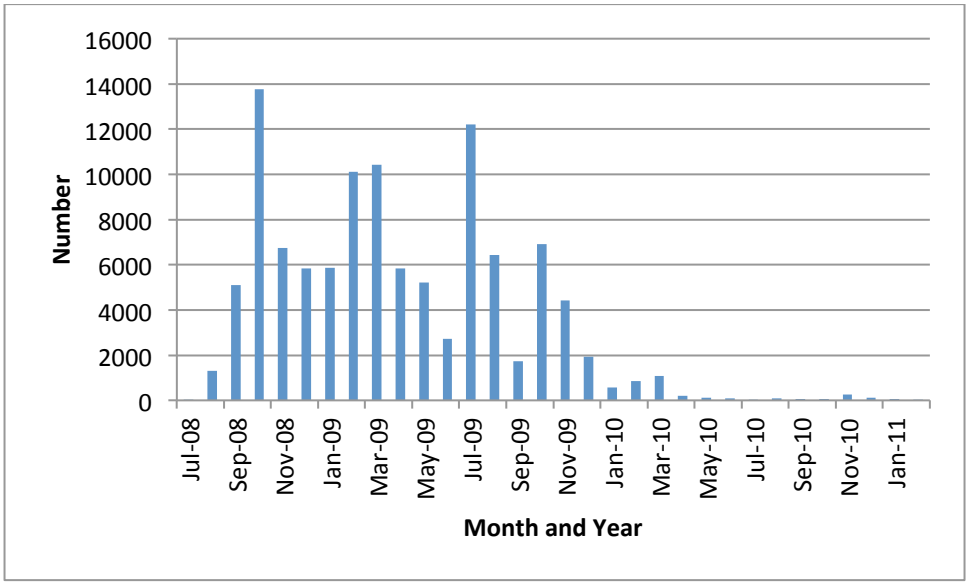

Figure S1. Distribution of GERA saliva sample collection dates, by month and year

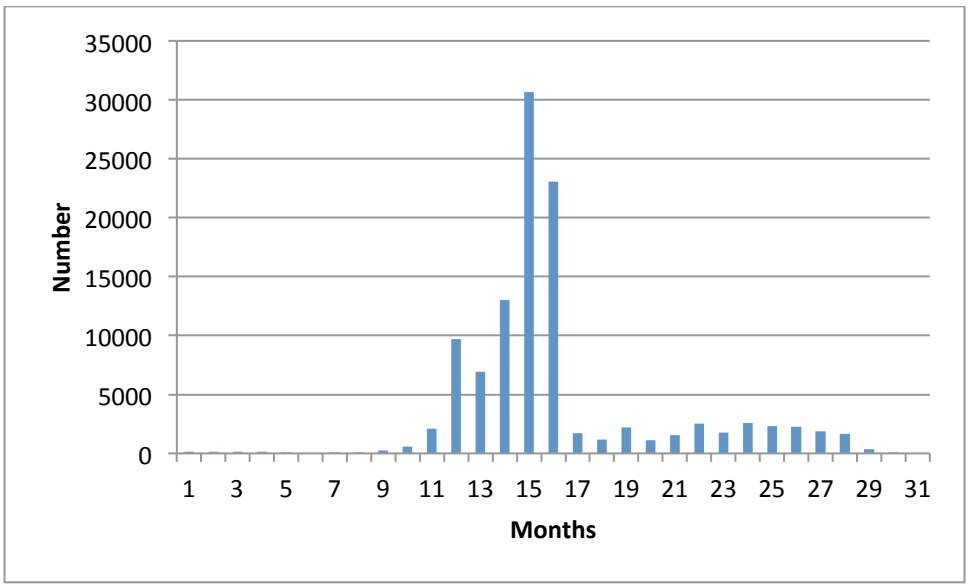

Figure S2. Distribution of saliva sample storage times prior to processing, in months

