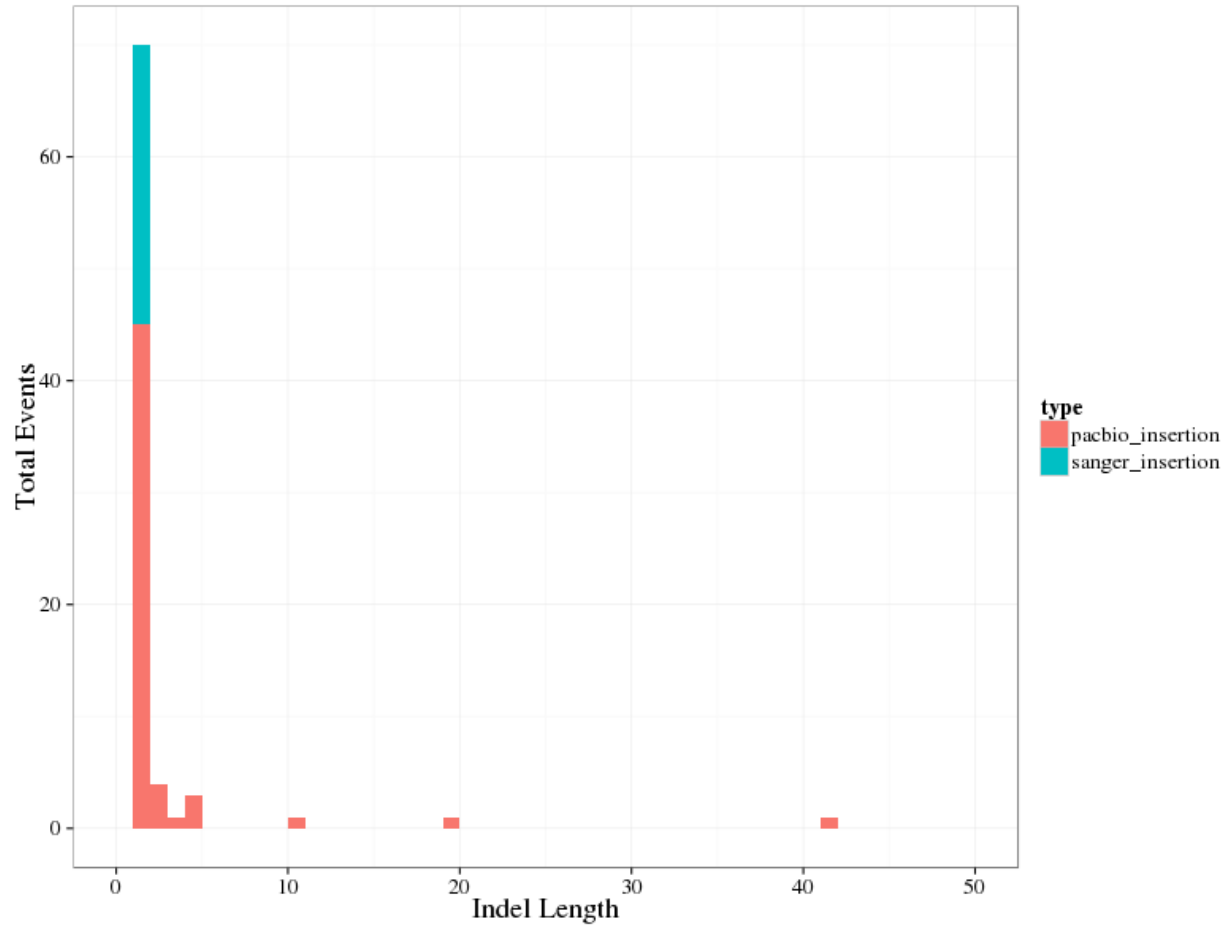
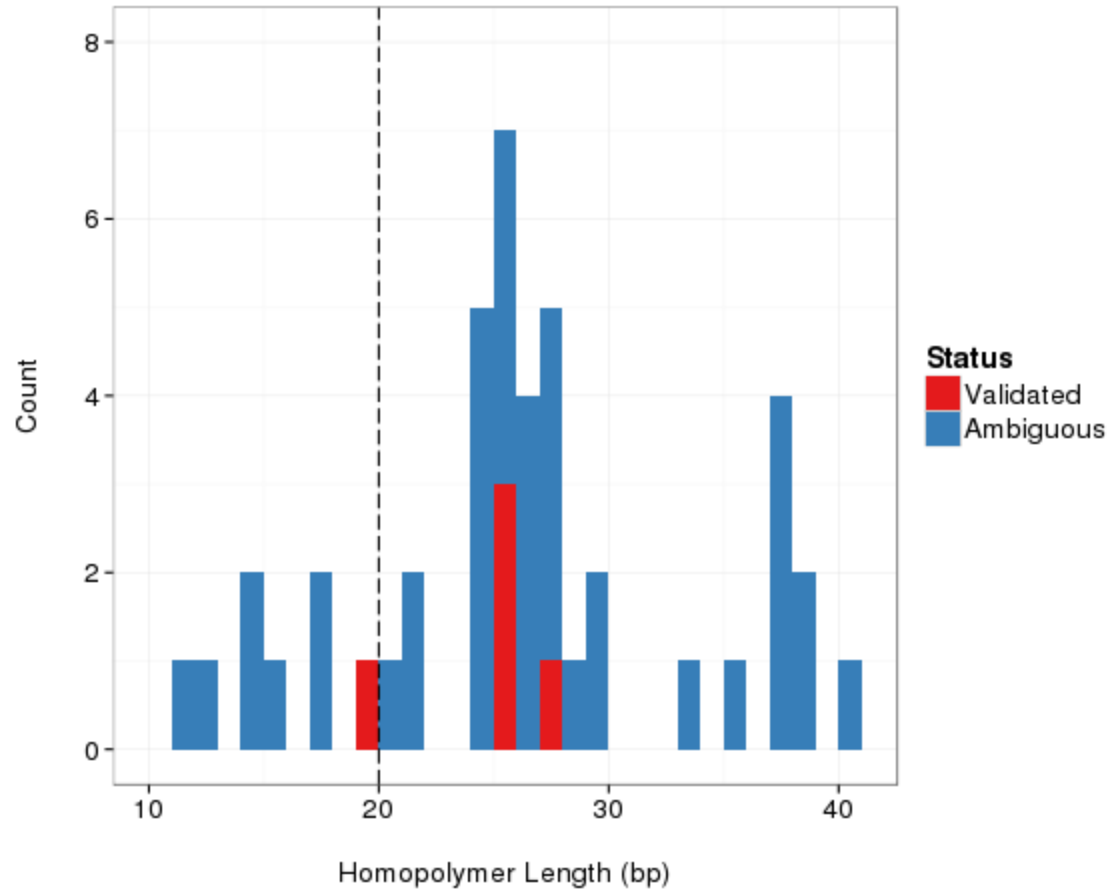


