**method flowchart: RBP aQTL analysis**

- PSAMs from MatrixREduce software
- sequence: either full mRNAs, 5' UTRs, ORFs or 3' UTRs

- calculate affinity scores
  AffinityProfile software

- calculate RBP activity levels by multivariate regression
  segregated mRNA expression data

- calculate LOD scores per markers using CIM method
  segregated genotype data

- calculate LOD score threshold at 1% FDR by 200 independent permutations

- for each RBP eliminate from expression data 3 sets of genes: its encoding gene, genes located near significant aQTL peaks and genes with significant eQTL at the peak

- calculate activity levels by multivariate regression for each processed expression
  Data and LOD scores and threshold

- Do new aQTL peaks appear?
  - Yes
  - No
    - search significant regions for genetic and physical interactions

**Figure S3** The flowchart representation of our aQTL analysis.