Cell line	Treatment	Hours	Experiment	Factor	Source	Library ID	Replicate	Combined into	Combined into	# of reads	Orig. Complexes (F>1)	Repetitive regions filtered	Entropy filtered (F=1)	Entropy filtered (F>1)	Enrich. Test FDR 0.1 (F=1)	Enrich. Test FDR 0.1 (F>1)	Enrich. Test FDR 0.2 (F=1)	Enrich. Test FDR 0.2 (F>1)
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG0210	Rep1-1	GM12878-CTCF-Rep1	GM12878-CTCF-pooled	53,809,034	791,544	618,965	1,041,038	150,101	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG0211	Rep1-2	GM12878-CTCF-Rep1	GM12878-CTCF-pooled	64,003,215	964,667	690,815	1,179,667	163,843	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG0212	Rep1-3	GM12878-CTCF-Rep1	GM12878-CTCF-pooled	87,724,974	1,341,844	1,027,220	1,745,852	266,143	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG0213	Rep1-4	GM12878-CTCF-Rep1	GM12878-CTCF-pooled	76,970,686	1,103,947	847,447	1,400,215	232,071	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG8113	Rep1-5	GM12878-CTCF-Rep1	GM12878-CTCF-pooled	89,647,949	2,583,586	2,099,266	3,729,833	535,011	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG8132	Rep1-6	GM12878-CTCF-Rep1	GM12878-CTCF-pooled	59,679,168	3,636,322	3,020,748	5,471,716	824,716	NA	NA	NA	NA
GM12878	**None**	**0**	**ChIA-Drop**	**CTCF**	**This study**		**Rep1**	**GM12878-CTCF-Rep1**	**SUM**	**431,835,026**	**10,421,910**	**8,304,461**	**14,568,321**	**2,171,885**	**1,446,321**	**172,209**	**3,829,611**	**524,532**
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG0214	Rep2-1	GM12878-CTCF-Rep2	GM12878-CTCF-pooled	95,786,946	1,838,463	1,469,135	2,644,685	331,473	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG0215	Rep2-2	GM12878-CTCF-Rep2	GM12878-CTCF-pooled	80,764,231	1,439,764	1,121,141	1,978,236	256,894	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG0216	Rep2-3	GM12878-CTCF-Rep2	GM12878-CTCF-pooled	72,844,914	1,188,792	935,629	1,632,757	212,748	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG0217	Rep2-4	GM12878-CTCF-Rep2	GM12878-CTCF-pooled	62,791,060	2,018,968	1,666,936	3,021,846	382,237	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG8117	Rep2-5	GM12878-CTCF-Rep2	GM12878-CTCF-pooled	89,781,816	1,486,451	1,210,392	1,965,824	359,772	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG8133	Rep2-6	GM12878-CTCF-Rep2	GM12878-CTCF-pooled	77,645,469	3,962,279	3,252,336	5,692,687	1,029,915	NA	NA	NA	NA
GM12878	**None**	**0**	**ChIA-Drop**	**CTCF**	**This study**		**Rep2**	**GM12878-CTCF-Rep2**	**SUM**	**479,614,436**	**11,934,717**	**9,655,569**	**16,936,035**	**2,573,039**	**1,574,468**	**202,948**	**4,372,322**	**636,262**
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG8033	Rep3-1	GM12878-CTCF-Rep3	GM12878-CTCF-pooled	51,695,102	733,738	543,326	875,400	142,541	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG8065	Rep3-2	GM12878-CTCF-Rep3	GM12878-CTCF-pooled	69,463,568	704,855	438,847	723,394	105,057	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG8098	Rep3-3	GM12878-CTCF-Rep3	GM12878-CTCF-pooled	64,024,493	715,163	560,346	927,602	134,599	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG8099	Rep3-4	GM12878-CTCF-Rep3	GM12878-CTCF-pooled	63,853,377	572,485	432,749	710,710	103,414	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG0193	Rep3-5	GM12878-CTCF-Rep3	GM12878-CTCF-pooled	50,095,683	520,952	412,727	731,855	70,338	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	CTCF	This study	SHG8035	Rep3-6	GM12878-CTCF-Rep3	GM12878-CTCF-pooled	83,797,446	2,750,133	2,205,832	4,488,489	244,101	NA	NA	NA	NA
GM12878	**None**	**0**	**ChIA-Drop**	**CTCF**	**This study**		**Rep3**	**GM12878-CTCF-Rep3**	**SUM**	**382,929,669**	**5,997,326**	**4,593,827**	**8,457,450**	**800,050**	**1,311,673**	**123,156**	**3,100,214**	**319,744**
