**Table S1: Fit of *A. arenosa* SNPs with simulated allo- and autotetraploid data**

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| --- | --- | --- | --- |
|  | χ2 Di (td =1.0) | χ2 Di (td = 0.2) | χ2 Tetr |
| Simplex (AAAa) | 2155.57 \*\*\* | 63.46 \* | 21.33 (ns) |
| Duplex (AAaa) | 61.26 \* | 27.31 (ns) | 10.49 (ns) |
| Triplex (Aaaa) | 12891.03 \*\*\* | 666.12 \*\*\* | 21.62 (ns) |
| Homozygote (aaaa) | 8166.50 \*\*\* | 178.28 \*\*\* | 37.87 (ns) |

Table S1 notes: χ2 values from comparing our actual data with genotype ratios in simulated datasets assuming complete and long-term disomic (allotetraploid) inheritance (Di; td =1.0), partial or recent allotetraploid inheritance (td = 0.2), or fully tetrasomic inheritance (Tetr); Significance: (ns) = not significant, \* = *p*<0.05, \*\* = *p*<0.01, \*\*\* = *p*<0.001; χ2 test, 46 df.