

S3 Table. Sample-specific features of non-validated CNVs.

Software	Total number	Median length [kb]	Median cumulated length [Mb]	Median number of markers in CNV	Median inter-marker distance [kp]	DDR
APT	43.0 (34.8 - 57.2)	8.1 (6.4 - 10.0)	1.9 (1.4 - 3.3)	6.2 (4.0 - 10.0)	0.30 (0.22 - 0.37)	4.7 (3.3 - 6.5)
GLAD	92.0 (63.5 - 127.8)	6.6 (5.7 - 7.5)	3.3 (1.9 - 4.9)	4.0 (4.0 - 5.5)	0.30 (0.23 - 0.40)	2.0 (1.2 - 2.9)
PennCNV	29.0 (18.0 - 35.2)	26.2 (17.3 - 44.8)	2.0 (1.5 - 3.4)	23.0 (19.4 - 29.0)	0.25 (0.17 - 0.35)	4.8 (3.7 - 6.6)
QuantiSNP	75.0 (60.0 - 92.2)	7.9 (6.9 - 10.2)	3.0 (2.1 - 5.8)	4.0 (4.0 - 5.5)	0.31 (0.26 - 0.40)	2.9 (2.4 - 4.1)
R-gada	130.0 (107.5 - 169.2)	7.6 (6.2 - 8.9)	100.6 (16.4 - 266.8)	6.0 (5.0 - 8.1)	0.35 (0.31 - 0.44)	5.5 (3.9 - 7.4)
VEGA	89.5 (72.8 - 120.2)	6.0 (5.2 - 7.4)	3.6 (2.5 - 5.9)	5.0 (4.0 - 6.0)	0.37 (0.29 - 0.43)	4.5 (3.1 - 6.2)
Algorithm Type						
HMM	43.0 (34.0 - 52.0)	9.3 (7.8 - 11.4)	2.2 (1.7 - 3.6)	7.0 (5.0 - 10.0)	0.29 (0.23 - 0.36)	4.3 (3.2 - 5.2)
Segmentation	103.0 (86.2 - 141.5)	6.7 (5.7 - 7.6)	4.2 (3.0 - 6.0)	5.0 (4.0 - 6.0)	0.35 (0.28 - 0.41)	4.3 (3.1 - 5.2)

Given are the median and, in parentheses, the inter-quartile range. **DDR**: Ratio of deletions to duplications.