GM12878	**None**	**0**	**ChIA-Drop**	**CTCF**	**This study**		**pooled**	**GM12878-CTCF-pooled**	**SUM**	**1,294,379,131**	**28,353,953**	**22,553,857**	**39,961,806**	**5,544,974**	**3,860,627**	**438,452**	**10,130,243**	**1,315,778**
GM12878	None	0	ChIA-Drop	RAD21	This study	SHG0180	Rep1-1	GM12878-RAD21-Rep1	GM12878-cohesin-pooled	86,737,328	5,114,489	4,396,204	9,438,034	619,616	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RAD21	This study	SHG0195	Rep1-2	GM12878-RAD21-Rep1	GM12878-cohesin-pooled	156,888,671	8,172,660	6,922,948	15,658,707	1,157,328	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RAD21	This study	SHG0198	Rep1-3	GM12878-RAD21-Rep1	GM12878-cohesin-pooled	56,143,013	3,451,076	2,971,641	6,186,579	386,731	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RAD21	This study	SHG0202	Rep1-4	GM12878-RAD21-Rep1	GM12878-cohesin-pooled	185,966,786	9,377,136	7,921,234	18,477,807	1,300,248	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RAD21	This study	SHG0205	Rep1-5	GM12878-RAD21-Rep1	GM12878-cohesin-pooled	130,723,974	8,069,067	7,027,539	16,154,497	1,035,487	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RAD21	This study	SHG0206	Rep1-6	GM12878-RAD21-Rep1	GM12878-cohesin-pooled	162,624,186	8,792,169	7,638,734	17,749,761	1,185,566	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RAD21	This study	SHG0207	Rep1-7	GM12878-RAD21-Rep1	GM12878-cohesin-pooled	62,793,728	4,378,656	3,794,757	7,909,865	587,478	NA	NA	NA	NA
GM12878	**None**	**0**	**ChIA-Drop**	**RAD21**	**This study**		**Rep1**	**GM12878-RAD21-Rep1**	**SUM**	**841,877,686**	**47,355,253**	**40,673,057**	**91,575,250**	**6,272,454**	**24,040,443**	**2,354,936**	**38,564,652**	**3,814,289**
GM12878	None	0	ChIA-Drop	RAD21	This study	SHG0181	Rep2-1	GM12878-RAD21-Rep2	GM12878-cohesin-pooled	84,530,899	5,855,167	5,066,326	10,806,732	857,395	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RAD21	This study	SHG0196	Rep2-2	GM12878-RAD21-Rep2	GM12878-cohesin-pooled	156,415,452	9,227,264	7,966,428	17,914,120	1,615,428	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RAD21	This study	SHG0199	Rep2-3	GM12878-RAD21-Rep2	GM12878-cohesin-pooled	102,445,657	5,881,573	4,992,295	11,148,999	901,052	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RAD21	This study	SHG0203	Rep2-4	GM12878-RAD21-Rep2	GM12878-cohesin-pooled	191,895,737	11,257,752	9,780,145	23,216,948	2,011,434	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RAD21	This study	SHG0208	Rep2-5	GM12878-RAD21-Rep2	GM12878-cohesin-pooled	68,451,827	4,531,214	3,915,771	8,216,029	601,217	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RAD21	This study	SHG0209	Rep2-6	GM12878-RAD21-Rep2	GM12878-cohesin-pooled	79,128,174	4,808,693	4,138,099	8,709,449	652,205	NA	NA	NA	NA
GM12878	**None**	**0**	**ChIA-Drop**	**RAD21**	**This study**		**Rep2**	**GM12878-RAD21-Rep2**	**SUM**	**682,867,746**	**41,561,663**	**35,859,064**	**80,012,277**	**6,638,731**	**19,156,824**	**2,049,377**	**30,243,718**	**3,641,468**
GM12878	None	0	ChIA-Drop	RNAPII	This study	SHG8034	Rep1-1	GM12878-RNAPII-Rep1	GM12878-RNAPII-pooled;	79,192,522	3,149,655	2,545,237	5,250,602	280,345	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RNAPII	This study	SHG8100	Rep1-2	GM12878-RNAPII-Rep1	GM12878-RNAPII-pooled;	65,226,738	2,035,305	1,681,315	3,390,414	175,460	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RNAPII	This study	SHG8101	Rep1-3	GM12878-RNAPII-Rep1	GM12878-RNAPII-pooled;	67,282,542	1,913,204	1,583,783	3,175,672	165,845	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RNAPII	This study	SHG8096	Rep1-4	GM12878-RNAPII-Rep1	GM12878-RNAPII-pooled;	68,385,904	1,475,063	1,180,104	1,939,470	337,391	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RNAPII	This study	SHG8097	Rep1-5	GM12878-RNAPII-Rep1	GM12878-RNAPII-pooled;	64,871,999	1,345,206	1,052,235	1,736,384	290,936	NA	NA	NA	NA
