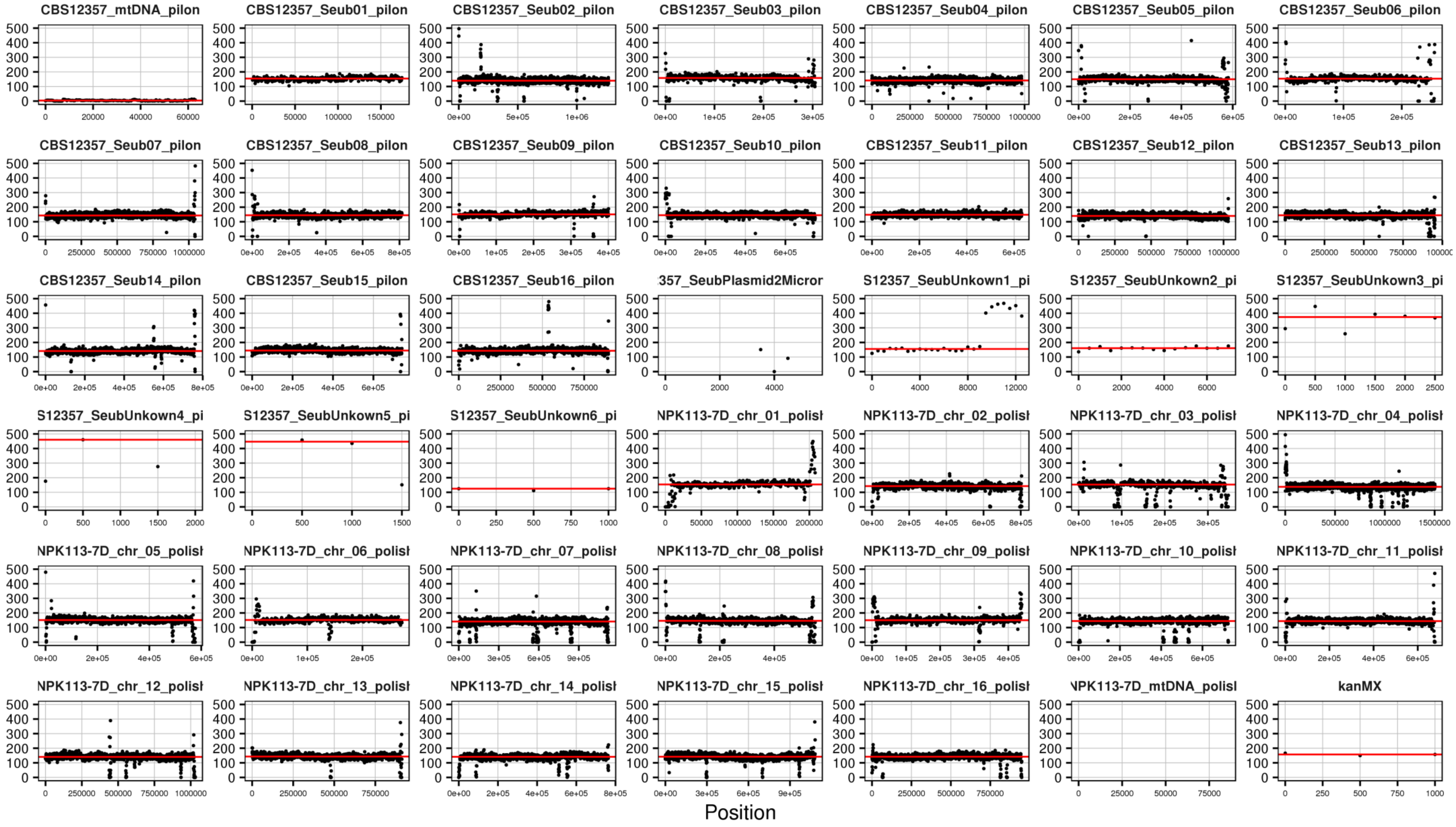
Supplementary Data File

Of the manuscript

Allele-specific genome editing using CRISPR-Cas9 causes off-target mutations in diploid yeast

Figure S1: Whole genome sequencing coverage plots of *S. cerevisiae* x *eubayanus* hybrid IMS0408 before and after targeting the *S. cerevisiae* specific gene *MAL11*. Genomic DNA was extracted from untransformed IMS0408 and from four randomly selected isolates obtained after attempting the deletion of MAL11 using Cas9 and a 120 bp repair fragment, called IMX1421 to IMX1424. Whole genome sequencing was performed using 150 bp paired-end reads on an Illumina HiSeq 2500, and the reads were aligned to reference genome composed of chromosome-level assemblies of *S. cerevisiae* strain CEN.PK113-7D and of *S. eubayanus* strain CBS12357 obtained using nanopore sequencing. On the graphs the local sequencing coverage across all contigs is shown by black dots and the median coverage is shown by a black line. While in IMS0408, the coverage of all chromosomes is approximately equal, IMX1421-1424 show no coverage on regions of *S. cerevisiae* chromosome VII including *MAL11* (1,100,203-1,102,053), and double coverage on the corresponding regions of *S. eubayanus* chromosome VII. The coordinates at which the coverage on *S. cerevisiae* chromosome VII disappeared were verified using IGV software: around 1,094,000 for IMX1421, 768, 000 for IMX1422, 968,300 for IMX1423 and 767,000 for IMX1424. In all cases, coverage increased on the corresponding region of *S. eubayanus* chromosome VII and read pairing indicated the duplicated segment of *S. eubayanus* chromosome VII was attached to the remaining segment of *S. cerevisiae* chromosome VII. In the case of IMX1422, the *S. cerevisiae* and *S. eubayanus* chromosomes merged into two copies of a chimeric chromosome, while for the others, the *S. eubayanus* chromosome is intact while the *S. cerevisiae* chromosome became chimeric, resulting in loss of heterozygosity.

