Gc2* locus, but does not have a 4BL counterpart that physically maps in 4BL-10. In inset D TC167916 is the closest codominant marker to the *Gc2* locus that also does not have a counterpart physically mapping in 4BL-10; however, the 4S^{sh}#7 line indicates that a 4B allele is missing.

Comparative mapping with rice 3S, and the ITMI 4BL map provided information about both colinearity and recombination within the 4BL-10 deletion bin. The region surrounding the *Gc2* locus is highly rearranged in comparison with the distal region of rice chromosome 3S. Proximal to the *Gc2* locus several inversions are observed in comparing the presumptive location of wheat EST along the rice chromosome 3S and their genetic location on the *Gc2* map. The ITMI 4BL map shows that without suppressed recombination the 4BL-10 deletion bin comprises 124.7 cM as defined by markers CA626486, BF482767 at the 4BL-10 breakpoint, and the distal

marker BF474826. Comparative mapping of BE497476 and BF474826 (BQ168434 in the *Gc2* map is the 5' sequence and BF474826 is the 3' sequence from the same cDNA; no polymorphism was detected in *Gc2* using BF474826). In ITMI these two markers are 11.9 cM apart. In *Gc2* they are 40.5 cM apart, showing a large genetic expansion, or high recombination rate surrounding the *Gc2* locus compared to the region in ITMI. Distal to the *Gc2* locus colinearity was observed with markers BQ168434, BJ303051 and TC167916. These markers are in the same order in rice at 1.6 cM at overlapping BACs OSJNBa0090O10 (ORF 21) and OSJNBb0005F16 (ORF 29, 26) respectively (Figure 10). The *Gc2* locus is flanked by the rice BAC OSJNBb0005F16, TC235627 (ORF23) and TC167916 (ORF26); ORF24 was screened by both SSCP and RFLP but it was monomorphic.

The physical-to-genetic distance ratio within the 4BL-10 region estimated using the ITMI mapping population was compared between ITMI and the *Gc2* map. Deletion bin 4BL-10 comprises 21.3 Mb of DNA and 124.7 cM of recombination distance giving this region a 170.8 Kb/cM ratio, accounting for 65.6% of the recombination of the long arm. In the *Gc2* map, this ratio can be estimated using the distal markers and rice. In this estimate, the physical to genetic ratio ranges from 35.6 Kb/cM to 4.3 Kb/cM (Figure 10). The most distal genetic marker that could be mapped was pAESKb52 which was derived from the subtelomeric repeat pGc1R-1.

The genetic mapping of pAESKb52 provided an anchor of the genetic map to physical position along the chromosome. As seen in Figure 4 the telomeric repeat pAtT4 and the tandem subtelomeric repeat pGc1R-1 (genetic marker pAESKb52) co-localize, with the probe pGc1R-1 hybridized directly adjacent and proximal to pAtT4. This physical anchoring of the telomeric repeat to the subtelomeric genetic marker (pAESKb52) indicates that the *Gc2* locus is in the distal 1% of the chromosome arm.

Differential display / candidate gene validation

A cDNA differential-display approach was used to identify expressed sequences present in the *Gc2/-* library but absent in CS, both to search for potential candidate genes and to enrich for markers in the physical proximity of the *Gc2* locus. Thirty-one clones were selected from the initial screening (Table 8) and used as probes in Southern or SSCP analysis. One cDNA clone 37H2O was polymorphic by SSCP; however, when it was applied to the *Gc2* map no discrete genetic location could be assigned due to many spurious genotypes. Four cDNA probes had dominant bands derived from DS4S^{sh}#7(4B), indicating their presence on chromosome 4S^{sh} but above the translocation.

To further investigate the gametocidal gene effect on whole-genome expression, four RNA samples, *Gc2*^{mut}#1/- and *Gc2*/-, at early and late meiosis were characterized for differential expression levels using microarrays. At a 10 fold level of difference, *Gc2*^{mut}#1, and *Gc2* were contrasted for constitutive expression in early and late meiosis (appendix table 1). *Gc2*^{mut}#1> Gc2 showed 24 genes at both early and late stages. In contrast *Gc2* > *Gc2*^{mut}#1 had 20. Within developmental stages more genes were present at 10 fold differences. Gc2^{mut}#1 early > *Gc2* early showed 995. In contrast *Gc2* early > *Gc2*^{mut}#1 early showed 911. At the late developmental stage of meiosis *Gc2*^{mut}#1 late > *Gc2* late showed 940. The only significant difference appeared in the comparison of *Gc2* late > *Gc2*^{mut}#1 late which had 514 (45.4%) fewer genes.

The selected cDNA differential display clones were screened against the microarray results (Table 8). Three cDNA clones showed significant >10 fold differential expression in the microarray. An additional five cDNA clones showed >2 fold expression difference in microarray as well.

Discussion

Genetic stocks

The genetic stocks developed to map the gametocidal gene from *Ae. sharonensis* were critical to this project. For more than three decades, the gametocidal genes and their distortion of segregation have been known in wheat. However without proper genetic stocks studying the gametocidal genes at a genetic level was impossible. The development of the *Gc2* mutant lines restored Mendelian segregation and made it possible to identify a discrete segregating phenotype. The development of the eight disomic addition lines provided a source for a polymorphic wild-type parent, and the subsequent disomic substitution lines made homologous pairing and recombination possible in the translocation region containing the *Gc2* locus. Given the genome size of wheat, chromosome deletion lines are a vital tool for targeting markers to specific regions in the genome, and defining a fine-scale physical map of the genomic location of the *Gc2* locus.

The Mendelian segregation observed in both $Gc2^{mut}$#1 and $Gc2^{mut}$#2 mapping populations indicates that the knockout mutants had complete penetrance in this cross; however, background effects showed incomplete penetrance in one mutant. The leaky phenotype observed in the second mutant when $Gc2^{mut}$#2 was crossed to $DS4S^{sh}$#7(4B) indicated that the mutation at this locus was not as complete as seen in $Gc2^{mut}$#1 described by Friebe et al. (2003). The underlying genetics responsible for the lack of complete penetrance is unknown. One explanation is that the $Gc2^{mut}$#2 is the result of a specific mutation event that does not completely suppress the function. The reason that this mutant is effectively suppressed in some backgrounds

and not others is unknown. A more likely explanation relies on the dual-function model. If the dual function model is correct, then a difference in protecting agents in different accessions of *Ae. sharonensis* could be responsible for the leaky phenotype, and not *Gc2^{mut}#2*. Evidence for this could be seen when *Gc2^{mut}#1* and *Gc2^{mut}#2* was crossed with *DS4^{sh}#1*(4B) (the original donor accession). Both *Gc2^{mut}#1* (Friebe et al. 2003) and *Gc2^{mut}#2* showed complete suppression of the gametocidal gene, indicating that *Gc2* gene in *Gc2^{mut}#2* is completely silenced. The results of the cross of *Gc2^{mut}#1* and *Gc2^{mut}#2* to CS, both with complete fertility, also supports this model. Allelic variation in the protecting agents between *4S^{sh}#1* and *4S^{sh}#7* would also explain why the cross of *Gc2^{mut}#2* and *DS4^{sh}#7* produced a leaky phenotype.

Previous research to tag the wheat–*Ae. sharonensis* translocation was unsuccessful. Nasuda (1999) had screened multiple AFLP and published RFLP markers, and found no RFLP markers linked to this region of 4BL. After our linkage analysis and defining the wheat–*Ae. sharonensis* breakpoint it is clear that the distal RFLP markers screened by Nasuda (1999) would not have tagged the *Ae. sharonensis* segment, as the most distal marker was ~ 30–40 cM proximal to the translocation breakpoint.

Comparative genomics

This project relied heavily on comparative genomics with rice. Using the additional deletion lines 4BL-11, 4BL-3, 4BL-7, 4BL-8, and 4BL-10 and the physically mapped EST from 4BL-5 bin, Qi et al. (2004) refined the region within rice for comparative analysis. Our results indicate a mix of both colinearity and disruption of colinearity at the macro and micro-synteny levels. At the macro-synteny level segments of 4BL-10, 4BL-8 and 4BL-11 were collinear with rice 3S. In contrast, part of 4Bl-11, all of 4BL-3, 4BL-7 and part of 4BL-8, together comprising a large physical segment (23.0%) of the long arm, was inverted. The mechanism causing this event

is unknown. The presence of the tandem and transposed duplication at the boundary may have played a role in the rearrangement or may have been just a byproduct of it. At the micro-synteny level genes distal to the *Gc2* locus were collinear. The disruption of synteny and the genetic block between TC235623 and TC167916 indicates a large segment of DNA not present in the orthologous region in rice. In addition several genetic markers in the proximal region were not collinear, as seen by the inversions of their order observed in Figure 8 between the *Gc2* map and rice. This disruption of synteny at the macro level is found throughout the wheat genome (Sorrells et al. 2003). At the micro level several examples of colinearity (Yan et al. 2003, 2004; Chantret et al. 2004) and disruption of colinearity (Spielmeyer and Richards 2004; Valárik et al. 2006) have been documented. In the distal regions of the chromosome this disruption is more pronounced. Akhunov et al. (2003b) observed a trend along the whole genome of reduced synteny towards the distal regions of the chromosome. Our previous work (See et al. 2006) confirmed this trend and showed that in 4BL-10 several genes have no orthologs in the rice genome.

Comparing the results presented in Tables 4, 5, 6 the distal region on 4BL has the highest number of restriction fragments, the most paralogous duplications, and the lowest percentage of homoeologous loci. A disruption of homoeology was also observed between ESTs in deletion bins 4BL-10 and 4BL-8 as compared with the two distal bins on 4DL-13 and 4DL-12. If the two homoeologous regions were collinear, restriction fragments within 4BL-10 should map to a discrete location in 4DL-12 with a transition of EST to the more proximal 4DL-13 higher up on the physical map of 4BL. However, ESTs in both deletion bin 4BL-10 and 4BL-8 show a mix of locations in both 4DL-13 and 4DL-12. It cannot yet be stated whether this rearrangement of ESTs is a result of an event on 4DL or on 4BL.

Comparative genomics using rice was useful in the development of markers flanking the *Gc2* locus, and using rice to develop markers useful in wheat. The overall success rate, 86.0% of amplification of EST selected from rice ORF was high. This result shows that even though rice and wheat have diverged and colinearity is not conserved at the micro-level, using expressed sequences from rice is beneficial in producing genetic markers useful in wheat.

Marker types

In the analysis of the ESTs several approaches were used, with SSCP being the most polymorphic. It must be noted that SSCP technology has some drawbacks. While SSCP is highly polymorphic, its window of detection is low, i.e. 600 bp or less. In some instances, PCR amplicons that were monomorphic by SSCP were polymorphic by RFLP.

After screening markers derived from comparative genomics that flanked the *Gc2* locus was completed, AFLP bulk segregant analysis was employed to select further markers. The development of additional markers in the recombinant *Ae. sharonensis* segment using AFLP bulk segregant approach produced 3 useful markers. This is a low return rate on 256 primer combinations. Haen et al. (2004) observed a similar low frequency of critical markers using a nonmethylated 6-base restriction enzyme *Eco*RI. In their screen of a methylation-sensitive restriction enzyme *Pst*I a higher frequency of polymorphic fragments was observed.

The difference between Haen's observed results and ours may be due to the size of the physical interval for critical marker selection. In targeting the *Tsn1* gene in the proximal 76 to 79% of the chromosome a larger physical region produced more critical markers. In our case while the *Ae. sharonensis* translocation is in the distal 5% of the long arm of 4B, the recombinants used in bulk segregant analysis are in the last 1 to 2% of the arm.

An additional result observed in our screening of AFLP probes complicates the recovery of useful markers. As seen in the genetic map, the region surrounding the *Gc2* locus is tagged with genetic markers having homology to subtelomeric repeats (proximal Ksuds1-6, distal pAESKb52). The AFLP clone Ksuds1-6 was similar to a previously reported telomere-associated repeat PSR2134 (Mao et al. 1997). The presence specifically in the proximal interval of five AFLP probes hybridizing to tandem repeats indicates that this region harbors many such tandem repeat elements.

The cosmid library screening indicated that chromosome walking could be done; however, the short distances that could be achieved did not make it a viable option. Its potential screening for mutant validation is still viable and will be used in the future. One key drawback to this library was its small size, at ~3X coverage, most probes only produced one or two hits against the library. For a more efficient tool, this library would need to be increased.

The BAC screening of *Ae. speltoides* did provide additional markers and is still a useful tool. However, it is the conclusion of this work, that any efficient map-based cloning, a target genome-specific BAC-based library must be in hand. Screening of the cDNA from *Gc2*/- for differentially displayed clones was not successful in providing additional marker close to the *Gc2* locus. While a few markers gave banding patterns that indicated their presence on the $4S^{sh}$#7 chromosome, this dominant banding pattern only indicated their location proximal to the T4BS·4BL-$4S^{sh}$#1L translocation.

Microarray analysis did validate a few of the clone selections however this is most likely only confirmation that genes within this interval govern the expression of other genes on $4S^{sh}$#7 or on other chromosomes. Conclusions from the microarray experiments can not be discussed at this point. The primary reason is due to a lack of biological replications needed to remove false

positives from these experiments. With over 3000 different transcripts with greater than 10 fold expression profiles, no discrete positive results could be obtained.

Recombination

Recombination within the 4BL-10 deletion bin is high. In defining the extent of the recombination described by the 4BL-10 deletion bin in the ITMI mapping population, this region accounted for 75% of the recombination on the long arm of the chromosome (See et al. 2006). Faris and Gill (2002) calculated a recombination ratio of the whole genome at 4.4 Mb/cM the 4BL-10 bin comprising only 5% of the long arm has 26-fold more recombination than the genomic average.

High recombination was not observed across the whole *Ae. sharonensis* translocation. Distal to the *Gc2* locus recombination was normal. Proximal to AFLP marker Paga/Mcgc2-14 recombination was suppressed. While codominant markers could be scored in the proximal region, indicating the presence of both T4BS‘4BL-4S^{sh}#1L and 4S^{sh}#7 chromosome segments, recombination within this region was suppressed as compared to the region distal to the *Gc2* gene. One explanation is that the proximal region within the *Ae. sharonensis* translocation is a gene rich region.

There are several examples of gene-rich regions in wheat (Gill et al. 1993, 1996a, 1996b); however, the high recombination usually associated with gene-rich regions is not present. A more likely explanation can be proposed. The presence of *Ph1* should restricted recombination to homologous chromosomes. This means suppressed above the CS/*Ae*. *sharonensis* boundary and normal in the *Ae*. *sharonensis* translocation between 4S^{sh}#1L and DS4S^{sh}#7. This is true for markers above the boundary, while proximal to the CS/*Ae. sharonensis* translocation recombination was highly suppressed due to the general inability of CS

to pair with *Ae. sharonensis*. In the proximal region above the *Gc2* locus and below the CS/*Ae. sharonensis* boundary additional factors are at work, DS4S^{sh}#7 is also in proximity to 4BL, causing a conflict between homologous (4S^{sh}#1L and DS4S^{sh}#7) and homoeologous (DS4S^{sh}#7 and 4BL) boundaries. This boundary causes suppression of the recombination machinery that prevents normal recombination and pairing between 4S^{sh}#1L and DS4S^{sh}#7 chromosomes. Recombination distal to the *Gc2* locus is not suppressed.

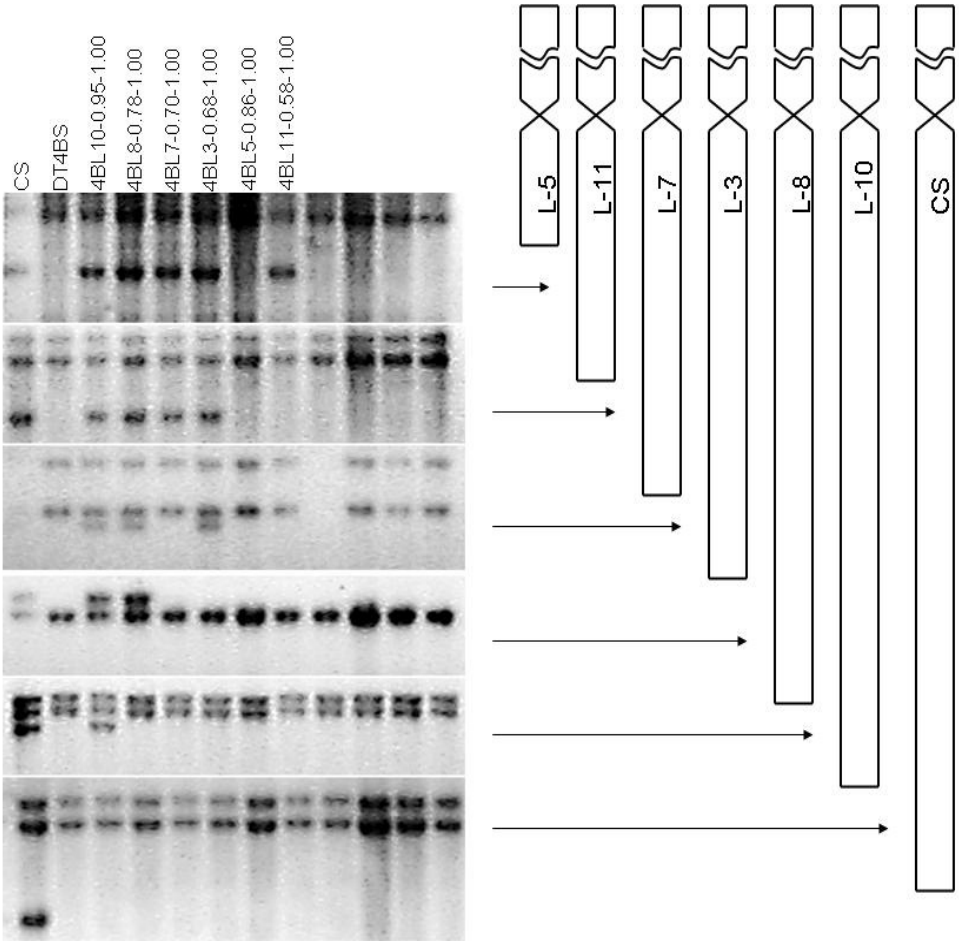
Evidence to support this theory can be seen in marker distribution within the *Ae. sharonensis* segment proximal to the *Gc2* locus where this same suppression of recombination is observed. Dubcovsky et al. (1995) observed a similar phenomenon close to homoeologous breakpoints between 1A of wheat and 1A^{m} from *T. monococcum*, and concluded that the boundary between homologous and homoeologous chromosome segments suppresses recombination. In maize, Burnham (1943) observed a reduction in crossing over associated with proximity to breakpoints. In *Drosophila*, Bridges and Brehme (1944) observed that when breakpoints were in proximal regions that are physically long but show little crossing-over, recombination is not reduced; however, if breakpoints are in the distal region recombination is greatly reduced.

Concluding remarks

The largest hurdle for this project was the lack of known genetic markers in the distal region of 4BL. While the sequenced rice genome was crucial to our ability to map this gene, synteny broke down in the critical region leaving a small gap on the distal side of the gene and a large gap in the proximal region. As previously stated in the discussion of the AFLP markers, and seen in the subtelomeric repeat genetic markers flanking the *Gc2* region (Ksud1-6 and pAESKb52), this region, and the large gap proximal to the *Gc2* locus may comprise nothing

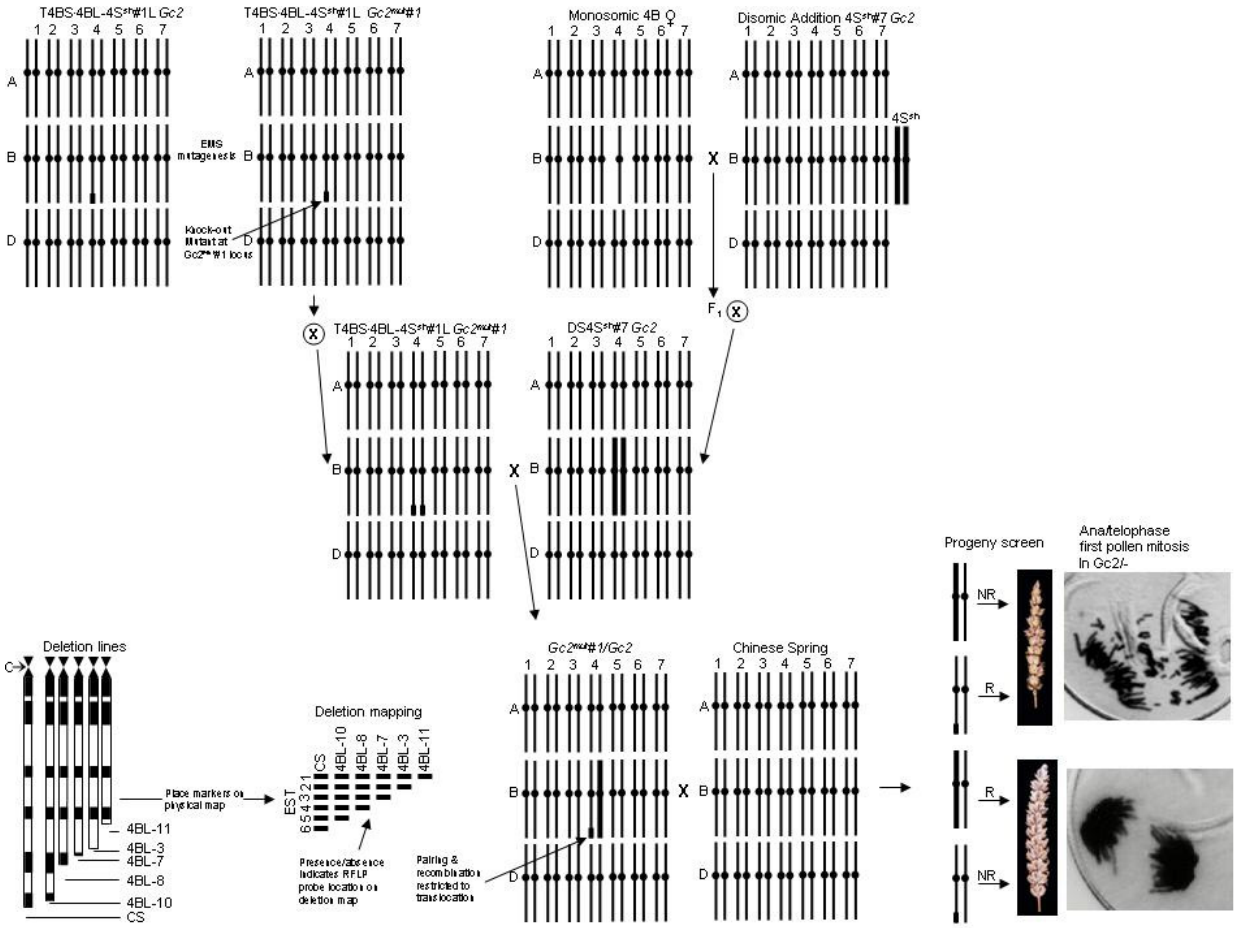
more than multiple tandem repeat elements, that would make walking through this region difficult. While these results demonstrate that it is possible to map a gametocidal gene in wheat, our objective to produce co-segregating markers and clone the gene were unsuccessful. However, the short genetic distance from the distal marker to the *Gc2* locus and the high recombination observed on this side of the locus indicates that walking towards the locus should be feasible using additional genetic material, specifically a BAC library from *Ae. sharonensis*.

Figure 2.1 Physical deletion mapping



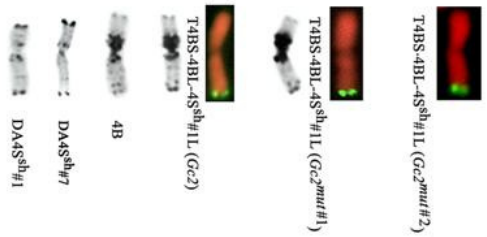
The presence-absence pattern of DNA hybridization signals from CS, DT4BS and the deletion stocks allows assignment of EST restriction fragments to one or more specific deletion bins refining the physical location within the 4BL-5 deletion bin.

Figure 2.2 Genetic stocks used in mapping the *Gc2* gene



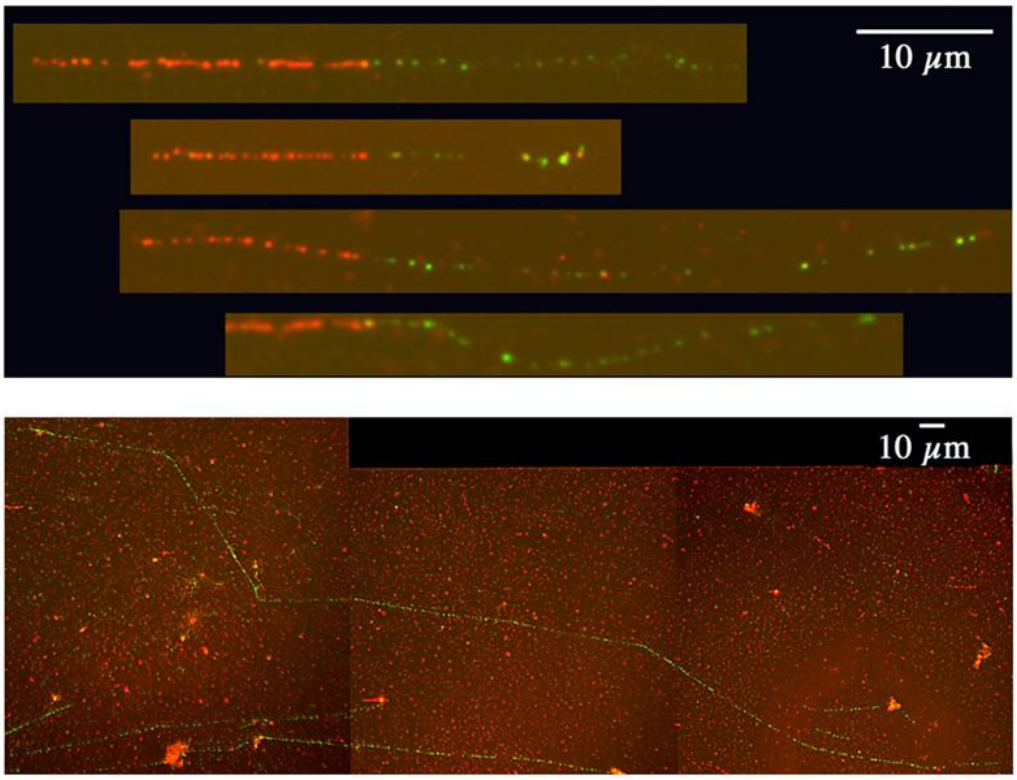
Mutagenesis of the hemizygous T4BS·4BL-4S^{sh}#1L *Gc2* stock produced a knockout mutant (*Gc2^{mut}*#1) at the *Gc2* locus. DA4S^{sh}#7(male) was crossed with CS monosomic 4B(female) then selfed to produce homozygous disomic substitution line DS4S^{sh}#7. T4BS·4BL-4S^{sh}#1L*Gc2^{mut}*#1 was crossed with DS4S^{sh}#7; the F_1 was then crossed to CS (-/-) to produce the mapping population. The spike phenotype was scored (fertile = *Gc2^{mut}*#1/-: semisterile = *Gc2*/-) and recombinants were genetically selected for mapping (R = recombinant: NR = no recombination). Ana/telophase of first pollen mitosis pollen mitosis is shown in the bottom right, indicating the extent of chromosome breakage which results in semisterility. Markers mapped to 4BL-5 deletion bin were hybridized to DNA of deletion lines 4BL-10, 4BL-8, 4BL-7, 4BL-3, and 4BL-11, affording finer coverage of markers, and the physical location of the *Gc2* locus.

Figure 2.3 C-banding and fluorescent *in situ* hybridization (FISH) analysis



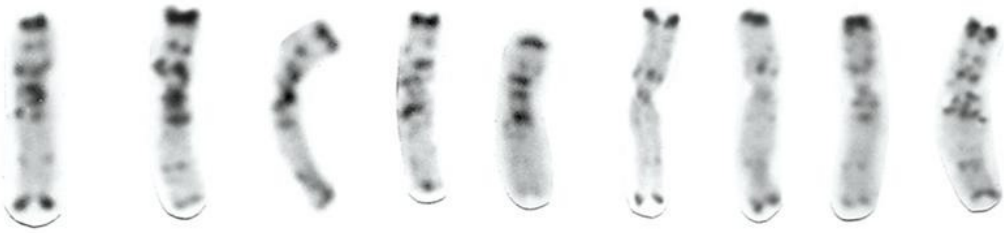
C-banding and fluorescent *in situ* hybridization (FISH) analysis of wild-type *Gc2* carrier chromosome DA4S^{sh}#1, chromosome 4B, and the translocation line T4BS·4BL-4S^{sh}#1L*Gc2*. Hybridization with the Gc1R-1 probe shows the FISH pattern of the *Gc2* carrier chromosome is identical to the *Gc2^{mut}#1* and *Gc2^{mut}#2*, indicating that the loss of function is not the result of a terminal deletion.

Figure 2.4 Fiber FISH of subtelomeric region of T4BS·4BL-4S^{sh}#1L



Top panel: Fiber FISH shows that the telomeric repeat pAtT4 (red) is localized at the distal tip of the long arm and has a size of 16.85 ± 1.6 µm on extended DNA fibers that correlates to a physical length of about 48 kb. The subtelomeric repeat pGc1R-1 hybridized directly adjacent and proximal to pAtT4 (green). Bottom panel: The longest fiber from pGc1R-1 could be followed over three photographic frames had a length of 400 µm, corresponding to 1,148 kb and 1,504 copies of this repeat (repeat length is about 763 bp).

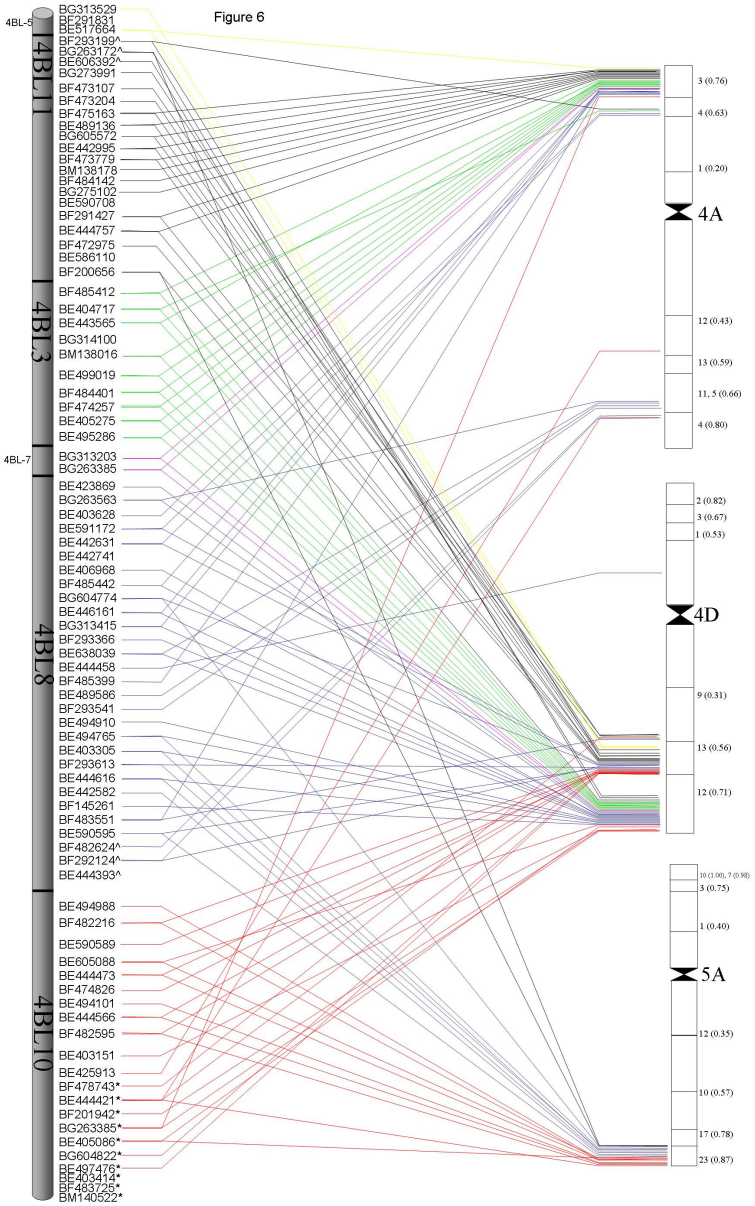
Figure 2.5 Pairing and polymorphism screen of parental lines



Polymorphism	56%	59%	63%	47%	56%	34%	65%	-/-
Metaphase I Pairing in L	56%	20%	79%	30%	69%	62%	36%	-/-

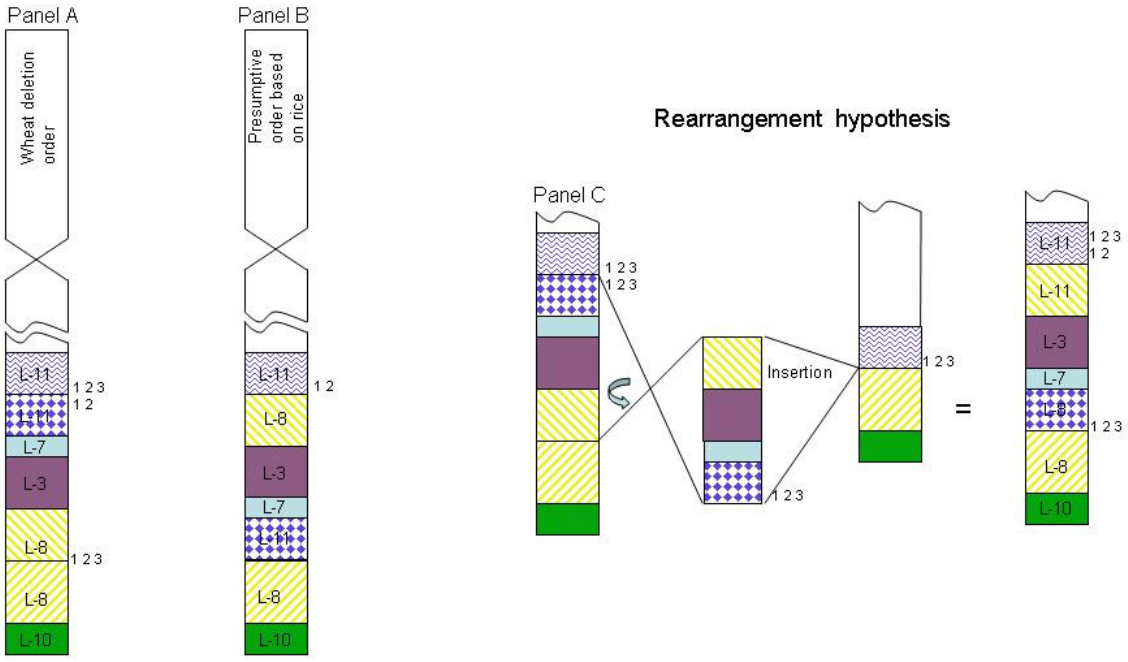
C-banding patterns, Amplified fragment length polymorphism (AFLP) of metaphase I pairing survey of the 4S^{sh} chromosomes DA4S^{sh}#1 (original *Gc2* donor) and the eight disomic addition lines DA4S^{sh}#3-10. Analysis of metaphase I pairing of the long arm was calculated against DA4S^{sh}#1 to determine which of the eight DA4S^{sh} lines would be used as the wild-type parent for the mapping of the *Gc2* gene.

Figure 2.6 Homoeologous location of 4BL ESTs



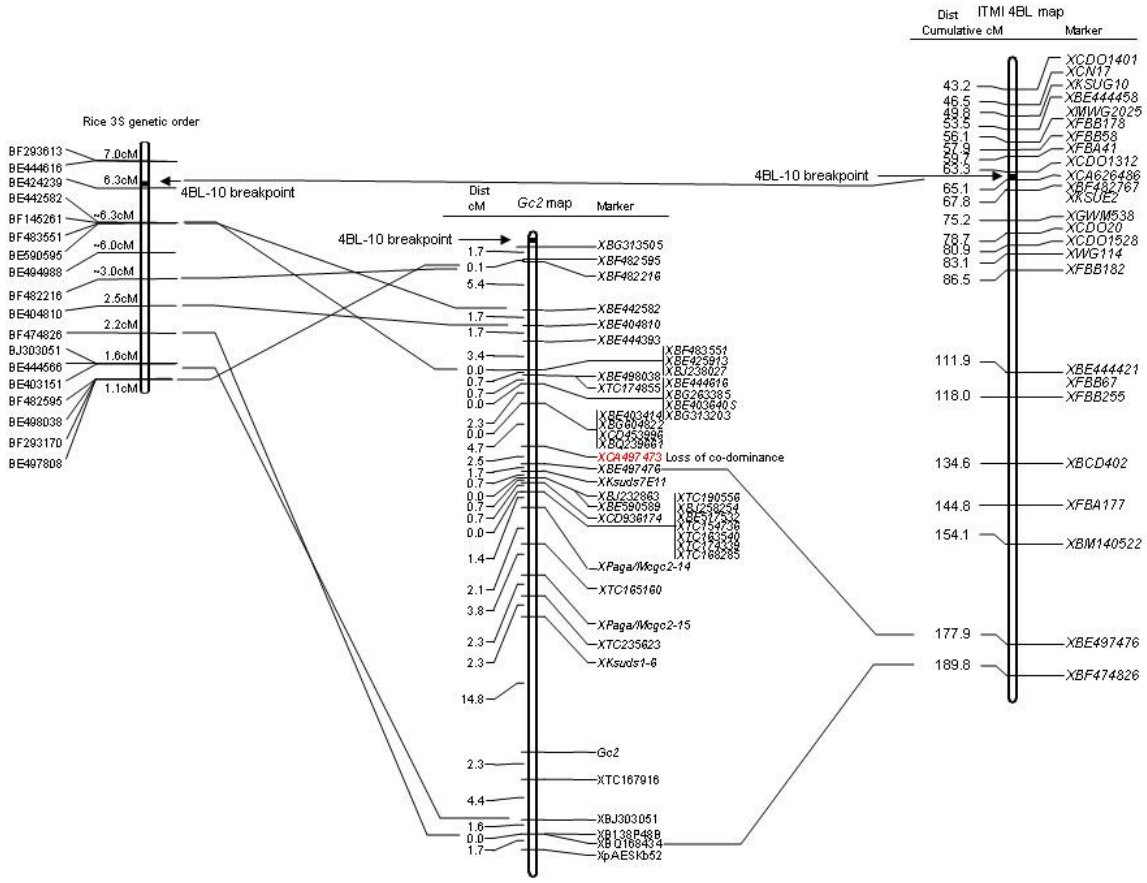
Wheat ESTs physically mapped in the 5 deletion bins were presumptively ordered based upon the sequenced rice genome within each deletion bin. The deletion bins on the right are the homoeologous chromosome regions to 4BL. Based upon deletion mapping results from the NSF project, the 4BL ESTs homoeologous locations were positioned on 4A, 4D, and 5A. The map lines are colored depending on which 4BL deletion bin they were in.

Figure 2.7 Rearrangement diagram of 4BL



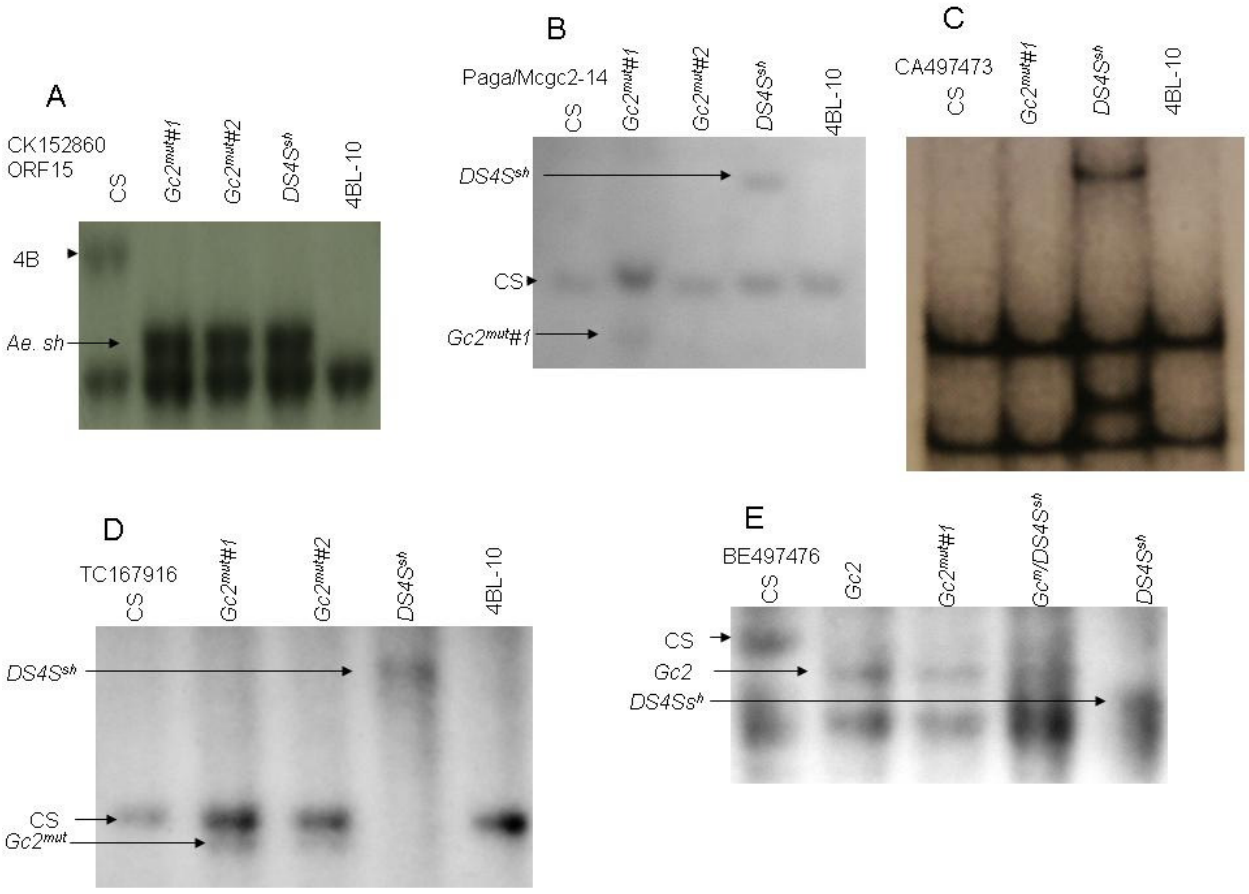
A proposed rearrangement diagram was drawn to explain the discrepancy between wheat physically mapped EST deletion bin assignments and their presumptive genetic location on rice chromosome 3S. Three EST with paralogous duplication; BG 605572 (4BL-8, 4BL-11), BE442995 (4BL-8, 4BL-11, 4BL-11), and BF473779 (4BL-8, 4BL-11, 4BL-11) define the boundary of this inversion event.
Panel A indicates the deletion bins as seen in wheat.
Panel B indicates the segmented deletion bins as ordered by rice genetic position.
Panel C indicates the ancestral order.

Figure 2.8 *Gc2* genetic map



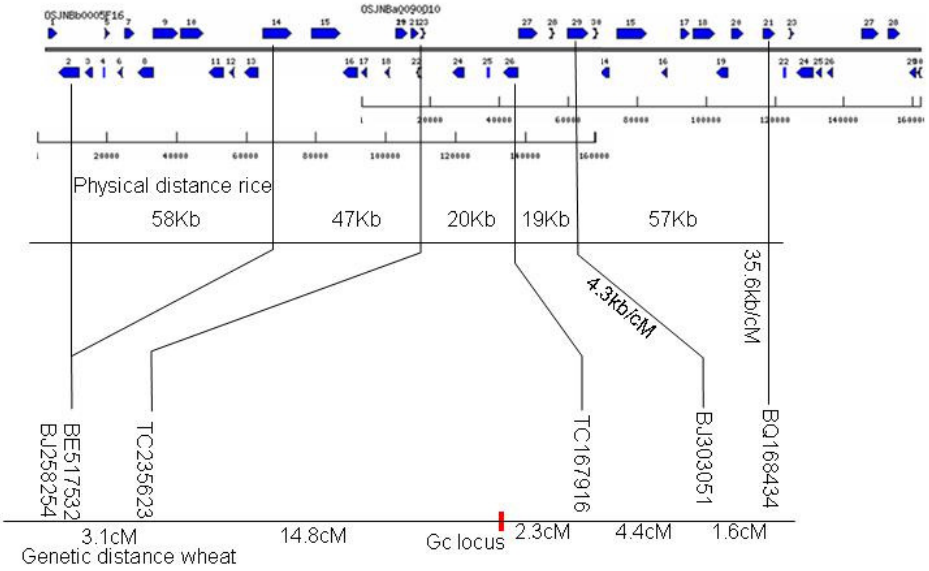
The genetic order of wheat physically mapped EST as seen in rice is on the left.
The genetic map of (DS4S^{sh}#7(*Gc2*) X T4BS·4BL-4S^{sh}#1L(*Gc2^{mut}*#1)) X CS in the middle, is confined to the 4BL-10 deletion bin. The EST BE497476 is the last marker that is codominant (DS4S^{sh}#7 and T4BS·4BL-4S^{sh}#1L), all markers proximal, starting with CA497473 are dominant for DS4S^{sh}#7 indicating the upper boundary of the 4BS·4BL-4S^{sh}#1L translocation. The wheat ITMI 4BL map is on the right, ESTs CA626486, and BF482767 indicate the 4BL-10 breakpoint boundary. ESTs BE497476 and BF474826 have flanking positions in the *Gc2* map.

Figure 2.9 Genetic marker profiles



Insets:
Inset A: CK152860 is a low-copy RFLP probe physically mapped in 4BL-10 with a compensating fragment in *Ae. sharonensis*.
Inset B: Paga/Mcgc2-14 is a codominant AFLP probe that maps proximal to the Gc2 locus.
Inset C: CA497473 defines the upper limit of the $4S^{sh}$#1L segment.
Inset D: TC167916 is the closest codominant marker to the GC2 locus.
Inset E: BE497476 is a codominant marker distal to CA497473 that defines the wheat-*Ae. sharonensis* translocation boundary.

Figure 2.10 Rice BAC region flanking the *Gc2* locus



The two overlapping BACs OSJNBa0090O10 and OSJNBb0005F16 in rice 3S at 1.6 cM show the markers flanking the *Gc2* locus. The genetic distance in wheat is compared to the physical distance in rice between open reading frames (ORF). Wheat EST that had sequence identity to rice ORF26, 29 (BAC OSJNBb0005F1) and ORF21 (BAC OSJNBa0090O10) were collinear in their genetic location in wheat. On the proximal side TC235623 (ORF23) flanks the *Gc2* locus. No polymorphism was detected in ORF24.

Table 2.1 AFLP primers used in polymorphism screening (*Eco*RI / *Mse*I), and in the bulk segregant analysis project (*Pst*I / *Mse*I).

