

Table S3. Concordance between duplicates and agreement between orthogonal genotyping methods.

	iCOGS SNPs	OncoArray Indels	TOTAL
Samples	13779	4320	
Polymorphic variants	37	80	
No found on sequencing	4	7	
Rare variants (MAF<0.01)			
Variants	26	70	
Correctly called by sequencing	716	543	1259
Incorrectly called by sequencing	5	11	16
Not called by sequencing	12	43	55
Variant not found by sequencing	13	15	28
Sensitivity (called genotypes only)	99.30%	98.00%	98.70%
Sensitivity (all known heterozygotes)	95.98%	88.70%	92.70%
Common variants (MAF>=0.01)			
Variants	11	10	21
Concordant	145744	42987	188731
Not concordant	71	2	73
Concordance	99.95%	99.995%	99.96%