

Table S4. CENP-A^{TAP} and H3.1^{TAP} sequence mapping onto α -satellite DNAs in human centromere reference models for each autosome and the X chromosome

hg38 chromosome number	Chromosome coordinates		GenBank Accession number	HuRef reference model length (bp)	CENP-A ^{TAP} G1		CENP-A ^{TAP} G2		H3.1 ^{TAP} RC	
	Start	End			reads	bp	reads	bp	reads	bp
chr1	122,026,459	122,224,535	GJ211836.1	198,076	1,461	196,166	1,564	207,416	597	87,974
chr1	122,224,635	122,503,147	GJ211837.1	278,512	23,360	3,045,996	30,786	4,004,255	4,410	646,038
chr1*	122,503,247	124,785,432	GJ212202.1	2,282,185	6,105,419	772,773,576	7,094,651	902,285,561	251,399	36,133,148
chr1	124,785,532	124,849,129	GJ211855.1	63,597	4,792	647,360	5,953	797,337	1,302	192,880
chr1	124,849,229	124,932,724	GJ211857.1	83,495	14,642	1,890,865	17,965	2,321,981	1,736	252,436
Sum chr1				2,905,865	6,149,674	778,553,963	7,150,919	909,616,550	259,444	37,312,476
chr2	92,188,145	94,090,557	GJ211860.1	1,902,412	1,114,799	143,974,336	1,275,294	164,799,540	20,700	3,036,769
chr3	90,772,458	91,233,586	GJ211866.1	461,128	10,584	1,409,525	9,509	1,264,645	5,167	743,841
chr3	91,233,686	91,247,622	GJ211867.1	13,936	412	54,717	352	47,378	205	29,556
chr3	91,553,419	93,655,574	GJ211871.1	2,102,155	1,163,381	144,645,366	1,325,682	166,520,218	94,142	10,440,534
Sum chr3				2,577,219	1,174,377	146,109,608	1,335,543	167,832,241	99,514	11,213,931
chr4	49,712,061	51,743,951	GJ211881.1	2,031,890	1,233,349	151,127,497	1,397,925	173,214,791	40,774	5,696,788
chr5	46,485,900	46,569,062	GJ211882.1	83,162	4,815	564,774	4,662	548,882	1,221	156,786
chr5	46,569,162	46,796,725	GJ211883.1	227,563	3,555	440,833	3,646	452,207	1,265	175,064
chr5	46,796,825	47,061,288	GJ211884.1	264,463	9,805	1,241,255	9,703	1,233,959	3,159	443,549
chr5	47,106,994	47,153,339	GJ211886.1	46,345	4,486	566,664	4,424	563,510	1,596	226,729
chr5	47,153,439	47,296,069	GJ211887.1	142,630	3,515	421,387	3,948	471,147	691	96,586
chr5*	47,309,184	49,591,369	GJ212203.1	2,282,185	6,105,419	772,773,576	7,094,651	902,285,561	251,399	36,133,148
chr5**	49,667,531	49,721,203	GJ211904.2	53,672	1,799	233,706	1,543	200,507	767	108,463
chr5	49,721,303	50,059,807	GJ211906.2	338,504	5,566	709,116	4,927	629,878	2,452	349,776
Sum chr5				3,438,524	6,138,960	776,951,311	7,127,504	906,385,651	262,550	37,690,101
chr6	58,553,888	59,829,934	GJ211907.1	1,276,046	2,228,578	274,542,041	2,725,427	339,244,461	67,157	9,501,112
chr7	58,169,653	60,828,234	GJ211908.1	2,658,581	1,890,684	234,734,200	2,299,673	288,818,995	41,138	5,818,872
chr7	61,377,788	61,528,020	GJ212194.1	150,232	5,737	709,234	6,011	746,119	1,614	222,269
Sum chr7				2,808,813	1,896,421	235,443,434	2,305,684	289,565,114	42,752	6,041,141
chr8	44,033,744	45,877,265	GJ211909.1	1,843,521	1,624,244	205,287,215	2,125,046	270,873,431	37,388	5,381,393

