

RNA-Seq Reads

Align reads to contigs
with Maq pipeline
2,263,279 SNPs



Filter SNPs for read depth, density,
and quality with Maq SNPFilter
575,340 SNPs (**Filtered SNPs**)



Align contigs to genome sequence and link
SNPs from each variety to a genomic position
80,986 SNPs



Remove SNPs that are not biallelic and
filter SNPs within 50bp of intron
69,011 SNPs (**High Confidence SNPs**)



Pick final SNPs for the BeadXpress SNP array

Sanger ESTs

Assemble ESTs per variety
using TGICL and call SNPs
8,327 SNPs



Filter SNPs for read depth and
density using custom perl script
2,358 SNPs (**Filtered SNPs**)



Align contigs to genome sequence and link
SNPs from each variety to a genomic position
80,986 SNPs



Remove SNPs that are not biallelic and
filter SNPs within 50bp of intron
69,011 SNPs (**High Confidence SNPs**)



Pick final SNPs for the BeadXpress SNP array