

**Table S2 Constitutive SNPs found in the U regions in the wild-type mutation accumulation lines**

Line	Chrom.	Position	ORF	Gene	Ref.	Variant	Aa change	Sequence Ontology term
wt_ABCE100	chrII	15 101	YBL105C	<i>PKC1</i>	T	G	I866L	missense_variant
wt_ABCE100	chrIII	143 131	Intergenic	-	T	C	-	intergenic_variant
wt_ABCE100	chrIII	162 361	Intergenic	-	T	C	-	intergenic_variant
wt_ABCE100	chrIII	162 640	YCR024C-B	YCR024C-B	T	G	S76R	missense_variant
wt_ABCE100	chrIII	162 694	YCR024C-B	YCR024C-B	G	A	synonymous	synonymous_variant
wt_ABCE100	chrIII	163 059	YCR024C-A	<i>PMP1</i>	T	C	synonymous	synonymous_variant
wt_ABCE100	chrV	48 384	Intergenic	-	T	C	-	intergenic_variant
wt_ABCE100	chrV	154 531	YER001W	<i>MNN1</i>	T	A	S338T	missense_variant
wt_ABCE100	chrV	352 394	YER096W	<i>SHC1</i>	A	G	K233E	missense_variant
wt_ABCE100	chrV	517 529	Intergenic	-	T	C	-	intergenic_variant
wt_ABCE100	chrXIII	448 333	Intergenic	-	G	A	-	intergenic_variant
wt_ABCE100	chrXIII	680 936	YMR207C	<i>HFA1</i>	T	C	K877E	missense_variant
wt_ABCE100	chrXIII	680 940	YMR207C	<i>HFA1</i>	C	T	synonymous	synonymous_variant