GM12878	**None**	**0**	**ChIA-Drop**	**RNAPII**	**This study**		**Rep1**	**GM12878-RNAPII-Rep1**	**SUM**	**344,959,705**	**9,918,433**	**8,042,674**	**15,492,542**	**1,249,977**	**498,661**	**49,328**	**1,625,961**	**176,301**
GM12878	None	0	ChIA-Drop	RNAPII	This study	SHG8112	Rep2-1	GM12878-RNAPII-Rep2	GM12878-RNAPII-pooled;	67,273,144	837,532	631,102	784,063	300,071	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RNAPII	This study	SHG8116	Rep2-2	GM12878-RNAPII-Rep2	GM12878-RNAPII-pooled;	63,420,334	2,040,875	1,649,997	2,681,333	538,143	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RNAPII	This study	SHG8130	Rep2-3	GM12878-RNAPII-Rep2	GM12878-RNAPII-pooled;	73,720,406	1,515,204	1,115,839	1,493,472	505,536	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RNAPII	This study	SHG8131	Rep2-4	GM12878-RNAPII-Rep2	GM12878-RNAPII-pooled;	50,726,668	3,737,580	3,107,110	5,080,082	1,208,344	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RNAPII	This study	SHG0218	Rep2-5	GM12878-RNAPII-Rep2	GM12878-RNAPII-pooled;	57,701,716	1,348,602	1,079,930	1,973,798	201,193	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RNAPII	This study	SHG0219	Rep2-6	GM12878-RNAPII-Rep2	GM12878-RNAPII-pooled;	57,662,440	1,402,528	1,157,338	2,129,293	209,548	NA	NA	NA	NA
GM12878	**None**	**0**	**ChIA-Drop**	**RNAPII**	**This study**		**Rep2**	**GM12878-RNAPII-Rep2**	**SUM**	**370,504,708**	**10,882,321**	**8,741,316**	**14,142,041**	**2,962,835**	**1,766,059**	**324,424**	**4,009,518**	**802,527**
GM12878	None	0	ChIA-Drop	RNAPII	This study	SHG0234	Rep3-1	GM12878-RNAPII-Rep3	GM12878-RNAPII-pooledv	77,820,387	1,783,676	1,516,515	2,835,101	266,791	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RNAPII	This study	SHG0235	Rep3-2	GM12878-RNAPII-Rep3	GM12878-RNAPII-pooledv	87,702,678	6,465,918	5,715,047	12,226,757	1,065,348	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RNAPII	This study	SHG0238	Rep3-3	GM12878-RNAPII-Rep3	GM12878-RNAPII-pooledv	78,539,454	617,441	438,423	750,148	89,533	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	RNAPII	This study	SHG0239	Rep3-4	GM12878-RNAPII-Rep3	GM12878-RNAPII-pooledv	94,222,395	2,919,656	2,447,198	4,779,894	425,597	NA	NA	NA	NA
GM12878	**None**	**0**	**ChIA-Drop**	**RNAPII**	**This study**		**Rep3**	**GM12878-RNAPII-Rep3**	**SUM**	**338,284,914**	**11,786,691**	**10,117,183**	**20,591,900**	**1,847,269**	**7,280,519**	**911,541**	**11,783,316**	**1,296,009**
GM12878	**None**	**0**	**ChIA-Drop**	**RNAPII**	**This study**		**pooledv2**	**GM12878-RNAPII-pooledv2**	**SUM**	**1,053,749,327**	**32,587,445**	**26,901,173**	**50,226,483**	**6,060,081**	**9,798,884**	**1,263,151**	**15,607,687**	**2,399,732**
GM12878	None	0	ChIA-Drop	SMC1A	This study	SHG0182	Rep1-1	GM12878-SMC1A-pooled	GM12878-cohesin-pooled	88,752,922	6,607,743	5,793,086	12,891,264	866,372	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	SMC1A	This study	SHG0197	Rep1-2	GM12878-SMC1A-pooled	GM12878-cohesin-pooled	149,720,829	9,006,846	7,879,794	18,316,671	1,300,389	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	SMC1A	This study	SHG0200	Rep1-3	GM12878-SMC1A-pooled	GM12878-cohesin-pooled	58,803,883	4,233,583	3,642,191	7,991,181	502,120	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	SMC1A	This study	SHG0204	Rep1-4	GM12878-SMC1A-pooled	GM12878-cohesin-pooled	177,247,438	12,688,027	11,316,882	28,633,048	2,177,644	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	SMC1A	This study	SHG0186	Rep1-5	GM12878-SMC1A-pooled	GM12878-cohesin-pooled	147,848,455	7,014,380	5,878,466	13,114,151	962,827	NA	NA	NA	NA
GM12878	None	0	ChIA-Drop	SMC1A	This study	SHG0201	Rep1-6	GM12878-SMC1A-pooled	GM12878-cohesin-pooled	57,751,339	3,872,026	3,276,503	6,829,458	496,042	NA	NA	NA	NA