Primer Name	Sequence	Primer Name	Sequence
*Eco*RI adapter E-Ad1	CTCGTAGACTGCGTACC	*Eco*RI adapter E-Ad2	AATTGGTACGCAGTCTAC
*Pst*I adaptor P-Ad1	CTCGTAGACTGCGTACATGCA	*Pst*I adaptor P-Ad2	TGTACGCAGTCTAC
*Mse*I adaptor M-Ad1	GACGATGAGTCCTGAG	*Mse*I adaptor M-Ad2	TACTCAGGACTCAT
Preamp *Eco*RI preA	GACTGCGTACCAATTCA	Preamp *Pst*I PreA	GACTGCGTACATGCAGA
Preamp *Mse*I PreC	GATGAGTCCTGAGTAAC	*Eco*RI 5'-/56-fam ACC	GACTGCGTACCAATTCACC
*Eco*RI 5'-/56-fam ACA	GACTGCGTACCAATTCACA	*Eco*RI 5'-/56-hex ACA	GACTGCGTACCAATTCACA
*Pst*I P-AAA	GACTGCGTACATGCAGAAA	*Pst*I P-AAT	GACTGCGTACATGCAGAAT
*Pst*I P-AAG	GACTGCGTACATGCAGAAG	*Pst*I P-AAC	GACTGCGTACATGCAGAAC
*Pst*I P-ATA	GACTGCGTACATGCAGATA	*Pst*I P-ATT	GACTGCGTACATGCAGATT
*Pst*I P-ATG	GACTGCGTACATGCAGATG	*Pst*I P-ATC	GACTGCGTACATGCAGATC
*Pst*I P-AGA	GACTGCGTACATGCAGAGA	*Pst*I P-AGT	GACTGCGTACATGCAGAGT
*Pst*I P-AGG	GACTGCGTACATGCAGAGG	*Pst*I P-AGC	GACTGCGTACATGCAGAGC
*Pst*I P-ACA	GACTGCGTACATGCAGACA	*Pst*I P-ACT	GACTGCGTACATGCAGACT
*Pst*I P-ACG	GACTGCGTACATGCAGACG	*Pst*I P-ACC	GACTGCGTACATGCAGACC
*Mse*I M-CAA	GATGAGTCCTGAGTAACAA	*Mse*I M-CAT	GATGAGTCCTGAGTAACAT
*Mse*I M-CAG	GATGAGTCCTGAGTAACAG	*Mse*I M-CAC	GATGAGTCCTGAGTAACAC
*Mse*I M-CTA	GATGAGTCCTGAGTAACTA	*Mse*I M-CTT	GATGAGTCCTGAGTAACTT
*Mse*I M-CTC	GATGAGTCCTGAGTAACTC	*Mse*I M-CTG	GATGAGTCCTGAGTAACTG
*Mse*I M-CGA	GATGAGTCCTGAGTAACGA	*Mse*I M-CGT	GATGAGTCCTGAGTAACGT
*Mse*I M-CGC	GATGAGTCCTGAGTAACGC	*Mse*I M-CGG	GATGAGTCCTGAGTAACGG
*Mse*I M-CCA	GATGAGTCCTGAGTAACCA	*Mse*I M-CCT	GATGAGTCCTGAGTAACCT
*Mse*I M-CCC	GATGAGTCCTGAGTAACCC	*Mse*I M-CCG	GATGAGTCCTGAGTAACCG

Table 2.2 STS primer names, orientation, annealing temperature (Tm), and primer sequences developed for the genetically mapped markers

Name	Tm	Sequence	Name	Tm	Sequence
BF482595F	57.0	GAGAGCATCAGAATGGGTTATAACG	BF482595R	59.1	GGCACCATAGACAGCCACATC
BE425913R	62.1	TGCTTGTGGTAGTCGTGGTAGTGG	BE425913F	60	TGCTGCTGGAGAAGAAGGAGTC
BE638039F	58.1	CACTTTCTTCTTCGCTGTTTGGAC	BE638039R	59.4	TTGTTAGTTGTTCCCGTGGCAC
BF145261F	57.8	CAACTGGCATCCGTGTTCTTTAC	BF145261R	57	GTTCCAATCCGACCAATCGTC
BG313203F	60.2	CACAAACAGCCGTGACACACAG	BG313203R	60.7	TTCTCCCCATTGACACCGTTCG
BG313505F	62.3	ATCACGACAGAGCCCAGGAACATC	BG313505R	57.5	GACCATCACCAGCAAAGATTCAG
BJ303051F	59.6	TTACTCCTCTGTTCCTTTCAGTCCC	BJ303051R	58.7	TTTTCTGTAGATGCCGCCCC
TC167916F	60.6	ACTGCTGCTGCTCTGTCTTATGG	TC167916R	57.6	GAACCTCATCAACTTCCTTTGTGG
TC174339F	55.4	GTCGTACCTGATATTCACCAAGC	TC174339R	54.3	ACGACATCAAACAACACAAACTG
TC165160F	54.3	CAGAGAATGCAACAGCTTATGTG	TC165160R	56.1	TTCGCTAGTTGCGAGTAGTATCC
TC168285F	52.6	TATGAAAAAGGTCAGCGATTGAT	TC168285R	53.8	CGAAAAGGTTGTAGTGATTCAGG
TC163540F	54.9	GGACTTGATCTCTGCATCTATGG	TC163540R	56.7	TCTTTGCTGTTAGCCCAGTCTAC
TC154736F	55	CAACAACTACCTCTACTGGTTCG	TC154736R	53.8	GATAATCCTCTGCAAGATCCTCT
BE517532F	52.8	CGTATTTTGATGGGTACTGATGT	BE517532R	51.5	CCTGGTGCCTTTTTATTATATCC
TC190556F	53.9	AAAAGCAAATGACGATGCTCTAC	TC190556R	57.7	AGTTGTACCCGACTAGCACAGAA
CD936174F	59.1	CCCCTATCTTCTCTCCCACTAATCC	CD936174R	59.4	CGCAGGTTGTCCAAGTTATCCG
BE590589F	55.8	ATCATCCATAGCCAGCAGC	BE590589R	54.9	ATCAACTCCAAGGGTGAGG
BJ232863F	51.1	TTTCGAATTAGGACGAAAAACAA	BJ232863R	54.4	CTATCGAAACAAGAGAGCTGGAA
BE497476F	58.4	TCGCCGCCAAAAGCAAATG	BE497476R	62.6	AATCCTCGCAAAGCCAAACGCC
CA497473F	52.4	GAAGAACATATCTGGAACCATCA	CA497473R	52.5	AGCACCATCAAAAGATAATTCCT
BQ239661F	60.2	AAGGGGTGAGGAGTTGGCTTAC	BQ239661R	59.4	CGGGCACTAACAAAGTCCATTCTC
CD453996F	59.7	CAAGGCAGTATTCCACACCAGTTG	CD453996R	59.4	AGGCAGAGCGTTCACAAAAGG
BG604822F	59.2	ACGACTTTTCCGCCAACTGG	BG604822R	58.7	CAACAACATTCAACCTCGCTGC
BE444616F	58.1	CATTCTCCGCCAAACTGTTGAAG	BE444616R	60.9	AAGGAAGCATCAGAGCCACCAC
TC174855F	52.5	GGCACTCCAAATGAACAAAC	TC174855R	53.5	ACCATCTCCATGTCCTTGAA
BE498038F	63.3	AAGGAGATGCAGCACGGCAACAT	BE498038R	60.9	CTGCAAAGATACAGCCCACTGACCAC
BJ238027F	58.4	CAGCAGGAGATTGAGGAAGGTATG	BJ238027R	60.1	GCACGAGGCAGAGAAAGCAAAG
BF483551F	57.7	TCGGTCGGACAAGATGATGG	BF483551R	57.6	CAGCAACCTTCTGGACATAAACG

BE404810F	61.5	TACTTCCACGACCAGGAGTCGTTC	BE404810R	59.8	GCTTTACAGGAGCAGAGCATGC
BE442582F	64.8	GGTGCTACGTGAACAGCCTCAAAGCT	BE442582R	61.8	GGATGAGCTGAGACCAAATGCACAC
BF482216F	60.8	CGCTTGACTGACCTGAGAGCTG	BF482216R	60.5	TCTCCAAGAACTTTAGGAGCCTTGC
BG263385F	60.7	AATCCCTGTCCCCAACCTTTCC	BG263385R	62.1	TAGAGTAAGAGCAAACCGCCGTCC
BQ168434F	61.4	TGGACGAAGATCTTGTAGCGTAT	BQ168434R	59.2	TGTCGCTGACCTAAACAAGCTAT
M13F	52.2	GGAAACAGCTATGACCATGA	M13R	55.8	TTGTAAAACGACGGCCAGTG
BE403414F	59.2	CGACCCAATCTCACATCAACCG	BE403414R	60.1	ATTTCCAGCGACAAGCGTGC
BE403640F	58.6	TGGGGACAAAGGGAACAAGAAG	BE403640R	59.2	TTAGCGGCAAAGTGACAACTCTG
pAEsKb52F	54.6	ACACAAACCGCACGAAAG	pAEsKb52R	55.2	CGTAACACCTGATGACCAAATG
Ksuds7E11F	55.2	ATGTCCCTCGTCACAATTCTTT	Ksuds7E11R	58.3	TTCTCCTCGGCGTATGTAGAAT
Ksuds1-6F	56.0	GTTACCCTTGACGAAAGCACTTC	Ksuds1-6F	55.3	CTTCTTCCTTGTTCATCGAGCTA

Table 2.3 *Gc2^{mut}*#2 chromosomal constitution and chromosomal breakage at ana-telophase of the first pollen mitosis of testcross progenies of the *Gc2^{mut}*#2 mutant.

M_2 constitution	Testcross	Testcross constitution	1st pollen mitosis	
			Normal	Fragments
Gc2^{mut}#2/*Gc2^{mut}*#2	*Gc2^{mut}*#2/*Gc2^{mut}*#2	*Gc2^{mut}*#2/*Gc2^{mut}*#2	188[a]	
Gc2^{mut}#2/*Gc2^{mut}*#2	-/-	*Gc2^{mut}*#2/-	384[b]	
Gc2^{mut}#2/*Gc2^{mut}*#2	*Gc2/Gc2* (DS4^{sh}#1)	*Gc2^{mut}*#2/*Gc2*	565[c]	
Gc2^{mut}#2/*Gc2^{mut}*#2	*Gc2/Gc2* (DS4^{sh}#7)	*Gc2^{mut}*#2/*Gc2*	284[d]	79 (27.8%)
Gc2^{mut}#2/*Gc2^{mut}*#2	*Gc2/Gc2* (DS4^{sh}#1)	*Gc2^{mut}*#2/*Gc2*	466[e]	

a = Data from 3 plants
b = Data from 5 plants
c = Data from 6 plants
d = Data from 4 plants
e = Data from 4 plants

Table 2.4 Restriction fragment analysis

Del. bin (EST)	Bands/bin	*Eco*RI Ave	*Hin*dIII Ave	Loci *Eco*RI	Loci *Hin*dIII
4BL-10 (21)	128E/151H	6.0	7.0	1.4	1.2
4BL-8 (29)	178E/151H	6.1	5.2	1.2	0.7
4BL-3 (10)	41E/33H	4.1	3.3	1.0	0.5
4BL-7 (2)	8E/10H	4.0	5.0	1.0	1.0
4BL-11 (20)	98E/108H	5.8	5.8	1.2	1.1
Total (82)	906	5.3	5.3	1.2	0.9

Ave = Average

Table 2.5 Chromosome 4BL paralogous duplications

EST	Del Bin	EST	Del Bin
BE444473*	4BL-10^2	BE442631*	4BL-8^2
BG604822	4BL-10^2	BE444616*	4BL-10^2; 4BL-8
BE403414*	4BL-10^2 ; 4BL-8	BE494765	4BL-8^2
BF482595	4BL-10^2	BE293541	4BL-8^2
BE605088	4BL-10^2	BG263385	4BL-10; 4BL-7
BF201942*	4BL-10^2	BG275102	4BL-11^2
BE425913	4BL-10^2	BE442995*	4BL-11^2; 4BL-8
BF482624	4BL-8; 4BL-11	BF473779*	4BL-11^2; 4BL-8
BE403628*	4BL-8^2	BG605572	4BL-11; 4BL-8
BG313415	4BL-8^2		

Asterisk indicates that the paralog was observed in both *Eco*RI and *Hin*dIII.
Superscript indicates the number of copies observed.

Table 2.6 Group 4 homoeologous loci detected

Del. Bin	EST	None	One	Two
4BL-10	21	(4) 19.0%	(8) 38.1%	(9) 42.8%
4BL-8	29	(7) 24.1%	(8) 27.6%	(14) 48.3%
4BL-3;4BL-7	12	(1) 8.3%	(0) 0.0%	(11) 91.7%
4BL-11	20	(2) 10.0%	(7) 35.0%	(11) 55.0%
Total	82	17.1%	28.1%	54.8%

In parenthesis is the number of EST per category, detection is split into three categories. None = only present on 4BL, or does not have an additional mapped loci in a homoeologous location.
One = only detecting one of the homoeologous chromosomes.
Two = mapped bands on both 4A-5AL and 4DL.

Table 2.7 Markers used in genetic mapping for *Ae. sharonensis* & *T. Aestivum*

Marker	CS	*Gc2^{mut}#1*	*4S^{sh}#7*(4B)	4BL-10	Detection
BG313505	A	A	C	NA	PCR
BE482595	A	A	C	ABS	CAPS *Rsa*I
BF482216	A	A	C	ABS	SSCP
BE442582	A	A	C	ABS	SSCP
BE404810	A	A	C	NA	SSCP
BE444393	A	A	C	PRE	SSCP
BF483551	A	A	C	NA	CAPS *Mse*I
BE425913	A	A	C	ABS	CAPS *Mse*I
BJ238027	A	A	C	NA	SSCP
TC174855	A	A	C	NA	SSCP
BE444616	A	A	C	NA	SSCP
BG263385	A	A	C	NA	SSCP
BE403640	A	A	C	NA	SSCP
BG313203	A	A	C	PRE	PCR *Mse*I
BE403414	A	A	C	NA	SSCP
BG604822	A	A	C	NA	SSCP
CD453996	A	A	C	ABS	SSCP
BQ239661	A	A	C	NA	SSCP
CA497473	A	A	C	PRE	SSCP
BE497476	A	B	C	ABS	SSCP, RFLP
Ksuds7E11	A	B	A	NA	PCR
BJ232863	A	A	C	NA	SSCP

BE590589	A	B	C	ABS	SSCP
CD936174	A	A	C	NA	SSCP
TC190556	A	A	C	ABS	PCR
BJ258254	A	B	C	ABS	SSCP
BE517532	A	B	C	ABS	SSCP
TC154736	A	A	C	ABS	SSCP
TC163540	A	A	C	NA	SSCP
TC174339	A	A	C	NA	SSCP
TC168285	A	A	C	NA	SSCP
PagaMcgc2-14	A	B	C	PRE	RFLP
TC165160	A	A	C	NA	PCR
PagaMcgc2-15	A	A	C	PRE	RFLP
TC235623	A	A	C	NA	SSCP
Ksuds1-6	A	B	X	NA	SSCP
TC167916	A	B	C	PRE	RFLP
BJ303051	A	B	C	ABS	SSCP, RFLP
B138P48BR	A	B	C	ABS	RFLP
BQ168434	A	B	C	ABS	SSCP
PAESKb52	A	A	C	NA	SSCP

A=CS allele present
B=*Gc2*^{mut}*#1* + CS allele present
C= *4Ssh#7*(4B) + CS allele present
X= absent
NA= not available
ABS = 4BL band is absent in 4BL-10 deletion line
PRE = 4BL band is present in 4BL-10 deletion line

Table 2.8 cDNA clones from differential display and microarray results with sequence homology to cDNA clones

cDNA	Detection	4BL	Microarray probe set	Signal strength/Tissue Type
31C10	RFLP/ 4.0	N	AFFX-Ta_Sucsyn_M_at	10 fold < *Gc2*/- early
37K12	RFLP/ 5.0	N	TaAffx.128585.4.S1_x_at	10 fold < $Gc2^{mut}$*#1*/- early
19O24	RFLP/ 6.2	N	Ta.28157.1.S1_at	10 fold < *Gc2*/- early
27N19	RFLP/ 5.6	N	Ta.22377.1.S1_at	2 fold > *Gc2*/- late
26K24	RFLP/ 4.8	N		
35P6	RFLP/ 5.8	N	Ta.27209.1.S1_at	2fold > *Gc2*/- ;$Gc2^{mut}$*#1*/- late
38B5	RFLP/ 5.8	Y		
26K9	RFLP/ 2.0	N		
23P22	RFLP/ 8.6	Y		
40D19	RFLP/ 1.2	N		
31G10	RFLP/ 4.4	N		
31C18	RFLP/ 5.6	N	TaAffx.92860.1.A1_at	2 fold > in *Gc2*/- late
82J15	RFLP/ 3	Y		
48I8	RFLP/ 4	N		
25M1	RFLP/ 3.2	N		
23P15	RFLP/ 3.6	N		
78B15	RFLP/ 3.8	N		
27M5	RFLP/ 2	N		
29N16	RFLP/ 5.2	N		
19P23	RFLP/ 3.8	N		
31H18	RFLP/ 7.0	N		
19B23	RFLP/ 4.4	N		
58J16	RFLP/ 4.4	Y		
22I22	SSCP	N	Ta.3644.2.S1_at	2 fold > *Gc2*/- late
43H10	SSCP	N		
42N2	SSCP	N		
40H14	SSCP	N		
40D19	SSCP	N		

37H20	SSCP	Y		
32F13	SSCP	N	Ta.28344.1.A1_x_at	2 fold > in *Gc2*/- early
31D21	SSCP	N		

References Chapter 2

Akhunov ED Goodyear AW Geng S Qi LL Echalier B Gill BS Miftahudin J Gustafson P Lazo G Chao S Anderson OD Linkiewicz AM Dubcovsky J La Rota M Sorrells ME Zhang D Nguyen HT Kalavacharla V Hossain K Kianian SF Peng J Lapitan NLV Gonzalez-Hernandez JL Anderson JA Choi DW Close TJ Dilbirligi M Gill KS Walker-Simmons MK Steber C McGuire PE Qualset CO Dvorak J (2003a) The organization and rate of evolution of wheat genomes are correlated with recombination rates along chromosome arms. Genome Res 5:753-763.

Akhunov ED Akhunova AR Linkiewicz AM Dubcovsky J Hummel D Lazo GR Chao S Anderson OD David J Qi L Echalier B Gill BS Miftahudin J Gustafson P La Rota M Sorrells ME Zhang D Nguyen HT Kalavacharla V Hossain K Kianian SF Peng J Lapitan NLV Wennerlind EJ Nduati V Anderson JA Sidhu D Gill KS McGuire PE Qualset CO Dvorak J (2003b) Synteny perturbations between wheat homoeologous chromosomes caused by locus duplications and deletions correlate with recombination rates. Proc Natl Acad Sci USA 100:10836-10841.

Akhunov ED Akhunova AR Dvorak J (2005) BAC libraries of *Triticum urartu*, *Aegilops speltoides* and *Ae. tauschii*, the diploid ancestors of polyploid wheat. Theor Appl Genet 111:1617-1622.

Anamthawat-Jónsson K Heslop-Harrison JS (1993) Isolation and characterization of genome-specific DNA sequences in Triticeae species. Mol Gen Genet 240:151-158.

Botstein D White RL Skolnick M Davis RW (1980) Construction of a genetic linkage map in man using restriction fragment length polymorphisms. Am J Hum Genet. 32:314-331.

Bridges CB and Brehme KS(1944) The mutants of *Drosophila melanogaster*. Carnegie Inst of Wash Publ 552, Wash., D.C.

Burnham CR (1943) Chromosomal interchanges in maize: reduction of crossing-over and the association of non-homologous parts. Amer Nat 68:81-82.

Burt A Trivers R (2006) Genes in conflict: the biology of selfish genetic elements. Harvard University Press. Cambridge, Massachusetts London, England.

Cameron DR Moav R (1957) Inheritance in *Nicotiana tabacum*. XXVII. Pollen killer, an alien genetic locus inducing abortion of microspores not carrying it. Genetics 42:326-335.

Chantret N Cenci A Sabot F Anderson O Dubcovsky J (2004) Sequencing of the *Triticum monococcum* Hardness locus reveals good microcolinearity with rice. Mol Gen Genomics 271:377-386.

Chao S Lazo GR You F Crossman CC Hummel DD Lui N Laudencia-Chingcuanco D Anderson JA Close TJ Dubcovsky J Gill BS Gill KS Gustafson JP Kianian SF Lapitan NL Nguyen HT Sorrells ME McGuire PE Qualset CO Anderson OD (2006) Use of a large-scale Triticeae expressed sequence tag resource to reveal gene expression profiles in hexaploid wheat (*Triticum aestivum* L.). Genome 49:531-544.

Dubcovsky J Lou MC Dvorak J (1995) Differentiation between homoeologous chromosomes 1A of wheat and $1A^m$ of *Triticum monococcum* and its recognition by the wheat *Ph1* locus. Proc Natl Acad Sci USA 92:6645-6649.

Endo TR (1978) On the *Aegilops* chromosomes having gametocidal action on common wheat. In: Ramanujam S (ed) Proceedings 5th Int. Wheat Genet Symp, New Delhi. 306-314.

Endo TR (1979) Selective gametocidal action of a chromosome of *Aegilops cylindrica* in a cultivar of common wheat. Wheat Inf Serv 50:24-28.

Endo TR (1982) Gametocidal chromosomes of three *Aegilops* species in wheat. Can J Genet Cytol 24:201-206.

Endo TR (1985) Two types of gametocidal chromosome of *Aegilops sharonensis* and *Ae. longissima*. Jpn J Genet 60:125-135.

Endo TR (1988a) Induction of chromosomal changes by a chromosome of *Aegilops cylindrica* L. in common wheat. J Heredity 79:366-370.

Endo TR (1988b) Chromosome mutations induced by gametocidal chromosomes in common wheat. In: Miller, TE, Koebner RMD (eds) Proceedings of the 7th international wheat genetics symposium. Institute of Plant Science Research. Cambridge laboratory, Cambridge. 259-265.

Endo TR (1990) Gametocidal chromosomes and their induction of chromosome mutations in wheat. Jpn J Genet 65:135-152.

Endo TR Gill BS (1996) The deletion stocks of common wheat. J Heredity 87:295-307.

Endo TR Tsunewaki K (1975) Sterility of common wheat with *Aegilops triuncialis* cytoplasm. J Heredity 66:13-18.

Endo TR Katayama Y (1978) Finding of a selectively retained chromosome of *Aegilops caudata* L. in common wheat. Wheat Inf Serv 47-48:32-35.

Faris JD Haen KM Gill BS (2000) Saturation mapping of a gene-rich recombination hot spot region in wheat. Genetics 154:823-835.

Faris JD Gill BS (2002) Genomic targeting and high-resolution mapping of the domestication gene Q in wheat. Genome 45:706-718.

Fossella J Samant SA Silver LM King SM Vaughan KT Olds-Clarke P Johnson KA Mikami A Vallee RB Pilder SH (2000) An axonemal dynein at the *hybrid sterility 6* locus: implications for *t* haplotype-specific male sterility and the evolution of species barriers. Mamm gen 11:8-15.

Friebe B Tuleen N Jiang J Gill BS (1993) Standard karyotype of *Triticum longissimum* and its cytogenetic relationship with *T. aestivum*. Genome 36:731-742.

Friebe B Tuleen NA Gill BS (1999) Development and identification of a complete set of *Triticum aestivum-Aegilops geniculata* chromosome addition lines. Genome 42:374-380.

Friebe B Zhang P Nasuda S Gill BS (2003) Characterization of a knock-out mutation at the *Gc2* locus in wheat. Chromosoma 111:509-517.

Gill BS Friebe B Endo TR (1991) Standard karyotype and nomenclature system for description of chromosome bands and structural aberrations in wheat (*Triticum aestivum*). Genome 34:830-839

Gill KS Gill BS Endo TR (1993) A chromosome region-specific mapping strategy reveals gene-rich telomeric ends in wheat. Chromosoma 102:374-381.

Gill KS Gill BS Endo TR Boyko EV (1996a) Identification and high-density mapping of gene-rich regions in chromosome group 5 of wheat. Genetics 143:1001-1012.

Gill KS Gill BS Endo TR Taylor T (1996b) Identification and high-density mapping of gene-rich regions in chromosome group 1 of wheat. Genetics 144:1883-1891.

Haen KM Lu H Friesen TL Faris JD (2004) Genomic targeting and high-resolution mapping of the *Tsn1* gene in wheat. Crop Sci 44:951-962.

Hammer MF Schimenti J Silver LM (1989) Evolution of mouse chromosome 17 and the origin of inversions associated with the *t* haplotype. Proc Natl Acad Sci USA 86:3261-3265.

Hartl DL Hiraizumi Y Crow JF (1967) Evidence from sperm dysfunction as the mechanism of segregation distortion in *Drosophila melanogaster*. Proc Natl Acad Sci USA 58:2240-2245.

Hartl DL (1974) Genetic dissection of segregation distortion. I. Suicide combinations of *SD* genes. Genetics 76:477-486.

Hayashi K Yandell DW (1993) How sensitive is PCR-SSCP? Hum. Mutat. 2:338-346.

Herrmann BG Kosxhorz B Wertz K McLaughlin KJ Kispert A (1999) A protein kinase encoded by the *t* complex *responder* gene causes non-Mendelian inheritance. Nature 402:141-146.

Houtchens K Lyttle TW (2003) Responder (*Rsp*) alleles in the segregation distorter (*SD*) system of meiotic drive in *Drosophila* may represent a complex family of satellite repeat sequences. Genetica 117:291-302

Hu F Xu P Deng X Zhou J Li J Tao D (2006) Molecular mapping of a pollen killer *S29*(*t*) in *Oryza glaberrima* and co-linear analysis with S22 in *O. glumaepatula*. Euphytica 151:273-278.

Jackson SA Zhang P Chen W Phillips R (2001) High-resolution structural analysis of biolistic transgene integration into the nuclear genome of wheat. Theor Appl Genet 103:56-62.

King IP Laurie DA (1993) Chromosome damage in early embryo and sndosperm development in crosses involving the preferentially transmitted $4S^l$ chromosome of *Aegilops sharonensis*. Heredity 70:52-59.

Kosambi DD (1944) The estimation of map distances from recombination values. Ann Eugen 12:172-175.

Kota RS Dvorak J (1988) Genomic instability in wheat induced by chromosome $6B^s$ of *Triticum speltoides*. Genetics 120:1085-1094.

Kusano A Staber C Ganetzky B (2001) Nuclear mislocalization of enzymatically active RanGAP causes segregation distortion in *Drosophila*. Dev Cell 1:351-361.

Kusano A Staber C Ganetzky B (2002) Segregation distortion induced by wild-type RanGAP in *Drosophila*. Proc Natl Acad Sci USA 99:6866-6870.

Lander ES Green P Abrahamson J Barlow A Daly MJ Lincoln SE Newburg L (1987) Mapmaker: an interactive computer package for constructing primary genetic linkage maps of experimental and natural populations. Genomics 1:174-181.

Li Z Pinson SR Paterson AH Park WD Stansel JW (1997) Genetics of hybrid sterility and hybrid breakdown in an intersubspecific rice (*Oryza sativa* L.) population. Genetics 145:1139-1148.

Li W Gill BS (2002) The colinearity of the Sh2/A1 orthologous region in rice, sorghum and maize is interrupted and accompanied by genome expansion in the Triticeae. Genetics 160:1153-1162.

Loegering WG Sears ER (1963) Distorted inheritance of stem-rust resistance of timstein wheat caused by a pollen killing gene. Can J Genet Cytol 5:67-72.

Lyon MF (1986) Male sterility of the Mouse t-complex is due to homozygosity of the Distorter genes. Cell 44:357-363.

Lyon MF Schimenti JC Evans EP (2000) Narrowing the critical regions for mouse *t* complex transmission ratio distortion factors by use of deletions. Genetics 155:793-801.

Lyon MF (2003) Transmission ratio distortion in mice. Annu rev genet 37:393-408.

Maan SS (1975) Exclusive preferential transmission of an alien chromosome in common wheat. Crop Sci 15:287-292.

Mao L Devos KM Zhu L Gale MD (1997) Cloning and genetic mapping of wheat telomere-associated sequences. Mol Gen Genet 254:584-591.

Merrill C Bayraktaroglu L Kusano A Ganetzky B (1999) Truncated RanGAP encoded by the segregation distorter locus of *Drosophila*. Science 283:1742-1745.

Messing J Llaca V (1998) Importance of anchor genomes for any plant genome project. Proc Natl Acad Sci USA 95:2017-2020.

Miller TE Hutchinson J Chapman V (1982) Investigation of a preferentially transmitted *Aegilops sharonensis* chromosome in wheat. Theor Appl Genet 61:27-33.

Mullis K Faloona F Scharf S Saiki R Horn G Erlich H (1986) Specific enzymatic amplification of DNA in vitro: The polymerase chain reaction. Cold Spring Harbor Symp Quant Biol 51:263.

Nasuda S Friebe B Gill BS (1998) Gametocidal genes induce chromosome breakage in the interphase prior to the first mitotic cell division of the male gametophyte in wheat. Genetics 149:1115-1124.

Nasuda S (1999) Molecular cytogenetic analysis of gametocidal genes in wheat. Ph.D thesis, Department of Plant Pathology, Kansas State University, Manhattan, Kansas, USA.

Pimpinelli S Dimitri P (1989) Cytogenetic analysis of segregation distortion in *Drosophila melanogaster*: the cytological organization of the responder (*Rsp*) locus. Genetics 121:765-772.

Planchart A You Y Schimenti JC (2000) Physical mapping of male fertility and meiotic drive quantitative trait loci in the mouse *t* complex using chromosome deficiencies. Genetics 155:803-812.

Qi L Echalier B Friebe B Gill BS (2003) Molecular characterization of a set of wheat deletion stocks for use in chromosome bin mapping of ESTs. Funct Integr Genomics 3:39-55.

Qi LL Echalier B Chao S Lazo GR Bulter GE Anderson OD Akhunov ED Dvorak J Linkiewicz AM Ratnasiri A Dubcovsky J Bermudez-Kandianis CE Greene RA Kantety R La Rota CM Munkvold JD Sorrells SF Sorrells ME Dilbirligi M Sidhu D Erayman M Randhawa HS Sandhu D Bondareva SN Gill KS Mahmoud AA Ma XF Miftahudin Gustafson JP Conley EJ Nduati V Gonzales-Hernandez JP Anderson JA Peng JH Lapitan NLV Hossain KG Kalavacharla V Kianian SF Pathan MS Zhang DS Nguyen HT Choi DW Fenton RD Close TJ McGuire PE Qualset CO Gill BS (2004) A chromosome bin map of 16,000 expressed sequence tag loci and distribution of genes among the three genomes of polyploid wheat. Genetics 168:701-712.

Rick CM (1966) Abortion of male and female gametes in the tomato determined by allelic interaction. Genetics 53:85-96.

Richards EJ and Ausubel FM (1988) Isolation of a higher eukaryotic telomere from *Arabidopsis thaliana*. Cell 53:127-136.

Sambrook J Fritsch EF Maniatis T (1989) Molecular cloning. Cold Springs Harbor Laboratory Press.

Sandler L Novitski E (1957) Meiotic drive as an evolutionary force. Am Nat 91:105-110.

Sano Y (1990) The genetic nature of gamete eliminator in rice. Genetics 125:183-190.

See D Kanazin V Kephart K Blake T (2002) Mapping genes controlling variation in barley grain protein concentration. Crop Sci 42:680-685.

See DR Brooks S Nelson JC Brown-Guedira G Friebe B Gill BS (2006) Gene evolution at the ends of wheat chromosomes Proc Natl Acad Sci USA 103:4162-4167.

Silver LM (1993) The peculiar journey of a selfish chromosome: *t*-haplotypes and meiotic drive. Trends Genet 9:250-254.

Sorrells ME La Rota M Bermudez-Kandianis CE Greene RA Kantety R Munkvold JD Miftahudin Mahmoud A Ma X Gustafson PJ Qi LL Echalier B Gill BS Matthews DE Lazo GR Chao S Anderson OD Edwards H Linkiewicz AM Dubcovsky J Akhunov ED Dvorak J Zhang D Nguyen HT Peng J Lapitan NLV Gonzalez-Hernandez JL Anderson JA Hossain K Kalavacharla V Kianian SF Choi DW Close TJ Dilbirligi M Gill KS Steber C Walker-Simmons MK McGuire PE Qualset CO (2003) Comparative DNA sequence analysis of wheat and rice genomes. Genome Res 13:1818-1827.

Southern EM (1975) Detection of specific sequences among DNA fragments separated by gel electrophoresis. J Mol Biol 98:503-517.

Spielmeyer W Richards RA (2004) Comparative mapping of wheat chromosome 1AS which contains the tiller inhibition gene (*tin*) with rice chromosome 5S. Theor Appl Genet 109:1303-1310.

Temin RG Ganetzky B Powers PA Lyttle TW Pimpinelli S Dimitri P Wu CI Hiraizumi Y (1991) Segregation distortion in *Drosophila melanogaster*: genetic and molecular analyses. Am Nat 137:287-331.

Tsujimoto H (1994) Two new sources of gametocidal genes from *Aegilops longissima* and *Ae. sharonensis*. Wheat Inf Serv 79:42-46.

Tsujimoto H (1995) Gametocidal genes in wheat and its relatives. IV. Functional relationships between six gametocidal genes. Genome 38:283-289.

Tsujimoto H Tsunewaki K (1983) Genetic analyses on a gametocidal gene originated from *Aegilops aucheri*. In: Sakamoto S (ed) Proc 6th Int Wheat Genet Symp, Plant Germplasm Institute, Kyoto Univ, Kyoto, Japan. 1077-1081.

Tsujimoto H Tsunewaki K (1985a) Gametocidal genes in wheat and its relatives. II. Suppressor of the chromosome 3C gametocidal gene of *Aegilops triuncialis*. Can J Genet Cytol 27:178-185.

Tsujimoto H Tsunewaki K (1985b) Hybrid dysgenesis in common wheat caused by gametocidal genes. Jpn J Genet 60:565-578.

Tsujimoto H Noda K (1988) Chromosome breakage in wheat induced by the gametocidal gene of *Aegilops triuncialis* L.: Its utilization for wheat genetics and breeding. Proc. 7th Int. Wheat Genet Symp, Cambridge, 455-460.

Valárik M Linkiewicz AM Dubcovsky J (2006) A microcolinearity study at the earliness *per se* gene *Eps-A^{m}1* region reveals an ancient duplication that preceded the wheat-rice divergence. Theor Appl Genet 112:945-957.

Vos P Hogers R Bleeker M Reijans M Van De Lee T Hornes M Frijters A Pot J Peleman J Kuiper M Zabeau M (1995) AFLP: A new technique for DNA fingerprinting. Nuc Acid Res 23:4407-4414.

Wang C Zhu C Zhai H Wan J (2005) Mapping segregation distortion loci and quantitative trait loci for spikelet sterility in rice (*Oryza sativa* L.) Genet Res 86:97-106.

Werner JE Endo TR Gill BS (1992) Toward a cytogenetically based physical map of the wheat genome. Proc Natl Acad Sci USA 89:11307-11311.

Williams ND Miller JD Klindworth DL (1992) Induced mutations of a genetic suppressor of resistance to wheat stem rust. Crop Sci 32:612-616.

Xu Y Zhu L Xiao J Huang N McCouch SR (1997) Chromosomal regions associated with segregation distortion of molecular markers in F2, backcross, doubled haploid, and recombinant inbred populations in rice (*Oryza sativa* L.) Mol Gen Genet 253:535-545.

Yan L Loukoianov A Tranquilli G Helguera M Fahima T Dubcovsky J (2003) Positional cloning of the wheat vernalization gene *VRN1*. Proc Natl Acad Sci USA 100:6263-6268.

Yan L Loukoianov A Blechl A Tranquilli G Ramakrishna W SanMiguel P Bennetzen JL Echenique V Dubcovsky J (2004) The wheat *VRN2* gene is a flowering repressor down-regulated by vernalization. Science 203:1640-1644.

Yu J Hu S Wang J Wong GK-S Li S Lui B Deng Y Dai L Zhou Y Zhang X Cao M Liu J Sun J Tang J Chen Y Huang X Lin W Ye C Tong W Cong L Geng J Han Y Li L Li W Hu G Huang X Li W Li J Liu Z Li L J Liu Qi Q Liu J Li L Li T Wang X Lu H Wu T Zhu M Ni P Han H Dong W Ren X Feng X Cui P Li X Wang H Xu X Zhai W Xu Z Zhang J He S Zhang J Xu, J Zhang K Zheng X Dong J Zeng W Tao L Ye J Tan J Ren X Chen X He J Liu D Tian W Tian C Xia H Bao Q Li G Gao H Cao T Wang J Zhao W Li P Chen W Wang X Zhang Y Hu J Wang J Liu S Yang J Zhang G Xiong Y Li Z Mao L Zhou C Zhu Z Chen R Hao B Zheng W Chen S Guo W Li G Liu S Tao M Wang J Zhu L Yuan L Yang H (2002) A draft sequence of the rice genome (*Oryza sativa* L. ssp. indica). Science 296:79-92.

Zhang P Friebe B Lukaszewski AJ Gill BS (2001) The centromere structure in Robertsonian wheat-rye translocation chromosomes indicates that centric breakage-fusion can occur at different positions within the primary constriction. Chromosoma 110:335-334.

Appendix A - Gene evolution at the ends of wheat chromosomes.

Gene evolution at the ends of wheat chromosomes

Deven R. See*, Steven Brooks†, James C. Nelson*, Gina Brown-Guedira†, Bernd Friebe*, and Bikram S. Gill*‡

*Department of Plant Pathology and †Agricultural Research Services Department of Agronomy, United States Department of Agriculture, Kansas State University, Manhattan, KS 66506

Communicated by Koichiro Tsunewaki, Kyoto University, Kyoto, Japan, October 17, 2005 (received for review July 16, 2005)

Wheat ESTs mapped to deletion bins in the distal 42% of the long arm of chromosome 4B (4BL) were ordered *in silico* based on BLASTN homology against rice pseudochromosome 3. The ESTs spanned 29 cM on the short arm of rice chromosome 3, which is known to be syntenic to long arms of group-4 chromosomes of wheat. Fine-scale deletion-bin and genetic mapping revealed that 83% of ESTs were syntenic between wheat and rice, a far higher level of synteny than previously reported, and 6% were nonsyntenic (not located on rice chromosome 3). One inversion spanning a 5-cM region in rice and three deletion bins in wheat was identified. The remaining 11% of wheat ESTs showed no sequence homology in rice and mapped to the terminal 5% of the wheat chromosome 4BL. In this region, 27% of ESTs were duplicated, and it accounted for 70% of the recombination in the 4BL arm. Globally in wheat, no sequence homology ESTs mapped to the terminal bins, and ESTs rarely mapped to interstitial chromosomal regions known to be recombination hot spots. The wheat–rice comparative genomics analysis indicated that gene evolution occurs preferentially at the ends of chromosomes, driven by duplication and divergence associated with high rates of recombination.

rice | synteny

Comparative genomics in crop species aims to characterize the genomic changes associated with their evolutionary divergence. Although the major cereal crop species wheat (*Triticum aestivum* L.), maize (*Zea mays* L.), rice (*Oryza sativa* L.), barley (*Hordeum vulgare* L.), rye (*Secale cereale* L.), and sorghum (*Sorghum vulgare* L.) diverged from a common ancestor >65 million years ago, they still show a high degree of conservation of gross gene order (1–8). At the DNA-sequence level, a more complex picture emerges. In some regions microcolinearity is conserved among wheat, rice, and sorghum (9–11), whereas in others it is violated, mainly by duplications, intergenic expansions, and inversions (12–14). The full-genome sequence comparisons reveal that related genomes are not completely identical in their gene content. Among the sequenced plant genomes of *Arabidopsis* and rice, only 71% of predicted rice genes show homology with *Arabidopsis thaliana* genes (15). Gene evolution appears to occur nonuniformly across the genome (16–19). Recent comparison of human with chimpanzee genomes revealed regions of disproportionate gene divergence (20, 21). Other comparative studies suggest that regions of chromosomal instability, often located near the telomeres, are hot spots of chromosome evolution (22), harboring extensive rearrangements (23) and segmental gene duplications (22). The emergence of novel genes appears to be associated with the high rates of recombination characterizing these regions (24).

The first deletion-bin maps of wheat using restriction fragment length polymorphism markers revealed that the distal telomeric, gene-rich regions of wheat chromosome arms account for most of the recombination, although they constitute only a small fraction of the physical length (25, 26). More recently, high-density deletion-bin maps of the 21 chromosomes of wheat have been produced by restriction fragment hybridization of 5,762 ESTs to a panel of 101 wheat deletion stocks, each missing a different terminal portion of a chromosome arm (http://wheat.pw.usda.gov/NSF/data.html) (27). These maps have been aligned to the sequenced genome of rice. While aligning bin-mapped ESTs with the rice genome to identify ESTs for chromosome walking, we observed an apparent decline of synteny toward the end of the long arm of wheat chromosome 4B (4BL). This decline led us to examine the chromosomal distribution of genes present in wheat but not found in rice, using fine-scale deletion-bin and genetic mapping of ESTs aligned at relaxed stringency with rice genome sequence.

Results

The analyzed wheat and rice chromosomal regions are shown in Fig. 1. The wheat 4BL region spanning the distal 42% of the arm consisting of 4 deletion bins is 179 megabases (Mb) in size [based on relative chromosome size and total genome size as given by Gill *et al.* (28)] and has a genetic length of 146 cM (based on the International Triticeae Mapping Initiative map; see Fig. 3). The corresponding homologous region in rice identified by BLAST search spans 29 cM and 5.9 Mb of the distal end of chromosome 3 short arm. These homologous regions were colinear (Fig. 1) except for an inversion in a region on rice chromosome 3 between 14.8 and 17.9 cM relative to a wheat region encompassing the 4BL-3 deletion bin along with parts of flanking bins 4BL-11 and 4BL-8. The boundaries of the inversion harbor duplications. Of the three ESTs BG605572, BE442995, and BF473779 located at the inversion site in the proximal region of 4BL-11 (Fig. 2), the last two are duplicated in the proximal region (4BL-11), and all three have transposed duplications in the interstitial region (4BL-8).

Based on synteny and sequence homology, we defined three classes among the 101 4BL-5 bin-specific wheat ESTs (wESTs). Class I, colored blue in Fig. 2, included wESTs having homologs on rice chromosome 3. The wESTs (83% of the total) falling into this class could be further divided into three subclasses: "wheat–rice orthologs" (56%), consisting of colinear wESTs with $E < 1.0 \times 10^{-15}$ whose best BLASTN hit was with rice chromosome 3; "colinear paralogs" (11%), representing ESTs aligning at $E < 1.0 \times 10^{-15}$ with a chromosome 3 sequence but not as the first BLASTN hit, indicating a paralogous location; and "low-sequence similarity" (16%), giving rice chromosome 3 BLASTN alignments that, although showing E values of $>1.0 \times 10^{-15}$, were still consistent with the EST locations on the wheat deletion map. Class II wESTs, colored green in Fig. 2, aligned only with non-chromosome-3 rice sequences and comprised 6% of wESTs. Class III wESTs, colored red in Fig. 2 (see also Table 1, which is published as supporting information on the PNAS web site), comprised 11% of the total and were unique to wheat, showing no sequence homology (NSH) with any known rice sequence on either BLASTN or TBLASTX alignment.

The distribution of different classes of wESTs among the 4BL chromosome bins was not uniform. Depending on their relative position in relation to the telomere–centromere axis, we designated bins as proximal (lying on the centromere side, spanning 0.58–0.78% fraction length of 4BL), interstitial (spanning 0.78–0.95% fraction length of 4BL), and telomeric [spanning 0.95–1.0% of

Conflict of interest statement: No conflicts declared.

Abbreviations: NSH, no sequence homology; Mb, megabase; TC, tentative contig; wEST, wheat expressed sequence tag; BAC, bacterial artificial chromosome; CE, coefficient of exchange; 4BL, long arm of wheat chromosome 4B.

Data deposition: The sequence reported in this paper has been deposited in the GenBank database (accession no. DQ220740).

‡To whom correspondence should be addressed. E-mail: bsgill@ksu.edu.

www.pnas.org/cgi/doi/10.1073/pnas.0508942102

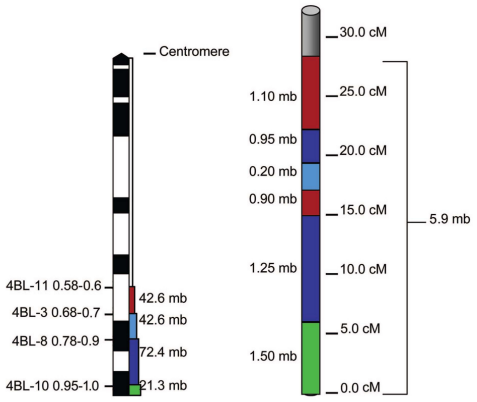


Fig. 1. Wheat deletion bin map of 4BL and the corresponding physical region of rice. (*Left*) The fraction length and estimated size (in DNA bases) of the physical deletion bins of wheat chromosome 4B used in this analysis. (*Right*) The corresponding region on the short arm of rice chromosome 3. The color-coded deletion bins and corresponding location on rice indicate the physical location and genetic distances correlating to the regions on the short arm of rice chromosome 3. We detected an inversion encompassing the 4BL-3 deletion bin along with parts of flanking bins 4BL-11 and 4BL-8 as seen by the broken segments of these two deletion bins in rice.

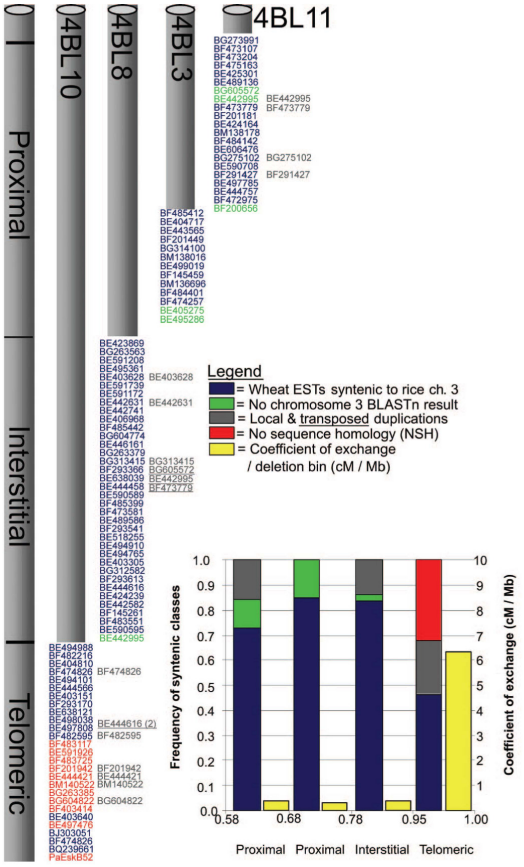


Fig. 2. Fine-scale deletion-bin map of the distal 42% of the wheat chromosome 4BL. wESTs are positioned on the four deletion lines based on their inferred genetic positions on the short arm of rice chromosome 3. EST labels are color-coded according to BLASTN *E* value. Blue ESTs have $E < 1.0 \times 10^{-15}$ with rice chromosome 3. Green ESTs have a BLASTN return from rice but no returns from chromosome 3. Gray ESTs show clustered and transposed gene duplications (gene duplications are underlined), revealed by restriction fragment length polymorphism analysis of the wESTs. Red ESTs showed no alignment with rice sequence at a BLASTN cutoff threshold of 10. The histogram shows the frequency of syntenic classes within each region and the CE within each bin.

fraction length including the telomere and the adjacent telomeric region (see Fig. 2)]. The interstitial region accounted for 69% of the wheat–rice ortholog subclass of colinear wESTs. The wESTs in the colinear, paralog class were randomly distributed throughout the deletion bins. The low-sequence similarity wESTs, although found in all bins, were more frequent in the telomeric deletion bin, 4BL-10. All NSH ESTs mapped in the telomeric bin with the exception of BG263385, which showed restriction fragment length polymorphism bands in the telomeric and proximal bins.

Of the wEST locus duplications identified (in gray, Fig. 2), 14 occurred within deletion bins and five occurred across deletion bins (Fig. 2, underlined). Although the duplications identified across deletion bins can be identified as transpositions, this experiment could not distinguish whether within-bin duplications were tandem or transposed. A few wESTs showed both within-bin (BE444616 and BE403414) and across-bin (BE442995 and BE473779) duplications, which may be associated with an inversion event described earlier. Duplication events also were not uniformly distributed over the wheat deletion map (Fig. 2), but they were more frequent in the telomeric region, with 27% of wESTs duplicated compared with only 8% in the interstitial region.

