

**Supplementary table 1.** Characterization of 454 shotgun sequences obtained from two independent sequencing libraries.

sample ID	tag	454 sequence coverage				differences to Sanger sequences					
		number of 454 sequences	average coverage [-fold]	uncovered positions	positions covered < 3-fold	Sanger sequence accession numbers	Number of 454 consensus positions	single base pair insertions / deletions	substitutional differences	frequency of indels [%]	frequency of substitutions [%]
WE4	ATCGAC	4154	21.9	0	0	AY289082	16569	15 / 11	0	0.16	0.000
SH19	TCGCTG	2071	11.1	2	26	AY289089	16538	12 / 36	0	0.29	0.000
SanC2	TATCGC	3026	16.0	49	16	EF184593	16578	26 / 26	1	0.31	0.006
SanC3	ACTCTC	2561	13.2	0	63	EF184611	16541	15 / 23	0	0.23	0.000
SanC5	TGTGAC	3645	18.3	0	9	EF184590	16582	21 / 17	1	0.23	0.006
SanC6	TCACAC	1995	9.7	23	265	EF184592	16594	48 / 21	2	0.42	0.012
						mean		23 / 22	0.67	0.27	0.004
human1	ATCGAC	4449	25.3	6	35	n/a					
human2	TCGCTG	3523	19.9	0	59	n/a					
human3	TATCGC	4657	26.2	0	62	n/a					
human4	ACTCTC	5731	31.6	0	0	n/a					
human5	AGATAG	3267	18.5	3	119	n/a					
human6	TAGACG	3474	20.3	0	106	n/a					

**Supplementary table 2.** Oligonucleotide sequences.

long range PCR primers		barcoding oligonucleotides	
huChrM-amp1-fwd	5'-GGCTTTCTCAACTTTTAAAGGATA-3'	BC1-ATCGAC	5'-GTCGATGCCCCGGGCATCGAC-3'
huChrM-amp1-fwd-blocked	5'-C6 Amino-GGCTTTCTCAACTTTTAAAGGATA-3'	BC2-TCGCTG	5'-CAGCGAGCCCGGGCTCGCTG-3'
huChrM-amp1-rev	5'-TGTCTTGATCCAACATCGAG-3'	BC3-TATCGC	5'-GCGATAGCCCGGGCTATCGC-3'
huChrM-amp1-rev-blocked	5'-C6 Amino-TGTCCTGATCCAACATCGAG -3'	BC4-ACTCTC	5'-GAGAGTGCCCCGGGCACTCTC-3'
huChrM-amp2-fwd	5'-CCGTGCAAAGGTAGCATAATC-3'	BC5-TGTGAC	5'-GTCACAGCCCGGGCTGTGAC-3'
huChrM-amp2-fwd-blocked	5'-C6 Amino-CCGTGCAAAGGTAGCATAATC -3'	BC6-TCACAC	5'-GTGTGAGCCCGGGCTCACAC-3'
huChrM-amp2-rev	5'-TTACTTTTATTTGGAGTTGCACCA-3'	BC7-AGATAG	5'-CTATCTGCCCCGGGCAGATAG-3'
huChrM-amp2-rev-blocked	5'-C6 Amino-TTACTTTTATTTGGAGTTGCACCA -3'	BC8-TAGACG	5'-CGTCTAGCCCCGGGCTAGACG-3'