

Figure S1. Marker-trait associations for maturity. The estimated magnitude of each allelic effect (in days) is depicted by circle symbol diameter, with negative and positive effects relative to the common parent (IA3023) respectively depicted by red and green. The observed $-\log_{10}(p)$ values for the each of the 19 marker-trait associations across the 39 founder families are column color-coded by magnitude in the row labeled JMp (acronym for Joint Mapping p value). Founder parent names are listed on Table 1.

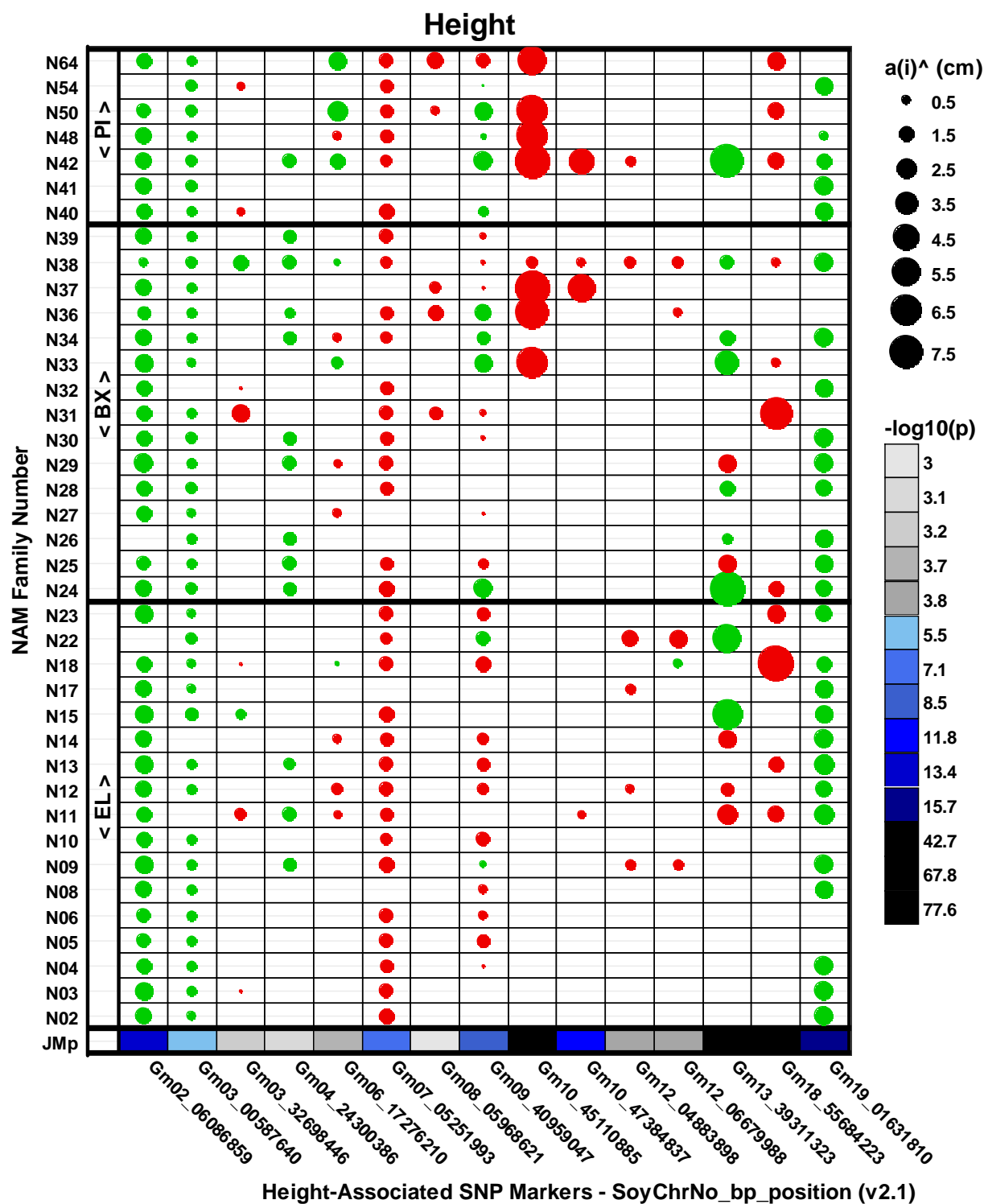


Figure S2. Marker-trait associations for plant height. The estimated magnitude of each allelic effect (in cm) is depicted by circle symbol diameter, with negative and positive effects relative to the common parent (IA3023) respectively depicted by red and green. The observed $-\log_{10}(p)$ values for the each of the 15 marker-trait associations across the 39 founder families are column color-coded by magnitude in the row labeled JMp (acronym for Joint Mapping p value). Founder parent names are listed on Table 1.

