

Supplementary Material

- 1 **A novel multivariate approach to phenotyping and association**
 2 **mapping of multi-locus gametophytic self-incompatibility reveals**
 3 ***S*, *Z* and other loci in a perennial ryegrass (*Poaceae*) population**

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7 **Supplementary Data**

8 **Supplementary Figures and Tables**

9 Supplementary Table 1. Correlation coefficients (*R*) of within and between half-sib family
 10 pollinations made in 2013 and 2015.

		♂				
		h-sib 1	h-sib 2	h-sib 3	h-sib 4	
13	h-sib 1					0.6
14		0.60	0.42	0.74	0.52	7
15	h-sib 2					0.6
16		0.43	0.64	0.54	0.63	9
16	h-sib 3					0.7
17		0.63	0.65	0.83	0.63	3

18 All correlations $P < 0.001$ (degrees of freedom ranging between 98 and 223)

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20Supplementary Table 2. Correlation coefficients (*R*) pollinations made of each genotype as female or male parent with other members of the 21population.

Genotyp							Genotype						
e	♀	df	P	♂	df	P		♀	df	P	♂	df	P
5	0.80	40	<.001	0.53	48	<.001	222	0.82	41	<.001	0.68	36	<.001
12	0.66	37	<.001	0.96	48	<.001	223	0.74	35	<.001	0.56	49	<.001
27	0.57	33	<.001	0.58	34	<.001	228	0.92	40	<.001	0.66	44	<.001
33	0.45	41	<.01	0.69	22	<.001	231	0.67	36	<.001	0.71	14	<.01
39	0.62	36	<.001	0.67	47	<.001	233	0.67	31	<.001	0.89	24	<.001
42	0.74	41	<.001	0.41	38	<.05	235	0.95	36	<.001	0.89	46	<.001
43	0.72	33	<.001	0.30	43	<.05	238	0.58	32	<.001	0.50	45	<.001
45	0.70	35	<.001	0.86	32	<.001	294	0.60	27	<.001	0.79	13	<.01
46	0.78	45	<.001	0.67	34	<.001	295	0.48	35	<.01	0.72	44	<.001
47	0.46	38	<.01	0.62	12	<.05	298	0.81	34	<.001	0.48	46	<.001
115	0.85	41	<.001	0.79	42	<.001	301	0.63	38	<.001	0.88	33	<.001
123	0.65	36	<.001	0.57	38	<.001	307	0.67	41	<.001	0.75	33	<.001
131	0.89	30	<.001	0.63	34	<.001	314	0.60	42	<.001	0.63	30	<.001
132	0.79	43	<.001	0.89	48	<.001	318	0.69	37	<.001	0.58	18	<.05
133	0.67	40	<.001	0.61	49	<.001	320	0.37	40	<.05	0.56	45	<.001
134	0.84	36	<.001	0.42	33	<.01	323	0.00	27	NS	0.91	41	<.001
136	0.50	35	<.01	0.76	34	<.001	329	0.83	40	<.001	0.71	47	<.001
138	0.69	45	<.001	0.90	46	<.001	331	0.90	39	<.001	0.69	42	<.001
143	0.64	27	<.001	0.70	48	<.001	332	0.80	37	<.001	0.69	46	<.001
145	0.53	42	<.001	0.83	27	<.001	334	0.45	26	<.05	0.15	15	NS
148	0.56	46	<.001	0.51	46	<.001	337	0.53	34	<.001	0.62	34	<.001
204	0.96	35	<.001	0.79	31	<.001	342	0.66	31	<.001	0.70	18	<.01
213	0.78	38	<.001	0.82	45	<.001	345	0.82	31	<.001	0.58	39	<.001
216	0.69	43	<.001	0.93	34	<.001	347	0.82	40	<.001	0.68	41	<.001
218	0.66	34	<.001	0.84	32	<.001	348	0.74	30	<.001	0.73	40	<.001

