

### Appendix 3. Erroneous SNPs identified.

GenomeStudio's heritability report algorithm was used to identify potentially discrepant parent-child relationships and reveal non-Mendelian genotyping errors. Erroneous SNPs were removed prior to homozygosity analysis with PLINK. More than 99.9% of SNPs are inherited in a Mendelian manner from unaffected mothers to probands verifying correct parent child relationship.

Proband	Unaffected Parent	Correct SNPs	Erroneous SNPs	Total SNPs	P-C Heritability Freq
1.III-1	1.II-2	591009	69	591078	0.9998832
2.V-2	2.IV-2	590820	83	590903	0.9998595
3.III-1	3.II-2	590903	95	590998	0.9998392
3.III-7	3.II-6	590934	67	591001	0.9998866