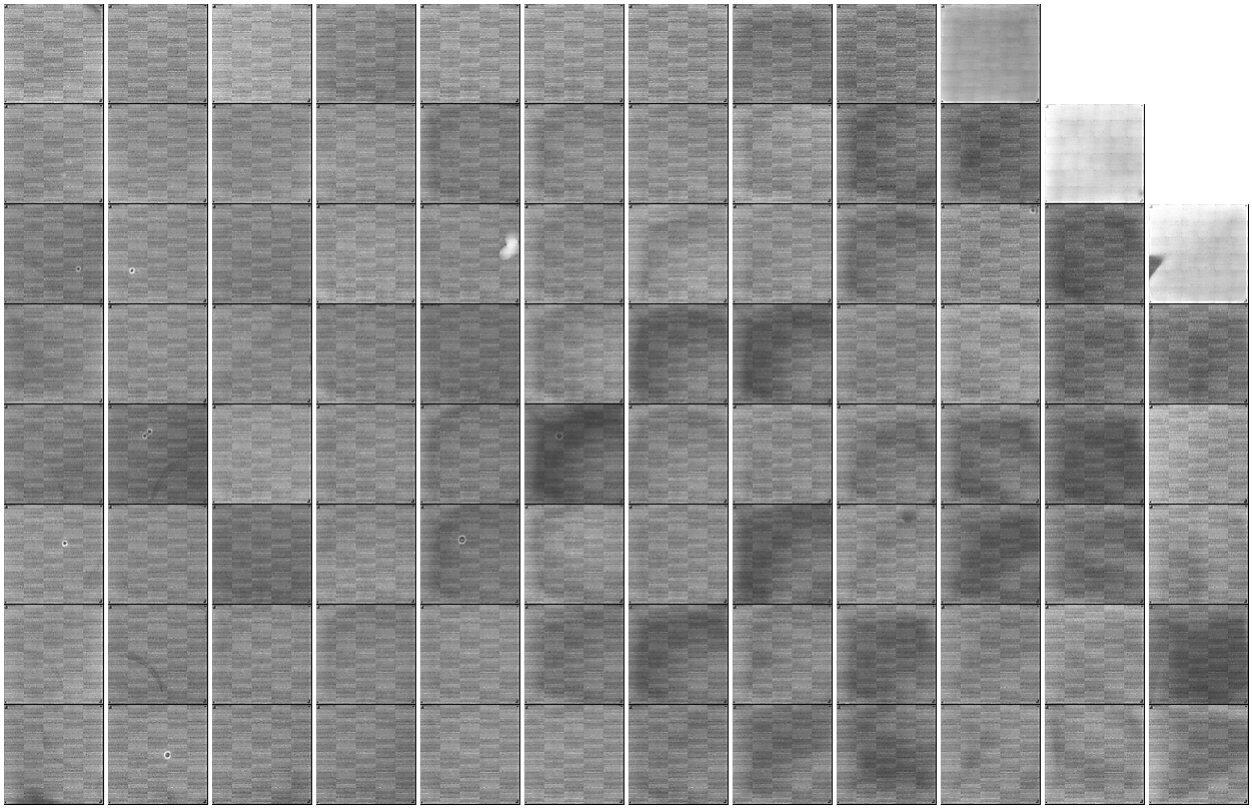

Figure S3. A montage of digital array images for an early Axiom plate assay. Note the problem in the upper right, due to an assay problem. Fast detection of such problems allowed us to fix them in a timely manner and avoid the problems in later plate assays.