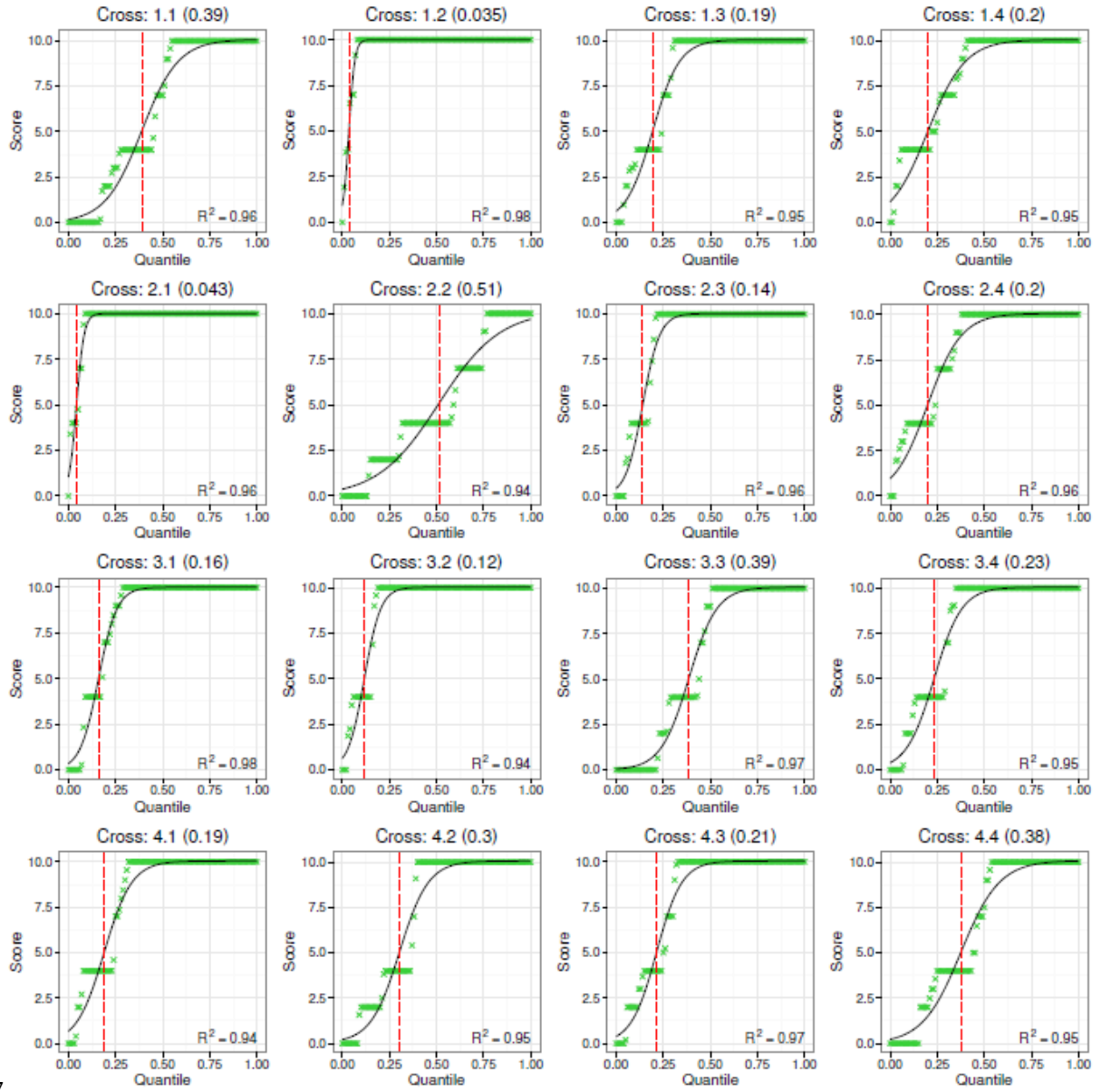
22Supplementary Table 3 Summary statistics for numbers and density of SNP markers mapped
 23using the integrated map of Blackmore et al. 2015).

Linkage group	Length (cM)	Number of markers	Mapped marker density (n/cM)	
			Number of markers	Mapped marker density (n/cM)
			2013	2015
1	87.6	236	2.69	237
2	127.0	251	1.98	251
3	99.2	257	2.59	257
4	131.2	330	2.52	331
5	89.2	153	1.72	153
6	114.0	267	2.34	267
7	106.0	278	2.62	278
Total mapped	754.2	1772	2.35	1774
Unmapped			689	690
Total mapped and unmapped			2461	2464