chr9	43,389,635	45,518,558	GJ211929.1	2,128,923	1,192,718	147,751,733	1,362,257	170,167,593	25,606	3,633,103
chr10	39,686,682	39,935,900	GJ211930.1	249,218	331,795	42,608,708	403,073	51,829,873	995	138,151
chr10	39,936,000	41,497,440	GJ211932.1	1,561,440	698,728	90,628,464	824,279	106,941,290	21,122	3,074,660
chr10	41,497,540	41,545,720	GJ211933.1	48,180	26,210	3,413,679	31,164	4,053,709	2,159	311,149
chr10	41,545,820	41,593,521	GJ211936.1	47,701	110,704	14,207,639	141,299	18,114,124	2,731	393,671
Sum chr10				1,906,539	1,167,437	150,858,490	1,399,815	180,938,996	27,007	3,917,631
chr11	51,078,348	51,090,317	GJ211938.1	11,969	73	9,546	104	13,749	50	7,168
chr11	51,090,417	54,342,399	GJ211943.1	3,251,982	1,476,032	192,834,230	1,929,625	252,756,395	56,978	8,358,125
chr11	54,342,499	54,425,074	GJ211948.1	82,575	161,983	20,677,761	216,313	27,681,784	4,836	697,457
Sum chr11				3,346,526	1,638,088	213,521,537	2,146,042	280,451,928	61,864	9,062,750
chr12	34,769,407	34,816,611	GJ211949.1	47,204	1,697	220,834	2,114	272,027	496	71,353
chr12	34,835,295	37,185,252	GJ211954.1	2,349,957	2,749,051	353,719,505	3,214,234	413,551,083	92,425	13,446,813
Sum chr12				2,397,161	2,750,748	353,940,339	3,216,348	413,823,110	92,921	13,518,166
chr13***	16,000,000	16,022,537	GJ211955.2	22,537	1,000	250,926	2,070	240,611	797	113,642
chr13***	16,022,637	16,110,659	GJ211961.2	88,022	1,125	303,218	2,449	273,296	893	126,055
chr13***	16,110,759	16,164,892	GJ211962.2	54,133	6,312	1,712,846	13,409	1,573,026	6,367	918,199
chr13***	16,164,992	16,228,527	GJ211963.2	63,535	3,147	829,391	6,524	758,925	2,836	388,560
chr13***	16,228,627	16,249,297	GJ211965.2	20,670	3,518	1,022,766	7,508	868,048	3,007	435,718
chr13***	16,249,397	16,256,067	GJ211967.2	6,670	3,571	938,762	7,461	899,828	2,975	428,703
chr13***	16,256,167	16,259,412	GJ211968.2	3,245	115	27,449	243	27,787	97	13,636
chr13***	16,259,512	16,282,073	GJ211969.2	22,561	626	166,478	1,305	153,843	451	65,214
chr13***	16,282,173	17,416,384	GJ211972.2	1,134,211	2,487,380	507,872,091	5,271,121	630,098,540	94,400	13,704,134
chr13***	17,416,484	17,416,824	GJ212205.1	340	8	935	20	2,293	0	0
chr13***	17,416,924	17,417,264	GJ212206.1	340	21	3,539	41	5,882	1	183
chr13***	17,417,364	17,418,562	GJ211986.2	1,198	760	204,870	1,618	192,384	637	91,165
chr13***	17,418,662	18,051,248	GJ211991.2	632,586	1,572,599	327,344,781	3,335,707	403,695,005	43,652	6,344,923
Sum chr13				2,050,048	4,080,182	840,678,052	8,649,476	1,038,789,468	156,113	22,630,132