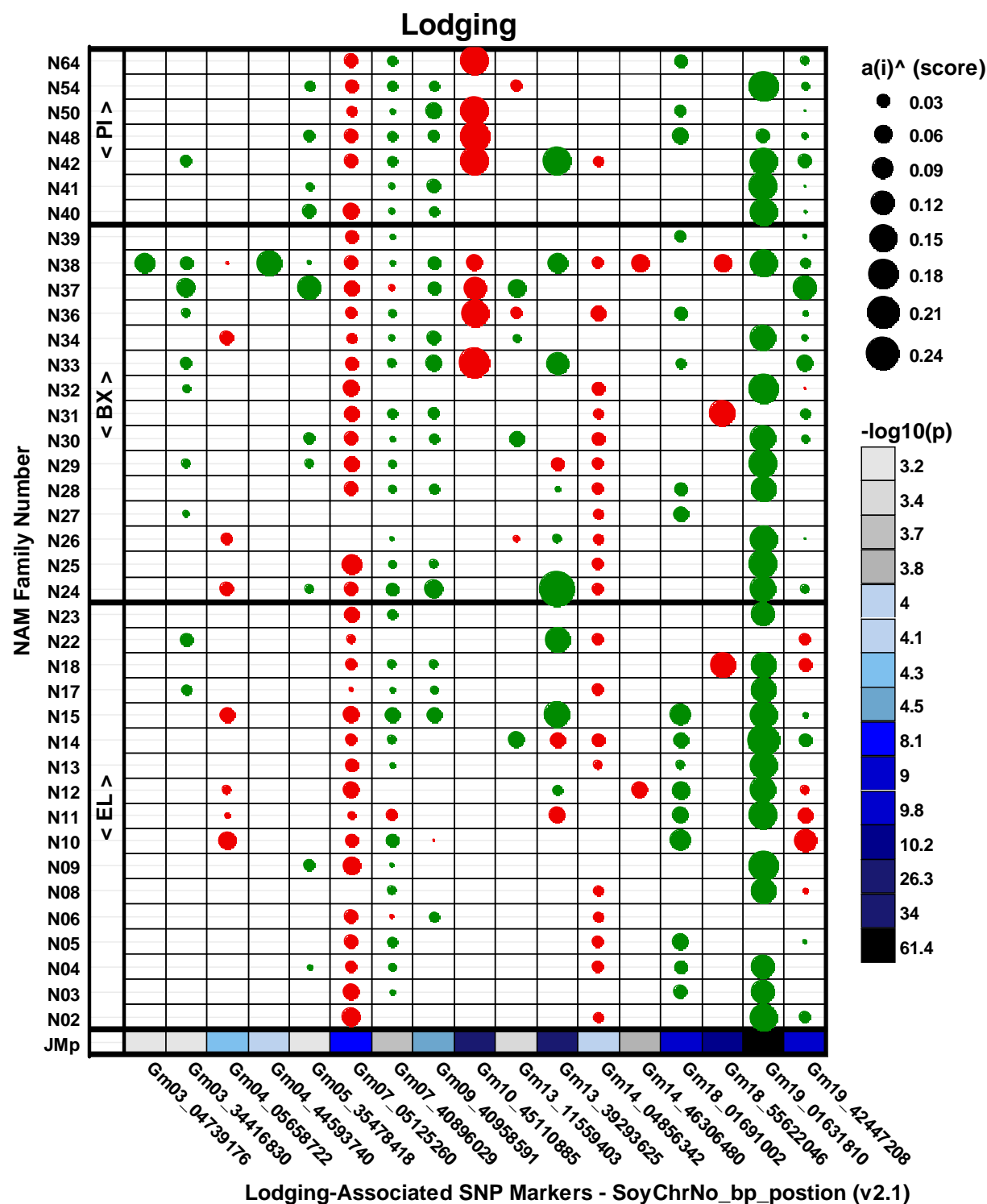


Figure S3. Marker-trait associations for plant lodging. The estimated magnitude of each allelic effect (score) is depicted by circle symbol diameter, with negative and positive effects relative to the common parent (IA3023) respectively depicted by red and green. The observed $-\log_{10}(p)$ values for the each of the 17 marker-trait associations across the 39 founder families are column color-coded by magnitude in the row labeled JMp (acronym for Joint Mapping p value). Founder parent names are listed on Table 1.