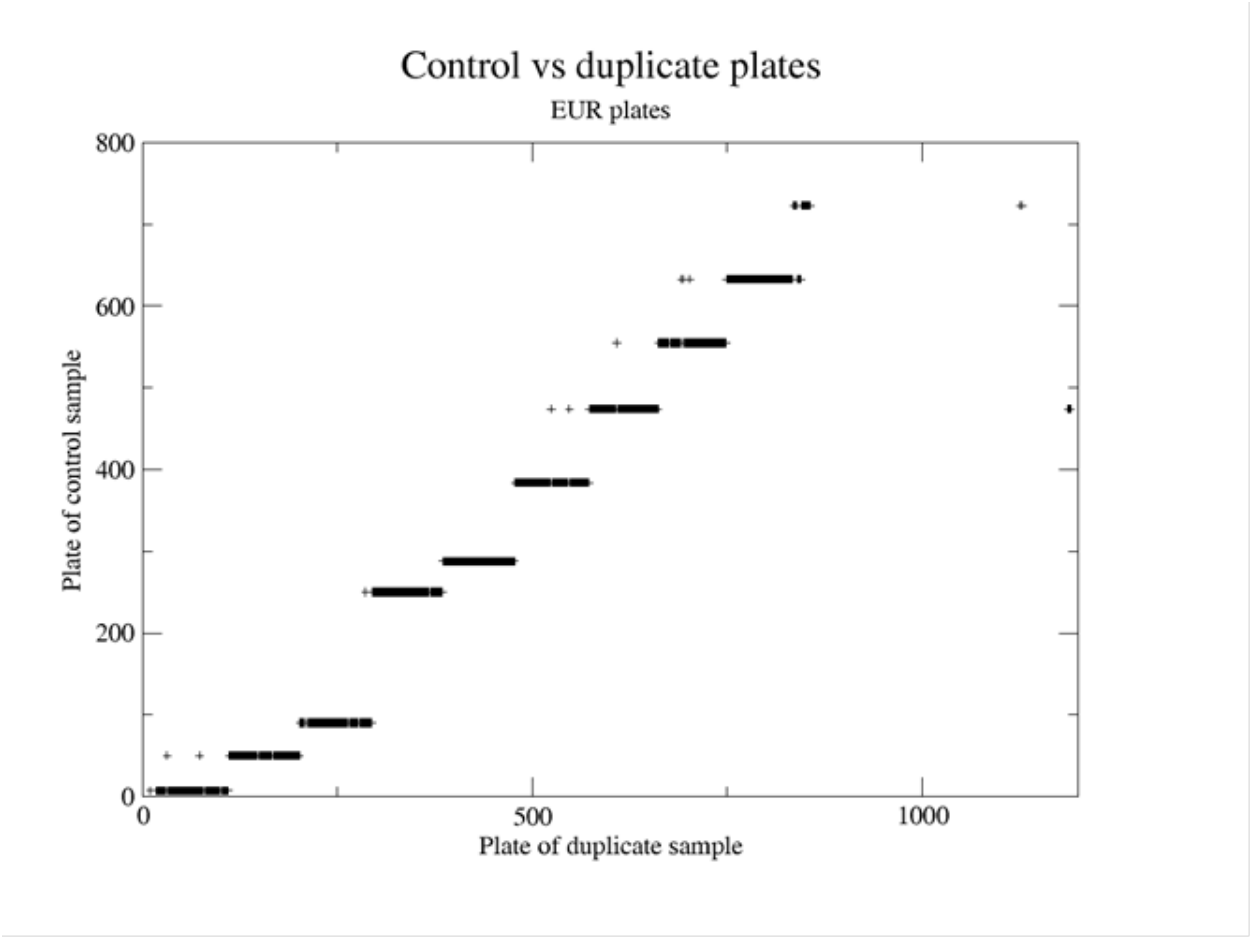

Figure S4. The distribution of Axiom plate numbers (up to plate 730) of duplicate control sample versus original control sample.

