

Supplementary Table 4. Linkage disequilibrium (r^2) between pairwise combinations of significant SNPs according to Bonferroni threshold at 5% and, if not included, the first SNP on the opposite side of the cloned gene for each of seven pea qualitative traits (flower pigmentation includes SNPs for both standard pigmentation and keel and wing pigmentation). Although not significant, the SNP featuring the lowest p value for cotyledon color was included due to its proximity to the significance threshold. Significant SNPs were identified by a GWAS based on 41,114 SNPs performed on a worldwide germplasm collection of 220 landraces from 19 regional pools and 11 modern cultivars.

Stipule pigmentation

	chr6LG2 _683704 59	chr6LG2 _683074 52	chr6LG2 _682653 55	chr6LG2 _678359 18	chr6LG2 _235650 075	chr6LG2 _274077 16
chr6LG2_683 70459	1	0.07	0.08	0.08	0	0
chr6LG2_683 07452	0.07	1	0.93	0.62	0.39	0.06
chr6LG2_682 65355	0.08	0.93	1	0.65	0.39	0.06
chr6LG2_678 35918	0.08	0.62	0.65	1	0.29	0.07
chr6LG2_235 650075	0	0.39	0.39	0.29	1	0.11
chr6LG2_274 07716	0	0.06	0.06	0.07	0.11	1

Cotyledon color

	chr2LG1 _419560 365	chr2LG1 _424229 115
chr2LG1_419 560365	1	0.05
chr2LG1_424 229115	0.05	1

Hilum pigmentation

	chr1LG6 _356439 618	chr1LG6 _356809 768
chr1LG6_356	1	0.10

439618
chr1LG6_356
809768 0.10 1

Flower pigmentation

	chr6LG2 _683704 59	chr6LG2 _683074 52	chr6LG2 _682653 55	chr6LG2 _682611 12	chr6LG2 _676417 87	chr6LG2 _678359 18	chr6LG2 _678360 00	chr6LG2 _235650 075
chr6LG2_683 70459	1	0.07	0.08	0.06	0.03	0.08	0.05	0
chr6LG2_683 07452	0.07	1	0.93	0.72	0.69	0.62	0.61	0.39
chr6LG2_682 65355	0.08	0.93	1	0.79	0.71	0.65	0.65	0.39
chr6LG2_682 61112	0.06	0.72	0.79	1	0.58	0.50	0.51	0.33
chr6LG2_676 41787	0.03	0.69	0.71	0.58	1	0.49	0.48	0.34
chr6LG2_678 35918	0.08	0.62	0.65	0.50	0.49	1	0.88	0.29
chr6LG2_678 36000	0.05	0.61	0.65	0.51	0.48	0.88	1	0.32
chr6LG2_235 650075	0	0.39	0.39	0.33	0.34	0.29	0.32	1

Seed coat pigmentation

	chr6LG2 _235739 982	chr6LG2 _683704 59	chr6LG2 _683074 52	chr6LG2 _682653 55	chr6LG2 _682611 12	chr6LG2 _676417 87	chr6LG2 _678359 18	chr6LG2 _678360 00	chr6LG2 _235650 075	chr6LG2 _235650 004	chr6LG2 _682702 46	chr6LG2 _682702 89	chr6LG2 _235738 439	chr6LG2 _682703 04
chr6LG2_235 739982	1	0.01	0.41	0.43	0.37	0.40	0.36	0.31	0.23	0.38	0.17	0.18	0.64	0.17
chr6LG2_683 70459	0.01	1	0.07	0.08	0.06	0.03	0.08	0.05	0	0	0.11	0.11	0.05	0.12
chr6LG2_683 07452	0.41	0.07	1	0.93	0.72	0.69	0.62	0.61	0.39	0.51	0.51	0.51	0.49	0.50
chr6LG2_682 65355	0.43	0.08	0.93	1	0.79	0.71	0.65	0.65	0.39	0.51	0.57	0.57	0.49	0.56
chr6LG2_682 61112	0.37	0.06	0.72	0.79	1	0.58	0.50	0.51	0.33	0.45	0.48	0.47	0.44	0.46

chr6LG2_676 41787	0.40	0.03	0.69	0.71	0.58	1	0.49	0.48	0.34	0.39	0.47	0.47	0.49	0.47
chr6LG2_678 35918	0.36	0.08	0.62	0.65	0.50	0.49	1	0.88	0.29	0.41	0.37	0.37	0.43	0.37
chr6LG2_678 36000	0.31	0.05	0.61	0.65	0.51	0.48	0.88	1	0.32	0.42	0.40	0.40	0.39	0.39
chr6LG2_235 650075	0.23	0	0.39	0.39	0.33	0.34	0.29	0.32	1	0.49	0.34	0.33	0.30	0.31
chr6LG2_235 650004	0.38	0	0.51	0.51	0.45	0.39	0.41	0.42	0.49	1	0.35	0.32	0.48	0.31
chr6LG2_682 70246	0.17	0.11	0.51	0.57	0.48	0.47	0.37	0.40	0.34	0.35	1	0.94	0.24	0.94
chr6LG2_682 70289	0.18	0.11	0.51	0.57	0.47	0.47	0.37	0.40	0.33	0.32	0.94	1	0.24	0.96
chr6LG2_235 738439	0.64	0.05	0.49	0.49	0.44	0.49	0.43	0.39	0.30	0.48	0.24	0.24	1	0.23
chr6LG2_682 70304	0.17	0.12	0.50	0.56	0.46	0.47	0.37	0.39	0.31	0.31	0.94	0.96	0.23	1

Cotyledon wrinkling

	chr3LG5 _655666 66	chr3LG5 _716706 71
chr3LG5_655 66666	1	0.30
chr3LG5_716 70671	0.30	1