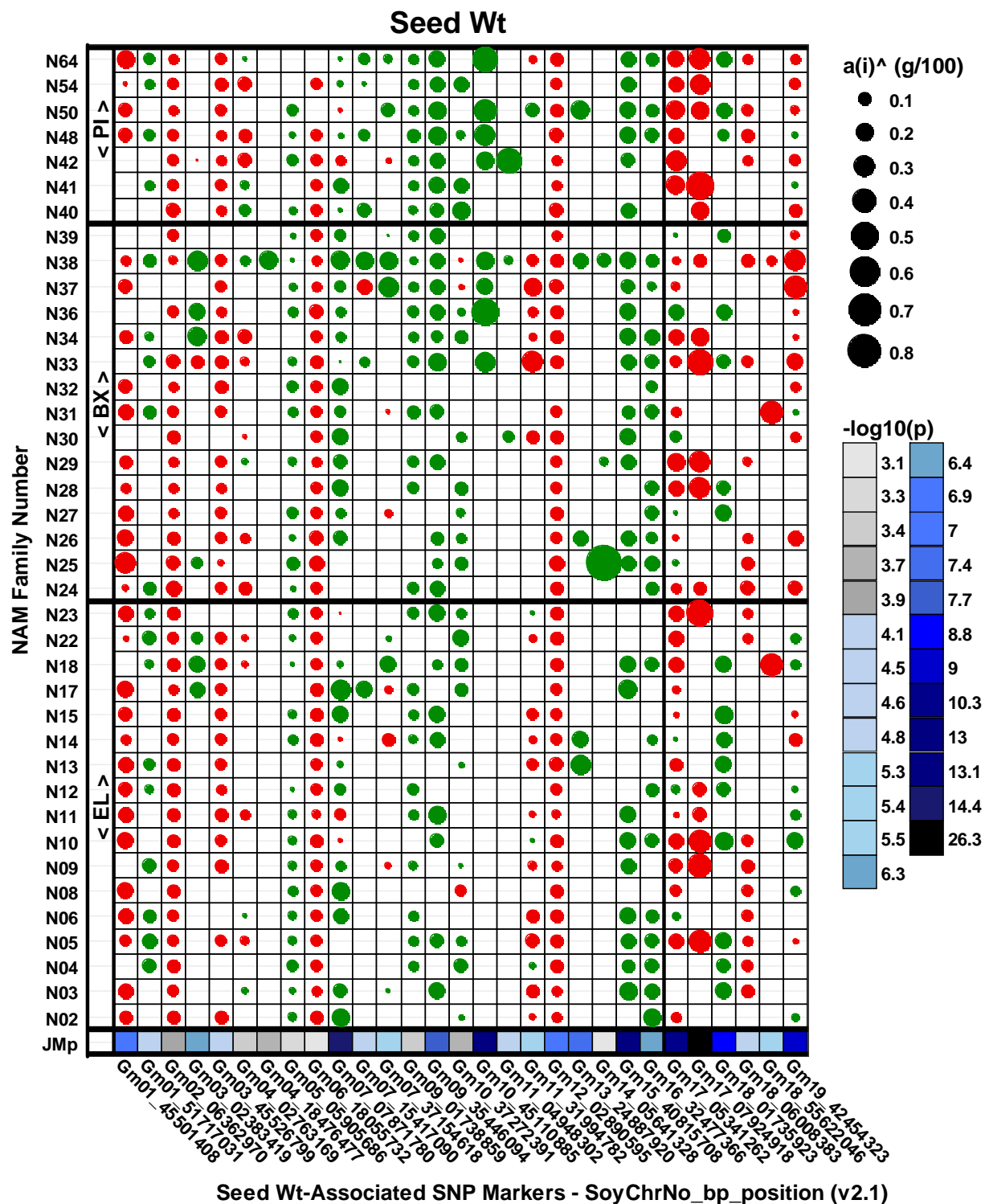


Figure S4. Marker-trait associations for seed weight. The estimated magnitude of each allelic effect (in g 100 seed⁻¹) is depicted by circle symbol diameter, with negative and positive effects relative to the common parent (IA3023) respectively depicted by red and green. The