

**Table S2.** Base call rates and accuracies of all individual samples with/without using user defined criteria.

Sample ID	Without Filters		With Filters	
	Call Rate (%)	Accuracy (%)	Call Rate (%)	Accuracy (%)
1	89.39	99.84	96.50	99.93
2	83.86	99.76	92.52	99.89
3	87.63	99.79	95.81	99.91
4	88.79	99.71	96.54	99.87
5	84.18	99.72	93.01	99.82
6	83.30	99.61	92.86	99.88
7	86.39	99.70	94.92	99.86
8	86.47	99.81	94.27	99.89
9	82.31	99.53	93.76	99.86
10	84.74	99.66	94.98	99.90
11	83.92	99.77	92.40	99.87
12	80.12	99.74	89.14	99.85
13	81.20	99.67	89.96	99.82
14	75.55	99.62	84.27	99.76
15	83.91	99.73	92.24	99.86
16	88.94	99.67	96.46	99.82
17	85.39	99.79	93.50	99.87
18	83.54	99.76	92.27	99.86
19	88.32	99.72	96.02	99.89
C1	88.65	99.71	96.15	99.89
C2	85.33	99.49	95.65	99.81
C3	88.61	99.80	95.82	99.91
C4	79.72	99.30	92.89	99.70
Average	84.79	99.69	93.56	99.86
Minimum	75.55	99.30	84.27	99.70
Maximum	89.39	99.84	96.54	99.93

Note: Without adopting user defined criteria, 267,550 bp (1508 exon fragments) per array were sequenced; with adopting user defined criteria, 181,897 bp (1050 exon fragments, ~70% of the tiled exon fragments) per array were efficiently sequenced. User defined criteria: filtering out fragments with consistently failed PCR assays at least for 8 samples; filtering out ones with a call rate of < 80% for at least for 4 samples. Sample #1-19, patient DNA; sample #C1-C4, CEPH control DNA.