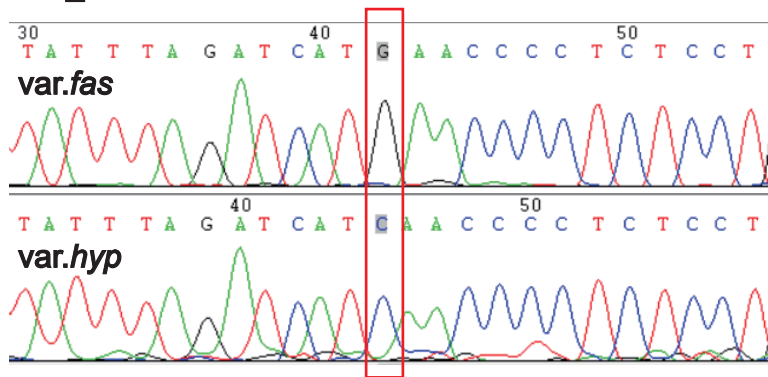
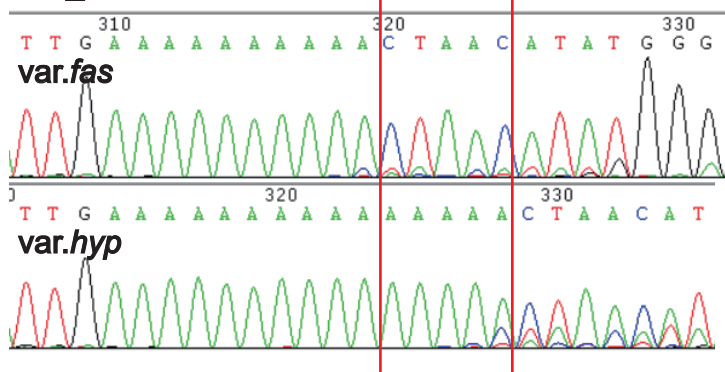