IMS0408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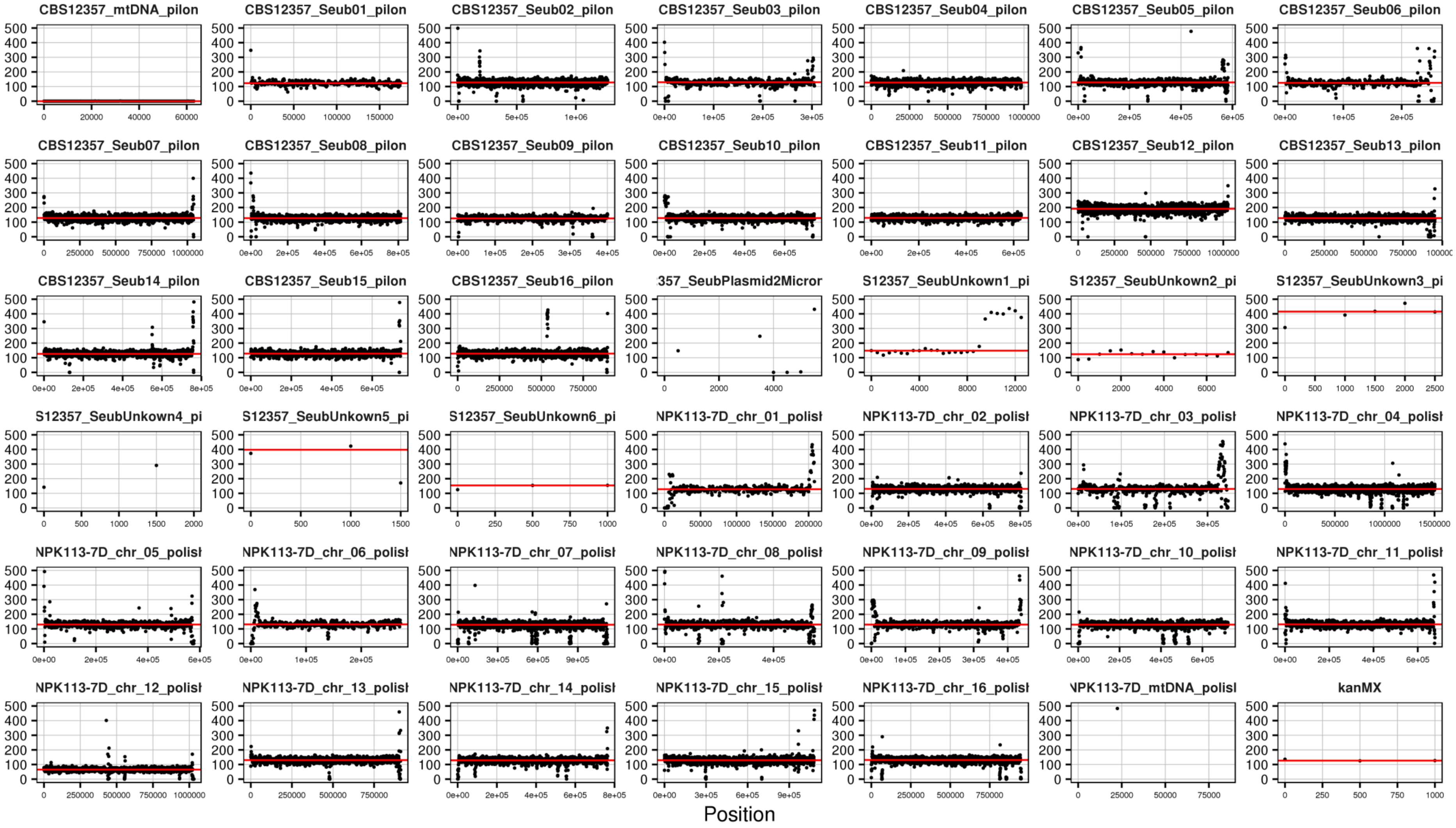
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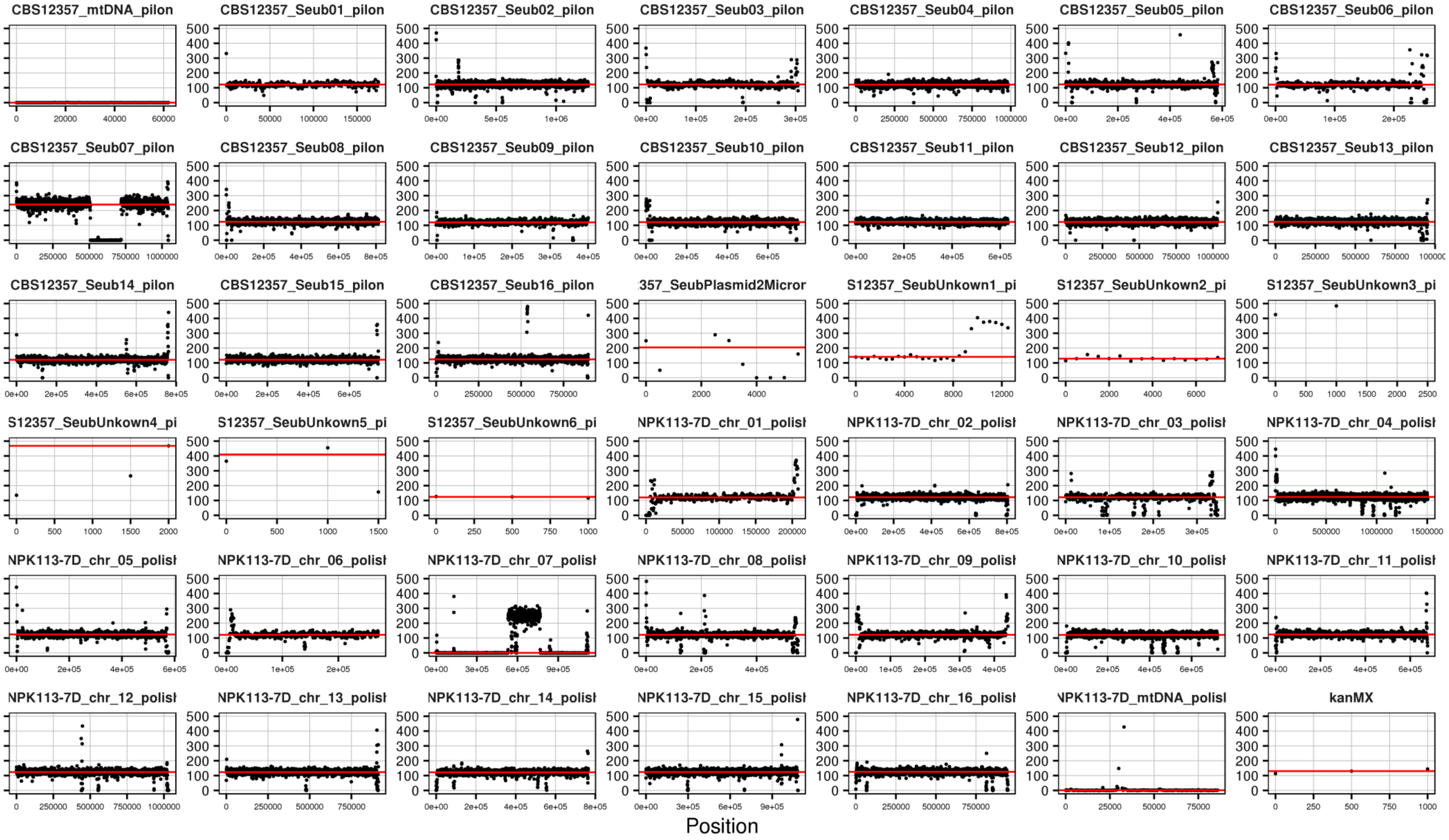
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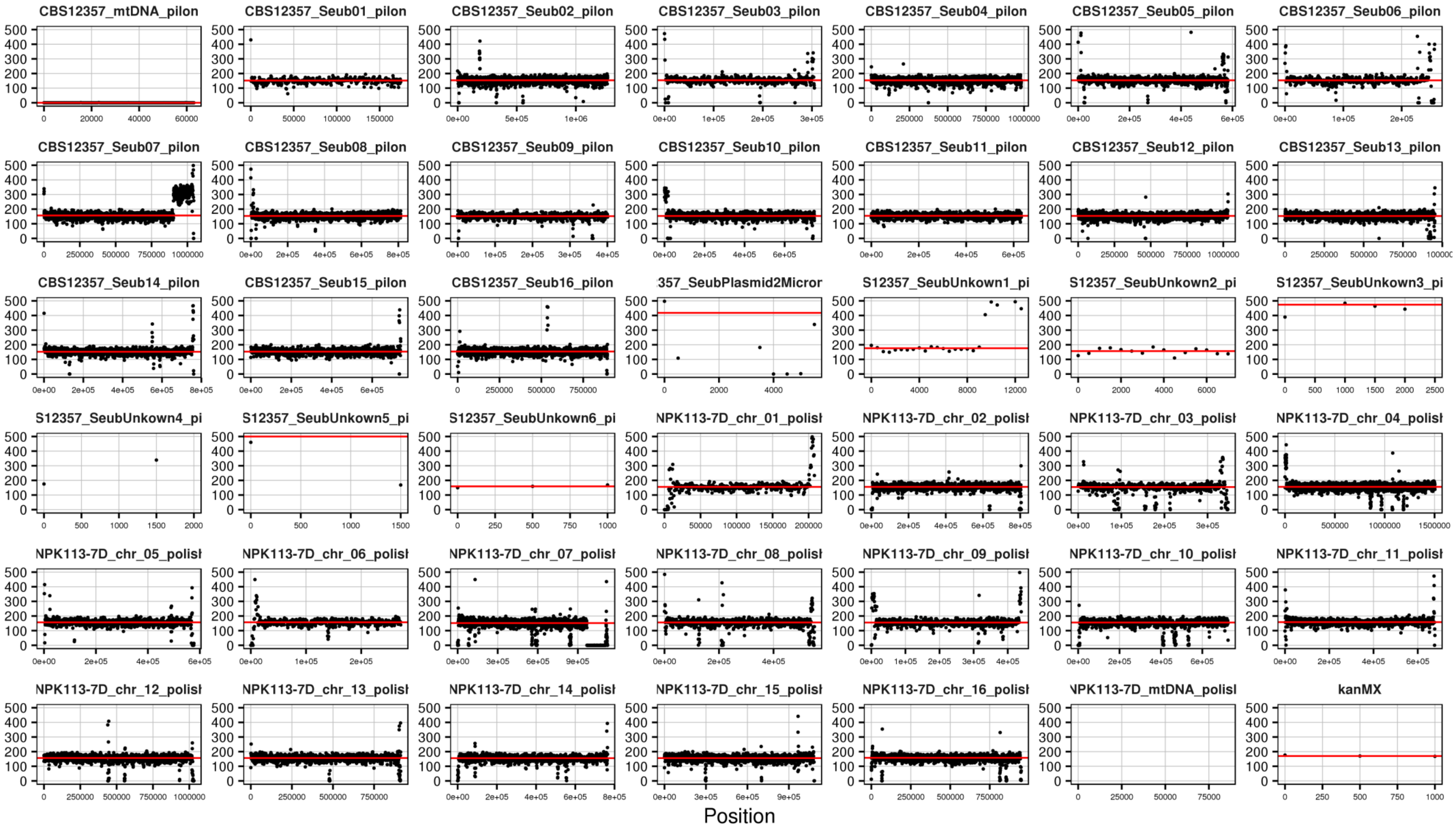
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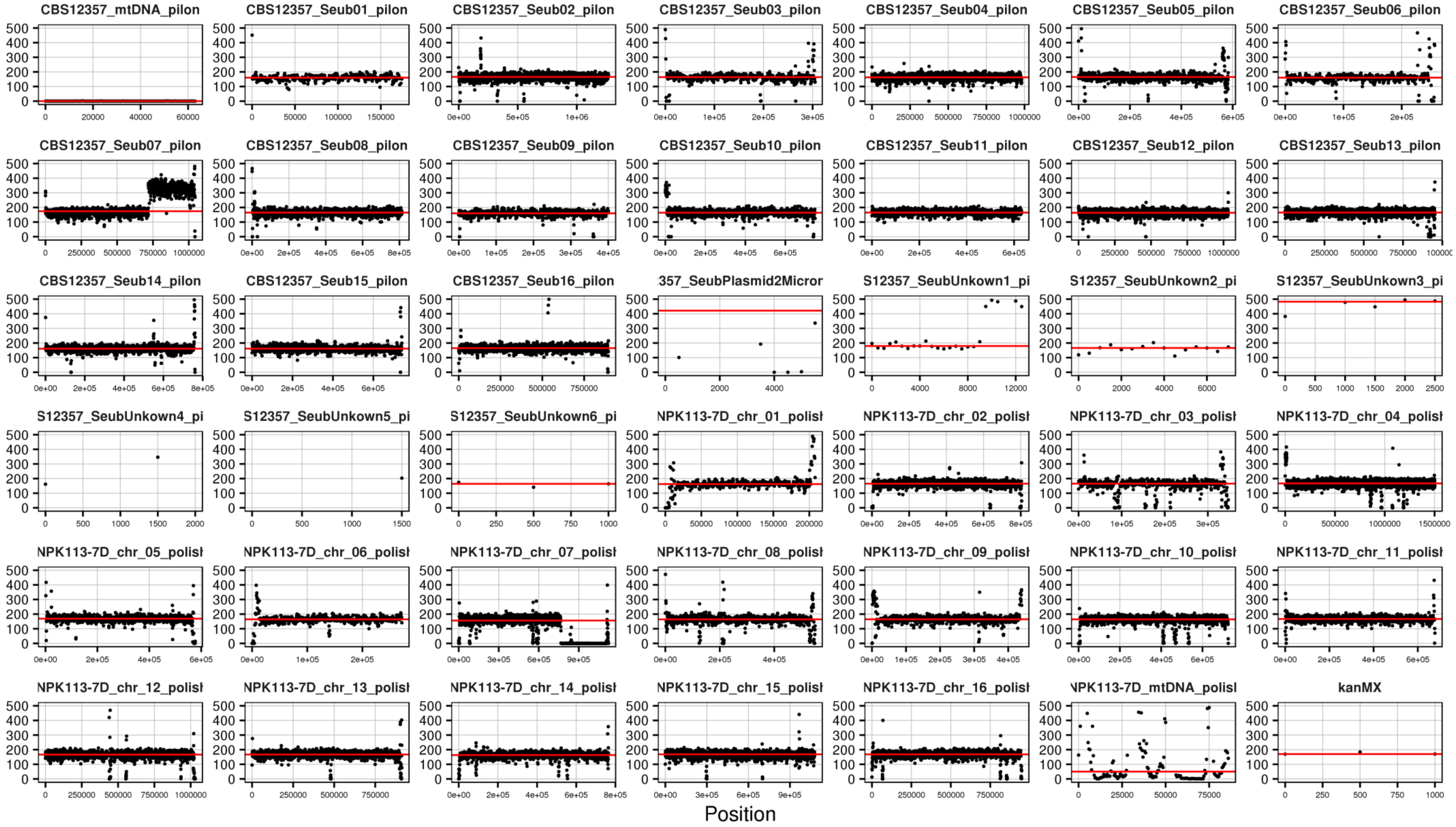
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Table S1. Fluorescence profiles of samples measured in this study. For each targeted locus, three replicates from independent transformations were measured both with and without repair fragment. Single cells were selected on a FSC-A/FSC-H graph, Venus+ cells on a Venus/FSC-A graph and quartiles with and without fluorescence were gated on a mRuby2/mTurquoise2 graph, as indicated in Figure 1. The exact gating differed per strain, but was kept uniform among strains. All numbers are indicated in percentage of the parental gating, which is indicated in the top row, except for the single cells column, which indicates the number of single cells measured. The percentage of having lost mRuby2 or mTurquoise2 was calculated by adding the corresponding quartiles. When targeting cas9 in IMX1555, one of the replicates without repair fragment did not grow at all, therefore flow cytometric data could not be acquired.

