FIGURE 1

Workflow of SNP Identification

RNA-Seq reads from high ranked and low rank families
(100 bp, average of 123,000,000 per group)

Map reads to the reference transcriptome
(average of 8,600,000 reads mapped per group)

SNP probabilistic variant detection
(127, 401 putative SNPs)

Filter to 31,419 SNPs
(coverage >20, probability ≥0.95, quality score >20)

Fisher exact test to compare high and low rank families
(147 SNP markers)

Validation by sequined genotyping in 20 individuals
(41 validated SNPs)

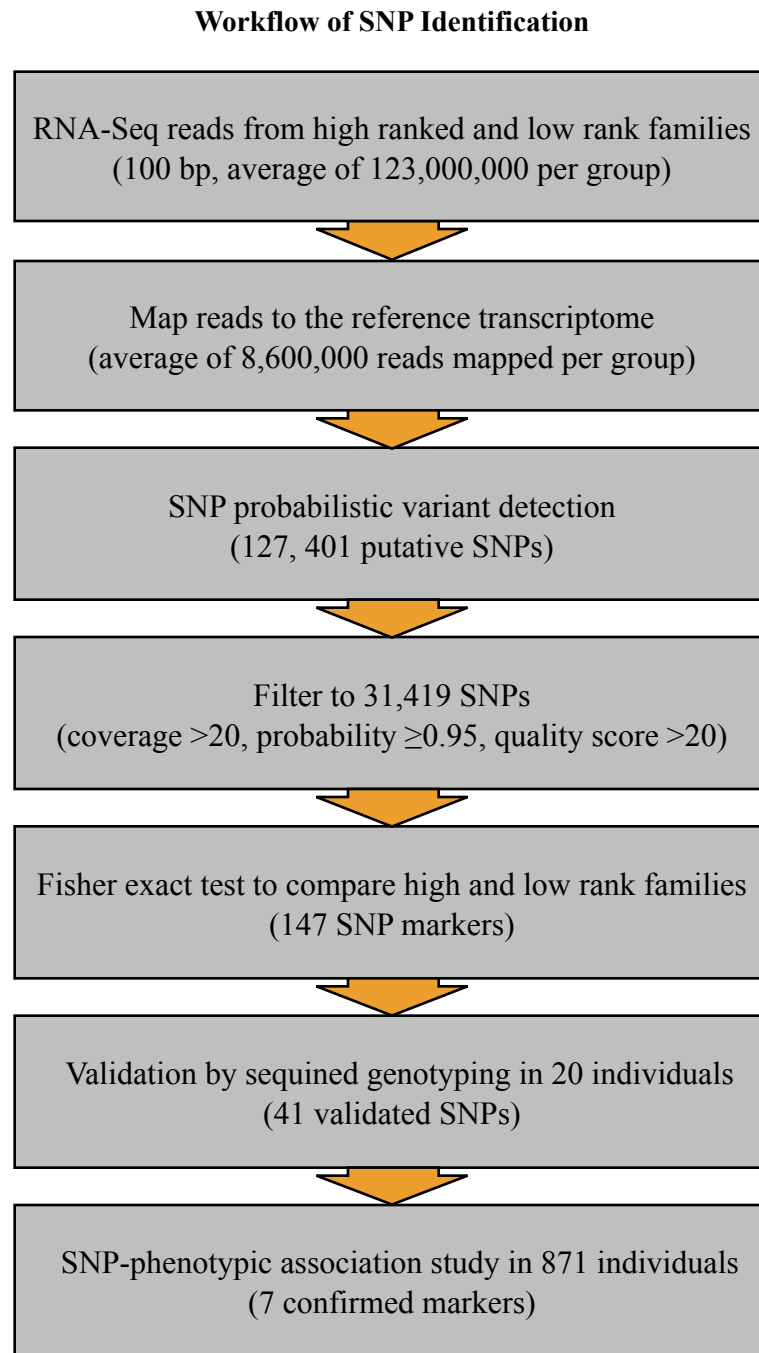SNP-phenotypic association study in 871 individuals
(7 confirmed markers)

This workflow was used for identification of SNPs associated with muscle mass, fat content, and flesh whiteness in rainbow trout.