Similar to the distinctive distribution of wESTs, the relative frequency of recombination [calculated as coefficient of exchange (CE)] was skewed among the deletion bins (Fig. 2). Mapping in the (DS4S^{sh}(4B) × *Gc2mut#1*) × CS population revealed the genetic position of the NSH ESTs as well as their inferred point of origin between 1.1 and 2.5 cM in rice (Fig. 3). Because this population showed suppressed recombination proximal to the alien translocation, the International Triticeae Mapping Initiative population was used to characterize further the recombination surrounding the NSH genes. Genetic mapping revealed that 70% of the recombination in 4BL is localized to the telomeric bin, which constitutes 5% of the chromosome arm length. Comparative mapping showed that in 4DL as well 50% of the recombination occurred in the telomeric region. The corresponding telomeric region in rice chromosome 3 spans 1.5 Mb and has a CE value of 4.2 cM/Mb. In contrast, the corresponding 21.3-Mb region of wheat 4BL-10 has a CE value of 6.2 cM/Mb. Recombination dropped sharply in the proximal end of the telomeric region, to 0.3 cM/Mb in the interstitial region. In rice, this region corresponds to two blocks of synteny at 1.1 and 2.5 cM from the telomere. One microscale inversion was observed distal to the gene expansion, with a small block of inverted colinearity indicated by ESTs BJ303051, genetically mapping in rice at 2.2 cM, and BQ239661, at 1.1 cM. The proximal end of gene expansion was not as clearly defined, because this region contains multiple ESTs, BG313203, BE444616, and BE482595, which arose from paralogous duplications. The region is, however, flanked by syntenic ESTs: BE404810, BF482216, BG313505, BJ238027, and BE482595 (Fig. 2).

NSH EST sequences were further investigated for evidence of homology to rice or other species. A Southern blot experiment indicated that they were absent or diverged substantially from the rice genome and were not due to gaps caused by missing sequences

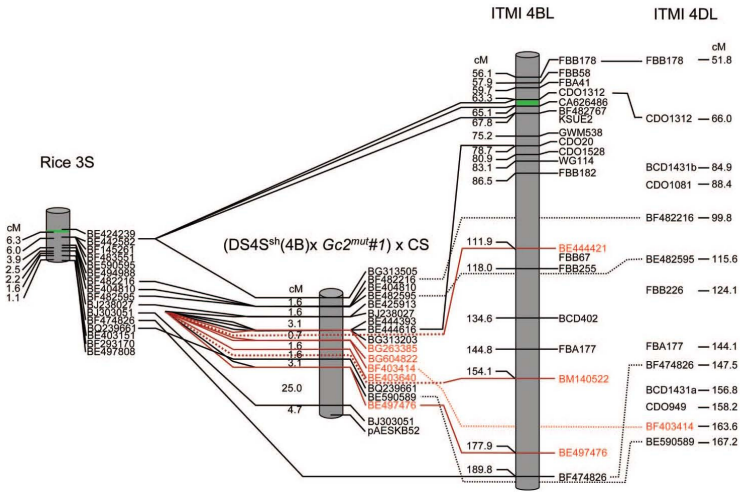


Fig. 3. The genetic maps of the distal 6.3 cM of the short arm of rice chromosome 3 and wheat 4BL and 4DL corresponding to the telomeric region in wheat reveal the genetic location of NSH ESTs.

in the published rice genome sequences. Although a wEST (BF474826) with 80% nucleotide similarity hybridized strongly to rice genomic DNA, BG263385, which has no amino acid similarity to rice, and BF201942, which has amino acid similarity only to maize, did not hybridize to rice (Fig. 5, which is published as supporting information on the PNAS web site). Table 1 describes the nucleotide and amino acid similarity found for NSH ESTs mapping to 4BL, half of which gave strong matches to sequences from other grass species. EST BE403640, originally designated as NSH, did not align with rice when BLASTed alone, but its tentative contig (TC) did align. This result is explained by the location of this EST in a part of the TC (the 3′ end of the ORF) lacking a sequence counterpart in rice.

To examine in more detail the genomic region around one of the NSH wESTs (BE497476), we sequenced 3.9 kb of a cosmid identified by hybridization of BE497476 to an *Aegilops sharonensis* library. Exon prediction programs FGENESH, GRAIL, and GENSCAN were used to identify exon and intron regions. The dicot model in FGENESH predicted five exons (Fig. 6, which is published as supporting information on the PNAS web site). Alignment with wheat TCs confirmed the exon predicted at ≈500 bp and the exon at ≈1,850 bp, the latter showing high similarity to the sequence of BE497476. The exon predicted at 3,260 bp matched no wESTs. The two main exons found encompassed the total length of the wheat TCs, suggesting that the genomic region sequenced spans the full length of this gene. As expected, TBLASTX analysis of this intron-containing 3.9 kb of genomic DNA gave the same results as those from the TCs: no homology with rice but homology with barley and sugarcane.

Genomewide Homology Search of NSH ESTs. Of the 290 NSH wESTs showing no BLASTN match with rice bacterial artificial chromosomes (BACs) or ESTs, 179 were members of TCs and 111 were singletons. Two NSH wESTs, one a TC and another a singleton, were removed after a search of the TREP and the Institute for Genomic Research repeat databases. When aligned at the amino acid level against rice, 54 of the 288 NSH ESTs gave significant E values $< 1.0 \times 10^{-5}$). Of the remaining 234 sequences, 122 (52%) aligned at the amino acid level with ESTs from plant species other than rice. The best-represented species was *Hordeum* (barley) with 86 (37%) matches, whereas *Saccharum* (sugarcane) and *Zea* (maize) matched more than 10 hits each, all of these graminaceous species being well represented in dbEST with EST numbers ≈300,000. Dicotyledonous species *Arabidopsis* and *Glycine* (soybean) with similarly high EST representation yielded only 10 matches between them. The 122 NSH ESTs, 58 singletons plus 54 TCs showed no match to any other plant species at $E < 1.0 \times 10^{-5}$.

Chromosome and Genome Distribution of NSH ESTs. The 5% of bin-mapped ESTs designated as NSH were in excess in the terminal regions of most wheat chromosomes, consistent with the 4BL distribution (Fig. 4). The frequencies of NSH ESTs (at $E \geq 10$) were higher ($P \approx 0.01$) in terminal than in nonterminal deletion bins after correction for overall EST distribution. This contrast grew more marked as E-value thresholds for declaring NSH were lowered. At the most liberal threshold of $E \geq 0.1$, the excess was significant at ($P < 0.00002$), and the number of ESTs assigned as NSH was triple that satisfying the $E \geq 10$ cutoff. Tests of NSH frequencies against those expected from overall EST frequencies, where each test included all bins on a single arm, showed deviation from expectation (at $P \leq 0.05$) on only one-fourth of the 42 arms (results not shown). When the same test was made for bin NSH frequencies individually against the summed NSH frequencies over the other bins in the same arm, approximately one-fifth deviated from expectation (at $P \leq 0.05$), and these corresponded in general to the terminal bins, as may be seen from the longer bars in Fig. 4. Although all ESTs were more abundant ($P < 0.0001$) in the B genome (0.36 of total NSH ESTs) than in the A and D genomes (where they occurred in equal proportions), NSH ESTs showed a still greater excess in the B genome than expected from the overall EST distribution ($P < 0.05$ to $P < 0.001$ depending on the E-value cutoff applied).

Discussion

Reducing Conservatism in Synteny Searching. The conservative approach of accepting only "best-BLAST-hit" high-stringency sequence alignments for characterizing wheat–rice synteny by plotting correspondences across genomes (8) may underestimate synteny and lose information provided by its absence. Here, substitution of the criterion "best rice-chromosome-3 BLAST hit" increased the per-

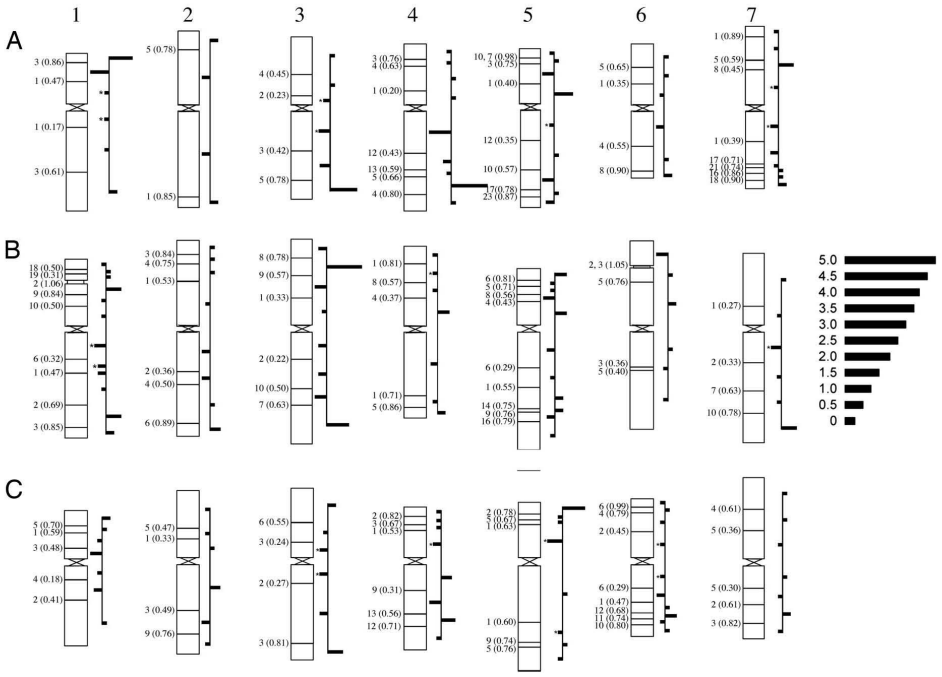


Fig. 4. Distribution trend in NSH wESTs in deletion bins along chromosome arms. Bars represent negative $\log_{10}$ of *P* values resulting from a χ^2 test for each bin that tested the null hypothesis that the proportion, with respect to that chromosome arm, of NSHs mapping to that bin is equal to that of all ESTs mapping to that bin. Bars extend to right for bins in which NSH frequency exceeds expectation and to left for those in which it is lower than expectation (asterisks indicate that the bin contained no observed NSHs).

centage of informative ESTs from 57% to 83%. The linear orders of the wheat deletion bins and rice BACs containing these ESTs were consistent (with the exception of the inversion already described), suggesting that, for this genomic region at least, wheat–rice colinearity is conserved at a much higher resolution than previously proposed (8). Possibly the most striking lesson is that the genomic distribution of wheat genes that match no rice sequence (and vice versa) may be equally as important to an understanding of genome divergence as that of genes common to these species.

Random vs. Localized Genome Evolution. Are all regions of the genome and chromosomes equally capable of undergoing rearrangements, such as inversions, translocations, insertion/deletions (indels), duplications, or DNA sequence divergence, over the evolutionary time scale? The emerging picture from comparative genomics is revealing genomic/chromosomal regions of either unusual conservation or dynamic change (22). For example at the level of chromosomes, synteny is best conserved between chromosomes of wheat groups 3 and 6 to rice chromosomes 1 and 2, respectively, breaking down only in centromeric regions. In contrast, group 5 chromosomes of wheat are highly rearranged relative to rice and are syntenic to parts of rice chromosomes 12, 9, and 3 (8, 29). Along the 4BL arm, which is essentially syntenic with rice chromosome 3 short arm (8), fine-scale deletion-bin mapping and wheat–rice sequence comparison has now allowed us to distinguish regions of gene conservation and gene evolution. The interstitial region showed the highest degree of conservation with rice. Of the 69% of orthologs reported in this region, 36% returned only chromosome 3 BLASTN results, indicating little if any gene duplication in this region either in rice or wheat. The telomeric region showed the lowest percentage of orthologs, which together with the duplication of 27% of the ESTs in this region and the excess of NSH ESTs indicated that this region is under positive selection contributing to divergence (16, 22, 30). In mammals and yeast, the telomeric regions are dynamic, undergoing duplications and harboring species-specific genes (23, 31, 32). The rapid evolution occurring in the telomeric regions may be due to the plasticity of this region as observed through duplications and ectopic recombination yielding new genes (24) and to the intrinsic high rates of recombination in these regions (see below). Over longer evolutionary time spans, such regions may become relocated in the genome so that a clear distinction between localized and random modes of evolution may be difficult to make.

Additional evidence of the plasticity within telomeric regions can be observed in the wheat–rice colinear region containing the grain hardness genes puroindolines *pinA* and *pinB* and the grain softness protein gene *Gsp* (33). These genes showed no homology with rice at the nucleotide level. However, *Gsp*, but not the puroindolines, showed a match at the amino acid level to a rice sequence predicted to be a nonfunctional gene, possibly indicating loss of this gene in rice. It is hypothesized that *Gsp* gene after the splitting of the wheat rice lineage was duplicated in the wheat lineage and gave rise to the puroindoline genes (33). A similar scenario has been proposed for the evolution of gluten genes that control bread-making properties in wheat and are missing in rice, but both lineages share related globulin genes (34).

Genetic Recombination and the Genomic Distribution of Divergent ESTs. A discussion of the role of recombination in gene evolution must distinguish between different types of recombination: general,

site-specific, ectopic, and gene conversion. General recombination (also called crossover recombination) occurs between homologous pairs of chromosomes (orthologous sequences) leading to chiasmate association that ensures proper chromosome segregation and gene reassortment. General recombination also maintains chromosome integrity; lack of recombination in regions, such as centromeres and human male chromosomes, can lead to rapid sequence divergence (22). Site-specific recombination is associated with the movement of transposable (cut-and-paste) or retrotransposable (copy-and-paste) elements and produces the commonly observed indel polymorphisms and paralogous gene duplications and perhaps other chromosomal rearrangements. Most of the transposed duplications observed in 4BL must have arisen from site-specific recombination. Ectopic recombination between duplicated sequences on the same chromosome or nonhomologous chromosomes can produce inversions or translocations. The observed inversion flanking duplicated ESTs (Figs. 1 and 2) most likely arose from ectopic intrachromatid recombination between segmental duplications. Intragenic conversion-type recombination can lead to rapid gene divergence, as was documented for the *Lr21* locus located in the telomeric region of 1DS of wheat (35). Evidence is mounting that telomeres are hot spots for all types of recombination (24) and that "extraordinary genomic churning . . . has a key role in rapidly creating phenotypic diversity over evolutionary time" (23).

In the present study, the trend of accumulation of NSH ESTs at the ends of chromosomes may be most prudently explained by the recombination gradients along the lengths of chromosomes of wheat (26, 36) and other plant species (15, 37, 38), and, as a result, most recombination occurs in the terminal regions. For 4BL, 70% of the recombination occurred in a small fraction of the 5% of the physical length of this arm represented by the telomeric deletion bin. The sharp recombination boundary proximal to the group of NSH ESTs suggests that the division between high and low recombination is reflected by evolutionary conservation, with low recombination maintained in conserved regions and evolutionary divergence taking place in high-recombination regions. A similar observation for wheat chromosome 3 and rice chromosome 1 led Akhunov *et al.* (39) to conclude that chromosomes lose synteny from each other at a faster rate in high-recombination regions. In *Plasmodium vivax* the telomerically located *var* genes show elevated recombination, which promotes the diversification of antigenic and adhesive phenotypes (40). Nonterminal regions of NSH EST concentration along the chromosome length might be explained by recombination hot spots (41). Increased frequency in the nonterminal 4AL5 deletion bin could be explained by the 4A, 5A, 7B cyclic translocation (42, 43) that moved the 5AL terminal segment to this site.

Along with recombination, mating system and evolutionary history may also influence the accumulation of NSH ESTs at the genome level. The wheat B genome, richer in NSH ESTs than the A and D genomes, originated from an outcrossing species closely related to *Aegilops speltoides*, whereas the other two genomes originated from self-pollinating species. After investigating synteny perturbation among the different genomes of wheat, Akhunov *et al.* (39) attributed the lower synteny levels in B-genome chromosomes to the higher recombination per generation characterizing the cross-pollinating mating system. On the evolutionary time scale we are considering (44), divergence between genomes within the same nucleus of polyploid wheat has not been accelerated by the whole genome duplication. If divergence were accelerated because of polyploidy, then the A and B genomes would be expected to show more gene novelty than the more recently acquired D genome.

Sources of Error in Evolutionary Speculation Based on Nonhomology. The apparent absence of a wEST sequence in rice did not always mean absence of the parent gene in rice or *de novo* origin in wheat. From the initial list of 290 ESTs assigned as NSH on this basis, 54 were later dropped when the contigs to which they belonged proved to align with rice ESTs. In at least the case of EST BE403640, the corresponding rice sequence was simply absent from the full-length wheat TC. In other cases, genes diverged more at the nucleotide level than at the amino acid level. The cases for which species more distant than rice shared ESTs with wheat but not with rice suggest gene loss in rice rather than gain in wheat. It would be of interest to study the distribution of these events in the rice genome. It might be objected that some of the missing genes could represent gaps in the rice sequence. For at least rice chromosome 3, there were no such gaps. In any case, our estimate of ≈5% NSH ESTs coincides with the proportion reported recently based on BLAST alignment of >4,000 full-length wheat cDNAs against rice.

Are these sequences all genes? Recent opinion articles (45, 46) caution that 30% or more of rice sequences annotated as genes, besides having unusual GC composition, show signatures of transposable elements and probably represent low-copy long-terminal-repeat retrotransposons. BLAST searches of our putative wheat-unique gene sequences against Triticeae Repeat Sequence Database and the Institute for Genomic Research repeat database resulted in rejection from the NSH category of only one TC and one singleton EST with E values as low as 10^{-5}. We could not reliably characterize G/C ratios between codon positions (46), as is feasible when large stretches of sequence are available for computational annotation. However, NSH sequences were overall significantly less GC-rich (47.6% vs. 52.3%; $P \ll 0.0001$) than other mapped ESTs. The proportion of NSH TCs and singleton ESTs matching loci in two or three homoeologous groups was ≈20%, similar to the 17% reported (27) for all physically mapped ESTs. Rapidly evolving low-copy retroelements would not be expected to retain homoeologous relationships after genome divergence. The 53% of TCs and 47% of singleton ESTs with similarity to cereal genomes other than rice are unlikely to represent conserved retroelements, and currently available evidence does not suggest that the sequences unique to wheat do either.

Conclusion. Against the background of the wheat deletion map, wEST alignments with rice genomic sequence afford a picture of the synteny and colinearity between the genomes of these grass relatives. When alignment stringencies are relaxed, a finer-scale picture can be drawn. It emerges that most ESTs that fail to find rice homologs are located near the ends of wheat chromosomes. These observations support a theory that the higher recombination rates in these genomic regions, by promoting gene duplication and subsequent divergence, make these regions hot spots of gene evolution.

Materials and Methods

Sequence Analysis. FASTA sequences from wESTs previously mapped to the 4BL5 deletion bin were compared by BLASTN against all rice BAC and P1 artificial chromosome sequences in GenBank at the default settings for WU-BLAST (Washington University BLAST), including a homology rejection threshold of $E \geq 10$. E values were recorded for all ESTs. The 138 ESTs aligning with BACs from rice chromosome 3 were presumptively ordered in wheat according to the relative positions of the BACs on chromosome 3. A reverse approach was taken for wESTs BJ238027, BQ239661, BJ303051, and CA626486, which were identified by BLAST of rice-chromosome-3 BAC putative ORFs against a wEST database (http://tigrblast.tigr.org/tgi).

The chromosomal distribution in wheat of NSH ESTs was determined by a WU-BLASTN search of 5,300 deletion-bin-mapped wESTs against rice BAC/P1 artificial chromosome sequences. (We call these ESTs NSH rather than "nonsyntenic" to distinguish them from genes having homologs on other rice chromosomes than predicted by synteny). Goodness-of-fit tests of distribution over the deletion map were made by χ^2 on the null hypothesis that NSH

ESTs occur in deletion bins at the same relative frequencies as all mapped ESTs.

To find sequence matches that might be missed by short alignments of ESTs or involve species other than rice, we searched at the amino acid level the 10 NSH ESTs found on 4BL and their TCs from the Institute for Genomic Research wEST assembly release 8 against the GenBank nr (GenBank nonredundant), HTGS (high-throughput genomic sequences), PDB (Protein Data Bank), and dbEST (EST database) databases by TBLASTX. To exclude false positives from 3′ UTRs, we confirmed these results by BLASTX of only the ORFs as predicted with the National Center for Biotechnology Information's ORF Finder. For each of the 280 NSH ESTs not from 4BL, we searched its TC (or the EST itself if it was a singleton) at the amino acid level by TBLASTX against all plant ESTs in dbEST, except for *Triticum* species and against the rice BAC/P1 artificial chromosomes. For each of the plant species with at least one EST, we tabulated the number of NSH ESTs that aligned at $E < 1.0 \times 10^{-5}$. To identify putative retroelements, we searched all TCs and singleton ESTs at the amino acid and nucleotide levels against the Triticeae Repeat Sequence Database (http://wheat.pw.usda.gov/ITMI/Repeats/index.shtml) and the Institute for Genomic Research Gramineae Repeat Database v3.1.

Deletion-Bin and Genetic Mapping. For deletion-bin mapping, EST sequences assigned to the 4BL-5 bin (http://wheat.pw.usda.gov/NSF/data.html) were hybridized to DNA of deletion lines 4BL-10-0.95, 4BL-8-0.78, 4BL-7-0.70, 4BL-3-0.68, and 4BL-11-0.58 (47), affording finer coverage than the original map. The deletion bin between 0.68 and 0.70 characterized by 4BL7-0.70, with only two ESTs (BG313203 and a transposed duplicated EST BG263385), was removed from the analysis. The presence–absence pattern of DNA hybridization signals among the stocks allows assignment of EST loci to one or more specific deletion bins (27).

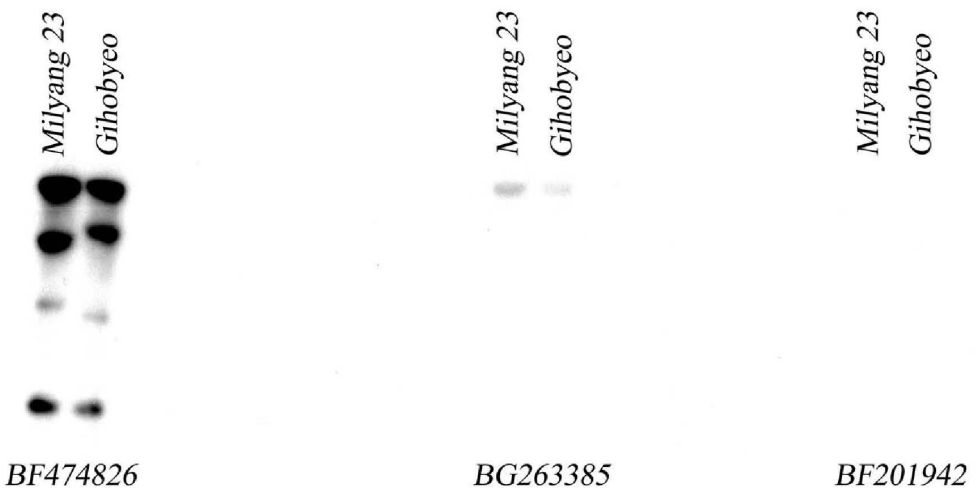
Fine-scale genetic mapping in the telomeric region was done with 180 testcross lines derived from a cross between a disomic substitution line from *Ae. sharonensis* DS4S^{sh}#7(4B) and homozygous translocation stock T4BS.4BL-4S^{sh}#1L plants (48) followed by a cross of the F_1 with CS. The second genetic mapping population used was a 50-line subset of the recombinant inbred 150-line International Triticeae Mapping Initiative population Synthetic × Opata 85 (49).

To increase polymorphisms for deletion-bin mapping, two sets of blots with restriction enzymes EcoRI or HindIII were used in all assays. For the rice Southern blots, 500 ng of genomic DNA from two varieties (Milyang 23, a Japonica/Indica hybrid, and Gihobyeo, a Japonica variety) was digested with EcoRI. All restriction fragment length polymorphism conditions were the same as used for wheat (27).

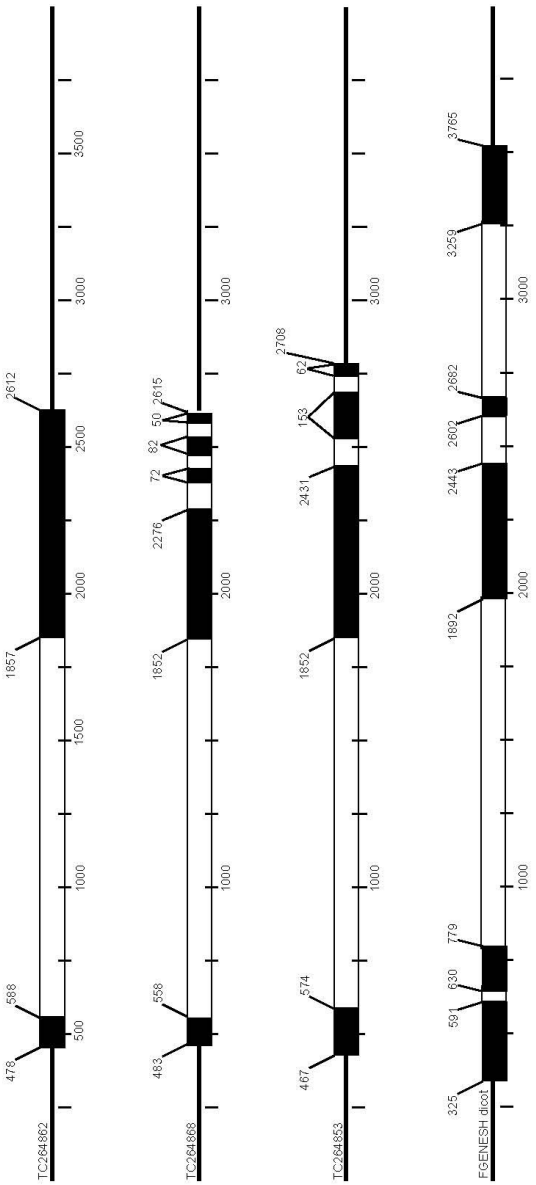
Sequences from ESTs and TCs were used for PCR primer design with MACVECTORTM 6.5.3 (Oxford Molecular, Madison, WI). Markers used in genetic mapping were screened by single-strand conformational polymorphism technology (50). Staining was done with a standard silver-staining protocol (51). Mapping was done with MAPMAKER 2.0 (52). An *Ae. speltoides* telomeric repeat probe, PaEskB52 (53), which hybridizes to the telomeric region of chromosome arm 4S^{sh} in *Ae. sharonensis* but not *T. aestivum* was converted to an sequence-tagged site marker and used as a genetic marker to define the chromosome end. The CE was calculated for each deletion bin as the recombination observed for the bin divided by its physical length.

We thank Robin Buell for reading the manuscript and suggesting some of the BLAST searches and reviewers and editors for pointing out the need to address potential error from several sources, including retrotransposon misannotation. This work was partially funded by a special U.S. Department of Agriculture grant to the Wheat Genetic and Genomic Resources Center and by National Science Foundation Grant DBI-9975989. D.R.S. was supported by a U.S. Department of Agriculture National Needs fellowship. This article is contribution number 04-315-J from the Kansas Agricultural Experimental Station.

1. Hulbert, S. H., Richter, T. E., Axtell, J. D. & Bennetzen, J. L. (1990) *Proc. Natl. Acad. Sci. USA* **87,** 4251–4255.
2. Ahn, S., Anderson, J. A., Sorrells, M. E. & Tanksley, S. D. (1993) *Mol. Gen. Genet.* **241,** 483–490.
3. Kurata, N., Moore, G., Nagamura, Y., Foote, T., Yano, M., Minobe, Y. & Gale, M. D. (1994) *Biotechnology* **12,** 276–278.
4. Moore, G., Devos, K. M., Wang, Z. & Gale, M. D. (1995) *Curr. Biol.* **5,** 737–739.
5. Van Deynze, A. E., Dubcovsky, J., Gill, K. S., Nelson, J. C., Sorrells, M. E., Dvořák, J., Gill, B. S., Lagudah, E. S., McCouch, S. R. & Appels, R. (1995) *Genome* **38,** 45–59.
6. Devos, K. M. & Gale, M. D. (1997) *Plant Mol. Biol.* **35,** 3–15.
7. Gale, M. D. & Devos, K. M. (1998) *Proc. Natl. Acad. Sci. USA* **95,** 1971–1974.
8. Sorrells, M. E., Rota, M. L., Kandianis, C. E., Greene, R. A., Kantety, R., Munkvold, J. D., Miftahudin., Mahmoud, A., Ma, X., Gustafson, P. J., *et al.* (2003) *Genome Res.* **13,** 1818–1827.
9. Dubcovsky, J., Ramakrishna, W., SanMiguel, P., Busso, C. S., Yan, L., Shiloff, B. & Bennetzen, J. (2001) *Plant Physiol.* **125,** 1342–1353.
10. SanMiguel, P., Ramakrishna, W., Bennetzen, J. L., Busso, C. S. & Dubcovsky, J. (2002) *Funct. Integ. Genomics* **2,** 70–80.
11. Ramakrishna, W., Dubcovsky, J., Park, Y. J., Busso, C. S., Emberton, J., SanMiguel, P. & Bennetzen, J. L. (2002) *Genetics* **162,** 1389–1400.
12. Feuillet, C. & Keller, B. (1999) *Proc. Natl. Acad. Sci. USA* **96,** 8265–8270.
13. Gaut, B. S. (2002) *New Phytol.* **154,** 15–28.
14. Guyot, R., Yahiaoui, N., Feuillet, C. & Keller, B. (2004) *Funct. Integ. Genomics* **4,** 47–58.
15. International Rice Genome Sequencing Project (2005) *Nature* **436,** 793–800.
16. Long, M. Y. & Langley, C. H. (1993) *Science* **260,** 91–95.
17. Carlson, M. & Botstein, D. (1983) *Mol. Cell. Biol.* **3,** 351–359.
18. Louis, E. J., Naumova, E. S., Lee, A., Naumov, G. & Haber, J. E. (2002) *Genetics* **136,** 789–802.
19. Treles, F. R., Tarrio, R. & Ayala, F. J. (2003) *Proc. Natl. Acad. Sci. USA* **100,** 13413–13417.
20. Britten, R. J. (2002) *Proc. Natl. Acad. Sci. USA* **99,** 13633–13635.
21. Anzai, T., Shiina, T., Kimura, N., Yanagiya, K., Kohara, S., Shigenari, A., Yamagata, T., Kulski, J. K., Naruse, T. K., Fujimori, Y., *et al.* (2003) *Proc. Natl. Acad. Sci. USA* **100,** 7708–7713.
22. Eichler, E. E. & Sankoff, D. (2003) *Science* **301,** 793–797.
23. Kellis, M., Patterson, N., Endrizzi, M., Birren, B. & Lander, E. S. (2003) *Nature* **423,** 241–254.
24. Mefford, H. C. & Trask, B. J. (2002) *Nat. Rev. Genet.* **3,** 91–102.
25. Werner, J. E., Endo, T. R. & Gill, B. S. (1992) *Proc. Natl. Acad. Sci. USA* **89,** 11307–11311.
26. Gill, K. S., Gill, B. S. & Endo, T. R. (1993) *Chromosoma* **102,** 374–381.
27. Qi, L. L., Echalier, B., Chao, S., Lazo, G. R., Butler, G. E., Anderson, O. D., Akhunov, E. D., Dvořák, J., Linkiewicz, A. M., Ratnasiri, A., *et al.* (2004) *Genetics* **168,** 701–712.
28. Gill, B. S., Friebe, B. & Endo, T. R. (1991) *Genome* **34,** 830–839.
29. La Rota, M. & Sorrells, M. E. (2004) *Funct. Integr. Genomics* **4,** 34–46.
30. Akhunov, E. D., Goodyear, A. W., Geng, S., Qi, L. L., Echalier, B., Gill, B. S., Miftahudin, J., Gustafson, P., Lazo, G., Chao, S., *et al.* (2003) *Genome Res.* **5,** 753–763.
31. Trask, B. J., Friedman, C., Martin-Gallardo, A., Rowen, L., Akinbami, C., Blankenship, J., Collins, C., Giorgi, D., Iadonato, S., Johnson, F., *et al.* (1998) *Hum. Mol. Genet.* **1,** 13–26.
32. Naumov, G., Turakainen, H., Naumova, E., Aho, S. & Korhola, M. (1990) *Mol. Gen. Genet.* **224,** 119–128.
33. Chantret, N., Cenci, A., Sabot, F., Anderson, O. & Dubcovsky, J. (2004) *Mol. Gen. Genomics* **271,** 377–386.
34. Kong, X. Y., Gu, Y. Q., You, F. M., Dubcovsky, J. & Anderson, O. D. (2004) *Plant Mol. Biol.* **54,** 55–69.
35. Huang, L., Brooks, S. A., Li, W., Fellers, J. P., Trick, H. N. & Gill, B. S. (2003) *Genetics* **164,** 655–664.
36. Dvořák, J., Ming-Chen, L. & Yang, Z. L. (1998) *Genetics* **148,** 423–434.
37. Stephan, W. & Langley, C. H. (1998) *Genetics* **150,** 1585–1593.
38. Schmidt, R., West, J., Love, K., Lenehan, Z., Lister, C., Thompson, H., Bouchez, D. & Dean C. (1995) *Science* **270,** 480–483.
39. Akhunov, E. D., Akhunova, A. R., Linkiewicz, A. M., Dubcovsky, J., Hummel, D., Lazo, G., Chao, S., Anderson, O. D., Jacques, D., Qi, L. L., *et al.* (2003) *Proc. Natl. Acad. Sci. USA* **100,** 10836–10841.
40. Freitas-Junior, L. H., Bottius, E., Pirrit, L. A., Deitsch, K. W., Scheidig, C., Guinet, F., Nehrbass, U., Wellems, T. E. & Scherf, A. (2000) *Nature* **407,** 1018–1022.
41. Faris, J. D., Haen, K. M. & Gill, B. S. (2000) *Genetics* **154,** 823–835.
42. Naranjo, T., Roca, A., Goicoechea, P. G. & Giraldez, R. (1987) *Genome* **29,** 873–882.
43. Mickelson-Young, L., Endo, T. R. & Gill, B. S. (1995) *Theor. Appl. Genet.* **90,** 1007–1011.
44. Huang, S., Sirikhachornkit, A., Su, X., Faris, J., Gill, B., Haselkorn, R. & Gornicki, P. (2002) *Proc. Natl. Acad. Sci. USA* **99,** 8133–8138.
45. Jabbari, K., Cruveiller, S., Clay, O., Le Saux, J. & Bernardi, G. (2004) *Trends Plant Sci.* **9,** 281–285.
46. Bennetzen, J. L., Coleman, C., Liu, R., Ma, J. & Ramakrishna, W. (2004) *Curr. Opin. Plant Biol.* **7,** 732–736.
47. Endo, T. R. & Gill, B. S. (1996) *J. Hered.* **87,** 295–307.
48. Friebe, B., Zhang, P., Nasuda, S. & Gill, B. S. (2003) *Chromosoma* **111,** 509–517.
49. Nelson, J. C., Van Deynze, A. E., Autrique, E., Sorrells, M. E., Lu, Y. H., Merlino, M., Atkinson, M. & Leroy, P. (1995) *Genome* **38,** 516–524.
50. Hayashi, K. & Yandell, D. W. (1993) *Hum. Mutat.* **2,** 338–346.
51. Sambrook, J., Fritsch, E. F. & Maniatis, T. (1989) *Molecular Cloning* (Cold Springs Harbor Lab. Press, Woodbury, NY).
52. Lander, E. S., Green, P., Abrahamson, J., Barlow, A., Daly, M. J., Lincoln, S. E. & Newburg, L. (1987) *Genomics* **1,** 174–181.
53. Anamthawat-Jónsson, K. & Heslop-Harrison, J. S. (1993) *Mol. Gen. Genet.* **240,** 151–158.



Supplemental figure 5



Supplemental Figure 6

Appendix B - Microarray results

Table B.1 *Gc2*/- over *Gc2^{mut}#1*/-

Probe set ID	*GC2* E	*GC^{mut}#1* E	*GC2* L	*GC^{mut}#1* L
Ta.12392.1.S1_at	4	125.4	8.2	184.1
TaAffx.13929.1.A1_at	6	121.1	5.1	62.4
Ta.22083.1.S1_at	6.7	78.7	4.8	56.2
Ta.16043.1.S1_at	7.2	78.2	6.4	81.3
TaAffx.24740.1.S1_at	3.1	66.6	6.7	96.9
Ta.8447.1.S1_x_at	4.4	61.1	2.8	50.3
TaAffx.53897.1.S1_at	3.7	56.2	8	109.9
TaAffx.121275.1.A1_at	4.2	47.6	4.8	59.8
TaAffx.87070.1.S1_at	4.2	43.5	6.3	110.2
Ta.22090.1.S1_at	1.6	40.9	2.1	25
TaAffx.92004.1.A1_at	3.7	40	5.4	63
TaAffx.59271.1.S1_at	3.2	38.7	3	33.2
TaAffx.31283.1.S1_at	1.7	37.1	1.5	28.6
TaAffx.26265.1.S1_at	2.7	35.7	1.6	44.6
TaAffx.105562.1.S1_at	2	35.7	2.2	24.6
Ta.14274.2.S1_at	2.9	32.7	1.3	50
TaAffx.22.1.A1_at	1.4	31.2	4	71.5
TaAffx.7116.1.S1_at	1.5	31.1	1.1	12.2
TaAffx.32098.1.S1_at	2.3	29.2	1.3	14
TaAffx.16883.2.S1_at	1.8	28.9	1.7	29.3
TaAffx.57990.1.S1_at	1.7	27.9	1.1	46.5
TaAffx.9188.1.S1_at	2.4	25.6	1.4	48.2
TaAffx.116491.3.S1_at	1.4	23.1	3.1	49
TaAffx.54207.1.S1_at	1.6	20.2	4	46.9

Table B.2 *Gc2^{mut}#1*/- over *Gc2*/-

Probe set ID	*GC2* E	*GC^{mut}#1* E	*GC2* L	*GC^{mut}#1* L
TaAffx.92710.1.A1_s_at	22.9	2	38.1	1.1
Ta.17978.1.S1_at	12.7	1	14	1.1
Ta.18672.2.S1_x_at	17.7	1.2	19.6	1.1
TaAffx.108845.2.S1_at	21.6	1.1	19.4	1.4
TaAffx.80217.2.S1_at	46	3.7	44.1	4.1
TaAffx.81628.1.S1_at	20	1.7	20.5	1.7
TaAffx.82452.1.S1_at	30.7	2.7	33.1	2.6
TaAffx.107383.1.S1_at	32.5	1.2	29.1	1.9
TaAffx.5632.1.S1_at	47.9	2.1	36.2	2.7
TaAffx.5003.1.S1_at	47.5	0.7	50.8	2.2
Ta.22610.2.S1_at	34.6	1.2	25.1	1.7
TaAffx.120036.1.S1_at	23.3	1.5	28	2.1
Ta.27548.1.S1_at	20.4	1.6	33.4	2.6
TaAffx.62591.1.S1_at	18.5	0.9	31.8	2.9
TaAffx.91530.1.S1_at	49.6	4.1	61.6	5.4
TaAffx.84214.1.S1_at	51.9	4.8	77.8	6.4
TaAffx.31991.1.S1_at	38.8	3.6	55.8	5
TaAffx.81498.1.S1_at	49.8	2.5	61.7	6.1
TaAffx.112550.1.S1_at	59.1	5	39.4	2.4
TaAffx.110201.1.S1_at	74.8	7.2	55	4.1

Table B.3 *Gc2^{mut}#1*/- early over *Gc2*/- early

Probe set ID	*GC2* E	*GC^{mut}#1* E	*GC2* L	*GC^{mut}#1* L
Ta.24618.2.S1_s_at	832.1	35353.8	39500.3	43462.1
TaAffx.59835.1.S1_x_at	98.5	34703.9	37961.2	34047.1
Ta.3079.1.S1_x_at	695.8	33074.4	37331.3	35805.8
Ta.3542.1.S1_at	90.2	30812.1	35292.2	36279.9
Ta.3485.1.S1_at	238.9	30260.6	38044.2	35612.4
Ta.3079.2.S1_s_at	1658.8	30082.5	35315.8	37610.6
Ta.3079.1.S1_at	503.3	29107.8	30368.7	29334.5
Ta.3079.2.S1_x_at	797.1	26585.3	29145.3	33233.3
Ta.24618.2.S1_at	230.7	23442.7	31724.9	28989.9
AFFX-Ta_Sucsyn_3_at	1796.1	22916.4	32064.3	21863.3
Ta.1725.1.S1_at	733.7	20608.5	24098.1	23456.3
Ta.4274.1.S1_at	1425.2	18196.4	27655.5	18408.8
Ta.4536.1.A1_at	1283.9	16242.2	25622.9	13728.2
TaAffx.106036.1.S1_at	134.4	15734.3	21137.3	7713.4
TaAffx.10772.1.A1_at	1132.8	15628.6	17539	16105.6
Ta.10648.1.S1_x_at	754	15548.7	19637.7	12018.6
Ta.4411.1.S1_at	277	13899.7	20098.1	15994.1
Ta.3409.1.S1_at	4.1	13614.2	18809.5	7524.4
TaAffx.78658.1.S1_at	512.3	13461.5	18939.2	14442.2
TaAffx.105858.1.S1_at	47.5	13355.4	24290.7	16876.6
AFFX-Ta_Sucsyn_M_at	533.6	12947.5	17169.3	7253.4

TaAffx.12525.2.A1_at	314	12665.5	17228.1	8790.2
Ta.8871.1.A1_at	166.1	12259.6	18247.3	9169
Ta.19013.1.S1_at	128	12139.5	19216.4	10563.5
Ta.11015.1.S1_at	174.9	11482	14692.2	11243.2
TaAffx.88201.1.A1_at	233.1	11425.7	12004.4	6876.4
TaAffx.9509.1.S1_at	9.5	10798.6	27621.6	19657.8
TaAffx.93263.1.A1_at	135	10527.9	18713.5	11695.7
Ta.998.1.A1_at	950.1	10274	11536.5	10984.2
Ta.11362.1.A1_at	665.1	8944.7	13627.7	10687.6
TaAffx.10772.1.A1_s_at	766.3	8646.6	11754.8	9858
Ta.18070.1.S1_at	752.2	8319.7	5512.1	3662.7
TaAffx.86985.1.S1_at	34.9	8252.1	16487.1	11370.4
Ta.14461.1.S1_x_at	470.3	8060	10911.2	4233.2
Ta.26042.1.S1_at	588.4	7838.6	9644.9	8087.7
TaAffx.92366.1.S1_at	310	7550.6	11300.3	4145
Ta.24037.1.A1_at	24.3	7511.7	10621.4	3025.4
Ta.8871.2.S1_at	10.3	7401.5	8784.2	3963.7
TaAffx.114330.1.S1_at	11.1	7320.9	13385.4	7450.4
Ta.92.1.S1_s_at	395	7277.6	12085	4978.3
Ta.4219.2.S1_a_at	18.3	7239.1	24425.6	20169
TaAffx.12525.1.S1_at	141.6	7107.3	8558.5	4193.5
Ta.5563.1.S1_at	139.9	6873.1	11086.8	7409
Ta.3869.1.S1_at	57.1	6702	9943.7	5974.3
Ta.10648.2.S1_x_at	285.6	6621.5	8103.9	3173.4
TaAffx.129145.2.S1_at	324	6499.3	9634.7	7154.7
Ta.18070.1.S1_x_at	567.9	6391.3	5460.6	3332
Ta.10532.1.A1_s_at	300.8	6131.8	201.6	112.3
TaAffx.87036.2.S1_s_at	152.8	6084.8	9805	5991
Ta.12339.1.S1_at	82.3	5833.5	7213.1	5399.3
TaAffx.5529.1.S1_at	194	5154.9	8477.1	7063.7
Ta.24801.1.S1_at	317.3	4930.4	1854.2	383.4
TaAffx.93191.1.S1_at	82.7	4923.4	5511.6	4276.7
TaAffx.13704.2.A1_at	445.1	4664.8	6178.2	3648.7
Ta.9577.1.S1_at	418.8	4640.5	6139.3	3382.8
Ta.8413.1.A1_at	339	4534	7819.9	4445.6
TaAffx.130510.1.S1_at	341.9	4395.7	6527.4	5313.2
Ta.12339.1.S1_s_at	131.4	4206.4	5719.2	3270.7
Ta.5888.1.S1_s_at	5.2	4163.4	4331.8	1641.3
Ta.1869.1.S1_at	66.2	4102.2	4792.6	1421.7
Ta.10656.1.S1_at	138.3	3827.2	3135.3	2155.8
TaAffx.66052.1.S1_at	64.1	3600.7	3967.4	3355.3
Ta.20686.1.A1_at	20.3	3588.6	7591.9	5065
Ta.9172.1.S1_at	57.5	3535.9	4267.7	2060.4
Ta.11389.1.A1_at	207.7	3528.7	2140.9	1955.8
Ta.3347.1.A1_at	41.4	3500.6	2714.6	1424
Ta.21881.2.S1_a_at	56.9	3360.6	6643.6	4258.3

Ta.28479.1.S1_at	111.7	3326.3	3801.9	3154.8
TaAffx.32486.1.S1_at	239.2	3265.5	6565.4	3528.1
Ta.3924.1.A1_at	185.9	3232.3	5733.9	3064.7
TaAffx.54414.1.S1_at	3.8	3096.8	4240.7	2180.6
Ta.23407.1.S1_at	280	2951.2	4455.5	1764.8
Ta.3432.1.S1_at	8	2838.2	1640.8	1179.7
Ta.9172.1.S1_x_at	49.6	2825.9	3847.2	1920.7
Ta.24738.3.A1_at	29.9	2762.2	2014.3	1190.4
TaAffx.105521.1.S1_at	187.6	2755.9	101.3	87.4
TaAffx.87061.1.S1_at	80.8	2739.1	4110.9	2026.7
TaAffx.96188.1.S1_at	216.8	2697.7	7898.3	4668.1
Ta.21591.1.A1_s_at	37.2	2681	3105.1	1406.2
Ta.6213.1.S1_at	77.8	2668.8	2826.6	1085
TaAffx.70822.1.A1_at	76.5	2603.9	1744.8	1186.4
Ta.11411.1.A1_at	7.3	2546.7	2744.2	1082.3
TaAffx.9019.1.S1_at	47.3	2534.4	2432.2	1587.3
Ta.10853.1.S1_at	34.4	2478	1500.7	732
Ta.202.1.S1_at	206.3	2435.9	973.1	197.2
Ta.9765.1.S1_x_at	9.8	2317.6	2834.4	1139.6
Ta.13941.1.S1_at	5.8	2302.3	4388.1	1332.3
AFFX-Ta_Sucsyn_5_at	159.8	2266.5	1724.4	687.9
Ta.23832.1.S1_at	88.1	2196.5	3615	3327.2
TaAffx.128418.32.S1_at	63.3	2178.2	3998	2270.5
TaAffx.87245.1.S1_at	39.7	2141	1224.3	762
TaAffx.59885.1.S1_at	59.3	2128.3	3490.8	2363.5
TaAffx.82312.1.S1_s_at	48.3	2125.4	2704.1	892.6
Ta.10746.1.S1_at	6.4	1967	2322.2	641.2
TaAffx.37720.1.S1_at	115.3	1888.1	1405.6	1107.8
Ta.6019.1.S1_at	18.7	1866.7	2477.6	1195.3
Ta.8879.1.A1_at	114.6	1835.7	3684.6	1336.9
TaAffx.120444.1.A1_at	30.5	1813.6	1767.9	1905.4
TaAffx.12039.1.S1_at	67.7	1720.6	2138.2	1142.6
Ta.25958.1.A1_at	32.1	1704.2	1348.8	1248.8
TaAffx.114275.1.S1_at	65	1699.8	2902.8	1742.7
Ta.201.1.S1_at	118.4	1666.1	415.5	90.3
Ta.16018.1.S1_at	135.1	1607	2034.7	1534.5
Ta.1454.1.S1_x_at	11.4	1601.8	1551.9	792.9
Ta.24738.2.S1_x_at	45	1595	1272.9	593
Ta.24332.1.S1_at	14	1583.1	449.3	163.5
Ta.15373.2.S1_x_at	3.9	1583.1	7966.3	5236
Ta.13503.1.S1_at	86.4	1525.8	1639.5	694.3
Ta.1454.2.S1_x_at	76.6	1448.6	1458	752.9
Ta.13573.1.A1_s_at	25.3	1443.2	1691.9	372.5
TaAffx.131309.1.S1_x_at	86.1	1440.9	1983.9	1202.7
Ta.22916.1.S1_x_at	17.8	1426.4	4418.5	3074.2
Ta.4439.1.A1_at	109.5	1321.9	1177.4	797.4