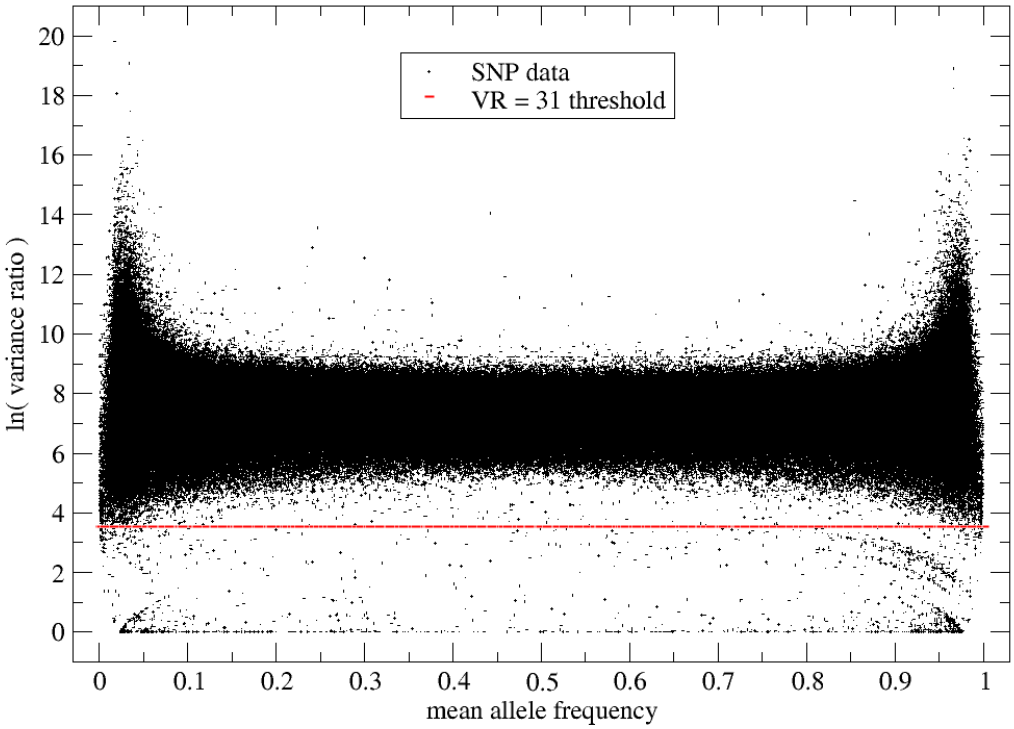

Figure S5. A scatterplot of the natural log of the variance ratio (VR) versus mean allele frequency for each SNP in the EUR dataset. The chosen variance ratio threshold of 31 is shown in red.