observed -log₁₀(p) values for the each of the 29 marker-trait associations across the 39 founder families are column color-coded by magnitude in the row labeled JMp (Joint Mapping p value). Founder parent names are listed on Table 1.

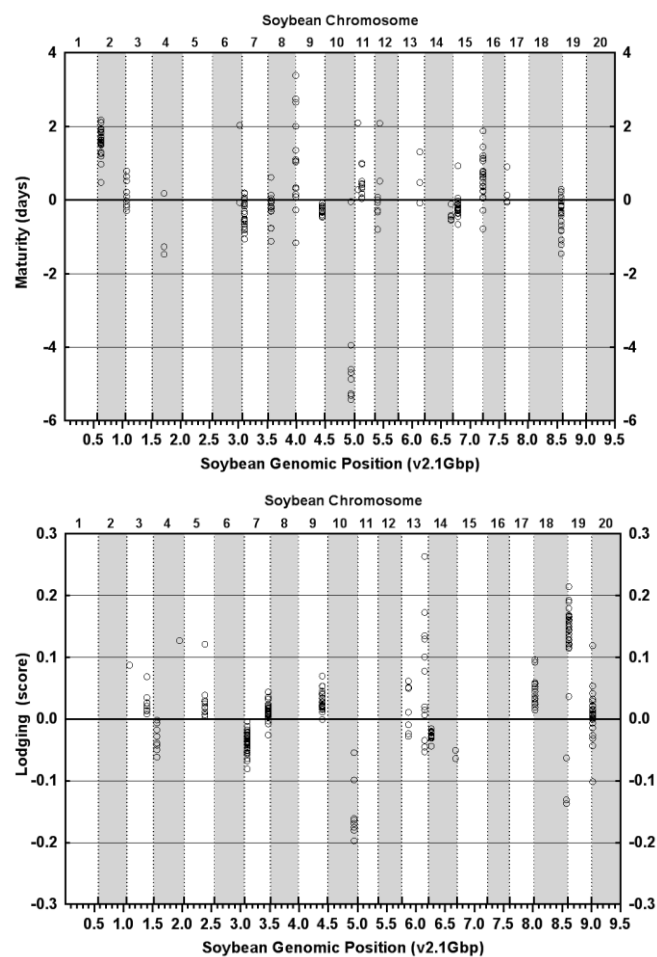
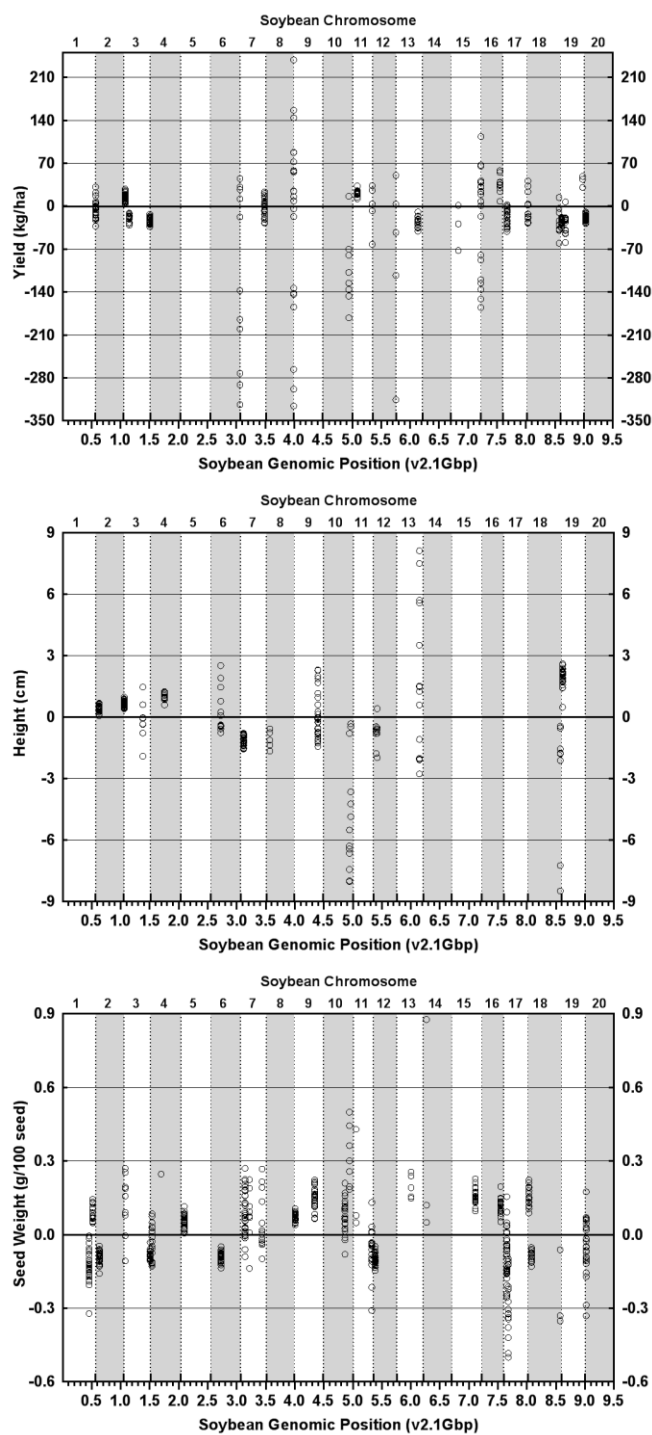


