Supplementary table 3. Number of InDels in various locations for each sample

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | downstream | exonic | intergenic | intronic | splicing | upstream | upstream;downstream | 3′ UTR | 5′ UTR |
| D-pool | 57,651 | 19,765 | 194,257 | 112,988 | 1,504 | 76,010 | 19,346 | 18,145 | 13,797 |
| dwarf | 44,487 | 14,977 | 149,246 | 85,605 | 1,174 | 58,778 | 14,893 | 13,747 | 10,438 |
| tall | 43,701 | 14,020 | 153,912 | 83,905 | 1,105 | 57,843 | 14,235 | 13,262 | 10,189 |
| T-pool | 57,725 | 19,790 | 193,801 | 113,279 | 1,514 | 76,215 | 19,473 | 18,225 | 13,889 |

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

Downstream: variant overlaps 1-kb region downstream of transcription end site (use -neargene to change this); 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 (use -splicing\_threshold to change this); 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.