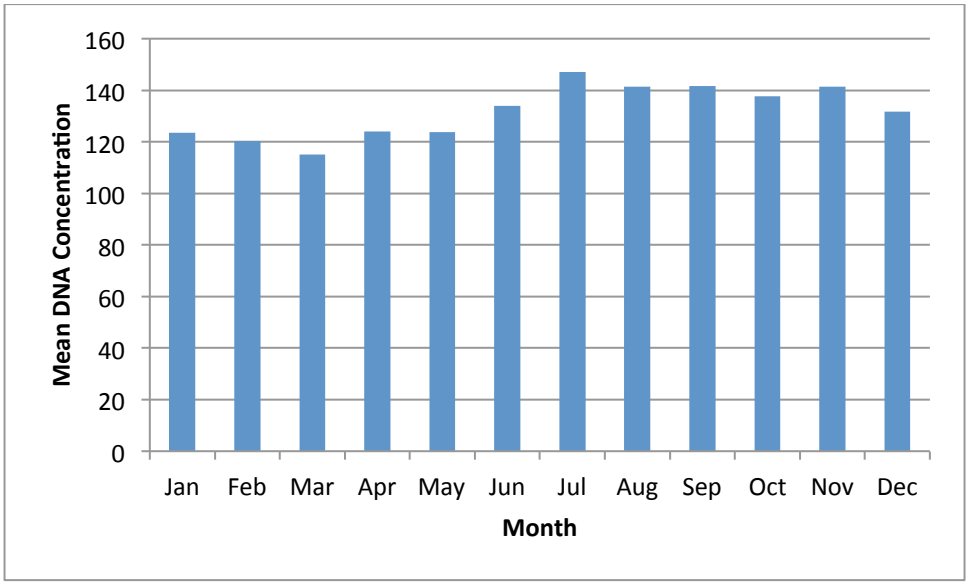

Figure S6. Mean DNA concentration by month of the year

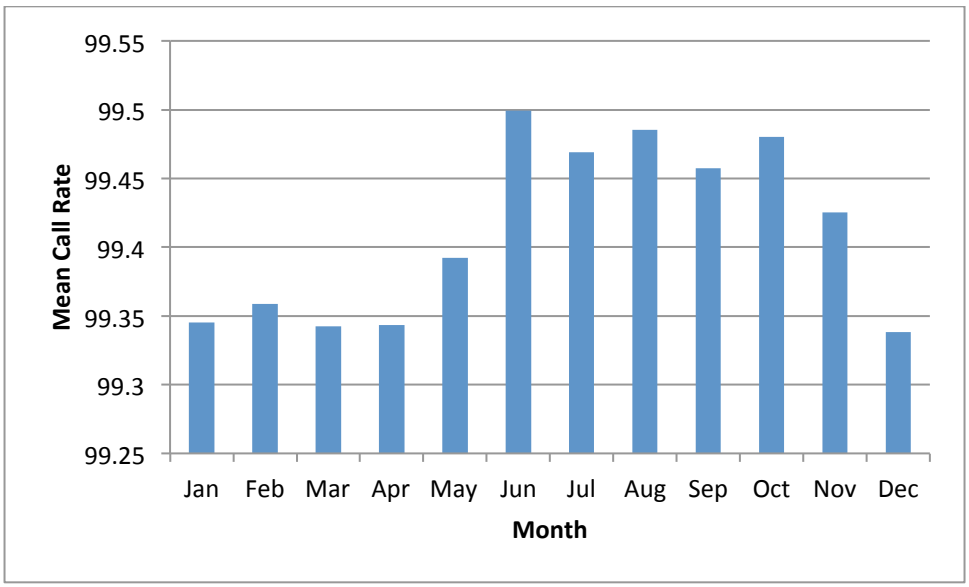

Figure S7. Mean initial call rate (CR1) by month of the year

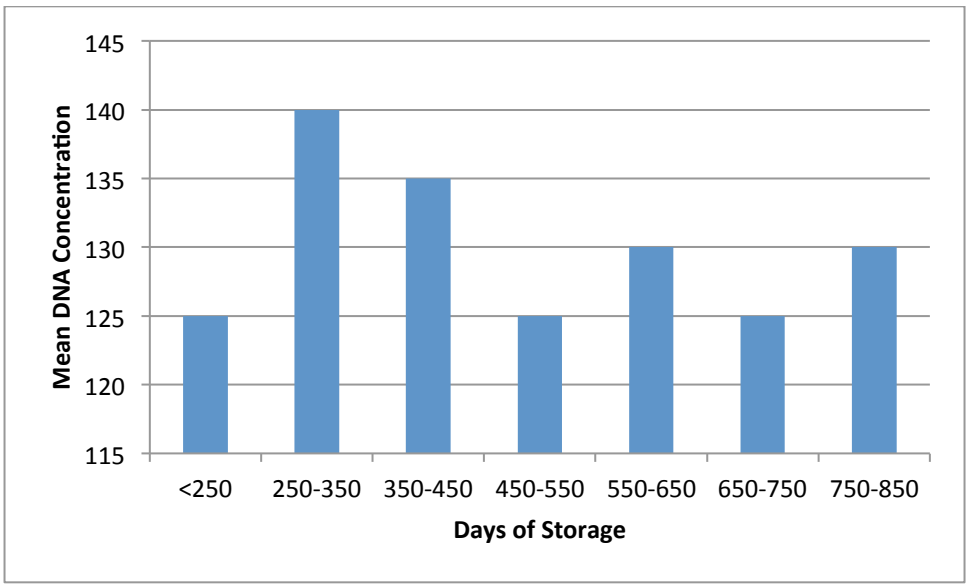

Figure S8. Mean DNA concentration by saliva sample storage time, in 100 day intervals

