

Table S1. Summary of results of all three large scale SLM screens.

		Strains with p-val<0.1		Strains with significant LogRatio		Strains with p-val<0.1 and significant LogRatio	
		Strain count	% of total*	Strain count	% of total*	Strain count	% of total*
1	Strains with elevated SLM at <i>CAN1 locus</i> (LogRatio SLM <i>CAN1</i> > 2)	4610	80,74	1250	21,89	748	13,10
2	Strains with elevated SLM at <i>URA3 locus</i> (LogRatio SLM <i>URA3</i> > 2)	2115	37,04	2670	46,76	998	17,48
3	Strains with elevated SLM at both <i>loci CAN1</i> and <i>URA3</i> [(LogRatio SLM <i>CAN1</i> > 2) AND (LogRatio SLM <i>URA3</i> > 2)]	<b>1694</b>	<b>29,67</b>	<b>757</b>	<b>13,26</b>	<b>158</b>	<b>2,77</b>
4	Strains which mate as <i>MATa</i> (LogRatio cross with <i>MATa</i> > 1)	5089	89,12	637	11,16	458	8,02
5	Strains which mate as <i>MATα</i> (LogRatio cross with <i>MATa</i> > 1)	4894	85,71	693	12,14	351	6,15
6	Strains which mate with <i>MATa</i> or <i>MATα</i> [(LogRatio cross with <i>MATa</i> > 1) OR (LogRatio cross with <i>MATa</i> > 1)]	4563	79,91	825	14,45	637	11,16
7	Strains with elevated SLM at <i>URA3 locus</i> , which mate with <i>MATα</i> or <i>MATa</i> , but with slight if any SLM at <i>CAN1 locus</i> , {[(LogRatio SLM <i>URA3</i> > 2) AND [(LogRatio cross with <i>MATα</i> > 1) OR (LogRatio cross with <i>MATa</i> > 1)] AND [LogRatio SLM <i>CAN1</i> < 2]}	<b>1442</b>	<b>25,25</b>	<b>264</b>	<b>4,62</b>	<b>74</b>	<b>1,30</b>
8	Strains with elevated SLM at <i>CAN1 locus</i> which mate with <i>MATα</i> or <i>MATa</i> , but slight if any SLM at <i>URA3 locus</i> , <b>might be haploid</b> {[(LogRatio SLM <i>CAN1</i> > 2) AND [(LogRatio cross with <i>MATα</i> > 1) OR (LogRatio cross with <i>MATa</i> > 1)] AND [LogRatio SLM <i>URA3</i> < 2]}	<b>1442</b>	<b>25,25</b>	<b>97</b>	<b>1,70</b>	<b>17</b>	<b>0,30</b>
9	Strains with elevated SLM at both <i>loci CAN1</i> and <i>URA3</i> , or with elevated SLM at <i>CAN1</i> or <i>URA3 loci</i> , which mate with <i>MATα</i> or <i>MATa</i> ; <b>potential mutator strains</b> (3 OR 7 OR 8)	<b>1694</b>	<b>29,67</b>	<b>1118</b>	<b>19,58</b>	<b>249</b>	<b>4,36</b>
10	Strains with significant signal in all experiments, <b>mutators</b> {[(LogRatio SLM <i>CAN1</i> > 2) AND (LogRatio SLM <i>URA3</i> > 2)] AND [(LogRatio cross with <i>MATα</i> > 1) OR (LogRatio cross with <i>MATa</i> > 1)]}	<b>1442</b>	<b>25,25</b>	<b>146</b>	<b>2,56</b>	<b>21</b>	<b>0,37</b>

\*) – Relative to total number of 5710 strains included in the analysis.