Fresh seed dormancy

ICGV 00350 (Non-dormant) X ICGV 97045 (Dormant)

Recombinant inbred lines (RILs)

20 Dormant RILs | 20 Non-dormant RILs

20 Dormant bulks | 20 Non-dormant bulks | ICGV 97045 (Dormant)

26.94 Gb 11.3 X | 27.96 Gb 11.7 X | 33.03 Gb 13.9 X

Mapping of reads to *A. duranensis* and *A. ipaensis* genome assembly

Construction of reference assembly for donor parent ICGV 97045

Mapping of bulk reads on the developed reference parent assembly for calculation of SNP Index and Δ SNP Index

A. ipaensis (B05):
- 114.45 Mb to 116.69 Mbp (2.24 Mb)
- 18 effective SNPs (Delta SNP-index = -1) at confidence ~99% with the read depth of 5
- 3 SNPs in 3 candidate genes *Araip.S6QRU*, *Araip.YHU92* and *Araip.X9V0W*

A. duranensis (A09)
- One non synonymous SNP in a ABA biosynthetic gene (*Aradu.D94AQ*)

Validation of markers
- Panel of dormant and non-dormant genotypes
- Validation of GMFSD1 (B05_8196)

Workflow steps:

1. Developing RILs mapping population
2. Phenotyping of mapping population
3. Selection of RILs with contrast phenotype
4. Construction of dormant and non-dormant bulks
5. Sequencing of bulks and dormant genotype
6. Sequencing data analysis with QTL-seq pipeline
7. Identification of genomic regions, SNPs and candidate genes
8. Validation of identified markers
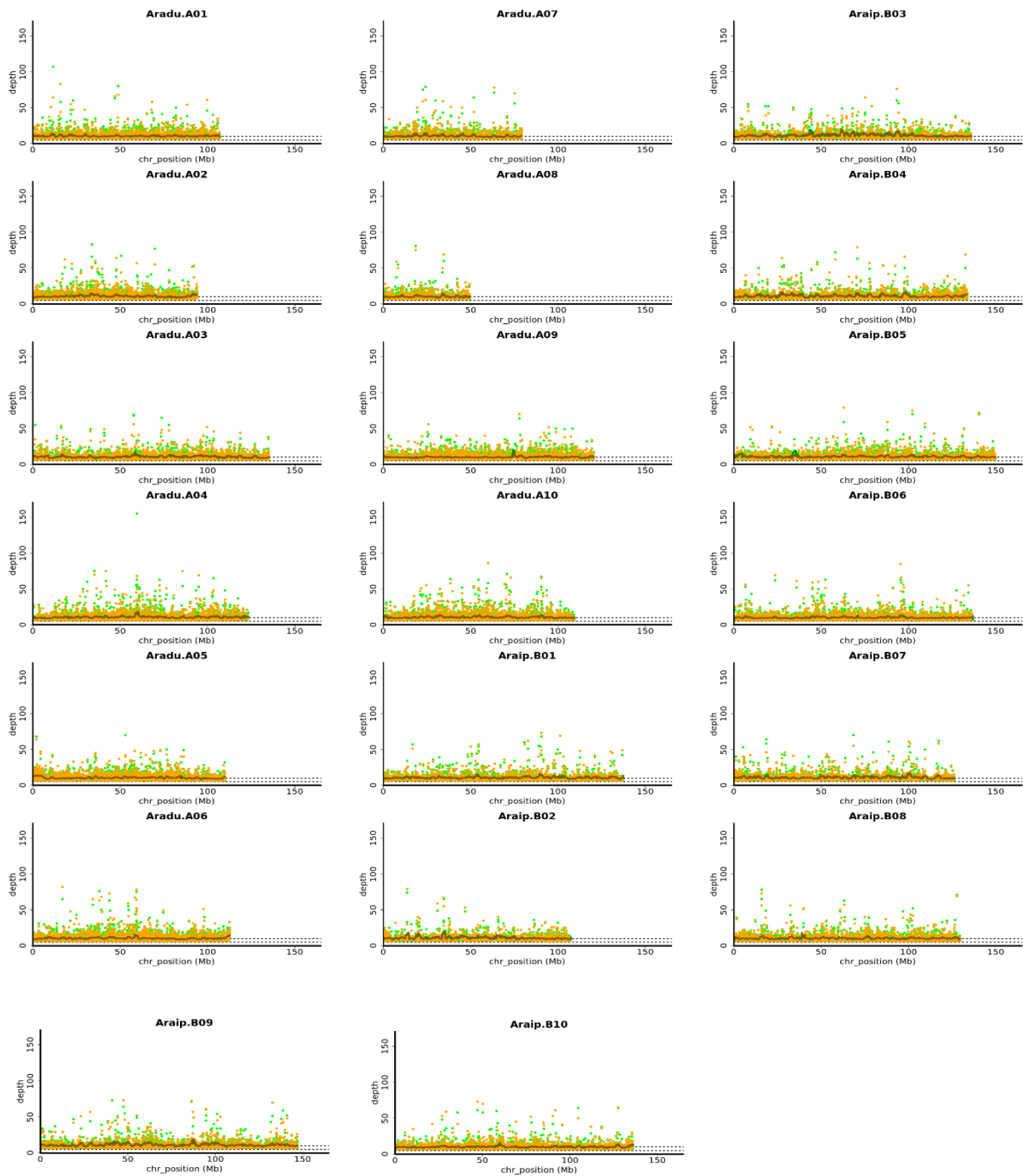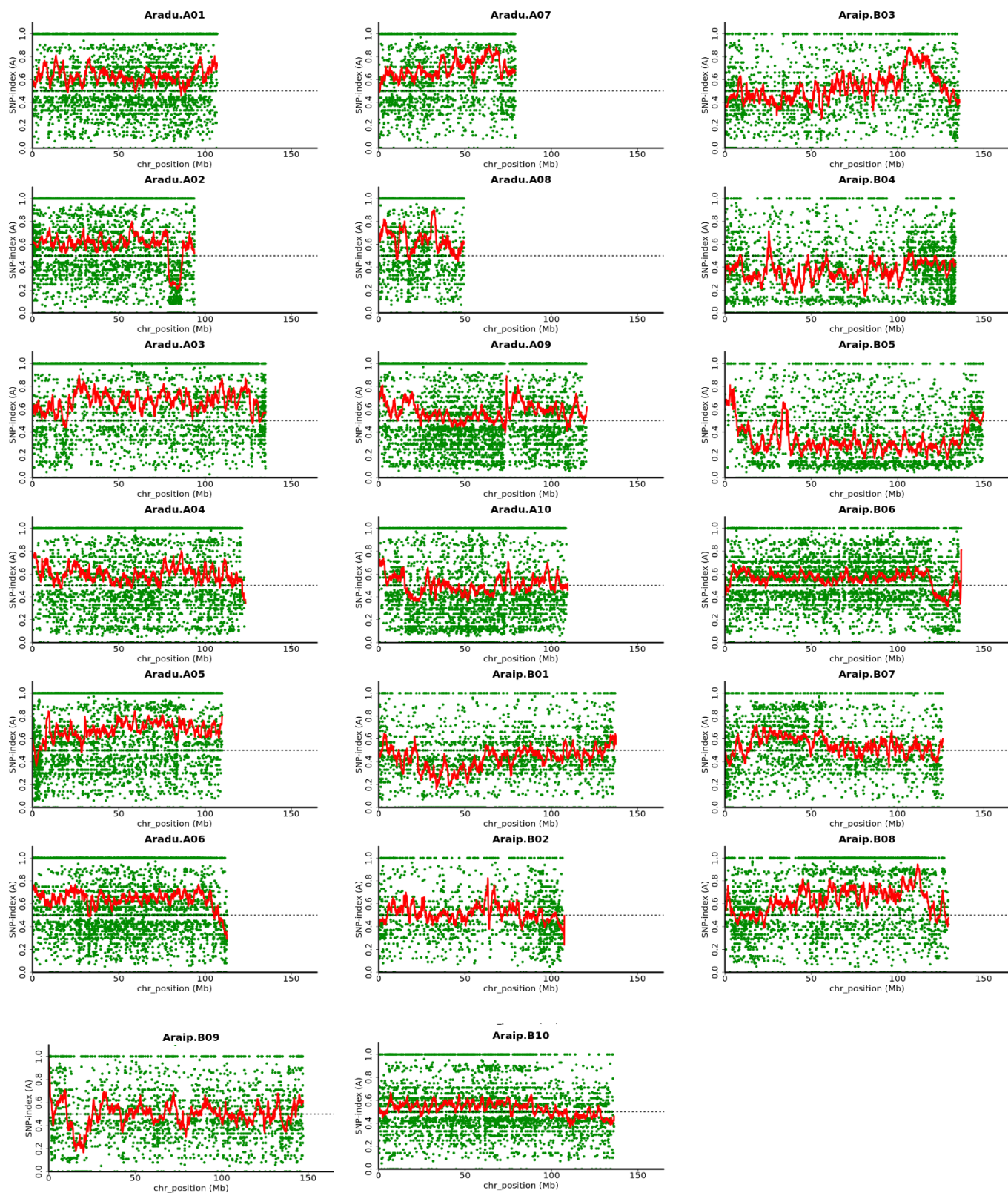
Supplementary Figure S1. QTL-seq approach used for trait mapping in groundnut for fresh seed dormancy

Supplementary Figure S2. Sequencing depth of the dormant parent ICGV 97045 Black line indicates the sliding window average of 2 Mb interval with 50 kb increment for SNP-index.