				Single Cells	Venus$^+$				Venus$^-$			
Strain	Target	Repair	Single Cells	Venus$^+$	mTurquoise$^-$ mRuby2$^+$	mTurquoise$^+$ mRuby2$^+$	mTurquoise$^+$ mRuby2$^-$	mTurquoise$^-$ mRuby2$^-$	mTurquoise$^-$ mRuby2$^+$	mTurquoise$^+$ mRuby2$^+$	mTurquoise$^+$ mRuby2$^-$	mTurquoise$^-$ mRuby2$^-$
IMX1555	*cas9*	+	84531	97,9	0,0	99,7	0,2	0,0	1,8	78,8	19,4	0,0
IMX1555	*cas9*	+	83772	99,7	0,0	99,9	0,1	0,0	12,2	84,2	3,2	0,5
IMX1555	*cas9*	+	84407	97,2	0,0	99,9	0,1	0,0	1,2	98,4	0,3	0,0
IMX1555	*cas9*	-	84161	0,1	1,9	95,3	2,8	0,0	0,1	92,0	7,8	0,0
IMX1555	*cas9*	-	82950	0,2	3,9	96,1	0,0	0,0	0,1	99,9	0,0	0,0
IMX1555	*cas9*	-	-	-	-	-	-	-	-	-	-	-
IMX1557	-	-	85567	0,0	20,0	80,0	0,0	0,0	8,3	91,6	0,1	0,1
IMX1557	-	-	85198	0,0	25,0	75,0	0,0	0,0	8,4	91,4	0,1	0,1
IMX1557	-	-	84060	0,1	8,2	91,8	0,0	0,0	2,3	97,5	0,1	0,1
IMX1557	*AIM9*	+	90511	97,6	0,0	97,9	2,1	0,0	40,4	49,6	9,5	0,5
IMX1557	*AIM9*	+	84385	98,3	1,6	97,8	0,4	0,2	70,2	19,6	3,0	7,3
IMX1557	*AIM9*	+	83120	99,8	18,8	81,2	0,0	0,0	67,2	32,4	0,5	0,0
IMX1557	*AIM9*	-	90555	0,0	0,0	100,0	0,0	0,0	1,5	23,4	73,3	1,8
IMX1557	*AIM9*	-	92034	0,0	0,0	100,0	0,0	0,0	2,2	17,3	80,1	0,4
IMX1557	*AIM9*	-	87529	0,0	0,0	0,0	0,0	0,0	1,3	9,0	89,1	0,6
IMX1557	*CAN1*	+	91519	0,8	0,1	98,7	1,1	0,0	1,2	95,5	3,2	0,1
IMX1557	*CAN1*	+	91767	1,7	0,1	98,7	1,2	0,0	0,8	93,1	6,1	0,1
IMX1557	*CAN1*	+	92089	0,4	0,0	99,4	0,6	0,0	0,5	95,3	4,0	0,2
IMX1557	*CAN1*	-	91970	0,0	0,0	0,0	0,0	0,0	1,5	93,5	4,9	0,1
IMX1557	*CAN1*	-	93115	0,0	0,0	0,0	0,0	0,0	0,9	92,4	6,6	0,1
IMX1557	*CAN1*	-	91297	0,0	0,0	0,0	0,0	0,0	0,6	94,1	5,0	0,3
IMX1557	*cas9*	+	85008	1,9	0,8	99,3	0,0	0,0	0,7	47,1	51,9	0,3
IMX1557	*cas9*	+	83723	8,0	0,2	99,8	0,0	0,0	0,3	51,9	47,7	0,1
IMX1557	*cas9*	+	82777	3,2	0,9	97,7	1,5	0,0	0,3	56,7	42,9	0,1
IMX1557	*cas9*	-	81166	0,1	4,4	95,6	0,0	0,0	0,4	43,9	55,5	0,1
IMX1557	*cas9*	-	83007	0,0	11,1	88,9	0,0	0,0	0,5	57,3	42,1	0,1
IMX1557	*cas9*	-	81313	0,0	22,7	77,3	0,0	0,0	0,3	46,5	53,0	0,2
IMX1557	*YCK3*	+	87009	98,9	26,9	73,0	0,1	0,0	83,0	14,3	0,5	2,2
IMX1557	*YCK3*	+	80983	98,9	0,9	99,0	0,1	0,0	74,9	21,4	1,0	2,7
IMX1557	*YCK3*	+	82570	99,7	0,1	99,8	0,1	0,0	51,6	47,6	0,4	0,4
IMX1557	*YCK3*	-	79957	0,0	45,7	54,3	0,0	0,0	97,6	0,1	0,0	2,3
IMX1557	*YCK3*	-	92277	0,0	0,0	100,0	0,0	0,0	89,0	9,0	0,6	1,6
IMX1557	*YCK3*	-	92256	0,0	0,0	0,0	0,0	0,0	89,2	8,7	0,6	1,6
IMX1585	-	-	84826	0,0	50,0	50,0	0,0	0,0	0,3	98,9	0,8	0,0
IMX1585	-	-	84777	0,0	0,0	100,0	0,0	0,0	0,4	98,8	0,8	0,0
IMX1585	-	-	80656	0,0	50,0	50,0	0,0	0,0	0,4	98,9	0,7	0,0
IMX1585	550K	-	78717	0,0	60,0	40,0	0,0	0,0	43,7	55,3	0,8	0,3
IMX1585	550K	-	80876	0,0	16,7	83,3	0,0	0,0	42,9	55,5	1,1	0,6
IMX1585	550K	-	76315	0,0	33,3	66,7	0,0	0,0	43,2	55,8	0,8	0,3
IMX1585	*AIM9*	-	80253	0,0	14,3	85,7	0,0	0,0	13,6	84,9	1,4	0,1
IMX1585	*AIM9*	-	81671	0,0	0,0	100,0	0,0	0,0	13,3	84,6	1,9	0,2
IMX1585	*AIM9*	-	78711	0,0	0,0	100,0	0,0	0,0	13,5	84,8	1,6	0,1
IMX1585	*cas9*	-	75002	0,0	7,7	92,3	0,0	0,0	0,4	55,6	43,8	0,2
IMX1585	*cas9*	-	80788	0,0	25,0	75,0	0,0	0,0	0,2	52,0	47,8	0,1
IMX1585	*cas9*	-	81085	0,0	0,0	100,0	0,0	0,0	0,2	51,4	48,3	0,0
IMX1585	*FIR1*	-	82063	0,0	50,0	50,0	0,0	0,0	12,1	86,1	1,7	0,1
IMX1585	*FIR1*	-	82033	0,0	0,0	100,0	0,0	0,0	11,6	86,0	2,3	0,2
IMX1585	*FIR1*	-	76748	0,0	0,0	100,0	0,0	0,0	12,5	86,1	1,3	0,1
IMX1585	*UTR2*	-	81225	0,0	0,0	100,0	0,0	0,0	0,2	88,5	11,3	0,0
IMX1585	*UTR2*	-	79212	0,0	20,0	80,0	0,0	0,0	0,2	88,7	11,0	0,0
IMX1585	*UTR2*	-	79061	0,0	0,0	0,0	0,0	0,0	0,3	88,6	11,1	0,0
IMX1585	*YCK3*	-	80034	0,0	0,0	100,0	0,0	0,0	12,5	85,7	1,7	0,1
IMX1585	*YCK3*	-	79346	0,0	0,0	100,0	0,0	0,0	12,4	86,0	1,5	0,1
IMX1585	*YCK3*	-	79874	0,0	12,5	87,5	0,0	0,0	12,8	85,7	1,4	0,1

