Supplementary Material

The paralogous genes *PDR18* and *SNQ2*, encoding multidrug resistance ABC transporters, derive from a recent duplication event, *PDR18* being specific to the *Saccharomyces* genus

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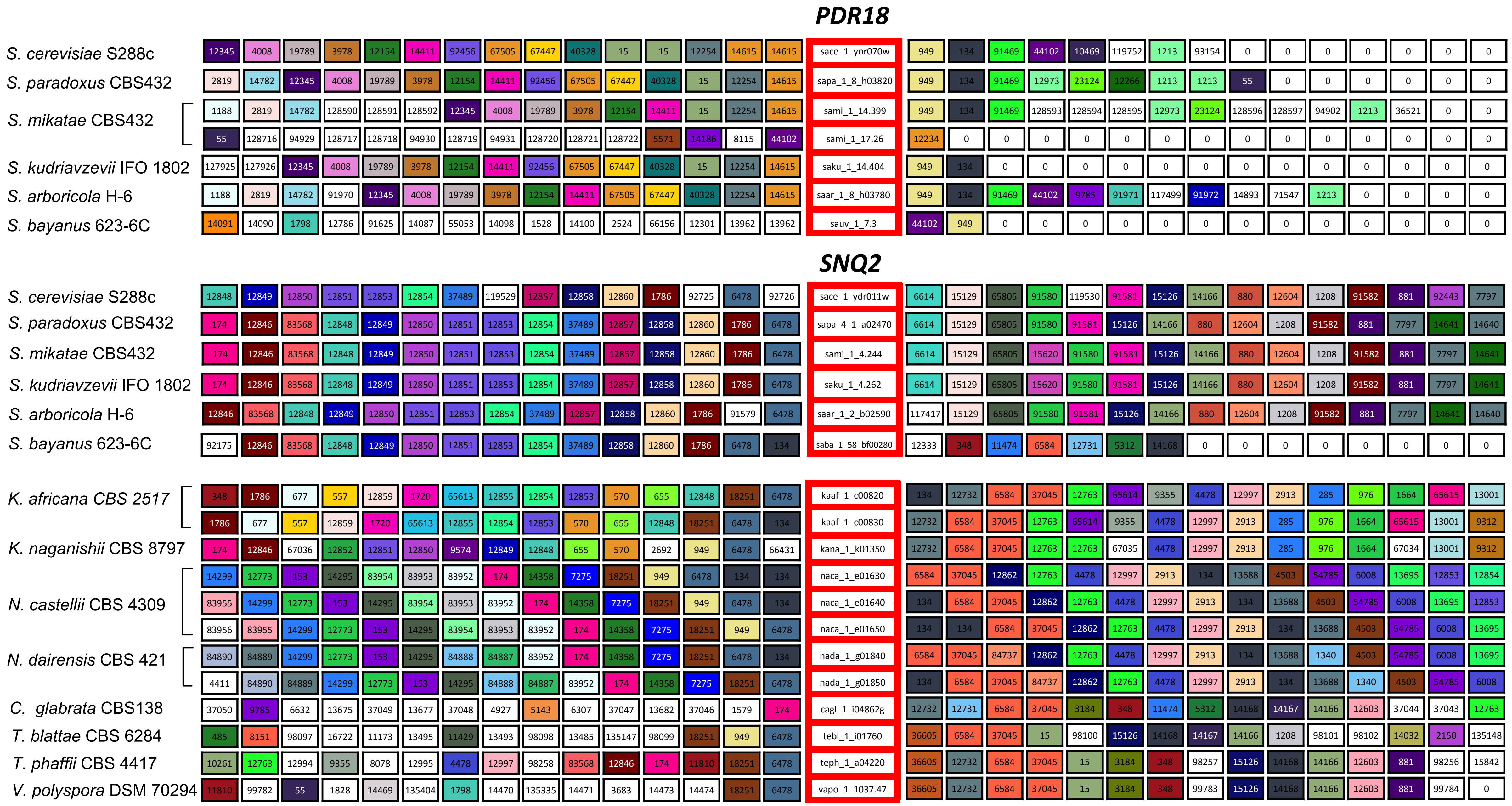
Supplementary figure S1. Gene neighborhood of the *ScPDR18* and *ScSNQ2* orthologs encoded in the Saccharomycetaceae species genomes examined. Central boxes represent Sc*PDR18/ScSNQ2* orthologs and the adjacent boxes represent gene neighbours. Homologous neighbours are highlighted in the same colour and identified with the same number. A white box represents genes with no homologous neighbours in the represented chromosome region and white boxes with a zero represent the end of the contig/chromosome.