Ta.5951.1.S1_x_at	10.8	1313.2	1067	501.9
Ta.13573.1.A1_at	61.3	1299.7	2254.6	451
Ta.9399.1.S1_at	87.7	1286.6	3306	1759.2
Ta.9765.1.S1_at	8.1	1250.7	1619.7	450.2
TaAffx.65033.1.A1_at	86.8	1203.2	1358.3	1338.1
TaAffx.16775.1.A1_at	89.2	1199.4	1615.4	1191.1
Ta.16788.1.S1_at	47.8	1177.7	1928.6	1176.2
TaAffx.114207.1.S1_at	64.5	1177.6	3353.8	2581
Ta.5951.1.S1_at	79.8	1169.7	1163.6	472.7
TaAffx.106029.1.S1_at	49.3	1147.1	1747.2	1452.6
TaAffx.106136.1.S1_at	36	1134.3	1283.3	1077.3
Ta.27095.1.S1_at	12	1114.2	1642.7	539.1
Ta.21385.1.S1_x_at	19.6	1085	1434	1078.4
Ta.13641.1.A1_at	11.7	1043.4	950.3	949.9
TaAffx.122511.2.S1_at	4.6	1030.8	3686	1169.5
Ta.18237.1.S1_at	41.7	1027.8	1122.6	628.9
Ta.712.1.S1_s_at	7.9	1023.2	1406.5	418.1
TaAffx.7032.1.S1_at	19.1	990.9	1001.8	379.4
TaAffx.113314.1.S1_x_at	79.4	959.9	1757.7	891.8
Ta.28621.1.S1_at	12.8	912.6	657.4	595.1
Ta.22760.1.A1_at	28.4	910.8	1142.6	1091.6
TaAffx.87185.1.S1_at	6.3	892.7	1953.7	1717.6
Ta.24832.1.S1_s_at	34.4	885.1	710.9	545.9
Ta.4188.1.A1_at	7.1	877.4	2013.5	988.8
Ta.25909.1.A1_at	67.2	859	2311.1	2077.1
Ta.11659.1.A1_at	10	858.9	601.9	465.9
Ta.15373.1.S1_at	13.8	858.5	2357	1517
Ta.1057.1.A1_x_at	12.6	854.4	911.8	382.1
Ta.7000.1.A1_x_at	10.6	850.8	983.7	145
TaAffx.16032.1.A1_at	16.4	845.1	1011.8	343.3
Ta.25964.1.A1_at	6.4	833.4	588.6	511
Ta.15373.2.S1_at	9.3	824.8	4810.5	2956.7
TaAffx.118353.1.A1_at	14.4	814.2	1532.5	784.7
Ta.30892.1.S1_at	63.4	809.1	864.9	683.9
Ta.4144.1.S1_at	52.8	801	1065.3	570.9
Ta.7000.1.A1_at	78.2	799.4	1071.9	209.7
Ta.13454.1.S1_at	48	796.5	2379.6	1183.7
Ta.27661.2.S1_at	56	778.6	309.5	139
Ta.3643.1.S1_at	9.2	749.9	568.2	431.4
Ta.3869.2.S1_at	1.9	724.5	490.5	518.3
Ta.13988.1.S1_at	13.6	658.1	1137.8	309.2
Ta.8665.1.S1_at	39.9	656	180.7	20.4
TaAffx.113701.1.S1_at	15	651.6	456.7	404
TaAffx.91293.1.A1_at	8.6	650.1	767.8	324.2
Ta.15373.3.S1_at	46.3	643.7	4700.6	2526.4
TaAffx.33701.1.S1_at	35.8	620.9	1156.5	629.9

TaAffx.64879.1.A1_at	2.3	596.4	311.7	350
Ta.18223.1.S1_at	46.8	581.7	728.7	689.4
TaAffx.93411.1.S1_at	22.1	579.2	412.3	642.1
Ta.16361.1.S1_at	29.3	574.8	668.3	587.8
TaAffx.133491.1.S1_x_at	25.9	572.8	902.9	493.3
Ta.9898.1.A1_at	7.2	560	885.3	278.4
Ta.3781.1.A1_a_at	1.6	551.2	2200.6	1043.3
Ta.9142.1.A1_at	16	543.9	526.6	354.9
Ta.23763.1.S1_at	12.3	535.4	327.7	270.2
TaAffx.32354.1.S1_at	24.9	528.3	702.3	339.1
TaAffx.65171.2.S1_at	40.6	517.6	832.1	707
TaAffx.70203.1.S1_s_at	28.3	512.3	1437.7	433.6
Ta.9172.2.S1_at	15.9	502.2	651.6	311.4
Ta.20402.1.S1_at	44.6	484.1	748.6	723.8
Ta.309.1.S1_at	14.1	477.3	1643.8	367.5
Ta.5597.1.S1_at	23.5	472.1	409	175.1
Ta.9348.1.S1_at	17.8	463.5	531.6	366.5
Ta.14461.3.S1_x_at	18.9	455.6	553.5	483.6
Ta.5345.2.S1_a_at	30.5	450.7	618.6	647.4
Ta.4286.1.S1_at	40.7	431.9	635.9	229.7
Ta.2632.1.S1_x_at	30	414.4	7.2	8.8
Ta.12080.1.A1_s_at	29.4	406.9	529.4	290.2
TaAffx.59846.1.S1_x_at	4.7	395.1	214.2	120.3
Ta.11618.1.S1_at	3	386.1	392.4	265.7
TaAffx.9296.1.S1_at	27.1	382.7	386.7	131.3
TaAffx.64985.1.S1_at	8.3	378.2	401.8	208.6
Ta.21350.1.S1_x_at	2.3	365.9	11.4	65.8
Ta.1630.3.S1_a_at	15.3	362.1	495.4	171.4
Ta.24734.1.S1_at	5.4	356.1	1345.5	661
Ta.9172.3.S1_at	2	355	425.5	222.8
Ta.27268.1.S1_at	1.8	350.3	367.2	256.5
TaAffx.105901.1.S1_at	12.3	350.3	335	339
Ta.4375.1.A1_at	28.9	345.2	1673.7	1227.1
TaAffx.119664.1.A1_at	13.6	338.8	296.1	282.2
TaAffx.114162.1.S1_at	5.1	335.2	348.7	331
Ta.25999.1.A1_at	26.5	328.4	315.8	226.1
Ta.12055.1.S1_x_at	28.6	323.3	391.8	240.7
Ta.20778.3.A1_at	31.7	321.5	255.8	273.5
TaAffx.79214.1.S1_at	15.9	319.4	860.3	435.6
TaAffx.12445.1.A1_at	3.6	317.2	444.4	244.3
Ta.19014.1.S1_s_at	11	312.5	211.1	116.7
Ta.5293.1.S1_at	5.3	294.1	199.5	153.6
TaAffx.85830.1.S1_at	22.9	292.5	296.9	172.2
Ta.25876.1.A1_at	12.9	292.3	258.1	144.6
TaAffx.115935.1.S1_x_at	12.5	277	293.8	352.2
TaAffx.119616.1.A1_at	12.1	273.2	487.7	530.5

TaAffx.43554.1.S1_at	3.6	273.1	3.2	5.5
Ta.22954.1.S1_a_at	20.2	266.4	381.8	147.4
TaAffx.17164.1.S1_at	9	266.3	265	128.2
Ta.9172.3.S1_x_at	3.2	263.7	329.9	144.1
TaAffx.131697.1.S1_x_at	5.3	258.6	366.7	111.4
TaAffx.65556.1.S1_at	4	258.2	237.2	183.3
TaAffx.12182.1.S1_at	9.4	257.2	246.9	104.6
Ta.28063.1.S1_x_at	6.2	253	226.8	275.4
Ta.3778.1.S1_at	13.1	251.7	98.2	225.3
TaAffx.59666.1.S1_at	15.6	251.3	371.9	330.4
TaAffx.59890.1.S1_x_at	10.9	249.9	466.3	419.7
TaAffx.131697.1.S1_s_at	13.6	249.2	621.5	306.8
Ta.1566.1.A1_at	23.3	248.8	197.3	140.1
Ta.11168.1.A1_x_at	16.1	246.7	590.7	396.6
TaAffx.82113.1.S1_x_at	24.5	246.2	216.9	325.6
TaAffx.112202.1.S1_s_at	19.3	245.6	61.6	17
TaAffx.42438.1.A1_at	24.3	243.1	172.2	301.7
Ta.22954.1.S1_at	17.6	242.9	266.2	80.6
TaAffx.27163.1.S1_at	17.5	242.5	135.5	124.7
Ta.27457.8.S1_x_at	20.8	242	76.5	59.4
TaAffx.91995.1.A1_at	8.8	235	538.4	161.1
Ta.5331.1.A1_x_at	9.8	234.8	35.5	6.9
Ta.24110.1.A1_s_at	8	233.6	131.5	8.6
TaAffx.57201.1.S1_at	13.9	229.6	88.8	44
TaAffx.111156.1.S1_at	21.2	226.8	89.3	93.6
TaAffx.59890.1.S1_at	5	218.3	165.5	34.7
Ta.5491.1.A1_at	7.8	213.4	28.5	14
TaAffx.90174.1.S1_at	17.2	212.7	252.6	56.4
Ta.18232.2.S1_a_at	5.5	210.6	322.1	304.6
Ta.11168.1.A1_at	12.9	206.7	476.8	493.8
TaAffx.59797.1.S1_at	7.5	204.5	249	325.9
TaAffx.59917.1.S1_at	16.9	203.3	167	83.9
Ta.3941.1.A1_at	6.7	202.1	159.4	231.7
Ta.14483.1.S1_x_at	7	200.4	166.9	20.7
Ta.30494.1.A1_at	10.1	197	118.1	151.4
TaAffx.113805.1.S1_at	14	196.9	228.9	224.9
TaAffx.110321.1.S1_at	2.8	196.5	134.3	69.1
TaAffx.122944.1.S1_at	17.5	195.6	148	101.5
TaAffx.35581.2.S1_s_at	7.4	194.4	13.1	38
Ta.5650.1.S1_a_at	7.4	193	341.9	180.7
Ta.16013.1.S1_at	7.6	193	459.9	247.9
Ta.19998.1.S1_at	18.3	188.1	136.6	162.8
Ta.21314.1.S1_x_at	17.6	186.5	72.7	41
Ta.3428.1.S1_s_at	17.8	185.9	182.6	26.1
Ta.8964.1.A1_at	18.2	184.4	286	218.5
TaAffx.114252.1.S1_at	12.5	184.4	166	140.4

Ta.28508.1.S1_at	15.8	178.6	266.6	276.4
TaAffx.70573.1.S1_at	16.6	178.5	109.2	12.5
Ta.28756.3.S1_x_at	17.4	177.6	106.7	44.2
TaAffx.92552.1.S1_at	5.4	175.8	181	115.5
TaAffx.59846.1.S1_at	3.1	174.8	103.4	35.4
Ta.22516.1.S1_at	7.1	172.5	114.8	118.4
Ta.1967.1.S1_x_at	2	171.4	3.4	22
TaAffx.78656.1.S1_at	12.5	171.3	80.6	12.2
Ta.881.2.S1_x_at	4.4	170.4	174.8	107.8
Ta.28942.2.A1_at	2.1	169.2	30.8	2.1
TaAffx.131379.1.A1_at	5.6	169	39.7	2.3
Ta.11464.1.A1_at	1.8	168.6	249.9	220.5
TaAffx.106865.1.S1_at	12.2	168.3	79.3	133.5
Ta.16046.1.S1_at	4.8	166.8	497.4	406.5
TaAffx.616.2.S1_s_at	8.9	166.4	80	46.3
TaAffx.58783.1.S1_at	13.5	165.4	158.2	104
TaAffx.133664.1.S1_at	1.4	164.6	61.7	201.8
Ta.23823.2.S1_at	11.7	161.2	35.3	15.2
Ta.20093.1.S1_at	13.5	160.6	125.8	205.6
Ta.22954.2.S1_x_at	7.9	160	237.3	166.2
Ta.19210.1.A1_at	4.7	158.4	141.9	39.2
TaAffx.15009.1.S1_at	13.8	156.1	169	140.1
Ta.19525.1.S1_at	11.9	156	75.4	6.5
TaAffx.128682.3.A1_at	4	155.6	139.9	84
Ta.18926.1.S1_at	11.8	154.6	193.5	46.1
TaAffx.107877.1.S1_at	9.6	154.1	103.6	158.2
Ta.10560.2.S1_x_at	9.5	153.7	123.8	92.4
Ta.11600.1.A1_at	11.4	153.7	206.5	138.7
TaAffx.120138.1.A1_at	4.2	149.5	1089.9	338.3
TaAffx.52141.1.S1_at	14.7	149.2	76.4	37.4
Ta.29365.1.S1_x_at	3.6	148.8	403.6	188
Ta.10042.1.S1_at	10.9	146.1	23.3	33.9
TaAffx.27822.1.S1_at	11.7	144.6	3.1	8.2
TaAffx.9641.1.S1_at	11.8	141.4	111.9	71.1
TaAffx.9518.1.S1_at	2.9	141	579.5	451.4
Ta.1725.3.S1_at	5	140.7	830.8	507.2
Ta.27457.1.S1_x_at	7	138.5	18.5	66.7
Ta.17827.1.S1_at	5.9	135.3	88.6	13.5
TaAffx.56820.1.S1_at	12.3	135.1	165.2	73
Ta.1057.1.A1_at	9.2	134.7	431.9	88.4
Ta.7401.3.S1_x_at	10.8	134.5	165.9	135.3
TaAffx.58927.1.S1_at	7	134.3	76.6	95.9
TaAffx.12558.1.A1_at	5.9	133.8	118.4	145.4
Ta.27744.1.S1_x_at	10.5	133.6	40.8	41.8
TaAffx.108455.1.S1_at	4.5	133.5	16.9	42.5
TaAffx.107027.1.S1_at	11.5	133.3	75.5	129

Ta.2904.1.S1_at	5.6	132.3	178.9	179.3
Ta.1282.4.S1_at	9.1	131.2	290.7	104.3
TaAffx.120389.1.S1_s_at	11.7	130.7	152.7	120.6
TaAffx.58282.1.S1_at	11.3	126.8	95.1	164.4
Ta.13191.2.S1_x_at	11.9	125.1	129.3	190.5
TaAffx.54060.1.S1_at	10.5	123.3	46.1	4.9
TaAffx.8335.1.S1_at	7.7	122.1	192.9	51.4
TaAffx.105764.1.S1_at	11.5	121.7	129.7	153.5
TaAffx.113255.1.S1_at	6.1	121.1	66.5	7.1
TaAffx.84557.1.S1_at	10	120.8	86	86.8
Ta.14164.1.S1_s_at	6.2	120.6	50.2	5.3
TaAffx.42799.1.S1_at	5.3	119.7	58.9	95.6
Ta.8255.1.A1_at	11	118.8	9.6	19.3
Ta.13232.1.S1_at	6	118.5	286.3	204.9
Ta.20722.1.S1_at	10.7	117.6	139.5	124.2
TaAffx.70904.1.A1_at	4.5	116.5	85.4	69
Ta.30408.1.A1_at	5	116.1	57.7	85.4
Ta.22981.3.S1_a_at	5.2	115	78.5	67.3
Ta.27754.2.S1_x_at	5.6	113.9	42.5	10.7
TaAffx.28992.1.S1_at	8.9	113.7	18.8	11.3
Ta.5571.1.S1_at	6.8	113.3	660.4	335.7
TaAffx.7030.1.S1_at	1.7	113	85.1	14.4
Ta.10528.2.S1_at	10.3	112.3	128.8	145.1
TaAffx.12481.1.S1_at	8.8	112.1	10.4	6.9
Ta.8604.1.A1_at	7	111.4	73.1	10.8
Ta.4843.2.S1_at	8.3	111.3	12.5	18.7
TaAffx.51521.1.S1_at	7.3	110.7	143.2	114.2
Ta.3812.3.S1_at	7.9	110.6	1266.8	1017
Ta.26978.1.A1_at	8.9	110.5	118.2	86.5
TaAffx.23900.1.S1_at	5.2	110.3	39.2	74.9
Ta.25039.2.S1_at	9	109.6	118.8	123.2
Ta.5150.1.S1_at	2.1	109.4	83.8	44.3
TaAffx.83223.1.S1_at	10.9	109.1	79.6	79.6
Ta.16956.1.A1_at	7.4	108.3	140.2	40.6
Ta.20361.1.A1_at	9	108.3	8.8	47.5
Ta.2746.2.S1_x_at	4.5	106.6	68.5	30.2
TaAffx.105543.1.S1_at	4.8	106	2.8	4.2
TaAffx.106230.1.S1_at	5.4	105.6	170.9	109.1
TaAffx.62609.1.S1_at	9.9	105.4	96.5	5.4
Ta.1700.1.S1_at	9.4	104.9	80.3	90.1
TaAffx.114256.2.S1_at	10	104.2	164.9	30.1
TaAffx.7434.1.S1_at	2.8	104.1	23.2	6.1
Ta.5497.1.A1_x_at	9.7	103.1	48.8	49.5
TaAffx.85652.1.S1_at	7.2	102.9	36.6	103.4
Ta.12188.1.A1_at	8.2	102.8	86.8	67
TaAffx.9566.1.S1_at	0.8	102.3	41.3	74.7

TaAffx.113607.2.S1_at	10	101.2	138.5	13.3
Ta.30934.1.A1_at	3.7	101	11.7	115.1
TaAffx.28505.1.S1_at	9.2	101	112.7	58.7
Ta.19210.1.A1_x_at	4.6	100.7	63.4	119.1
TaAffx.105516.1.S1_at	4.5	100.3	50.8	67.5
TaAffx.5530.1.S1_at	5.1	100.2	13.1	11
TaAffx.15836.1.S1_at	7.5	100.1	27.8	18.5
TaAffx.80350.1.S1_at	2	100	4.1	8.2
TaAffx.58536.1.S1_at	6.4	98.6	31	20.9
TaAffx.81300.1.S1_at	8.5	98.6	186	101.5
TaAffx.117195.1.S1_at	3.1	98.3	42.7	13.7
TaAffx.11994.1.S1_at	8.7	98.2	81.4	71.1
Ta.22184.1.S1_at	9	97.3	99.8	124.9
Ta.12340.1.A1_at	5.6	97.2	103.8	72.4
TaAffx.51591.1.S1_at	5.5	96.6	41.9	25.2
TaAffx.37197.1.A1_at	9.3	96.4	6.2	11.3
TaAffx.128643.5.S1_at	4.1	96.2	116	138.9
Ta.17557.1.S1_at	7.7	95.9	81.1	17.1
Ta.25471.1.S1_at	3.8	95.7	47.3	12.6
TaAffx.51313.1.S1_at	7.8	94.5	131	63.2
Ta.22363.1.S1_at	5.3	94.4	371.6	285.3
TaAffx.119521.1.S1_at	3.8	94.2	33.4	83.6
TaAffx.65939.1.A1_at	3.7	93.9	95.3	68.5
TaAffx.143995.19.A1_at	9.3	93.5	57.2	93.3
TaAffx.111334.1.S1_at	6	93.5	107.7	133.6
Ta.10390.1.S1_at	5.9	92.4	21.8	2.9
Ta.21711.1.S1_at	7.1	91.3	48	55.8
Ta.4073.3.S1_a_at	4.3	90.5	121.3	46.7
TaAffx.55056.1.S1_at	7.8	90.1	7.5	20.7
Ta.25800.1.A1_x_at	8.9	90	71.5	66.3
TaAffx.84034.1.S1_s_at	7.1	89.4	207.8	73
Ta.19805.2.S1_at	7.4	88.7	86.2	42.2
TaAffx.80550.1.S1_at	8	88.7	33.5	18.4
Ta.25932.1.A1_at	8.4	88.5	90	73.8
TaAffx.25313.1.S1_at	7.5	88.2	9.5	36.1
Ta.10251.2.S1_at	4.6	87.8	10.4	102.9
Ta.26999.1.S1_x_at	4.9	87.4	523.8	231.6
TaAffx.114344.1.S1_at	4.9	86.4	103.3	29.2
TaAffx.116158.1.S1_at	8.1	86.2	145.1	35.6
TaAffx.17421.1.A1_at	6.2	85.8	65	9.6
Ta.14269.1.A1_at	5.3	84.8	11.2	3.4
TaAffx.98425.1.S1_x_at	3.8	84.7	222	48.8
TaAffx.55262.1.S1_at	2.2	84.7	62.1	29.6
TaAffx.161.1.S1_at	5.5	83.4	35.2	12.2
TaAffx.109525.1.S1_at	7.5	83	39.4	84.5
TaAffx.104885.1.S1_at	7	82.9	27	23.8

Ta.12228.1.A1_at	5.3	82.7	84.4	71.2
TaAffx.106117.1.S1_at	4.3	82.4	91.8	65.9
Ta.3640.2.S1_s_at	6.5	82.3	77.2	34.4
TaAffx.84937.1.S1_at	5.8	81.8	94.6	83.2
Ta.9251.2.A1_at	6.5	81.5	52.8	28.4
TaAffx.31625.1.S1_at	3	81.2	47	33.7
TaAffx.30561.2.A1_at	4	81.1	9.4	21
Ta.2167.2.S1_at	7.3	80.9	156.1	161.5
Ta.8400.1.A1_at	3.8	80.5	98.7	61.4
Ta.9212.2.S1_at	4.4	80.4	5.2	22.9
Ta.4063.1.S1_at	3.6	80.3	34.6	54.5
TaAffx.110208.2.A1_at	8	80.3	4	36
Ta.13161.2.A1_s_at	1.1	80.1	850.4	454.7
TaAffx.70447.1.A1_at	4.1	79.9	115.1	58.8
TaAffx.15436.2.S1_at	7.6	79.8	72.4	83.4
TaAffx.121181.1.S1_at	7.7	79.5	64.8	70.6
Ta.16709.1.S1_at	6.3	78.8	64	49.1
Ta.14578.1.S1_at	1.7	78.2	63.2	114.6
TaAffx.25664.1.S1_at	7.7	77.6	128.2	99.3
TaAffx.8970.1.S1_at	3.7	77	76.5	53.3
Ta.6239.3.S1_x_at	6.4	76.6	77.5	72.3
Ta.15619.1.S1_at	6	76.3	4	12.2
Ta.19461.1.S1_at	4.4	76.2	27.4	79.4
Ta.29607.1.S1_at	7.1	75.2	9.8	13.6
Ta.4371.3.S1_at	7	75.1	85.9	46.3
TaAffx.26518.1.S1_at	1.2	74.7	62.5	30.2
TaAffx.31447.1.S1_at	6	74.5	106.7	122.3
Ta.1338.1.S1_at	7.1	74.3	28.5	9.9
Ta.11022.1.S1_x_at	4.6	74.3	20	6.5
TaAffx.50101.1.S1_at	3	74	86.3	69.3
Ta.9274.3.S1_s_at	6.9	73.8	42.4	6.9
TaAffx.113282.1.S1_s_at	3.8	73.6	3.1	18.8
Ta.8748.1.A1_at	5.1	73.6	49.1	19.3
TaAffx.506.1.A1_at	6.4	73.4	112.3	129.1
Ta.14383.1.A1_at	2.9	73.2	15.7	14.3
Ta.9990.2.S1_at	6.7	72.8	11.1	22.9
TaAffx.25602.1.S1_s_at	3	72.7	20.1	2.3
Ta.26148.1.S1_at	6.2	72.6	146.2	84.9
Ta.25635.2.S1_at	6.2	71.7	2.9	11.3
TaAffx.93376.1.S1_x_at	6.9	71.6	30	108.2
Ta.5636.2.S1_x_at	3.7	71.2	70.6	102.6
Ta.15441.1.S1_at	4.8	71.1	35.4	29
Ta.761.1.S1_at	5.3	71	11.6	5
TaAffx.85834.1.S1_at	7	70.8	106.9	121.3
Ta.24660.2.A1_at	3.5	70.6	43.7	11.8
TaAffx.4412.1.S1_s_at	4	70.6	9.5	16.5

TaAffx.122333.1.S1_at	4.2	70.5	75.4	74.5
TaAffx.23665.1.S1_at	4.8	69.7	5.5	15.9
Ta.1149.1.A1_at	2.8	69.6	76.3	8.4
TaAffx.128713.1.S1_at	3.9	69.5	54.4	21.9
TaAffx.54378.1.S1_at	3.9	69.5	33.6	64
TaAffx.32390.1.S1_at	4.4	69.3	76.3	6.8
TaAffx.106905.1.S1_at	3.7	69.2	18.8	13.6
Ta.303.1.S1_x_at	5.9	69.1	7.5	7.9
TaAffx.77603.1.S1_at	1.6	68.8	40.9	43.4
Ta.17681.1.S1_at	5.3	68.6	76.8	87.2
TaAffx.128414.147.S1_x_at	5.8	68.6	11.2	73.6
TaAffx.131747.1.S1_x_at	3.4	68.4	8.9	1.8
Ta.17452.1.S1_at	5	68.3	49.9	42.7
TaAffx.110017.1.S1_at	5.6	68.3	9.8	47.3
Ta.19368.1.S1_at	3.4	68.2	35.7	3.7
Ta.12805.1.S1_at	4.1	67.9	26.7	94.4
TaAffx.12088.2.S1_at	4.9	67.7	50	90.1
TaAffx.107992.1.S1_at	3.3	67.4	17.6	51
Ta.8027.2.S1_at	4	67.4	36.6	90.6
Ta.12520.1.A1_at	2.4	67.3	43.9	43
TaAffx.31831.1.S1_at	4.5	66.8	46.5	33.3
TaAffx.116833.1.S1_at	5	66.4	27.1	81.7
TaAffx.8951.1.S1_at	6.2	66.4	61.8	38.6
Ta.5200.1.A1_at	5.9	65.9	49.5	70.3
Ta.18693.1.A1_at	5.3	65.8	57.3	79
TaAffx.84393.1.S1_at	5.3	65.8	6.7	30.2
TaAffx.27005.1.S1_at	3.7	65.6	140.5	97.7
Ta.12302.1.A1_at	5.4	65.4	68.1	68.1
Ta.16388.1.S1_at	3.7	65.1	10	40.8
TaAffx.29052.2.S1_at	3.7	65.1	29.8	10.2
TaAffx.85486.1.S1_at	2.6	64.9	25.7	8.6
Ta.22466.1.S1_at	6.1	64.7	88.2	101
Ta.21069.2.S1_a_at	5.1	64.6	52	40.3
TaAffx.55076.1.S1_at	4.9	64.5	34.3	69.3
Ta.22565.1.S1_x_at	3.9	63.8	67.9	53.3
TaAffx.107508.2.S1_at	5.7	63.8	63.2	18.7
Ta.3827.1.S1_at	4.5	63.6	11.9	97.2
TaAffx.53704.1.S1_at	6.1	63.6	12.8	70.1
TaAffx.104648.1.S1_at	2.9	63.5	50.7	47.5
TaAffx.9192.1.S1_at	2.8	63.1	49.7	38.8
Ta.178.2.S1_x_at	3.6	62.7	1.6	3.1
Ta.20602.1.S1_at	5.2	62.7	17.9	57.1
TaAffx.64719.1.A1_at	4.9	62.4	41.6	43.7
TaAffx.84028.1.S1_at	2.6	62.3	9.5	20.6
Ta.20768.1.S1_at	5.3	62.2	86.7	117.7

Ta.1729.3.A1_at	4.9	62.2	35	56.5
TaAffx.112026.1.S1_at	1.8	61.6	4.9	7.1
Ta.23693.1.S1_at	5.1	61.2	24.4	20.4
Ta.27744.2.S1_a_at	4.4	61.1	80	108.3
TaAffx.16062.1.A1_at	0.7	60.6	38.1	51.6
TaAffx.110663.1.S1_at	5.4	60.4	58	96.8
Ta.27576.1.A1_at	4.4	60.2	83.1	34.6
TaAffx.65642.1.S1_at	2.8	60.2	43	3.7
Ta.28063.2.S1_at	2.6	60.1	203.6	204.3
TaAffx.84095.1.S1_at	5.8	60	44	6.2
Ta.27557.1.S1_at	1.2	59.9	144.8	18.3
TaAffx.113461.1.S1_at	3.4	59.9	23.7	45.6
Ta.26145.1.A1_at	5.6	59.7	65.5	80.8
TaAffx.105712.1.S1_at	4.4	59.6	58.2	2.5
Ta.11690.1.S1_at	4.1	59.5	306.1	93.9
TaAffx.97381.2.S1_at	2.3	59.2	86.3	74
TaAffx.108275.1.S1_at	1.9	58.8	43.1	19.6
Ta.13069.1.A1_at	3	58.7	17.4	32
TaAffx.26981.1.S1_at	5.3	58.6	25.4	5.6
TaAffx.110174.1.S1_at	2.3	58.6	41.9	16.1
TaAffx.113486.2.S1_at	4.5	58.4	63.8	7.7
TaAffx.56450.1.S1_at	5	58.4	62.1	53.6
TaAffx.108638.1.S1_at	3.3	58.1	50.4	12.8
TaAffx.111829.1.S1_x_at	3.4	58	13.7	13.3
Ta.5257.2.S1_x_at	3.8	57.8	29.2	56.2
Ta.24736.1.S1_at	1.3	57.5	66.2	41.9
Ta.26973.1.S1_at	5.5	57.5	88.2	68.3
TaAffx.87036.2.S1_at	1.9	57.4	74.3	77.6
TaAffx.81495.2.S1_s_at	4.5	57.4	19.2	9.1
Ta.21213.1.S1_x_at	1.4	57.1	66.2	52.5
TaAffx.112386.1.S1_at	4.2	57	51.6	67.6
TaAffx.24723.1.S1_at	4.6	56.7	15.2	78
TaAffx.24287.1.S1_at	4.9	56.5	15.5	72.3
Ta.19477.3.S1_x_at	3.4	56.4	30	28
Ta.15159.1.S1_at	5.3	56	45.5	25.9
TaAffx.60746.2.A1_s_at	2.3	55.8	19.8	85.4
Ta.9086.3.S1_at	5.5	55.7	50.4	27.2
TaAffx.78273.1.S1_at	5.1	55.6	35.7	87.3
TaAffx.5059.1.S1_at	1.4	55.6	10.7	11.5
Ta.4048.3.S1_at	5.3	55.5	12.2	8.5
TaAffx.23112.1.S1_at	2.3	55.2	14.6	23.7
TaAffx.84466.1.S1_at	1.8	55	61.1	52
Ta.16896.1.A1_at	4.5	54.8	12.6	9.2
Ta.9336.2.S1_x_at	4.9	54.8	39.5	15.1
TaAffx.25732.1.S1_at	4.8	54.7	15.6	86.1
TaAffx.8946.1.A1_at	3	54.6	37.6	45.3

Ta.13327.3.S1_a_at	2.5	54.1	16.6	8.7
TaAffx.55066.1.S1_at	2.4	53.9	12.9	3.5
TaAffx.54490.1.S1_at	1.1	53.9	15	3.8
Ta.1247.1.S1_at	3.5	53.8	34.6	8
Ta.11776.2.S1_at	2.5	53.8	40.9	15.3
Ta.712.1.S1_x_at	1.8	53.7	62.4	65
TaAffx.25977.1.S1_at	2.9	53.7	47.8	91
Ta.21124.2.S1_x_at	4.2	53.5	10.2	37
TaAffx.69846.1.S1_at	4.1	53.4	13.2	22.1
Ta.28700.1.S1_at	4.3	53.3	8.4	78.1
TaAffx.25475.1.S1_at	2.1	53.2	8.3	28
TaAffx.38872.2.A1_at	5	53	38.4	31.7
Ta.1938.2.S1_at	2.5	52.9	9.4	61.7
TaAffx.58397.1.S1_at	3	52.9	47	68
Ta.17177.1.S1_a_at	2.3	52.8	78.3	72.2
Ta.28161.2.S1_at	5.1	52.8	59.8	19.3
Ta.10216.2.S1_at	4.3	52.7	71.4	57.4
TaAffx.82970.1.S1_at	2.3	52.7	28.8	7.6
Ta.14595.2.A1_at	4.9	52.6	35.6	9.7
Ta.26427.1.A1_at	4.1	52.6	13.8	13.1
Ta.18517.1.S1_at	4.3	52.6	15.9	5.7
Ta.8877.1.A1_at	4.1	52.6	18.3	47.2
TaAffx.92173.1.S1_s_at	2.6	52.5	43	13.4
TaAffx.5470.1.S1_at	2.9	52.3	2.7	7.2
Ta.556.1.S1_at	1.1	52.2	50.7	1.4
TaAffx.32248.1.S1_at	1.9	52.2	23.1	51.8
TaAffx.31630.1.S1_at	3.8	52.1	10.7	80.2
TaAffx.112279.1.S1_at	4.3	52.1	2.5	17.7
TaAffx.128894.1.S1_at	4.1	52	24.1	54
Ta.9038.1.S1_at	4.5	51.7	29.1	53.4
TaAffx.110642.1.S1_x_at	1.7	51.5	8.3	60.9
TaAffx.82078.1.S1_at	3.4	51.2	37.4	42
TaAffx.94038.1.S1_at	3.8	51.1	71.9	69.3
TaAffx.128619.3.S1_x_at	3.8	51	73.9	47.7
TaAffx.59568.1.S1_at	4.4	50.8	40.4	9
AFFX-r2-TagJ-5_at	4.7	50.7	21.8	4.4
TaAffx.107556.1.S1_at	4.8	50.5	75.7	61.8
Ta.21342.1.S1_x_at	2.4	50.4	21.4	5.3
Ta.20596.1.A1_at	5	50.3	5.9	27.4
TaAffx.84156.1.S1_at	2.3	50.2	59.1	47.9
TaAffx.24214.1.S1_at	3.1	50.2	22.1	44.2
TaAffx.38194.1.S1_at	3.1	49.9	21.1	3.3
TaAffx.5829.1.S1_at	4.8	49.9	34.9	22.2
TaAffx.111527.1.S1_at	3.6	49.7	6.2	11.7
TaAffx.110994.2.S1_at	3.3	49.6	5.5	29.6
Ta.18675.1.S1_at	3.4	49.5	86.6	3.4

Ta.24632.1.S1_at	1.8	49.3	29.6	2.6
TaAffx.136701.3.S1_x_at	3.1	49.3	15.6	32
TaAffx.71684.1.A1_at	3.5	49.1	42.2	11
TaAffx.28302.2.S1_at	3.4	49	87.2	70.8
Ta.9084.2.S1_at	3.4	48.9	6.8	16.6
Ta.6059.1.S1_at	4.5	48.5	41.6	32.6
Ta.21438.2.A1_x_at	2.2	48.4	0.8	2.5
Ta.22711.1.S1_at	3.7	48.3	79.7	7.8
TaAffx.85843.1.S1_at	0.8	48.3	2.1	9.8
Ta.8082.1.A1_at	4.2	48.2	4.8	14.2
TaAffx.6128.1.S1_at	3.3	48.2	19.1	10.9
Ta.26359.1.A1_at	2.2	48.1	4.7	12.8
TaAffx.120174.1.S1_at	3.3	48	2.4	6.4
Ta.16858.1.S1_at	3.6	47.9	6.5	50.7
TaAffx.108225.1.S1_at	2.3	47.8	47.7	43.3
TaAffx.111067.3.S1_at	1.7	47.8	57.8	30.9
TaAffx.83988.2.S1_at	4.7	47.8	66.1	31.9
Ta.24179.3.S1_at	3.3	47.8	92.8	38.3
TaAffx.81914.1.S1_at	2.8	47.7	30.6	80.5
Ta.25886.1.A1_at	4.5	47.6	10.4	46.2
Ta.9005.2.S1_at	4.4	47.4	72.9	62.9
TaAffx.37201.1.S1_at	4.2	47.4	11.7	17.2
TaAffx.109002.1.S1_at	1.3	47.3	4.3	34.1
TaAffx.53419.1.S1_x_at	4	47.3	11.7	13.8
TaAffx.31404.1.S1_at	4.2	47.3	5.8	3.3
TaAffx.57100.1.S1_at	3.1	47.3	9	39.7
Ta.26902.1.S1_at	3.2	47.1	8.4	50.3
TaAffx.81379.1.S1_at	2.2	47.1	30	26.2
Ta.9401.3.S1_x_at	2.9	46.8	43.9	30.1
Ta.17775.1.S1_at	3.7	46.8	17.5	2
Ta.4969.2.S1_x_at	2.5	46.8	2.3	3.8
Ta.13008.1.S1_at	2	46.7	4.1	18.2
Ta.14965.2.S1_at	3	46.6	3.6	5.1
Ta.15432.1.S1_at	2.1	46.5	9.7	22.6
TaAffx.8301.1.S1_at	4.4	46.4	92.6	34.8
Ta.4141.1.A1_at	2.3	46.1	4.5	7.6
Ta.17212.1.S1_at	2.5	46.1	23.7	3.4
TaAffx.128798.2.S1_x_at	3.5	46.1	3.6	18.5
TaAffx.57703.1.S1_at	3.6	45.9	11.2	6.8
Ta.26615.1.A1_at	2.6	45.8	7.9	15.2
TaAffx.47704.1.S1_at	2.9	45.8	38.6	5.1
Ta.20117.1.S1_at	2.8	45.6	29.4	32.4
Ta.15422.1.S1_at	3.3	45.6	50.4	44.8
TaAffx.79972.1.S1_at	3.7	45.6	31.5	67.3
TaAffx.111759.2.S1_at	4	45.5	53.2	34.4
Ta.3466.1.S1_at	2.9	45.3	10	14.1

Ta.25755.2.A1_x_at	4.4	45.3	17.6	39
TaAffx.89472.1.S1_x_at	1.3	45	17.2	18.7
TaAffx.8413.1.S1_at	2.4	45	7.2	7
TaAffx.82080.1.S1_at	2.9	44.9	23	5
TaAffx.23383.1.S1_at	2.5	44.8	20.7	14.6
TaAffx.8712.1.S1_at	3.7	44.7	5.2	9
TaAffx.58912.1.S1_at	4.1	44.7	37.1	25
TaAffx.131298.1.S1_at	1.6	44.7	36.7	40.6
Ta.16996.1.S1_at	1.6	44.4	23.7	58.6
TaAffx.111048.1.S1_at	2.2	44.3	83.8	55.5
Ta.6020.3.S1_at	3.8	44.3	20.5	49.4
Ta.4516.1.A1_at	4.4	44.2	92.9	161.2
TaAffx.80573.1.S1_at	3.8	44.2	44	31.9
Ta.26134.1.A1_at	3.9	44.1	11.1	8.2
Ta.14946.1.S1_at	2.9	44.1	7.2	7.7
TaAffx.111476.1.S1_at	3.3	44.1	29.3	3.4
TaAffx.55231.1.S1_at	1.1	44	29.3	4.6
TaAffx.71465.1.S1_at	3.1	43.9	11.6	1.9
TaAffx.28598.1.S1_at	3.3	43.9	40	6.6
TaAffx.26106.1.S1_at	2.4	43.9	20.5	3.5
TaAffx.113192.1.S1_at	3.8	43.9	28.9	65.1
Ta.5263.1.S1_at	3.4	43.6	6	10.7
TaAffx.131043.1.S1_at	1.8	43.6	31.5	38.3
TaAffx.135168.5.S1_at	1.6	43.6	28.8	44.4
TaAffx.38186.1.S1_at	4	43.5	12.3	3.6
TaAffx.107998.1.S1_at	3.5	43.5	31	52.1
TaAffx.108400.1.S1_at	2.9	43.3	25.9	10.4
TaAffx.82624.1.S1_at	4	43.3	1.8	5.5
Ta.28398.2.S1_x_at	3.7	43.2	43.6	52
TaAffx.80584.1.S1_at	3.7	43.2	6.3	28.5
Ta.18334.1.S1_s_at	3.3	43.1	64	2.8
TaAffx.64059.1.S1_at	4	43.1	90.5	18
TaAffx.56398.1.S1_at	1.9	43	29.9	82.5
TaAffx.76.1.S1_at	3.2	42.7	7.6	36.4
Ta.590.2.S1_x_at	3.7	42.7	24.6	32.1
TaAffx.6710.1.S1_at	3.3	42.7	67.6	9.4
TaAffx.7497.1.S1_at	3.2	42.6	38.9	32.9
Ta.8553.1.S1_at	4	42.5	24.7	19.8
TaAffx.83100.1.S1_at	3.2	42.5	4.2	5.7
TaAffx.105416.1.S1_at	3	42.4	43.9	7.2
TaAffx.6251.1.S1_at	2.3	42.3	55.1	45.6
TaAffx.81506.1.S1_at	3.8	42.2	1.8	8.7
Ta.19253.1.S1_at	3.1	42.1	3.9	7.9
TaAffx.86295.1.S1_at	3.4	42.1	2.8	17.7
Ta.6269.2.S1_x_at	3.7	42	50.5	70.5
TaAffx.50271.1.S1_at	4.1	42	16	41.8

Ta.27064.1.S1_at	3.8	41.9	32.2	7.8
TaAffx.111495.1.S1_x_at	3.8	41.9	15.8	49.1
Ta.27571.1.S1_at	2.3	41.7	4.6	5.2
TaAffx.31688.1.S1_at	2.7	41.7	14.1	11.2
TaAffx.12607.1.S1_at	4.1	41.6	93.7	95.2
TaAffx.86325.1.S1_at	0.6	41.5	21.8	48.1
TaAffx.26458.1.S1_at	3.4	41.5	56.7	65.3
TaAffx.54386.2.S1_at	2.8	41.5	7	2.1
Ta.6025.2.S1_at	3.7	41.4	39	63.2
TaAffx.112897.1.S1_at	4.1	41.4	39.4	55.7
Ta.21682.1.S1_x_at	3.5	41.3	55.5	5.5
TaAffx.83284.1.S1_s_at	3.7	41.1	38.8	9.1
TaAffx.80831.1.S1_at	2.2	41	1.7	14.3
TaAffx.53057.1.S1_at	2.7	40.8	24.4	36.2
TaAffx.129494.1.S1_at	3.7	40.7	47.4	27.8
TaAffx.30561.1.S1_x_at	2.1	40.7	27.7	19.4
TaAffx.109049.1.S1_at	1.3	40.7	17.1	5.7
Ta.27865.1.A1_at	1.8	40.5	46.9	73.3
Ta.22630.1.S1_at	0.8	40.4	46.6	48.2
TaAffx.29085.1.S1_at	2.5	40.2	4.4	4.3
TaAffx.57969.1.S1_at	3.9	40.2	11.5	17.5
TaAffx.2929.2.A1_at	3.3	40.1	47.5	58.6
TaAffx.9092.2.S1_at	3.9	39.9	18.2	11.1
Ta.11428.1.A1_at	3.8	39.8	82.6	3.9
TaAffx.105828.1.S1_at	2.7	39.8	16	10.5
TaAffx.113947.1.S1_at	3	39.7	37.4	50.4
Ta.8117.1.S1_at	1.6	39.6	6	11.5
Ta.24662.1.A1_at	1.5	39.5	7.3	39.2
TaAffx.31590.1.S1_at	3.2	39.4	19.4	36.8
Ta.16933.1.S1_at	3.6	39.3	7.2	42.1
Ta.16190.1.A1_x_at	1.6	39.3	39.5	19
Ta.9975.2.S1_at	3	39.3	42.5	4.6
TaAffx.13367.1.A1_at	3.2	39.3	32.8	44.8
TaAffx.32060.1.S1_at	3	39.2	33.1	41.1
TaAffx.54491.1.S1_at	3	39.1	4.1	7.2
Ta.8304.1.S1_a_at	3.8	39	34.6	3.4
Ta.26347.1.A1_at	2.1	39	4.1	7.1
TaAffx.119923.1.A1_at	2.7	39	11.8	12.9
TaAffx.5802.2.S1_at	3.1	39	13.1	14
TaAffx.81277.1.S1_at	1.5	38.9	21	2.8
Ta.10099.1.S1_at	2.8	38.7	34.3	76.4
TaAffx.80605.1.S1_at	2.9	38.7	6.6	13.2
Ta.20928.2.A1_at	3.5	38.6	36.3	20.9
Ta.18398.1.S1_at	1.2	38.4	27.4	8.1
TaAffx.121567.1.S1_at	2.5	38.3	2.2	4
TaAffx.23849.1.S1_at	1.3	38.3	4.9	4.8

TaAffx.83141.1.S1_at	3.6	38.3	7.1	1.6
Ta.775.1.A1_at	1.7	38.1	3.6	3.4
TaAffx.111313.1.S1_at	3.6	38	7.3	6.4
TaAffx.78802.1.S1_at	1.7	37.7	49.5	102.6
TaAffx.85382.1.S1_at	1.4	37.7	19.8	6
Ta.15547.1.S1_at	3.3	37.6	15.3	34.6
TaAffx.9061.2.S1_at	3.5	37.6	29.9	21.3
Ta.30507.1.S1_at	1.4	37.4	103.8	80.5
TaAffx.32378.1.S1_at	3.4	37.2	36.2	15.7
Ta.5490.3.S1_at	1.9	37.1	8.8	18.9
Ta.21362.2.S1_x_at	2.8	37.1	2.8	2.8
TaAffx.108836.1.S1_at	2.6	37.1	37.1	17.2
Ta.30765.2.S1_s_at	3.5	37	8.1	8.8
Ta.30633.1.A1_at	2.3	36.9	21.4	1.7
Ta.27806.1.A1_at	1.2	36.9	4.8	24.1
TaAffx.26778.1.S1_s_at	3	36.9	1.1	0.6
TaAffx.118625.1.S1_at	0.9	36.8	2.7	20.7
Ta.10826.1.A1_a_at	2.9	36.7	9.2	7.4
Ta.11962.1.A1_at	2.6	36.6	40.5	46.8
Ta.16845.1.S1_at	0.9	36.4	3	29.5
Ta.27882.1.S1_x_at	1.3	36.1	22.3	4.6
TaAffx.38592.1.S1_at	2.4	35.9	39.9	16.2
TaAffx.26414.1.S1_at	2.1	35.9	14.7	9.2
TaAffx.112375.1.S1_at	2.8	35.7	96.5	6.6
TaAffx.64652.1.S1_at	3.1	35.5	11.3	24.7
TaAffx.58211.1.S1_at	1.1	35.3	10.3	77.4
TaAffx.27074.1.S1_at	1.8	35.3	16.9	3.8
RPTR-Ta-X58791-1_s_at	1.3	35.2	36.8	6.8
TaAffx.52278.1.S1_at	2.9	35.2	26.7	18.8
Ta.1106.1.A1_at	1.7	34.9	8.5	30.9
TaAffx.5261.1.S1_at	2	34.9	30.9	19.7
TaAffx.128729.1.S1_at	2.4	34.8	2.4	6.4
Ta.15668.1.S1_at	2.9	34.8	25.5	71.2
Ta.6093.2.S1_at	1.7	34.8	1.6	4.7
Ta.4797.2.S1_at	1.9	34.6	40	11.9
Ta.1682.1.S1_at	2.9	34.5	2.7	6.6
TaAffx.50233.1.S1_at	2.7	34.3	8.1	24
TaAffx.83806.1.S1_at	1.3	34.2	4.5	2.3
Ta.10617.2.S1_x_at	3.2	34.1	6.1	3.5
Ta.408.2.S1_at	2.5	33.7	5.9	23.9
TaAffx.78900.2.S1_at	2.1	33.6	28.5	18.5
Ta.24799.1.A1_at	2.3	33.4	22.3	6.1
Ta.1727.1.A1_at	2.9	33.4	129.4	28.6
TaAffx.82306.1.S1_x_at	1.8	33.4	3	23.5
TaAffx.59228.1.S1_at	2.6	33.4	14.8	2
Ta.24496.1.S1_at	1.2	33.3	8.5	20.2