Table S2: Loss of heterozygosity at the nucleotide level on chromosome V of the heterozygous diploid IMX1585 and in IMX1585-derived isolates in which the CEN.PK113-7D derived alleles of the *UTR2* or *FIR1* loci were targeted using Cas9. Upon targeting of *UTR2* and *FIR1*, 10 isolates having conserved fluorescence of mRuby2 and mTurquoise2 were and 10 isolates having lost the fluorophore located on the targeted fluorophore were isolated for each targeted locus using FACS. Purified DNA of each isolate was sequenced using 150 bp pair-end Illumina reads. After alignment of the reads to the genome assembly of CEN.PK113-7D, heterozygous and homozygous SNPs and INDELs were called and used to identify nucleotides which had become homozygous for the S288C allele in the isolates which were heterozygous in IMX1585. Since there were ca. 4 heterozygous nucleotides per kbp in IMX1585, the resolution at which loss of heterozygosity could be detected was dependent upon the presence of heterozygous nucleotides at that location in IMX1585. Nucleotides which became homozygous for the CEN.PK113-7D allele were never observed. The number of hemizygous SNPs and INDELs called in S288C (Supplementary information X) which were lost due to the loss of heterozygosity is shown as "Mutations".

Strain	**Targeted Locus**	**Fluorescence**	**Homozygous nucleotides**	**Heterozygous nucleotides**	**Mutations**
IMX1585	-	Ruby^{+}/mTurquoise2^{+}	1-577607		0
IMX1596	*UTR2*	Ruby^{-}/mTurquoise2^{+}	1-84628	86629-577607	443
IMX1597	*UTR2*	Ruby^{-}/mTurquoise2^{+}	1-110289	143879-577607	502
IMX1598	*UTR2*	Ruby^{-}/mTurquoise2^{+}	1-79859	80023-577607	387
IMX1599	*UTR2*	Ruby^{-}/mTurquoise2^{+}	1-80609	81042-577607	401
IMX1600	*UTR2*	Ruby^{-}/mTurquoise2^{+}	1-92729	97030-577607	459
IMX1601	*UTR2*	Ruby^{-}/mTurquoise2^{+}	1-79859	80023-577607	387
IMX1602	*UTR2*	Ruby^{-}/mTurquoise2^{+}	1-92729	97030-577607	459
IMX1603	*UTR2*	Ruby^{-}/mTurquoise2^{+}	1-92729	97030-577607	459
IMX1604	*UTR2*	Ruby^{-}/mTurquoise2^{+}	1-92729	97030-577607	459
IMX1605	*UTR2*	Ruby^{-}/mTurquoise2^{+}	1-77600, 78882-79859	78423-78522, 80023-577607	385
IMX1606	*UTR2*	Ruby^{+}/mTurquoise2^{+}	78423-80377, 80609	1-77600, 80469-80587, 81042-577607	15
IMX1607	*UTR2*	Ruby^{+}/mTurquoise2^{+}	68797-82144	1-47413, 82157-577607	121
IMX1608	*UTR2*	Ruby^{+}/mTurquoise2^{+}	75235-80609, 82012-82652, 83580-92729	1-74650, 81042-81700, 83201, 97030-577607	80
IMX1609	*UTR2*	Ruby^{+}/mTurquoise2^{+}	79857-79859	1-79751, 80023-577607	2
IMX1610	*UTR2*	Ruby^{+}/mTurquoise2^{+}	73657-79859	1-73052, 80023-577607	2
IMX1611	*UTR2*	Ruby^{+}/mTurquoise2^{+}	78423-82091	1-77600, 82144-577607	41
IMX1612	*UTR2*	Ruby^{+}/mTurquoise2^{+}	79857-79859	1-79751, 80023-577607	2
IMX1613	*UTR2*	Ruby^{+}/mTurquoise2^{+}	78423-80377, 80609	1-77600, 80469-80588, 81042-577607	15
IMX1614	*UTR2*	Ruby^{+}/mTurquoise2^{+}	74385-79859	1-74094, 80023-577607	33
IMX1615	*UTR2*	Ruby^{+}/mTurquoise2^{+}	79857-83201	1-79751, 83580-577607	43
IMX1616	*FIR1*	Ruby^{+}/mTurquoise2^{-}	216993-577607	1-216630	1687
IMX1617	*FIR1*	Ruby^{+}/mTurquoise2^{-}	214818-577607	1-204146	1697
IMX1618	*FIR1*	Ruby^{+}/mTurquoise2^{-}	217767-577607	1-217602	1681
IMX1619	*FIR1*	Ruby^{+}/mTurquoise2^{-}	216993-218163, 220098-577607	1-216360, 218645-219357	1681
IMX1620	*FIR1*	Ruby^{+}/mTurquoise2^{-}	217767-577607	1-217602	1681
IMX1621	*FIR1*	Ruby^{+}/mTurquoise2^{-}	216993-577607	1-216360	1687
IMX1622	*FIR1*	Ruby^{+}/mTurquoise2^{-}	216993-577607	1-216360	1687
IMX1623	*FIR1*	Ruby^{+}/mTurquoise2^{-}	214818-577607	1-204146	1697
IMX1624	*FIR1*	Ruby^{+}/mTurquoise2^{-}	214818-577607	1-204146	1697
IMX1625	*FIR1*	Ruby^{+}/mTurquoise2^{-}	216993-577607	1-216360	1687
IMX1626	*FIR1*	Ruby^{+}/mTurquoise2^{+}	217767-217767	1-217602, 217908-577607	1
IMX1627	*FIR1*	Ruby^{+}/mTurquoise2^{+}	217767-217767	1-217602, 217908-577607	1

IMX1628	*FIR1*	Ruby$^+$/mTurquoise2$^+$	217458-219121	1-217338, 219357-577607	10
IMX1629	*FIR1*	Ruby$^+$/mTurquoise2$^+$	217602-217767	1-217458, 217908-577607	2
IMX1630	*FIR1*	Ruby$^+$/mTurquoise2$^+$	217767-217767	1-217602, 217908-577607	1
IMX1631	*FIR1*	Ruby$^+$/mTurquoise2$^+$	216993-217767	1-216360, 217908-577607	7
IMX1632	*FIR1*	Ruby$^+$/mTurquoise2$^+$	214818-226717	1-204146, 227223-577607	80
IMX1633	*FIR1*	Ruby$^+$/mTurquoise2$^+$	217458-219357	1-217338, 220098-577607	11
IMX1634	*FIR1*	Ruby$^+$/mTurquoise2$^+$	217458-217908	1-217338, 218163-577607	4
IMX1635	*FIR1*	Ruby$^+$/mTurquoise2$^+$	217767-219121	1-217602, 219357-577607	8