GM12878	**None**	**0**	**ChIA-Drop**	**cohesin**	**This study**		**pooled**	**GM12878-cohesin-pooled**	**SUM**	**2,204,870,298**	**132,339,521**	**114,319,043**	**259,363,300**	**19,216,579**	**54,701,855**	**5,705,174**	**93,673,795**	**10,211,318**
GM12878	None	0	ChIA-PET	CTCF	This study	LHG0052H	Rep1	N/A	N/A	358,752,218								
GM12878	None	0	ChIA-PET	SMC1A	This study	LHG0051H	Rep1	N/A	N/A	356,152,208								
GM12878	None	0	ChIA-PET	RAD21	This study	LHG0104V	Rep1	N/A	N/A	459,140,632								
GM12878	None	0	ChIA-PET	Cohesin	This study	LHG0051H_0104V	pooled	N/A	N/A	815,292,840								
GM12878	None	0	ChIA-PET	RNAPII	This study	LHG0035N	Rep1	N/A	N/A	132,169,141								
GM12878	None	0	ChIA-PET	RNAPII	This study	LHG0035V	Rep1	N/A	N/A	253,204,012								
GM12878	None	0	ChIA-PET	RNAPII	This study	LHG0045V	Rep2	N/A	N/A	494,494,353								
GM12878	None	0	ChIA-PET	RNAPII	This study	LHG0035N_0035V_0045V	pooled	N/A	N/A	879,867,506								
GM12878	None	0	SPRITE	None	4D Nucleome	4DNESI1U7ZW9	pooled	N/A	N/A	1,610,209,838								
GM12878	None	0	Hi-C	None	4D Nucleome	4DNFI7J8BQ4P	pooled	N/A	N/A	826,414,879								
GM19239	None	0	Hi-C	None	4D Nucleome	4DNESVKLYDOH	pooled	N/A	N/A	750,185,985								
HCT116	None	0	ChIA-PET	CTCF	This study	LHH0118V	Rep1	N/A	N/A	293,527,935								
HCT116	None	0	ChIA-PET	CTCF	This study	LHH0127V	Rep2	N/A	N/A	306,988,032								
HCT116	None	0	ChIA-PET	CTCF	This study	LHH0118V_0127V	pooled	N/A	N/A	600,515,967								
HCT116	None	0	ChIA-PET	RNAPII	This study	LHH0098V	Rep1	N/A	N/A	517,207,217								
HCT116	None	0	ChIA-PET	RNAPII	This study	LHH0128V	Rep2	N/A	N/A	316,087,217								
HCT116	None	0	ChIA-PET	RNAPII	This study	LHH0098V_0128V	pooled	N/A	N/A	833,294,434								
HCT116	None	0	ChIA-PET	RAD21	This study	LHH0139	Rep1	N/A	N/A	48,523,665								
HCT116	None	0	ChIA-PET	RAD21	This study	LHH0139V	Rep1	N/A	N/A	90,562,053								
HCT116	None	0	ChIA-PET	RAD21	This study	LHH0140	Rep2	N/A	N/A	42,973,485								
HCT116	None	0	ChIA-PET	RAD21	This study	LHH0140V	Rep2	N/A	N/A	110,921,989								
HCT116	None	0	ChIA-PET	RAD21	This study	LHH0139_0139V_0140_01	pooled	N/A	N/A	292,981,192								
HCT116	RAD-mAC-auxin	0	Hi-C	None	This study	LHH0146V	Rep1	N/A	N/A	360,397,636								
HCT116	RAD-mAC-auxin	6	Hi-C	None	This study	LHH0147V	Rep1	N/A	N/A	372,697,334								
HCT116	RAD-mAC-auxin	0	Hi-C	None	4D Nucleome	4DNFIP71EWXC	Rep1	N/A	N/A	3,475,834,764								
HCT116	RAD-mAC-auxin	6	Hi-C	None	4D Nucleome	4DNFILIM6FDL	Rep1	N/A	N/A	3,365,153,349								
HCT116	RAD-mAC-auxin	0	ChIA-PET	CTCF	This study	LHH0157	Rep1	N/A	N/A	366,508,457								
HCT116	RAD-mAC-auxin	0	ChIA-PET	CTCF	This study	LHH0172	Rep2	N/A	N/A	569,205,831								
HCT116	RAD-mAC-auxin	0	ChIA-PET	CTCF	This study	LHH0157_0172	pooled	N/A	N/A	935,714,288								
HCT116	RAD-mAC-auxin	6	ChIA-PET	CTCF	This study	LHH0158	Rep1	N/A	N/A	401,699,562								
HCT116	RAD-mAC-auxin	6	ChIA-PET	CTCF	This study	LHH0173	Rep2	N/A	N/A	460,564,094								
HCT116	RAD-mAC-auxin	6	ChIA-PET	CTCF	This study	LHH0158_0173	pooled	N/A	N/A	862,263,656								
HCT116	RAD-mAC-auxin	0	ChIA-PET	RNAPII	This study	LHH0170	Rep1	N/A	N/A	557,061,917								
HCT116	RAD-mAC-auxin	0	ChIA-PET	RNAPII	This study	LHH0159	Rep2	N/A	N/A	343,180,214								
HCT116	RAD-mAC-auxin	0	ChIA-PET	RNAPII	This study	LHH0159V	Rep2	N/A	N/A	483,901,014								
HCT116	RAD-mAC-auxin	0	ChIA-PET	RNAPII	This study	LHH0170_0159_0159V	pooled	N/A	N/A	1,384,143,145								
HCT116	RAD-mAC-auxin	6	ChIA-PET	RNAPII	This study	LHH0171	Rep1	N/A	N/A	565,251,115								
HCT116	RAD-mAC-auxin	6	ChIA-PET	RNAPII	This study	LHH0160	Rep2	N/A	N/A	363,275,787								
HCT116	RAD-mAC-auxin	6	ChIA-PET	RNAPII	This study	LHH0160V	Rep2	N/A	N/A	533,711,372								
HCT116	RAD-mAC-auxin	6	ChIA-PET	RNAPII	This study	LHH0171_0160_0160V	pooled	N/A	N/A	1,462,238,274								
H1	None	0	ChIA-PET	RNAPII	ENCODE	LHES0007H; ENCSR782EKZ	Rep1	N/A	N/A	302,061,532								
K562	None	0	ChIA-PET	RNAPII	ENCODE	LHK0009H_0011V_0012V;	pooled	N/A	N/A									