TaAffx.38105.1.A1_at	1.9	33.2	60	43.6
TaAffx.78291.1.S1_at	2.3	33.2	6.8	27.7
Ta.26492.1.S1_at	2.6	33.1	51.3	37.9
TaAffx.86316.1.S1_at	3.2	33	2.5	11.4
TaAffx.86540.1.S1_at	2.3	32.6	17.8	38.1
TaAffx.81642.1.S1_at	2.9	32.5	20.4	45.4
TaAffx.30607.1.S1_at	1.7	32.5	18.3	43.9
Ta.13949.1.A1_at	1.1	32.3	17.4	16.2
Ta.6278.3.S1_at	1.8	32.3	27.1	2.4
TaAffx.120321.1.A1_s_at	2.8	32.3	34	3.6
TaAffx.85802.11.S1_at	1.8	32.3	1.8	1.8
Ta.9957.1.S1_at	2	32.2	39.4	4.6
Ta.13391.1.S1_at	2.9	32.2	7.3	16.6
TaAffx.112708.1.S1_at	3.2	32.2	8.2	6
TaAffx.31810.1.S1_at	1.7	32.2	7.2	3.2
Ta.28316.2.S1_x_at	2.8	32.1	2.7	20.1
TaAffx.128414.42.S1_at	2.8	32	14.8	10.9
Ta.28061.2.S1_at	1.4	31.9	3.2	6.1
TaAffx.85397.2.S1_at	1	31.8	24.9	44.6
TaAffx.12323.1.A1_at	2.8	31.7	10.2	9.8
Ta.5662.3.A1_x_at	2.2	31.7	2.2	10.4
TaAffx.31651.1.S1_at	0.7	31.6	5	32.1
Ta.25659.1.A1_at	2.6	31.5	35.8	85.6
TaAffx.97045.1.S1_at	0.8	31.4	10.5	17
TaAffx.24062.1.S1_at	2.4	31.3	9.2	19.1
TaAffx.84648.1.S1_at	2.8	31.3	9.3	32.7
TaAffx.78193.1.S1_at	2.1	31.2	7.2	9.3
TaAffx.78595.1.S1_at	1.5	31.1	5	22.6
Ta.29955.1.A1_at	2.5	31	10.5	22.2
Ta.11272.2.S1_at	1	31	13.9	24.1
Ta.22361.1.S1_at	2.7	30.9	49.6	12.7
Ta.11899.1.A1_at	3	30.8	13.6	28.4
Ta.4081.3.S1_at	2.2	30.8	9.2	3.4
Ta.27229.1.A1_at	1.5	30.7	5.3	11.3
Ta.10919.1.S1_at	1.9	30.7	24.4	2.9
TaAffx.28557.1.S1_at	2.9	30.6	5.5	6.8
Ta.13341.2.S1_x_at	0.8	30.5	2.9	4.5
TaAffx.58033.1.S1_at	3	30.5	27.6	10
TaAffx.109794.1.S1_x_at	2.9	30.5	14.7	4.5
TaAffx.28222.2.S1_at	1.8	30.5	8.7	74.5
TaAffx.25725.1.S1_at	2.2	30.4	7.6	8.4
TaAffx.54299.1.S1_at	2.4	30.4	2.5	3.6
TaAffx.4382.1.S1_at	2.3	30.3	7.2	4.7
TaAffx.109978.2.S1_at	2	30.2	15.1	30.4
TaAffx.1849.1.S1_at	1	30	19.7	2.2
TaAffx.7479.1.S1_at	2.6	30	28.4	14

Ta.963.3.S1_at	2.1	30	3.1	10
TaAffx.85049.1.S1_at	2.9	29.8	8.1	8.3
Ta.4117.1.S1_at	1	29.7	15.5	23
TaAffx.26805.1.S1_at	2.5	29.6	6.6	3.8
Ta.24738.1.S1_x_at	1.5	29.5	19.9	20.5
Ta.13076.1.S1_at	2.1	29.3	11.6	2.1
Ta.17483.1.S1_at	1.5	29.2	19.7	42.6
TaAffx.30781.1.S1_at	2.6	29	23.8	7
TaAffx.112773.1.S1_at	2.8	28.9	2.9	6.3
Ta.4306.1.S1_at	2.6	28.7	1.7	2.3
TaAffx.46015.1.A1_at	2.3	28.7	13.3	60.1
Ta.22461.2.S1_at	2.2	28.7	23	52.1
Ta.16385.1.S1_at	0.9	28.7	5.3	4.2
Ta.9664.2.A1_at	1.5	28.7	6.1	5.9
TaAffx.98423.1.A1_at	2.4	28.6	26.7	36.6
TaAffx.6820.1.S1_at	2.5	28.6	2.8	2.4
Ta.20650.2.S1_at	1.7	28.5	1	1.6
TaAffx.96538.1.S1_at	2.3	28.4	7.3	33.9
TaAffx.55604.1.S1_at	1.4	28.4	35.8	36.5
TaAffx.113419.1.S1_at	1.9	28.3	12.8	9.5
TaAffx.117141.1.S1_at	2.1	28.3	5.6	3.1
TaAffx.31824.1.S1_at	1.7	28.3	4.3	3.7
TaAffx.117280.1.S1_at	2.8	28.3	31	62.2
TaAffx.79711.2.S1_at	1.5	28.3	37.6	10.7
Ta.26563.1.S1_at	1.3	28.2	3.2	1
Ta.10243.2.S1_at	1.6	28.2	29.1	51.5
TaAffx.92860.2.S1_at	2.7	28.1	4	5.6
Ta.18530.1.S1_a_at	1.3	27.8	52.2	4.7
TaAffx.104761.1.S1_at	2.7	27.7	3.4	9.8
TaAffx.31746.1.S1_at	0.9	27.7	27.4	5.6
TaAffx.25602.1.S1_x_at	2.4	27.5	1.6	11.3
Ta.24934.2.S1_a_at	2.4	27.4	20.2	3.9
Ta.4554.2.S1_at	1.7	27.2	2.3	22.8
Ta.16779.2.S1_x_at	2.7	27.2	28.6	32.4
Ta.29602.2.S1_a_at	2.6	27.2	21.9	16.3
TaAffx.81595.1.S1_at	2	27.2	9.4	2.4
Ta.14866.1.S1_at	1.5	27.1	22.3	2.7
TaAffx.85884.1.S1_at	1.8	27.1	59.5	12.3
Ta.10092.1.S1_at	1.2	27	7.2	15.7
TaAffx.50141.3.S1_s_at	1.3	27	37.3	18.7
TaAffx.132498.1.S1_at	2.5	26.9	3.5	3
TaAffx.6187.1.S1_at	2.1	26.9	2.7	8.2
TaAffx.108841.1.S1_at	1.9	26.9	6.5	33.6
TaAffx.112828.1.S1_at	1.4	26.8	7.3	19.9
TaAffx.86449.3.S1_at	1.4	26.8	5.1	5.3
TaAffx.12145.1.S1_at	2.2	26.8	20.2	5.8

TaAffx.83275.3.S1_s_at	1.9	26.6	10.1	27
Ta.17697.1.S1_at	1	26.5	6.1	12.8
Ta.21115.3.A1_s_at	2.4	26.2	5.8	16.2
TaAffx.12279.2.S1_at	2.2	26.2	61.6	48.7
TaAffx.57988.1.S1_at	2.1	26	1.1	8.1
Ta.3743.1.A1_s_at	2.4	25.8	35.5	3.5
Ta.16714.1.S1_at	2.3	25.8	26.3	3.3
Ta.28606.1.A1_at	1.8	25.7	10.1	50.6
Ta.23031.1.A1_at	1.1	25.7	12.5	7.9
TaAffx.93270.1.A1_at	2.5	25.7	41.3	66.5
TaAffx.30492.1.S1_at	1.7	25.7	45.4	10.3
TaAffx.111106.1.S1_at	0.7	25.5	10.2	8.4
TaAffx.24038.1.S1_at	1.7	25.4	16.7	3.8
TaAffx.25951.1.S1_at	1.4	25.3	18.4	6.4
TaAffx.85001.1.S1_at	2.3	25.2	24.7	4.9
Ta.30538.1.S1_at	1.5	25	21.6	5.5
TaAffx.106000.1.S1_at	2	25	6.1	4.5
Ta.15654.1.S1_at	1.7	24.9	17.2	11.9
Ta.3419.3.S1_at	1.2	24.8	26.5	35.4
Ta.28547.1.S1_at	2.1	24.6	9.1	5.9
Ta.22433.1.S1_at	0.4	24.3	15.1	5.5
TaAffx.77596.1.S1_at	1.6	24.2	2.3	2
Ta.22415.1.S1_x_at	2.2	24.1	6.7	12.2
TaAffx.31925.1.S1_at	2.2	24.1	19	22.6
Ta.5873.1.S1_x_at	2	24	17.4	3.6
Ta.22428.1.S1_at	1.3	24	56.3	24.6
TaAffx.80687.1.S1_at	2.3	24	2.4	2.6
TaAffx.110081.1.S1_x_at	1.5	23.6	7.1	5.1
TaAffx.6790.1.S1_at	1.1	23.5	3	1.7
TaAffx.119327.1.A1_at	1.9	23.5	2	6.8
TaAffx.82807.1.S1_at	1.8	23.5	5.4	7.4
TaAffx.77834.1.S1_at	1.4	23.4	1.6	2.5
TaAffx.1861.5.S1_x_at	2.2	23.2	6.6	47.2
Ta.26744.1.A1_at	1.6	23.1	9.4	24.2
TaAffx.11930.2.S1_at	1.9	23	34.2	30.7
TaAffx.114312.1.S1_x_at	1.9	22.9	44.4	23.3
TaAffx.81088.1.S1_at	2	22.8	8.3	22.3
Ta.20624.1.S1_at	2.1	22.7	4.4	5.9
TaAffx.29286.1.S1_at	2.1	22.7	1.2	2.3
TaAffx.28482.1.S1_at	0.8	22.6	6.4	56.9
Ta.23293.1.S1_at	1.1	22.5	1.7	11
Ta.24690.2.S1_at	2.1	22.5	15.4	2.9
Ta.5898.1.S1_at	1.9	22.4	7.5	24.6
Ta.18878.1.S1_at	0.6	22.1	16.5	26.7
TaAffx.129484.1.A1_at	1.8	21.9	12.6	3.2
TaAffx.30021.1.S1_at	0.6	21.8	20	3.3

TaAffx.109621.1.S1_at	0.7	21.8	6.1	3.7
TaAffx.52730.1.S1_at	1.9	21.6	8.6	38.1
TaAffx.93101.1.S1_at	1	21.6	23.9	52.7
TaAffx.53532.1.S1_at	2.1	21.4	9	15.6
Ta.8788.1.A1_a_at	2	21.3	21.6	24.8
Ta.9944.1.S1_at	1.1	21.2	18.6	30.6
Ta.1751.2.S1_x_at	1.5	21.2	2.8	1.4
TaAffx.72060.1.A1_at	1.9	21.2	7.8	24.4
TaAffx.30262.1.S1_at	0.3	20.8	12	11.3
Ta.27142.1.S1_at	1.6	20.7	5.8	5.5
TaAffx.24874.1.S1_at	1.3	20.6	7.5	2.3
Ta.87.1.S1_x_at	2	20.5	2.7	1.7
TaAffx.82672.1.S1_at	1.5	20.5	2	2.1
TaAffx.113486.1.S1_at	1.7	20.3	3.8	4
TaAffx.106701.1.S1_at	1.6	20.3	39.2	65.8
Ta.12328.1.S1_at	1.2	20.2	4	3.2
Ta.8486.2.S1_at	1.7	20.2	4.2	3.6
TaAffx.113774.3.S1_at	1.1	20.1	55.9	1.6
TaAffx.105869.1.S1_at	1	20	3.9	2
TaAffx.15910.1.S1_at	0.7	19.7	3.3	1.5
TaAffx.106318.1.S1_at	0.8	19.7	27.1	63
TaAffx.110934.1.S1_at	0.7	19.5	1.3	2.5
TaAffx.53329.1.S1_at	1.2	19.5	23.6	31.5
Ta.17613.1.S1_at	1	19.4	2.6	3.2
TaAffx.29357.1.S1_at	1.4	19.4	68.3	45.3
TaAffx.85616.1.S1_at	1.7	19.4	4.4	14.5
TaAffx.120208.1.S1_at	1.7	19.3	2.9	2
TaAffx.83341.1.S1_at	1.4	19.1	3.1	7.9
Ta.686.1.S1_x_at	0.9	19	1251.4	574.8
TaAffx.25963.1.A1_at	0.8	19	34.9	34.3
TaAffx.57030.1.S1_at	1.8	19	2.5	4.5
Ta.9346.2.S1_at	1.4	18.9	29.9	2.9
TaAffx.118497.1.A1_at	1.6	18.9	19.8	25.5
Ta.30908.1.S1_at	1.6	18.8	28	5.6
Ta.28860.1.S1_at	1.1	18.6	19.6	7.6
TaAffx.105262.1.S1_at	1.8	18.4	21.4	8.9
Ta.23271.2.S1_a_at	1.6	18.3	10.6	4.8
Ta.12980.1.S1_at	1.7	18.2	18.9	29.8
TaAffx.24160.1.S1_at	1.8	18.2	2.7	9.2
Ta.10109.2.S1_x_at	1.1	18.2	4.2	17.4
Ta.20865.1.S1_at	0.9	18.1	1.3	1.8
TaAffx.113469.1.S1_at	1.4	18	25.3	34.9
TaAffx.55554.1.S1_at	1.4	18	25.9	44
TaAffx.112134.1.S1_at	1.6	17.9	35.9	28.7
Ta.18027.1.S1_at	0.9	17.7	7.3	15.9
Ta.12381.1.A1_at	1	17.6	22.2	1.7

TaAffx.7107.1.S1_x_at	1.2	17.6	2.8	4
Ta.10761.1.S1_at	1.5	17.5	15.7	9.8
Ta.6877.3.S1_at	1.1	17.5	32.5	3
Ta.1840.1.S1_a_at	1.3	17.4	4.1	10.8
TaAffx.36917.1.A1_at	1.2	17.4	4.4	9.9
TaAffx.122543.1.S1_at	1.7	17.4	4.2	5.5
TaAffx.24732.1.S1_at	1.7	17.4	3.8	16.6
TaAffx.6422.1.S1_s_at	1.6	17.3	20	1.8
Ta.9923.1.S1_x_at	1.3	16.8	3.4	31.1
Ta.16323.2.S1_at	1	16.7	8.1	2
TaAffx.29723.1.S1_at	1.4	16.6	4.9	21.6
Ta.10276.1.A1_at	1	16.4	1.5	3.9
TaAffx.54527.1.S1_at	1.3	16.4	24.8	27.9
TaAffx.10719.2.S1_at	1.4	16.4	3.2	1.9
TaAffx.83913.1.S1_at	1.6	16.3	69.8	4.6
Ta.23290.1.S1_at	1.3	16.2	32	1.8
TaAffx.109389.1.S1_x_at	0.9	16.2	19.2	32.9
Ta.10866.1.A1_at	1	15.9	1.6	4.7
TaAffx.108626.1.S1_at	0.9	15.8	1.5	2.2
TaAffx.81438.1.S1_at	0.7	15.5	1.9	1.5
TaAffx.81008.1.S1_at	1	15.5	0.9	3.4
Ta.22062.1.S1_at	1.5	15.3	1.5	13.6
TaAffx.82716.1.S1_at	0.4	15.3	8.7	13
TaAffx.108274.9.S1_at	1.2	15.2	5.4	2.8
TaAffx.122459.1.A1_at	1.2	15.1	15.7	3.6
TaAffx.104724.1.S1_at	0.8	15	3.3	1.5
Ta.16384.1.S1_at	0.9	14.7	5.1	26.6
Ta.12959.1.A1_at	1.3	14.5	3.9	7.4
Ta.15126.2.S1_x_at	1.3	14.5	30.1	34.4
Ta.17289.1.S1_at	1.2	14.4	3.5	10
TaAffx.82074.1.S1_at	0.9	13.9	2.2	9.1
TaAffx.25579.1.S1_at	1.1	13.9	21.6	41.1
Ta.5049.1.A1_at	1.3	13.8	57.6	4.7
TaAffx.128414.54.S1_x_at	0.8	13.6	2.1	1.4
TaAffx.54242.1.S1_at	1.3	13.5	29.8	7.8
Ta.21419.1.S1_at	1.1	13.1	29.8	22.6
TaAffx.102783.1.A1_at	0.9	13.1	2.7	12.3
TaAffx.111105.1.S1_at	1.1	13	5.1	23.8
TaAffx.117200.1.S1_at	1.1	12.8	13.8	12.3
TaAffx.98753.1.S1_at	0.8	12.1	3.3	2.6
TaAffx.80971.1.S1_x_at	0.8	12	62.2	11.5
TaAffx.111857.3.S1_at	0.9	11.8	17.1	18.9
TaAffx.69933.1.S1_at	1	11.7	5.9	21.5
TaAffx.112541.1.S1_at	1	11.6	8	7.5
Ta.27184.1.S1_at	0.7	11.1	38.4	1.5

TaAffx.58861.1.S1_at	0.7	10.1	0.3	0.3
RPTR-Ta-AF292559-1_at	0.8	9.9	17.3	36.6
TaAffx.37427.1.A1_at	0.7	9.9	53.7	26.5
TaAffx.113152.1.S1_at	0.5	9.1	0.1	0.3
Ta.18862.3.S1_at	0.9	9.1	8.8	4.2
TaAffx.38378.1.S1_at	0.3	7.6	14.2	16.1
Ta.18741.1.S1_at	0.6	7.5	12.7	32.2
TaAffx.96931.2.S1_at	0.5	6.2	26.7	2.5
TaAffx.4060.1.A1_at	0.2	5.2	5.4	1.7
Ta.17417.1.S1_at	0.1	1.2	10.7	1.1

Table B.4 *Gc2*/- early over *Gc^{mut}#1*/- early

Probe set ID	***GC2* E**	***GC^{mut}#1* E**	***GC2* L**	***GC^{mut}#1* L**
TaAffx.12865.1.S1_at	960.5	51.7	4.7	17.2
Ta.3611.1.S1_at	904.1	62.5	39.6	78.4
Ta.15832.1.S1_at	746.5	63	47.5	44.8
TaAffx.59898.1.S1_s_at	662.7	37.8	20.9	58.3
TaAffx.113100.1.S1_at	596.8	54.6	89	176.4
Ta.14156.1.S1_at	492	30.8	2.7	35.6
TaAffx.120614.1.S1_at	469.8	43.8	39.7	19.7
Ta.13056.2.A1_at	360.6	14.2	6	26
TaAffx.58299.1.S1_x_at	338.1	18.1	153.4	39.1
TaAffx.9378.1.S1_at	328.9	16	6.9	18.3
Ta.21427.1.S1_at	285.2	6.4	23.7	19.5
TaAffx.57418.1.S1_at	273.7	22.2	71	77.8
TaAffx.51327.1.S1_at	257.8	16.4	2	4.3
TaAffx.27500.1.S1_at	257.7	22	162.4	288.4
TaAffx.55901.1.S1_at	242.8	20	72.4	126.2
TaAffx.31324.1.S1_at	242.7	20.1	61.5	74.1
TaAffx.32413.1.S1_at	198.6	17.2	6.2	14.5
Ta.3561.1.A1_at	198	16.9	13.5	18.1
TaAffx.38536.1.A1_at	194.8	15.2	4.5	3
TaAffx.54727.1.S1_at	194.3	15.2	37.6	117
Ta.5503.1.S1_s_at	186.2	5.6	10.4	11.5
TaAffx.121733.1.S1_at	183.8	15.2	11.3	18.1
Ta.15217.1.S1_at	180.1	16.2	158.7	20.8
Ta.6668.2.S1_at	177.6	11.1	18.7	16.7
Ta.17785.1.S1_at	177.1	15	163.1	222.9
Ta.2990.1.S1_at	177.1	5.6	3.6	2.2
Ta.16070.1.S1_at	172.4	11.6	9.8	15.6
TaAffx.30081.1.S1_at	168.6	10.7	98.1	76
TaAffx.112428.1.S1_at	154.2	3.4	5.6	86.4
Ta.10107.3.S1_at	152.5	6.4	157.9	30.8
Ta.25243.2.S1_at	151.7	15.1	65.8	126.5

TaAffx.86450.1.S1_at	149.9	11.2	42.5	38.6
Ta.3535.1.S1_at	149.2	5.8	8.8	47.1
Ta.5448.2.S1_x_at	148	9.3	75.1	131.2
TaAffx.9604.1.S1_at	144.8	11.7	180.9	212.2
TaAffx.56645.1.S1_at	143.3	12.7	69.6	191.5
Ta.4850.2.S1_at	143.2	5.5	19.3	16.5
TaAffx.123378.1.S1_at	143	10.1	22.6	19
Ta.5568.2.S1_at	142.7	11.7	11.5	38.2
TaAffx.76317.1.S1_s_at	140.8	12.2	14.1	106.5
TaAffx.66650.1.S1_at	139.3	11.1	16.5	27.5
TaAffx.78499.1.S1_at	137.2	13.5	31	33.9
TaAffx.59561.1.S1_at	135.3	3.7	163.9	296
Ta.7555.3.S1_at	134.7	5.6	12.5	83.6
TaAffx.57792.1.S1_at	134.6	8.4	27.7	92.1
TaAffx.8165.1.S1_at	133.9	11.9	60.4	104
Ta.4100.1.S1_at	133.4	0.7	206.3	87.1
TaAffx.83179.1.S1_at	132.5	8.1	65.1	63.4
TaAffx.80666.1.S1_x_at	131	12.8	16.8	59.7
Ta.28983.1.S1_at	130.2	11.1	6.7	9.2
Ta.19425.1.S1_at	129.6	12.7	17.5	52.2
TaAffx.105474.1.S1_at	128.3	8.6	146.4	155.2
TaAffx.86128.1.S1_at	127.1	9.2	149.1	81.6
Ta.16323.1.S1_a_at	124	8.3	14	14.7
TaAffx.6404.1.S1_at	123.4	5.1	28.2	17.9
Ta.20517.1.S1_a_at	122.6	10.7	10.8	100.4
Ta.5847.1.S1_at	122.6	11.2	49.9	24.1
TaAffx.107325.2.S1_x_at	122.2	8.3	95.4	55
TaAffx.113127.1.S1_at	119.8	4.6	41	55
TaAffx.47284.1.A1_at	119.8	10.9	62.7	126.7
TaAffx.9033.1.S1_at	119.1	7.6	18.8	179.1
Ta.9864.1.S1_at	118.1	7.6	46.3	25.1
TaAffx.31829.1.S1_at	116.9	10.8	25.3	100.5
TaAffx.29220.1.S1_at	116.2	11.5	126.1	201.1
Ta.29585.2.S1_at	115.8	9.4	10.8	135.8
TaAffx.31498.1.S1_s_at	114.1	9.9	10.5	19.6
TaAffx.55844.1.S1_at	113.1	10.3	14.3	18.1
TaAffx.106262.1.S1_at	112	2.2	24.3	52.6
Ta.15897.1.S1_at	111.9	9	66.8	107.5
Ta.1031.3.S1_at	111.8	10.9	28.9	55.1
TaAffx.7960.1.S1_at	111.8	4.1	79.9	82.5
TaAffx.18065.1.S1_at	111.3	10.9	84	109.2
Ta.14344.1.S1_at	111.1	7.2	29	9.7
TaAffx.87253.3.S1_at	110.1	9.4	4474.5	2884.1
TaAffx.38829.1.S1_at	110	7.8	54	31.9
TaAffx.53294.1.S1_at	109.9	5.9	13.9	29.3
Ta.13298.1.S1_at	109.7	8.6	109.7	59.8

TaAffx.7239.1.S1_at	109.3	7.6	86.8	57
Ta.30650.1.S1_at	108.6	10.1	50	75.2
Ta.6223.1.S1_at	107.3	8.8	37	18.9
TaAffx.27069.1.S1_at	107.2	6	26.1	55.8
Ta.27259.1.S1_at	105.8	5.6	15.7	59.7
TaAffx.86807.1.S1_at	105	6.9	31.2	58.3
TaAffx.38017.1.A1_at	104.8	3.9	8.8	39.9
TaAffx.24281.1.S1_at	104.7	4.6	41.8	70.3
TaAffx.78732.1.S1_at	104.5	3.7	70	40.9
TaAffx.62693.1.S1_at	104.3	6.7	72	20
TaAffx.85839.1.S1_at	104.2	8.2	79.2	57.6
TaAffx.56934.1.S1_at	103.2	9.4	8.2	54.6
TaAffx.81144.1.S1_at	103	5.5	68.5	84
TaAffx.22829.1.S1_at	102.8	7.2	3.9	54
TaAffx.64725.1.S1_at	102.6	4.3	24.4	35.1
TaAffx.28365.1.S1_at	100.7	9.9	14.6	36.8
Ta.12417.1.A1_at	99.9	9	35.6	27.9
TaAffx.90179.2.S1_s_at	98.9	6.9	17.7	8.4
TaAffx.38705.1.A1_at	97.9	4.2	98.4	75.1
Ta.24044.1.A1_at	97.6	8.8	12.4	9
TaAffx.24725.1.S1_at	97.1	3.3	3.3	74.1
TaAffx.65948.1.A1_at	95.4	3.6	40.1	40.5
TaAffx.5502.1.S1_at	95.1	3.3	6.8	31.1
Ta.10390.2.A1_a_at	94.1	8.9	61.8	30.1
Ta.397.1.A1_at	93.8	4.6	31.8	28.8
TaAffx.112967.1.S1_at	93.8	2.9	75.2	101.2
TaAffx.128712.11.S1_at	93.7	3.6	41.7	38
TaAffx.118642.1.S1_at	93.4	6	14.2	59.1
TaAffx.26235.1.S1_at	92.8	5.3	11.6	9.9
TaAffx.111355.1.S1_at	92.5	6.1	82.4	10.2
Ta.5685.1.S1_at	91.5	7.9	23.7	70.8
TaAffx.57193.1.S1_at	90.8	8.2	22.6	24.5
Ta.25364.1.S1_at	90.1	7.1	57.3	26.4
TaAffx.31169.1.S1_at	90.1	4.1	38.8	51.7
TaAffx.97953.1.S1_at	89	4.8	56.1	15.3
TaAffx.51106.1.S1_at	89	3.3	3.2	43.8
TaAffx.80327.1.S1_at	88.1	5.2	11.6	26.1
Ta.26184.1.S1_at	87.1	6	30.2	48.3
Ta.26584.1.A1_at	86.9	8	83.4	19.4
TaAffx.80072.1.S1_x_at	86.9	4.7	148.3	97.9
Ta.7967.1.A1_at	86.8	4.3	36.8	113.3
Ta.1971.3.S1_at	86.6	8.5	58.7	53.2
Ta.7330.1.S1_a_at	86.5	4.3	4.4	11.5
Ta.12328.2.A1_at	86.3	5.7	6	45.8
TaAffx.4858.1.S1_at	86	5.3	32.7	26.4
TaAffx.57188.1.S1_at	86	3.3	12.1	6.9

TaAffx.53241.1.S1_at	85.4	7.5	42.3	67.6
Ta.18723.2.S1_a_at	84.8	2.6	8.3	9
TaAffx.26553.1.S1_at	84.7	1.8	42.7	44
TaAffx.84006.1.S1_at	84.3	6.8	41.1	53.5
TaAffx.77811.1.S1_at	83.1	7.4	32.2	68.9
TaAffx.85676.1.S1_at	83	4.4	22.6	101
Ta.4660.1.S1_at	82.9	7.9	6.2	37.2
Ta.3840.2.S1_at	82.8	6	43.4	25
TaAffx.23460.1.S1_at	82.5	5.7	66.7	58.7
Ta.26789.1.S1_at	82.3	3	48.7	19.1
TaAffx.51407.1.S1_at	81.8	5.9	50.2	55.4
Ta.20674.2.S1_x_at	81.7	7.1	154.3	52.9
TaAffx.121618.3.S1_at	81.7	8.1	8.1	26.5
TaAffx.123816.3.S1_at	81.6	5.6	19.1	13.3
Ta.10.1.S1_a_at	81.4	3.8	21.4	5
Ta.25675.1.A1_at	81.4	7.6	6.8	36.9
TaAffx.87235.1.S1_at	81.4	5.4	17.8	8.1
TaAffx.128541.39.S1_at	80.3	4.9	27.1	34
TaAffx.110720.1.S1_at	79.4	5.9	6	82.7
Ta.10054.1.S1_at	79.2	3.7	17	67.5
Ta.6899.3.S1_at	79.1	6.9	10.2	28.2
Ta.4218.3.S1_at	78.5	1.8	39.6	17.1
TaAffx.106028.1.S1_x_at	78.3	5.1	42	75.7
TaAffx.27234.1.S1_at	78	4	31.3	9.4
TaAffx.91968.1.S1_at	78	4.5	22.7	54.9
TaAffx.24701.1.S1_at	77.6	4.6	8.9	39
Ta.8284.1.S1_at	77.5	5.7	49	25.3
Ta.16942.1.S1_a_at	77.1	5.8	11.4	10.5
TaAffx.69653.1.S1_at	76.8	5.7	4.4	52.7
TaAffx.38749.1.S1_at	76.8	4.1	12.5	46
Ta.28659.3.S1_x_at	76.5	6.6	10.7	18.4
TaAffx.128585.4.S1_x_at	76.5	5.9	24.1	137.7
Ta.8129.1.S1_s_at	76.2	6.7	13.7	16.5
TaAffx.30903.1.S1_at	76	6.9	41.3	24.3
Ta.8281.1.S1_at	75.6	5.3	4.6	7
TaAffx.80867.1.S1_at	75.5	6.2	44.7	10.6
Ta.17756.1.S1_at	75.4	5.7	30.8	5.7
TaAffx.1074.1.S1_at	75	3	39.1	29.3
TaAffx.50680.1.S1_at	74.9	5.3	7.5	63.9
TaAffx.5846.1.S1_at	74.6	7.4	8.6	11.8
Ta.22411.1.S1_at	74.4	5.4	37	87.6
TaAffx.108668.1.S1_at	74.4	2.2	3.3	2.9
TaAffx.37181.1.A1_at	74.3	6.8	9.3	12.9
TaAffx.97914.1.S1_at	74.2	3.1	35.7	28.5
TaAffx.25367.1.S1_at	73.9	6.4	29.8	68.3
TaAffx.54887.1.S1_at	73.8	5.3	4.1	5

TaAffx.56838.1.S1_at	73.8	4.5	45.6	33.5
TaAffx.31046.1.S1_at	73.4	4.6	14.8	21.1
TaAffx.87228.1.S1_at	73.2	4.7	2.7	9.8
Ta.14780.1.S1_at	73.1	6.7	51.8	44.3
Ta.7190.3.S1_at	73	6.3	67.1	81.2
Ta.26474.1.A1_at	72.5	5.3	9.1	55.7
TaAffx.83020.2.S1_at	72.3	2.5	8.1	38
TaAffx.35356.1.S1_at	72.3	4.3	47	96.6
TaAffx.85660.1.S1_at	72.3	7.1	12.8	10.2
Ta.29460.3.S1_at	72.2	5.7	63.7	58.4
Ta.18560.1.S1_at	71.7	3.8	7.6	6.3
TaAffx.84344.1.S1_at	71.7	6	48.5	12.3
TaAffx.24573.1.S1_x_at	71.5	6	3.1	4.1
Ta.3520.1.S1_at	71.4	6.4	38.8	21.9
TaAffx.8903.1.S1_at	71.1	4.9	35	62.5
TaAffx.54318.1.S1_at	71	1.7	4.1	47.2
TaAffx.56982.7.S1_at	71	3.7	31.5	10.1
TaAffx.105909.1.S1_at	70.9	6.4	5.8	5.3
TaAffx.86926.1.S1_at	69.8	4.8	52.8	84.7
TaAffx.30954.2.S1_at	69.7	6.4	4.3	40.6
Ta.17438.1.S1_at	69.1	6.9	43.3	35
TaAffx.80491.1.S1_at	69.1	4.2	73.3	57.4
TaAffx.26866.1.S1_at	68.5	4.8	6.9	3
TaAffx.55665.2.S1_at	68.5	2.7	5	9.5
Ta.22673.1.S1_s_at	68.3	5.2	9.3	40.4
Ta.15491.1.S1_at	68.3	4.9	41.6	7.5
TaAffx.22967.1.S1_at	68	3.2	3.7	4.7
Ta.27185.1.S1_at	67.8	4.9	17.4	14.8
TaAffx.83422.1.S1_at	67.7	2.5	56.7	54.8
TaAffx.113363.1.S1_at	67.7	2.9	9	34.7
TaAffx.53168.1.S1_at	67.5	5.2	11.9	16
Ta.10910.1.A1_at	67.3	3.5	17.5	35.2
Ta.5148.1.S1_a_at	67.2	6.4	51.1	47
Ta.8173.2.A1_at	67.2	6.4	29.9	13.6
TaAffx.106854.1.S1_at	66.9	4.3	24.8	70.6
TaAffx.53790.1.S1_at	66.8	5	3.6	49.6
TaAffx.81169.1.S1_at	66.3	3.6	10.1	4.5
TaAffx.59206.1.S1_x_at	66.3	2.2	18.5	13.1
TaAffx.109038.1.S1_at	66.2	3.2	14.1	11.4
TaAffx.32049.1.S1_at	66.1	3.3	5.5	38.5
TaAffx.53195.2.S1_at	66.1	2	9.6	13
TaAffx.9253.1.S1_at	65.9	5.7	31.1	7.5
Ta.27952.1.S1_at	65.8	4.5	58.1	20.1
TaAffx.65239.1.A1_at	65.2	6.2	22.9	8
TaAffx.85637.1.S1_at	65.2	4.2	69.4	24.8
TaAffx.9167.1.S1_at	65.2	5.8	44.9	81.9

TaAffx.111092.1.S1_at	65	6	9.9	34.7
Ta.9963.1.S1_at	64.9	2.6	15.1	21.7
Ta.5954.2.S1_at	64.7	5.2	61.4	10.7
TaAffx.56854.1.S1_at	64.7	4	77.6	75.1
TaAffx.57191.1.S1_at	64.5	6.3	6.5	72.2
TaAffx.108453.1.S1_at	64.3	3	7.8	31
Ta.9308.3.A1_at	64.1	3.8	37.7	70.3
Ta.26377.1.A1_at	64	2.1	62.6	10.4
TaAffx.59823.1.S1_at	64	5.4	8.3	65.8
Ta.27559.1.S1_at	63.9	3.6	70.9	87.2
TaAffx.79698.1.S1_at	63.7	4.6	23.6	7.4
Ta.17233.1.S1_at	63.6	5.9	12.4	80.3
TaAffx.81481.1.S1_at	63.6	3.3	11.5	30.2
TaAffx.85980.1.S1_at	63.6	5.7	47.5	19.7
TaAffx.58906.1.S1_at	63.6	5.8	6.8	10.1
Ta.3133.1.S1_x_at	63.5	3.6	2.1	36.9
AFFX-r2-TagO-5_at	63.3	1.8	21.5	54.3
TaAffx.24911.1.S1_at	63.3	3.6	32.9	62.3
Ta.19089.1.S1_at	63.2	5.9	6.3	11.8
TaAffx.98090.1.A1_at	62.4	3.4	87.3	58.5
TaAffx.23589.1.S1_at	62.4	3.5	37.6	7.7
TaAffx.121217.1.A1_at	62.3	1.4	5.9	24.4
Ta.1106.2.S1_at	62.2	2.7	32.2	41.7
TaAffx.84002.1.S1_at	61.9	2.9	27.9	66.1
Ta.147.1.S1_at	61.5	5.7	20.9	53.9
Ta.26643.1.A1_at	61.5	3.4	9.2	19.3
Ta.17850.1.S1_at	61.2	3.7	21.6	17.3
TaAffx.108824.1.S1_at	61.2	5.9	70.1	18.2
Ta.20878.3.S1_at	61.2	2.8	1.4	14.8
Ta.12851.1.A1_at	61.1	3.3	19.5	15.8
TaAffx.71190.1.S1_at	60.7	4.6	4.8	13.3
TaAffx.11842.2.S1_at	60.6	1.5	47.4	72.2
Ta.4407.2.A1_at	60.2	2.4	39.8	47
Ta.23967.1.S1_x_at	60.1	4	105.1	23.3
TaAffx.86371.1.S1_at	60.1	5	16.2	14.9
TaAffx.59899.1.S1_at	59.9	4.4	43.4	22.1
TaAffx.57689.1.S1_at	59.9	2.9	19.4	6.8
Ta.19188.1.S1_at	59.7	4.8	7.9	16
Ta.2919.1.A1_at	59.7	5.8	7.1	32.2
Ta.20867.1.S1_at	59.5	4.1	67	20.2
TaAffx.108528.1.S1_at	59.5	2.7	50.1	16.8
TaAffx.30925.1.S1_at	59.5	5.4	71.2	36.2
TaAffx.53229.1.S1_at	59.5	3.8	7.1	38.4
Ta.10301.1.A1_at	59.4	4.9	75.5	73.1
TaAffx.57212.1.S1_at	59	3.2	22.8	23
Ta.4272.1.S1_at	58.9	5.8	101.3	16.1

Ta.26699.1.A1_at	58.8	1	19.1	69.6
TaAffx.12607.2.S1_at	58.7	5.2	45.7	23
TaAffx.56048.1.S1_at	58.6	3.8	4.8	3.6
Ta.25531.2.A1_x_at	58.5	4.5	34.4	59.3
TaAffx.25879.1.S1_x_at	58.4	2.1	6.7	16.1
Ta.15394.1.S1_at	58.3	4.4	137.1	109
TaAffx.108119.1.S1_at	58.1	3.6	2.9	23.7
TaAffx.113764.1.S1_at	58.1	2.6	3	8.3
TaAffx.59060.1.S1_at	58	1.5	55.2	22.1
TaAffx.82932.1.S1_at	58	4.4	24.3	11.7
Ta.26352.1.A1_at	57.7	2.6	49.8	19
TaAffx.81466.1.S1_at	57.6	1	44.4	19.1
TaAffx.112764.1.S1_at	57.6	0.8	37.2	29.8
TaAffx.77695.1.S1_at	57.4	3.7	26.4	31.5
TaAffx.30642.1.S1_at	57.4	4.3	11.1	24.9
TaAffx.83636.1.S1_at	57.4	3.1	26.1	9
TaAffx.30338.1.S1_at	57.4	5	41.7	84
TaAffx.85962.1.S1_at	57.3	2.7	49.4	99.4
TaAffx.113058.1.S1_at	57.2	3.5	2.9	3.4
TaAffx.78849.1.S1_at	57.2	4.2	4.5	2.5
RPTR-Ta-U46493-1_s_at	57.1	1	28.2	13.5
Ta.27542.1.A1_at	56.9	5.5	8.9	43.4
TaAffx.112028.1.S1_at	56.8	2.5	4.1	84.5
TaAffx.105861.1.S1_at	56.7	4.9	24.8	65.5
Ta.12938.1.S1_at	56.7	3.5	18.4	4.4
TaAffx.81668.1.S1_at	56.7	3.8	22.6	7.7
TaAffx.53858.1.S1_at	56.7	5.4	10.2	75.1
Ta.30858.1.S1_at	56.3	4.7	4.2	25.3
Ta.1875.3.A1_at	56.3	4.1	6	4.6
Ta.15492.1.A1_at	56.2	4.2	10.6	26.7
Ta.10781.1.A1_at	56.2	4.6	21.9	11.9
TaAffx.77975.1.S1_at	56.2	2.7	1.3	5
TaAffx.85411.1.S1_at	55.8	3.9	74	23.5
TaAffx.118664.1.S1_at	55.7	1.7	10.4	6.2
Ta.14686.1.S1_at	55.7	2	28	64.7
TaAffx.32174.1.S1_at	55.7	2.2	27.9	43.2
TaAffx.58590.1.S1_at	55.7	3.9	47.3	95.6
TaAffx.121954.3.S1_at	55.7	1.5	2.7	89.7
TaAffx.58548.1.S1_at	55.7	4.9	5.5	7.8
Ta.22587.2.S1_at	55.6	2.6	9.5	23.1
TaAffx.107335.1.S1_at	55.6	4.2	63.7	62.3
TaAffx.37962.1.S1_at	55.6	3.5	6.1	45.9
TaAffx.5232.1.S1_at	55.5	3.2	9.9	61.2
Ta.14035.1.S1_at	55.4	2.4	7.2	20.5
TaAffx.261.1.S1_at	55.3	4.1	17.3	12.6
TaAffx.107703.1.S1_at	55.3	2	5.2	3.6

TaAffx.22878.2.S1_at	55.2	5.1	52.1	13.2
TaAffx.30267.1.S1_at	55.1	3.6	3.3	52.5
TaAffx.90216.1.S1_at	55	3.8	39.9	54.3
TaAffx.104915.1.S1_at	55	5.1	10.3	8.9
TaAffx.110275.1.S1_at	54.9	5.1	53.3	53.2
Ta.17552.1.S1_at	54.7	4.7	43.8	95.6
TaAffx.113666.3.S1_x_at	54.7	3.5	8.3	33.9
TaAffx.128593.2.S1_at	54.7	2.8	13.1	7.6
TaAffx.42587.1.A1_at	54.5	5.2	10	64.1
TaAffx.53974.1.S1_at	54.4	2.6	26.4	3.4
TaAffx.29385.1.S1_at	54.2	3.2	9.5	11.4
Ta.20597.1.S1_at	54.1	4.6	38.6	98.2
TaAffx.108105.1.S1_at	54.1	5.1	57.2	32.8
TaAffx.77851.1.S1_at	54.1	4.8	23	67.4
TaAffx.26605.1.S1_at	54.1	2	35.8	4.1
Ta.26308.1.A1_at	54	1.3	6.9	50.7
Ta.30672.1.S1_at	53.8	4.3	31.7	47.9
TaAffx.7335.1.S1_at	53.7	2.3	14.7	41.8
Ta.20874.2.S1_x_at	53.6	3.4	6.1	6.6
Ta.17546.1.S1_at	53.6	3.2	17.5	11.8
Ta.18028.1.S1_at	53.5	4.9	7.6	17.5
Ta.12354.2.S1_at	53.5	5	20	7.9
Ta.12647.3.S1_at	53.4	5	28.4	82.2
TaAffx.53705.1.S1_at	53.2	4.6	40.8	34.8
TaAffx.83181.1.S1_at	53.2	2	27.4	18.6
TaAffx.108211.1.S1_at	52.9	3	4.9	5.1
TaAffx.84842.1.S1_at	52.9	3.8	36.9	12
TaAffx.59876.1.S1_at	52.8	4.1	49.2	10.3
Ta.278.1.S1_x_at	52.6	5	45.5	62.4
TaAffx.110716.1.S1_at	52.6	2.2	42.8	48.6
TaAffx.77809.1.S1_at	52.6	2	4.8	4.8
Ta.27520.1.S1_at	52.5	4.4	37.5	30.8
TaAffx.26623.1.S1_at	52.5	1.6	38.4	60.9
TaAffx.8388.1.S1_at	52.3	2.4	77	24.2
Ta.15798.1.S1_at	52.2	1.8	6.1	61.3
Ta.26198.1.A1_at	52.1	5	44	27.7
Ta.8614.2.S1_x_at	52.1	4.1	102.3	99.5
TaAffx.30797.2.S1_s_at	52.1	4.1	3.2	10
TaAffx.6123.1.S1_at	52.1	4.4	9.1	6.5
TaAffx.53122.1.S1_at	52	1.8	16.1	68.6
TaAffx.107686.1.S1_at	51.9	4.4	3.1	3
Ta.5691.1.S1_at	51.8	4.3	3.9	10.3
TaAffx.31416.1.S1_at	51.7	2.3	8.4	10.2
TaAffx.9012.1.S1_at	51.7	2.9	46.6	75.6
TaAffx.92871.1.S1_at	51.6	3.3	17.5	66.3
TaAffx.113265.1.S1_at	51.6	4.9	39.5	42.9

TaAffx.104826.1.S1_at	51.6	3	2.4	48.2
TaAffx.113032.1.S1_at	51.5	4.2	16.1	6.3
Ta.20620.1.S1_at	51.2	3.6	16.4	20.7
Ta.20253.1.S1_at	51.2	2.4	2.8	26
Ta.8611.1.A1_at	51.1	1.8	30.5	33.8
TaAffx.112973.1.S1_at	51.1	4.9	12.2	73.2
TaAffx.106964.1.S1_at	51.1	4.2	11.4	54.6
TaAffx.52381.1.S1_at	51	3.3	3.5	22.6
Ta.6056.3.S1_at	50.7	1.8	33.7	69.7
Ta.22659.3.A1_at	50.6	4.5	42.7	6.4
TaAffx.39401.1.S1_at	50.6	5	49.4	120.9
TaAffx.80699.1.S1_at	50.5	1.7	35.6	56.8
TaAffx.81742.1.S1_at	50.2	1.1	4.5	72.8
TaAffx.8781.1.S1_at	50.2	3.5	23.6	10.1
Ta.23988.1.A1_at	50.1	1.3	4.7	54.7
TaAffx.70654.1.A1_at	50.1	3.3	11.1	2.7
TaAffx.113138.1.S1_at	50	4.4	4.8	4.4
Ta.8090.1.A1_at	49.9	4.9	46.6	11.9
TaAffx.54440.1.S1_at	49.9	2.9	33.3	3.5
TaAffx.128682.2.S1_at	49.7	2.7	2.5	11.2
Ta.26630.1.A1_at	49.7	4.6	5.1	10.2
TaAffx.53406.1.S1_at	49.6	1.8	5.4	19.5
TaAffx.83784.1.S1_at	49.6	3.8	47.3	5.9
Ta.13485.1.A1_at	49.5	3.6	24.4	45.1
Ta.8637.1.S1_s_at	49.5	2.3	51	17.6
TaAffx.112914.1.S1_at	49.4	3.1	23.8	73.1
Ta.25145.1.S1_s_at	49.3	1.2	3.8	2.4
Ta.17784.1.S1_at	49.3	4.4	1.5	17.9
Ta.1936.1.S1_at	49	1.8	10.8	43.6
TaAffx.78384.1.S1_at	49	4.8	77.5	31.4
TaAffx.110589.3.S1_s_at	49	4.1	13.1	36.4
TaAffx.82685.1.S1_at	48.8	4.3	12.8	5.1
TaAffx.111193.1.S1_at	48.8	3.3	12.5	3.7
Ta.11486.1.A1_at	48.7	4.4	9.7	16.3
Ta.9046.1.S1_at	48.6	3.3	8.7	23.8
TaAffx.54078.1.S1_at	48.5	3.2	29.5	43.8
Ta.11704.3.A1_x_at	48.4	4.2	6.7	6.1
Ta.21382.1.S1_at	48.3	4.5	6	47.5
TaAffx.58964.1.S1_at	48.3	4.2	2.8	2.5
Ta.23256.3.S1_at	48.2	3.2	30.3	60.6
TaAffx.37448.1.S1_at	48.2	3.9	21.8	77.7
TaAffx.52728.1.S1_at	48.2	3.2	8.5	4.3
TaAffx.30593.1.S1_at	48.2	3.3	3.4	4.9
TaAffx.108425.1.S1_at	48.1	3.7	9.2	2.1
TaAffx.5349.1.S1_at	48.1	4.6	10.7	49.8
TaAffx.112257.1.S1_at	48	4.6	3.6	9.1