Table S3: ***Saccharomyces*** **strains used throughout this study.**

Name	Species	Ploidy	Strain background	Relevant Genotype	Source
CEN.PK113-7D	*S. cerevisiae*	1N	CEN.PK	*MATa SIT1 CAN1 UTR2 URA3 FIR1 AIM9 YCK3 FAU1*	[1]
IMX581	*S. cerevisiae*	1N	CEN.PK	*MATa SIT1 can1::cas9-natNT2 UTR2 ura3-52 FIR1 AIM9 YCK3 FAU1*	[2]
IMX1544	*S. cerevisiae*	1N	CEN.PK	*MATa sit1::mRuby2 can1::cas9-natNT2 UTR2 ura3-52 FIR1 AIM9 YCK3 FAU1*	This study
IMX1555	*S. cerevisiae*	1N	CEN.PK	*MATa sit1::mRuby2 can1::cas9-natNT2 UTR2 ura3-52 FIR1 AIM9 YCK3 fau1::mTurquoise2*	This study
IMK439	*S. cerevisiae*	1N	CEN.PK	*MATα SIT1 CAN1 UTR2 ura3::KanMX FIR1 AIM9 YCK3 FAU1*	[3]
IMX1557	*S. cerevisiae*	2N	CEN.PK CEN.PK	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52 ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
S288C	*S. cerevisiae*	1N	S288C	*MATα SIT1 CAN1 UTR2 URA3 FIR1 AIM9 YCK3 FAU1*	[4]
IMX1585	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1596	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα SIT1/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1597	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα SIT1/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1598	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα SIT1/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1599	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα SIT1/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1600	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα SIT1/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1601	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα SIT1/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1602	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα SIT1/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1603	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα SIT1/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1604	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα SIT1/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1605	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα SIT1/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1606	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1607	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1608	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1609	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1610	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3*	This study

				fau1::mTurquoise2/FAU1	
IMX1611	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1612	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1613	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1614	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1615	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1616	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 FAU1/FAU1*	This study
IMX1617	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 FAU1/FAU1*	This study
IMX1618	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 FAU1/FAU1*	This study
IMX1619	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 FAU1/FAU1*	This study
IMX1620	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 FAU1/FAU1*	This study
IMX1621	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 FAU1/FAU1*	This study
IMX1622	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 FAU1/FAU1*	This study
IMX1623	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 FAU1/FAU1*	This study
IMX1624	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 FAU1/FAU1*	This study
IMX1625	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 FAU1/FAU1*	This study
IMX1626	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1627	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1628	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1629	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1630	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study

IMX1631	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1632	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1633	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1634	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
IMX1635	*S. cerevisiae*	2N	CEN.PK/S288C	*MATa /MATα sit1::mRuby2/SIT1 can1::cas9-natNT2/CAN1 UTR2/UTR2 ura3-52/ ura3::KanMX FIR1/FIR1 AIM9/AIM9 YCK3/YCK3 fau1::mTurquoise2/FAU1*	This study
CBS12357	*S. eubayanus*	2N	CBS12357	*MATa /MATα* wildtype	[5]
IMS0408	*S. cerevisiae x eubayanus*	2N	CEN.PK/CBS12357	*MATa /MATα ura3::KanMX/URA3* MAL11	[6]
IMX1421	*S. cerevisiae x eubayanus*	2N	CEN.PK/CBS12357	*MATa /MATα ura3::KanMX/URA3*	This study
IMX1422	*S. cerevisiae x eubayanus*	2N	CEN.PK/CBS12357	*MATa /MATα ura3::KanMX/URA3*	This study
IMX1423	*S. cerevisiae x eubayanus*	2N	CEN.PK/CBS12357	*MATa /MATα ura3::KanMX/URA3*	This study
IMX1424	*S. cerevisiae x eubayanus*	2N	CEN.PK/CBS12357	*MATa /MATα ura3::KanMX/URA3*	This study

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Table S4: Plasmids used throughout this study. Plasmid parts used for the assembly of pUD429-pUD431 and pUDE480-pUDE482 were standard pYTK plasmids[1].

Name	Relevant genotype	Origin
pUD429	ori amp^R ARS4/CEN6 hyg^R GFP	This study
pUD430	ori amp^R ARS4/CEN6 hyg^R GFP	This study
pUD431	ori amp^R ARS4/CEN6 hyg^R GFP	This study
pUD574	ori amp^R gRNA-MAL11	GeneArt™
pUDE480	ori amp^R ARS4/CEN6 hyg^R ScPGK1p-mRuby2-ScPGK1t	This study
pUDE481	ori amp^R ARS4/CEN6 hyg^R ScTDH3p-mTurquoise2-ScADH1t	This study
pUDE482	ori amp^R ARS4/CEN6 hyg^R ScTEF1p-Venus-ScENO2t	This study
pMEL11	ori amp^R 2µm amdSYM gRNA-CAN1.Y	[2]
pROS11	ori amp^R 2µm amdSYM gRNA-CAN1.Y gRNA-ADE2.Y	[2]
pUDR323	ori amp^R 2µm amdSYM gRNA-SIT1	This study
pUDR324	ori amp^R 2µm amdSYM gRNA-FAU1	This study
pUDR325	ori amp^R 2µm amdSYM gRNA-Cas9	This study
pUDR358	ori amp^R 2µm amdSYM gRNA-UTR2	This study
pUDR359	ori amp^R 2µm amdSYM gRNA-FIR1	This study
pUDR360	ori amp^R 2µm amdSYM gRNA-AIM9	This study
pUDR361	ori amp^R 2µm amdSYM gRNA-YCK3	This study
pUDR362	ori amp^R 2µm amdSYM gRNA-550K	This study
pUDP004	ori amp^R panARSopt amdSYM cas9	[3]
pUDP045	ori amp^R panARSopt amdSYM cas9 gRNA-MAL11	This study

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Table S5: Primers used in this study.

name	Sequence (3' to 5')	Purpose
1084	AGGCACAAGTACCAGGTGCTAAAG	Amplification *MAL11*
1148	GCAAGCTTGCCGGCACTAATTTTATTTGACGAG	Amplification *MAL1*
1470	GCGAGTTGCAAGAATCTCTACG	Amplification *MAL11*
1657	CACCACTAGTATGACTTTAACTAAGCAAACATGCGCC	Amplification *MAL1*
6005	GATCATTTATCTTTCACTGCGGAGAAG	Amplification pROS11 backbone
9457	TGCGCATGTTTCGGCGTTCGAAACTTCTCCGCAGTGAAAGATAAATGATCCTAGGCTGTCCAAATCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	Introduction of gRNA-*cas9* in pROS11
10813	TTGGTGTTTCTTTCTGATGCTACATAGAAGAACATCAAACAACTAAAAAAATAGTATAATGTAAAAGGGTTGTTTTTTTTTTTTTGGAAGAAATAAGGAATCCCTTTGACTGCTCCCAAA	Repair fragment *MAL11*
10814	TTTGGGAGCAGTCAAAGGGATTCCTTATTTCTTCCAAAAAAAAAAAAACAACCCTTTTACATTATACTATTTTTTTAGTTGTTTGATGTTCTTCTATGTAGCATCAGAAAGAAACACCAA	Repair fragment *MAL11*
12228	AGAACATCGTAGTGCTTTGTAAAAGAACTGTTAAAGACCCAGTACGAAAATTTTTCCATAGCCGATAATTGCAGACG	Integration of mRuby2 in *FAU1*
12229	ATGTTCTTGACTATGTAGTAGCTATATGTGCATGTATGAAATTATTTGGGTGAGATAATACGTCTCATTGGCAGC	Integration of mRuby2 in *FAU1*
12230	TGCGCATGTTTCGGCGTTCGAAACTTCTCCGCAGTGAAAGATAAATGATCATTCATTACAACTTATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	Introduction of gRNA-*SIT1* in pROS11
12231	GGCACAGAATGACTTGCAGC	Amplification *SIT1* locus
12232	AACTGATTGGGGCCACTACG	Amplification *SIT1* locus
12233	AAATGGCAAAAATAAAAATTACTGTCAGCTACGCTATCTTTATATAGCTACAAAAAATTACAGATGTCAACACAGCTAC	Integration of mTurquoise2 in *SIT1*
12234	TACTTATTTATTTATTTATTTATACAATAGCTGTACCATGTAAATAATACATATATGAAATCGTCTCACATCCAGC	Integration of mTurquoise2 in *SIT1*
12235	TGCGCATGTTTCGGCGTTCGAAACTTCTCCGCAGTGAAAGATAAATGATCTCAGGCTCTTTTAGTTGATAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	Introduction of gRNA-*FAU1* in pROS11
12236	CTTGCGAACCCGAAGCTTTC	Amplification *FAU1* locus
12237	TGCTCTACCCAAGAACGCAG	Amplification *FAU1* locus
12238	TTTCAGAGTTCTTCAGACTTCTTAACTCCTGTAAAAACAAAAAAAAAAAAAGGCATAGCACACACTGGCTTAAGATGAC	Integration of Venus in *CAN1*
12239	TATGAGGGTGAGAATGCGAAATGGCGTGGGAATGTGATTAAAGGTAATAAAACGTCATATCGTCTCATGCTCAGC	Integration of Venus in *CAN1*
12805	TGCGCATGTTTCGGCGTTCGAAACTTCTCCGCAGTGAAAGATAAATGATCTGAAATTAATTGGGACGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	Introduction of gRNA-*UTR2* in pROS11
12806	TGCGCATGTTTCGGCGTTCGAAACTTCTCCGCAGTGAAAGATAAATGATCAACAAAAAGTGTTCCATCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	Introduction of gRNA-*FIR1* in pROS11
12807	TGCGCATGTTTCGGCGTTCGAAACTTCTCCGCAGTGAAAGATAAATGATCTGACCTGAAGTTGGGCATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	Introduction of gRNA-*AIM9* in pROS11
12808	TGCGCATGTTTCGGCGTTCGAAACTTCTCCGCAGTGAAAGATAAATGATCGGAGAGAACATTCTTCATTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	Introduction of gRNA-*YCK3* in pROS11
12809	TGCGCATGTTTCGGCGTTCGAAACTTCTCCGCAGTGAAAGATAAATGATCAGTGGAGTAGGTGTGCTTTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	Introduction of gRNA-550K in pROS11
12810	TGTTCCCTTTGTAAAACTTCTATTTATTGTCCTGCAAATAAGCTAATTATATAATTAATACACTGGCTTAAGATGAC	Integration of Venus in *UTR2*
12811	ATTAATACTTTTTTTTTTGAGAGTCCTGTGTAGCCTATTTGTTCTTAGATGCAGATCCTCCGTCTCATGCTCAGC	Integration of Venus in *UTR2*
12812	CCTCTTTCTCTAATTTAGCACCCGCACACCGCAGCGGTCTGTGATATTCCGCATTGGAAACACTGGCTTAAGATGAC	Integration of Venus in *FIR1*
12813	CATGCGATGAGCTGGTCAAATCTGTTTACCAGAACAATTTGTAGGGTTTTTTTTTTTTTTCGTCTCATGCTCAGC	Integration of Venus in *FIR1*
12814	CAGCGAAGAAGAAGTAGCAAAAGCTGTTTAGCAAGCAAGACAGCAATACGAAGACCAAGCCACTGGCTTAAGATGAC	Integration of Venus in *AIM9*
12815	ACGTTATATACAGTTGAGTGAGGTAAAGAAAACGAAAAAATATTTCATTTTTAGTATAGACGTCTCATGCTCAGC	Integration of Venus in *AIM9*
12816	CCGCTAATCAAAAGTGGTATCTCATTCTGAAGAAAAAGTGTAAAAGGACGATAAGGAAAGCACTGGCTTAAGATGAC	Integration of Venus in *YCK3*
12817	AAGGAAACAGCCAATCAAAAAAAAAAAAAAGGAAAAAGAGAAAAGTATAAAAATCGCTTTACGTCTCATGCTCAGC	Integration of Venus in *YCK3*
12818	ATCTCTTATACAACATTTCACAAAAAACGTGTGATATGCTTACAATTGATCCTATCAATACACTGGCTTAAGATGAC	Integration of Venus in 550K
12819	GGAAATAAAATCCCTTGATTTAGACGAATACTGTAGAATGCAATAAAAGGTTTTGTGATTCGTCTCATGCTCAGC	Integration of Venus in 550K