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26Supplementary Figures



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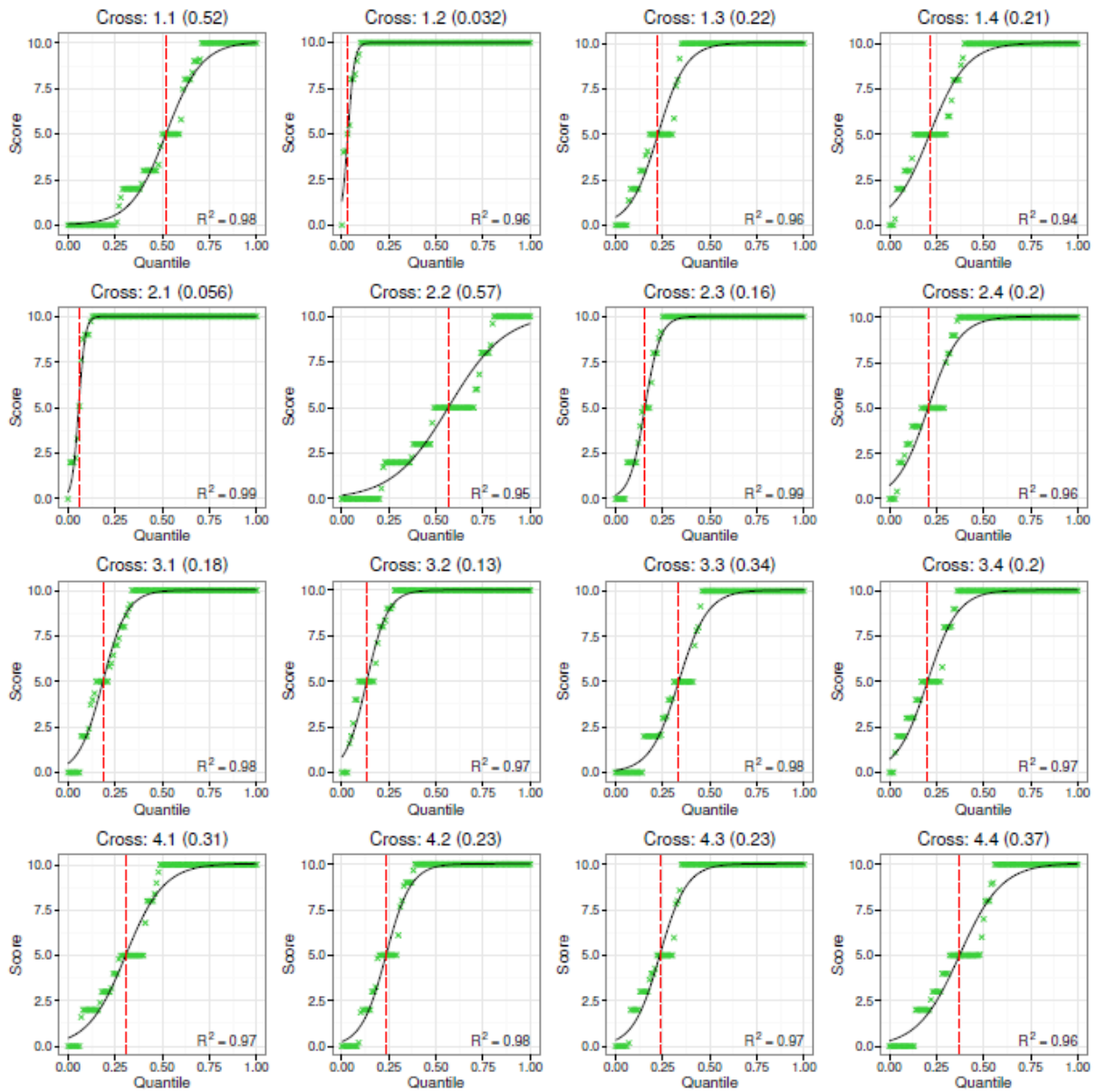
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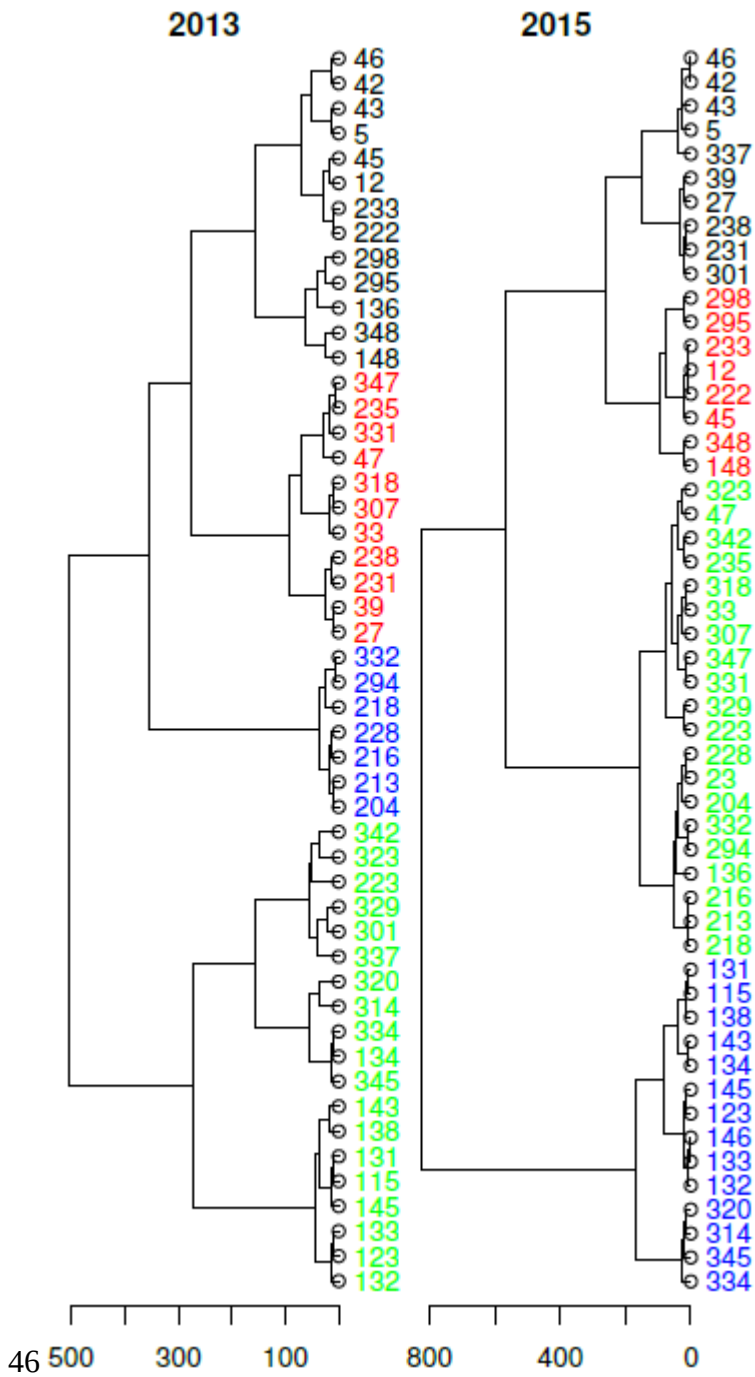
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49**Supplementary Figure 1.** 2013 cross-compatibility quantiles within and between half-sib families.
50Compatibility score (1-10, y-axis) is plotted against quantile (every 0.01, x-axis). Cross numbers in
51each graph title are given as two numbers (x.y), the first designating the maternal half-sib family and
52the second, the paternal half-sib family and is then followed by the SI_{50} score in brackets. The
53quantiles are shown as green crosses and the predictions of the modelling as a solid black line. The
54 SI_{50} is shown as a vertical red dashed line. R^2 for the model is shown in the lower right corner of each
55graph.

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57**Supplementary Figure 2.** 2015 cross-compatibility quantiles within and between half-sib families.
58Compatibility score (1-10, y-axis) is plotted against quantile (every 0.01, x-axis). Cross numbers in
59each graph title are given as two numbers (x.y), the first designating the maternal half-sib family and
60the second, the paternal half-sib family and is then followed by the SI_{50} score in brackets. The
61quantiles are shown as green crosses and the predictions of the modelling as a solid black line. The
62 SI_{50} is shown as a vertical red dashed line. R^2 for the model is shown in the lower right corner of each
63graph.

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65**Supplementary Figure 3.** Dendrograms showing principal components for 2013 and 2015 of
66cross-compatibility scores. The genotype numbers (5-47 = half-sib family 1; 115-148 = half-sib
67family 2; 204-298 = half-sib family 3; 301-348 = half-sib family 4) are coloured based on hierarchical
68clustering into four groups using the Ward method.

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