chr14***	16,000,000	16,022,537	GJ211992.2	22,537	1,000	250,926	2,070	240,611	797	113,642
chr14***	16,140,627	16,228,649	GJ211998.2	88,022	1,125	303,218	2,449	273,296	893	126,055
chr14***	16,228,749	16,282,882	GJ211999.2	54,133	6,312	1,712,846	13,409	1,573,026	6,367	918,199
chr14***	16,282,982	16,346,517	GJ212000.2	63,535	3,147	829,391	6,524	758,925	2,836	388,560
chr14***	16,346,617	16,367,287	GJ212002.2	20,670	3,518	1,022,766	7,508	868,048	3,007	435,718
chr14***	16,367,387	16,374,057	GJ212004.2	6,670	3,571	938,762	7,461	899,828	2,975	428,703
chr14***	16,374,157	16,377,402	GJ212005.2	3,245	115	27,449	243	27,787	97	13,636
chr14***	16,377,502	16,400,063	GJ212006.2	22,561	626	166,478	1,305	153,843	451	65,214
chr14***	16,404,448	17,538,659	GJ212009.2	1,134,211	2,487,380	507,872,091	5,271,121	630,098,540	94,400	13,704,134
chr14***	17,538,759	17,539,099	GJ212210.1	340	8	935	20	2,293	0	0
chr14***	17,539,199	17,539,539	GJ212211.1	340	21	3,539	41	5,882	1	183
chr14***	17,539,639	17,540,837	GJ212023.2	1,198	760	204,870	1,618	192,384	637	91,165
chr14***	17,540,937	18,173,523	GJ212028.2	632,586	1,572,599	327,344,781	3,335,707	403,695,005	43,652	6,344,923
Sum chr14				2,050,048	4,080,182	840,678,052	8,649,476	1,038,789,468	156,113	22,630,132
chr15	17,083,673	17,498,951	GJ212036.1	415,278	7,253	969,682	7,469	994,275	2,616	380,692
chr15	17,499,051	18,355,008	GJ212042.1	855,957	33,063	4,389,529	39,351	5,196,438	8,654	1,259,441
chr15	18,355,108	19,725,254	GJ212045.1	1,370,146	1,901,942	245,093,841	2,297,489	296,436,842	23,967	3,460,063
Sum chr15				2,641,381	1,942,258	250,453,052	2,344,309	302,627,555	35,237	5,100,196
chr16	36,311,158	36,334,460	GJ212046.1	23,302	1,052	138,509	1,186	155,577	262	37,717
chr16	36,337,666	38,265,669	GJ212051.1	1,928,003	1,364,770	177,007,725	1,662,383	215,520,357	33,302	4,860,437
Sum chr16				1,951,305	1,365,822	177,146,234	1,663,569	215,675,934	33,564	4,898,154
chr17	22,813,679	23,194,918	GJ212053.1	381,239	131,078	17,144,482	163,528	21,424,575	7,138	1,045,717
chr17	23,195,018	26,566,633	GJ212054.1	3,371,615	1,175,357	149,015,569	1,570,089	199,125,688	30,175	4,276,747
chr17	26,566,733	26,616,164	GJ212055.1	49,431	260,307	34,317,742	334,081	44,133,348	7,764	1,145,164
Sum chr17				3,802,285	1,566,742	200,477,793	2,067,698	264,683,611	45,077	6,467,628
chr18	15,460,899	15,780,377	GJ212060.1	319,478	39,230	5,098,489	49,169	6,356,770	5,562	808,354
chr18	15,797,855	20,561,439	GJ212062.1	4,763,584	806,190	105,354,159	954,066	124,696,905	23,253	3,377,317
chr18	20,603,247	20,696,289	GJ212066.1	93,042	5,616	736,749	6,487	844,777	1,351	195,531
chr18	20,696,389	20,736,025	GJ212067.1	39,636	1,129	146,130	1,257	163,045	237	34,042
chr18	20,736,125	20,813,083	GJ212069.1	76,958	1,786	232,850	2,177	282,722	311	45,337
chr18	20,839,797	20,861,206	GJ212071.1	21,409	266	33,935	301	38,480	60	8,390
Sum chr18				5,314,107	854,217	111,602,312	1,013,457	132,382,699	30,774	4,468,971

