Supplementary table 1. Number of SNPs in various locations for each sample

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | downstream | exonic | intergenic | intronic | splicing | upstream | upstream;downstream | 3′ UTR | 5′ UTR |
| D-pool | 221,265 | 475,383 | 1,329,736 | 350,208 | 1,783 | 258,956 | 56,840 | 46,461 | 30,316 |
| Dwarf | 167,236 | 357,693 | 970,382 | 261,987 | 1,321 | 195,168 | 42,841 | 34,755 | 22,692 |
| Tall | 165,384 | 336,831 | 1,047,012 | 254,205 | 1,272 | 194,209 | 41,135 | 33,362 | 21,693 |
| T-pool | 221,986 | 476,055 | 1,336,930 | 351,450 | 1,778 | 259,910 | 57,049 | 46,715 | 30,408 |

Tall: tall parental line G184-189; Dwarf: dwarf parental line YA2016-12; T-pool: bulked DNA pool for extreme tall individuals from the F2 population; D-pool: bulked DNA pool for extreme dwarf individuals from the F2 population.

Downstream: variant overlaps 1-kb region downstream of transcription end site; exonic: variant overlaps a coding exon; intergenic: variant is in intergenic region; intronic: variant overlaps an intron; splicing: variant is within 2-bp of a splicing junction; upstream: variant overlaps 1-kb region upstream of transcription start site; 3′ UTR: variant overlaps a 3' untranslated region; 5’ UTR: variant overlaps a 5' untranslated region.