HepG2	None	0	ChIA-PET	RNAPII	ENCODE	LHH0123_0123V_0124_01	pooled	N/A	N/A									
MCF7	None	0	ChIA-PET	RNAPII	ENCODE	LHM0011_0011H_0014_0	pooled	N/A	N/A									

Cell line	Treatment	Hours	Experiment	Factor	Source	Library ID	# of reads
GM12878	None	0	ChIP-seq	NIPBL	This study	CHG0030	61,848,343
GM12878	None	0	ChIP-seq	CTCF	This study	CHG0031	77,693,935
GM12878	None	0	ChIP-seq	WAPL	This study	CHG0032	47,004,834
GM12878	None	0	ChIP-seq	Input	This study	CHG0033	57,104,734
GM12878	None	0	ChIP-seq	RAD21	This study	CHG0034	56,474,262
GM12878	None	0	ChIP-seq	H3K27ac	ENCODE consortium	ENCFF340JIF	36,793,809
GM12878	None	0	ChIP-seq	H3K4me1	ENCODE consortium	ENCFF831ZHL	63,144,095
GM12878	None	0	chromHMM	N/A	Broad inst. UCSC	N/A	N/A
GM12878	None	0	Super-enhancer	N/A	Hsniz et al., 2013	N/A	N/A
GM12878	None	0	CTCF motif	N/A	Tang et al., 2015	N/A	N/A
HCT116	RAD-mAC-auxin	0	ChIP-seq	RAD21	This study	CHH0056	78,476,992
HCT116	RAD-mAC-auxin	6	ChIP-seq	RAD21	This study	CHH0057	90,082,366
HCT116	RAD-mAC-auxin	9	ChIP-seq	RAD21	This study	CHH0058	76,173,734
HCT116	RAD-mAC-auxin	12	ChIP-seq	RAD21	This study	CHH0059	99,661,912
HCT116	RAD-mAC-auxin	0	ChIP-seq	CTCF	This study	CHH0060	86,801,317
HCT116	RAD-mAC-auxin	6	ChIP-seq	CTCF	This study	CHH0061	93,779,737
HCT116	RAD-mAC-auxin	9	ChIP-seq	CTCF	This study	CHH0062	68,463,927
HCT116	RAD-mAC-auxin	12	ChIP-seq	CTCF	This study	CHH0063	96,902,097
HCT116	RAD-mAC-auxin	0	ChIP-seq	RNAPII	This study	CHH0064	90,338,263
HCT116	RAD-mAC-auxin	6	ChIP-seq	RNAPII	This study	CHH0065	76,276,878
HCT116	RAD-mAC-auxin	9	ChIP-seq	RNAPII	This study	CHH0066	82,799,502
HCT116	RAD-mAC-auxin	12	ChIP-seq	RNAPII	This study	CHH0067	95,021,331
HCT116	RAD-mAC-auxin	0	Repli-seq	N/A	4D Nucleome	4DNESNGZM5FG	N/A
HCT116	RAD-mAC-auxin	6	Repli-seq	N/A	4D Nucleome	4DNES92AU9JR	N/A
HCT116	None	0	chromHMM	N/A	ENCODE consortium	ENCFF513PJK	N/A
HCT116	None	0	Super-enhancer	N/A	Hsniz et al., 2013	N/A	N/A
MCF7	None	0	chromHMM	N/A	ENCODE consortium	ENCFF506GEX	N/A
K562	None	0	chromHMM	N/A	Broad inst. UCSC	N/A	N/A
HepG2	None	0	chromHMM	N/A	Broad inst. UCSC	N/A	N/A
H1	None	0	chromHMM	N/A	Broad inst. UCSC	N/A	N/A

Cell line	Treatment	Hours	Experiment	Source	Library ID	# of reads
GM12878	None	0	RNA-seq	ENCODE consortium	ENCLB555AQG	117,876,320
HCT116	RAD-mAC-auxin	0	RNA-seq	This study	RHH0001	41,471,532
HCT116	RAD-mAC-auxin	0	RNA-seq	This study	RHH0005	69,861,080
HCT116	RAD-mAC-auxin	6	RNA-seq	This study	RHH0002	54,085,738
HCT116	RAD-mAC-auxin	6	RNA-seq	This study	RHH0006	74,474,501
HCT116	RAD-mAC-auxin	9	RNA-seq	This study	RHH0003	56,290,599
HCT116	RAD-mAC-auxin	9	RNA-seq	This study	RHH0007	57,358,596
HCT116	RAD-mAC-auxin	12	RNA-seq	This study	RHH0004	52,650,577
HCT116	RAD-mAC-auxin	12	RNA-seq	This study	RHH0008	66,396,860
H1	None	0	RNA-seq	ENCODE consortium	ENCLB555AMA	125,395,196
K562	None	0	RNA-seq	ENCODE consortium	ENCLB555AKN	113,588,758
HepG2	None	0	RNA-seq	ENCODE consortium	ENCLB555AQD	124,172,649
MCF7	None	0	RNA-seq	ENCODE consortium	ENCLB555AQN	128,178,110

Cell line	Treatment	Hours	Experiment	Source	Probe loci	# of nuclei	# of pairs	# of distances	Supp. Videos
HCT116/RAD21-mAC/dCas9	None	0	Casilio	This study	*BCL6*	21	27	1107	S1
HCT116/RAD21-mAC/dCas9	Auxin	24	Casilio	This study	*BCL6*	26	38	1484	S2
HCT116/RAD21-mAC/dCas9	None	0	Casilio	This study	*SOX9*	17	31	1166	S3
HCT116/RAD21-mAC/dCas9	Auxin	24	Casilio	This study	*SOX9*	15	23	943	S4

Cell line	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878
IP-factor	CTCF	CTCF	CTCF	CTCF	CTCF	CTCF	CTCF	CTCF	CTCF	CTCF	CTCF
lib	SHG0193	SHG0210	SHG0211	SHG0212	SHG0213	SHG0214	SHG0215	SHG0216	SHG0217	SHG8033	SHG8035
Ref. Genome	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38
pcr_duplication	0.02846304	0.02232472	0.02911794	0.03511322	0.02911747	0.03527989	0.03000722	0.02844855	0.02422908	0.02405731	0.0474847