chr19**	24,498,980	24,552,652	GJ212072.2	53,672	1,799	233,706	1,543	200,507	767	108,463
chr19	24,552,752	24,891,256	GJ212077.2	338,504	5,760	774,057	5,091	683,177	2,843	413,366
chr19*	24,908,689	27,190,874	GJ212201.1	2,282,185	6,105,419	772,773,576	7,094,651	902,285,561	251,399	36,133,148
Sum chr19				2,674,361	6,112,978	773,781,339	7,101,285	903,169,245	255,009	36,654,977
chr20	26,436,232	26,586,955	GJ212091.1	150,723	17,666	2,297,742	21,441	2,779,583	3,694	544,832
chr20	26,608,145	28,494,539	GJ212093.1	1,886,394	1,028,819	134,137,851	1,327,549	173,241,417	20,219	2,955,762
chr20	28,508,997	28,556,953	GJ212095.1	47,956	10,395	1,361,132	10,378	1,346,938	3,262	474,587
chr20	28,648,108	28,728,874	GJ212105.1	80,766	1,315	176,013	1,185	158,311	647	92,644
chr20	29,125,793	29,204,668	GJ212107.1	78,875	739	96,683	590	76,896	376	52,678
chr20	29,917,404	30,038,348	GJ212117.1	120,944	986	131,855	887	117,505	414	59,632
Sum chr20				2,365,658	1,059,920	138,201,276	1,362,030	177,720,650	28,612	4,180,135
chr21***	10,864,560	10,887,097	GJ212118.2	22,537	1,000	250,926	2,070	240,611	797	113,642
chr21***	10,887,197	10,975,219	GJ212124.2	88,022	1,125	303,218	2,449	273,296	893	126,055
chr21***	10,975,319	11,029,452	GJ212125.2	54,133	6,312	1,712,846	13,409	1,573,026	6,367	918,199
chr21***	11,029,552	11,093,087	GJ212126.2	63,535	3,147	829,391	6,524	758,925	2,836	388,560
chr21***	11,093,187	11,113,857	GJ212128.2	20,670	3,518	1,022,766	7,508	868,048	3,007	435,718
chr21***	11,113,957	11,120,627	GJ212130.2	6,670	3,571	938,762	7,461	899,828	2,975	428,703
chr21***	11,120,727	11,123,972	GJ212131.2	3,245	115	27,449	243	27,787	97	13,636
chr21***	11,124,072	11,146,633	GJ212132.2	22,561	626	166,478	1,305	153,843	451	65,214
chr21***	11,146,733	12,280,944	GJ212135.2	1,134,211	2,487,380	507,872,091	5,271,121	630,098,540	94,400	13,704,134
chr21***	12,281,044	12,281,384	GJ212204.1	340	8	935	20	2,293	0	0
chr21***	12,281,484	12,281,824	GJ212207.1	340	21	3,539	41	5,882	1	183
chr21***	12,281,924	12,283,122	GJ212149.2	1,198	760	204,870	1,618	192,384	637	91,165
chr21***	12,283,222	12,915,808	GJ212154.2	632,586	1,572,599	327,344,781	3,335,707	403,695,005	43,652	6,344,923
Sum chr21				2,050,048	4,080,182	840,678,052	8,649,476	1,038,789,468	156,113	22,630,132
chr22***	12,954,788	12,977,325	GJ212155.2	22,537	1,000	250,926	2,070	240,611	797	113,642
chr22***	13,021,422	13,109,444	GJ212161.2	88,022	1,125	303,218	2,449	273,296	893	126,055
chr22***	13,109,544	13,163,677	GJ212162.2	54,133	6,312	1,712,846	13,409	1,573,026	6,367	918,199
chr22***	13,163,777	13,227,312	GJ212163.2	63,535	3,147	829,391	6,524	758,925	2,836	388,560
chr22***	13,227,412	13,248,082	GJ212165.2	20,670	3,518	1,022,766	7,508	868,048	3,007	435,718
chr22***	13,248,182	13,254,852	GJ212167.2	6,670	3,571	938,762	7,461	899,828	2,975	428,703
chr22***	13,254,952	13,258,197	GJ212168.2	3,245	115	27,449	243	27,787	97	13,636
chr22***	13,258,297	13,280,858	GJ212169.2	22,561	626	166,478	1,305	153,843	451	65,214

chr22***	13,285,243	14,419,454	GJ212172.2	1,134,211	2,487,380	507,872,091	5,271,121	630,098,540	94,400	13,704,134
chr22***	14,419,554	14,419,894	GJ212208.1	340	8	935	20	2,293	0	0
chr22***	14,419,994	14,420,334	GJ212209.1	340	21	3,539	41	5,882	1	183
chr22***	14,420,434	14,421,632	GJ212186.2	1,198	760	204,870	1,618	192,384	637	91,165
chr22***	14,421,732	15,054,318	GJ212191.2	632,586	1,572,599	327,344,781	3,335,707	403,695,005	43,652	6,344,923
Sum chr22				2,050,048	4,080,182	840,678,052	8,649,476	1,038,789,468	156,113	22,630,132
chrX	58,605,579	62,412,542	GJ212192.1	3,806,963	1,314,380	163,946,028	1,670,542	210,615,299	28,485	4,075,538

Column 1: chromosome information. Column 2: chromosome start position. Column 3: chromosome end position. Column 4: Genbank accession. Column 5: length in bp of each reference model as represented in the human assembly. Columns 6-11: list of mapping data (number of bases aligned and number of reads aligned) from each experimental ChIP-seq dataset to the α -satellite reference models. A summary of the reads and bases is given for those chromosomes that have several α -satellite reference models. Arrays that are identical between different chromosome locations are indicated as the following: *, Sum of three near-identical arrays on chr1, 5, and 19; **, Sum of two near-identical arrays on chr5 and 19; ***, Sum of acrocentric near-identical arrays on chr13, 14, 21, and 22). Centromere reference models are from K.H. Miga and W.J. Kent (unpublished data). Sequence coordinates refer to the human GRCh38 assembly.