Supplemental files

Global analysis of furfural-induced genomic instability using yeast model

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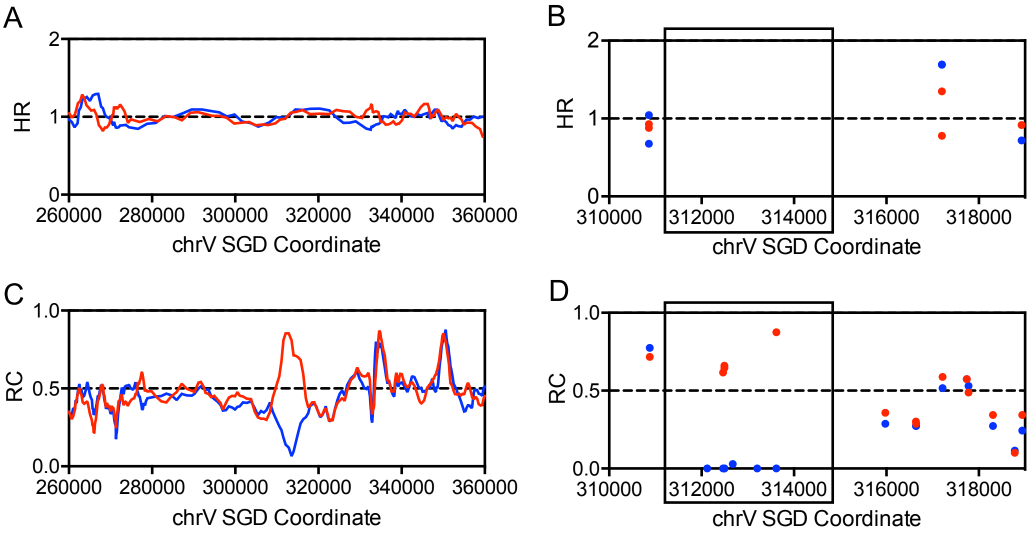

Fig. S1. A new gene conversion event detected by whole genome sequencing. Red and blue lines/points represent normalized hybridization ratio of genomic DNA to YJM789-derived and W303-1A-derived SNPs. (A) High- and (B) low-resolution depiction of the 260 kb to 360 kb region of chromosome V in QLF11 detected by SNP microarray. (C) High- and (D) low-resolution depiction of same region detected by whole genome sequencing.

Table S1 New LOH events detected in the 7 sequenced JSC25-derived isolates

Colony name	**NO.**	**Chr**	**Event type**	**Class[a]**	**Markers flanking transitions**		**Event window**	
					Left	**Right**	**Left**	**Right**
QLF2	1	II	CON	b1	18175	18513	18175	19557
					19218	19557		
	2	IV	CON	b1	117925	117968	117925	118488
					117968	118488		
	3	VII	CON	b1	648198	649406	648198	653157
					650619	653157		
	4	VIII	CON	b2	211729	212293	211729	212499
					212293	212499		
	5	XVI	CON	b1	377336	377648	377336	377765
					377648	377765		
QLF5	6	XIII	CON	b1	132751	132818	132751	152476
					152033	152476		
QLF8	7	IV	CON	b2	317793	320064	317793	321142
					320064	321142		
QLF11	8	V	CON	b1	310877	312122	310877	315976
					313619	315976		
	9	VII	CON	b1	20940	20941	20940	21081
					21077	21081		
	10	XIII	CON	b2	149883	150027	149883	150108
					150027	150108		
QLF18	11	VII	CON	b1	742148	747273	742148	751202
					751065	751202		
	12	X	CON	b1	196634	197018	196634	206537
					204641	206537		
QLF19	13	V	CON	b2	169761	171549	169761	173217
					171549	173217		
	14	VII	CON	b1	360816	361541	360816	364120
					362516	364120		
	15	VIII	CON	b2	369183	369483	369183	370842
					370707	370842		
	16	IX	CON	b2	405945	405973	405945	409106
					408244	409106		
	17	XI	CON	b2	634031	634150	634031	638417
					637017	638417		

[a] LOH classes were depicted in Dataset S4.

Table S2. Small DNA changes detected in 7 sequenced JSC25-derived isolates

No.	Isolates	chromosome	Location	Reference	Mutations
1	QLF5	chr2	328607	C	T
2	QLF5	chr2	529698	T	C
3	QLF5	chr7	127766	A	AT
4	QLF5	chr10	101417	A	G
5	QLF5	chr15	490308	T	C
6	QLF5	chr16	354387	C	A
7	QLF8	chr2	108598	G	A
8	QLF8	chr9	127612	A	C
9*	QLF8	chr11	356900	C	T
10	QLF8	chr15	408037	G	C
11	QLF11	chr2	100815	C	T
12*	QLF11	chr7	431798	T	C
13	QLF11	chr7	585208	T	C
14	QLF11	chr8	13021	C	T
15	QLF18	chr2	410711	C	T
16	QLF18	chr9	383036	G	A
17	QLF18	chr11	580901	G	A
18	QLF18	chr13	863678	C	T
19	QLF18	chr15	505667	C	T
20	QLF18	chr16	431727	C	A
21	QLF19	chr8	405975	C	A
22	QLF19	chr10	122651	T	C
23*	QLF19	chr13	35335	G	A
24*	QLF19	chr15	205706	T	C
25	QLF19	chr16	479612	G	A
26	QLF1	chr8	378808	G	A
27	QLF1	chr15	197651	T	A
28	QLF1	chr16	744245	C	T
29	QLF1	chr2	779167	GA	G
30*	QLF2	chr2	550748	G	A
31	QLF2	chr2	550749	G	A
32	QLF2	chr11	137099	T	C
33	QLF2	chr12	715373	T	C

*These SNVs were also verified by Sanger sequencing.