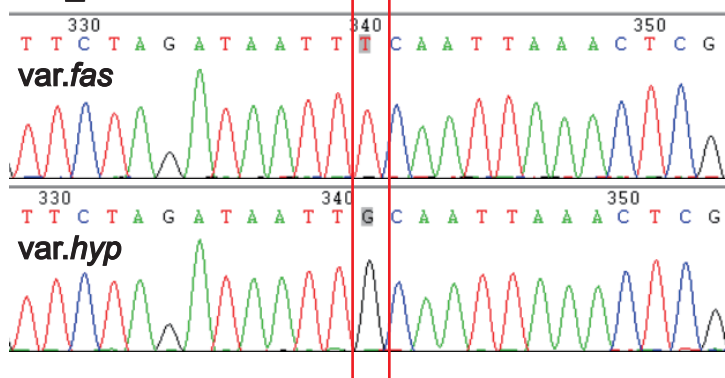
a YLT_29089



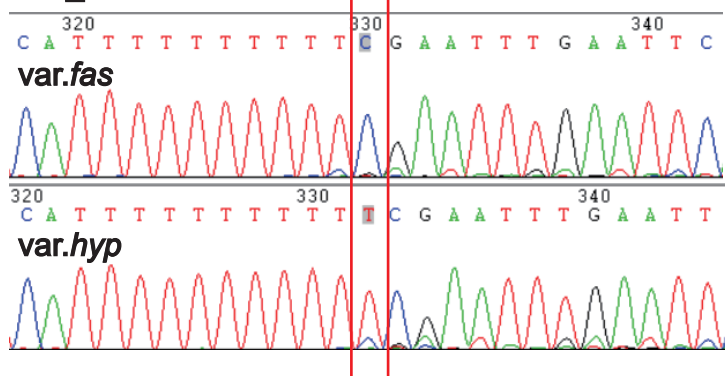
b YLT_73768



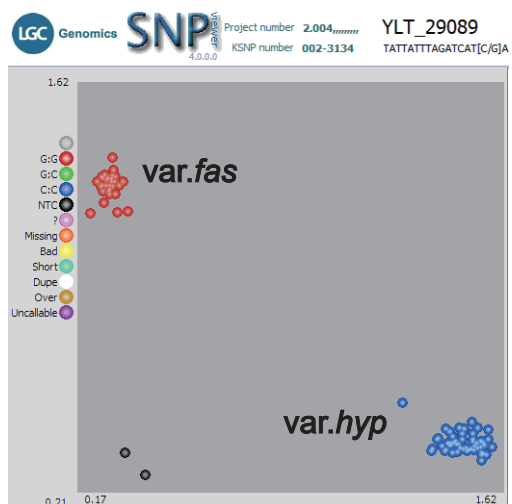
C YLT_82368



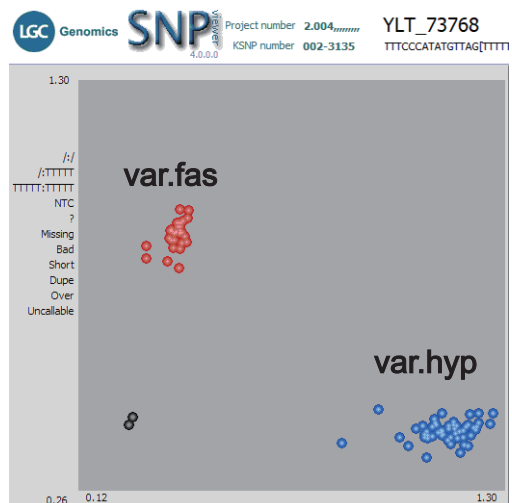
d YLT_82771



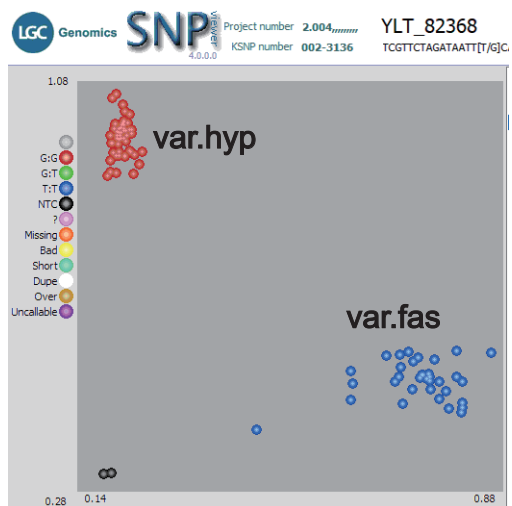
e



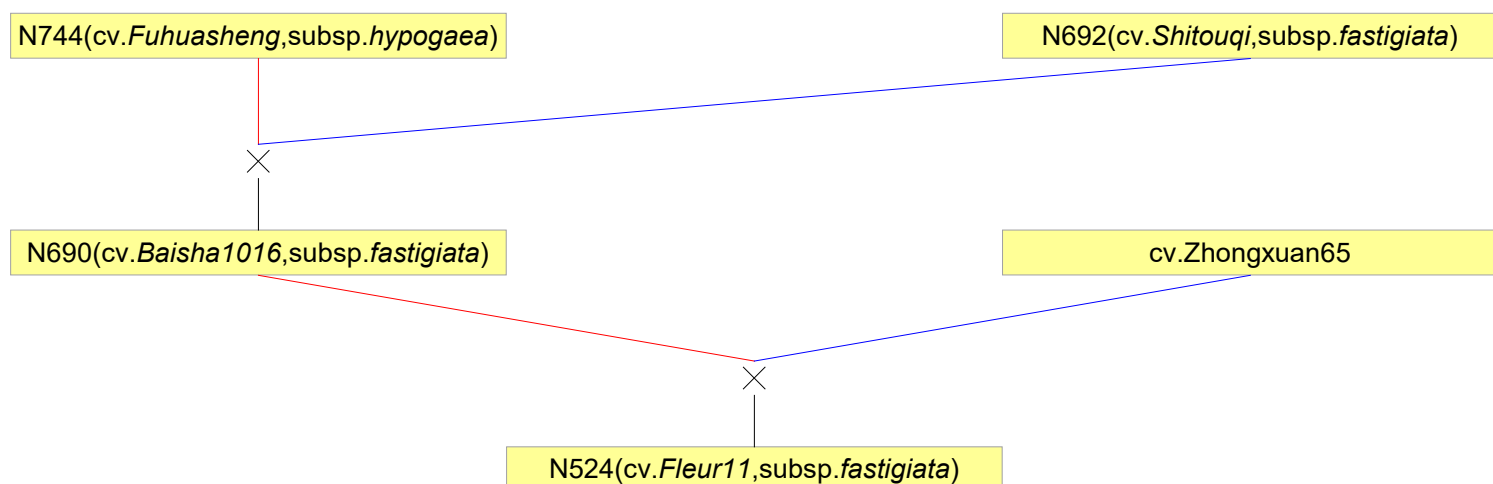
f



