Table S1 *Ds* insertion sites in yeast

Ade^{+}rev	Chr	Position	*Ds* target site[a]	Accession	E-value[d]	Gene
***Ac*TPase$_{4x}$**						
1	XIII	311423	TTGGCCAA	NM_001182514.1	3e -19	S288c Putative protein with similarity to human PEX5Rp
2	XII	458235	CAAAGAGT	FN554374.1	8e -144	Partial 5S rRNA gene
3	XI	264064	CCCCAGAT	X71133.1	1e -75	HAP4, AAT1, GFA1, LAP4 and MBR1 genes
4	XV	323245	**GCACTTTC**	Z74744.1	0.0	Chromosome XV reading frame ORF YOL002c
5	XII	693673	**GTTTCATC**	U09242.1	0.0	DNA replication protein Cdc46p (CDC46) gene
6	VII	440638	CTTATTTT	Z72551.1	3e -32	Chromosome VII reading frame ORF YGL029w
7	II	792133	**AAAATGTT**	AB200246.1	0.0	BIO6 gene for biotin biosynthesis enzyme
8	XI	478727	**GACTCTTT**	NM_001179810.1	7e -112	S288c Component of GARP (Golgi associated retrograde protein) complex
9	VII	465531	**GAGAATAG**	S58126.1	7e -51	LEU1-ATE1 loci: LEU1...YGL029
10	IV	302350	AAAAAAGG	Z74134.1	1e -105	Chromosome IV reading frame ORF YDL086w
11	XV	637133[e]	GCCCTAAT	NM_001183580.1	7e -170	S288c Pns1p (PNS1)
12	XVI	688009	TAGAAAAT	NM_001184168.1	2e -85	S288c Putative membrane protein
13	XV	552278[e]	**AGTTTTCT**	M23369.1	0.0	Profilin (PFY) gene
14	XII	390865	**AAAATACG**	Z73293.1	0.0	Chromosome XII reading frame ORF YLR121c
15	IV	239896	**GTGGCCAA**	X56956.1	4e -80	CDC48 gene for cell cycle protein CDC48p
16	XV	525094[e]	ATCCGAAT	NM_001183528.1	0.0	S288c Inp53p (INP53)
17	IX	388640	GTACAGAA	BK006942.2	8e-34	S288c chromosome IX complete sequence
18	XV	170355	CCCCTTGC	M83139.1	1e -101	RAS1 and RAS2 attenuator (IRA2) gene, 5' end
19	XII	457081	**GCCAACCG**	BK006945.1	0.0	Isolate OC21 18S ribosomal RNA gene
20	II	466515	GTCCACGT	X66247.1	5e -146	YSA1, SSN6, RAD16, and LYS2 genes
21	XV	226759	TTCATATG	Z74797.1	5e -146	Chromosome XV reading frame ORF YOL055c
22	V	41348	CATTTGGG	NM_001178875.1	0.0	S288c Prb1p (PRB1), mRNA, (Protease B)
23	X	106834	**ATTTATTT**	U15300.1	7e -22	Hal5p (HAL5) mRNA
24	XVI	501953	CTGCCGGC	U30613.1	0.0	Suppressor kinase of snf3, Sks1p (SKS1) gene
25	XV	587811[e]	**GGCATGGT**	NM_001183559.1	0.0	S288c Sfl1p (SFL1)
26	II	10413	TTTCTAAG	NM_001178347.1	199	S288c Putative protein of unknown function
27	VII	871291	GAGCTCAA	U27358.1	6e -130	Hgh1p (HGH1) gene
28	VII	73860	TTAATTAC	Z72748.1	0.0	Chromosome VII reading frame ORF YGL226w
29	XII	790299	AATTCATT	Z49198.1	2e -72	CHS5 (CAL3) gene
30	IV	352297	TGAATGTC	NM_001180116.1	1e -06	S288c Putative protein of unknown function
31	VII	84707	GGTAAAAT	Z72741.1	3e -81	Chromosome VII reading frame ORF YGL219c
32	X	78731	**GCCTCGTA**	NM_001181620.1	4e -59	S288c Protein kinase
33	VII	514478	TAATTACT	Z72797.1	7e -72	Chromosome VII reading frame ORF YGR012w
34	XVI	901730	**GGCAGAAT**	J04184.1	1e -63	Dolichol phosphate mannose synthase (DPM1) gene
35	-[b]	-	**TATGAATG**	NM_001184395.1	1e -121	S288c Retrotransposon TYA Gag gene
***Ac*TPase**						
1	VI	204983	**CACACGCC**	U09479.1	4e -147	Histidinolphosphatase (HIS2) gene
2	XV	256401	ATTTCCAC	Z74779.1	0.0	Chromosome XV reading frame ORF
3	X	210344	GAGACGAG	NM_001181543.1	3e -26	S288c GATA zinc finger protein and Dal80p homolog
4	XII	1078175	GGTACAGA	NM_001182321.1	8e -50	S288c Calcineurin A
5	XVI	230894	**ACTCTAAG**	Z73525.1	4e -42	CXVI reading frame ORF YPL169c
6	XII	611863	CATGGTTT	M24939.1	0.0	DNA topoisomerase (TOP3) gene
7	VIII	167614	**TGTATATA**	X15484.1	1e -14	Dipeptidyl aminopeptidase B (DPAP B)
8	VII	842662	GTTTGAAA	X14629.1	5e -24	MSM1 gene for mitochondrial methionyl-tRNA synthase
9	XII	445181	**AGGATATT**	S79456.1	7e -93	tRNA-Gln, ACS2=acetyl-coenzyme A synthetase 2
10	XIII	287458	AAAGAAAC	M33270.1	1e -94	High affinity hexose transporter-2 (HXT2) gene
11	II	410391	TCTAGCGC	J03724.1	0.0	Mitochondrial C-1-Tetrahydrofolate synthase gene (MIS1)
12	IV	778863	**GCTTTACG**	NM_001180467.1	1e -41	S288c SPS plasma membrane sensor system (Ssy1p-Ptr3p-Ssy5p)
13	VII	503923	AATATGGG	NM_001181133.1	0.0	S288c Peroxisomal integral membrane protein