Table S6: list of SNPs between chromosome VII of CEN.PK113-7D and of S288C

Position	In CEN.PK113-7D	In S288C
125	ACCCACAC	A
1589	T	TC
1740	TC	T
3761	A	AT
4319	T	C
4388	A	G
4772	A	G
5958	C	A
5961	T	C
5978	G	A
5986	C	T
5992	G	A
6008	T	C
6009	T	C
6047	A	G
6052	AT	A
6150	A	AG
6179	T	C
6184	T	G
6206	T	C
6218	A	G
6227	G	T
6236	A	G
6258	C	T
6260	C	T
6821	C	T
6831	T	C
6835	T	C
6840	C	T
6843	G	A
6854	A	G
6937	A	G
6948	G	A
6956	A	G
6957	T	C
6964	G	A
6967	T	C
6990	G	T
6999	T	C
7090	A	G
7095	T	C
7102	T	A
7106	T	C
7107	G	T
7111	A	C
7183	T	A
7185	C	T

8225	T	C
8226	A	G
8244	A	G
8270	C	T
8273	A	G
8275	A	G
8278	G	C
8279	G	A
8291	A	T
8301	G	A
8306	C	T
8326	G	A
8341	T	C
8352	T	C
8368	G	A
8374	A	T
8491	A	AC
8539	A	C
8850	C	T
8885	C	T
8964	T	C
8991	AT	A
9151	C	A
9246	G	A
9563	C	T
9649	A	G
10091	C	T
10136	G	GA
10236	C	T
10250	T	C
10846	C	T
11163	A	G
11198	G	A
11506	T	A
11925	C	T
11957	A	T
12004	A	T
12035	T	C
12083	C	T
12250	C	T
12353	C	T
12404	G	A
12490	C	T
12499	G	T
12655	C	T
12674	A	C
12743	G	C
12800	T	C
13045	A	G
13060	T	C

13089	T	G
13151	G	T
13328	A	G
13332	C	A
13340	A	C
13375	C	A
13490	A	G
13519	C	T
13562	C	A
13613	C	T
13717	T	A
13815	A	T
13836	T	C
13875	T	C
13904	T	C
13916	T	C
13920	CAG	C
13931	A	G
13935	A	G
14175	T	C
14243	T	C
14310	C	A
14315	C	CT
14472	G	T
14520	A	G
14612	G	A
14751	A	T
14752	T	C
14754	T	G
14759	T	C
14798	C	CT
14806	C	T
15329	G	A
15365	G	A
15479	T	A
15712	A	G
15742	A	T
15780	A	G
15786	G	A
15816	G	C
15883	A	T
15896	G	A
15914	G	A
15964	A	T
15980	G	A
16156	T	C
16211	G	A
16461	C	T
16549	A	G
16590	T	C

16680	A	T
16808	C	T
16948	A	G
17054	AT	A
18048	T	C
18303	A	G
18383	A	T
18901	A	T
18994	G	A
19018	T	C
19079	A	AT
19156	T	A
19267	T	A
19321	A	G
19325	A	G
19484	A	C
19591	C	T
19618	A	C
19968	A	G
20118	C	T
20210	A	C
20411	A	AT
20477	C	T
20486	T	C
20490	T	A
20515	AGAAAAG	A
20553	CAAAAAA	C
20645	G	C
21175	T	C
21592	T	C
21642	C	T
21745	T	C
21768	C	T
21790	A	G
21841	T	C
21895	G	C
21984	T	C
22136	C	T
22295	T	C
22316	C	A
22320	A	AATTG
22321	C	A
22334	T	G
22338	C	T
22360	G	A
22741	A	C
22855	T	C
23061	G	A
23275	T	A
23305	G	A

23311	C	T
23328	A	C
23356	T	C
23369	T	C
23401	A	G
23411	A	G
23478	T	C
23521	C	G
23623	A	T
23650	C	T
23833	G	A
24097	A	G
24130	C	T
24139	A	G
24171	T	C
24288	G	A
24473	T	C
24952	C	T
24953	C	T
25004	C	G
25114	C	T
25211	T	C
25649	T	C
25849	A	G
25881	A	G
26036	T	C
26085	G	A
26099	A	T
26216	T	C
26311	T	C
26376	GA	G
26387	A	G
26551	T	A
26570	G	A
27402	C	T
27574	A	G
27658	T	C
27665	T	C
32643	G	A
32652	T	C
32847	C	T
33982	C	A
34324	T	C
34455	CT	C
34532	G	A
34763	A	C
34832	T	C
35021	G	A
35031	A	G
35033	A	T

35305	TA	T
35475	T	C
35604	C	T
35793	T	C
36021	C	T
36681	T	C
37035	C	A
37227	A	T
37271	G	GTT
37539	T	C
38016	A	G
38387	C	T
38421	T	A
38519	C	T
38727	A	G
39656	G	A
39696	T	C
40158	A	G
40284	A	G
40631	A	T
40845	G	A
40874	T	TAA
40986	G	GA
41497	T	C
41600	G	A
41965	G	A
42016	A	G
42409	G	C
42522	C	T
42664	C	A
42688	G	C
43232	T	C
43373	AT	A
43396	A	G
43468	A	G
43822	GTA	G
44054	C	T
44222	T	C
44465	T	C
44474	G	A
44558	G	A
44639	A	G
44724	T	C
44726	G	A
44818	G	A
44939	A	G
45548	C	T
45581	G	T
45593	C	T
45743	G	A

45979	G	C
46188	C	T
47413	T	A
65125	C	A
68797	A	G
69601	G	A
69660	G	C
69671	C	G
69672	G	C
69676	G	T
69954	A	G
70017	G	A
70041	C	T
70111	GC	G
70161	G	T
70168	C	A
70188	T	C
70202	GT	G
70211	T	C
70270	T	C
70419	T	C
70428	C	T
70528	G	T
70965	G	A
71295	C	A
71342	GA	G
71448	C	T
71648	G	A
71815	C	T
71875	G	A
71917	G	A
71932	C	A
71949	T	C
71961	T	C
72017	A	G
72025	T	C
72145	C	G
72160	C	T
72242	G	A
72385	C	A
72448	A	G
72454	C	T
72487	G	A
72553	T	C
72556	G	A
72749	A	C
72805	G	T
72934	A	G
72979	G	A
73000	C	A