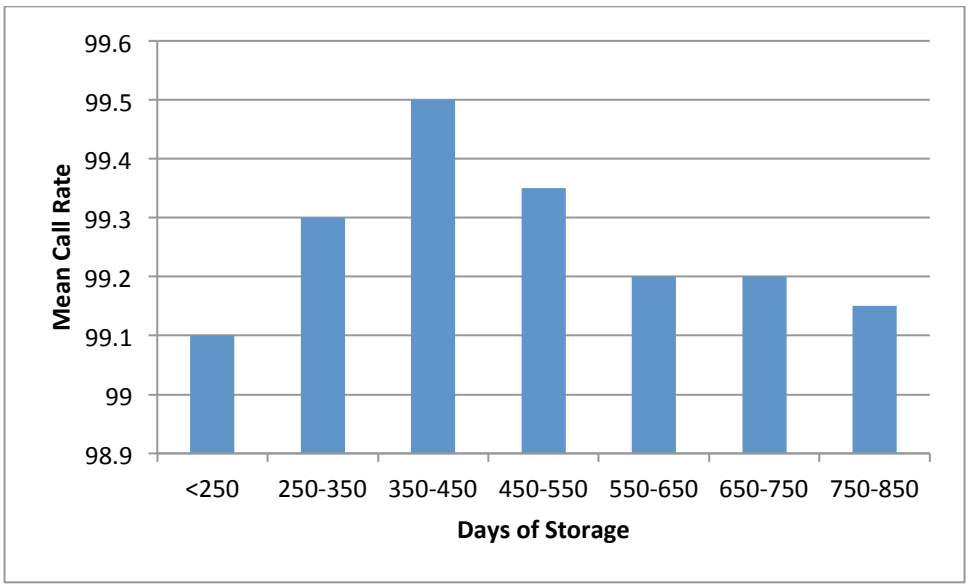

Figure S9. Mean initial call rate (CR1) by saliva sample storage time, in 100 day intervals