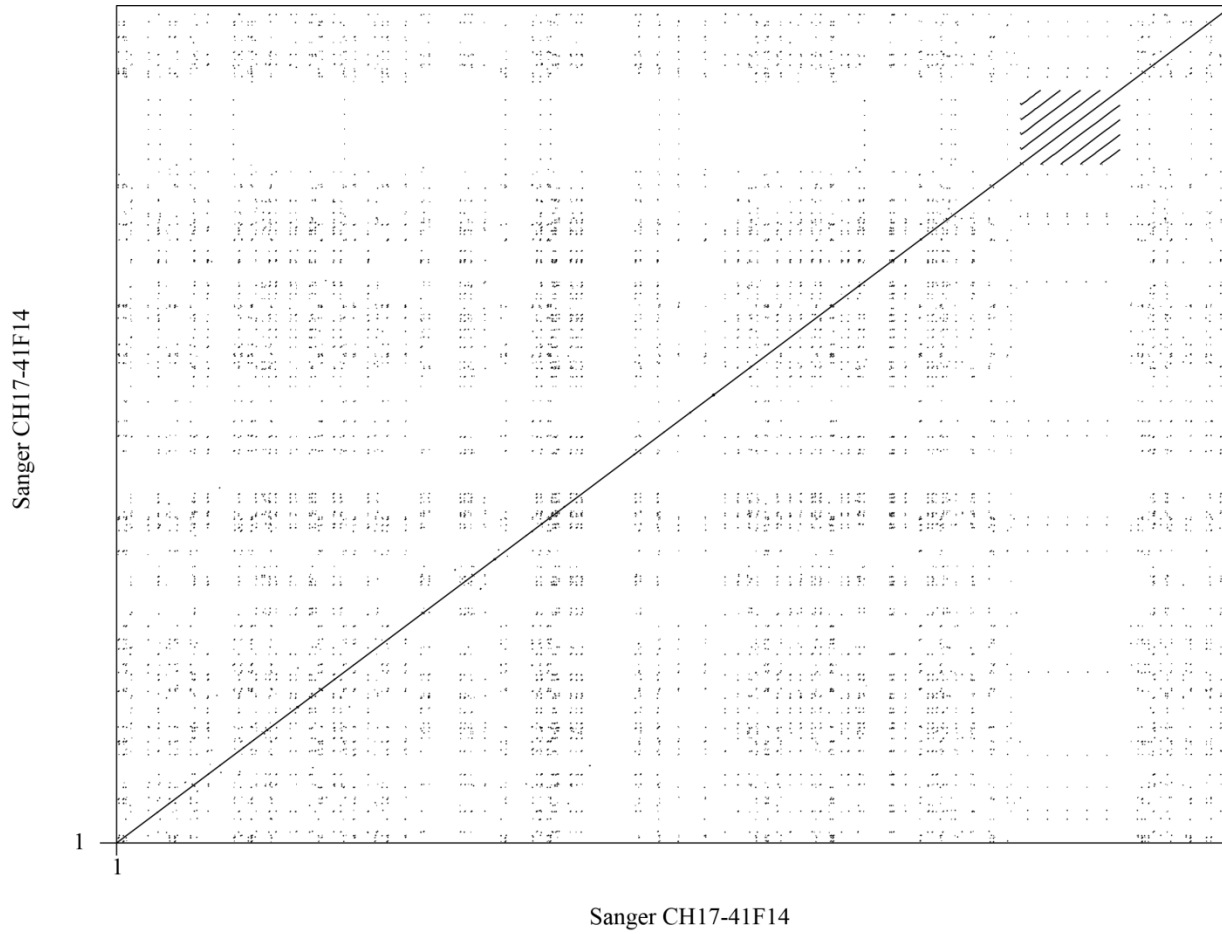
Supplementary Figure 1



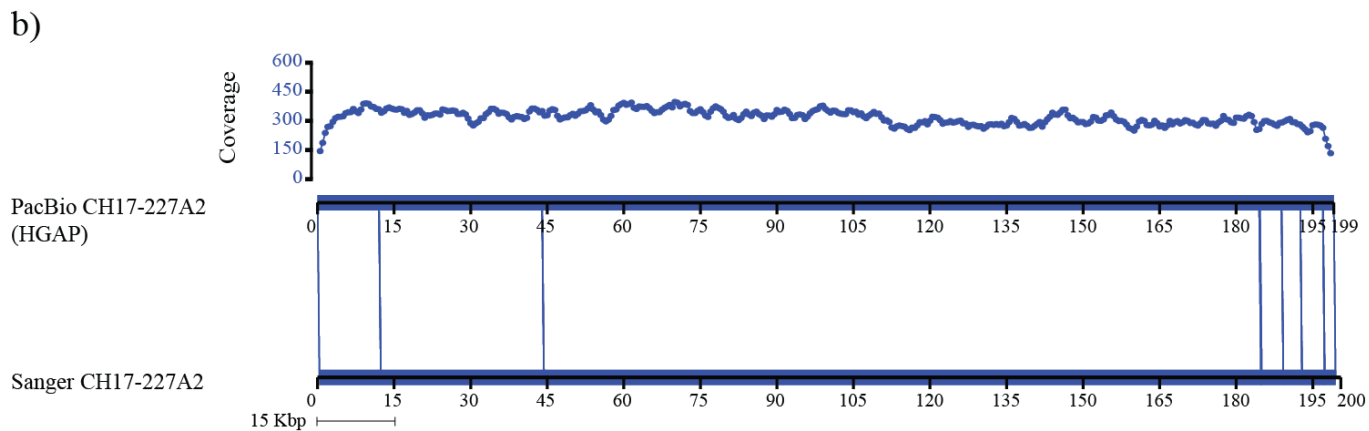
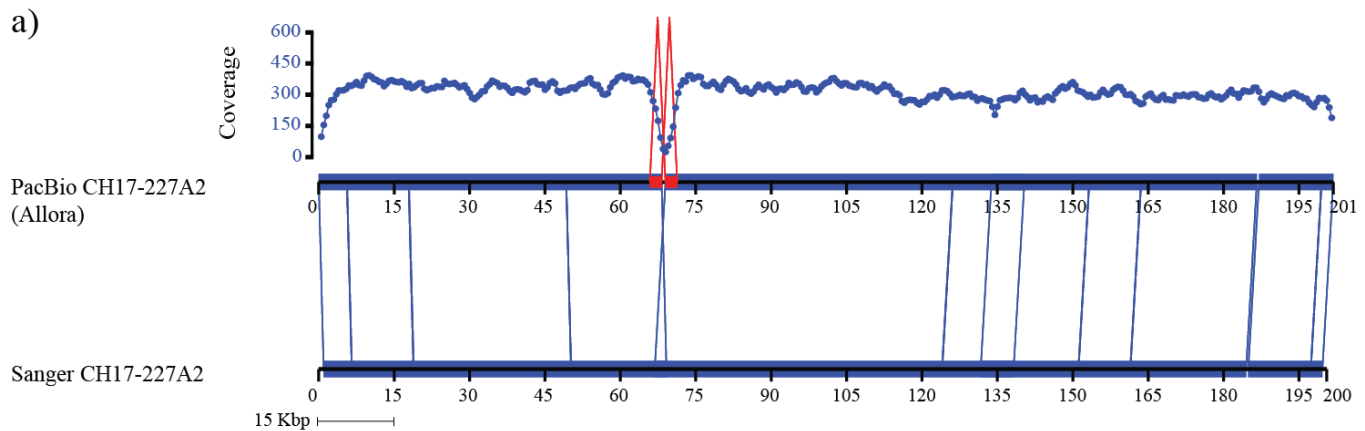
Supplementary Figure 2