Total_PET_(Paired_end_reads)	50,095,683	53,809,034	64,003,215	87,724,974	76,970,686	95,786,946	80,764,231	72,844,914	62,791,060	51,695,102	83,797,446
PET_with_BC_(BarCode)	39,872,030	42,176,374	50,948,959	69,070,748	60,371,463	78,497,190	65,747,475	57,541,619	55,393,822	36,833,007	71,371,861
Uniq_Mappable_reads (R1)	37,204,747	39,818,903	48,053,958	64,921,051	56,875,230	73,763,730	61,661,275	53,795,101	52,562,678	35,146,861	69,353,579
Reads_mapq>=30	27,457,413	29,156,604	34,244,792	47,531,107	41,776,872	55,753,439	45,905,695	39,568,073	41,989,305	24,343,565	53,326,491
Reads_q>=30_&_len>=50bp	25,969,870	27,773,006	32,681,246	45,168,473	39,719,788	53,002,068	43,632,326	37,493,110	40,221,986	23,192,800	51,497,910
Reads_q>=30_&_len>=50bp_&_3'ext500	25,547,959	27,378,204	32,165,303	44,540,686	39,178,246	52,265,577	43,001,284	36,975,642	39,888,849	22,970,144	50,900,386
Reads_q>=30_&_len>=50bp_&_3'ext500_&_MAJOR_CHROM	25,547,959	27,378,204	32,165,303	44,540,686	39,178,246	52,265,577	43,001,284	36,975,642	39,888,849	22,970,144	50,900,386
BC_count_of_PET-w/-BC_(BarCode)	1,772,481	1,762,747	1,865,890	2,016,988	1,917,566	2,089,977	1,959,526	1,937,727	1,829,715	2,102,213	2,386,536
BC_of_Uniq_Mappable_reads_(R1)	1,747,622	1,741,282	1,839,903	1,990,117	1,892,314	2,060,361	1,930,980	1,910,217	1,807,211	2,083,999	2,369,710
BC_of_Reads_q>=30 & len>=50bp & 3'ext500 & MAJOR_CHROM	1,596,356	1,594,196	1,679,722	1,817,450	1,728,402	1,903,802	1,778,739	1,759,094	1,688,512	1,940,561	2,243,710
GEM_TOTAL	1,596,356	1,594,196	1,679,722	1,817,450	1,728,402	1,903,802	1,778,739	1,759,094	1,688,512	1,940,561	2,243,710
GEM_singleFrag	444,317	440,807	519,437	527,685	491,659	544,079	516,730	502,183	405,159	620,589	564,290
GEM_multiFrags	1,152,039	1,153,389	1,160,285	1,289,765	1,236,743	1,359,723	1,262,009	1,256,911	1,283,353	1,319,972	1,679,420
GEM_of_intra_chrom	18,514	14,662	13,683	12,180	13,282	9,194	9,651	11,347	5,367	25,332	10,573
GEM_of_inter_chrom	1,133,525	1,138,727	1,146,602	1,277,585	1,223,461	1,350,529	1,252,358	1,245,564	1,277,986	1,294,640	1,668,847
GEM_of_inter_chrom_divby_chrom_has_multiFrags	502,438	776,882	950,984	1,329,664	1,090,665	1,829,269	1,430,113	1,177,445	2,013,601	708,406	2,739,560
GEM_of_inter_chrom_divby_chrom_has_singleFrag	3,811,330	4,209,325	4,486,721	5,343,336	4,833,333	6,257,545	5,482,278	5,136,950	6,347,235	4,321,196	8,633,129
GEM_of_TOTAL_SA_[SingleFrag+IntraFrags]	4,776,599	5,441,676	5,970,825	7,212,865	6,428,939	8,640,087	7,438,772	6,827,925	8,771,362	5,675,523	11,947,552
GEM_with_Frags=1	4,255,647	4,650,132	5,006,158	5,871,021	5,324,992	6,801,624	5,999,008	5,639,133	6,752,394	4,941,785	9,197,419
GEM_with_Frags=2	451,522	646,944	766,429	1,033,107	863,940	1,385,716	1,107,676	938,347	1,506,691	598,865	2,090,724
GEM_with_Frags=3	55,895	109,882	145,283	219,748	172,215	322,728	239,076	184,496	363,299	97,114	488,682
GEM_with_Frags=4	9,078	23,185	34,360	56,084	42,740	84,639	60,090	43,415	96,960	22,565	119,319
GEM_with_Frags=5	2,222	6,630	10,230	18,052	13,413	26,072	18,461	12,864	30,163	7,850	32,645
GEM_with_Frags=6	851	2,286	3,805	6,770	5,138	9,502	6,721	4,680	10,949	3,494	10,364
GEM_with_Frags=7	472	1,077	1,737	3,164	2,482	4,110	3,010	2,034	4,748	1,581	3,784
GEM_with_Frags=8	259	539	939	1,682	1,388	2,059	1,615	1,038	2,395	849	1,747
GEM_with_Frags=9	193	333	534	1,032	766	1,162	908	618	1,309	541	985
GEM_with_Frags=10	128	182	390	639	517	698	589	387	810	284	509
GEM_with_Frags=11	67	126	265	415	346	470	405	216	486	184	376
GEM_with_Frags=12	57	108	157	265	243	300	308	194	353	107	229
GEM_with_Frags=13	52	70	128	196	187	240	187	119	212	96	177
GEM_with_Frags=14	39	47	91	168	129	155	162	88	157	46	120
GEM_with_Frags=15~19	79	90	225	358	291	412	364	197	344	123	243
GEM_with_Frags=20~29	25	42	88	150	137	164	163	84	88	33	164
GEM_with_Frags=30~39	11	2	5	14	12	28	28	13	2	5	45
