

Table S1 PCR-RFLP analysis of 10 colonies isolates from the different hybrids obtained by sporulation

	<i>APM3</i> (II)	ITS (XII)	<i>UGA3</i> (IV)	<i>GSY1</i> (VI)	<i>BRE5</i> (XIV)
H3 D1	U	U	U	U	U
H3 D2	U	U	U	U	U
H3 D3	U	U	U	U	U
H3 D4	U	U	U	U	U
H3 F2	U	U	U	U	U
H3 F3	U	U	U	U	U
H3 G6	U	U	U	U	U
H3 G7	U	U	U	U	U
H3 G8	U	U	U	U	U
H3 G9	U	U	U	U	U
H4 A6	U	U	U	U	U
H4 A7	U	U	U	U	U
H4 A8	U	U	U	U	U
H4 A9	U	U	U	U	U
H4 I2	U	U	U	U	U
H4 I3	U	U	U	U	U
H4 I4	U	U	U	U	U
H4 I6	U	U	U	U	U
H4 I7	U	U	U	U	U
H4 I8	U	U	U	U	U
H14 A6	CU	CU			
H14 A7	CU	CU			
H14 A8	C	C	C	CU	
H14 A9	C	CU			
H14 B1	C	C	C	CU	
H14 C1	C	CU			
H14 D6	C	C	C	C	C
H14 D7	C	C	C	CU	
H14 D8	CU	CU			

Note: The isolates that remained being hybrids are marked in bold. U means that at this genomic region both alleles show *S. uvarum* pattern, C *S. cerevisiae* pattern and CU both species patterns.