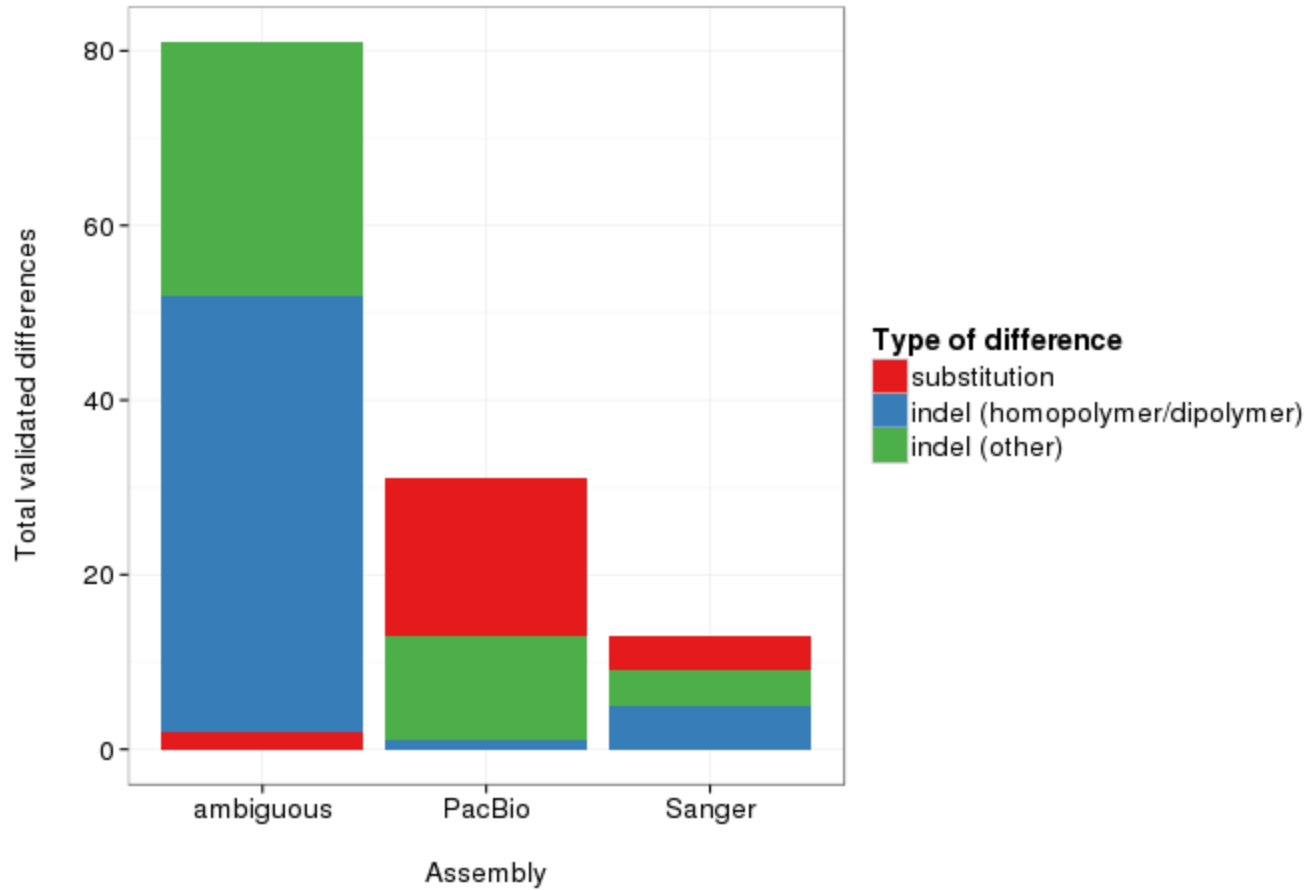
Supplemental Figure 3



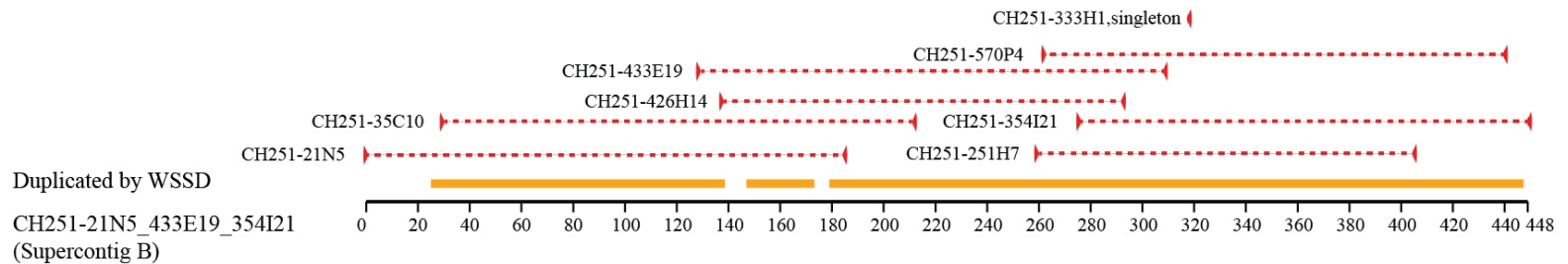
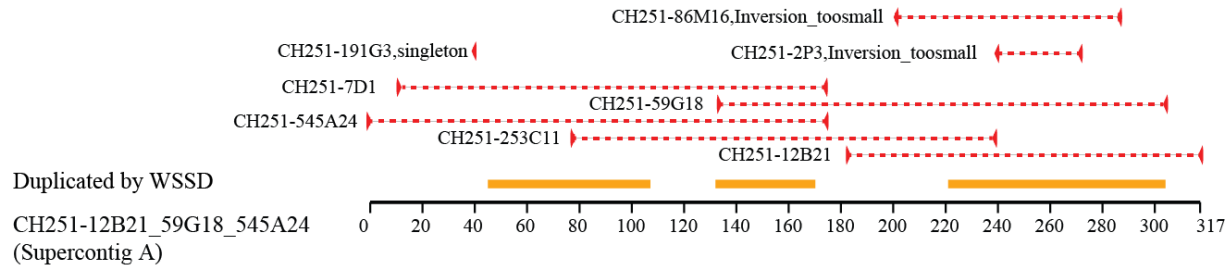
Supplementary Figure 4