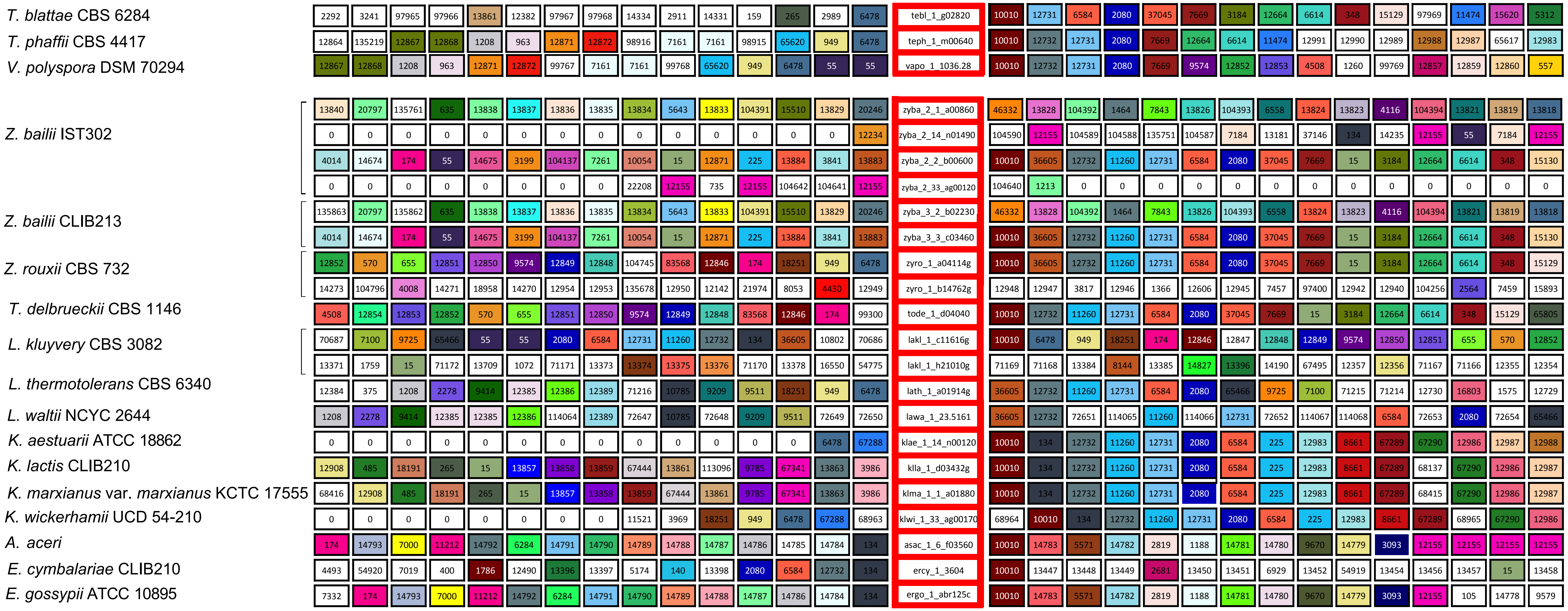
PDR18

S. cerevisiae S288c	12345	4008	19789	3978	12154	14411	92456	67505	67447	40328	15	15	12254	14615	14615	sace_1_ynr070w	949	134	91469	44102	10469	119752	1213	93154	0	0	0	0	0	0	0
S. paradoxus CBS432	2819	14782	12345	4008	19789	3978	12154	14411	92456	67505	67447	40328	15	12254	14615	sapa_1_8_h03820	949	134	91469	12973	23124	12266	1213	1213	55	0	0	0	0	0	0
S. mikatae CBS432	1188	2819	14782	128590	128591	128592	12345	4008	19789	3978	12154	14411	15	12254	14615	sami_1_14.399	949	134	91469	128593	128594	128595	12973	23124	128596	128597	94902	1213	36521	0	0
	55	128716	94929	128717	128718	94930	128719	94931	128720	128721	128722	5571	14186	8115	44102	sami_1_17.26	12234	0	0	0	0	0	0	0	0	0	0	0	0	0	0
S. kudriavzevii IFO 1802	127925	127926	12345	4008	19789	3978	12154	14411	92456	67505	67447	40328	15	12254	14615	saku_1_14.404	949	134	0	0	0	0	0	0	0	0	0	0	0	0	0
S. arboricola H-6	1188	2819	14782	91970	12345	4008	19789	3978	12154	14411	67505	67447	40328	12254	14615	saar_1_8_h03780	949	134	91469	44102	9785	91971	117499	91972	14893	71547	1213	0	0	0	0
S. bayanus 623-6C	14091	14090	1798	12786	91625	14087	55053	14098	1528	14100	2524	66156	12301	13962	13962	sauv_1_7.3	44102	949	0	0	0	0	0	0	0	0	0	0	0	0	0

SNQ2

S. cerevisiae S288c	12848	12849	12850	12851	12853	12854	37489	119529	12857	12858	12860	1786	92725	6478	92726	sace_1_ydr011w	6614	15129	65805	91580	119530	91581	15126	14166	880	12604	1208	91582	881	92443	7797
S. paradoxus CBS432	174	12846	83568	12848	12849	12850	12851	12853	12854	37489	12857	12858	12860	1786	6478	sapa_4_1_a02470	6614	15129	65805	91580	91581	15126	14166	880	12604	1208	91582	881	7797	14641	14640
S. mikatae CBS432	174	12846	83568	12848	12849	12850	12851	12853	12854	37489	12857	12858	12860	1786	6478	sami_1_4.244	6614	15129	65805	15620	91580	91581	15126	14166	880	12604	1208	91582	881	7797	14641
S. kudriavzevii IFO 1802	174	12846	83568	12848	12849	12850	12851	12853	12854	37489	12857	12858	12860	1786	6478	saku_1_4.262	6614	15129	65805	15620	91580	91581	15126	14166	880	12604	1208	91582	881	7797	14641
S. arboricola H-6	12846	83568	12848	12849	12850	12851	12853	12854	37489	12857	12858	12860	1786	91579	6478	saar_1_2_b02590	117417	15129	65805	91580	91581	15126	14166	880	12604	1208	91582	881	7797	14641	14640
S. bayanus 623-6C	92175	12846	83568	12848	12849	12850	12851	12853	12854	37489	12858	12860	1786	6478	134	saba_1_58_bf00280	12333	348	11474	6584	12731	5312	14168	0	0	0	0	0	0	0	0
