Supplemental Table 1: Further classification based on sequence similarity to previously characterized reference databases for satellite repeats: alpha, beta, gamma, HSat 1-6, and subtelomeric repeats.

		GRCh37/hg19 Mapping Targets				**GRCh38/hg38 Mapping Targets**			
	Total Reads	**Align to hg19**	**Filtered Reads based on Parology to Reference Assembly**	**Remaining**	**Est Genome %**	**Align to hg38**	**Filtered Reads based on Parology to Reference Assembly**	**Remaining**	**Est Genome %**
Alpha Satellite (ALR,ALR1,ALR2,ALRa,b)	826394	172295	9486	816908	2.58248125	172301	64305	762089	2.58248125
HSAT II, III (GGAAT)	456231	391016	52968	403263	1.425721875	391033	66231	390000	1.425721875
HSAT I (HSATI,SAR)	39270	35790	130	39140	0.12271875	35827	378	38892	0.12271875
Gamma Satellite (GSAT, GSATII, GSATX)	42311	833	187	42124	0.132221875	836	258	42053	0.132221875
Beta Satellite (BSR,BSRa,BSRb,BSRd,BSRf,LSAU)	6858	6791	1414	5444	0.02143125	6818	1873	4985	0.02143125
rDNA	214862	210941	105855	109007	0.67144375	211288	141555	73307	0.67144375
HSAT IV	8	7	5	3	0.000025	7	5	3	0.000025
ACRO1	3538	3519	171	3367	0.01105625	3519	1765	1773	0.01105625
CER	2596	2588	977	1619	0.0081125	2588	1586	1010	0.0081125
D20S16	102	100	44	58	0.00031875	100	46	56	0.00031875
MSR1	51	50	29	22	0.000159375	50	30	21	0.000159375
REP522	442	439	250	192	0.00138125	439	295	147	0.00138125
SATR1,2	873	868	587	286	0.002728125	868	628	245	0.002728125
SN5	131	131	83	48	0.000409375	131	84	47	0.000409375
TAR1	296	293	143	153	0.000925	293	187	109	0.000925