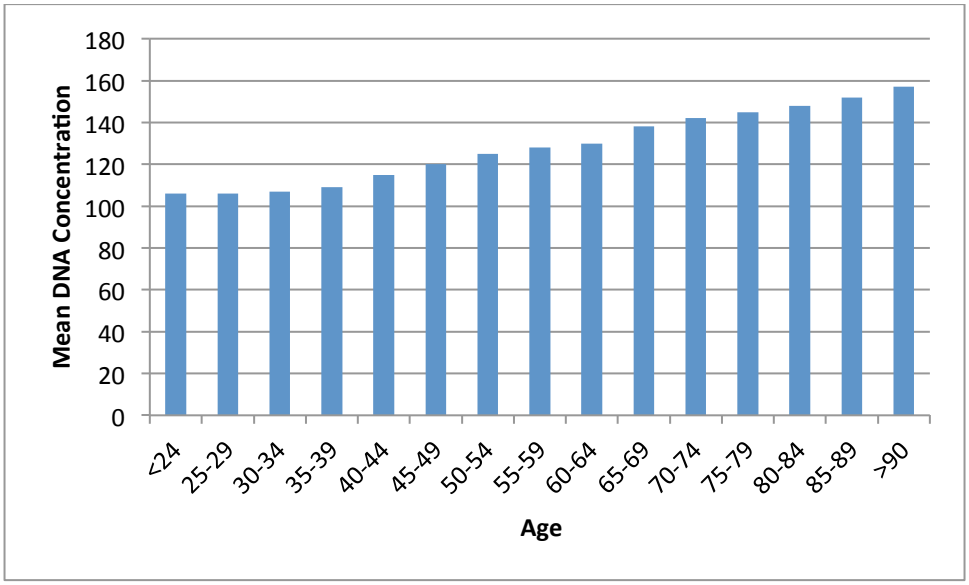

Figure S10. Mean DNA concentration by age of study subject

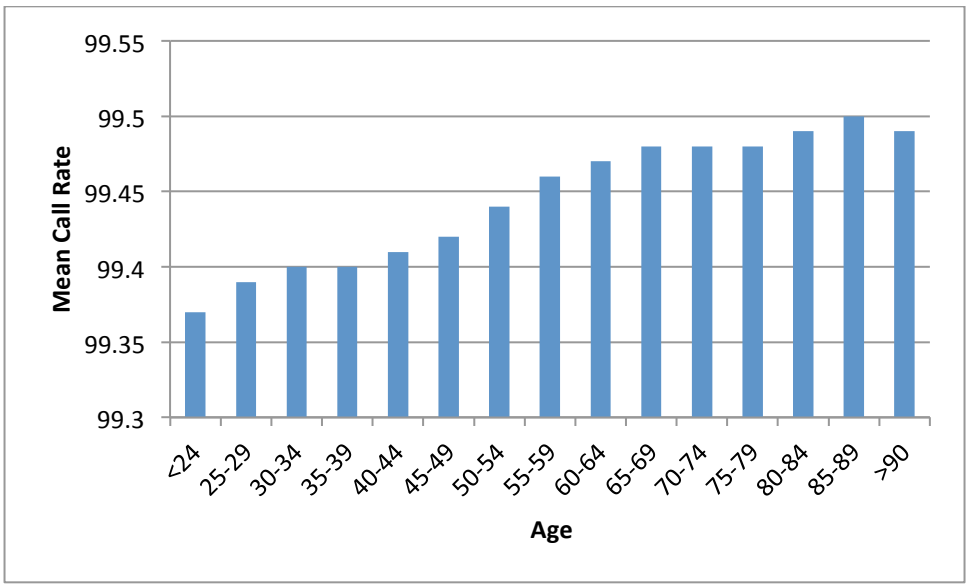

Figure S11. Mean initial call rate (CR1) by age of study subject

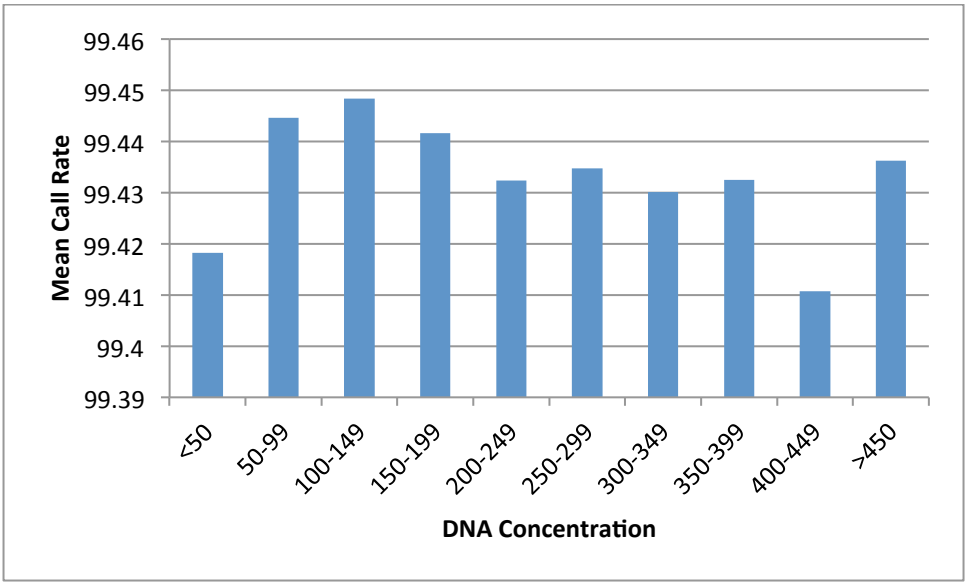

Figure S12. Mean initial call rate (CR1) by DNA concentration.