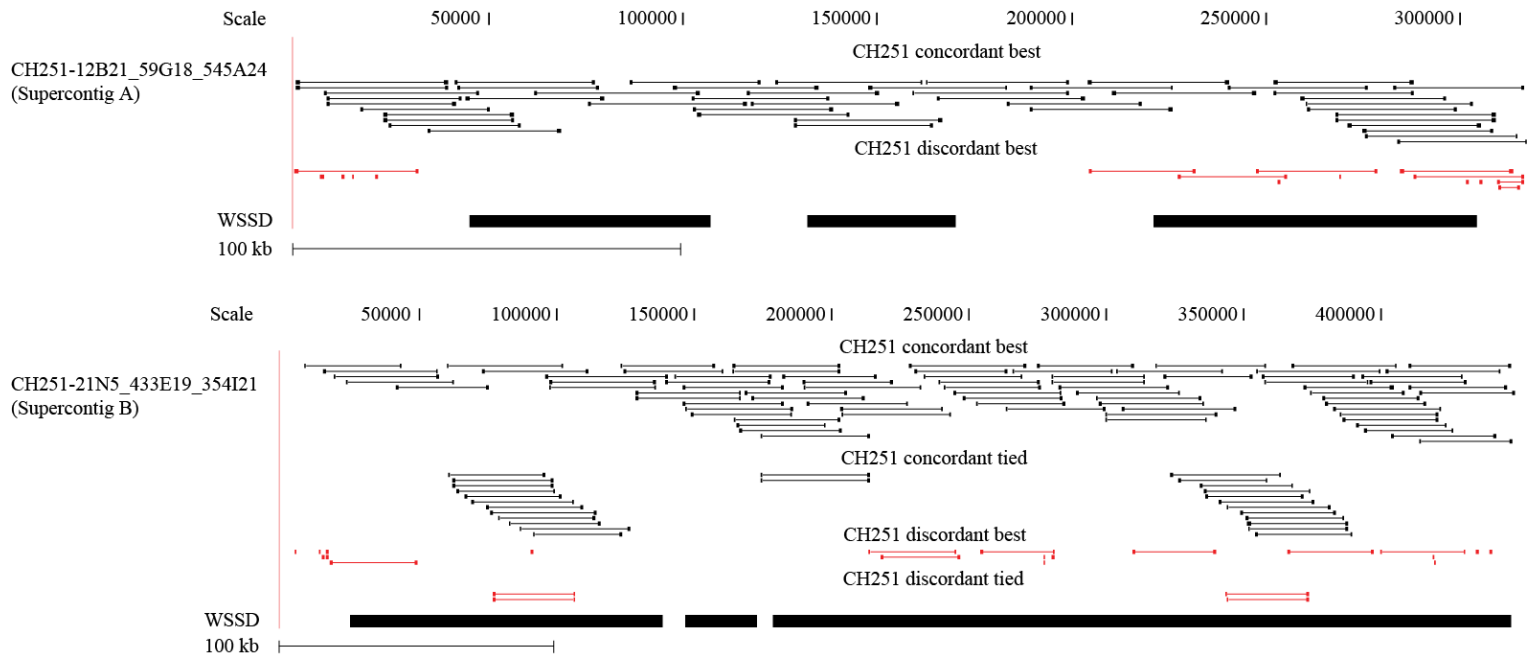
Supplementary Figure 5



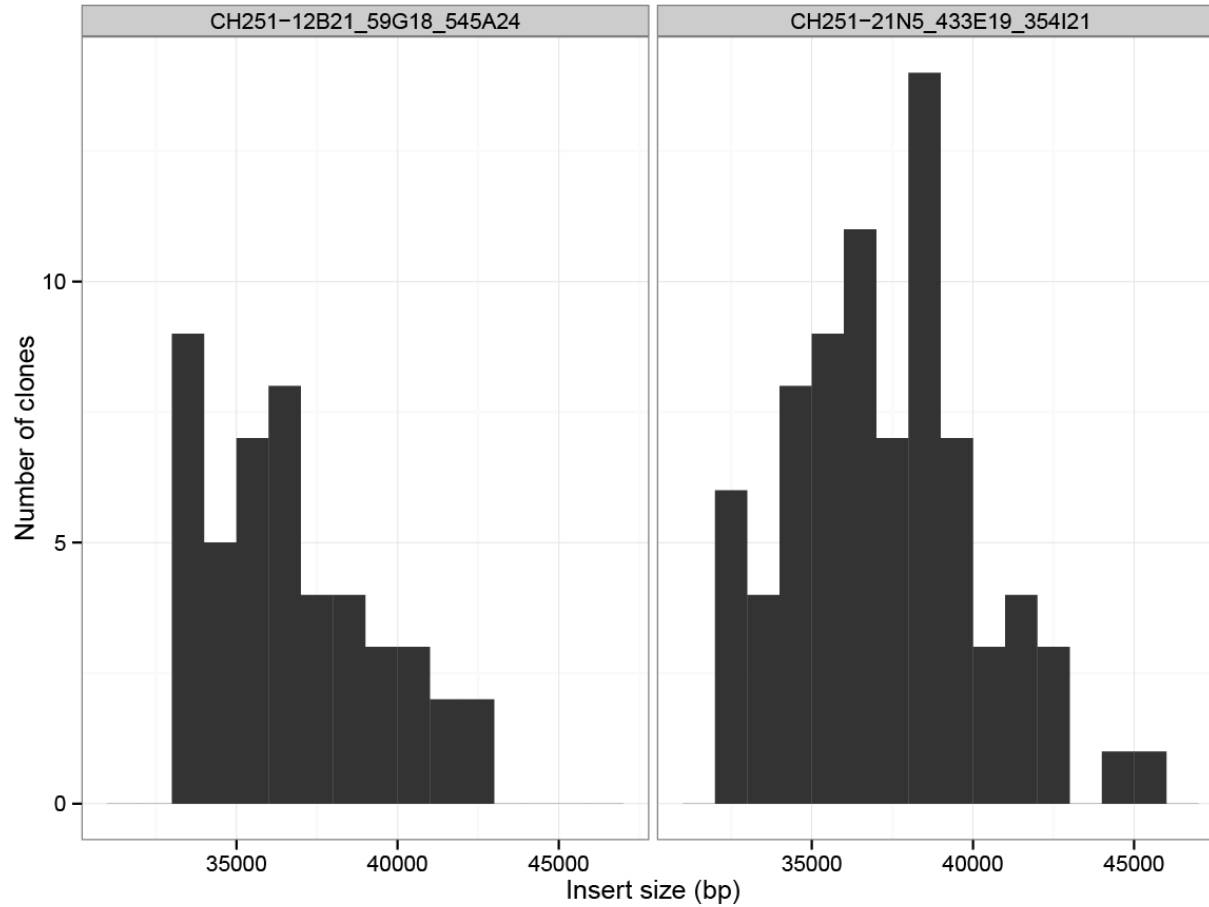
Supplementary Figure 7a



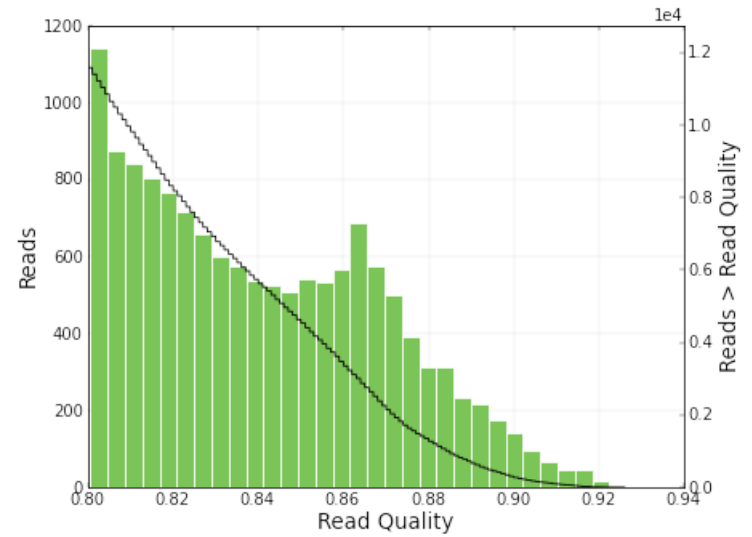
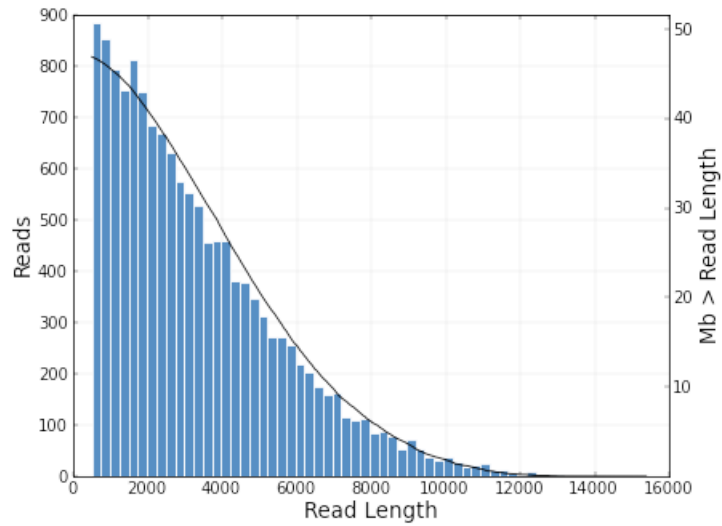
Supplemental Figure 7b



Supplemental Figure 8

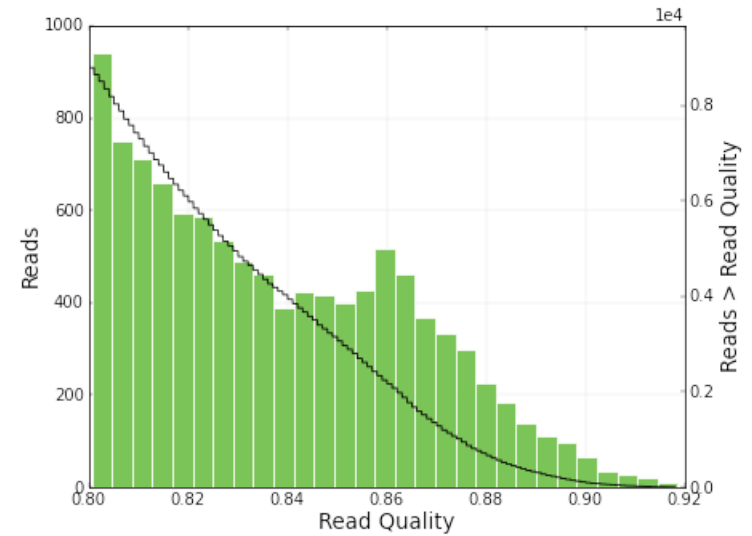
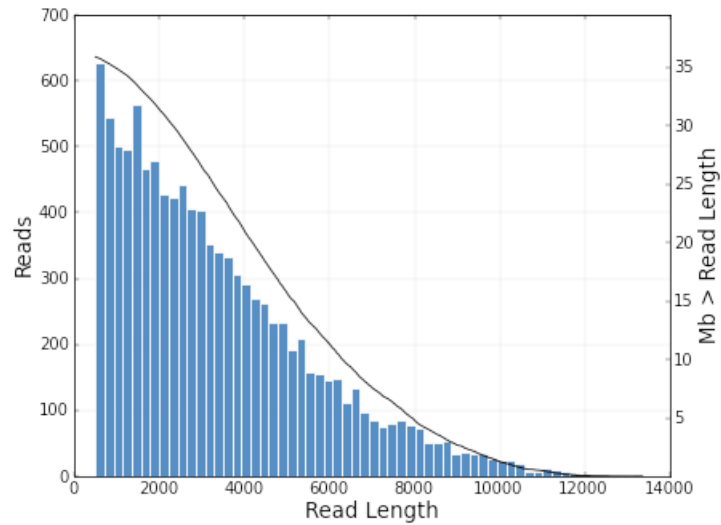


Supplementary Figure 9a



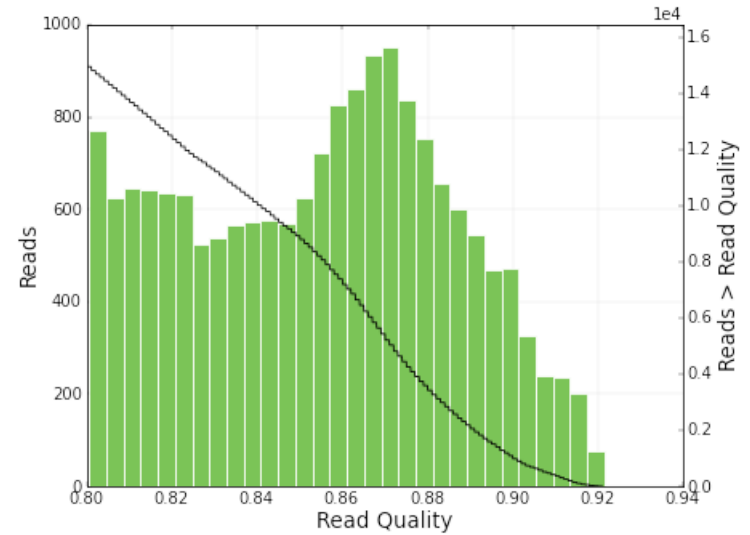
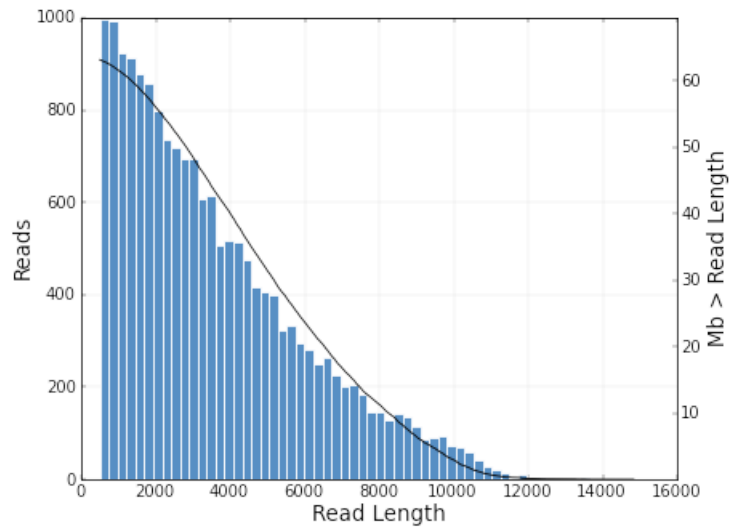
CH17-124M20

Supplementary Figure 9b



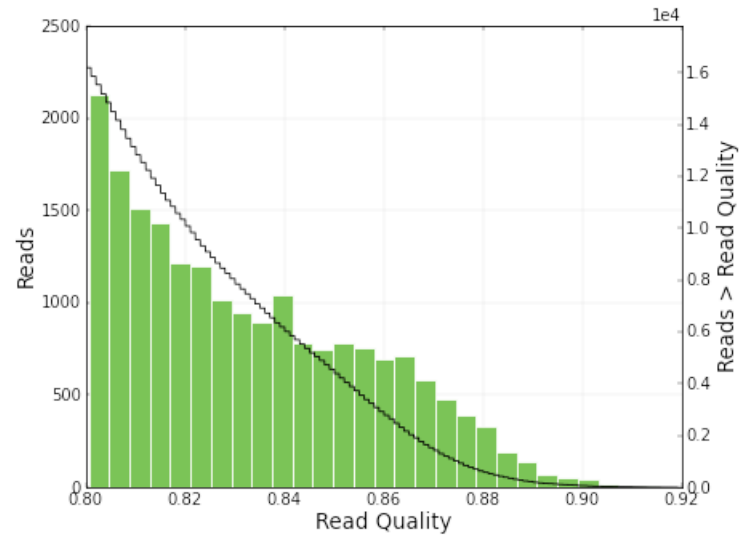
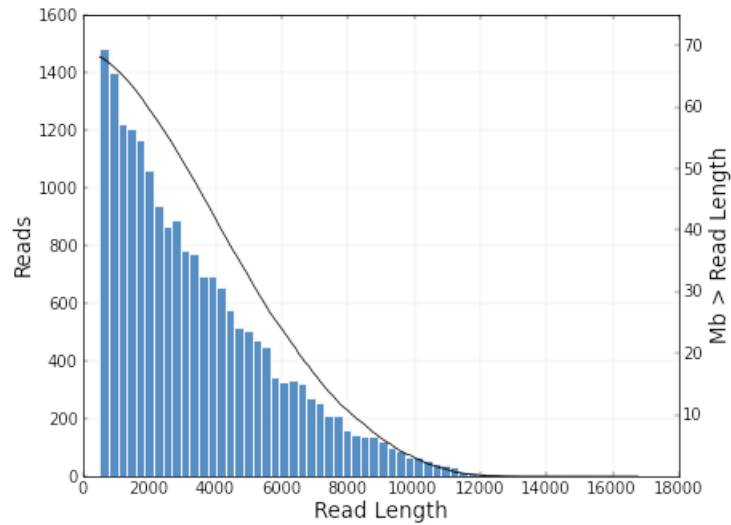
CH17-157L1

