Supporting Table 2. Chromosome-wise validation of SCNAs detected by COPS using whole genome SNP microarray.

Chr	CNA sizes from sequencing reads using COPS	CNA sizes found by using whole genome SNP microarray	% Overlap after adjusting coverage >= 1.5X	% Overlap after adjusting coverage >= 2.5X	% Overlap after adjusting coverage >= 5X	% Overlap after adjusting coverage >= 7.5X	% Overlap after adjusting coverage >= 10X	% Overlap after adjusting coverage >= 15X
1	39456276	10773720	87.43	93.97	98.99	99.84	99.97	100.00
2	55481916	23368947	87.19	93.73	98.92	99.81	99.97	100.00
3	32994154	198544	68.59	78.09	89.17	93.75	96.12	97.81
4	123756785	112241762	87.68	93.88	98.83	99.70	99.87	99.91
5	36875208	8142814	89.63	94.94	99.09	99.83	99.96	99.99
6	25221070	835279	70.19	79.35	91.91	96.92	98.97	99.89
7	2973684	8751693	84.33	92.36	98.64	99.74	99.93	99.98
8	20361798	388438	83.51	90.70	97.11	98.84	99.43	99.81
9	28267798	22242420	90.67	95.65	99.29	99.81	99.89	99.93
10	52298975	34672569	88.25	94.07	98.79	99.64	99.80	99.87
11	30253616	6978704	75.56	86.68	97.05	99.38	99.87	99.99
12	19433592	8511	89.27	94.13	99.41	100.00	100.00	100.00
13	15064650	NA*	NA	NA	NA	NA	NA	NA
14	14471659	745161	88.88	93.59	98.26	99.58	99.88	99.97
15	30176985	15184678	88.70	94.53	99.07	99.85	99.98	100.00
16	12237383	177784	61.05	71.88	85.57	91.37	94.32	97.19
17	23814203	15674745	87.48	93.98	99.00	99.83	99.97	100.00
18	11703900	NA	NA	NA	NA	NA	NA	NA
19	13122559	3015860	83.03	91.30	98.27	99.55	99.87	99.97
20	21331257	14209770	85.15	92.56	98.63	99.75	99.96	100.00
21	5182301	66771	9.81	14.23	26.13	37.11	45.50	61.81
22	5395036	NA	NA	NA	NA	NA	NA	NA
X	3811262	20231	93.60	96.79	98.76	99.51	99.75	100.00
Y	1074159	470352	97.01	98.75	99.84	99.99	100.00	100.00
All	651523026	278168753	80.81	87.39	93.85	95.90	96.81	97.91

*Not Applicable

Overlapping loci involved in SCNA events were estimated using COPS on tumor:normal mate-pair sequencing data and CNVPartitition2.4.4 plugin in GenomeStudio on Omni2.5M SNP array data for the same samples. The overlap was also estimated after systematically omitting reads not satisfying sequencing coverage thresholds of 1.5X, 2.5X, 5X, 7.5X, 10X and 15X, respectively, for either normal or tumor samples.