# S4 Table The sequence of filters to remove false-positive 90k iSelect SNP calls in GenomeStudio.

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| Steps | Filters | Description | Threshold to  keep markers | Num. of SNPs left |
| 1 | Allele Freq. | Remove all monomorphic markers | Allele frequency < 1 | 48,248 |
| 2 | Cluster Sep. | Cluster separation – genotypic clusters separated into two discrete groups | Cluster Sep >= 0.2 | 47,830 |
| 3 | Call Freq. | Removal of SNP markers with > 5% missing data | Call Freq >= 0.95 | 36,813 |
| 4 | AB R Mean | Remove SNP markers with low signal intensity | AB R Mean >= 0.2 | 36,618 |
| 5 | AB T Mean | Remove SNP markers where AB clusters has shifted toward the AA or BB | 0.2 < AB T Mean < 0.8 | 35,175 |
| 6 | Minor Freq. | Removed markers with a minor allele frequency of less than 10% | Minor Freq >= 0.1 | 13,539 |