Supplementary Figure S3. SNP-index plots for 20 pseudomolecules Dormant pool with the dormant parent. Red lines indicate the sliding window average of 2 Mb interval with 50 kb increment for SNP-index.
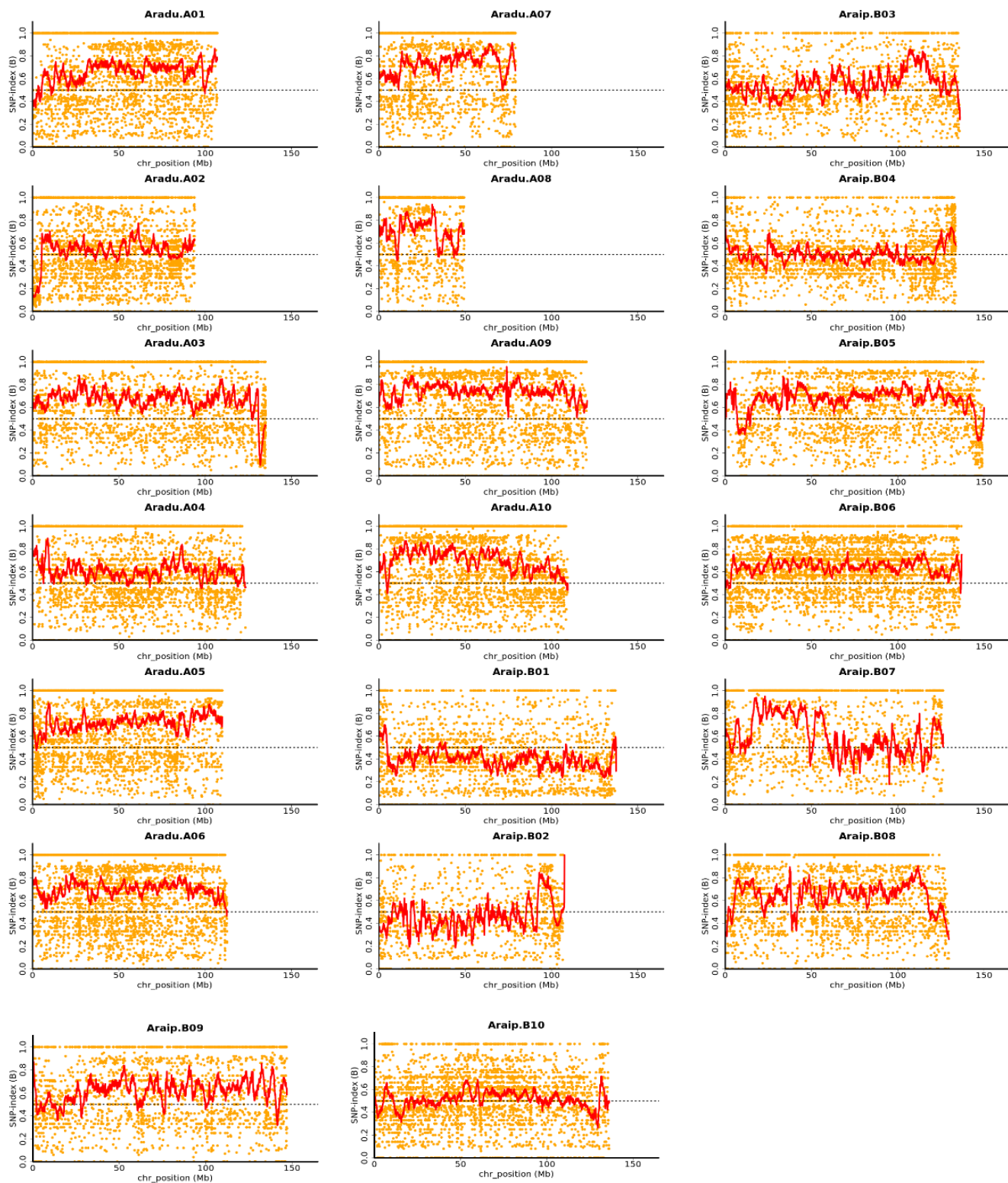
Supplementary Figure S4. SNP-index plots for 20 pseudomolecules of Non–dormant pool with dormant parent. Red lines indicate the sliding