TaAffx.78234.1.S1_at	47.9	1.6	5.6	9.6
TaAffx.85340.1.S1_at	47.8	2.6	8.9	11.4
TaAffx.108734.1.S1_at	47.7	2.9	11.1	28.7
TaAffx.38211.1.S1_at	47.6	4.5	9	8.7
Ta.21709.1.S1_at	47.6	3.8	5.3	13.8
Ta.11019.1.A1_at	47.5	2.5	5.7	5.6
TaAffx.80791.1.S1_at	47.5	1.5	2.1	13
Ta.3133.3.S1_x_at	47.5	2.8	4.6	24.9
TaAffx.59196.1.S1_at	47.4	2.7	10.2	43
Ta.9952.1.S1_at	47.3	3.6	7	9.9
TaAffx.26009.1.S1_at	47.2	2.7	56.6	35.7
TaAffx.79041.1.S1_at	47.1	4	3.5	8.7
TaAffx.57408.1.S1_at	47	4.3	3.9	16.8
TaAffx.29881.1.S1_at	46.9	3.7	13.2	72.2
TaAffx.57603.1.S1_at	46.9	3.7	11.1	54.8
TaAffx.111152.1.S1_at	46.9	3.6	24.7	11.1
TaAffx.12742.1.S1_at	46.7	3.9	16.1	85
TaAffx.27142.1.S1_at	46.5	4.6	11.7	25.1
Ta.26038.1.A1_at	46.3	4.3	4.7	37.2
TaAffx.83850.1.S1_at	46.3	2.8	41.6	21.7
TaAffx.55492.1.S1_at	46.3	1.2	1.5	7.2
Ta.12787.1.S1_at	46.2	4.4	43.5	18.8
Ta.21622.1.S1_at	46.2	4	9.5	53.8
TaAffx.84246.1.S1_at	46.1	3.7	2.9	4.5
TaAffx.121914.3.S1_at	45.8	4	47.8	25.9
Ta.5922.1.S1_at	45.7	2.7	38.7	11.8
TaAffx.52613.1.S1_at	45.6	3.7	14.2	4
TaAffx.26959.1.S1_at	45.5	2.9	44.6	27.3
TaAffx.24928.1.S1_at	45.4	3.1	87	92.8
TaAffx.108696.3.S1_at	45.4	1.6	11.7	5.4
Ta.22775.3.S1_at	45.3	4.1	7.3	19
TaAffx.85823.1.S1_at	45.2	4.1	6	8.6
TaAffx.108418.1.S1_at	45.1	1.4	20.6	27.9
Ta.14488.2.S1_at	45.1	2.3	14	18
TaAffx.85838.1.S1_at	45.1	3.2	2.6	2.6
TaAffx.56198.1.S1_at	45	2.7	27.6	8.8
TaAffx.83792.1.S1_at	45	3.9	13.3	2.8
Ta.6916.3.A1_at	44.9	2.7	63.4	11.9
TaAffx.56537.2.S1_at	44.9	4	35.8	7.4
TaAffx.85542.1.S1_at	44.8	3.6	4.4	49.2
TaAffx.65565.1.A1_at	44.7	2	16.1	54.5
TaAffx.12181.3.S1_at	44.7	1.4	15.2	44.4
TaAffx.5839.1.S1_at	44.7	2.2	23.2	11.8
TaAffx.51457.1.S1_at	44.7	3.3	37.2	50.4
TaAffx.110196.3.S1_at	44.6	4.4	3.5	14.6
Ta.26563.2.S1_s_at	44.4	4.4	6.2	5.4

TaAffx.111013.1.S1_at	44.4	2.5	48.1	32.6
TaAffx.6594.1.S1_at	44.4	2.7	1.6	43.9
Ta.10100.2.S1_x_at	44.3	2.6	5.2	3.7
Ta.5590.3.S1_at	44.3	2.6	16.5	27.7
TaAffx.80726.1.S1_at	44.3	2.9	46.1	13.3
TaAffx.2515.1.S1_at	44.2	3.2	8.8	68.8
Ta.5778.2.S1_at	44.2	2.6	6.2	73.9
TaAffx.110404.2.S1_at	44	0.6	16.6	1.7
TaAffx.6263.1.S1_at	44	2.7	10.3	1.9
TaAffx.84382.1.S1_at	43.7	1.4	2	1.7
Ta.19482.1.S1_at	43.6	1.2	22.7	10.7
Ta.485.2.S1_at	43.5	3.7	8.6	19.5
TaAffx.117169.1.S1_at	43.5	2.9	17.5	63.9
TaAffx.81531.1.S1_at	43.5	2	60.9	38
TaAffx.31865.1.S1_at	43.4	3.1	38.9	4.2
TaAffx.83949.1.S1_s_at	43.3	4.1	4.7	36.3
Ta.26659.1.A1_at	43.3	2.8	79.5	18.3
TaAffx.78852.1.S1_at	43.3	2.1	8.4	3.9
TaAffx.57233.1.S1_at	43.3	2.4	39.5	43.5
Ta.7432.2.S1_at	43.1	2.1	9.6	16.2
TaAffx.8570.1.S1_at	43.1	4	18.1	2.8
Ta.24114.8.S1_at	42.7	1.9	40.5	4.7
TaAffx.12830.1.A1_at	42.7	2.6	20.8	23.1
TaAffx.128541.8.S1_at	42.7	3.7	4	34.5
TaAffx.83459.1.S1_at	42.7	4	52	12.6
TaAffx.113161.1.S1_at	42.5	4	5	7.7
TaAffx.90215.1.S1_at	42.5	2.8	5.2	5
Ta.8897.1.A1_at	42.4	4.1	5.4	42.6
Ta.15642.1.S1_at	42.4	3.8	6.1	55.4
TaAffx.118897.1.S1_at	42.4	2.5	20.1	33
TaAffx.113158.1.S1_x_at	42.4	2.8	5.7	28.4
RPTR-Ta-XXU09476-1_at	42.3	1.8	12.5	5.7
TaAffx.108308.1.S1_at	42.3	2.3	11.5	7.2
TaAffx.30988.1.S1_at	42.1	2.4	25.6	35.6
TaAffx.132337.1.S1_at	42	3.3	9.3	29
Ta.16200.1.S1_at	42	3.2	6.4	15.7
Ta.7994.2.S1_at	42	1.3	2	4.8
TaAffx.129374.2.S1_x_at	41.9	0.5	4.2	0.9
TaAffx.81967.2.S1_at	41.9	3.6	63.9	35.3
TaAffx.56165.1.S1_at	41.9	0.8	3.4	24.9
TaAffx.38460.1.S1_at	41.7	2.2	3.5	5.7
TaAffx.111067.1.S1_s_at	41.7	3.3	14.4	39.7
Ta.26813.1.A1_at	41.7	2.3	34.6	32.5
TaAffx.54085.1.S1_at	41.7	2.9	15.4	17.7
TaAffx.117155.2.S1_at	41.6	2	2	3.6
TaAffx.120660.1.S1_at	41.6	1.2	2.1	6.8

Ta.11580.2.S1_at	41.4	4	16.5	8.4
TaAffx.26067.1.S1_at	41.4	1.3	34	21.7
TaAffx.24411.1.S1_at	41.4	3.4	77.1	28.8
TaAffx.80154.3.S1_at	41.4	4	12.9	10
TaAffx.6797.2.S1_at	41.4	4.1	3.7	4.9
Ta.15793.1.S1_at	41.3	2.1	8.6	34.2
TaAffx.106057.1.S1_at	41.3	2.5	2.7	8.9
Ta.4125.1.A1_at	40.9	3.8	40.2	44
Ta.3235.1.S1_at	40.9	3	3.9	23
TaAffx.86490.1.S1_s_at	40.9	3.3	10.7	3.2
TaAffx.53431.1.S1_at	40.9	0.7	1.4	1.8
Ta.28162.1.S1_at	40.8	3.9	26.5	29.3
TaAffx.105530.1.S1_at	40.7	2.8	24.4	8.6
TaAffx.83430.1.S1_at	40.7	2.5	3	40.8
TaAffx.31349.1.S1_at	40.5	2.2	14.5	31.1
Ta.26551.1.A1_at	40.3	2.1	34.9	31.8
Ta.20767.1.S1_x_at	40.2	3.2	5.4	42.8
TaAffx.38234.1.S1_at	40.2	1.4	25.6	5.6
TaAffx.27084.1.S1_at	40	3.5	11.6	43.6
TaAffx.107319.1.S1_at	40	1.1	1.4	15
TaAffx.53174.1.S1_at	39.9	1.2	18.4	5.5
Ta.19805.1.S1_at	39.6	1.7	2.9	23.2
TaAffx.86158.1.S1_at	39.6	2.3	2.1	1.6
TaAffx.12611.1.S1_at	39.5	3.1	3.1	10.3
TaAffx.7023.4.S1_at	39.5	1.3	10.1	17.7
Ta.13319.2.S1_x_at	39.4	3	7	26.8
Ta.27530.1.S1_at	39.1	3.6	55	16.8
Ta.22987.1.A1_at	39.1	3.6	11.7	38.9
Ta.28857.1.S1_at	39.1	1	35.3	8.2
TaAffx.107478.1.S1_at	39	1.9	10.5	4.4
Ta.12875.1.A1_at	39	1.4	2	10.9
TaAffx.54017.1.S1_at	39	3.8	2.7	2.1
Ta.26338.1.A1_x_at	38.9	1.8	5.8	7.6
Ta.20663.1.S1_at	38.9	2.6	4.4	3.8
TaAffx.29095.1.S1_at	38.9	2.8	3.7	45.4
TaAffx.65598.1.S1_at	38.8	3	54.8	41.6
TaAffx.30831.1.S1_at	38.7	2.8	2.4	4.8
Ta.1249.3.S1_at	38.6	2.2	44.5	51.1
TaAffx.25029.1.S1_at	38.4	2.7	10.2	43.4
Ta.10411.1.A1_at	38.3	2.1	32	9.4
TaAffx.80705.1.S1_at	38.3	1.7	10.1	7.2
Ta.24957.2.A1_s_at	38.2	0.8	0.7	20.6
TaAffx.30461.1.S1_at	38.2	3.1	7.6	21.1
TaAffx.114092.1.S1_at	38.2	2.9	17.9	10.1
TaAffx.8364.1.S1_at	38.2	1.8	32.5	44.1
TaAffx.50667.1.S1_at	38.1	2.9	9.3	35.7

TaAffx.52046.1.S1_at	38.1	0.8	37.1	4.5
TaAffx.29023.1.S1_at	37.8	3.1	21.8	8.2
TaAffx.54516.1.S1_at	37.8	3.2	10.1	3.5
Ta.10643.1.S1_at	37.7	3.1	22.4	5.5
TaAffx.56743.1.S1_at	37.7	2.3	10.3	11.4
TaAffx.56903.1.S1_at	37.6	0.6	24	7.2
Ta.11465.1.A1_at	37.5	2	7.2	75.2
TaAffx.5067.1.S1_at	37.5	1.9	59.8	50.5
TaAffx.7732.1.S1_at	37.4	2.1	4.6	2.9
TaAffx.53724.1.S1_at	37.4	2.7	3.4	9
Ta.3464.1.S1_at	37.3	2.3	8.2	8.5
TaAffx.22603.1.S1_at	37.3	2.9	5.7	5.4
TaAffx.78001.1.S1_at	37.2	2.9	32.2	17.6
TaAffx.113839.1.S1_at	37.2	3.2	4.4	6.8
TaAffx.111169.2.S1_at	36.8	2.6	9.5	43.5
TaAffx.113274.1.S1_at	36.8	1.7	10.1	7.5
Ta.14813.1.S1_at	36.5	2	31.5	35.3
TaAffx.42802.1.A1_at	36.5	2.3	2.7	43.4
Ta.9990.1.S1_x_at	36.4	2.8	9.7	61.7
TaAffx.8725.1.S1_at	36.4	1.2	28.8	9.8
TaAffx.24243.1.S1_at	36.4	2.8	50.5	72.8
Ta.14815.1.S1_at	36.3	1.3	2.9	4
TaAffx.108644.1.S1_at	36.3	2.7	4.7	76.1
TaAffx.56551.1.S1_at	36.3	2.8	6.3	9.8
Ta.20869.1.S1_at	36.2	1.1	4.7	43.6
Ta.14854.1.S1_at	36.2	3	22.2	15.2
TaAffx.109027.1.S1_x_at	36.1	2.2	5.3	11.9
Ta.23904.1.S1_at	36	2.4	53	43.3
Ta.26297.1.A1_at	36	2.4	30	15.1
TaAffx.80858.1.S1_at	36	1	14.4	12.4
TaAffx.82923.1.S1_at	36	3.1	2.9	12.1
TaAffx.28132.1.S1_at	35.9	3.2	30.4	17
Ta.23798.1.S1_at	35.8	3.2	50.6	25.7
TaAffx.108971.1.S1_at	35.8	1.6	4.6	4.2
TaAffx.55677.1.S1_at	35.8	1.7	15.8	34.3
TaAffx.111754.1.S1_at	35.7	3	9.6	11
TaAffx.114128.1.S1_at	35.7	2.7	7	4.3
TaAffx.83664.1.S1_at	35.7	1.3	33.6	4
TaAffx.6369.1.S1_at	35.7	0.7	1.4	4.2
Ta.9396.2.S1_at	35.5	2.4	39.9	9.4
Ta.20518.3.S1_at	35.3	2.5	44.7	75.2
Ta.25912.1.A1_at	35.2	2.1	7.3	51.7
TaAffx.53776.1.S1_at	35.1	1.7	1	2.7
Ta.20841.2.S1_at	35	3.4	2.5	18.7
TaAffx.85899.2.S1_at	34.8	2.6	43.4	13.5
TaAffx.128414.56.S1_at	34.7	2	57.8	21.3

Ta.11671.3.S1_at	34.7	0.6	4.7	17.7
TaAffx.8717.1.S1_at	34.7	1.9	38.4	13.5
TaAffx.53037.1.S1_at	34.7	3.3	74.2	74.9
TaAffx.128414.49.S1_at	34.6	2.4	39.5	5.2
Ta.22471.1.S1_at	34.5	2.5	58.4	68.3
TaAffx.58974.1.S1_at	34.5	1.9	13.9	4.9
TaAffx.9221.2.S1_at	34.4	2.6	33.6	42.4
TaAffx.32093.2.S1_at	34.4	2.2	3.6	51.8
TaAffx.23513.1.S1_at	34.4	2.6	8	5.2
TaAffx.53676.1.S1_x_at	34.4	2.4	8.7	7.4
RPTR-Ta-NC_001669-2_at	34.3	2.9	17.2	10.6
TaAffx.31983.1.S1_at	34.3	3.2	35.8	33.1
TaAffx.108909.2.S1_at	34.3	1.9	18.3	34.3
TaAffx.50313.1.S1_at	34.2	2.1	13	16.6
TaAffx.6366.1.S1_at	34	2.4	3.9	27.4
TaAffx.113703.1.S1_at	34	1.1	2.1	14.1
TaAffx.93961.1.S1_at	33.9	2.9	35.3	9.5
Ta.27060.1.S1_at	33.8	2.1	46.9	9.7
TaAffx.73741.1.S1_at	33.8	2.4	34.9	61.6
TaAffx.6095.1.S1_at	33.8	2.5	6.8	42.8
TaAffx.29454.1.S1_at	33.7	1.4	34	5.9
TaAffx.121261.1.A1_at	33.6	2	30.9	31.3
TaAffx.108124.1.S1_at	33.6	1	5.2	10.9
TaAffx.112360.1.S1_at	33.5	1.2	3.9	9.8
TaAffx.27405.1.S1_at	33.5	3.1	4.2	10.2
TaAffx.80891.1.S1_at	33.5	2.5	22.5	11.7
TaAffx.4999.1.S1_at	33.5	0.9	9.1	24.3
Ta.24471.1.S1_x_at	33.4	2.7	33.7	57.6
Ta.10092.3.A1_at	33.4	2.8	6.5	4.4
TaAffx.105054.1.S1_at	33.3	3.2	14.1	43.8
TaAffx.113105.1.S1_at	33.2	1.6	38.7	8.2
TaAffx.103569.1.A1_at	33.1	3.3	16.1	19.9
TaAffx.25765.1.S1_at	33	2.4	24.1	9
TaAffx.110624.2.S1_at	33	2.9	3.1	3.4
TaAffx.128796.1.S1_at	32.9	2.2	27.7	5.1
Ta.5414.2.S1_at	32.9	2	44.4	43.9
TaAffx.77700.1.S1_at	32.8	2.4	29.9	78.4
TaAffx.128478.2.S1_at	32.7	1.6	10.9	3.2
TaAffx.53330.1.S1_at	32.7	2.8	5	26.5
TaAffx.112935.1.S1_at	32.7	0.9	41.9	61.9
Ta.26600.1.A1_at	32.6	3.1	6.6	15.6
Ta.27909.1.A1_at	32.6	1.3	36	8.2
TaAffx.7097.1.S1_at	32.6	2.6	4.8	8.1
Ta.15684.1.S1_at	32.5	1.6	1.8	35.5
TaAffx.113042.1.S1_at	32.5	1.6	3.1	1.7

TaAffx.113316.1.S1_at	32.5	3	25.2	4.5
TaAffx.128896.13.S1_x_at	32.5	1.9	9.1	33.2
Ta.14586.2.A1_at	32.4	1.8	26.4	34.4
Ta.20385.1.S1_x_at	32.3	2	2.4	2.7
Ta.21449.1.S1_at	32.3	3	1.7	3.7
Ta.12653.1.S1_at	32.2	2.6	21.9	58.6
TaAffx.78961.1.S1_at	32.2	2.8	60.1	44.2
Ta.1840.1.S1_at	32.1	1.3	27.2	33.8
Ta.16234.1.S1_at	32.1	1.5	1.9	10.8
TaAffx.6297.1.S1_at	32.1	1.9	50	9.2
TaAffx.56954.1.S1_at	32.1	3.1	52.8	51.9
TaAffx.108186.1.S1_at	32.1	2.4	27.6	10.4
Ta.5839.1.S1_at	32	1.8	4.8	4
TaAffx.72768.1.S1_at	32	2.5	7	61.5
Ta.15969.1.S1_at	31.8	1.4	44.8	18
TaAffx.24491.1.S1_at	31.7	2.6	8.4	13.7
Ta.8447.1.S1_a_at	31.6	2.1	5.8	5
Ta.11439.1.A1_at	31.6	3.1	21.6	15.7
TaAffx.9493.1.S1_at	31.6	1	34.8	39.9
TaAffx.85672.3.S1_at	31.6	1.4	52.3	68.9
TaAffx.106609.1.S1_at	31.6	1.5	6.4	8.2
Ta.15494.1.S1_at	31.4	1.2	28.8	15.7
Ta.22406.1.S1_at	31.4	2.8	3.9	16.5
Ta.7125.2.S1_at	31.4	3.1	6.6	27.1
Ta.21094.3.S1_at	31.4	1.9	6.3	40.9
Ta.25568.2.A1_at	31.4	2.6	2.2	53.5
TaAffx.57554.1.S1_at	31.4	3.1	26	15.4
TaAffx.27092.1.S1_at	31.4	2.6	36	4.9
Ta.24085.1.A1_x_at	31.3	2.3	24	26.9
Ta.9883.1.S1_x_at	31.3	2.3	14	28.6
Ta.18362.2.S1_at	31.3	3.1	8.1	41.5
TaAffx.85307.1.S1_at	31.2	2.6	3.1	36
TaAffx.12397.1.S1_at	31.1	2.2	41.1	12.7
Ta.21829.1.S1_at	30.7	1.6	30.9	8
Ta.17901.1.S1_at	30.5	2.6	27.5	30
Ta.16715.1.S1_at	30.5	1.3	11	8.9
TaAffx.56486.1.S1_at	30.4	2.4	5.9	7.1
TaAffx.86208.1.S1_at	30.4	2.7	17.7	43.4
Ta.16515.1.S1_at	30.3	1.1	20.4	3.9
Ta.16999.2.S1_at	30.3	2	2.1	19.2
TaAffx.15432.1.A1_at	30.3	2.8	7.2	8.2
TaAffx.26057.1.S1_at	30.2	2.5	4.4	4.4
TaAffx.110463.1.S1_at	30.2	2.7	2.9	3.6
Ta.26862.1.A1_at	30.1	2	6.7	3.9
TaAffx.93935.1.A1_at	30	1.7	7.8	6.2
Ta.15766.1.S1_at	30	1.8	0.4	22.2

Ta.8157.3.S1_s_at	29.9	2.7	18.3	9.6
TaAffx.108970.2.S1_at	29.9	2.3	6.6	8.9
TaAffx.8350.1.S1_at	29.8	1.8	15.2	30.7
Ta.15757.1.A1_at	29.7	1.8	7	42
TaAffx.22902.1.S1_at	29.6	1.1	18.1	27
TaAffx.25611.1.S1_at	29.6	2.2	13.4	12.3
Ta.18347.1.S1_at	29.5	1.3	3.3	5.5
TaAffx.106752.1.S1_at	29.5	1.2	26.8	28.2
TaAffx.53518.1.S1_at	29.5	2.3	32.4	44.8
TaAffx.26103.1.S1_at	29.5	2.6	5.6	42.1
TaAffx.8396.1.S1_at	29.4	2.5	30.3	12.9
TaAffx.82029.1.S1_at	29.3	1.3	8.7	7.3
TaAffx.111033.2.S1_at	29.2	1.5	10.4	108
TaAffx.83951.1.S1_at	29	1.7	10.3	6.9
Ta.26876.1.A1_at	28.9	2.6	2.3	3.4
TaAffx.82683.1.S1_at	28.8	1.8	31.3	44.2
TaAffx.84241.1.S1_at	28.7	2	43.7	4.8
TaAffx.112264.1.S1_at	28.7	2.4	4.1	16.6
TaAffx.85904.1.S1_at	28.7	1.4	2.6	3.4
TaAffx.109945.1.S1_at	28.7	2.2	36.8	64.4
Ta.16835.1.A1_at	28.5	2.7	41	12
Ta.17062.1.S1_at	28.5	1.9	41.8	31.8
TaAffx.5270.1.S1_at	28.2	0.9	4.8	44.3
Ta.20627.1.S1_at	28	2.7	50.2	23.1
TaAffx.108024.2.S1_at	27.9	2.2	5.6	28.3
Ta.26618.1.A1_at	27.8	1.1	11.7	52.2
TaAffx.85597.2.S1_x_at	27.8	1.4	14.2	4.8
TaAffx.27099.1.S1_at	27.8	1.6	5.4	2
TaAffx.53650.1.S1_at	27.8	2.5	2.6	56.1
TaAffx.28211.1.S1_at	27.7	1.3	34.1	19.9
TaAffx.78394.1.S1_at	27.7	0.4	12.4	27.4
Ta.14263.1.S1_at	27.6	2.7	23.3	5.5
TaAffx.52593.1.S1_at	27.4	1.3	16.3	3.7
TaAffx.128848.3.S1_s_at	27.3	1.9	28.7	47
Ta.26851.1.A1_at	27.3	2.7	5.7	4.5
Ta.3710.2.S1_at	27.3	2.7	19.3	7.3
TaAffx.108123.1.S1_at	27.3	1.2	3.1	24.5
TaAffx.113984.1.S1_at	27.3	1.9	24.7	27.4
TaAffx.107607.1.S1_at	27.1	2.3	24.9	5.4
TaAffx.54698.1.S1_at	26.7	0.8	21.7	15.4
TaAffx.52049.1.S1_at	26.6	0.9	21	12.4
TaAffx.79327.1.S1_at	26.5	1	30	33.7
Ta.30900.1.S1_at	26.4	1.8	23	36.5
TaAffx.107742.1.S1_at	26.3	2.4	37.1	51.1
Ta.15671.1.S1_at	26.1	2.6	2.1	2.7
TaAffx.81666.1.S1_at	26.1	1.3	19.1	11.8

Ta.29679.1.S1_at	26.1	1.7	10.2	1.7
Ta.28856.1.S1_at	25.9	1.3	2.9	6.7
Ta.26457.1.A1_at	25.9	1.6	0.9	36.4
Ta.15068.1.S1_at	25.8	1.6	39.5	26.6
Ta.29596.1.S1_at	25.8	1.9	26.4	2.9
TaAffx.56343.1.S1_at	25.8	2.4	27.2	54.1
RPTR-Ta-M62653-1_at	25.7	1	16	31
Ta.13157.1.S1_at	25.7	1.9	1.6	4.5
TaAffx.58407.1.S1_at	25.7	0.8	2.8	21.8
TaAffx.82977.1.S1_at	25.6	1.6	6.9	43.2
Ta.25441.1.S1_at	25.6	2.1	12.9	6
TaAffx.136696.1.S1_at	25.6	1.6	9	2.8
TaAffx.81062.1.S1_at	25.6	1.2	1.9	5.3
TaAffx.108713.1.S1_at	25.6	0.9	3.9	37.7
TaAffx.70438.1.A1_at	25.5	2.5	2.8	5
TaAffx.30810.2.S1_at	25.5	1.8	8.4	2.8
TaAffx.81541.1.S1_at	25.2	1.7	13.1	3.2
TaAffx.72199.2.S1_at	25.2	1.4	20.7	9.9
TaAffx.57522.2.S1_at	25	1.8	10.6	4.2
TaAffx.120459.1.A1_at	24.8	0.9	21.6	5.1
TaAffx.54973.1.S1_at	24.8	0.7	2.1	3.2
TaAffx.124262.1.S1_at	24.8	2.3	20.8	5.5
TaAffx.4447.1.S1_at	24.6	1	35.7	38.9
Ta.25024.1.S1_x_at	24.5	2.4	7.3	6.3
Ta.7235.2.S1_at	24.4	1.4	49.1	43.8
TaAffx.107944.1.S1_at	24.3	0.7	7.6	1.6
Ta.13841.3.S1_at	24.3	2.2	38.8	6.9
TaAffx.6588.1.S1_at	24.3	2.4	25.2	18
Ta.18871.1.S1_at	24.1	0.2	13.4	2.7
Ta.17211.1.S1_at	24.1	1.4	2	2
TaAffx.7023.5.S1_at	24.1	1.7	7.8	33.1
Ta.27780.1.S1_at	24	1.3	27.3	3.1
Ta.11340.1.A1_at	24	0.9	3.9	10.8
TaAffx.85700.1.S1_at	24	1.8	28.8	27.1
Ta.9139.3.A1_at	24	1	7	17.3
TaAffx.24457.1.S1_at	24	1.1	9.7	23.1
TaAffx.79794.1.S1_at	24	1.4	10.3	52.2
TaAffx.53291.1.S1_at	23.9	1.9	7.5	5.6
TaAffx.86226.1.S1_at	23.9	2.2	4.2	8.1
TaAffx.80402.1.S1_at	23.8	2.2	2.8	9.1
TaAffx.16911.2.S1_at	23.7	1.3	5.8	9
Ta.17252.1.S1_at	23.6	2	2.9	7.8
TaAffx.6790.3.S1_at	23.6	2.1	29.4	40.3
TaAffx.23438.1.S1_at	23.6	1.1	1.1	12.8
TaAffx.53321.1.S1_at	23.5	1.1	13.2	14.8
TaAffx.82672.1.S1_x_at	23.5	0.9	4.1	29.7

TaAffx.30387.1.S1_at	23.5	1	35.4	37.4
Ta.12919.1.A1_at	23.4	2	4.1	9
TaAffx.29185.1.S1_at	23.1	1.1	21.1	34.3
Ta.22627.1.S1_at	23	1.9	6.3	7.5
TaAffx.57208.1.S1_at	23	1.4	8	2
TaAffx.80197.1.S1_at	22.9	1.5	62.6	70.9
TaAffx.53829.1.S1_at	22.9	1.3	6.5	13.4
TaAffx.85490.1.S1_at	22.8	1.8	2.2	20.3
TaAffx.25985.1.S1_at	22.8	1.7	5	8.8
Ta.11442.1.A1_at	22.7	1.8	8.5	10.9
TaAffx.6548.1.S1_at	22.7	1.3	4	1.7
TaAffx.27810.1.S1_at	22.7	1	5	30.9
Ta.14074.2.S1_at	22.6	1.3	1.4	2.2
TaAffx.80440.1.S1_at	22.6	1.8	5	11
TaAffx.84751.1.S1_at	22.2	1.9	4.5	1.9
Ta.16371.1.S1_at	22.1	1.7	6.1	54.8
TaAffx.57023.1.S1_at	22.1	1.8	3.9	76.7
Ta.28247.1.S1_at	22	0.6	0.7	28.9
TaAffx.108286.1.S1_at	21.7	1.9	3.4	14.6
TaAffx.84475.1.S1_at	21.7	2	2	32.1
TaAffx.81288.1.S1_at	21.7	1.4	3.8	2.5
RPTR-Ta-J01347-1_s_at	21.6	1.3	16.1	13.1
TaAffx.81998.1.S1_at	21.6	0.9	19.7	26.4
TaAffx.29165.1.S1_x_at	21.6	1.2	6.7	17.9
Ta.22666.2.S1_at	21.5	1.8	5.1	48.3
Ta.2941.1.A1_at	21.4	1.9	6.9	4.2
TaAffx.108262.2.S1_at	21.4	1.2	6	5.7
TaAffx.106265.1.S1_at	21.4	1.5	62.6	68
TaAffx.82807.2.S1_at	21.2	0.5	2.6	19.8
TaAffx.24522.1.S1_at	21.2	2.1	4.5	16.3
TaAffx.3194.2.S1_at	21.1	0.7	1.4	2.6
TaAffx.8801.1.S1_at	21.1	2	34.4	22.2
TaAffx.80680.1.S1_at	21	1	1.2	2
Ta.12091.1.S1_at	20.8	0.6	18.6	3
Ta.20756.1.S1_at	20.7	1	29.7	5.8
TaAffx.37317.1.A1_at	20.7	1.1	3.5	4.4
TaAffx.80775.1.S1_at	20.7	1	1.2	34.3
TaAffx.29817.1.S1_at	20.6	1.2	25.8	26.7
TaAffx.112466.1.S1_at	20.6	2	14.1	6.8
TaAffx.7858.1.S1_at	20.6	0.9	29.5	4.5
TaAffx.82512.1.S1_at	20.4	1	59.8	8.8
TaAffx.112045.1.S1_at	20.4	1.4	6.1	19.7
Ta.18692.1.S1_at	20.4	0.8	3.1	13
TaAffx.85795.1.S1_at	20.3	0.2	23.2	11.7
TaAffx.108525.1.S1_at	20.3	1.6	47.1	22.9
TaAffx.51287.3.S1_x_at	20.3	2	1.9	51.5

Ta.26731.1.A1_at	20.1	1.2	7.5	24.5
Ta.30854.1.S1_at	20.1	1.9	5.5	76
TaAffx.53072.1.S1_at	20.1	1.2	8.5	38.1
Ta.4943.3.S1_at	20.1	2	18.8	32.3
TaAffx.26304.1.S1_at	19.8	1.7	24.6	3.8
Ta.9836.1.A1_at	19.6	1.6	1.1	1.5
Ta.17823.1.S1_at	19.5	1.1	5.1	45
TaAffx.36994.1.S1_at	19.5	0.8	14.9	37.4
TaAffx.5836.1.S1_at	19.5	0.8	2.5	4.3
TaAffx.110225.1.S1_at	19.4	1.5	26.2	3.4
TaAffx.83959.1.S1_at	19.2	1.5	19	33.9
TaAffx.85515.1.S1_at	19.2	1.9	40	6.4
TaAffx.7997.1.S1_at	19	1.7	4.9	20.2
TaAffx.118913.1.S1_at	19	1.4	5.5	2.5
TaAffx.112993.1.S1_at	19	1.1	10.7	2.8
TaAffx.27112.1.S1_at	18.9	1.6	4.5	4.8
Ta.24275.1.A1_at	18.8	0.5	25.7	20
TaAffx.86505.2.S1_at	18.7	1.1	8.2	55.9
TaAffx.16379.1.A1_at	18.6	1.8	25.8	3.1
TaAffx.112045.1.S1_x_at	18.5	1.4	43.6	5.9
TaAffx.26241.1.S1_at	18.5	1.6	31	46.9
Ta.14056.1.S1_x_at	18.4	1.2	24.9	22.9
Ta.6906.1.A1_at	18.4	1.8	6.8	17.2
Ta.18871.1.S1_x_at	18.3	1.1	2.5	1.4
Ta.22678.2.S1_a_at	18.2	0.7	3.1	21
TaAffx.58561.1.S1_at	17.9	1.5	8	29.5
Ta.3326.1.S1_at	17.8	0.8	5.3	38.8
Ta.19346.1.S1_at	17.8	1.1	16.8	3.7
Ta.11017.1.A1_at	17.5	1.6	2.6	66.4
TaAffx.23393.1.S1_at	17.5	1.2	24.7	26.1
Ta.9903.3.S1_at	17.2	1.7	3.3	3.6
TaAffx.29487.1.S1_at	16.9	1.3	9	5.1
TaAffx.54157.1.S1_at	16.8	1.1	8.4	21.2
Ta.5461.2.S1_at	16.8	1.3	8.4	6.1
TaAffx.59777.1.S1_at	16.8	1.1	4.4	4.7
TaAffx.8766.1.S1_at	16.7	0.8	18.7	32
TaAffx.135342.1.S1_at	16.6	1	16.8	4.4
TaAffx.26014.1.S1_at	16.6	1.3	3.5	40.1
TaAffx.6691.1.S1_at	16.5	1.6	3.3	4
Ta.13132.2.A1_x_at	16.4	1.5	7.5	3.5
TaAffx.7919.1.S1_at	16.4	1.1	25.2	36.7
Ta.17098.1.S1_at	16.2	1.1	3.6	1.2
TaAffx.115144.1.S1_at	15.9	0.7	0.7	1.3
TaAffx.5864.1.S1_at	15.9	1.1	1.4	6.3
TaAffx.53696.1.S1_at	15.6	0.9	2.3	3.1
TaAffx.111448.4.S1_at	15.5	1.5	5	28.7

TaAffx.59562.1.S1_at	15.4	1.1	12.5	41.7
TaAffx.89353.2.S1_at	15.3	1.4	2.6	14
TaAffx.107986.1.S1_at	15.1	0.8	2.5	3
Ta.17209.1.S1_s_at	15	0.9	13.8	10.6
TaAffx.113686.1.S1_at	15	1	28.2	8.4
TaAffx.107582.1.S1_at	14.8	1.4	4.9	17.1
TaAffx.110627.1.S1_at	14.7	1	27.5	16
Ta.7645.3.S1_at	14.6	1.4	8.4	3.5
TaAffx.80921.1.S1_at	14.5	1.2	3	1.5
TaAffx.53503.1.S1_at	14.3	0.8	2.4	10.5
TaAffx.111829.1.S1_at	14.2	0.7	4.2	26.1
TaAffx.83153.1.S1_at	14.1	1.2	4.6	3.7
Ta.5506.2.S1_at	14.1	0.4	23.2	17.9
Ta.1120.1.S1_x_at	14	1.1	4.9	31.8
Ta.20901.1.S1_at	13.7	1.1	1	6.4
Ta.398.2.S1_at	13.3	1.3	2.5	6.4
TaAffx.31003.1.S1_at	13.2	0.5	11.9	20.6
TaAffx.86014.1.S1_at	13.2	1.2	8.1	11.2
TaAffx.98485.5.S1_s_at	13.1	1.2	2.8	22.9
Ta.17274.1.S1_at	13.1	1.2	26.6	41
TaAffx.6795.1.S1_at	12.9	1.1	6.5	6.8
TaAffx.30318.2.S1_at	12.9	0.6	2.9	5.2
TaAffx.4330.1.S1_at	12.8	1.2	18.9	11.1
TaAffx.35302.1.S1_at	12.7	0.9	2	3.4
TaAffx.105465.2.S1_at	12.3	1	8.5	21.2
Ta.15540.1.S1_at	12.2	1.1	1	8.5
Ta.26689.1.A1_at	12.2	0.8	7.3	12.8
TaAffx.112350.3.S1_at	12.1	1.1	5.2	7.1
TaAffx.24625.1.S1_at	12	1.1	25.8	33.1
TaAffx.23403.1.S1_at	11.9	1	18.7	33.5
TaAffx.70061.16.S1_at	11.7	0.7	3.5	20.4
TaAffx.79247.2.S1_at	11.6	0.9	2.3	3.6
TaAffx.117318.1.S1_at	11.5	0.6	1.3	16.2
Ta.24774.2.S1_at	11.4	1.1	3.6	3.4
Ta.5376.1.S1_at	11.3	0.9	31.4	32.7
TaAffx.65280.1.A1_at	11.1	1.1	13.8	9.5
Ta.17312.1.S1_at	11.1	0.8	30.8	23
Ta.22668.3.S1_x_at	11	0.6	20.9	20.7
TaAffx.108138.1.S1_at	10.7	0.5	37.7	23.7
TaAffx.112959.1.S1_at	10.1	0.7	1.8	17.8
TaAffx.86178.1.S1_at	9.7	0.9	5.9	10.3
TaAffx.83820.1.S1_at	9.7	0.8	13.6	8.4
TaAffx.27098.1.S1_at	9.7	0.7	13.6	26.5
TaAffx.108135.1.S1_at	9.3	0.8	3.6	21.7
TaAffx.116915.2.S1_at	9.1	0.8	2.3	5.2
TaAffx.86512.1.S1_at	9.1	0.8	22.7	25.2

TaAffx.85165.1.S1_at	7.8	0.7	15.2	9.2
TaAffx.106405.1.S1_at	7.5	0.7	1.4	1.6
TaAffx.83910.1.S1_at	7.1	0.7	10.2	20.1
Ta.14852.1.S1_at	6.4	0.6	15	31.1
Ta.22732.1.S1_s_at	4.5	0.4	5.9	1.4
TaAffx.77755.1.S1_at	4.4	0.4	0.7	3.5
TaAffx.6041.3.S1_at	1.2	0.1	0.9	3.1

Table B.5 *Gc2^{mut}#1*/- late over *Gc2*/- late

Probe set ID	***GC2* E**	***GC^{mut}#1* E**	***GC2* L**	***GC^{mut}#1* L**
Ta.4753.1.S1_at	153.7	162.3	36.7	583.4
Ta.20780.3.S1_at	348.4	154.9	20	463.7
TaAffx.113329.2.S1_at	169.1	94.8	39.1	413.4
TaAffx.57046.1.S1_at	112.3	142.7	29.7	389.2
TaAffx.4694.1.S1_at	82.1	76.1	33.2	352.1
Ta.20105.1.S1_at	33.3	19.6	23.6	328.8
Ta.5257.2.S1_s_at	34.3	21.5	26.1	281
TaAffx.112639.1.S1_at	25.1	93.8	13.7	279.9
AFFX-Ta_18SrRNA_at	199.6	136.1	21.9	270.4
TaAffx.110006.1.S1_at	180.2	86.2	25.1	267.1
Ta.23129.1.S1_x_at	119.7	162.4	14.3	263
TaAffx.131077.1.S1_x_at	12.6	73.8	14.8	231.7
TaAffx.79439.1.S1_at	29.4	33	18.7	211.7
TaAffx.55879.1.S1_at	30.6	204.3	15	206.6
TaAffx.82826.1.S1_at	37.5	118.8	19.1	204.6
TaAffx.132349.1.A1_at	88.5	102.2	12.2	200.4
Ta.15177.2.S1_at	157.4	167.2	15.2	198.1
Ta.14422.1.S1_at	27.4	92.9	12.9	197.1
Ta.26670.1.A1_at	130	134.6	7.6	193.5
Ta.22872.3.S1_at	25.2	119.8	18.7	193.4
Ta.26607.1.A1_at	86.2	100.5	5.4	190.9
TaAffx.8613.1.S1_at	110.7	68.6	12.8	186.8
TaAffx.112567.1.S1_at	30.6	20.5	13.3	180.8
TaAffx.132703.1.S1_at	24.1	76.7	6.2	180.6
TaAffx.111621.1.S1_at	128.1	18.5	15.5	175.9
Ta.27774.1.S1_x_at	160.6	86.9	14.8	174.6
Ta.3708.3.S1_x_at	192.6	85	15	173.4
Ta.25578.1.S1_x_at	201.4	82.3	14.2	169.4
TaAffx.113459.1.S1_at	8.4	4.9	8.6	165.6
TaAffx.3790.1.A1_at	149.7	133.3	16.3	164.7
TaAffx.54035.1.S1_at	36.6	99.1	12	163.6
TaAffx.39307.1.S1_at	6.5	20.4	15.5	160.9
Ta.27028.1.S1_at	125	107.2	11.4	160.7
TaAffx.106370.1.S1_at	34.9	145.1	14	157.6
Ta.7320.2.S1_at	118.9	67.1	4.1	156.1

TaAffx.117197.1.S1_at	63.2	36.1	9.2	154.4
Ta.9151.3.S1_at	91.6	43.5	8.4	153.2
Ta.6690.2.A1_x_at	206.7	231.4	10	152
Ta.30875.1.S1_at	117.8	44.8	7	150.5
TaAffx.77468.1.S1_at	68.2	10.6	14.6	149.3
TaAffx.92615.1.S1_at	31.9	110.1	6.6	147.7
TaAffx.5621.1.S1_at	85	44.8	9.8	146.9
Ta.23342.3.A1_at	81.1	55.5	2.7	145.7
TaAffx.53644.1.S1_at	61.4	104.8	5	145.1
Ta.26992.1.A1_at	38.1	57	9.2	144.9
TaAffx.79154.1.S1_at	25.3	41.1	3.5	143.9
TaAffx.91818.1.S1_at	54.6	109.6	12.7	143.5
TaAffx.84623.1.S1_at	26.2	20.6	10.3	141.8
Ta.18832.1.S1_at	57.6	30.4	9	140.2
Ta.17513.1.S1_at	57.4	26.2	12.9	139.6
Ta.5004.3.S1_at	76.3	95.2	13.5	138.7
TaAffx.24122.1.S1_at	73.8	44.8	12.2	137.7
TaAffx.29182.1.S1_at	73.8	9.4	11.2	136.9
Ta.29585.2.S1_at	115.8	9.4	10.8	135.8
TaAffx.56925.1.S1_at	90	11.4	9.9	133.5
TaAffx.50332.1.S1_at	44.7	35.9	8.5	132.9
TaAffx.8365.1.S1_at	55.4	23.7	9.7	132.1
TaAffx.128563.3.S1_at	143.9	135.1	7.6	131.5
TaAffx.86194.1.S1_at	82.9	8.8	3.6	129
TaAffx.112712.1.S1_at	51.4	5.2	12.2	128.4
TaAffx.27372.1.S1_at	168.9	41.2	7.4	126.4
TaAffx.29448.1.S1_at	59	72	6.1	126.4
TaAffx.26908.1.S1_x_at	26.3	132.9	8.3	126.3
TaAffx.110190.1.S1_at	16.5	14.6	11.3	125.8
TaAffx.57808.1.S1_at	126.1	95.9	10.6	125.6
TaAffx.86528.1.S1_at	65	7.2	12.2	125.4
TaAffx.56327.1.S1_at	7.3	15.7	7.8	125.4
TaAffx.12261.1.A1_at	15.8	27.9	10.9	124.2
Ta.19209.1.S1_at	65.1	6.7	5.4	124
TaAffx.111214.1.S1_at	136.1	115.4	7.7	123.6
Ta.15028.1.S1_at	41.6	22.8	10.9	123.4
TaAffx.7972.1.S1_at	11.8	32.7	4.5	122.6
TaAffx.143995.16.A1_at	118.5	71.9	8.5	122.4
TaAffx.113333.1.S1_at	33.4	13	6.7	122
TaAffx.26139.5.S1_at	35.3	84.1	8.6	122
Ta.10172.2.S1_x_at	55.3	20.1	3.5	120.8
TaAffx.28894.2.S1_at	10.4	27.1	10	120.6
Ta.30612.1.S1_x_at	94.9	61.2	9.6	119.9
TaAffx.11984.1.A1_at	108.1	60.5	11.8	119.9
TaAffx.31902.1.S1_s_at	90	65.8	9.4	119.5
TaAffx.122623.3.S1_at	49.1	69.3	11.5	118.6

TaAffx.113653.1.S1_at	66.6	11.6	9.2	118.5
Ta.9886.2.S1_at	44.6	49.6	11.1	117.8
Ta.20603.1.S1_at	49.5	31.1	10.2	117.1
TaAffx.25069.1.S1_at	61	95.4	9.2	116.6
TaAffx.140923.1.S1_at	41.9	15	2.7	115.6
TaAffx.110229.1.S1_at	116.7	86.1	8.6	114.9
Ta.5004.3.S1_a_at	12	7.2	6.8	114.3
Ta.30728.3.S1_a_at	78.5	59.7	9.3	113.8
TaAffx.111445.1.S1_at	84.4	29.2	10.6	113.6
TaAffx.5649.1.S1_at	58.3	59.4	8.7	113.1
TaAffx.85645.1.S1_at	8	9.3	10.9	111.6
TaAffx.77852.1.S1_at	19.4	53	10.2	111.2
TaAffx.112829.1.S1_at	25.9	4.8	6	111.1
TaAffx.52953.1.S1_at	120.8	68	9.8	111
Ta.13785.1.S1_at	29.4	36.8	5.2	110.1
TaAffx.111033.2.S1_at	29.2	1.5	10.4	108
Ta.28791.1.S1_at	12.8	22.3	9.3	107.3
TaAffx.99141.1.S1_at	21.5	5.4	6.1	107.1
Ta.23167.1.S1_at	14.3	8	9.8	106.6
TaAffx.28669.1.A1_at	23.4	39.7	6.2	106.6
Ta.19145.1.S1_at	38	4.9	2.3	106.5
TaAffx.26915.1.S1_at	13.2	33.4	7.1	106.2
TaAffx.29890.1.S1_at	53	38.9	10.3	106.2
TaAffx.22825.1.S1_at	60.3	9.1	9.3	106
Ta.27962.2.A1_x_at	92.9	76.5	3.6	105.8
Ta.2962.2.S1_a_at	15.7	36.6	7.6	105.6
Ta.17572.1.S1_at	93.1	72.8	7.1	105.4
TaAffx.84620.1.S1_at	36	35.7	9.9	104.5
Ta.17272.1.S1_at	15.9	8.7	4.7	104.4
Ta.1092.2.S1_at	49.8	24.1	8.5	104.3
TaAffx.122376.2.A1_at	73.9	53.9	9.8	103.8
Ta.12236.1.A1_at	44	82.3	9.1	103.7
TaAffx.95386.1.A1_at	17.4	22.6	8.7	103.7
Ta.15411.1.S1_at	69.1	45.8	9.6	103.4
TaAffx.5894.1.S1_at	20.7	16.1	7.1	103.2
Ta.5389.3.A1_at	7	29.5	9.1	103
TaAffx.55189.1.S1_at	18.3	63	8.9	103
TaAffx.44650.1.A1_at	39.3	27.1	8.5	102.2
Ta.9233.2.S1_a_at	81.9	97.6	4.6	101.4
TaAffx.112636.1.S1_at	13	101.9	10	101.2
TaAffx.32045.1.S1_at	8.6	44.3	9.5	101.2
TaAffx.28991.1.S1_at	20.1	12.3	7.6	100.6
Ta.3671.2.S1_at	42.5	5.1	8.4	100.1
TaAffx.29174.1.S1_at	56.3	12.4	7.8	99.6
Ta.15514.1.S1_at	43.3	6.2	6.3	99.3
Ta.18348.1.S1_at	46	59	4.5	99.3

TaAffx.93048.1.S1_at	16	88	7.5	98.8
TaAffx.80403.1.S1_at	4.2	10.5	4.4	98.8
Ta.18637.1.S1_at	78.6	80.3	6.9	98.5
Ta.9225.1.S1_at	4.7	3	7.9	98.2
Ta.30350.1.A1_at	37.2	25.7	9.4	97.7
TaAffx.53452.1.S1_at	52.5	54.7	5.2	96.7
TaAffx.86053.1.S1_at	73.5	28.1	7.2	96.4
TaAffx.27406.1.S1_at	5.9	32.5	5.5	96.4
TaAffx.30309.1.S1_at	7.1	51.9	4.3	96.4
TaAffx.111246.3.S1_at	89.2	59	5.6	95.8
Ta.15768.1.A1_at	8.2	16.1	5.6	95.6
Ta.10516.2.S1_at	56.9	53.5	7.8	95.6
TaAffx.85283.1.S1_at	47.6	7.3	7.6	95.3
Ta.29551.1.A1_at	9.6	69.8	4.5	95.3
Ta.17125.1.S1_at	38	16.8	8	94.9
Ta.4127.2.S1_at	15.5	27.4	2.5	94.4
TaAffx.128719.2.A1_at	31.1	46.6	8.6	93.4
Ta.9918.2.S1_at	12.4	56.6	8.8	93.3
Ta.6391.2.A1_at	22.6	33.8	4.3	92.6
Ta.26792.1.A1_at	70.9	66.7	7.7	92.4
TaAffx.623.1.A1_at	16.9	19	9.1	92.1
TaAffx.112688.1.S1_at	56.3	20.1	5.6	92.1
TaAffx.90045.1.S1_at	31.7	37.5	5.7	92.1
Ta.26680.1.S1_at	26.1	7.7	3.7	91.8
Ta.11994.1.A1_at	62.7	11.3	8.1	91.7
Ta.24142.2.A1_at	97.1	40.9	8.7	91.6
Ta.7330.1.S1_at	144.5	66	3.2	91.5
Ta.24597.1.S1_x_at	60.6	63.1	4.1	91.4
TaAffx.37113.2.S1_at	143.2	51.6	6.2	90.3
TaAffx.16883.2.S1_x_at	55.5	72.6	2.3	90.3
TaAffx.50171.1.S1_at	51.6	11.6	6.2	89.9
TaAffx.121954.3.S1_at	55.7	1.5	2.7	89.7
TaAffx.80037.1.S1_x_at	51.2	33.7	8.5	89.6
Ta.22618.2.S1_at	91.6	58	5.9	89
Ta.1034.2.S1_at	39.2	9.8	6.7	88.9
Ta.10953.1.A1_at	42.1	29	6	88.8
TaAffx.112317.1.S1_s_at	8.3	8.6	4.9	88.8
Ta.9401.3.S1_at	27.3	77.8	6.4	88.3
TaAffx.95810.1.S1_at	7.8	11.6	6.9	88.1
TaAffx.7979.4.S1_at	45.5	103.3	8.6	88.1
TaAffx.131624.1.S1_at	73.4	31.4	6.1	87.9
TaAffx.108674.1.S1_at	1.6	3.3	3	87.5
TaAffx.37635.1.S1_at	56.3	110	4.5	87.2
TaAffx.85181.1.S1_at	16.5	22.2	3.7	87.1
Ta.7370.2.S1_a_at	20.6	28	3.9	87
Ta.5362.1.S1_at	107.4	49.9	6	86.9