K. africana CBS 2517	348	1786	677	557	12859	1720	65613	12855	12854	12853	570	655	12848	18251	6478	kaaf_1_c00820	134	12732	6584	37045	12763	65614	9355	4478	12997	2913	285	976	1664	65615	13001
	1786	677	557	12859	1720	65613	12855	12854	12853	570	655	12848	18251	6478	134	kaaf_1_c00830	12732	6584	37045	12763	65614	9355	4478	12997	2913	285	976	1664	65615	13001	9312
K. naganishii CBS 8797	174	12846	67036	12852	12851	12850	9574	12849	12848	655	570	2692	949	6478	66431	kana_1_k01350	12732	6584	37045	12763	12763	67035	4478	12997	2913	285	976	1664	67034	13001	9312
N. castellii CBS 4309	14299	12773	153	14295	83954	83953	83952	174	14358	7275	18251	949	6478	134	134	naca_1_e01630	6584	37045	12862	12763	4478	12997	2913	134	13688	4503	54785	6008	13695	12853	12854
	83955	14299	12773	153	14295	83954	83953	83952	174	14358	7275	18251	949	6478	134	naca_1_e01640	134	6584	37045	12862	12763	4478	12997	2913	134	13688	4503	54785	6008	13695	12853
	83956	83955	14299	12773	153	14295	83954	83953	83952	174	14358	7275	18251	949	6478	naca_1_e01650	134	134	6584	37045	12862	12763	4478	12997	2913	134	13688	4503	54785	6008	13695
N. dairensis CBS 421	84890	84889	14299	12773	153	14295	84888	84887	83952	174	14358	7275	18251	6478	134	nada_1_g01840	6584	37045	84737	12862	12763	4478	12997	2913	134	13688	1340	4503	54785	6008	13695
	4411	84890	84889	14299	12773	153	14295	84888	84887	83952	174	14358	7275	18251	6478	nada_1_g01850	134	6584	37045	84737	12862	12763	4478	12997	2913	134	13688	1340	4503	54785	6008
C. glabrata CBS138	37050	9785	6632	13675	37049	13677	37048	4927	5143	6307	37047	13682	37046	1579	174	cagl_1_i04862g	12732	12731	6584	37045	3184	348	11474	5312	14168	14167	14166	12603	37044	37043	12763
T. blattae CBS 6284	485	8151	98097	16722	11173	13495	11429	13493	98098	13485	135147	98099	18251	949	6478	tebl_1_i01760	36605	6584	37045	15	98100	15126	14168	14167	14166	1208	98101	98102	14032	2150	135148
T. phaffii CBS 4417	10261	12763	12994	9355	8078	12995	4478	12997	98258	83568	12846	174	11810	18251	6478	teph_1_a04220	36605	12732	6584	37045	15	3184	348	98257	15126	14168	14166	12603	881	98256	15842
V. polyspora DSM 70294	11810	99782	55	1828	14469	135404	1798	14470	135335	14471	3683	14473	14474	18251	6478	vapo_1_1037.47	36605	12732	6584	37045	15	3184	348	99783	15126	14168	14166	12603	881	99784	0