window average of 2Mb interval with 50 kb increment for SNP-index.
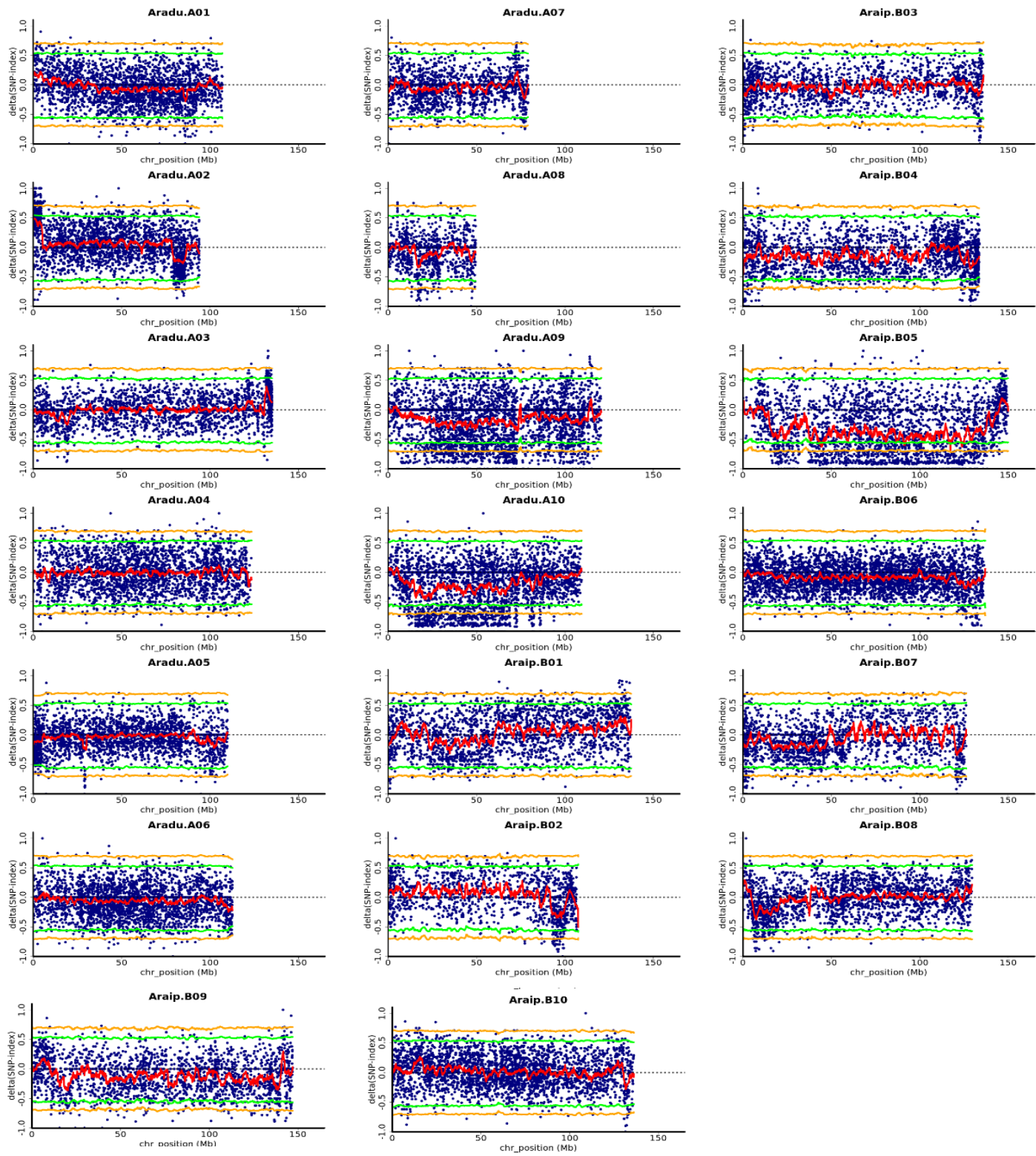
Supplementary Figure S5. The Δ(SNP index) plot obtained by subtraction of dormant pool SNP-index from non-dormant pool SNP-index Statistical confidence intervals under the null hypothesis of no QTL are shown (gray: $P < 0.1$; green: $P < 0.05$; pink: $P < 0.01$).