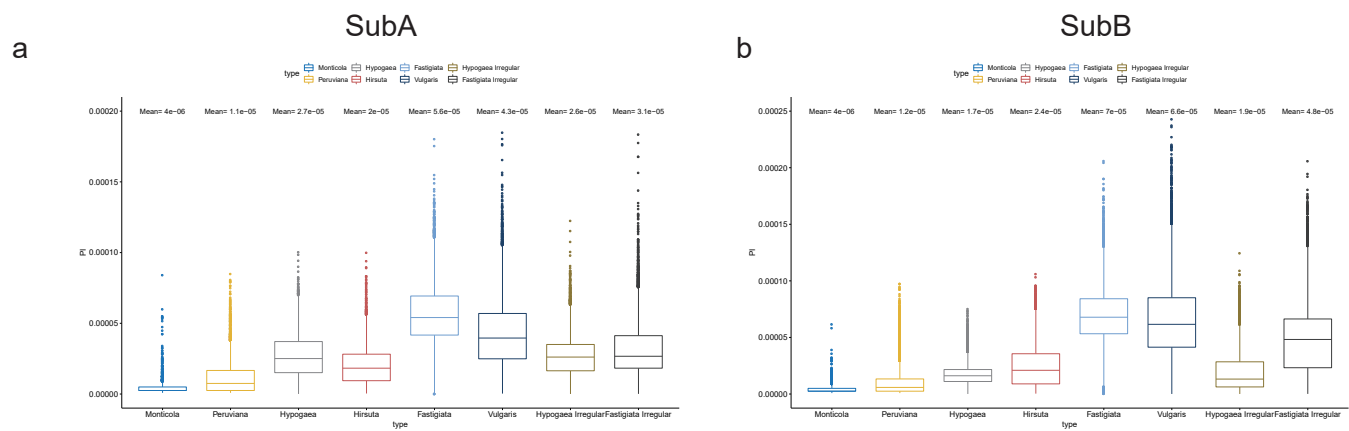
g



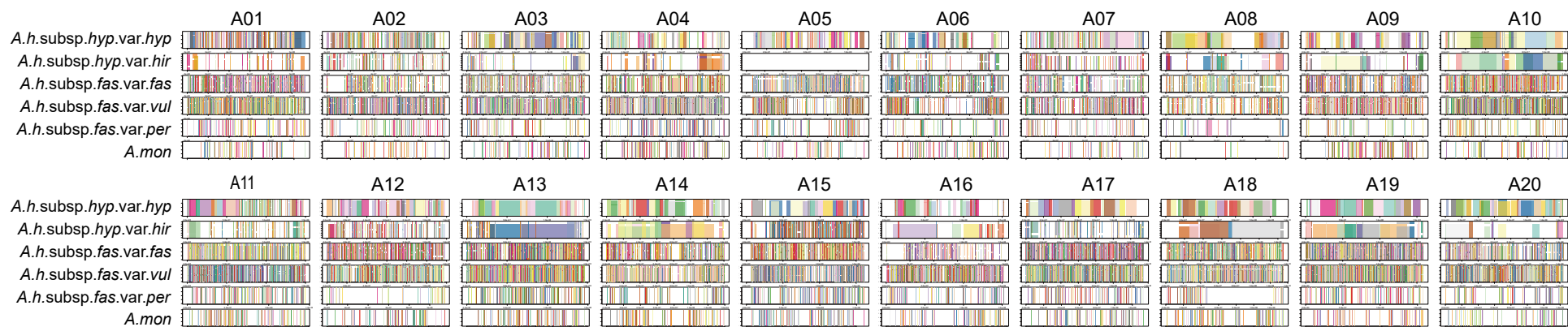
Supplementary Figure S1. Validation of chloroplast DNA polymorphisms. Four randomly chosen variations were confirmed by Sanger sequencing (a-d). Three of them were also validated by Kompetitive allele specific PCR (KASP) assays (e-g).



