

77,814,868
(78M)

- SNP discovery stage
- SNP calling criteria: mapping quality ≥ 20 , base quality ≥ 20 , SNP quality ≥ 20 , coverage ≥ 5

23,997,764
(24M)

- SNP quality ≥ 60 in within-line analysis and MAF $\geq 5\%$

10,028,579
(10M)

- SNP clusters removed
- *In-silico* analysis of SNPs to predict the conversion performance of SNPs in the array

1,829,290
(1.8M)

- SNPs selected for validation in pre-screen arrays
- SNPs placed evenly according to genetic map distance
- 1:1 ratio of broiler and layer SNPs

580,954
(600K)

- Final panel for array selected from validated list of SNPs
- 3:2 ratio of broiler and layer SNP
- SNPs placed uniformly according to genetic map distance
- Contains 21,534 exonic SNPs