Supplementary figure S1 (continued)



T. blattae CBS 6284	2292	3241	97965	97966	13861	12382	97967	97968	14334	2911	14331	159	265	2989	6478	tebl_1_g02820	10010	12731	6584	2080	37045	7669	3184	12664	6614	348	15129	97969	11474	15620	5312
T. phaffii CBS 4417	12864	135219	12867	12868	1208	963	12871	12872	98916	7161	7161	98915	65620	949	6478	teph_1_m00640	10010	12732	12731	2080	7669	12664	6614	11474	12991	12990	12989	12988	12987	65617	12983
V. polyspora DSM 70294	12867	12868	1208	963	12871	12872	99767	7161	7161	99768	65620	949	6478	55	55	vapo_1_1036.28	10010	12732	12731	2080	7669	9574	12852	12853	4508	1260	99769	12857	12859	12860	557
Z. bailii IST302	13840	20797	135761	635	13838	13837	13836	13835	13834	5643	13833	104391	15510	13829	20246	zyba_2_1_a00860	46332	13828	104392	1464	7843	13826	104393	6558	13824	13823	4116	104394	13821	13819	13818
	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12234	zyba_2_14_n01490	104590	12155	104589	104588	135751	104587	7184	13181	37146	134	14235	12155	55	7184	12155
	4014	14674	174	55	14675	3199	104137	7261	10054	15	12871	225	13884	3841	13883	zyba_2_2_b00600	10010	36605	12732	11260	12731	6584	2080	37045	7669	15	3184	12664	6614	348	15130
	0	0	0	0	0	0	0	0	22208	12155	735	12155	104642	104641	12155	zyba_2_33_ag00120	104640	1213	0	0	0	0	0	0	0	0	0	0	0	0	0
Z. bailii CLIB213	135863	20797	135862	635	13838	13837	13836	13835	13834	5643	13833	104391	15510	13829	20246	zyba_3_2_b02230	46332	13828	104392	1464	7843	13826	104393	6558	13824	13823	4116	104394	13821	13819	13818
	4014	14674	174	55	14675	3199	104137	7261	10054	15	12871	225	13884	3841	13883	zyba_3_3_c03460	10010	36605	12732	11260	12731	6584	2080	37045	7669	15	3184	12664	6614	348	15130
Z. rouxii CBS 732	12852	570	655	12851	12850	9574	12849	12848	104745	83568	12846	174	18251	949	6478	zyro_1_a04114g	10010	36605	12732	11260	12731	6584	2080	37045	7669	15	3184	12664	6614	348	15129
	14273	104796	4008	14271	18958	14270	12954	12953	135678	12950	12142	21974	8053	4430	12949	zyro_1_b14762g	12948	12947	3817	12946	1366	12606	12945	7457	97400	12942	12940	104256	2564	7459	15893
T. delbrueckii CBS 1146	4508	12854	12853	12852	570	655	12851	12850	9574	12849	12848	83568	12846	174	99300	tode_1_d04040	10010	12732	11260	12731	6584	2080	37045	7669	15	3184	12664	6614	348	15129	65805
L. kluyvery CBS 3082	70687	7100	9725	65466	55	55	2080	6584	12731	11260	12732	134	36605	10802	70686	lakl_1_c11616g	10010	6478	949	18251	174	12846	12847	12848	12849	9574	12850	12851	655	570	12852
