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)

[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.