Exome sequencing: 13,102 high confidence SNVs in genome

5,329 high confidence heterozygous SNVs (4,709 are known SNPs) in coding sequence of 3,123 genes

Transcriptome sequencing detecting 14,397 genes with at least 1x average coverage across the gene

2,534 heterozygous SNV loci in 1,591 genes covered by transcriptome sequences with at least 20x coverage

86 genes expressed preferentially from one allele indicated by 221 SNVs in the transcriptome