Supplementary table 2. Statistics of different functions of SNPs in each sample

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| --- | --- | --- | --- | --- |
| Sample | nonsynonymous SNV | stopgain | stoploss | synonymous SNV |
| D-pool | 185,083 | 2,261 | 687 | 287,352 |
| Dwarf | 138,597 | 1,661 | 509 | 216,926 |
| Tall | 132,330 | 1,610 | 513 | 202,378 |
| T-pool | 185,421 | 2,278 | 692 | 287,664 |

Tall: tall parental G184-189; Dwarf: dwarf parental 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.

Nonsynonymous SNV: a single nucleotide variant that cause an amino acid change; stopgain: a nonsynonymous SNV, frameshift insertion/deletion, nonframeshift insertion/deletion or block substitution that lead to the immediate creation of stop codon at the variant site. For frameshift mutations, the creation of a stop codon downstream of the variant will not be counted as "stopgain"; stoploss: a nonsynonymous SNV, frameshift insertion/deletion, nonframeshift insertion/deletion or block substitution that leads to the immediate elimination of a stop codon at the variant site; synonymous SNV: a single nucleotide variant that does not cause an amino acid change.