GEM_with_Frags=40~49	1	1	0	0	2	5	1	2	2	1	12
GEM_with_Frags=50~99	1	0	1	0	1	3	0	0	0	0	8
GEM_with_Frags=100~199	0	0	0	0	0	0	0	0	0	0	0
GEM_with_Frags=200~499	0	0	0	0	0	0	0	0	0	0	0
GEM_with_Frags=500~999	0	0	0	0	0	0	0	0	0	0	0
GEM_with_Frags>=1000	0	0	0	0	0	0	0	0	0	0	0
GEM_with_Frags>=2	520,952	791,544	964,667	1,341,844	1,103,947	1,838,463	1,439,764	1,188,792	2,018,968	733,738	2,750,133

GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878
CTCF	CTCF	CTCF	CTCF	CTCF	CTCF	CTCF	RAD21	RAD21	RAD21	RAD21	RAD21	RAD21	RAD21
SHG8065	SHG8098	SHG8099	SHG8113	SHG8117	SHG8132	SHG8133	SHG0180	SHG0181	SHG0195	SHG0196	SHG0198	SHG0199	SHG0202
hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38
0.02039344	0.01942816	0.01845405	0.02347501	0.02144112	0.0490809	0.06331885	0.04587731	0.0423211	0.07546764	0.06999088	0.02459719	0.04832803	0.06393175
69,463,568	64,024,493	63,853,377	89,647,949	89,781,816	59,679,168	77,645,469	86,737,328	84,530,899	156,888,671	156,415,452	56,143,013	102,445,657	185,966,786
42,913,924	41,494,304	38,705,371	68,003,364	59,499,825	45,518,623	56,416,833	81,245,068	79,961,732	145,105,015	146,085,990	53,219,658	96,778,952	174,291,034
39,628,989	39,246,156	36,291,400	65,265,888	56,746,979	44,097,839	54,504,978	77,257,629	76,226,127	137,567,545	139,079,600	51,039,139	92,936,861	166,767,800
23,129,640	26,565,428	23,160,539	49,161,136	40,069,067	34,851,418	42,275,084	61,759,016	61,074,010	107,831,916	110,441,419	41,192,989	72,508,767	136,516,711
21,664,710	25,101,266	21,702,443	47,035,308	37,995,117	34,018,551	41,136,175	59,549,310	58,978,852	103,697,647	106,442,199	39,859,302	70,336,480	131,809,441
21,415,272	24,880,328	21,492,394	46,471,646	37,529,466	33,664,036	40,720,911	59,256,727	58,715,139	103,054,513	105,909,846	39,694,561	69,945,102	131,148,769
21,415,272	24,880,328	21,492,394	46,471,646	37,529,466	33,664,036	40,720,911	59,256,727	58,715,139	103,054,513	105,909,846	39,694,561	69,945,102	131,148,769
1,870,026	1,908,267	1,816,956	2,153,502	2,180,138	1,900,443	1,907,343	2,038,467	2,037,963	2,724,084	2,683,085	1,890,494	2,210,317	2,921,118
1,846,019	1,892,738	1,799,767	2,137,020	2,165,412	1,894,014	1,899,338	2,017,770	2,017,626	2,701,969	2,661,243	1,875,073	2,183,052	2,889,612
1,650,217	1,753,372	1,629,261	2,007,376	2,023,825	1,838,423	1,832,873	1,902,013	1,905,534	2,562,403	2,521,212	1,781,341	2,009,871	2,715,025
1,650,217	1,753,372	1,629,261	2,007,376	2,023,825	1,838,423	1,832,873	1,902,013	1,905,534	2,562,403	2,521,212	1,781,341	2,009,871	2,715,025
484,442	468,648	441,258	411,650	453,143	200,641	204,899	357,600	352,028	698,983	680,411	330,641	722,801	829,390
1,165,775	1,284,724	1,188,003	1,595,726	1,570,682	1,637,782	1,627,974	1,544,413	1,553,506	1,863,420	1,840,801	1,450,700	1,287,070	1,885,635
22,281	20,868	23,235	7,420	16,759	4,367	3,559	3,548	3,186	15,075	13,452	2,993	9,979	15,848
1,143,494	1,263,856	1,164,768	1,588,306	1,553,923	1,633,415	1,624,415	1,540,865	1,550,320	1,848,345	1,827,349	1,447,707	1,277,091	1,869,787
682,574	694,295	549,250	2,576,166	1,469,692	3,631,955	3,958,720	5,110,941	5,851,981	8,157,585	9,213,812	3,448,083	5,871,594	9,361,288
3,814,982	4,327,109	3,787,752	7,730,734	6,187,010	8,673,167	8,711,157	9,732,819	10,028,458	11,013,824	11,094,276	8,526,621	7,757,077	11,157,778
5,004,279	5,510,920	4,801,495	10,725,970	8,126,604	12,510,130	12,878,335	15,204,908	16,235,653	19,885,467	21,001,951	12,308,338	14,361,451	21,364,304
4,299,424	4,795,757	4,229,010	8,142,384	6,640,153	8,873,808	8,916,056	10,090,419	10,380,486	11,712,807	11,774,687	8,857,262	8,479,878	11,987,168
539,816	596,225	480,188	1,877,831	1,148,503	2,488,683	2,624,917	3,439,261	3,797,704	4,777,764	5,170,163	2,501,133	3,444,020	5,245,974
100,830	90,974	69,233	480,013	239,804	738,695	827,338	1,120,698	1,325,357	1,988,666	2,281,151	681,673	1,441,837	2,338,256