Supplementary Figure 9c



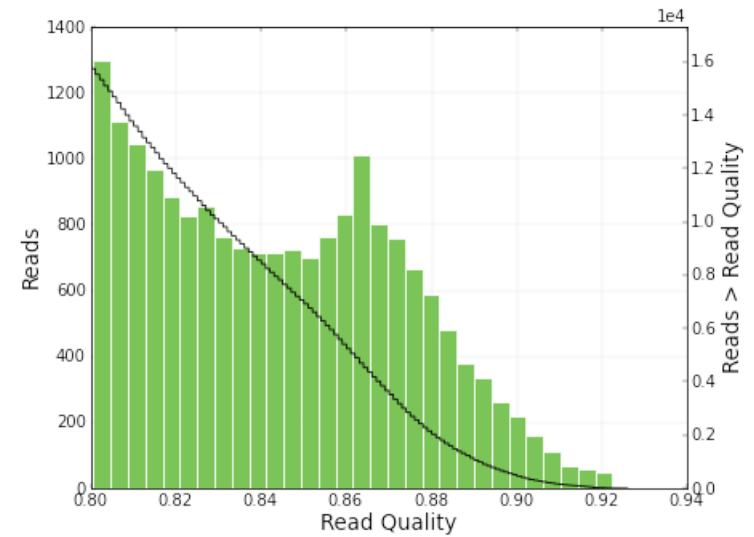
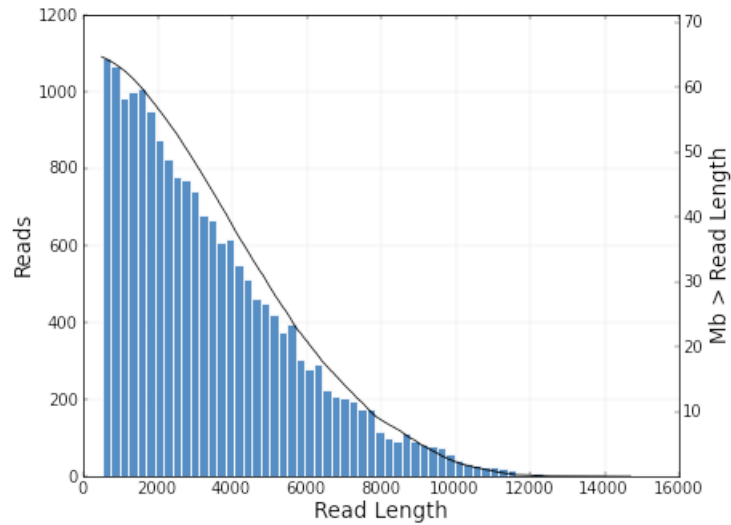
CH17-169A24

Supplementary Figure 9d



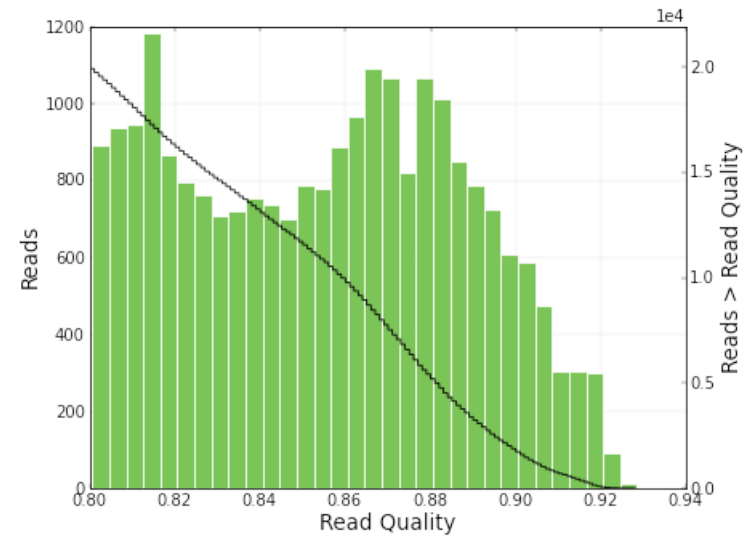
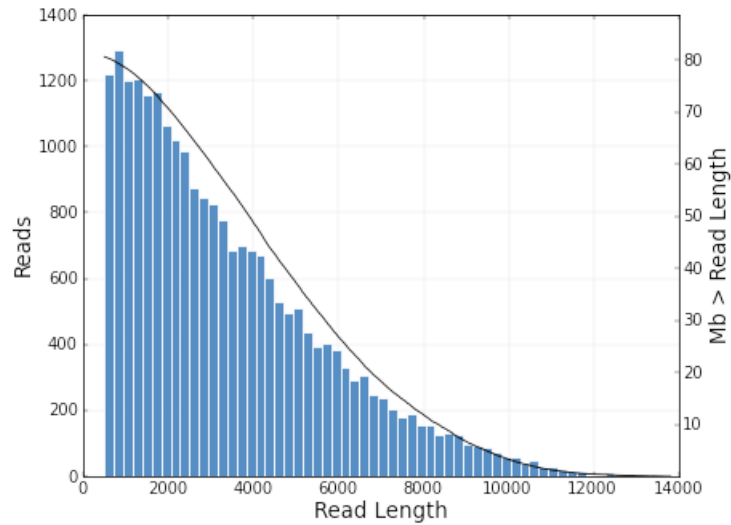
CH17-170H8

Supplementary Figure 9e



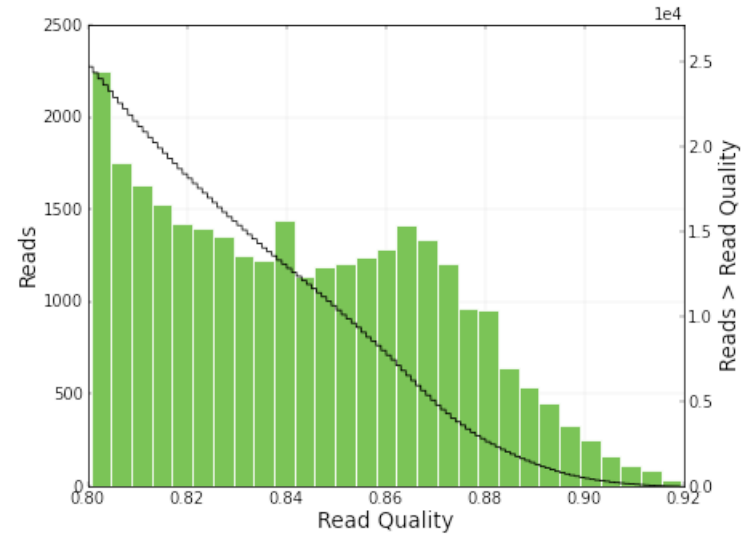
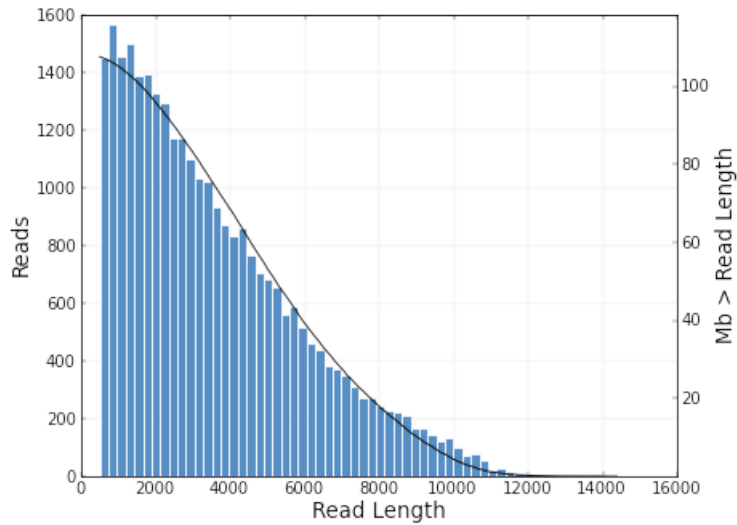
CH17-202L17

Supplementary Figure 9f



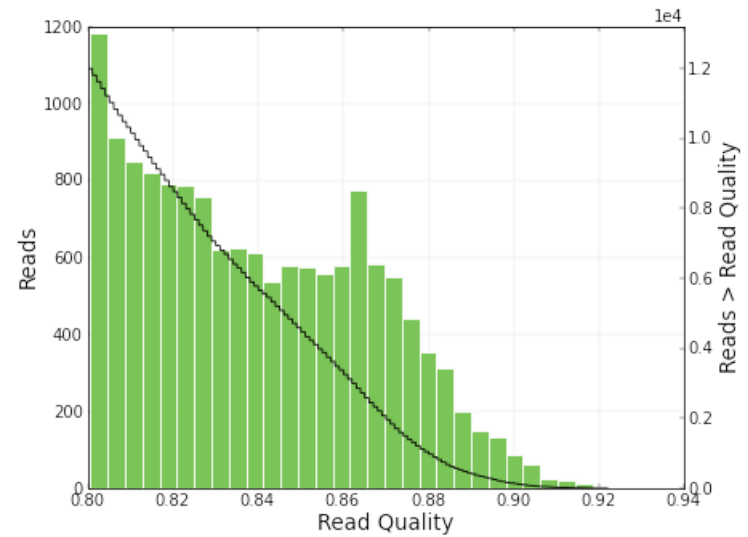
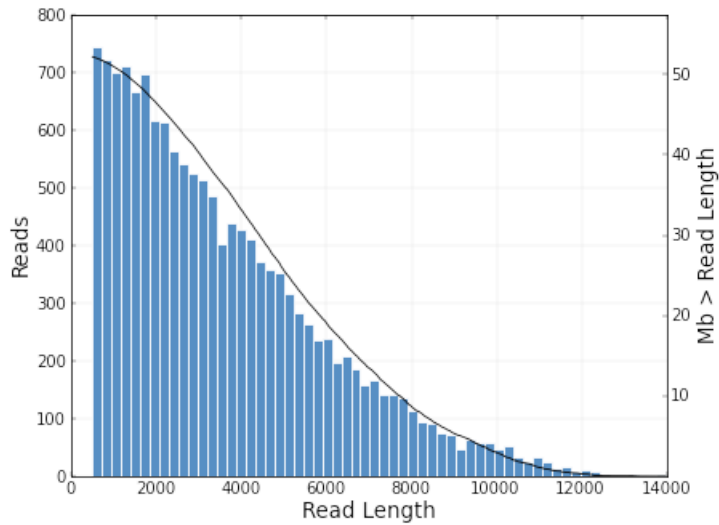
CH17-227A2

