Supplementary Table 1. Comparison between frequencies of previously reported CNVs in the DGV database and the identified CNV in our study

CNV region	Type	Frequency (%)	No. of samples	Population
chr20: 43307048–43308657[a]	Loss	8.76	181	African (92) Asian (29) European (60)
chr20: 43305884–43308885[a]	Loss	45.56	1169	African (235) Asian (460) European (224) Mexican (32) Native American (72) North American (16) South American (130)
chr20: 43304545–43310592[a]	Loss	11.50	210	African (34) Asian (54) European (73) South American (49)
chr20: 43296138–43309931[a]	Loss	0.08	2	Asian (1) European (1)
chr20: 43306032–43308125[b]	Loss Normal	38.27 61.73	1,537	Korean

The positions of each CNV were defined based on hg19/NCBI build 37.

CNV, copy number variation; DGV, Database of Genomic Variant.

[a]CNVs reported in DGV (http://dgv.tcag.ca/dgv/app/home).

[b]A CNV identified in our study.