**Table S2.** Distant eQTL hotspots of the four seed germination stages. These hotspots were identified by dividing the genome into bins of 2 Mbp and performing a test to determine whether the number of distant eQTLs on a particular bin is higher than expected (p > 0.0001) assuming a Poisson distribution. Seed germination phenotype and metabolite data were taken from Joosen et al. (2012) and Joosen et al. (2013), respectively. †Abbreviations in the phenotypes are as follows: AR, after-ripened; CD, controlled deterioration; NS, no stratification; WS, with stratification; Gmax, maximum percentage of seed germination; t10, time required for 10% of seeds to germinate; t50, time required for 50% of seeds to germinate; U8416, uniformity of germination that is the time interval between 84% and 16% of seeds to germinate; AUC, the area under the curve that is a parameter that combines Gmax, t50, and U8416. More information about the phenotypes can be seen in Joosen et al. (2012).

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| --- | --- | --- | --- | --- | --- | --- |
| hotspot ID | position | distant eQTLs | enriched GO terms1 | metabolite | phenotype† | |
| PD1 | ch1:6-10Mb | 43 | negative regulation of seed germination, alpha-ketoglutarate transport, oxaloacetate transport, RNA secondary structure unwinding, medium-chain fatty acid metabolic process, gibberellin biosynthetic process, alternative mRNA splicing via spliceosome, ammonia assimilation cycle, malate transmembrane transport, response to carbon dioxide, regulation of seed dormancy process | Sinapate | | Stratification.AR.AUC, Stratification.AR.t50, ABA.NS.Gmax, Cold.NS.Fresh.t10 |
| PD2 | ch3:8-12Mb | 69 | positive regulation of protein export from nucleus, detection of brassinosteroid stimulus, galactose catabolic process | two unknown metabolites | | Heat.NS.AR.t50 |
| AR1 | ch2:12-14Mb | 16 | none | none | | none |
| AR2 | ch3:2-4Mb | 20 | response to oxidative stress, response to light intensity, translation, phospholipid transfer to membrane, proline catabolic process, asparagine biosynthetic process, glutamate biosynthetic process, protein folding, response to heat | Sinapate | | Heat.NS.AR.Gmax, Heat.NS.AR.AUC, Heat.WS.AR.AUC |
| IM1 | ch5:6-8Mb | 19 | Lewis a epitope biosynthetic process, DNA catabolic process | D-maltose and 23 unknown metabolites | | NaCl.NS.t10 |
| IM2 | ch5:22-26Mb | 69 | negative regulation of chromatin silencing, seed germination, response to karrikin, entrainment of circadian clock by photoperiod, proline catabolic process, glutamate biosynthetic process | L-isoleucine, pyruvic acid, 2-hydroxybutyric acid, alanine, urea, oxoglutaric acid | | NaCl.NS.Gmax, NaCl.WS.U8416, Mannitol.WS.AUC, CD.NS.AR.Gmax, Stratification.AR.Gmax, Mannitol.WS.t50, Stratification.AR.U8416, Stratification.Fresh.Gmax, Stratification.Fresh.AUC, Mannitol.NS.t10, Mannitol.NS.U8416, ABA.NS.AUC, Stratification.Fresh.t50, ABA.NS.Gmax, ABA.NS.t50, AfterRipening.t10, AfterRipening.t50, Stratification.Fresh.t10, Heat.NS.AR.AUC, ABA.NS.t10, ABA.WS.Gmax, ABA.WS.AUC, ABA.WS.t10, ABA.WS.t50, ABA.WS.U8416, Size.imbibed.seed.Area, Mannitol.NS.t50, Heat.WS.AR.U8416, AR.Gmax.ns, Heat.NS.AR.Gmax, Cold.NS.Fresh.Gmax |
| RP1 | ch1:0-2Mb | 23 | medium-chain fatty acid metabolic process | none | | AR.U8416.ns |
| RP2 | ch1:6-8Mb | 18 | none | none | | Stratification.AR.AUC, Stratification.AR.t50, ABA.NS.Gmax |
| RP3 | ch5:14-16Mb | 21 | response to karrikin, pigment biosynthetic process, response to far red light, response to UV-B, response to red light, positive regulation of catalytic activity, response to blue light, flavonoid biosynthetic process, maltose metabolic process, pentose-phosphate shunt, starch biosynthetic process, response to sucrose, photosynthetic electron transport in photosystem II, membrane disassembly, rRNA processing, cellular response to calcium ion, photosynthesis, light harvesting in photosystem II, fructose 1,6-bisphosphate metabolic process, fructose metabolic process, cellular response to UV-A, photoprotection, cellular response to high light intensity, phenylpropanoid biosynthetic process, monosaccharide transmembrane transport, cytidine deamination, regulation of stomatal closure, photosystem II assembly, de-etiolation | none | | CD.NS.AR.t50 |
| RP4 | ch5:24-26Mb | 96 | seed development, lipid storage, response to acid chemical, seed germination, response to inorganic substance, response to freezing, toxin metabolic process, response to cyclopentenone, response to osmotic stress, defense response to fungus incompatible interaction, response to hypoxia, sugar mediated signaling pathway, abscission, protein homooligomerization, fatty acid catabolic process, leaf senescence, D-serine biosynthetic process, inorganic anion transport | Alanine, fumaric acid, glycine, L-aspartic acid, L-glutamine, L-lysine, L-methionine, L-phenylalanine, L-serine, L-tyrosine, L-valine, malic acid, sucrose, and other 7 unknown metabolites | | Stratification.AR.U8416, Stratification.Fresh.Gmax, Stratification.Fresh.AUC, Mannitol.NS.t10, Mannitol.NS.U8416, ABA.NS.AUC, Stratification.Fresh.t50, ABA.NS.Gmax, ABA.NS.t50, AfterRipening.t10, AfterRipening.t50, Stratification.Fresh.t10, Heat.NS.AR.AUC, ABA.NS.t10, ABA.WS.Gmax, ABA.WS.AUC, ABA.WS.t10, ABA.WS.t50, ABA.WS.U8416, Size.imbibed.seed.Area, Mannitol.NS.t50, Heat.WS.AR.U8416, AR.Gmax.ns, Heat.NS.AR.Gmax, Cold.NS.Fresh.Gmax |