Supplementary Figure 9g



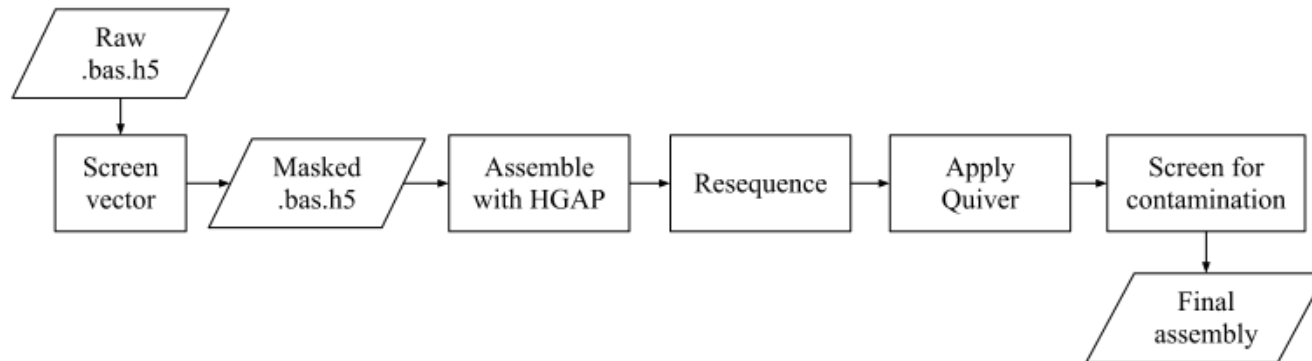
CH17-33G3

Supplementary Figure 9h

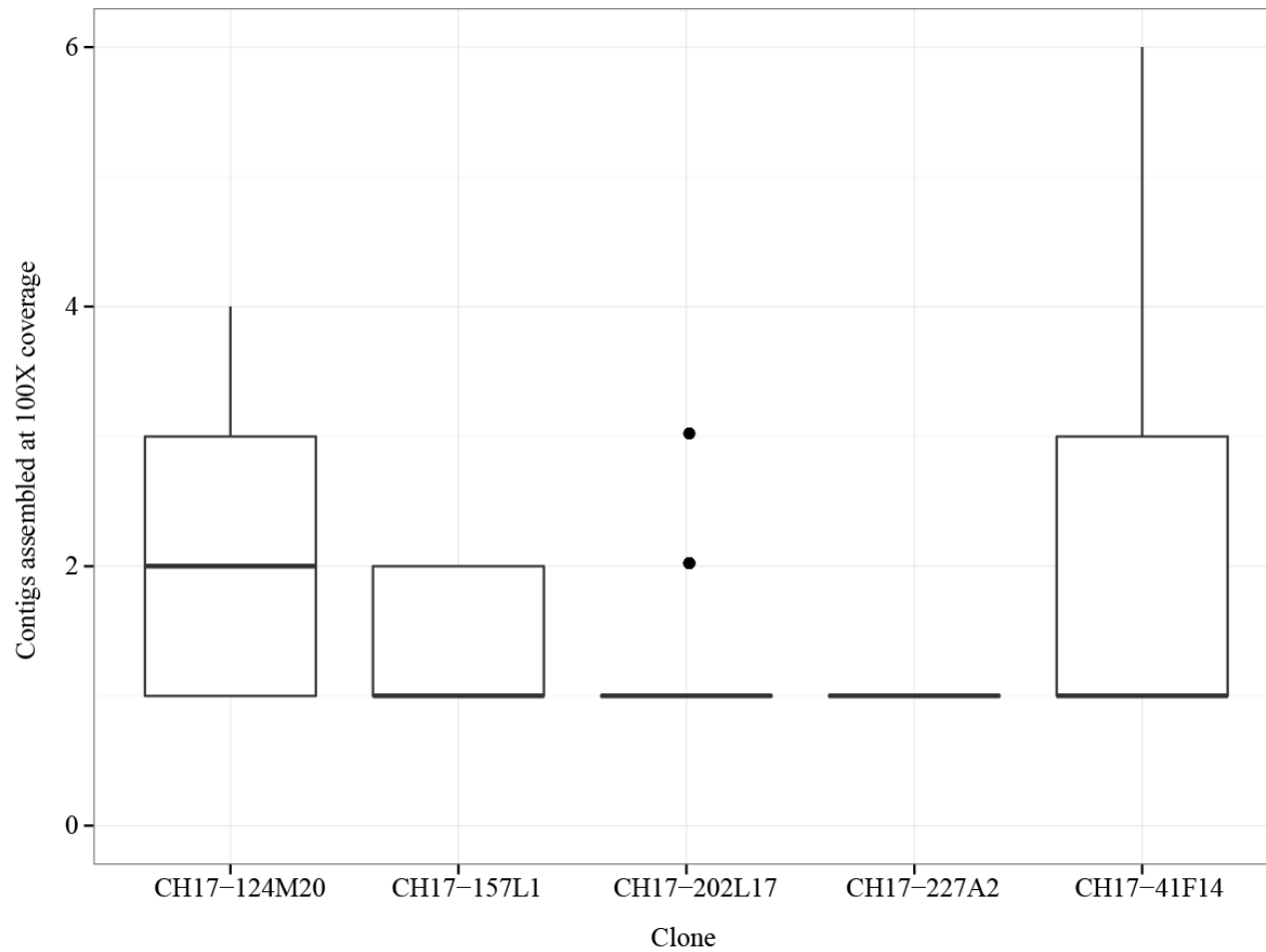


CH17-41F14

Supplementary Figure 10



Supplemental Figure 11



Supplemental Figure 12

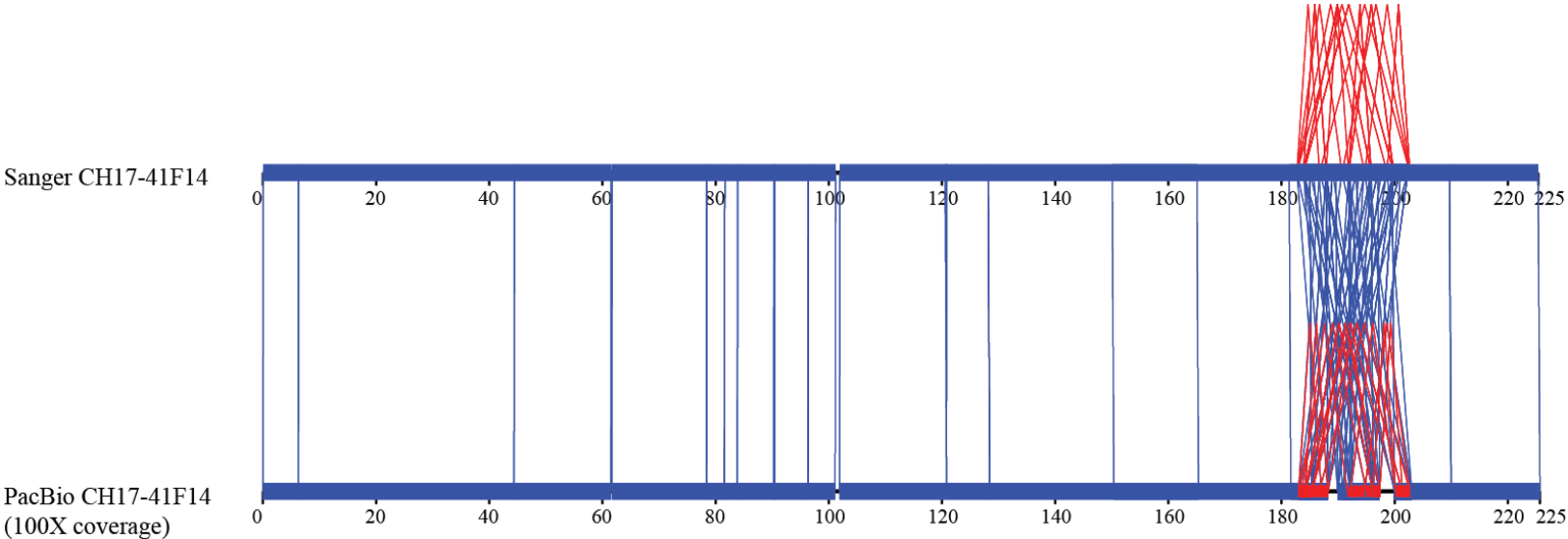


Table S1. Assembly details for clones.