14	XV	369772	**CGACCCAT**	NM_001183438.1	9e -92	S288c Protein of unknown function
15	XI	354898	TACATATC	X71621.1	0.0	Genes ELM1 and PRI2
16	VII	757585	**AATGTGTC**	X65470.1	7e -40	PAS2 gene
17	XV	586815[e]	GCCACAGT	Z75047.1	9e -87	Chromosome XV reading frame ORF YOR139c
18	-[c]	-	TGAACGTT	M18354.1	2e -35	Sigma repetitive element (TY3)

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[a] *Ds* insertion sites where 5’ and 3’ flanking sequences were isolated are bold typed.

[b] In case of insertion into TYA retrotransposon the exact chromosomal localization is not possible (XVI, XV,XII, XVII, V, IV or I).

[c] In case of insertion into yeast sigma repetitive element (TY3) the exact chromosomal localization is not possible (XIV, XI, IX, VII or I).

[d] Sequences were BLASTed against GenBank (All GenBank+EMBL+DDBJ+PDB sequences but no EST, STS, GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)

[e] Short range transposition; *Ds* reintegration occurred on the same chromosome in a maximal distance of 72 kb from the donor site.

Table S2 Distribution of *Ds* insertions on yeast chromosomes

Yeast chromosome			*Ds* insertions					
		% of	*Ac*TPase$_{4x}$		*Ac*TPase		Total	
No.	Size in kb	genome	Observed	Expected[b]	Observed	Expected[b]	Observed	Expected[b]
I	230	1.9	-	0.6	-	0.3	-	1
II	813	6.7	3	2.3	1	1.1	4	3
III	315	2.6	-	0.9	-	0.4	-	1
IV	1522	12.6	3	4.3	1	2.1	4	6
V	575	4.8	1	1.6	-	0.8	1	2
VI	270	2.2	-	0.8	1	0.4	1	1
VII	1091	9.0	6	3.1	3	1.5	9	5
VIII	562	4.7	-	1.6	1	0.8	1	3
IX	440	3.7	1	1.2	-	0.6	1	2
X	745	6.2	2	2.1	1	1.0	3	3
XI	666	5.5	2	1.9	1	0.9	3	3
XII	1078	8.9	5	3.0	3	1.5	8	5
XIII	924	7.7	1	2.6	1	1.3	2	4
XIV	784	6.5	-	2.2	-	1.1	-	3
XV[a]	1091	9.1	7	3.1	3	1.5	10	5
XVI	948	7.9	3	1.3	1	1.3	3	4
Σ	12057	100	34	34	17	17	51	51

[a] Yeast chromosome with *Ds* launch pad in *ade2* locus.

[b] Number of expected insertions was calculated based on the size of each chromosome.

Table S3 Primer sequences (5’ to 3’)

Primers for site directed mutagenesis	
E249A	CAATATTGTAGAACATGCGTACTTTGTTGAG CTCAACAAAGTACGCATGTTCTACAATATTG
D301A	CTCGCTTCAGTACAACTATGGCTATGTGGACA ACTGAACATCTTTTAGTTTTCCATACAACTTTTCTTTTTC
E336A	GCTTTTTTCATGTTGCAGGGCGCCACACTGG CCAGTGTGGCGCCCTGCAACATGAAAAAAGC
D367A	TGCCTTGTCTTTGGCTAATGCTAGTGC AACAATTTTTTCTCAATGTTCCACTTAACCA
D459A	GGGATCTCATATGCTGTCTCAACTAGATGG CCATCTAGTTGAGACAGCATATGAGATCCC
D545A	GGATTTGATTGCCCAATGGTGTGTTC GAACACACCATTGGGCAATCAAATCC
E719A	CTGTTGCTTCTGCGTCTGCGTTCAGTGC GCACTGAACGCAGACGCAGAAGCAACAG
Splinkerette-PCR gene specific primers	
primary PCR *Ds* 5’ end	GGATAAAACTAACAAAATCGGTTATACG
primary PCR *Ds* 3’ end	CCGTATTTATCCCGTTCGTTTTCGTTA
secondary PCR *Ds* 5’ end	CGATAACGGTCGGTACGGGATTTTC
secondary PCR *Ds* 3’ end	CCCGTTTTCGTTTCCGTCCCGCAAG
Primers for amplification of empty *Ds* donor sites in *Arabidopsis*	
P1	GGAAGTTCATTTCATTTGGAG
P2	TCGCCCTCGCCCTCGCCGGAC
P3	GATCTCGGTGACGGGCAGGAC