TaAffx.85400.2.S1_at	12.8	39	3.5	86.6
TaAffx.79648.1.S1_at	88.8	54.7	5.9	86.5
TaAffx.112428.1.S1_at	154.2	3.4	5.6	86.4
TaAffx.86388.1.S1_at	6.3	21	3.1	86.1
TaAffx.80399.1.S1_at	42.3	95.8	2.4	85.9
Ta.3748.1.A1_at	17.7	66.2	8.2	85.8
TaAffx.116570.1.S1_at	4.9	5.3	7.6	85.8
TaAffx.84226.1.S1_at	33.7	22.9	7.9	85.6
TaAffx.117301.1.S1_at	14.6	27.2	7.3	85.3
TaAffx.94519.1.S1_at	64.9	129.7	6	84.9
TaAffx.104657.1.S1_at	67.3	121.3	8.2	84.8
TaAffx.128510.15.S1_at	2.9	17.5	4.9	84.7
TaAffx.112028.1.S1_at	56.8	2.5	4.1	84.5
Ta.9430.1.S1_at	68.3	169.1	6.9	84.5
TaAffx.87844.1.S1_at	4.5	11	4.1	84.4
Ta.30294.1.S1_at	44.9	14	3.1	84.2
TaAffx.8093.1.S1_at	20.8	4.4	4.1	84
TaAffx.58733.1.S1_at	54.5	107.9	7.7	84
TaAffx.56970.1.S1_at	8.1	32.7	5.9	83.9
TaAffx.38131.1.S1_at	13.4	40.3	5.9	83.9
Ta.24911.1.S1_at	75.7	64.5	4.5	83.7
TaAffx.113773.1.S1_at	74.5	95.2	5.9	83.7
TaAffx.31040.1.S1_at	65.3	8.1	6.7	83.3
Ta.3275.1.S1_at	7.6	4.2	3.5	83.2
TaAffx.85514.1.S1_at	27.4	68.4	1.4	83.2
TaAffx.28567.1.S1_at	75	78.9	8.2	83.2
AFFX-r2-TagG_at	68	58.6	2.7	83.1
Ta.21049.2.S1_at	74.6	54.3	6.6	83.1
Ta.21673.1.S1_at	21.4	5.5	6.3	82.8
Ta.22464.1.S1_at	47.1	5.1	8	82.8
TaAffx.110720.1.S1_at	79.4	5.9	6	82.7
Ta.8608.1.A1_x_at	42.8	10.6	6.3	82.5
Ta.30832.1.S1_at	70.5	14.3	6.2	82.5
TaAffx.37861.1.A1_at	36.5	46.6	3.2	82.3
TaAffx.84743.1.S1_s_at	49.2	5.6	5.9	82.3
TaAffx.111386.1.S1_at	34.9	57.1	6.1	82.3
Ta.12398.2.S1_s_at	15.3	43.2	4.9	82.1
TaAffx.84518.1.S1_at	40.9	31.7	7	82.1
TaAffx.59323.1.S1_at	32.9	10.2	5.9	82
TaAffx.29276.1.S1_at	12.7	38	7.5	82
TaAffx.107217.1.S1_at	91.1	13.4	8.1	81.6
Ta.17158.1.S1_at	26.4	30.5	7.9	81.1
Ta.10543.1.A1_at	11.1	5.7	8	81
TaAffx.85659.1.S1_at	9.7	35.8	5.5	80.9
TaAffx.82999.1.S1_at	5.4	3	1.6	80.5
TaAffx.52035.1.S1_at	79.8	53.7	5.1	79.9

TaAffx.11930.3.S1_at	56.5	29.7	2.4	79.8
TaAffx.52495.1.A1_at	188.7	89.8	7.9	79.6
TaAffx.108347.1.S1_x_at	11.5	10.5	5.5	79.6
Ta.10037.2.S1_at	82.5	44.9	7.1	79.6
TaAffx.532.1.S1_at	72.5	38	2	79.1
TaAffx.12403.1.S1_at	67.3	57.8	7.5	78.9
TaAffx.56613.1.S1_at	40.2	31.7	7.7	78.9
TaAffx.56491.1.S1_at	18.5	51.2	6.2	78.8
TaAffx.86303.1.S1_at	5.5	37.3	7.8	78.5
TaAffx.86814.1.S1_s_at	10.6	49.1	6.4	78.5
Ta.9474.3.S1_at	53.9	71.3	7.5	78.4
TaAffx.31135.1.S1_at	33.7	6.1	7.4	78.4
Ta.26898.1.A1_at	46.2	64.7	7	78.3
Ta.20175.2.S1_at	6.2	46.7	5.7	77.9
Ta.25602.2.S1_x_at	70.2	45.2	1.8	77.7
TaAffx.31834.1.S1_at	46.7	19.1	7.5	77.6
Ta.22978.1.S1_x_at	23.9	19.7	6.2	77.5
TaAffx.55899.1.S1_at	51.6	44.5	6.4	77.4
TaAffx.30367.1.S1_at	12.4	3.3	5.2	77.1
TaAffx.77976.1.S1_at	61.6	92	6	77.1
TaAffx.135629.1.S1_at	40.3	42.2	1.8	76.9
TaAffx.57023.1.S1_at	22.1	1.8	3.9	76.7
TaAffx.108644.1.S1_at	36.3	2.7	4.7	76.1
Ta.30854.1.S1_at	20.1	1.9	5.5	76
TaAffx.4991.1.S1_at	21	50.5	6.2	75.8
Ta.24862.1.S1_x_at	9.2	5.2	7.3	75.7
TaAffx.112741.1.S1_at	7.2	15.8	5.4	75.7
TaAffx.23325.1.S1_at	37.5	81	2.5	75.4
Ta.11465.1.A1_at	37.5	2	7.2	75.2
TaAffx.25791.1.S1_at	50.2	59.4	4.7	74.9
TaAffx.29665.1.S1_at	54.3	26.1	6.2	74.8
Ta.17945.1.S1_at	32.7	32.3	2	74.4
TaAffx.24725.1.S1_at	97.1	3.3	3.3	74.1
TaAffx.86050.1.S1_at	41.5	25.2	4.1	74
TaAffx.29151.1.S1_at	6.9	25.6	6.8	74
Ta.5778.2.S1_at	44.2	2.6	6.2	73.9
TaAffx.7189.1.S1_at	47.4	17.3	6.9	73.9
Ta.20366.3.S1_at	55.3	47.1	3.2	73.9
TaAffx.94056.1.S1_at	4.6	3.3	4.3	73.7
TaAffx.61822.2.S1_at	40.9	18.7	6.7	73.6
TaAffx.79247.1.S1_at	43.3	13.1	3.8	73.5
TaAffx.30896.1.S1_at	47.1	35.6	2.4	73.3
TaAffx.83718.1.S1_at	8.5	44.2	1.4	73.3
TaAffx.31560.1.S1_at	57.3	13.3	6.9	73.2
TaAffx.23818.1.S1_at	76.6	48.3	6.7	73
TaAffx.81742.1.S1_at	50.2	1.1	4.5	72.8

TaAffx.54283.1.S1_at	8.9	33.2	4.1	72.7
TaAffx.107215.1.S1_at	39.8	4.1	1.3	72.5
TaAffx.57191.1.S1_at	64.5	6.3	6.5	72.2
TaAffx.104857.1.S1_at	76	25.6	2.2	72.2
TaAffx.55834.2.S1_at	122.8	25.4	3.2	72
Ta.19407.1.S1_at	56.4	14.9	4.8	71.9
TaAffx.28320.1.S1_at	20.7	25	5.9	71.9
TaAffx.112266.1.S1_at	3	5.1	3	71.9
Ta.13197.2.S1_at	9.2	29.3	6.4	71.8
TaAffx.108274.4.S1_at	61.7	26	4.6	71.7
TaAffx.77859.1.S1_at	31.2	26.5	5.4	71.7
TaAffx.56452.1.S1_at	13.1	36.5	4.7	71.5
TaAffx.91909.1.S1_at	85.7	67	5.6	70.9
TaAffx.51258.1.S1_at	8.8	15.7	4.6	70.9
Ta.30606.1.A1_at	56.5	76.3	6.3	70.8
Ta.30927.1.A1_at	3.7	25.4	6.7	70.7
Ta.20775.1.A1_x_at	21.1	9.7	4	70.7
TaAffx.57809.1.S1_at	22.6	6.4	4.5	70.7
TaAffx.29093.1.S1_at	20.8	31.3	2.8	70.3
TaAffx.54443.1.S1_at	24.7	39	6.7	70.1
TaAffx.138393.1.A1_at	47.9	23.5	4.7	70
TaAffx.58468.1.S1_at	9.2	12.3	4	70
TaAffx.111153.1.S1_at	11	9.3	3.9	69.9
Ta.5407.3.S1_x_at	97.8	81.5	3.8	69.8
TaAffx.112726.2.S1_at	58.8	25.2	4.6	69.3
Ta.28497.1.A1_at	86.7	92.5	6.2	69.2
TaAffx.29549.2.S1_at	26.4	4.2	6.6	69.2
TaAffx.31891.1.S1_at	5.2	39.2	4.4	69.2
TaAffx.71021.1.A1_at	55.5	32.3	5.1	68.9
Ta.17333.1.S1_at	6.3	43.3	5.8	68.6
Ta.15662.1.S1_at	21.2	26.8	1.1	68.5
TaAffx.112642.1.S1_at	56.6	29.2	2.7	68.4
TaAffx.107726.1.S1_at	6.7	14.4	2.5	68.4
Ta.13404.1.A1_at	28.6	13.5	4.4	68.3
Ta.20376.1.S1_at	49	20.4	6.5	68.3
TaAffx.86605.1.S1_at	50.7	20.7	2.3	68.3
Ta.27996.1.S1_at	149.7	166.5	6.6	68.2
TaAffx.84030.1.S1_at	65.5	35.1	2.7	67.6
Ta.26740.1.A1_at	11.8	19.1	5.1	67.4
TaAffx.26174.1.S1_at	8.9	14.5	5.4	67.4
Ta.9717.1.A1_x_at	5	35.8	6.7	67.3
TaAffx.6176.1.S1_at	23.6	40.8	6.2	67.2
TaAffx.109307.1.S1_at	58.5	20.2	4.9	67
TaAffx.107191.1.S1_at	10.5	39	5.3	66.9
Ta.15176.1.S1_at	8	22.3	5	66.8
TaAffx.81753.1.S1_at	4.1	19.9	5.4	66.8

Ta.26259.1.S1_at	64.8	30.4	5.7	66.6
Ta.11017.1.A1_at	17.5	1.6	2.6	66.4
Ta.7741.1.S1_at	35.4	9.8	3.1	66.4
Ta.649.2.S1_x_at	2.5	5.1	3.4	66.4
Ta.26655.1.S1_at	3.1	5.8	1.2	66.3
TaAffx.93070.1.S1_at	27.1	3.6	4	66.3
TaAffx.109268.1.S1_x_at	35.2	43.5	2.5	66
TaAffx.116175.3.S1_at	27	29.8	4	66
Ta.11083.1.A1_at	21.7	9.5	6.4	65.9
TaAffx.58583.1.S1_at	11.1	3.6	3.3	65.9
Ta.10361.2.S1_at	30.7	29.9	5.3	65.8
TaAffx.108309.1.S1_x_at	34.2	41	1.9	65.8
TaAffx.120246.1.A1_at	43	26.6	3.6	65.7
Ta.10114.2.S1_at	41.2	40.7	4.8	65.7
TaAffx.86567.1.S1_at	11.6	30.5	4.5	65.4
TaAffx.110932.1.S1_at	45.9	27.5	4.4	65.3
TaAffx.105579.1.S1_at	91.2	32.6	3.4	65.2
TaAffx.57803.1.S1_at	23.7	26.4	4.7	65.2
TaAffx.113223.1.S1_at	61.1	8.1	5.7	65
TaAffx.22878.1.S1_at	40	81.3	4.1	64.9
TaAffx.13063.1.S1_at	25	24.8	5.3	64.9
TaAffx.56922.1.S1_at	2.4	4.7	5.1	64.9
TaAffx.104641.1.S1_at	6.6	7	3.2	64.9
TaAffx.110134.1.S1_at	10.5	3.6	3.4	64.8
TaAffx.15048.1.A1_at	21.6	2.8	2.2	64.7
Ta.14810.1.S1_at	6.8	21.5	4.6	64.4
TaAffx.69877.1.A1_at	79.3	107.8	6.4	64.3
Ta.9990.1.S1_at	10.6	40.8	4	64.2
TaAffx.29660.2.A1_at	26.4	5	0.7	64.1
TaAffx.53024.1.S1_at	31	32.5	4.1	63.9
TaAffx.52688.1.S1_at	97.4	41.2	4.4	63.9
Ta.590.1.S1_x_at	27.7	17	3	63.7
TaAffx.32555.1.S1_at	9.3	42.3	3.4	63.6
TaAffx.16900.1.A1_at	38.7	51.1	5.7	63.5
TaAffx.112447.1.S1_at	46.9	7.8	2	63.5
TaAffx.117314.1.S1_at	58.4	82.4	4.2	63.4
TaAffx.93995.2.S1_at	45.1	38	5.5	63.2
Ta.30403.1.A1_at	61.9	9.7	6.1	63.2
TaAffx.113568.1.S1_at	15	34.8	5.4	63.2
Ta.4641.1.S1_at	68.9	64.6	6.2	63.1
TaAffx.129569.2.S1_s_at	5	38.9	3.3	63.1
Ta.10921.1.A1_at	4.4	22.3	3.7	62.9
TaAffx.53649.1.S1_at	7.2	5.6	3.7	62.9
TaAffx.119753.1.S1_at	32.2	72.3	6	62.8
TaAffx.25621.1.S1_at	10.4	5.8	5.6	62.7
TaAffx.50254.1.S1_at	54.9	58.5	3.9	62.5

TaAffx.104622.1.S1_at	74.2	75.9	4.8	62.4
TaAffx.25489.1.S1_at	7	12.7	3.7	62.4
Ta.28817.2.S1_at	76.7	35	4	62.2
TaAffx.108782.1.S1_at	2.1	12.6	2.2	62.1
TaAffx.29200.1.S1_at	41.3	19.7	5.3	62
TaAffx.58786.1.S1_at	3.5	14.6	5.5	62
TaAffx.8473.1.S1_at	54.2	10.5	5.3	62
TaAffx.22952.1.S1_at	6.1	16.3	2.8	62
TaAffx.78235.1.S1_at	5	13.9	4.4	61.9
Ta.23334.3.S1_at	18.4	5.5	5.7	61.8
TaAffx.109103.1.S1_at	6.5	53.6	5.8	61.8
Ta.20825.3.S1_at	15.9	5.2	2.6	61.7
TaAffx.111132.1.S1_at	53.8	45.2	5.1	61.7
TaAffx.9221.1.S1_at	3.3	8.5	4.2	61.5
Ta.22626.1.S1_at	7.7	1.4	3.1	61.5
TaAffx.27202.1.S1_at	16.3	21.9	2.1	61.5
Ta.15798.1.S1_at	52.2	1.8	6.1	61.3
TaAffx.26325.1.S1_at	38.4	33.2	3.6	61.3
Ta.23390.1.S1_at	9.8	33.6	5.1	61
Ta.6482.3.S1_at	7.5	47	3.8	60.8
TaAffx.30821.1.S1_at	35.3	50.3	3.6	60.8
TaAffx.30175.1.S1_at	35.8	21.2	5.2	60.8
TaAffx.602.1.A1_at	38.5	14	4.7	60.7
TaAffx.53094.1.S1_at	36.6	44.9	5.3	60.7
TaAffx.52665.1.S1_at	34.7	46.9	2.9	60.4
TaAffx.86775.1.S1_at	7.3	31.7	4.6	60.1
TaAffx.108764.1.S1_at	5.1	32.2	4.8	60
TaAffx.36729.1.S1_at	61.4	21.7	5.5	59.7
TaAffx.25849.1.S1_at	27.9	27.4	2.9	59.7
Ta.1934.3.S1_x_at	68.9	44.5	3.8	59.6
Ta.16174.1.S1_at	14	3.1	3.1	59.6
TaAffx.91897.1.S1_at	57.4	37	5.2	59.4
Ta.20872.1.S1_x_at	4.9	1.7	3.6	59.4
Ta.27521.1.S1_at	5.5	25.2	3.4	59.3
TaAffx.108965.1.S1_at	9.4	14.7	4.3	59.3
TaAffx.30076.1.S1_at	5.4	15.5	2.1	59.3
Ta.26768.1.A1_at	27.8	17.4	4.1	59.2
TaAffx.111581.1.S1_at	15.9	2.7	2.6	59
Ta.18239.2.S1_a_at	30.2	33.2	3.3	59
TaAffx.30672.1.S1_at	42.7	35	3.8	59
Ta.29396.2.A1_at	5.4	40.2	4.6	59
Ta.14539.3.S1_at	63	49.7	3.3	58.9
TaAffx.12798.1.S1_at	5.2	9.8	4.6	58.9
Ta.16729.1.S1_at	55.4	71.4	4.7	58.8
TaAffx.59159.1.S1_at	5.3	5.4	4	58.8
TaAffx.104831.1.S1_at	5.8	34.1	2.7	58.8

TaAffx.84129.1.S1_s_at	8.9	3	5.6	58.7
TaAffx.85864.1.S1_at	7.7	7.3	4.4	58.6
TaAffx.93075.1.S1_at	4.2	9.4	3.5	58.6
Ta.17804.1.S1_at	24	26.3	4.1	58.5
Ta.22474.1.S1_at	2.8	4	4.8	58.4
TaAffx.24738.1.S1_at	5.9	15.1	2.4	58.1
TaAffx.23912.1.S1_at	3.7	24.4	4.1	57.7
Ta.3528.1.S1_at	67.5	24.6	4.8	57.6
TaAffx.36438.1.A1_at	6	7.1	4.9	57.6
TaAffx.58270.1.S1_at	42	20.1	4.2	57.2
TaAffx.81765.1.S1_at	67.1	35	2	57.2
Ta.7791.3.S1_at	21.5	4.5	3.9	56.9
TaAffx.58216.1.S1_at	40.2	140.9	2.5	56.8
TaAffx.64082.1.S1_at	75.2	9.7	5.6	56.8
Ta.26401.1.A1_at	8.1	41.5	2.2	56.7
TaAffx.37997.1.S1_at	4.3	2.7	5.3	56.7
TaAffx.83462.1.S1_at	29.8	61.8	4.1	56.5
Ta.30691.2.S1_at	11.6	30.1	3.6	56.4
TaAffx.28435.1.S1_at	117.1	34.9	3	56.4
TaAffx.109047.1.S1_at	3.2	5.3	3.4	56.2
TaAffx.53650.1.S1_at	27.8	2.5	2.6	56.1
TaAffx.50186.1.S1_at	9.5	7.7	5.3	56
TaAffx.59400.1.S1_at	8.8	4.8	4.2	56
TaAffx.91475.1.S1_at	12.1	11.3	5.1	55.8
Ta.13723.1.S1_at	8	10.8	3.9	55.8
Ta.20618.1.A1_at	18.4	39.7	3.9	55.7
Ta.17194.1.S1_at	42	15.3	4.6	55.6
TaAffx.22849.1.S1_at	13.2	44.9	2.3	55.6
TaAffx.32099.1.S1_at	2.2	4.5	3.6	55.6
TaAffx.120526.1.S1_at	31.7	25.1	2.5	55.4
Ta.28183.3.S1_at	4.7	1.5	2	55.4
TaAffx.80316.1.S1_at	6.1	29.5	4.4	55.4
TaAffx.79641.1.S1_at	9.6	1.8	5.4	55.3
TaAffx.128541.15.S1_at	43.2	11.3	5.4	55.2
TaAffx.30659.1.S1_at	4.1	31.7	2.4	55.2
Ta.18082.2.A1_at	9.8	36.3	5.3	55.2
Ta.11614.1.A1_at	73.5	40.3	4.2	55.1
TaAffx.112984.2.S1_at	10.1	28.5	2.1	55.1
TaAffx.104787.1.S1_at	15.6	14.4	5.3	55.1
TaAffx.54143.1.S1_at	1.8	4.5	2.4	55.1
TaAffx.31444.1.S1_at	2.4	2	3.6	55
TaAffx.111146.1.S1_at	37.9	32.3	3.2	55
TaAffx.118770.1.A1_at	35	9.3	2.4	54.8
TaAffx.30895.1.S1_at	3.1	3.9	3.7	54.8
Ta.23988.1.A1_at	50.1	1.3	4.7	54.7
TaAffx.84525.1.S1_at	77.6	38.8	5.1	54.7

Ta.15186.1.S1_at	1.9	17.2	1.2	54.6
Ta.21998.2.S1_at	40.2	4.1	5.3	54.6
TaAffx.80488.1.S1_at	10.9	1.9	3.6	54.5
Ta.9141.2.S1_at	11.7	6.6	3.2	54.4
TaAffx.30272.2.S1_at	15.7	7.5	4.6	54.2
Ta.13314.1.S1_at	44.8	34.1	4.8	54.2
TaAffx.119320.2.S1_at	6.7	4.1	2.8	54.2
TaAffx.53119.1.S1_at	6.4	22.7	5.3	54.2
Ta.3133.2.S1_at	25	5	4.2	54.1
TaAffx.112541.2.S1_at	7.6	34.3	2.4	54.1
TaAffx.22829.1.S1_at	102.8	7.2	3.9	54
TaAffx.28917.1.S1_at	71.4	56.1	5.1	54
Ta.27284.1.S1_at	23.1	27.5	1.9	53.9
Ta.1613.1.S1_at	37.6	39.9	3.8	53.9
Ta.4642.1.A1_at	46.4	11.3	4.1	53.8
Ta.25568.2.A1_at	31.4	2.6	2.2	53.5
TaAffx.112701.1.S1_at	8.1	12.4	3.2	53.5
TaAffx.87282.1.S1_at	1.5	3.8	4.9	53.5
TaAffx.25063.1.S1_at	20.2	5.7	3.5	53.4
Ta.12737.1.S1_at	3.3	7.3	4	53.4
TaAffx.37179.1.A1_at	20.6	4.7	4	53.4
TaAffx.137341.1.S1_at	38.7	43.5	4.6	53.4
TaAffx.59280.1.S1_at	2.5	2.5	4.8	53.4
TaAffx.81593.1.S1_at	26	7.3	2	53.2
Ta.30219.2.S1_at	12.6	5.5	2.5	53.2
TaAffx.90063.1.S1_at	3.9	38.3	3.2	53.1
TaAffx.113039.1.S1_at	3.2	16.7	1.6	53.1
Ta.5235.1.S1_at	22.2	6.8	4.8	52.9
TaAffx.25368.1.S1_at	73.6	10.8	3.3	52.9
TaAffx.69653.1.S1_at	76.8	5.7	4.4	52.7
Ta.28353.2.S1_at	37.1	8.9	4.2	52.7
Ta.10546.1.A1_at	26.6	18.9	4.2	52.7
TaAffx.78085.1.S1_at	3.9	33.8	4.9	52.7
TaAffx.38195.1.S1_at	9	41.2	5.1	52.7
TaAffx.30267.1.S1_at	55.1	3.6	3.3	52.5
TaAffx.112406.1.S1_at	8.5	1.2	2.6	52.5
Ta.8977.1.A1_at	23.8	21.7	4.1	52.4
TaAffx.8419.1.S1_at	28.9	32.3	3.3	52.4
Ta.19202.1.S1_at	57.2	8.3	3	52.3
TaAffx.94339.2.S1_at	93.1	33.4	4.3	52.3
TaAffx.19604.5.S1_at	6.7	32.3	1.9	52.3
Ta.26803.1.A1_at	7.2	65.1	4	52.1
TaAffx.59514.1.S1_at	46.4	5.6	4.3	52.1
TaAffx.78631.1.S1_x_at	35.1	6.1	5.2	52.1
TaAffx.70800.1.S1_at	10.4	15	4.8	51.9
TaAffx.32093.2.S1_at	34.4	2.2	3.6	51.8

Ta.17387.1.S1_at	4.6	2	1.6	51.8
Ta.17604.1.S1_at	2.4	2.5	4.1	51.7
TaAffx.114024.1.S1_at	7	2.9	4.4	51.7
TaAffx.9160.1.S1_at	6.3	30.8	5.1	51.6
TaAffx.57250.1.A1_at	27.5	66.8	3.4	51.6
TaAffx.8775.4.S1_at	4.4	1.5	1.8	51.6
TaAffx.51287.3.S1_x_at	20.3	2	1.9	51.5
Ta.17564.1.S1_at	34.8	4.2	4.3	51.5
Ta.223.1.S1_at	1.9	1.9	2.5	51.4
TaAffx.106422.1.S1_at	56.8	6.1	3.8	51.3
TaAffx.120709.1.S1_at	37.6	49.9	3.5	51.2
TaAffx.110827.1.S1_at	3.1	17.5	2.2	50.9
Ta.22854.2.S1_at	3.3	28.2	4.2	50.9
TaAffx.105405.1.S1_at	55.1	43.8	2.8	50.7
Ta.12926.1.S1_at	37.4	10.8	4.1	50.6
Ta.14406.1.A1_at	6.6	48.5	4.7	50.4
Ta.8835.1.A1_at	4.2	8.1	4.3	50.2
Ta.25348.1.A1_at	4.8	31.2	4.4	50.2
TaAffx.30059.1.S1_at	53.1	47.1	4.7	50.2
TaAffx.28241.1.S1_at	40.9	19.5	4.5	50
Ta.20299.1.S1_at	1.2	1.5	2.2	49.9
TaAffx.84500.1.S1_at	5.4	6	4.8	49.9
TaAffx.53790.1.S1_at	66.8	5	3.6	49.6
Ta.12945.1.S1_at	3.9	3.3	3.3	49.6
Ta.21049.3.S1_at	4.7	19.4	4.7	49.6
TaAffx.64234.1.S1_at	80.7	38.8	4.2	49.5
TaAffx.29175.1.S1_at	6.4	29	2.8	49.5
TaAffx.7831.1.S1_at	35.2	34.8	2.9	49.5
TaAffx.26468.1.S1_at	26.4	8	3.6	49.4
Ta.10562.2.S1_at	34.5	31.3	2.2	49.3
TaAffx.85542.1.S1_at	44.8	3.6	4.4	49.2
TaAffx.106424.1.S1_at	41.6	37	4.1	49.1
TaAffx.56544.1.S1_at	20.6	18.2	2.9	49.1
TaAffx.84162.1.S1_at	13.2	8.3	2.3	49
TaAffx.90204.1.S1_at	29.4	64.6	3.8	48.9
TaAffx.107663.1.S1_at	2.3	3.9	3.6	48.9
Ta.22228.1.S1_at	2.1	17.8	2.4	48.8
TaAffx.78146.1.S1_at	2.2	5.1	3	48.8
TaAffx.38331.1.S1_at	4.8	30.6	1.4	48.7
TaAffx.56719.2.S1_at	36.9	29.8	4.3	48.7
Ta.19650.1.S1_at	44	84.9	4.7	48.6
TaAffx.114276.1.S1_at	54.7	36.7	2.6	48.5
TaAffx.128517.2.S1_at	21.5	11.2	3.6	48.5
TaAffx.26243.1.S1_at	64.7	11.3	2.4	48.5
Ta.30480.1.A1_at	4.6	2.2	3.2	48.3
TaAffx.84329.1.S1_at	45.4	13.2	4.1	48.3

TaAffx.104826.1.S1_at	51.6	3	2.4	48.2
Ta.22529.1.S1_at	38.9	23.3	4.8	48.2
TaAffx.26353.1.S1_at	16.5	2.2	2	48.2
TaAffx.30494.1.S1_at	5.3	43.5	2.9	48.2
TaAffx.51672.1.S1_at	15.9	29.4	3.2	48.2
TaAffx.65414.1.S1_at	33.8	4.1	2.4	48.1
TaAffx.29223.1.S1_at	13.7	17.6	4.2	48.1
TaAffx.26743.1.S1_at	40.1	66.3	4.1	47.9
Ta.22094.2.A1_at	10.2	45.6	4.4	47.7
TaAffx.58751.1.S1_at	5.3	9.3	1.9	47.7
TaAffx.109706.1.S1_at	4.4	6.3	4.4	47.7
Ta.26848.1.A1_at	9	10.3	2.1	47.6
TaAffx.58084.1.S1_at	5.1	5.5	1.8	47.6
TaAffx.1100.1.S1_at	9.5	23.4	4.3	47.5
TaAffx.25014.1.S1_at	17.7	28	1.6	47.4
TaAffx.106478.1.S1_at	4	32.7	4.2	47.4
Ta.20368.1.S1_at	2	1.1	3.7	47.3
Ta.15167.1.A1_at	3.1	2.3	3.6	47.3
TaAffx.54318.1.S1_at	71	1.7	4.1	47.2
Ta.2299.2.S1_at	35.2	21.4	4	47.2
TaAffx.58753.2.S1_at	16.8	47.1	3.3	47.2
Ta.19591.1.A1_at	34.9	27.5	2.6	47.1
Ta.19687.1.S1_at	43.4	4.6	3.7	47
TaAffx.59251.1.S1_at	18.6	10	4.6	46.8
Ta.22667.1.A1_at	2.1	6.9	3.6	46.8
TaAffx.108556.1.S1_at	47.5	20.9	4.1	46.6
TaAffx.38827.1.S1_at	11.2	2.6	3.9	46.6
TaAffx.12442.1.A1_at	5.9	19.1	2.8	46.6
TaAffx.27937.1.S1_at	25.5	8.1	4.3	46.5
TaAffx.6375.1.S1_at	41.5	12.7	4.3	46.5
TaAffx.111343.1.S1_at	8.8	9.8	3.1	46.4
TaAffx.53265.1.S1_at	32.9	4.1	3.5	46.4
TaAffx.109541.1.S1_x_at	4.6	25.5	3.8	46.4
Ta.8970.1.A1_x_at	5	23.1	2.4	46.3
TaAffx.108095.1.S1_at	5.9	21.2	4.2	46.3
TaAffx.30131.1.S1_at	5.1	31.3	4	46.2
Ta.24357.1.S1_at	45.3	26.9	2	46
TaAffx.31370.1.S1_at	6	2.5	2.2	46
TaAffx.104743.1.S1_at	3.6	6.8	2.6	45.9
Ta.18512.1.S1_at	4.1	2.8	2	45.8
TaAffx.496.1.S1_at	20	28.3	4.2	45.8
TaAffx.58753.1.S1_at	5.3	4.9	4.2	45.6
TaAffx.29095.1.S1_at	38.9	2.8	3.7	45.4
TaAffx.107478.1.S1_x_at	32	3.6	1.8	45.4
TaAffx.64528.2.S1_at	48	7.6	2.4	45.4
TaAffx.120312.1.S1_at	24.3	25.8	4.5	45.3

Ta.958.1.S1_at	7.9	6.9	3.7	45.3
TaAffx.54350.2.S1_at	2.7	4.5	1.4	45.3
Ta.10665.1.A1_at	26	18.9	2.8	45.2
Ta.26755.1.S1_at	22.3	7.3	3.1	45.1
TaAffx.9580.1.S1_at	37.2	33.2	3.9	45.1
Ta.16173.1.S1_at	15.3	2.5	2.1	45
Ta.9326.2.S1_at	3	2.2	1.8	45
TaAffx.57522.2.S1_x_at	8.2	27.7	2.8	44.9
Ta.8446.2.S1_at	9	2.5	2.6	44.8
TaAffx.86606.1.S1_at	3.6	1.9	4.1	44.7
TaAffx.28843.1.S1_at	8.6	45.2	3	44.5
TaAffx.79804.1.S1_at	51.3	88.6	1.9	44.4
RPTR-Ta-AF323980-1_at	1.9	4.8	3.8	44.3
TaAffx.27696.1.S1_at	40.3	4.4	3.3	44.3
TaAffx.30889.1.S1_at	60.1	40.8	3.2	44.3
TaAffx.117186.1.S1_at	20.1	10.3	3.9	44
TaAffx.113186.2.S1_at	32.5	7.9	4.2	44
TaAffx.6594.1.S1_at	44.4	2.7	1.6	43.9
Ta.8128.3.A1_at	34.5	27.1	2.3	43.9
TaAffx.108898.1.S1_at	10.5	30.1	4.2	43.9
TaAffx.51106.1.S1_at	89	3.3	3.2	43.8
Ta.24107.1.S1_at	39	25.9	2	43.8
Ta.10076.3.S1_at	21.8	2.6	3.6	43.7
Ta.16310.1.S1_at	17.3	3	2.2	43.6
Ta.8169.1.A1_at	31.6	25.5	1.9	43.6
TaAffx.39466.1.S1_at	3	1.5	1.8	43.6
TaAffx.53783.1.S1_at	7.4	4.3	3.7	43.5
TaAffx.42802.1.A1_at	36.5	2.3	2.7	43.4
TaAffx.121298.1.S1_at	66.7	18.2	2.2	43.3
TaAffx.38377.1.S1_at	8.3	53	2.2	43.1
Ta.29462.2.A1_at	14.3	50.7	3	42.7
Ta.17337.1.S1_at	46.1	15.2	2.1	42.5
TaAffx.81775.1.S1_x_at	43	25	3.3	42.3
TaAffx.84360.1.S1_at	44.4	48	4.1	42.3
Ta.28440.2.S1_at	10.7	47.4	3.4	42.2
Ta.12558.1.A1_at	27	6.9	3.7	42.2
Ta.12319.1.A1_at	19.4	54.3	2.9	41.9
TaAffx.107550.1.S1_at	42.3	25.3	3.3	41.9
TaAffx.111772.1.S1_at	2.6	10.6	2.2	41.9
Ta.17063.2.S1_at	8	30.5	3.1	41.7
Ta.24857.2.S1_x_at	39.4	9.2	4.1	41.7
TaAffx.48328.1.S1_at	9.7	6.2	3.7	41.5
TaAffx.14405.2.S1_at	4.3	31.3	2	41.5
Ta.21353.3.S1_at	4.4	20.6	4.1	41.4
TaAffx.108390.1.S1_at	21.8	17.9	2.4	41.4
TaAffx.78800.1.S1_at	15.1	2.1	1.8	41.3

Ta.22222.1.S1_at	22.6	2.6	1.6	41.2
TaAffx.85116.1.S1_at	16.6	26	0.4	41.1
TaAffx.11970.3.S1_at	4.3	30.7	3.8	41
TaAffx.56570.1.S1_at	2.3	9.4	3.2	41
TaAffx.83430.1.S1_at	40.7	2.5	3	40.8
Ta.22654.1.S1_at	7.2	5.9	2	40.8
Ta.12684.1.S1_at	52.4	34.1	1.4	40.7
TaAffx.111759.3.S1_s_at	18.8	3.8	2.7	40.7
TaAffx.120368.1.A1_x_at	45.2	12.1	3.2	40.6
TaAffx.57891.1.S1_at	26.6	4.5	3.7	40.6
TaAffx.108681.1.S1_at	22.5	6.4	3.7	40.6
TaAffx.84394.1.S1_at	3.6	2.3	3.2	40.5
TaAffx.80375.1.S1_at	32.8	13.5	1.2	40.5
TaAffx.108079.1.S1_at	6.1	9.6	3.9	40.5
TaAffx.30505.1.S1_at	2.6	3	3	40.4
Ta.22422.1.S1_at	28.6	41.9	2.4	40.3
TaAffx.26201.1.S1_at	17.2	3.7	2	40.3
TaAffx.90243.1.S1_at	49.7	13.6	3.6	40.3
TaAffx.7700.1.S1_at	26	19.7	2.2	40.3
TaAffx.4337.1.S1_at	7.9	9.9	1.9	40.3
TaAffx.26014.1.S1_at	16.6	1.3	3.5	40.1
Ta.22284.1.S1_at	21.8	22.3	3.2	40.1
TaAffx.128414.53.S1_at	14.1	7.8	2.7	40
TaAffx.82110.1.S1_at	10.6	34.5	2.8	40
Ta.25687.1.S1_at	8	10.1	2.5	39.9
Ta.5861.2.S1_at	2.8	1.6	1.9	39.9
Ta.20631.2.S1_at	2	18	0.8	39.9
TaAffx.57581.1.S1_at	22.7	46.7	3.7	39.9
TaAffx.107684.1.S1_at	21.8	12.1	3.8	39.9
Ta.2358.2.A1_at	11	17.7	3.5	39.7
TaAffx.7491.1.S1_at	39	26.6	1.9	39.7
TaAffx.128493.2.A1_at	3	18.8	3.7	39.6
Ta.5510.1.S1_at	5.2	20.5	3.5	39.5
Ta.9334.1.S1_s_at	7.6	30.6	2.2	39.3
Ta.4950.2.S1_at	39.3	5	2.4	39.3
TaAffx.26113.1.S1_at	2.8	1.4	3.4	39.1
Ta.14614.1.S1_at	67	8.5	3.7	39
Ta.26884.1.A1_at	25.6	17	2.4	39
TaAffx.32438.1.S1_at	31.9	25.9	3.7	39
TaAffx.82026.1.S1_at	58.7	45.1	3.4	39
TaAffx.52690.1.S1_at	22.1	4.9	0.5	39
Ta.22644.1.S1_at	35.6	19.1	3.2	38.9
Ta.8515.2.A1_at	31	19.4	3.7	38.8
TaAffx.30710.1.S1_at	4	21.1	2.8	38.8
TaAffx.113447.1.S1_at	15.7	19.1	1	38.7
TaAffx.50641.1.S1_at	36.9	28	3.2	38.7

TaAffx.39325.1.A1_at	14.5	18.8	2	38.5
Ta.9613.3.S1_at	1.3	11.4	1.7	38.5
TaAffx.29342.1.S1_at	26.9	48.5	3.4	38.5
Ta.428.3.S1_at	2.6	1.7	2.7	38.4
Ta.97.2.S1_x_at	4.3	19.1	3.7	38.2
Ta.29424.1.A1_a_at	10.2	23	2.9	38.1
TaAffx.91673.1.A1_at	14.2	17.4	2.6	38
Ta.28355.1.S1_at	92.6	31.1	2.3	37.9
TaAffx.107664.1.S1_x_at	4.4	3.6	1.5	37.9
TaAffx.112337.1.S1_at	4.5	34.1	2.4	37.8
TaAffx.58774.1.S1_at	23.5	2.6	3	37.8
TaAffx.6372.1.S1_at	42.1	42.6	2.2	37.7
TaAffx.71736.1.A1_at	17.9	13.4	3.4	37.6
TaAffx.51614.1.S1_at	4.9	2.9	3.3	37.5
Ta.15603.1.S1_at	2.3	6	1.9	37.4
TaAffx.109096.1.S1_at	6.9	2.6	2.6	37.4
TaAffx.27070.1.S1_at	17	16.2	0.8	37.4
TaAffx.26742.1.S1_at	4.5	1.7	1.8	37.3
TaAffx.8909.1.S1_at	49.9	38.4	3.5	37.3
TaAffx.81465.1.S1_at	5.4	29.5	2	37.3
TaAffx.77494.1.S1_at	35.2	9.1	3.6	37
Ta.3133.1.S1_x_at	63.5	3.6	2.1	36.9
TaAffx.53933.1.S1_at	9.7	10.8	2.9	36.7
TaAffx.52312.1.S1_at	0.8	2.2	2.6	36.7
TaAffx.85866.1.S1_at	8.5	6	2.6	36.6
TaAffx.97029.1.S1_at	4.7	3	3.3	36.5
TaAffx.109027.1.S1_at	29.9	5.8	0.8	36.5
Ta.26457.1.A1_at	25.9	1.6	0.9	36.4
Ta.16612.1.S1_at	30.9	34.7	3.6	36.4
TaAffx.124251.1.S1_at	3.2	6.9	3.6	36.4
Ta.9599.1.S1_a_at	6.4	3.2	1.5	36.3
Ta.22734.2.S1_x_at	5.3	1.5	1.6	36.3
Ta.24344.1.S1_at	115	74.4	3.1	36.1
TaAffx.85307.1.S1_at	31.2	2.6	3.1	36
Ta.30782.4.S1_at	21	2.4	1.9	36
Ta.14010.1.S1_at	7.7	3.3	1.7	36
TaAffx.25585.1.S1_at	11.7	15.1	1.6	36
TaAffx.121219.1.S1_at	9.8	27.7	2.1	36
TaAffx.81080.1.S1_at	3.1	9.7	3.3	36
TaAffx.53954.1.S1_at	38.2	8.9	2.7	35.8
Ta.27503.1.S1_at	29.9	3.7	3.1	35.7
Ta.8974.1.A1_at	6.7	3.3	2.3	35.7
Ta.14156.1.S1_at	492	30.8	2.7	35.6
TaAffx.25077.1.S1_at	63.7	42.2	3.4	35.6
Ta.15684.1.S1_at	32.5	1.6	1.8	35.5
Ta.15562.1.S1_at	23.9	33.1	2.5	35.4

Ta.11408.1.S1_at	10	4.2	1.6	35.4
TaAffx.102293.1.S1_at	21.4	25.4	1.7	35.4
TaAffx.26980.1.S1_at	3.3	0.9	1.3	35.2
TaAffx.5007.1.S1_at	2	18.3	2	35.1
TaAffx.84950.2.S1_at	10.6	18.4	3.5	35.1
TaAffx.30561.1.S1_at	2.4	1.2	2	34.9
Ta.22650.2.S1_at	35.7	71.5	2.6	34.9
TaAffx.5866.1.S1_at	7.7	22.4	1.5	34.9
TaAffx.111755.1.S1_at	24.3	7.4	1	34.9
Ta.5267.2.S1_x_at	17.2	12.6	1.7	34.5
Ta.15024.1.S1_at	4.6	24.9	2.9	34.4
Ta.12794.2.S1_at	3.5	4.3	2.2	34.4
TaAffx.80775.1.S1_at	20.7	1	1.2	34.3
TaAffx.7449.1.S1_x_at	22.4	19.4	0.6	34.3
TaAffx.106780.1.S1_at	21.9	2.3	1.3	34.1
TaAffx.128418.107.S1_at	18.6	9.9	2.8	34.1
Ta.7667.1.S1_at	44.8	13.5	2.3	34
Ta.8029.1.A1_at	41.8	25.5	2.5	34
TaAffx.66594.1.A1_at	17.3	12.6	2.4	33.9
TaAffx.78595.1.S1_x_at	3	14.6	1.6	33.9
TaAffx.105350.1.S1_at	5.7	10.5	3.1	33.7
TaAffx.134808.1.S1_at	16.7	20.5	0.5	33.6
TaAffx.112378.2.S1_s_at	25.3	3.4	2.7	33.5
Ta.17127.1.A1_at	2.7	6.8	2.8	33.4
Ta.9366.3.S1_at	8.6	26.1	1.5	33.4
TaAffx.83241.1.S1_at	2.7	13.6	2.7	33.4
TaAffx.108158.1.S1_at	0.5	0.9	1.3	33.3
TaAffx.85539.1.S1_at	14.1	48.3	3.3	33.3
TaAffx.30780.1.S1_at	3.1	2.3	2.1	33.3
TaAffx.51229.1.S1_x_at	12.7	2.4	3.2	33.3
Ta.8027.3.S1_at	4.6	2.7	2.3	33.2
TaAffx.28452.1.S1_at	1.5	12.3	1.6	33.2
TaAffx.56989.1.S1_at	8.1	20.2	2.3	33.1
Ta.4391.1.S1_at	47.3	36.9	2	33.1
TaAffx.65601.1.S1_at	11.9	2.8	2.4	33
Ta.27373.1.S1_at	1.8	7.5	1.8	32.9
TaAffx.107859.1.S1_at	31.9	12.1	3.1	32.8
TaAffx.7704.1.S1_at	60.5	45.9	1.9	32.8
TaAffx.106080.1.S1_at	5.1	5.1	2.7	32.7
Ta.6110.1.S1_x_at	2.7	6.4	2.8	32.6
TaAffx.53555.1.S1_at	21.7	56.8	3.1	32.5
TaAffx.112513.1.S1_at	48.5	28.2	2.2	32.4
TaAffx.65435.1.S1_at	46.9	47.8	2.5	32.4
TaAffx.54055.1.S1_at	30.3	9.9	1.7	32.3
TaAffx.30460.1.S1_at	41.3	4.4	2.6	32.2
TaAffx.24731.1.S1_at	8	44.4	1.7	32.2

TaAffx.84475.1.S1_at	21.7	2	2	32.1
TaAffx.98930.1.A1_at	9.6	28.3	2.8	31.9
TaAffx.85975.1.S1_at	27.6	43.6	2.9	31.8
TaAffx.57113.1.S1_at	37.5	32.1	2.5	31.8
TaAffx.24497.1.S1_at	19	3.9	1.3	31.7
TaAffx.78859.1.S1_at	2.2	0.5	2.7	31.7
TaAffx.25587.1.S1_at	5.6	3.4	2	31.6
TaAffx.28232.1.S1_at	14.1	11.4	2.8	31.6
TaAffx.23739.1.S1_at	18.7	8.7	2.3	31.5
TaAffx.128414.229.A1_x_at	82.2	51.2	2.5	31.5
TaAffx.51365.1.S1_at	6.2	31.9	2.8	31.3
TaAffx.12601.2.S1_at	20.6	39.3	2.9	31.2
Ta.19630.1.S1_at	61.3	25.8	2.8	31.1
Ta.18008.1.S1_at	29	6.8	1.5	31.1
TaAffx.110498.1.S1_at	9.1	5.7	2.8	31
TaAffx.79066.1.S1_at	25.7	17.7	1.1	31
TaAffx.545.1.S1_at	21.5	4.7	1.7	30.9
TaAffx.85537.3.S1_at	11.8	19	2.8	30.9
Ta.28507.2.S1_at	60.2	25.3	1.6	30.8
TaAffx.111016.1.S1_at	1.5	10.4	3	30.8
TaAffx.53394.1.S1_at	2.4	2.1	1.9	30.8
TaAffx.108166.1.S1_at	1.2	0.9	1.3	30.6
Ta.15652.1.S1_at	2.3	3	1	30.4
Ta.19615.1.S1_at	2.5	23	2.1	30.4
TaAffx.108958.1.S1_at	5.1	23.3	1.5	30.4
TaAffx.4544.2.S1_at	3.2	17.7	1.7	30.4
Ta.19642.2.A1_at	32.1	3.3	2.7	30.2
Ta.17577.1.S1_at	27.1	7.3	1.5	30.2
Ta.1308.1.S1_x_at	2.8	2.7	2.9	30
Ta.109.1.S1_at	11	1.5	2.4	30
Ta.26417.1.A1_at	25.8	4.3	2.6	30
Ta.21768.1.S1_at	4	3.1	2.7	29.7
TaAffx.81568.1.S1_at	2.8	3.2	2.7	29.7
TaAffx.52739.1.S1_at	6.4	9.2	2.8	29.5
TaAffx.58718.1.S1_at	18.9	4.7	2.9	29.4
TaAffx.40107.2.S1_at	2.7	3	1.5	29.3
Ta.26710.1.A1_at	43.7	16.4	2.8	29.3
TaAffx.30255.1.S1_at	2.6	10	2.9	29.3
TaAffx.108526.1.S1_at	26.7	27.7	2.1	29.1
TaAffx.84330.1.S1_at	25.3	4.6	1.2	29.1
Ta.28247.1.S1_at	22	0.6	0.7	28.9
TaAffx.79691.1.S1_at	5.2	31.5	1.7	28.7
Ta.28907.3.S1_x_at	16.2	13.9	2.3	28.5
TaAffx.86435.1.S1_at	12.1	6	1.3	28.3
TaAffx.58848.1.S1_at	6.3	7.2	2.8	28.2
TaAffx.43688.1.S1_at	2.8	21.4	2.7	28.1