Clone	Duplications ^a (Kbp)	PacBio coverage	Illumina coverage	Sanger size (bp)	PacBio size (bp)	SMRT cells	Mean subread length	Max subread length	Total bases	Vector bases removed	% vector	Contigs	Notes
CH17-124M20	184	475	117	202,892	202,859	1	1,710	11,790	258,873,314	40,855,804	0.16	1	
CH17-157L1	210	186	95	230,865	230,921	1	1,659	12,876	261,636,427	7,909	0.00	1	
CH17-169A24	0	78	68	243,129	242,237	1	1,988	11,835	211,316,606	106,110,557	0.50	1	Two BACs accidentally pooled into one SMRT cell
CH17-170H8	74	240	91	223,520	222,143	5	1,933	12,505	1,159,041,444	211,359,923	0.18	1	Sequenced to higher coverage due to contamination in DNA library
CH17-202L17	204	263	95	217,579	217,211	1	1,855	12,554	320,330,385	92,344,343	0.29	1	
CH17-227A2	110	312	109	200,520	201,802	1	2,153	12,538	270,130,585	94,166,352	0.35	1	
CH17-33G3	87	177	82	244,867	244,942	2	1,422	12,702	548,725,138	175,974,038	0.32	1	Sequenced to higher coverage due to contamination in DNA library
CH17-41F14	123	226	92	225,391	212,292	1	1,709	12,279	279,992,566	75,122,287	0.27	1	
Mean	124	245	94	223,595	221,801	2	1,804	12,385	413,755,808	99,492,652	0.26	1	

^a Duplications annotated by DupMasker

Table S2. Large misassemblies (>50 bp) based on alignments between PacBio and Sanger assemblies.

Assembly	Clone	Start	End	Size of event (bp)	Type of event
Sanger	CH17-169A24	226,467	226,829	372	misassembled sequence in Sanger assembly validated by Illumina in PacBio assembly
Sanger	CH17-41F14	120,770	120,781	357	deletion of sequence in Sanger that is present in PacBio
PacBio	CH17-41F14	185,978	186,032	7,991	collapsed tandem duplication in PacBio that is present in Sanger

Table S3. Illumina validation results per mismatch base between assemblies including homopolymer, dipolymer, and GC-rich region status.

PacBio clone	PacBio start	PacBio end	PacBio base	Group id	Read depth	Sanger start	Sanger end	Sanger base	Group id	Read depth	PacBio supported	Homopolymer run	Dipolymer run	GC rich
CH17-124M20	21528	21529	A	1	58	Sanger_CH17-124M20	21569	21570 A	1	3 Y	N	N	N	N
CH17-124M20	43240	43241 A	2	8	Sanger_CH17-124M20	43282	43283 -	2	6 -	N	N	Y	N	N
CH17-124M20	43241	43242 C	3	7	Sanger_CH17-124M20	43282	43283 -	3	6 -	N	Y	N	N	N
CH17-124M20	43242	43243 A	4	6	Sanger_CH17-124M20	43282	43283 -	4	6 -	N	Y	N	N	N
CH17-124M20	43243	43244 C	5	5	Sanger_CH17-124M20	43282	43283 -	5	6 -	N	Y	N	N	N
CH17-124M20	73777	73778 A	6	7	Sanger_CH17-124M20	73615	73616 -	6	7 -	Y	N	N	N	N
CH17-124M20	76180	76181	7	25	Sanger_CH17-124M20	76217	76218 -	7	25 -	N	Y	N	N	N
CH17-124M20	76182	76183 A	8	22	Sanger_CH17-124M20	76218	76219 -	8	24 -	N	Y	N	N	N
CH17-124M20	76183	76184 A	9	22	Sanger_CH17-124M20	76218	76219 -	9	24 -	N	Y	N	N	N
CH17-124M20	82165	82166 A	10	3	Sanger_CH17-124M20	82446	82447 -	10	3 -	N	Y	N	N	N
CH17-124M20	82740	82741 A	11	10	Sanger_CH17-124M20	82773	82774 -	11	10 N	Y	N	N	N	N
CH17-124M20	103275	103276 -	12	0	Sanger_CH17-124M20	103307	103308 C	12	0 -	N	N	N	Y	N
CH17-124M20	114547	114548 T	13	2	Sanger_CH17-124M20	114580	114581 -	13	2 -	Y	N	N	N	N
CH17-124M20	116680	116681 -	14	0	Sanger_CH17-124M20	116712	116713 G	14	0 -	N	N	N	Y	N
CH17-124M20	143336	143337 T	15	9	Sanger_CH17-124M20	143369	143370 -	15	8 Y	Y	N	N	N	N
CH17-124M20	148221	148222 -	16	0	Sanger_CH17-124M20	148253	148254 G	16	0 -	N	N	N	Y	N
CH17-124M20	151859	151860 T	17	2	Sanger_CH17-124M20	151892	151893 -	17	6 -	Y	N	N	N	N
CH17-124M20	152720	152721 T	18	6	Sanger_CH17-124M20	152752	152753 -	18	7 -	Y	N	N	N	N
CH17-124M20	186608	186609 A	19	4	Sanger_CH17-124M20	186639	186640 -	19	5 -	Y	N	N	N	N
CH17-157L1	15088	15089 A	1	12	Sanger_CH17-157L1	15138	15139 -	1	12 -	Y	N	N	N	N
CH17-157L1	18792	18793 A	2	0	Sanger_CH17-157L1	18841	18842 -	2	0 -	N	N	N	N	N
CH17-157L1	18805	18806 -	3	0	Sanger_CH17-157L1	18853	18854 A	3	1 -	N	N	N	N	N
CH17-157L1	24483	24484 A	4	4	Sanger_CH17-157L1	24532	24533 -	4	3 -	Y	N	N	N	N
CH17-157L1	51162	51163 -	5	0	Sanger_CH17-157L1	51210	51211 C	5	0 -	N	N	N	Y	N
CH17-157L1	53272	53273 A	6	3	Sanger_CH17-157L1	53321	53322 -	6	3 -	Y	N	N	N	N
CH17-157L1	55812	55813 A	7	18	Sanger_CH17-157L1	55860	55861 -	7	18 -	Y	N	N	N	N
CH17-157L1	55826	55827 T	8	17	Sanger_CH17-157L1	55874	55875 -	8	17 -	Y	N	N	N	N
CH17-157L1	64579	64580 -	9	0	Sanger_CH17-157L1	64625	64626 C	9	0 -	N	N	N	Y	N
CH17-157L1	85395	85396 T	10	3	Sanger_CH17-157L1	85442	85443 -	10	3 -	Y	N	N	N	N
CH17-157L1	94243	94244 T	11	1	Sanger_CH17-157L1	94290	94291 -	11	1 -	N	Y	N	N	N
CH17-157L1	106920	106921 T	12	8	Sanger_CH17-157L1	106965	106966 -	12	7 -	Y	N	N	N	N
CH17-157L1	106922 T	13	8	Sanger_CH17-157L1	106965	106966 -	13	7 -	Y	N	N	N	N	N
CH17-157L1	182853	182854 A	14	5	Sanger_CH17-157L1	182896	182897 -	14	6 N	Y	N	N	N	N
CH17-157L1	182854	182855 T	15	5	Sanger_CH17-157L1	182896	182897 -	15	6 -	Y	N	N	N	N
CH17-169A24	8721	8722 A	1	11	Sanger_CH17-169A24	8778	8779 -	1	7 -	N	N	N	N	N
CH17-169A24	8722	8723 A	2	11	Sanger_CH17-169A24	8778	8779 -	2	7 -	N	N	N	N	N
CH17-169A24	8724	8725 G	3	11	Sanger_CH17-169A24	8779	8780 -	3	7 -	N	N	N	N	N
CH17-169A24	8725	8726 G	4	10	Sanger_CH17-169A24	8779	8780 -	4	7 -	N	N	N	N	N
CH17-169A24	8726	8727 T	5	9	Sanger_CH17-169A24	8779	8780 -	5	7 -	N	N	N	N	N
CH17-169A24	8728	8729 T	6	8	Sanger_CH17-169A24	8780	8781 -	6	7 -	N	N	N	N	N
CH17-169A24	8729	8730 T	7	8	Sanger_CH17-169A24	8780	8781 -	7	7 -	N	N	N	N	N
CH17-169A24	8731	8732 T	8	7	Sanger_CH17-169A24	8781	8782 -	8	7 -	N	N	N	N	N
CH17-169A24	8733	8734 A	9	5	Sanger_CH17-169A24	8782	8783 -	9	7 -	N	N	N	N	N
CH17-169A24	8735	8736 T	10	4	Sanger_CH17-169A24	8783	8784 -	10	5 -	N	N	N	N	N
CH17-169A24	8737	8738 G	11	3	Sanger_CH17-169A24	8784	8785 -	11	5 -	N	N	N	N	N
CH17-169A24	8738	8739 A	12	3	Sanger_CH17-169A24	8784	8785 -	12	5 -	N	N	N	N	N
CH17-169A24	8739	8740 G	13	5	Sanger_CH17-169A24	8784	8785 -	13	6 -	N	N	N	N	N
CH17-169A24	41163	41164 -	14	0	Sanger_CH17-169A24	41207	41208 G	14	0 -	N	N	N	Y	N
CH17-169A24	41175	41176 -	15	0	Sanger_CH17-169A24	41219	41220 G	15	0 -	N	N	N	Y	N
CH17-169A24	54179	54180 T	16	1	Sanger_CH17-169A24	54226	54227 T	16	1 -	N	Y	N	N	N
CH17-169A24	194562	194563 -	17	1	Sanger_CH17-169A24	194609	194610 A	17	6 -	Y	N	N	N	N
CH17-169A24	198592	198593 -	18	0	Sanger_CH17-169A24	198640	198641 C	18	0 -	N	N	N	N	N
CH17-169A24	209938	209939 T	19	10	Sanger_CH17-169A24	209987	209988 -	19	20 -	N	Y	N	N	N
CH17-169A24	209939	209940 A	20	10	Sanger_CH17-169A24	209987	209988 -	20	20 -	N	Y	N	N	N
CH17-169A24	209941	209942 G	21	10	Sanger_CH17-169A24	209988	209989 -	21	20 -	N	Y	N	N	N
CH17-169A24	213169	213170 T	22	0	Sanger_CH17-169A24	213215	213216 G	22	22 -	N	N	N	N	N
CH17-169A24	213204	213205 A	23	0	Sanger_CH17-169A24	213335	213336 -	23	0 -	N	N	N	N	N
CH17-169A24	213293	213294 G	24	0	Sanger_CH17-169A24	213339	213340 T	24	9 N	N	N	N	N	N
CH17-169A24	213352	213353 T	25	0	Sanger_CH17-169A24	213398	213399 -	25	11 N	N	N	N	N	N
CH17-169A24	213355	213356 T	26	0	Sanger_CH17-169A24	213399	213400 A	26	11 N	N	N	N	N	N
CH17-169A24	213373	213374 C	27	1	Sanger_CH17-169A24	213418	213419 A	27	8 N	N	N	N	N	N
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CH17-169A24	226517	226518 T	31	67	Sanger_CH17-169A24	226561	226562 G	31	0 Y	N	N	N	N	N
CH17-169A24	226524	226525 A	32	66	Sanger_CH17-169A24	226568	226569 -	32	0 Y	N	N	N	N	N
CH17-169A24	226529	226530 T	33	69	Sanger_CH17-169A24	226572	226573 -	33	0 Y	N	N	N	N	N
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CH17-169A24	226575	226576 A	35	74	Sanger_CH17-169A24	226616	226617 -	35	0 Y	N	N	N	N	N
CH17-169A24	226587	226588 A	36	68	Sanger_CH17-169A24	226627	226628 -	36	0 Y	N	N	N	N	N
CH17-169A24	226591	226592 A	37	70	Sanger_CH17-169A24	226630	226631 -	37	0 Y	N	N	N	N	N
CH17-169A24	226615	226616 T	38	64	Sanger_CH17-169A24	226653	226654 G	38	0 Y	N	N	N	N	N
CH17-169A24	226620	226621 T	39	61	Sanger_CH17-169A24	226658	226659 -	39	0 Y	N	N	N	N	N
CH17-169A24	226639	226640 A	40	63	Sanger_CH17-169A24	226676	226677 G	40	0 Y	N	N	N	N	N
CH17-169A24	226680	226681 C	41	72	Sanger_CH17-169A24	226717	226718 G	41	0 Y	N	N	N	N	N
CH17-169A24	226682	226683 A	42	71	Sanger_CH17-169A24	226719	226720 T	42	0 Y	N	N	N	N	N
CH17-169A24	226690	226691 A	43	77	Sanger_CH17-169A24	226728	226729 T	43	0 Y	N	N	N	N	N
CH17-169A24	226694	226695 A	44	78	Sanger_CH17-169A24	226730	226731 G	44	0 Y	N	N	N	N	N
CH17-169A24	226702	226703 T	45	76	Sanger_CH17-169A24	226738	226739 G	45	0 Y	N	N	N	N	N
CH17-169A24	226725	226726 T	46	82	Sanger_CH17-169A24	226761	226762 G	46	0 Y	N	N	N	N	N
CH17-169A24	226748	226749 C	47	88	Sanger_CH17-169A24	226784	226785 G	47	0 Y	N	N	N	N	N
CH17-169A24	226780	226781 A	48	93	Sanger_CH17-169A24	226816	226817 T	48	0 Y	N	N	N	N	N
CH17-169A24	226782	226783 T	49	92	Sanger_CH17-169A24	226818	226819 G	49	0 Y	N	N	N	N	N
CH17-169A24	226785	226786 C	50	92	Sanger_CH17-169A24	226821	226822 G	50	0 Y	N	N	N	N	N
CH17-169A24	226792	226793 T	51	92	Sanger_CH17-169A24	226828	226829 G	51	0 Y	N	N	N	N	N
CH17-170H8	46419	46420 T	1	3	Sanger_CH17-170H8	46461	46462 -	1	3 -	Y	N	N	N	N
CH17-170H8	70848	70849 T	2	22	Sanger_CH17-170H8	70890	70891 -	2	16 -	N	N	N	N	N
CH17-170H8	70852	70853 G	3	22	Sanger_CH17-170H8	70892	70893 -	3	16 -	N	N	N	N	N
CH17-170H8	75501	75502 A	4	5	Sanger_CH17-170H8	75540	75541 -	4	5 -	Y	N	N	N	N
CH17-170H8	78214	78215 T	5	7	Sanger_CH17-170H8	78252	78253 -	5	7 -	Y	N	N	N	N
CH17-170H8	81939	81940 A	6	16	Sanger_CH17-170H8	81976	81977 -	6	15 -	Y	N	N	N	N
CH17-170H8	109277	109278 A	7	3	Sanger_CH17-170H8	109313	109314 -	7	3 -	Y	N	N	N	N
CH17-170H8	141334	141335 A	8	8	Sanger_CH17-170									

