

S6 Table. Segregation of the homoeolog types at the Ibit12692 in the F2 population from self-crossing of the “AAABBBC” parental genotype.

Genotypes	Observed Counts	^D Expected Counts (Freq.)	^R Expected Counts (Freq.)	Notes
AAAAAA	0	0	0 (1/30625)	Multinomial goodness of fit test (Monte Carlo method) p-value: <0.0001 At 5% Significance level, and with 10000 simulations:
AAAAAB ¹	4	0	0(18/30625)	
AAAABB ²	9	15 (0.0278)	2(99/30625)	
AAAAAC	1	0	0(6/30625)	
AAAABC ¹	7	0	1(72/30625)	
AAABBC ²	36	30(0.0556)	4(222/30625)	
AAABBB ²	37	30(0.0556)	3(164/30625)	
AABBBBC ²	47	30(0.0556)	4(222/30625)	
AABBBB ²	25	15 (0.0278)	2(99/30625)	
ABBBBC ¹	17	0	1(72/30625)	
ABBBBB ¹	4	0	0(18/30625)	
AAAACC	2	0	0(9/30625)	
AAABCC ¹	6	0	1(54/30625)	
AABBC ²	24	15 (0.0278)	2(99/30625)	
ABBCC ¹	12	0	1(54/30625)	
BBBCC	4	0	0(9/30625)	
BBBBBC	3	0	0(6/30625)	
BBBBBB	0	0	0(1/30625)	
AAAAAAB	0	0	0(24/30625)	
AAAAAAC	0	0	0(8/30625)	
AAAAAB ¹	3	0	5(288/30625)	
AAAAABC ¹	2	0	4(216/30625)	
AAAABBB ²	19	30(0.0556)	16(888/30625)	
AAAABBC ²	21	30(0.0556)	21(1224/30625)	
AAABBB ²	54	89(0.1667)	37(2104/30625)	
AAABBBB ²	22	30(0.0556)	16(888/30625)	
AABBBBC ²	32	30(0.0556)	21(1224/30625)	
AABBBBB	3	0	5(288/30625)	
ABBBBBBC	8	0	4(216/30625)	
AAAAACC	0	0	0(24/30625)	
AAAABCC ¹	6	0	5(288/30625)	
AAABBC ²	22	30(0.0556)	16(888/30625)	
AABBBCC ²	18	30(0.0556)	16(888/30625)	
ABBBCC ¹	6	0	5(288/30625)	
BBBBBCC	0	0	0(24/30625)	
ABBBBBB	1	0	0(24/30625)	
BBBBBBC	0	0	0(8/30625)	
AAAAAABB	2	0	3(144/30625)	
AAAAAABC	0	0	2(96/30625)	
AAAAABBB	3	0	15(864/30625)	
AAAAABBC	0	0	20 (1152/30625)	
AAAABBBB ²	6	15 (0.0278)	28(1584/30625)	
AAAABBBBC ²	11	30(0.0556)	62(3552/30625)	
AAABBBBC ²	15	30(0.0556)	62(3552/30625)	
AAAAAAC	0	0	0(16/30625)	
AAAAABCC	2	0	5(288/30625)	
AAAABBC ²	8	15 (0.0278)	28(1584/30625)	
AAABBBCC ²	14	30(0.0556)	46(2624/30625)	
AAABBBBB ¹	1	0	15(864/30625)	
AABBBBBBC ¹	1	0	20(1152/30625)	
AABBBBCC ²	12	15 (0.0278)	28(1584/30625)	
AABBBBBB	4	0	3(144/30625)	
ABBBBBBC ¹	0	0	2 (96/30625)	
ABBBBCC ¹	1	0	5(288/30625)	
BBBBBBCC	0	0	0(16/30625)	
Unexpected				
AABBBBBCC	1	0	0	Carrying two pairs of “C” from either IDR, or partially unreduced gamete
AAABBBCCC	1	0	0	
AAAABBBCCC	1	0	0	
AAAAABBBBC	1	0	0	Aneuploidy/Dysploidy
AAAAABBBCC	2	0	0	
AAABBBBBBC	1	0	0	
AAABBBBCC	1	0	0	
AAABB	1	0	0	
AABBB	3	0	0	
AABBC	1	0	0	
BBBCC	1	0	0	

^R: Under a random pairing of the homoeolog-types in bivalent configuration.^D: Under autosyndesis (AA, BB pairing) and allosyndesis (AB or AC) in bivalent configuration and random distribution of the unpaired one.¹: Involving one gametic genotype that may be derived from preferential pairing.²: Involving one gametic genotype that were derived from preferential pairing.

IDR: Identical-by Double-Reduction.