

Mendel Error (All parental genotypes)

father	mother	R/R	R/A	A/A	Error %	HomHet	Het %
R/R	R/R	14889	210	38	1.64	nan	nan
R/R	R/A	3403	3497	74	1.06	0.97	50.68
R/R	A/A	176	1482	155	18.26	nan	nan
R/A	R/R	3665	3652	68	0.92	1.00	49.91
R/A	R/A	1015	3151	990	0.00	0.64	61.11
R/A	A/A	43	1300	1401	1.57	1.08	48.13
A/A	R/R	172	1365	147	18.94	nan	nan
A/A	R/A	47	1164	1183	1.96	1.02	49.60
A/A	A/A	20	78	5637	1.71	nan	nan

Mendel Error (Collapsed genotypes)

Parental		R/R	R/A	A/A	Error %	HomHet	Het %
R/R	R/R	14889	210	38	1.64	nan	nan
R/R	R/A	7068	7149	142	0.99	0.99	50.28
R/R	A/A	348	2847	302	18.59	nan	nan
R/A	R/A	1015	3151	990	0.00	0.64	61.11
R/A	A/A	90	2464	2584	1.75	1.05	48.81
A/A	A/A	20	78	5637	1.71	nan	nan

Mendel Error (Collapse parental allelotypes)

Parental		R/R	R/A	A/A	Error %	HomHet	Het %
HOM	HOM	14909	288	5675	1.66	nan	nan
HOM	HET	7158	9613	2726	1.19	1.00	49.90
HET	HET	1015	3151	990	0.00	0.64	61.11
HOMREF	HOMALT	348	2847	302	18.59	nan	nan

Mendel Error Overall Summary

total mendelian error	2.505 %
no. of trios	2
no. of variants	25346