Raw sequence data 24Gb

MAQ read mapping 7.4 fold coverage

MAQ SNP calling n=7,102,734

MAQ SNP filter n=2,921,556

Custom script SNP filter n=2,443,037

Randomly selected SNPs checked with MALDI-TOF n=196

False positive rate: 1.1% (2/196)
Heterozygous under-calls: 4% (8/196)

Comparison with BovineSNP50 array n=25,726

False positive rate: 0.16% (46/25742)
Heterozygous under-calls: 6.6% (1720/25742)

False negative rate:
Homozygotes: 26%
Heterozygotes: 70%

High coverage, coding SNPs checked with MALDI-TOF n=75

False positive rate: 24% (18/75)