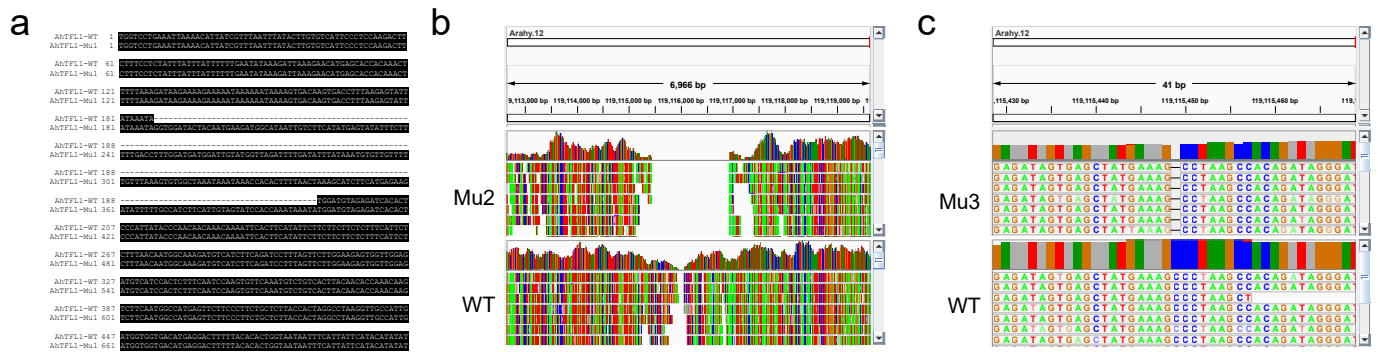
Supplementary Figure S2. Pedigree information of the accession N524. The red and blue lines indicate the female and male parent, respectively. The accession N524 inherited the chloroplast genome from N744.



Supplementary Figure S3. Nucleotide diversity (π) for different botanical types of peanut. The A and B sub-genomes were analyzed separately. Sub-A for AA genome (a) and Sub-B for BB genome (b).

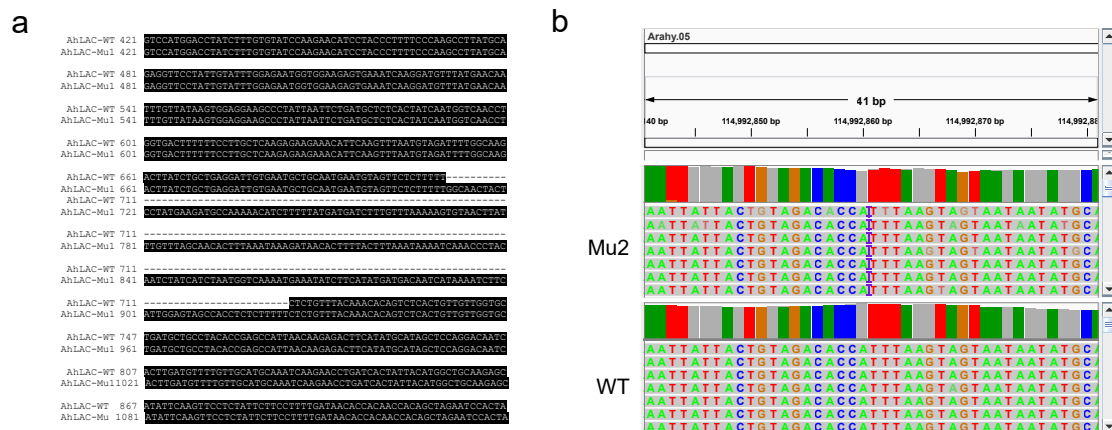


Supplementary Figure S4. Haplotype blocks for different peanut botanical types. Graphical block structure representation of 20 chromosomes. Haplotypes were computed with adaptive mode using window sizes of 5, 10, 20 and 50 markers and target coverage of 90%.