Figure S5. Range of allelic effects of significant MTAs detected in each family in the SoyNAM population for yield, maturity, plant height, plant lodging, and seed weight.

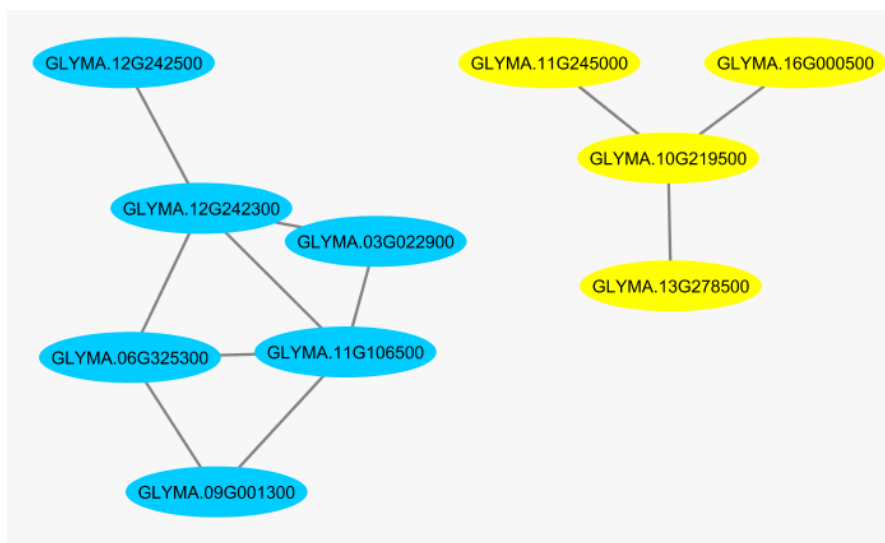


Figure S6. Candidate genes underlying yield MTA peaks. Edges represents a Z-score of 2.0 or greater between genes. Module one is colored in blue and module two is colored in yellow.