

a

Number of characterized SNPs with $\geq 10\%$ discordant genotypes (LOD 2)

Metric	Apparent Array Err (867 SNPs)	Apparent Seq Err (2245 SNPs)	Unresolved (204 SNPs)
In duplicated region	246	89	29
SNP neighbor within 50bp	340	784	89
SNP neighbor within 5bp	103	337	33
Mislabeled probe	8	118	24
Allele balance	0	191	4
Similar het/ref sequence base qualities	0	0	0
Homopolymer run	0	0	0
At most 2 haplotypes	2	38	24
Sequence read mapping quality	5	1	3
Sequence read mapping quality of zero	2	1	0
Similar het/ref read mapping qualities	0	0	0
Confidence of sequence call	0	0	0
Similar het/ref read position bias	3	117	15
Likelihood of strand bias	1	1	1
Total	528	1114	143

b

Number of characterized SNPs with $\geq 25\%$ discordant genotypes (LOD 2)

Metric	Apparent Array Err (351 SNPs)	Apparent Seq Err (225 SNPs)	Unresolved (96 SNPs)
In duplicated region	142	13	10
SNP neighbor within 50bp	131	77	38
SNP neighbor within 5bp	33	25	18
Mislabeled probe	6	53	22
Allele balance	0	0	0
Similar het/ref sequence base qualities	0	0	0
Homopolymer run	0	0	0
At most 2 haplotypes	2	19	19
Sequence read mapping quality	3	0	1
Sequence read mapping quality of zero	1	1	0
Similar het/ref read mapping qualities	0	0	0
Confidence of sequence call	0	0	0
Similar het/ref read position bias	0	4	3
Likelihood of strand bias	0	6	0
Total	241	148	72