

Table S3. Detailed information of BAC clone assemblies generated from SMRT sequencing data.

BAC Clones	Assembly Size (bp)	#Scaffolds	Min (bp)	Max (bp)	GC^a%	Lab.^b	Assembly Fraction^c (%)
194E12 ^d	155,628	1	155,628	155,628	59.7	WSM	72
288L23 ^d	186,195	7	886	57,130	58.3	SciLife	NA
50P17 ^d	147,467	1	147,467	147,467	58.6	WSM	70
52P20	66,939	2	852	66,087	54.4	SciLife	34
159K1 ^d	47,668	4	1,660	27,250	53.5	SciLife	NA
442L16	58,892	1	58,892	58,892	55.9	WSM	31
291B18 (1)	107,104	3	23,331	45,533	54.7	WSM	60
291B18 (2)	67,454	2	899	66,555	53.5	SciLife	38
712C2 ^d	140,175	1	140,175	140,175	55.8	WSM	NA
419P11 ^d	73,186	1	73,186	73,186	57.9	WSM	37

^a GC content of assembly.

^b Labs that sequenced BAC clones. WSM: Washington School of Medicine, Washington, United States of America. SciLife: Science for Life laboratory, Uppsala, Sweden.

^c Fraction of BAC assembled based on anticipated size from BAC end sequence alignment. NA=not applicable because the anticipated size of the BAC is not known.

^d These BACs were included in the previously published PAR BAC contig map (see Raudsepp et al., 2008).