Table S4. Assembly statistics for de novo assembly of Illumina 151 bp paired-end reads.

Clone	Illumina coverage	Sanger size (bp)	Illumina size (bp)	% assembled	Contigs	% identity
CH17-124M20	752	202,892	196,359	0.968	20	0.999617
CH17-157L1	655	230,865	227,946	0.987	22	0.999631
CH17-169A24	389	243,129	239,054	0.983	7	0.999703
CH17-170H8	569	223,520	221,714	0.992	7	0.999814
CH17-202L17	497	217,579	216,500	0.995	7	0.999746
CH17-227A2	598	200,520	198,788	0.991	8	0.999755
CH17-33G3	539	244,867	241,209	0.985	8	0.999762
CH17-41F14	458	225,391	205,054	0.91	10	0.999734
Mean	557	223,595	218,328	0.976	11	0.999720

Table S5. Assembly details for clones subsampled to 100X coverage and assembled with HGAP.

Clone ^a	Length	Bases sampled	Iterations	Mean identity (SD) ^b	Median total contigs (SD)	Median assembled bases (SD)
CH17-124M20	202,828	20,282,800	28	0.999824 (0.000025)	2.00 (1.03)	204146 (2287)
CH17-157L1	230,794	23,079,400	26	0.999863 (0.000017)	1.00 (0.49)	230757 (605)
CH17-202L17	217,484	21,748,400	25	0.999924 (0.000111)	1.00 (0.61)	217485 (2142)
CH17-227A2	200,447	20,044,700	22	0.999941 (0.000022)	1.00 (0.00)	200420 (9)
CH17-41F14	217,747	21,774,700	19	0.999849 (0.000016)	1.00 (1.50)	217658 (8801)

^a CH17-169A24 and CH17-170H8 were excluded due to accidental pooling and DNA contamination, respectively.

^b Identity was calculated between each clone's Sanger assembly and single-contig subsampled assemblies.

Table S6. Assembly details for pooled BAC clones.

Pool	Clone	Single			Pooled			Change in size	Single and pooled alignment identity	
		Coverage	Contigs	Assembled bases	Coverage	Contigs	Assembled bases			
1	CH251-75B17		141	1	108,163	231	1	109,699	1,536	99.8826
1	CH277-30K2		464	1	141,376	282	2	151,466	10,090	93.8439
2	CH251-75B17		141	1	108,163	241	1	107,919	-244	99.8592
2	CH251-182P19		404	1	166,051	147	1	166,049	-2	99.9958
2	CH277-80C4		87	5	190,243	143	1	203,336	13,093	98.2199

Table S7. Clone names, lengths, and supercontig composition for chimpanzee clones sequenced with PacBio.

Clone name	GenBank accession	Length	Supercontig	Supercontig size
CH251-545A24 ^a	AC183294.3	173,991	A	317,362
CH251-12B21	AC254815.1	134,512	A	
CH251-59G18	AC254826.1	169,700	A	
CH251-354I21	AC254823.1	172,941	B	448,927
CH251-433E19	AC254816.1	179,540	B	
CH251-21N5	AC254819.1	184,664	B	
Total		1,015,348		766,289

^a Previously sequenced Sanger clone (Accession: AC183294)

Table S8. Accessions and positions of clones in build36 and build37 based on BAC end-sequence mapping.

Clone name	Sanger accession	PacBio accession	Chromosome	build36		Chromosome	build37		Orientation
				Start	End		Start	End	
CH17-124M20	AC243899.3	AC254814.1	chr17	41572075	41956911	chr17	44216298	44601595	-
CH17-157L1	AC243627.3	AC254825.1	chr17	41607034	41802370	chr17	44251257	44446626	+
CH17-169A24	AC243621.2	AC254822.1	chr17	41176257	41419306	chr17	43820486	44063469	+
CH17-170H8	AC243658.3	AC254824.1	chr17	41404195	41627621	chr17	44048359	44271844	+
CH17-202L17	AC243659.3	AC254817.1	chr17	41929796	42147513	chr17	44574480	44792330	+
CH17-227A2	AC243685.2	AC254818.1	chr17	42087500	42287969	chr17	44732184	44932970	+
CH17-33G3	AC243807.3	AC254821.1	chr17	40970511	41215341	chr17	43614728	43859578	-
CH17-41F14	AC244207.2	AC254820.1	chr17	40762162	40975967	chr17	43406379	43620184	+