



**Supplementary figure S1. The mean level of linkage disequilibrium in 470 BLG accessions.** The mean linkage disequilibrium (LD) was estimated using all pairs of loci located in a window of 100 SNPs. The X-axis indicates the distance between marker pairs and the Y-axis indicates LD level. The red line denotes mean  $r^2$ , and the black line represents the half of maximum value.

**Supplementary table S1.** Hundred seed weight and missense mutation from GRIN database and publicly available genome sequences.

GRIN accession	Seed weight	Missense mutation <sup>1</sup>	Type
PI372418	12.9	G110S	cultivar
PI404198B	8.5	G110S	cultivar
PI437321	8.7	G110S	cultivar
PI437485	14.1	G110S	cultivar
PI437654	10.1	G110S	cultivar
PI437655	11.7	G110S	cultivar
PI437690	7.5	G110S	cultivar
PI437793	14.6	G110S	cultivar
PI437944	8.4	G110S	cultivar
PI438309	9.6	G110S	cultivar
PI506862	15.0	G110S	cultivar
PI548316	15.6	G110S	cultivar
PI548402	7.8	G110S	cultivar
PI567230	4.8	G110S	cultivar
PI567298	8.9	G110S	cultivar
PI567307	6.7	G110S	cultivar
PI567346	8.0	G110S	cultivar
PI567353	10.5	G110S	cultivar
PI567361	10.8	G110S	cultivar
PI567407	6.1	G110S	cultivar
PI567416	10.4	G110S	cultivar
PI567426	13.4	G110S	cultivar
PI567428	7.7	G110S	cultivar
PI567439	12.4	G110S	cultivar
PI597476	12.8	G110S	cultivar
PI567336B	4.6	G110S	landrace
PI567352A	10.6	G110S	landrace
PI567410B	15.0	G110S	landrace
PI567516C	4.4	G110S	landrace
PI587588A	10.3	G110S	landrace
PI587804	9.9	G110S	landrace
PI592937	12.2	G110S	landrace
PI594880	8.5	G110S	landrace
PI597478B	12.0	G110S	landrace
PI602991	15.1	G110S	landrace
PI603420	6.6	G110S	landrace
PI603488	12.1	G110S	landrace
PI603495B	12.8	G110S	landrace
PI603555	16.5	G110S	landrace
PI603556	10.0	G110S	landrace

PI062203	10.2	G110S	landrace
PI089772	9.6	G110S	landrace
PI090479P	13.9	G110S	landrace
PI090763	9.8	G110S	landrace
PI416890	17.6	A105T	cultivar

<sup>1</sup> G110S and A105T indicates the Williams 82 reference genome for *Glyma.02G119600*.