73052	G	A
73657	G	T
73763	G	C
73905	T	C
73953	G	T
73966	A	T
74094	A	G
74385	C	T
74437	CT	C
74556	T	C
74564	C	G
74634	A	G
74650	T	C
75235	G	T
75610	C	T
76189	G	A
76480	C	A
76503	C	T
76553	A	G
76558	T	C
76569	G	T
76695	G	T
76709	G	A
76824	C	A
76993	G	A
77042	T	C
77071	C	G
77196	A	C
77237	C	A
77321	G	A
77346	G	A
77436	G	A
77600	A	G
78423	A	G
78522	T	C
78882	T	C
79559	G	C
79751	T	C
79857	G	T
79859	G	C
80023	C	T
80180	T	TTCA
80195	T	A
80246	G	A
80270	T	C
80357	T	C
80377	A	G
80469	A	T
80505	C	T
80510	T	C

80568	A	G
80582	G	C
80587	G	A
80609	T	C
81042	T	C
81044	T	C
81057	G	A
81089	C	A
81093	GAT	G
81145	C	T
81266	A	T
81379	A	T
81400	C	G
81448	T	C
81472	A	G
81504	C	T
81520	G	T
81596	G	A
81634	A	G
81680	A	G
81691	G	C
81700	G	A
82012	T	C
82091	G	A
82144	G	A
82157	G	GTTATTATTATTATTATTGTTATTA
82272	A	T
82295	G	A
82340	G	A
82652	A	G
83201	A	T
83580	A	T
83608	A	G
83721	G	A
83814	G	T
83862	T	A
83867	A	G
83909	G	A
84077	A	G
84106	T	C
84139	C	CTGT
84265	T	G
84409	A	G
84484	T	C
84553	C	T
84628	A	G
85849	T	A
86629	C	T
87125	G	A
88244	C	T

88475	C	T
89942	T	G
89969	A	T
91640	T	C
91641	T	C
91751	G	A
92243	A	G
92417	T	A
92558	T	C
92636	T	C
92672	A	G
92729	T	C
97030	T	C
97360	T	G
98337	A	G
98550	A	C
98616	G	A
98961	G	A
99010	GA	G
99919	T	C
100377	C	T
100444	A	G
100506	GTCA	G
100718	G	GA
100998	A	G
101032	T	A
101137	A	T
101227	AC	A
101232	C	T
101237	C	G
101277	G	A
101285	T	C
101291	C	T
101297	T	A
101314	G	T
101316	G	A
101325	A	T
101331	G	T
101376	G	A
101548	G	T
101594	T	A
101931	C	T
102278	C	T
102556	A	T
102600	G	A
102617	AT	A
102733	T	C
102934	A	G
103099	C	T
103117	G	A

103451	T	G
103801	C	T
103913	A	G
104050	G	A
110289	T	C
116874	C	CT
116875	A	T
116886	A	G
116902	T	C
116910	C	T
116941	A	G
116999	A	G
117490	A	G
117557	T	G
133478	C	CAT
143879	T	TAATAATAAC
160912	C	T
184766	C	T
184771	G	A
184812	G	C
184859	G	A
184929	G	A
185170	C	T
185193	C	A
185586	C	T
186657	T	C
186885	C	T
187181	C	G
187326	G	A
187493	T	C
187512	T	C
187524	C	T
187551	G	A
187693	G	T
187714	G	A
187929	C	T
187973	T	G
188026	C	T
188058	T	C
188148	A	G
188170	T	C
188211	C	A
188259	A	G
188368	A	G
188384	A	T
188421	C	T
188461	T	C
188469	C	G
188533	G	A
188544	C	T

188547	C	T
188550	A	G
188581	T	C
188607	G	A
188653	T	A
188676	A	T
188686	AC	A
188708	T	C
188720	A	T
188727	G	C
188741	G	A
188788	C	T
188823	T	TTGCCTAGAACAA
188830	G	A
188907	C	T
188909	C	T
188931	A	G
188942	T	C
189045	G	A
189326	G	A
189623	C	T
189665	A	G
189666	T	C
189992	C	T
190553	G	A
190961	G	A
191246	T	C
191896	T	C
191900	A	T
196541	T	C
196637	G	A
196656	G	A
196721	G	T
196763	C	G
196766	C	T
196866	C	T
197081	G	A
197087	A	G
197162	T	C
197243	C	T
197246	C	T
197276	G	A
197282	A	G
197380	G	C
197417	T	C
197444	T	C
197445	C	T
197460	A	T
197850	C	T
197853	T	C

197969	T	A
197970	C	T
198012	A	G
198189	G	A
198219	C	T
198282	G	A
198360	A	G
198618	A	G
198684	G	C
198783	A	C
198993	A	G
199405	C	T
199496	G	A
199536	T	G
199608	TA	T
199668	TC	T
199734	G	A
199773	C	T
199831	A	G
199968	T	C
200922	C	T
201263	T	A
201606	T	C
201628	G	T
201720	A	G
201777	C	T
202097	T	A
202337	T	C
202451	G	T
202595	A	G
202748	T	C
202857	C	T
203041	A	T
203101	A	G
203154	C	T
203183	C	T
203339	T	C
203381	T	C
203704	G	A
204080	G	A
204095	C	T
204107	T	C
204146	C	T
214818	T	C
215621	T	G
215762	T	C
215928	C	G
215953	A	G
216006	C	T
216072	A	G

216096	G	A
216310	G	A
216360	A	G
216993	A	G
217080	A	G
217130	G	C
217338	C	T
217458	G	C
217602	T	C
217767	G	A
217908	C	T
218163	A	T
218574	A	AC
218645	C	T
218880	A	G
218997	A	G
219121	C	A
219357	G	C
220098	C	T
220124	T	C
220149	A	G
220174	T	C
220227	C	T
220233	C	T
220278	T	A
220471	T	C
220476	C	T
220827	A	G
220941	C	T
220976	T	C
221034	G	A
221494	A	G
221588	T	G
221841	G	A
222262	T	TA
222273	G	A
222405	G	T
222553	T	C
222566	A	G
222677	A	C
222694	G	C
222859	G	T
223074	G	A
223149	C	T
223157	A	C
223160	C	A
223261	G	A
223297	G	A
223339	A	G
223412	C	A

223459	A	T
223718	C	T
223808	A	G
223871	A	G
223889	C	G
223994	ATTTT	A
224035	T	C
224044	A	G
224112	T	C
224122	C	T
224123	A	C
224673	A	G
225147	G	A
225399	C	G
225552	A	G
226100	T	C
226268	A	G
226284	G	A
226315	T	TC
226355	A	T
226648	G	A
226652	TTATATA	T
226717	G	A
227223	A	G
227277	C	T
227376	A	G
227737	T	C
227980	G	A
227981	T	C
228118	C	T
228148	A	G
228203	C	T
228217	C	T
228259	A	G
228277	G	A
228410	C	T
228516	C	T
228712	A	G
228880	T	G
228988	A	G
228991	C	A
229268	A	T
229587	G	A
229614	A	G
229650	G	A
229819	T	A
229995	G	A
230141	G	A
230369	T	C
230445	C	T

230471	G	A
230479	A	G
230654	T	C
231084	T	C
231220	T	C
231282	C	T
231297	T	C
231459	G	A
231760	T	C
231785	A	G
231790	T	C
231799	T	G
231903	T	A
231972	G	C
232258	A	G
232284	T	C
232597	A	G
232765	A	G
232876	G	A
233063	A	G
233114	A	G
233157	C	CTTT
233221	G	A
233237	C	G
233265	A	G
233272	G	C
233453	C	T
233675	A	G
233742	T	A
233747	C	T
234128	C	T
234229	G	A
235112	A	G
235172	C	T
235192	T	C
235393	G	C
235452	G	A
235499	C	T
235527	A	G
235617	T	A
235622	A	G
235624	C	A
235800	C	T
235804	A	G
236368	C	T
236515	C	T
236646	G	A
236685	G	A
237075	G	A
237545	A	G

238064	TG	T
238267	A	G
238355	C	G
238926	T	C
239070	CT	C
239188	A	G
239850	A	G
240043	G	A
240081	C	T
240113	T	C
240657	T	C
240685	C	G
240691	T	C
240750	G	A
240824	A	G
240883	T	C
240884	T	C
240910	C	T
240961	T	C
240962	A	C
240975	G	T
241071	G	A
241168	T	C
241420	G	A
241606	A	G
241639	A	G
241836	G	T
241922	G	A
241934	A	G
241959	A	G
241984	A	G
242131	G	A
242200	A	G
242246	G	A
242397	T	C
242453	GA	G
242842	A	G
243021	C	T
243029	A	G
243066	G	A
243103	C	T
243223	G	C
243247	T	A
243275	C	T
243299	G	GT
243317	G	A
243322	A	T
243333	C	T
243342	A	G
243551	T	TG