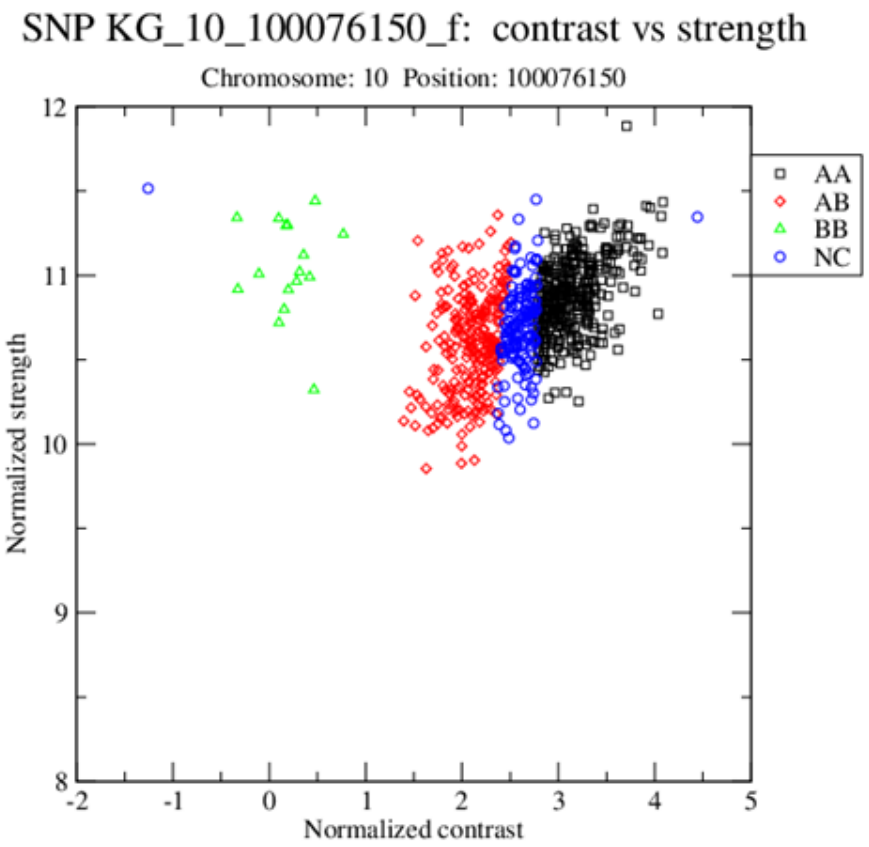

Figure S13. A normalized log intensity plot showing an example of a cluster split of a dominant AA cluster into incorrect AA and AB clusters. The cluster split also forces the miscall of the AB cluster as an incorrect BB cluster.

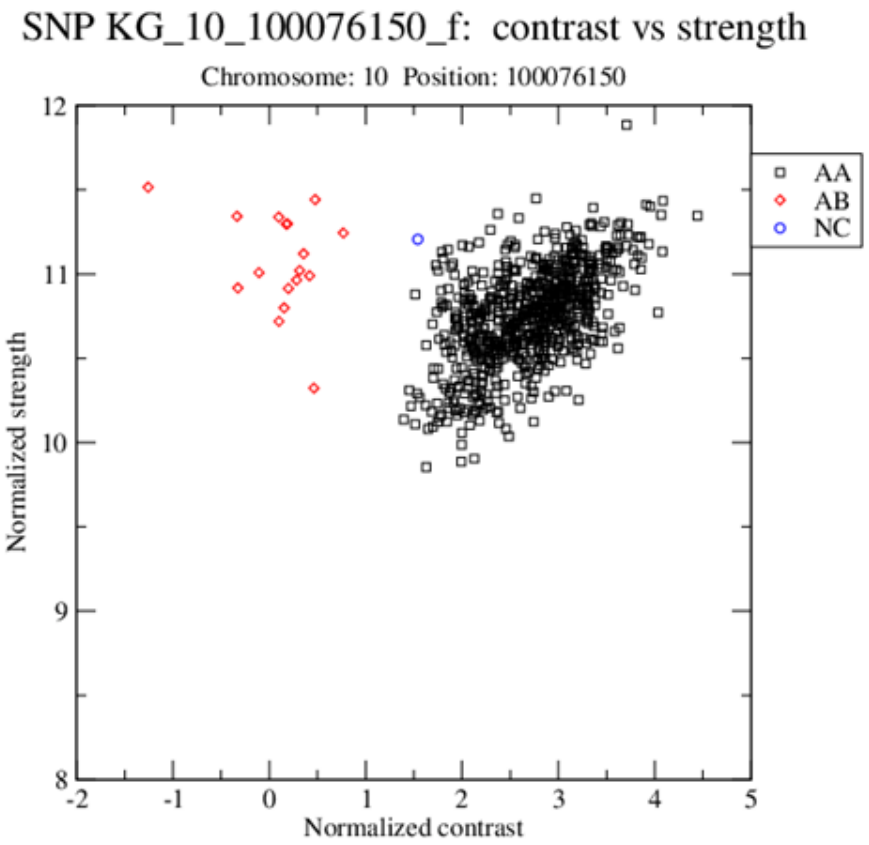

Figure S14. The same probe set as in Figure S13 but with the APT CSepPen parameter set at 0.15 instead of 0.10. The altered parameter avoids a cluster split and yields more accurate AA and AB clusters.