TaAffx.54558.1.S1_at	31.3	32.5	1.8	28.1
TaAffx.86018.1.S1_at	1.4	1	1.8	28
TaAffx.4219.1.S1_at	23.7	51	2.6	27.9
TaAffx.85901.2.S1_at	23.1	2.6	2.6	27.8
Ta.5642.1.A1_at	14.4	1.8	2.3	27.6
Ta.18672.1.S1_x_at	2.2	1.7	2	27.6
Ta.22620.1.S1_at	26.7	3.2	2.2	27.6
TaAffx.106390.1.S1_at	8.7	9.6	1.3	27.6
TaAffx.51497.1.S1_at	17.1	34.7	2.5	27.4
TaAffx.104577.1.A1_at	5.6	9.8	2.7	27.3
TaAffx.80489.1.S1_at	2.5	2.6	0.8	27.3
Ta.15633.1.S1_at	3.2	4.5	2.7	27.1
Ta.27457.4.S1_x_at	57.5	116.8	1.3	27
Ta.17688.1.S1_at	1.3	5.4	1.9	26.9
TaAffx.128570.3.S1_at	43.9	74.7	2	26.9
TaAffx.81833.1.S1_at	3.5	2	1.6	26.8
TaAffx.4455.1.S1_at	1	0.8	1.6	26.6
TaAffx.4520.1.S1_at	1.3	2	1.2	26.5
TaAffx.128541.24.S1_at	7.5	2.1	1.8	26.4
Ta.21281.2.A1_at	8.4	4.1	2.2	26.4
TaAffx.78369.1.S1_at	23.3	11.9	2.2	26.4
TaAffx.79302.1.S1_at	23.4	2.8	1.2	26.3
TaAffx.56796.1.S1_at	30.8	5.3	2.3	26
TaAffx.6172.1.S1_at	2.3	10.3	1.8	25.9
Ta.16159.1.S1_at	18.8	8	2.3	25.5
TaAffx.5957.1.S1_x_at	2.1	11.9	1.6	25.5
TaAffx.24073.1.S1_at	10.4	11.3	1.3	25.4
Ta.23243.1.S1_a_at	54	23.4	2.2	25.3
TaAffx.85981.1.S1_at	23.3	32.1	2.1	25.3
TaAffx.55398.1.S1_at	2.1	5.1	1.7	25.2
TaAffx.26575.1.S1_at	26.3	14.8	1.6	25.1
TaAffx.32459.1.S1_at	4.3	3.5	2.2	25
Ta.15752.1.S1_at	9.4	1	2.1	24.9
TaAffx.22995.1.S1_at	6.9	1.6	2.1	24.9
TaAffx.85998.1.S1_at	4.5	30.3	2.1	24.9
TaAffx.32222.1.S1_at	0.8	0.4	1.3	24.9
TaAffx.28761.1.S1_at	12.9	32.7	1.5	24.8
Ta.20617.1.S1_at	0.2	0.9	1.4	24.6
TaAffx.120225.1.S1_at	6.7	30.5	1.6	24.6
TaAffx.4545.1.S1_at	4.3	3.8	2.3	24.5
RPTR-Ta-X03453-1_at	4	15	1.3	24.4
TaAffx.22969.1.S1_at	6	22.4	2.1	24.3
TaAffx.37267.1.S1_at	24.6	19.8	2.4	24.3
Ta.1834.3.S1_at	4.6	18.4	2.3	24.2
TaAffx.70722.1.S1_at	3.7	2.7	1.5	24.1
Ta.25038.2.S1_at	0.5	1.1	0.9	24

TaAffx.108451.1.S1_s_at	4.4	19.7	1.4	23.7
TaAffx.6179.1.S1_at	1.9	5.9	2.3	23.4
Ta.27774.2.S1_at	57.6	8.9	2.3	23.2
TaAffx.30698.1.S1_at	7.2	16.9	1.7	23.2
Ta.9346.1.S1_x_at	15.6	2.7	1.8	23.1
TaAffx.79900.1.S1_at	16.7	11	1.6	22.8
TaAffx.111376.1.S1_at	27.5	15.8	2	22.7
Ta.12671.2.S1_x_at	8.1	16.2	1.9	22.7
TaAffx.48201.1.S1_x_at	20.7	9.3	1	22.7
Ta.15766.1.S1_at	30	1.8	0.4	22.2
Ta.26780.1.A1_at	3.6	8.5	1.8	22.1
TaAffx.59361.1.S1_at	8	42	1.6	21.8
TaAffx.86677.1.S1_at	3.5	2	2.1	21.6
Ta.27477.1.S1_at	7.2	10.1	1.6	21.4
TaAffx.112949.2.S1_at	20.2	5.5	1.1	21.3
TaAffx.86410.1.S1_at	12.4	25.8	1.6	21.3
TaAffx.106461.1.S1_at	3.5	19.6	1.8	21.2
Ta.14968.1.A1_at	10.4	21.7	2	21.2
Ta.26393.1.A1_at	2	1.7	2	21.2
TaAffx.80987.1.S1_at	7.6	3.6	1.8	21.1
TaAffx.12000.1.S1_at	3.5	2.6	2	21.1
TaAffx.65112.1.A1_at	3.2	3.1	1.9	20.8
TaAffx.105614.1.S1_at	3.9	5.5	1.7	20.7
Ta.24957.2.A1_s_at	38.2	0.8	0.7	20.6
TaAffx.55342.1.S1_at	11.3	20.1	1.1	20.6
TaAffx.53966.1.S1_at	6.5	2.6	0.8	20.4
Ta.26486.1.A1_at	34.5	18.5	1.4	20.3
Ta.25515.2.S1_at	2.5	22.7	1.6	20.2
TaAffx.57942.1.S1_at	7.3	12.9	1.8	20.2
TaAffx.132743.5.S1_at	2.8	1.1	1.9	20
TaAffx.112906.1.S1_at	2.7	0.8	0.7	19.8
TaAffx.30174.1.A1_at	4.2	1.2	1.6	19.4
TaAffx.54320.1.S1_at	5.4	5	1.9	19.3
Ta.17493.1.S1_at	26.3	8.6	1.5	19.2
Ta.492.1.S1_at	29.7	55.4	1.6	18.6
Ta.14650.1.S1_at	5.4	1.6	1.7	18.6
TaAffx.90048.1.S1_at	12.8	7.7	1.1	18.4
TaAffx.58617.1.S1_at	15.7	5.4	1.2	18.2
Ta.10690.2.S1_at	1.1	0.6	1.1	18.2
TaAffx.107554.1.S1_at	30.6	26.5	1.1	18
Ta.17784.1.S1_at	49.3	4.4	1.5	17.9
TaAffx.56496.1.S1_at	3.1	10.8	1	17.7
TaAffx.55188.1.S1_at	15.4	9.5	1.4	17.4
Ta.15169.1.S1_at	19.4	2.1	1.4	17.2
TaAffx.56365.1.S1_at	2.8	1.3	1.4	17.1
TaAffx.109255.1.S1_at	10.1	1.1	1.6	17

TaAffx.104950.1.S1_at	30.1	10.2	1.5	17
Ta.5839.2.S1_at	1.1	2.4	0.6	16.9
TaAffx.43393.1.S1_at	4.9	0.6	0.8	16.6
Ta.2962.3.S1_at	8.6	2.9	0.8	16.5
TaAffx.117318.1.S1_at	11.5	0.6	1.3	16.2
TaAffx.15085.5.S1_x_at	0.8	2.7	1	16.2
TaAffx.23652.1.S1_at	0.9	4.7	0.9	15.7
Ta.24818.1.S1_x_at	2.9	2.3	1.1	15.4
TaAffx.483.1.S1_at	19.4	2.3	1	15.3
TaAffx.53434.1.S1_at	3.2	1	1.5	15.1
TaAffx.107319.1.S1_at	40	1.1	1.4	15
Ta.11004.1.S1_at	2.3	11.7	1.3	15
TaAffx.48523.3.S1_at	2.9	2.3	0.9	14.9
Ta.20878.3.S1_at	61.2	2.8	1.4	14.8
TaAffx.50758.1.S1_at	2.2	6.5	1.4	14.8
TaAffx.78825.1.S1_at	2.4	9.4	1.3	14.6
Ta.20727.2.S1_x_at	12.4	9.9	0.9	13.4
TaAffx.29620.1.S1_at	1.7	1.6	1	13.2
TaAffx.23438.1.S1_at	23.6	1.1	1.1	12.8
TaAffx.128896.20.S1_at	0.3	1.1	0.8	12.7
TaAffx.43326.1.S1_at	3.8	1.3	1	12.6
TaAffx.81750.1.S1_at	15.1	9.7	0.6	12.4
Ta.16731.1.S1_x_at	20.5	10.3	1	12
TaAffx.115169.1.A1_at	1.3	3.7	0.8	11.6
TaAffx.5957.1.S1_at	2.4	6.3	1	11.6
TaAffx.108987.1.S1_at	73	94.7	1.1	11.4
TaAffx.105707.1.S1_at	28.3	18.7	1	11.2
TaAffx.108895.1.S1_at	20.5	12.6	0.8	11.1
TaAffx.53629.1.S1_at	47.3	5.9	0.9	9.3
TaAffx.106160.1.S1_at	13.2	1.7	0.6	6.6
TaAffx.27336.2.S1_at	2.4	0.4	0.4	5.4

Table B.6 *Gc2*/- late over *Gc^{mut}#1*/- late

Probe set ID	***GC2* E**	***GC^{mut}#1* E**	***GC2* L**	***GC^{mut}#1* L**
Ta.4138.1.A1_at	4.1	3.3	599.8	5.4
Ta.16011.1.S1_at	4.4	3.6	549.3	11.9
TaAffx.86222.1.S1_at	59.5	217.3	395.7	34.7
TaAffx.106899.1.S1_at	41.4	203.9	354.9	28.3
Ta.25315.1.A1_at	19	27.2	246.5	16.3
Ta.9361.2.S1_x_at	315.9	354.1	245.9	17.9
Ta.13302.1.S1_at	137.3	366	236.6	8.7
Ta.19529.1.S1_a_at	98.4	135.2	214.2	20.1
TaAffx.89243.1.S1_at	301.5	310	205.7	15.4
Ta.15371.1.S1_at	4.3	5.3	197.3	16.5
Ta.24656.1.S1_at	61.5	9.8	190.4	16.9

TaAffx.55265.1.S1_at	42.3	18.5	182.1	13.8
Ta.4307.1.S1_at	2	15.4	182	13.7
TaAffx.12142.1.S1_at	30.2	129.6	180.4	18
Ta.12754.1.S1_s_at	8.8	14.1	176.3	5.6
TaAffx.50712.1.S1_at	65.7	129.1	170.2	16
TaAffx.117264.1.S1_at	77.9	44.4	166	15.3
Ta.5539.1.S1_at	251.5	219.2	162.2	4.9
TaAffx.86350.1.S1_at	130.8	20.4	154.6	13.7
TaAffx.29188.1.S1_at	40.7	99.2	149.5	5.7
Ta.26235.1.A1_at	23.3	170.1	148.4	4.4
Ta.23376.2.S1_s_at	4.1	5	148.1	11
Ta.2747.1.S1_at	75.5	419	144.4	8
Ta.10729.2.S1_x_at	132.9	128.2	143.7	9.9
TaAffx.42638.1.S1_at	72.9	118.2	142.9	11.6
Ta.9251.1.S1_x_at	87.3	269.4	140	9.9
TaAffx.113607.2.S1_at	10	101.2	138.5	13.3
TaAffx.92731.1.A1_at	24.1	134.7	137.8	11.9
Ta.11643.1.A1_at	4.9	1.3	135.8	6.6
Ta.17862.1.S1_s_at	15.1	92.8	133	5.6
Ta.24110.1.A1_s_at	8	233.6	131.5	8.6
Ta.15177.2.S1_x_at	14.2	20.3	130.7	12.8
TaAffx.38238.1.S1_s_at	14.1	44.4	129.7	9.6
Ta.3726.1.S1_at	28	24.6	128.7	4.9
Ta.10015.1.A1_at	4.9	8.9	128	6.7
TaAffx.3993.1.S1_at	72.9	24.2	125.1	10.6
TaAffx.24260.1.S1_at	39.6	14.4	125	10.2
TaAffx.9032.1.S1_at	71.9	60.4	124.3	12.1
Ta.12059.1.S1_at	73.6	168.1	120.4	10.2
TaAffx.80201.1.S1_at	81.8	9.1	120.2	10.2
TaAffx.37079.1.S1_at	41.3	78.1	120	8.1
Ta.28775.1.S1_at	23.9	30.4	119.9	10.1
TaAffx.110693.2.S1_at	43.4	25.7	119.7	11.1
Ta.23797.1.S1_x_at	59.6	57.8	119.2	8.6
TaAffx.89521.1.S1_x_at	79.8	86.7	117.5	10.9
TaAffx.65216.1.S1_at	254.7	120.2	115.2	10.7
Ta.231.1.S1_at	42	86.9	110.7	8.5
TaAffx.7477.1.S1_at	46.8	6.7	110.3	10.4
TaAffx.50948.1.S1_at	7.4	11.2	110	7.2
Ta.7206.2.A1_x_at	112.4	57.7	109.7	9.7
TaAffx.113675.1.S1_at	2.8	10.2	108.6	9.5
Ta.7791.2.A1_s_at	85.8	89.2	107.4	6.7
Ta.17257.2.S1_at	6.6	63.1	107.2	5.7
TaAffx.22189.1.S1_at	51.5	51.3	107.1	10.1
TaAffx.136997.2.S1_at	77.6	69.3	106	6.4
Ta.22365.2.S1_a_at	2.1	5.2	104.2	3.4
TaAffx.55556.1.S1_at	88.5	111.6	103.1	7.7

Ta.9534.3.S1_at	143.5	111.7	102	8.3
TaAffx.105261.1.S1_at	24.6	63.7	102	8
TaAffx.38755.1.S1_at	151.1	60.2	101.6	8
TaAffx.12886.1.S1_at	8.7	31	101.2	4.8
Ta.18805.1.A1_a_at	50.8	92	98.7	9.2
TaAffx.56333.1.S1_at	20.3	85.8	97.3	8.8
TaAffx.107532.1.S1_at	3.3	10	96.6	5.3
TaAffx.112375.1.S1_at	2.8	35.7	96.5	6.6
TaAffx.62609.1.S1_at	9.9	105.4	96.5	5.4
TaAffx.22998.1.S1_at	9.2	36.3	93.6	8
Ta.24625.2.S1_a_at	14.1	23.2	93.3	9.2
TaAffx.94042.1.A1_at	10.5	86	92.7	4.6
Ta.26877.1.A1_at	15.1	7.5	92.6	7.1
TaAffx.82926.1.S1_s_at	18.2	113.6	92.3	5.9
TaAffx.84302.1.S1_at	47.8	56.5	91.7	7.1
Ta.22585.2.S1_x_at	56.3	70.2	90.7	9
Ta.15997.1.S1_at	9.9	8.5	90.5	3.4
Ta.6734.2.S1_x_at	69.1	71.6	90	5.3
TaAffx.122153.1.S1_at	126.8	178.6	89.8	6.9
Ta.15247.1.S1_at	55.8	70.8	89.3	3.3
TaAffx.84528.1.S1_at	57.7	71.7	89	5.2
TaAffx.85186.1.S1_at	88	9.7	88.5	6.9
TaAffx.15760.1.A1_at	58	68	88.2	7
TaAffx.90020.1.S1_at	16.8	56.3	87.7	7
Ta.15678.1.S1_at	12.5	12.5	87.2	8.4
Ta.9283.2.S1_a_at	14.9	16	87	7.5
Ta.18675.1.S1_at	3.4	49.5	86.6	3.4
Ta.14033.1.S1_at	63.5	67.7	86.5	4.7
TaAffx.85658.1.S1_at	239.3	118.9	86.5	8.6
Ta.654.2.S1_x_at	9.5	45.9	86.4	4.4
TaAffx.24363.1.S1_at	85.1	133.1	86.2	3.4
Ta.12754.1.S1_x_at	7.1	14.9	85.7	5.6
Ta.30425.1.A1_at	50.7	61.9	85.2	8.2
TaAffx.86760.1.S1_at	19.4	5.6	84.9	7.8
TaAffx.113724.1.S1_at	60.5	55.2	84.6	3.2
TaAffx.54266.1.S1_at	28.1	67.4	84.5	5.9
Ta.16423.2.S1_at	5.7	6	84.4	6.5
Ta.23463.2.S1_a_at	41.3	61.9	84.4	4.7
TaAffx.31763.1.S1_at	61.2	30.8	84.2	7.6
Ta.11428.1.A1_at	3.8	39.8	82.6	3.9
TaAffx.58481.1.S1_at	47.1	36.7	82.4	6.2
TaAffx.11851.1.A1_at	63.4	71.1	81.6	7
TaAffx.128418.76.S1_at	40.2	28	81.5	5.9
Ta.15638.2.S1_a_at	10.6	12.7	81.1	7.8
Ta.24615.1.S1_x_at	16.6	6	80.7	7
Ta.22711.1.S1_at	3.7	48.3	79.7	7.8

TaAffx.59648.1.S1_at	58.7	13.5	79.4	5.3
Ta.10441.1.S1_at	51.2	64	78.3	3.6
TaAffx.119626.1.A1_at	67.6	71.8	77.9	7.4
Ta.26372.1.A1_at	39.4	6.6	77.5	5
TaAffx.4830.1.S1_at	110.9	30.1	77.3	5.1
TaAffx.78350.1.S1_at	26.7	21.3	77	5.6
TaAffx.29260.1.S1_at	65.9	9.8	76.6	6.5
TaAffx.32390.1.S1_at	4.4	69.3	76.3	6.8
Ta.19525.1.S1_at	11.9	156	75.4	6.5
TaAffx.86839.1.S1_at	56.5	123.5	75.3	7.1
TaAffx.31963.1.S1_at	84.1	8.8	74.7	4.4
TaAffx.24963.1.S1_at	8.3	23.4	74.5	6.3
TaAffx.108506.1.S1_at	2.8	13.7	74.4	7
TaAffx.35484.1.S1_at	15.2	41	74.3	5.5
TaAffx.30142.1.S1_at	57.5	32.2	74.3	5.3
TaAffx.109058.1.S1_at	45.7	38.3	74.3	6.7
TaAffx.90014.1.S1_at	3.6	4.8	73.4	3.3
TaAffx.110021.1.S1_at	37.5	30.2	73.3	5
TaAffx.13354.1.A1_at	73.8	53.3	73	5.4
Ta.26947.1.A1_at	10.8	38.3	73	5.7
TaAffx.28931.1.S1_at	31.9	50.7	73	3.7
Ta.27232.1.S1_at	3.4	6.4	72.6	6.1
TaAffx.78045.1.S1_at	94	23.3	71.7	5.5
TaAffx.38164.1.S1_at	9	57.4	71.5	5.7
TaAffx.17257.3.A1_at	64.7	95	71.5	4.5
Ta.25685.1.S1_at	12.2	39.8	71.3	2.9
TaAffx.55846.1.S1_at	18.7	4.1	70.3	2.9
Ta.13310.1.S1_at	35.5	43.2	70.1	3.1
TaAffx.8264.2.S1_at	11.8	4.5	70.1	4.9
TaAffx.19575.1.S1_at	3.6	6.7	70	5.7
TaAffx.37763.1.A1_at	41.5	39.4	70	4.2
TaAffx.26663.1.S1_at	27.4	26	69.9	3.4
TaAffx.83913.1.S1_at	1.6	16.3	69.8	4.6
Ta.12173.1.A1_at	61.3	59.9	69.7	4.9
Ta.12808.2.S1_at	10.8	35.5	69.7	5.4
TaAffx.35525.1.S1_at	67.7	96.5	69.5	5.7
TaAffx.80376.1.S1_at	32.4	69.5	69.5	5.8
Ta.24639.2.S1_at	48.5	60.8	69.4	5.7
TaAffx.7031.3.S1_at	24.8	23.2	69	4.4
Ta.15465.1.S1_at	4.5	6.3	68.9	5.6
Ta.9369.3.S1_at	34.9	9.8	68.9	6.6
TaAffx.7136.1.S1_at	49.3	38.6	68.7	5.9
TaAffx.54029.1.S1_at	17.9	88.6	68.4	5.5
TaAffx.32482.1.S1_at	49	32.9	67.9	3.3
Ta.13281.1.S1_at	114.4	108.3	67.2	6.7
Ta.20564.2.S1_x_at	6.4	3.7	66.9	0.8

TaAffx.64607.1.A1_at	7.2	9.3	66.9	5.3
TaAffx.106622.2.S1_at	24.2	4.8	66.9	5.9
Ta.24114.1.S1_x_at	34.8	12.1	66.6	5.1
TaAffx.59015.1.S1_at	61.7	35.5	66.3	2.4
TaAffx.26007.1.S1_at	22.9	20.3	65.7	4.4
TaAffx.28399.1.S1_at	42	54.1	65.5	5.7
TaAffx.107268.1.S1_at	34.7	27.8	65.4	3.7
TaAffx.82906.1.S1_at	4	35.5	65.3	5.8
Ta.28480.1.S1_at	5.7	8.5	64.6	5.4
TaAffx.113163.2.S1_at	47.9	6.1	64.6	5.3
TaAffx.110222.1.S1_x_at	35.2	54.1	64.5	3.4
TaAffx.106787.1.S1_at	142.2	66.9	64.5	6.3
Ta.18334.1.S1_s_at	3.3	43.1	64	2.8
TaAffx.53833.1.S1_at	29.6	21.7	64	4.8
TaAffx.11919.2.S1_at	89.4	36.6	63.7	5.6
TaAffx.53091.1.S1_at	10.2	5.4	63.7	4
TaAffx.27943.1.S1_at	61	32.1	63.5	3.8
TaAffx.138332.1.S1_at	24.8	59	63.5	6.1
Ta.24294.1.A1_at	14.2	51.3	63.4	6.1
Ta.13956.1.S1_at	13.9	21.5	63.1	4.6
Ta.5252.3.S1_at	70.3	37	63.1	6.2
Ta.9264.3.S1_at	39.1	32.6	63	4.6
Ta.15698.1.S1_at	34.5	24.1	63	6
TaAffx.57382.1.S1_at	16.5	5.1	63	3.7
TaAffx.27111.1.S1_at	5.3	43	62.9	5.6
Ta.26787.1.A1_at	2.9	4.1	62.6	2.8
TaAffx.52643.1.S1_at	50.2	17.8	62.5	2.5
TaAffx.53061.1.S1_at	4.1	0.8	62.5	4.8
TaAffx.59101.1.S1_at	52.5	90.3	62.4	4.5
TaAffx.81428.1.S1_at	57.5	32.5	62.3	3.6
Ta.6172.2.S1_at	8.4	15.8	62.1	4.7
TaAffx.107704.1.S1_at	48.5	46.9	62.1	4.3
Ta.15759.1.S1_at	21.3	51.9	61.8	4.3
TaAffx.5541.1.S1_at	35.9	59.5	61.6	4.3
Ta.26322.1.A1_at	19.6	11.3	61.4	3.5
TaAffx.113289.1.S1_at	31.8	35.9	61.3	3.1
Ta.9924.1.S1_at	24.2	5.8	61	3.2
Ta.25004.1.A1_at	41.3	31.8	60.9	2.3
Ta.9150.2.S1_at	33.1	22.2	60.8	3.7
TaAffx.32444.1.S1_at	69.7	21.7	60.8	3.9
Ta.9226.1.S1_at	8.4	6.7	60.5	3.4
TaAffx.28845.1.S1_at	66.1	65	60.2	4.3
TaAffx.77641.1.S1_at	50.9	47.1	60	4.9
Ta.20582.2.S1_x_at	7.7	43.1	59.6	5.9
TaAffx.54069.1.S1_at	41.9	39.7	59.6	5.1
TaAffx.86814.3.S1_at	34	20.7	59.6	4

Ta.12895.1.A1_at	37.3	37	59.4	5.7
TaAffx.83608.1.S1_at	28.2	11.9	59.3	5.5
Ta.25381.1.S1_s_at	51.2	61	59.1	5.1
TaAffx.65044.1.A1_at	7.9	12.7	59.1	5.1
TaAffx.85682.1.S1_at	56	31.5	59	4.7
TaAffx.24983.1.S1_at	50.4	7	59	5.6
TaAffx.35355.1.S1_at	38.3	13	58.7	5.2
Ta.1840.2.S1_x_at	21.4	6.3	58.6	5
Ta.10672.1.S1_at	20.8	82.4	58.6	5.8
Ta.17862.1.S1_at	52.8	20.5	58.6	4.9
Ta.16951.1.S1_x_at	38.5	20.6	58.6	5.7
TaAffx.54026.1.S1_at	2.9	24.3	58.6	5.6
TaAffx.105712.1.S1_at	4.4	59.6	58.2	2.5
TaAffx.37918.1.S1_at	115.7	134.1	58.1	4.1
TaAffx.115102.1.S1_at	8.4	64.3	58	5.1
Ta.8820.1.A1_at	34.5	81.3	57.9	2.9
Ta.30764.2.S1_at	5	36.6	57.9	3
TaAffx.85751.1.S1_at	24	43.1	57.9	5.7
Ta.5049.1.A1_at	1.3	13.8	57.6	4.7
Ta.18930.1.A1_at	10.8	21.4	57.5	4.9
TaAffx.6393.1.S1_at	28.9	6.6	57.5	5.6
Ta.25119.1.S1_x_at	5.5	16.4	57.4	4.3
Ta.25360.1.A1_at	29.9	55.2	57.4	5.1
TaAffx.112236.1.S1_x_at	16.2	24.7	57.4	3.6
TaAffx.28679.1.S1_at	5.5	50.2	57.3	5.7
TaAffx.90006.1.S1_at	30.3	24.3	57.2	3.9
Ta.12652.2.S1_at	3.8	1.6	56.5	3.1
TaAffx.122153.2.S1_at	30.1	33	56.4	4.9
TaAffx.57558.1.S1_at	17.3	6.6	56	4.5
TaAffx.110859.1.S1_at	27.7	23.6	56	1.9
TaAffx.113774.3.S1_at	1.1	20.1	55.9	1.6
Ta.14018.3.S1_at	29.2	5.6	55.7	4.7
TaAffx.81392.1.S1_at	28.5	7.1	55.7	5.1
TaAffx.93308.1.S1_at	42.9	49.4	55.6	5.2
TaAffx.8537.1.S1_at	5.6	7.2	55.6	3.9
Ta.21682.1.S1_x_at	3.5	41.3	55.5	5.5
TaAffx.86486.1.S1_at	4.3	35.8	55.4	2.9
Ta.5490.1.S1_s_at	4.1	14	55.3	4.8
Ta.655.2.A1_x_at	16.3	56.5	55.3	4.9
TaAffx.70835.1.A1_at	8.1	31.3	55.1	5.5
Ta.17132.1.S1_at	4.9	6.3	54.8	3.2
Ta.26557.1.A1_at	40	33.8	54.4	3.5
Ta.29479.1.A1_at	27.8	56.4	54.1	5.4
Ta.5216.1.S1_x_at	4.6	2.1	54	3.3
TaAffx.114119.1.S1_at	33.8	6.7	54	3.7
TaAffx.128418.134.A1_at	80.8	34	53.8	4

Ta.25443.1.A1_at	4.3	8.3	53.7	5.1
Ta.24477.3.A1_at	40.8	66.3	53.5	4
TaAffx.42139.1.S1_at	7	31.9	53.3	3.6
TaAffx.5532.1.S1_at	57.8	18.4	52.9	4.8
TaAffx.28209.1.S1_at	11.7	13.7	52.9	5.2
TaAffx.66358.1.S1_at	50.6	6.9	52.8	3.6
TaAffx.56116.1.S1_at	5.3	5	52.8	3.7
TaAffx.84235.1.S1_at	84.7	46.6	52.7	4.9
TaAffx.104874.1.S1_at	44.1	47.6	52.5	5.1
Ta.18530.1.S1_a_at	1.3	27.8	52.2	4.7
TaAffx.101191.1.A1_at	6.4	41.3	52.2	4.8
TaAffx.22629.1.A1_at	29.6	30.3	52.1	2.8
Ta.26199.2.S1_at	17.4	39	52.1	3.5
Ta.5640.2.A1_x_at	16.6	9.1	52	3.7
TaAffx.58298.1.S1_at	44.1	36.3	52	3.7
TaAffx.120290.2.S1_at	24.6	46.3	52	4
TaAffx.29804.1.S1_at	12.6	8.2	51.9	4.2
TaAffx.112371.1.S1_at	4	3.3	51.7	4.1
TaAffx.80790.1.S1_at	7.3	11.4	51.6	3.3
TaAffx.26210.1.S1_at	21.1	17.9	51.6	4.6
TaAffx.12791.2.S1_at	32.3	17.9	51.3	2.9
Ta.10094.1.S1_at	35	25.1	51.2	3.8
Ta.556.1.S1_at	1.1	52.2	50.7	1.4
TaAffx.78867.1.S1_at	14.8	17.6	50.7	4.9
Ta.23256.2.S1_at	40	20.7	50.6	5
Ta.949.1.S1_at	3.3	1.7	50.4	3.2
Ta.20430.1.A1_at	6.2	5.8	50.3	3.8
TaAffx.55593.1.S1_at	6.8	3.7	49.6	4.5
TaAffx.22655.1.S1_at	2.3	6.1	49.3	3
Ta.26763.1.A1_at	6.1	17.3	49.1	4.2
TaAffx.128414.82.S1_at	4.9	21.5	49.1	2.3
Ta.17225.1.S1_at	11.7	2.7	49	3.2
Ta.13120.1.A1_at	4.8	5.6	48.9	1.8
TaAffx.4394.1.S1_at	46	13.1	48.7	2.5
Ta.17968.1.S1_at	47	9.7	48.6	2.9
TaAffx.79809.1.S1_at	15.4	49.3	48.4	3.7
Ta.18699.1.S1_at	20.3	6.5	48.3	4
TaAffx.79541.1.S1_at	30.9	49	48.3	4.3
TaAffx.4329.1.S1_at	17	14.6	48.2	2
TaAffx.108023.1.S1_at	6.9	17.7	47.8	2.1
TaAffx.4711.1.S1_at	103.4	70.1	47.7	4.6
TaAffx.109143.1.S1_at	12.8	48.5	47.3	4
TaAffx.31379.1.S1_x_at	15.8	23.4	47.1	2.9
TaAffx.4248.1.S1_at	49.2	11.5	47	4.4
Ta.30857.1.S1_at	31.1	10.8	46.9	4.1
TaAffx.112194.1.S1_at	14.4	2.8	46.9	1.7

TaAffx.117142.1.S1_at	64.3	55.3	46.9	2
AFFX-r2-TagB_at	13.5	3.8	46.7	2.7
TaAffx.26120.1.S1_at	11.2	4	46.7	2.2
TaAffx.113701.1.S1_s_at	54.1	67.4	46.3	2.8
TaAffx.62632.1.S1_at	34.8	68.5	46.1	3.9
TaAffx.6406.1.S1_at	10.3	41.8	46.1	4.3
TaAffx.6518.1.S1_at	17.9	3.6	46.1	3.9
Ta.14931.1.S1_at	19.1	20.3	45.9	3.9
TaAffx.23632.1.S1_at	45.6	40	45.9	2
TaAffx.28503.1.S1_at	1.8	3.8	45.9	4.5
TaAffx.26970.1.S1_at	25.1	27.4	45.8	2.7
TaAffx.24079.1.S1_at	5.3	7.4	45.7	4.4
TaAffx.9243.1.S1_at	5.7	13	45.7	4.3
TaAffx.4412.1.S1_at	26.6	5.2	45.6	3.8
TaAffx.56148.1.S1_at	19.7	20.4	45.6	4.2
TaAffx.97381.1.S1_at	3.7	34.7	45.3	1.4
Ta.26648.1.A1_at	9	18.8	45	2.3
TaAffx.4553.3.S1_at	65.3	50	45	2.1
TaAffx.91363.1.A1_x_at	10.9	70.8	44.9	4.2
Ta.26105.1.A1_at	2.8	24.2	44.8	3.7
Ta.6990.1.S1_at	44.4	98.1	44.2	4.4
TaAffx.124266.1.S1_at	59.4	88.2	44.1	4.2
TaAffx.79196.1.S1_at	7.3	2.2	44.1	3.1
TaAffx.56984.1.S1_at	2.4	23.4	44.1	3.5
TaAffx.55262.2.S1_at	33.1	23.7	43.7	3.6
Ta.28040.1.A1_at	33.4	57.2	43.6	3.3
Ta.552.2.S1_at	48.4	46.5	43.5	1.3
TaAffx.108314.1.S1_at	5.7	39.5	43.3	3.8
TaAffx.4398.1.S1_at	4.7	1.1	43.3	2.9
TaAffx.86413.1.S1_at	3.1	18.6	43.3	3.7
TaAffx.109192.1.S1_at	3.6	1.8	43.2	2.9
TaAffx.32578.1.S1_at	36.6	21.3	43.2	3.3
TaAffx.11955.2.S1_at	57.6	40.9	43.1	3.1
TaAffx.65642.1.S1_at	2.8	60.2	43	3.7
TaAffx.120446.1.A1_at	27.1	40.7	43	3
TaAffx.83378.1.S1_at	3.1	7.1	43	3.8
Ta.17175.1.S1_at	32.6	11.2	42.9	2.2
Ta.24539.2.S1_at	3.8	7.5	42.8	2.3
TaAffx.53043.1.S1_at	6.9	5.3	42.5	3
TaAffx.53588.1.S1_at	43.2	14.6	42.5	3.4
TaAffx.110509.3.S1_at	17.9	16.6	42.4	2.3
Ta.4928.1.S1_at	40.1	4.7	42.3	2.9
Ta.22360.1.S1_at	4.4	15.1	42.1	3
TaAffx.53617.1.S1_at	58.7	14.6	42.1	2.7
TaAffx.31242.1.S1_at	26.6	26	41.6	1.9
Ta.7916.1.S1_at	4.3	9.5	41.5	3.9

TaAffx.108656.1.S1_at	1	1.6	41.3	4.1
Ta.23219.1.A1_x_at	0.6	0.9	41.2	1.4
TaAffx.9183.1.S1_at	44.5	42.3	41.2	3.5
TaAffx.78423.1.S1_at	28	31.8	41.2	4.1
TaAffx.83167.1.S1_at	22.6	4.1	41.2	1.9
Ta.18041.1.S1_at	47.6	30.6	41.1	3.3
Ta.15228.1.S1_at	30.7	48.3	41	2.5
TaAffx.78962.1.S1_at	3.7	10.1	41	4
Ta.13089.1.S1_at	46.9	17.4	40.9	2.1
Ta.4214.1.A1_at	27.3	47.6	40.7	2.9
TaAffx.70666.1.S1_at	13.8	10.9	40.6	2.3
TaAffx.137.1.S1_at	39.4	23.7	40.1	3.7
TaAffx.53684.1.S1_at	15.1	9.3	40.1	3.4
TaAffx.131379.1.A1_at	5.6	169	39.7	2.3
TaAffx.5516.1.S1_at	23.9	28.1	39.7	2.3
TaAffx.54759.1.S1_at	7.5	13.6	39.6	2.6
TaAffx.113349.1.S1_at	2.8	3.9	39.2	2.6
TaAffx.81521.1.S1_at	48.1	24.4	39.2	3.2
Ta.5645.2.S1_at	22.2	52.3	39.1	3.7
TaAffx.54083.1.S1_at	18.2	15.8	38.8	2.6
Ta.20634.1.S1_at	3	19.4	38.6	3.8
Ta.12550.1.A1_at	15.2	5	38.6	2.6
TaAffx.79822.1.S1_at	11.5	3.9	38.6	2.4
Ta.27184.1.S1_at	0.7	11.1	38.4	1.5
TaAffx.6592.1.S1_at	54.1	7.3	38.3	2
TaAffx.56932.1.S1_at	43	62.6	38	3.1
Ta.5049.2.S1_at	20.6	18.4	37.9	2.1
TaAffx.23402.1.S1_at	1.3	10.4	37.7	2.5
TaAffx.85851.1.S1_at	17.2	6.7	37.7	3
TaAffx.111458.1.S1_at	8.1	30.6	37.6	2.2
TaAffx.50506.1.S1_at	43.6	37.9	37.6	2.1
TaAffx.64122.1.S1_at	41.5	50.7	37.5	3.7
TaAffx.51280.1.S1_at	6	14.6	37.5	2.5
Ta.13636.1.A1_at	51.7	32	37.4	3.2
TaAffx.53798.1.S1_at	5.4	6.3	37.3	3.6
Ta.23376.3.S1_at	35.5	48.3	36.9	3.5
TaAffx.109220.1.S1_at	2.3	2.1	36.7	1.3
Ta.4585.2.A1_at	46.9	52.1	36.6	3.1
Ta.15580.1.S1_at	4.4	0.8	36.5	2.1
TaAffx.83612.1.S1_at	48	6.9	36.5	2.4
TaAffx.86468.1.S1_at	32.5	33.7	36.1	1.9
TaAffx.78136.1.S1_at	5	4.6	36.1	3.4
TaAffx.65643.1.S1_at	16.9	39.4	35.8	2.7
TaAffx.78884.1.S1_at	7.2	1.5	35.7	2.2
Ta.3743.1.A1_s_at	2.4	25.8	35.5	3.5
TaAffx.83258.1.S1_at	7.5	24.3	35.5	2.3

TaAffx.70472.1.A1_at	5	3.3	35.2	0.8
Ta.15893.1.S1_at	6.5	6	34.9	3
TaAffx.29204.1.S1_at	18.4	24.5	34.8	1.8
Ta.8304.1.S1_a_at	3.8	39	34.6	3.4
Ta.17405.1.S1_at	13.5	36.2	34.6	3.1
TaAffx.26582.1.S1_at	6.6	1.6	34.6	1.9
TaAffx.82075.1.S1_at	1.8	3.1	34.4	1.8
Ta.12254.2.S1_at	35.8	38.5	34.4	1.8
Ta.30219.1.S1_at	3.6	3.2	34.2	2.5
TaAffx.92693.1.A1_at	27.8	44	34.2	1.9
TaAffx.128883.4.S1_at	28.4	9.8	34.1	1
TaAffx.83992.1.S1_at	18.9	4.6	34.1	1.1
TaAffx.27305.1.S1_at	42.7	5.3	34.1	1.7
Ta.9815.1.S1_at	25.2	17.7	34	2.6
TaAffx.51783.1.S1_at	10.1	3.8	34	3.3
Ta.10172.1.S1_at	14.6	20.9	33.7	2.8
TaAffx.113619.1.S1_at	0.6	2.4	33.7	1
Ta.29603.1.A1_at	3.4	1.4	33.3	3.1
TaAffx.129577.2.S1_at	1.1	4.3	33.3	1.7
TaAffx.30223.1.S1_at	22.5	17.9	33.1	1
TaAffx.79744.1.S1_at	6.3	13.6	33.1	3.3
Ta.3189.3.S1_at	17.8	28.2	33	3.2
TaAffx.111732.1.S1_at	9.3	37.6	32.6	3.2
Ta.6877.3.S1_at	1.1	17.5	32.5	3
TaAffx.113158.1.S1_at	5.3	4.1	32.5	2.4
TaAffx.95750.1.S1_at	8.9	55.2	32.3	2.3
Ta.16744.2.S1_at	6.1	9.5	32.2	2.7
Ta.23290.1.S1_at	1.3	16.2	32	1.8
Ta.30715.2.S1_at	3.8	4.8	31.5	2.2
TaAffx.112332.1.S1_at	9.4	6.7	31.5	2.9
Ta.18588.1.S1_s_at	2.3	20	31.4	1.2
Ta.26662.1.A1_a_at	2.5	19.9	31.3	2.7
Ta.5117.2.S1_at	40	21.9	31.3	2.9
Ta.13132.1.A1_at	12.5	2.6	31.2	2.6
Ta.11443.2.S1_x_at	0.6	1.8	30.9	3
Ta.28942.2.A1_at	2.1	169.2	30.8	2.1
TaAffx.29268.1.S1_at	3	13.2	30.6	3
TaAffx.89472.1.S1_at	40.9	13.8	30.5	1
TaAffx.29677.1.S1_at	1.4	4.7	30.4	2.2
TaAffx.79293.1.S1_at	15.2	10.3	30.1	1.5
Ta.9346.2.S1_at	1.4	18.9	29.9	2.9
Ta.15717.1.S1_at	43	59.9	29.9	2.2
TaAffx.78877.1.S1_at	1.6	6.6	29.7	1.9
Ta.24632.1.S1_at	1.8	49.3	29.6	2.6
TaAffx.83272.1.S1_at	2.2	2.1	29.5	2.8
Ta.30705.2.S1_at	1.2	1.8	29.4	1.6

Ta.26840.1.A1_at	3	6.6	29.1	1.6
Ta.12007.2.S1_at	28.7	11.6	29.1	1.9
TaAffx.39568.3.S1_at	13.8	1.8	29	1
TaAffx.81387.1.S1_at	2.9	19	28.9	1.9
TaAffx.86672.1.S1_at	51.8	46.4	28.5	1.9
Ta.27981.1.S1_at	21.8	16	28.4	1.8
TaAffx.42793.1.A1_at	1.6	10.7	28.4	1.8
TaAffx.92023.1.A1_at	36.3	24.2	28.3	2.6
TaAffx.53242.1.S1_at	3.9	1	27.9	2.7
TaAffx.5362.1.S1_at	7.4	12.3	27.6	2.5
TaAffx.6380.1.S1_at	1.6	7.2	27.5	1.5
Ta.25174.1.S1_at	1	0.4	27.2	1.3
TaAffx.11615.2.S1_at	34.5	44.2	27.2	1.8
Ta.6278.3.S1_at	1.8	32.3	27.1	2.4
Ta.27351.1.S1_at	36.7	44	26.9	1.2
TaAffx.129166.1.A1_at	19.1	15.8	26.8	2
Ta.27882.3.S1_at	2.7	1.8	26.8	2.4
TaAffx.83696.1.S1_at	3	24	26.8	0.9
TaAffx.96931.2.S1_at	0.5	6.2	26.7	2.5
Ta.6687.2.S1_at	34.6	32	26.6	2.6
Ta.26702.1.A1_at	49.1	9	26.5	1.9
TaAffx.80878.1.S1_at	14.5	24.8	26.5	1.9
Ta.264.1.S1_at	1.7	11.3	26	2.4
TaAffx.29001.1.S1_at	49.8	14.8	26	2.2
TaAffx.30542.1.S1_at	5.3	3.4	25.9	1.8
TaAffx.85597.4.S1_x_at	17.8	19	25.8	1.5
TaAffx.85861.1.S1_at	2.6	1.7	25.6	2
TaAffx.534.1.S1_at	41.6	19.3	25.6	1.7
TaAffx.81361.1.S1_at	2.5	1.4	25.6	1.6
TaAffx.24914.1.S1_at	4.5	21.1	25.5	1.3
Ta.5509.3.S1_at	0.8	0.7	25.3	1
Ta.15000.1.S1_at	7.6	3.3	24.7	2.1
TaAffx.109558.1.S1_at	1.6	2.1	24.7	0.8
TaAffx.92425.1.S1_at	3.9	1.6	24.7	2.3
TaAffx.90054.1.S1_at	1.3	1.1	24.7	1.1
TaAffx.4275.6.S1_at	2.6	1.1	24.7	1.9
TaAffx.53970.1.S1_at	1.3	1.2	24.3	1.5
TaAffx.112617.3.S1_at	16.1	7.5	24.3	1.4
Ta.4007.1.A1_at	2.3	1.6	24.1	1.3
Ta.13234.2.S1_at	3.4	0.8	24	1.5
Ta.14943.1.S1_at	1.4	4.1	23.6	0.8
TaAffx.109268.1.S1_at	28.9	39.6	23.6	0.6
TaAffx.107567.4.S1_at	28.9	33.1	23.6	0.4
TaAffx.25638.1.S1_at	3.2	11.5	23.2	2.1
Ta.11704.3.A1_at	1.8	1.2	23.2	1.4
TaAffx.107442.1.S1_at	0.4	0.5	23.1	0.5

Ta.28680.1.S1_at	32	39	22.7	1.9
Ta.2853.2.S1_at	3.9	2.6	22.7	1.7
Ta.5461.2.S1_x_at	11.7	3.4	22.5	1.8
Ta.12381.1.A1_at	1	17.6	22.2	1.7
TaAffx.5238.1.S1_at	3.9	10.6	21.9	1.2
TaAffx.83588.1.S1_at	46.9	31	21.7	1.7
Ta.22571.1.S1_x_at	26.2	5.1	21.6	1.1
Ta.30633.1.A1_at	2.3	36.9	21.4	1.7
TaAffx.115613.2.S1_at	3.1	2.3	21.1	1
Ta.15501.1.S1_at	2.5	5.9	20.9	1.5
TaAffx.62.2.S1_at	3.3	2.3	20.9	1.9
TaAffx.98485.6.S1_at	46.4	24.4	20.8	1.6
Ta.28316.3.S1_at	6.4	7.7	20.5	1.6
Ta.840.1.S1_at	1.5	1.7	20.4	1.4
Ta.10864.2.S1_x_at	26.8	5.2	20.4	1.8
TaAffx.29757.1.S1_at	6.2	24.8	20.4	1.7
TaAffx.23755.1.S1_at	2.3	3.8	20.3	1.6
TaAffx.29758.1.S1_at	8.2	8	20.3	2
TaAffx.109215.1.S1_at	15.9	8.6	20.3	1.8
TaAffx.110945.1.S1_at	1.9	1.4	20.1	1.5
TaAffx.111397.1.S1_at	6.4	51.4	20.1	1.8
TaAffx.6422.1.S1_s_at	1.6	17.3	20	1.8
TaAffx.106704.1.S1_at	12.1	5.4	20	1.8
Ta.23265.2.S1_at	24.3	14	19.7	1.3
TaAffx.85366.1.S1_at	2.9	14.2	19.5	1.4
Ta.15645.1.S1_at	2	6.8	19.4	1.4
TaAffx.23169.1.S1_at	3.5	5.1	19.4	1.4
TaAffx.85301.1.S1_at	19.9	27.5	18.3	1.5
Ta.9039.2.S1_at	20.6	3.4	18.1	1.2
TaAffx.29387.1.S1_at	1	3.2	18	1
Ta.26402.1.A1_at	7.1	13.1	17.8	1.1
Ta.15707.1.S1_at	5.5	8.1	17.2	1.7
TaAffx.27002.2.S1_at	18.5	11.5	17.1	1.3
TaAffx.110915.1.S1_at	3.2	7.4	17	1.5
TaAffx.6827.1.S1_x_at	20.2	11.7	16.7	1.5
Ta.21281.3.A1_at	29.4	4.5	15.1	1
Ta.10109.2.S1_at	0.9	0.7	12.7	1.1
TaAffx.29101.1.S1_at	41.7	5.9	11.7	0.2
TaAffx.81046.1.S1_at	0.7	1.2	11.6	0.9
TaAffx.112691.2.S1_at	5.7	1.1	10.5	0.9
Ta.502.3.A1_at	0.6	0.4	9.4	0.9
TaAffx.53270.1.S1_x_at	24	14.4	9.4	0.7
TaAffx.24500.1.S1_at	0.5	0.5	8.7	0.3