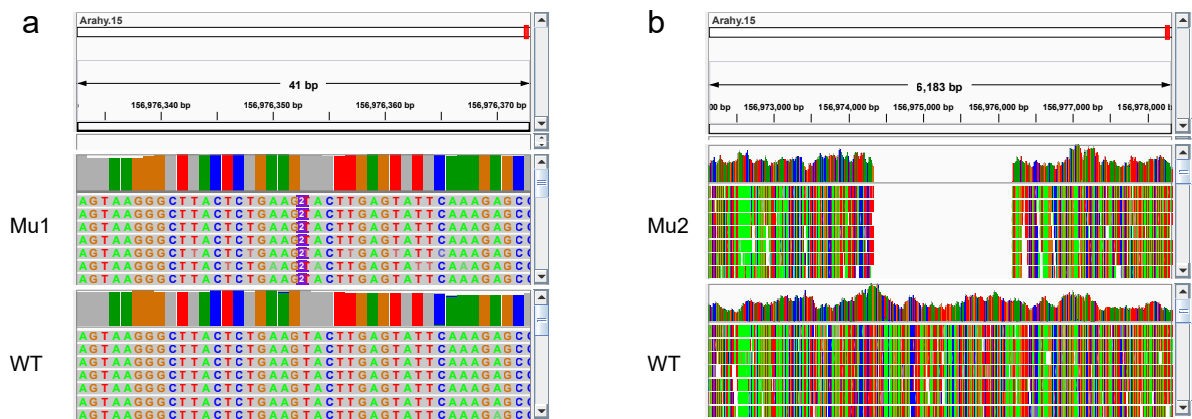


Supplementary Figure S5. Features of the mutations (Mu) identified for the gene *AhTFL1*.

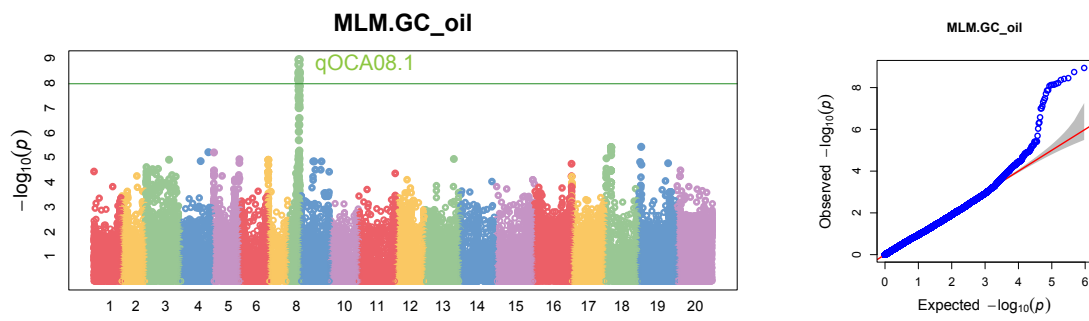
- Sequence alignment showing the 214 bp MITE insertion of the mutation type 1 (Mu 1);
- Integrative Genomics Viewer (IGV) image of the genomic region showing paired-end reads mapped on the candidate gene with a 1492 bp deletion described as mutation type 2 (Mu 2);
- the paired-end reads mapped on the candidate gene with a 1 bp deletion (with a C missing) described as mutation type 3 (Mu 3).



Supplementary Figure S6. Features of the mutations (Mu) identified for the gene *AhLAC*. a) Sequence alignment showing the 214 bp insertion of the mutation type 1 (Mu 1); b) Integrative Genomics Viewer (IGV) image of the genomic region showing paired-end reads mapped on the candidate gene with a 1 bp insertion (purple I) described as mutation type 2 (Mu 2).



Supplementary Figure S7. Features of the mutations (Mu) identified for the gene *AhMADs-box transcription factor 6*. a) Integrative Genomics Viewer (IGV) image of the genomic region showing paired-end reads mapped on the candidate gene with a 2 bp insertion (purple 2) described as mutation type 1 (Mu 1); b) Integrative Genomics Viewer (IGV) image of the genomic region showing paired-end reads mapped on the candidate gene with a 1870 bp deletion described as mutation type 2 (Mu 2).



Supplementary Figure S8. GWAS for seed oil content. Manhattan plot (left) and quantile-quantile (Q-Q) plot (right). The horizontal line in the Manhattan plot indicates the significance threshold for association ($p < 0.05$) after a Bonferroni correction on the number of markers.