243553	A	G
243661	C	T
243694	A	G
243767	G	A
243776	A	G
243800	T	A
243950	G	C
243995	G	A
244017	C	A
244159	C	T
244231	C	T
244576	CCGCTT	C
244582	T	A
244648	TATC	T
244716	A	C
244741	T	A
245166	G	A
245253	A	T
245499	T	C
245698	A	G
245700	A	G
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280558	G	A
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376638	C	T
376683	C	T
376746	T	G
376795	G	A
376882	A	G
376949	C	T
377020	A	G
377052	C	T
377213	C	A
377546	C	T
377631	G	A
377812	G	A
377847	C	T
377935	C	T
378026	T	C
378194	A	ACTGCTGTTGCTGCTGTTGCTGCTG
378720	G	A
378757	C	A
378767	C	T
378861	T	A
378888	C	T
378990	A	G
379083	A	G
379115	G	A
379116	C	A
379307	T	C
379764	C	T
380053	A	C
380614	A	G
380662	A	C
380701	A	G
380785	T	C
381223	A	G
381920	A	G
382080	C	T

382296	G	A
382440	C	T
382573	G	T
383031	A	G
383075	T	C
383176	T	C
383207	C	CA
383221	C	T
383464	T	A
384094	T	C
384181	T	C
384244	G	T
384475	C	T
384604	A	G
384687	G	A
384736	G	A
384859	A	G
385114	A	T
385198	A	G
385527	CATG	C
385565	A	G
385789	C	T
386029	T	C
386037	T	A
386062	C	T
386554	A	G
386660	T	C
386934	G	A
387058	A	AT
387111	C	T
387165	G	A
387189	C	T
387206	A	G
387211	T	C
387232	T	C
387291	C	T
387326	A	G
387373	G	A
387395	T	C
387418	T	C
387476	C	T
387527	G	A
387587	T	A
387668	T	C
387755	G	T
387758	G	A
387789	A	G
387891	C	T
387915	T	C
388398	A	T

388632	G	A
388715	C	T
389244	A	G
389259	G	C
389349	T	A
389685	A	G
390234	G	A
390264	C	G
390279	T	C
390381	G	A
390525	T	C
390606	T	C
390692	A	G
390764	T	G
390796	A	G
391140	T	C
391273	A	C
391370	C	T
391554	A	C
391626	A	G
391803	G	A
391995	T	C
392292	A	G
392617	C	T
392793	G	A
392815	T	C
392955	C	T
393008	T	C
393029	G	T
393516	C	T
393570	A	G
393727	A	G
393820	G	A
394044	G	A
394260	G	A
394333	A	G
394558	G	A
394605	G	A
394724	T	C
394786	A	T
395060	G	A
395477	G	A
395578	C	T
395714	T	C
395778	G	A
395905	C	CAAA
395927	G	C
396047	A	G
396147	T	C
396414	G	T

396486	T	C
396513	T	C
396838	T	C
397128	AT	A
397165	A	G
397190	C	T
397646	A	T
397806	G	T
398102	G	A
398454	G	T
398593	A	G
399676	G	T
400100	T	C
400706	G	A
400734	T	C
401182	C	T
401557	T	C
401583	G	A
401616	C	T
401689	C	CT
401806	T	G
402245	G	A
402362	T	C
402848	A	G
402868	T	C
402968	A	T
403021	C	T
403100	T	A
403422	A	G
403712	A	C
403754	G	A
403778	A	G
404257	C	T
404390	T	A
404478	C	T
405017	C	T
405222	T	A
405233	A	G
405447	G	A
405616	G	T
405768	T	C
406908	C	T
407110	CTTT	C
407326	G	A
407424	G	A
407445	T	C
407448	A	G
407449	A	G
407531	T	A
407630	T	G

407713	T	C
407758	T	C
407835	A	C
407836	T	C
407848	A	T
407894	C	T
407900	C	T
408114	C	T
408652	T	G
408839	G	C
409084	A	G
409162	A	G
410876	G	GA
411011	A	G
411212	T	C
411440	C	G
411641	A	G
411920	G	A
413326	AT	A
413587	G	A
413664	G	T
413806	C	T
413824	A	G
413855	A	G
413856	A	G
413928	A	G
413976	A	T
414554	A	C
414882	A	T
414935	G	A
415213	C	T
415291	T	C
415351	C	T
415641	A	G
415881	C	T
415982	A	C
416055	T	A
416228	T	G
416229	G	A
416465	C	A
417085	A	C
417115	T	C
417147	T	C
417153	A	G
417363	T	C
417386	G	A
417498	A	C
417881	T	C
417891	G	A
418082	A	G

418481	C	T
419075	G	A
419363	A	G
419439	G	A
419445	A	G
419675	G	A
419777	T	G
420107	G	T
420139	A	G
420202	G	T
420398	A	T
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420746	C	T
420770	C	T
420837	C	T
420850	G	A
420863	T	C
420947	G	A
421003	G	A
421049	A	C
421167	A	C
421190	C	T
421315	A	ATGTTAATCAGATATATGGTAGAAAGCTCTAACTTTTTACCCT
421557	T	C
421569	T	C
421644	C	T
421952	T	A
422163	G	A
422550	T	C
422712	T	C
423142	C	G
423519	C	CA
423887	G	GT
423928	A	G
424199	A	AT
424353	G	A
424980	C	T
425197	C	T
425528	A	G
425592	G	A
425860	G	A
426359	C	G
426462	T	C
426769	G	A
426857	A	C
426874	G	A
426959	G	A
427007	T	C
427038	T	G
427337	G	A

427466	T	G
427487	C	T
428153	A	T
428446	G	A
428753	A	G
428777	G	T
429033	A	G
429119	C	T
429137	T	C
429170	G	A
429217	C	T
429386	C	T
429474	G	A
429620	G	A
429934	T	C
429986	C	A
429992	T	C
430115	G	A
430349	T	A
430535	A	G
430559	A	G
430855	T	C
430980	T	A
431100	G	A
431123	G	A
431146	G	T
431178	A	G
431348	G	A
431363	A	G
431411	T	G
431425	C	T
431453	A	T
431493	C	T
431541	GA	G
431577	A	C
431641	A	G
431751	T	C
431981	T	G
432125	T	TC
432566	G	GA
432774	G	A
434810	C	T
436050	T	A
436759	T	C
438417	A	T
438701	C	G
438853	T	TTC
438855	T	A
438869	A	C
439440	G	A

439470	T	C
441327	G	T
442396	G	A
442728	G	A
442750	A	G
442753	G	T
442954	A	G
443146	G	A
444191	G	A
444642	T	C
449932	C	T
464509	T	C
464515	A	G
464648	T	C
464739	C	T
464839	C	T
465495	T	C
465609	C	T
465663	A	G
465911	T	C
465946	C	T
465979	C	T
466015	A	G
466038	T	C
466054	A	G
466063	T	C
466141	T	A
466307	T	C
466393	A	G
466451	G	T
466501	G	A
466704	G	A
466709	A	G
466720	T	G
466738	C	T
466756	G	A
466833	T	C
466920	A	G
466994	C	T
467009	T	A
467012	G	A
467215	T	C
467465	T	C
467537	C	T
468077	A	G
468146	C	G
468149	G	C
468206	T	C
468276	G	A
468287	T	C

468333	C	T
505921	C	T
514762	T	G
540310	C	T
540325	A	G
540363	A	G
540434	C	T
540506	G	A
540610	C	T
540655	G	T
541308	T	C
541323	A	G
541950	C	T
541970	T	TA
542146	T	A
542186	G	A
542206	A	G
542213	G	A
542233	G	A
542335	C	T
542450	T	A
543135	G	A
543177	A	G
543300	A	G
543473	A	C
543496	C	T
543762	A	G
543804	G	C
543817	T	C
543899	T	C
544065	T	G
544098	G	A
544172	C	T
544229	C	T
544269	G	A
544296	C	A
544722	T	C
544982	A	G
545018	A	T
545150	G	C
545156	G	A
545172	TA	T
545274	G	T
545300	C	T
545524	A	T
545550	C	T
545719	T	C
545883	A	G
545978	A	C
545996	C	T

546491	G	A
546573	C	T
546599	T	C
546791	T	C
546905	A	G
547115	C	T
547150	C	T
547151	C	T
547161	C	CTTAT
547444	T	C
547651	A	T
547734	T	C
547945	T	G
548042	T	C
548045	A	G
548047	G	A
548073	G	C
548085	T	C
548215	A	G
548223	A	G
548291	G	T
548294	A	G
548299	T	C
548301	G	A
548307	A	C
548322	T	C
548375	T	C
548605	T	C
548704	T	A
548707	G	A
548708	C	T
548768	C	T
548816	C	T
548834	T	C
548840	A	G
548867	T	A
548908	T	C
548950	A	G
548974	T	A
548991	C	T
549049	G	A
549062	A	T
549119	A	G
549300	T	A
549329	C	T
549338	A	C
549603	G	A
549836	T	C
549844	A	G
549945	T	C

549994	C	T
550227	G	C
550482	C	T
550676	A	G
550922	C	T
550929	T	C
550961	C	T
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551092	C	T
551150	A	G
551201	C	A
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551291	C	G
551405	G	T
551459	C	G
551501	T	C
551727	C	T
551762	C	T
565747	T	C
565790	C	CA
567054	C	T
567145	G	A
567397	A	G
568423	TG	T
569044	T	C
569315	G	A
569988	G	C
570400	A	C
570548	C	T
570584	G	C
570644	T	C
570656	A	G
570660	T	A
570662	AAAT	A
571379	GC	G
573160	A	AT
575501	C	T
577340	T	TA
577519	T	TGTG
577526	G	GGT