	13371	1759	15	71172	13709	1072	71171	13373	13374	13375	13376	71170	13378	16550	54775	lakl_1_h21010g	71169	71168	13384	8144	13385	14827	13396	14190	67495	12357	12356	71167	71166	12355	12354
L. thermotolerans CBS 6340	12384	375	1208	2278	9414	12385	12386	12389	71216	10785	9209	9511	18251	949	6478	lath_1_a01914g	36605	12732	11260	12731	6584	2080	65466	9725	7100	71215	71214	12730	16803	1575	12729
L. waltii NCYC 2644	1208	2278	9414	12385	12385	12386	114064	12389	72647	10785	72648	9209	9511	72649	72650	lawa_1_23.5161	36605	12732	72651	114065	11260	114066	12731	72652	114067	114068	6584	72653	2080	72654	65466
K. aestuarii ATCC 18862	0	0	0	0	0	0	0	0	0	0	0	0	0	6478	67288	klae_1_14_n00120	10010	134	12732	11260	12731	2080	6584	225	12983	8661	67289	67290	12986	12987	12988
K. lactis CLIB210	12908	485	18191	265	15	13857	13858	13859	67444	13861	113096	9785	67341	13863	3986	klla_1_d03432g	10010	134	12732	11260	12731	2080	6584	225	12983	8661	67289	68137	67290	12986	12987
K. marxianus var. *marxianus* KCTC 17555	68416	12908	485	18191	265	15	13857	13858	13859	67444	13861	9785	67341	13863	3986	klma_1_1_a01880	10010	134	12732	11260	12731	2080	6584	225	12983	8661	67289	68415	67290	12986	12987
K. wickerhamii UCD 54-210	0	0	0	0	0	0	0	0	11521	3969	18251	949	6478	67288	68963	klwi_1_33_ag00170	68964	10010	134	12732	11260	12731	2080	6584	225	12983	8661	67289	68965	67290	12986
A. aceri	174	14793	7000	11212	14792	6284	14791	14790	14789	14788	14787	14786	14785	14784	134	asac_1_6_f03560	10010	14783	5571	14782	2819	1188	14781	14780	9670	14779	3093	12155	12155	12155	12155
E. cymbalariae CLIB210	4493	54920	7019	400	1786	12490	13396	13397	5174	140	13398	2080	6584	12732	134	ercy_1_3604	10010	13447	13448	13449	2681	13450	13451	6929	13452	54919	13454	13456	13457	15	13458
E. gossypii ATCC 10895	7332	174	14793	7000	11212	14792	6284	14791	14790	14789	14788	14787	14786	14784	134	ergo_1_abr125c	10010	14783	5571	14782	2819	1188	14781	14780	9670	14779	3093	12155	105	14778	9579

Supplementary figure S2: Phylogenetic tree of the Pdr18 and Snq2 orthologs from the left sub-lineage of figure 4, encoded in the genomes of the post-WGD species. (A) Radial phylogram showing the amino acid sequence similarity distances between the protein homologs of Pdr18 and Snq2 under study **(B)** Cladogram showing the tree topology.