

Synthetic two-species allodiploid and three-species allotetraploid *Saccharomyces* hybrids with euploid (complete) parental subgenomes

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Table 1S: Restriction patterns generated by virtual digestion of the amplified fragments with restriction endonucleases

Marker/gene	Restriction endonuclease	Band pattern (bp)	<i>S. cerevisiae</i>	<i>S. kudriavzevii</i>	<i>S. uvarum</i>
<i>AFG1</i>	<i>RsaI</i>	372, 364, 80	502, 173, 130	251, 194, 131, 121, 119	
<i>ATF1</i>	<i>HaeIII</i>	635, 235, 40	635, 275	435, 275, 200	
<i>BCK2 (Sc/Su)</i>	<i>RsaI</i>	274, 176, 131, 128, 127, 109, 6		590, 361	
<i>BCK2 (Sk)</i>			425, 331, 163, 70		
<i>BUD14</i>	<i>MspI</i>	475, 310, 230, 95, 40	720, 310, 110	875, 160, 130	
<i>CAT8</i>	<i>MspI</i>	690, 50	450, 205, 80	280, 250, 200	
<i>CDC27</i>	<i>TaqI</i>	498, 312, 83	677, 128, 85, 72	657, 108, 105, 92	
<i>CHS2</i>	<i>TaqI</i>	452, 428, 223	710, 223, 170	325, 258, 223, 127, 105, 65	
<i>CYR1</i>	<i>HindIII</i>	385, 155	540	385, 155	
<i>DAL4</i>	<i>EcoRV</i>	390, 265, 260, 80	390, 280, 260, 170, 80	890, 390, 330, 280, 180	
<i>ECM25</i>	<i>RsaI</i>	337, 319	657, 172	477, 172, 7	
<i>FUS1</i>	<i>TaqI</i>	342, 269, 262	473, 276, 43	371, 336	
<i>GND1(Sc/Su)</i>	<i>HinfI</i>	640, 266		435, 210, 205	
<i>GND1(Sk)</i>	<i>HinfI</i>		359, 210, 205, 136, 56		
<i>GND2</i>	<i>HaeIII</i>	581, 247, 50	528, 272, 50	581, 290,	
<i>GSY1</i>	<i>TaqI</i>	292, 237, 221, 17	392, 358, 17	441, 309, 17	
<i>HCM1</i>	<i>MspI</i>	890, 380, 85	500, 430, 400	735, 680	
<i>KIN82</i>	<i>HinfI</i>	495, 400, 40	400, 300, 135	700, 130, 95	
<i>LEM3</i>	<i>HaeIII</i>	563, 229, 186, 96, 77	563, 229, 96, 77, 48	818, 74, 65, 21, 10	
<i>LEU3 (Sc/Su)</i>	<i>MseI</i>	276, 193, 115, 96, 95, 50, 45, 14, 1		422, 391, 64, 7	
<i>LEU3 (Sk)</i>			289, 276, 95, 66, 63, 52, 45, 1		
<i>LRO1 (Sc/Su)</i>	<i>RsaI</i>	553, 336, 82, 58, 11		282, 271, 216, 80, 62, 9	
<i>LRO1 (Sk)</i>			618, 282, 99, 60, 13		
<i>MAG2</i>	<i>MspI</i>	480, 400, 110	600, 225, 175	835, 175	
<i>MET2</i>	<i>SacI</i>	410, 170	410, 170	580	
<i>MNT2</i>	<i>MspI</i>	838, 135	429, 356, 188	543, 279, 148	
<i>OCA5 (Sc/Su)</i>	<i>MseI</i>	743	405, 331	627, 123	
<i>OCA5 (Sk)</i>			462, 405	759, 123	
<i>OPY1</i>	<i>HaeIII</i>	750	505, 245	405, 345	
<i>PRP4 (Sc/Su)</i>	<i>HaeIII</i>	702, 153, 54		469, 386, 54	
<i>PRP4 (Sk)</i>			262, 247, 208, 139, 54		
<i>PTR2</i>	<i>HaeIII</i>	487, 481, 309, 39	448, 270, 232, 216, 126, 116, 33	498, 448, 171, 120, 36, 33	
<i>RDR1</i>	<i>HaeIII</i>	569, 133, 56, 16	441, 321	489, 266, 16	
<i>SAM3</i>	<i>HaeIII</i>	452, 258, 143, 125, 55, 43	703, 199, 180, 43	1100, 700, 400	
<i>SNF1</i>	<i>MseI</i>	291, 237, 219, 47, 7	582, 62	308, 226, 201	

<i>STE2</i>	<i>HaeIII</i>	687, 262	661, 168, 148	511, 262
<i>STE6 (Sc)</i>	<i>HaeIII</i>	1007, 57		
<i>STE6 (Sk)</i>	<i>HaeIII</i>		438, 314, 262, 24	
<i>STE6 (Su)</i>	<i>HaeIII</i>			582, 399
<i>SWH1</i>	<i>MseI</i>	578, 348, 30	484, 233, 55	533, 228, 123, 69
<i>TDA1 (Sc/Sk)</i>	<i>HaeIII</i>	708, 271, 153, 27		516, 451, 192
<i>TDA1 (Su)</i>			708, 462, 27	
<i>UBP7</i>	<i>HinfI</i>	810, 150	700, 150, 110	405, 405, 160, 76
<i>UGA3 (Sc/Su)</i>	<i>RsaI</i>	438, 322		601, 162
<i>UGA3 (Sk)</i>		458, 251, 103	788, 24	354, 257, 204