30,937	18,531	14,548	139,186	61,630	239,827	286,280	362,041	459,430	811,731	981,888	187,276	582,009	1,005,485
13,881	5,267	4,484	47,287	19,841	88,648	112,004	121,582	164,105	333,657	425,887	54,273	235,059	431,837
7,539	2,041	1,904	18,838	7,863	37,086	48,652	42,413	62,006	140,874	189,997	16,858	97,222	190,166
4,124	941	831	8,660	3,579	17,296	24,007	15,851	24,355	61,690	87,118	5,472	41,603	85,052
2,467	440	500	4,493	2,005	9,132	12,963	6,343	10,490	28,567	41,800	2,083	18,879	39,759
1,713	288	276	2,588	1,101	5,388	7,730	2,631	4,844	13,266	20,665	863	8,945	18,890
1,118	140	149	1,556	650	3,365	4,907	1,218	2,351	6,562	10,742	460	4,441	9,355
729	101	96	928	404	2,273	3,302	703	1,297	3,351	5,921	245	2,415	4,659
482	69	70	637	253	1,505	2,339	419	800	1,776	3,335	163	1,306	2,570
321	34	50	434	185	1,032	1,653	247	490	1,184	2,110	112	829	1,418
244	19	23	300	158	794	1,228	188	362	693	1,411	60	601	822
480	63	84	606	318	1,805	3,067	484	887	1,503	2,770	242	1,295	1,704
144	27	39	184	130	666	1,407	260	465	886	1,548	125	775	816
17	3	5	38	21	100	294	83	117	280	417	27	201	208
8	0	3	5	5	18	86	30	60	105	148	6	68	87
5	0	2	2	1	9	86	36	47	101	170	5	64	70
0	0	0	0	0	0	15	1	0	4	22	0	3	8
0	0	0	0	0	0	4	0	0	0	1	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
704,855	715,163	572,485	2,583,586	1,486,451	3,636,322	3,962,279	5,114,489	5,855,167	8,172,660	9,227,264	3,451,076	5,881,573	9,377,136

GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878
RAD21	RAD21	RAD21	RAD21	RAD21	RAD21	SMC1A	SMC1A	SMC1A	SMC1A	SMC1A	SMC1A	RNAPII	RNAPII
SHG0203	SHG0205	SHG0206	SHG0207	SHG0208	SHG0209	SHG0182	SHG0186	SHG0197	SHG0200	SHG0201	SHG0204	SHG0218	SHG0219
hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38
0.06507599	0.04080005	0.05103529	0.0272089	0.02739122	0.02925437	0.03681377	0.05813272	0.04303481	0.02459852	0.02701237	0.03288814	0.02927647	0.02712616
191,895,737	130,723,974	162,624,186	62,793,728	68,451,827	79,128,174	88,752,922	147,848,455	149,720,829	58,803,883	57,751,339	177,247,438	57,701,716	57,662,440
181,580,861	123,784,145	153,072,139	59,211,581	64,680,345	74,251,010	86,265,518	139,345,536	144,916,276	56,903,448	54,925,050	173,467,548	47,703,440	47,582,400
174,244,222	118,072,681	145,811,190	56,587,584	61,714,453	70,710,360	83,689,009	133,177,422	140,949,358	55,412,659	52,788,350	169,298,401	44,780,648	44,727,208
142,866,662	97,255,562	119,664,193	46,028,720	49,078,393	55,920,819	70,352,994	103,749,435	118,986,672	46,604,769	42,174,020	147,103,752	31,953,228	32,058,056
138,316,876	93,862,760	115,339,163	44,521,320	47,427,796	53,963,819	68,703,503	100,205,515	116,115,293	45,681,378	40,943,087	144,187,673	30,478,266	30,510,648
137,637,355	93,454,012	114,829,001	44,331,077	47,222,452	53,726,175	67,918,010	98,814,463	114,538,527	44,911,203	40,483,176	142,558,840	30,299,353	30,347,279
137,637,355	93,454,012	114,829,001	44,331,077	47,222,452	53,726,175	67,918,010	98,814,463	114,538,527	44,911,203	40,483,176	142,558,840	30,299,353	30,347,279
2,800,485	2,618,896	2,798,679	2,204,312	2,095,451	2,178,202	1,914,369	2,532,457	2,298,015	1,825,199	2,076,666	2,446,515	2,029,433	2,016,268
2,769,385	2,586,966	2,764,032	2,180,309	2,075,332	2,156,250	1,897,061	2,507,478	2,278,233	1,803,937	2,053,586	2,419,741	1,999,990	1,990,892
2,593,084	2,424,384	2,586,355	2,049,577	1,954,728	2,024,006	1,799,976	2,368,735	2,147,125	1,681,152	1,914,466	2,283,339	1,780,041	1,793,040
2,593,084	2,424,384	2,586,355	2,049,577	1,954,728	2,024,006	1,799,976	2,368,735	2,147,125	1,681,152	1,914,466	2,283,339	1,780,041	1,793,040
801,145	722,533	802,303	511,059	442,773	489,157	286,266	681,109	527,349	461,177	489,631	651,260	423,117	386,400
1,791,939	1,701,851	1,784,052	1,538,518	1,511,955	1,534,849	1,513,710	1,687,626	1,619,776	1,219,975	1,424,835	1,632,079	1,356,924	1,406,640
13,357	10,142	13,514	4,943	4,025	4,763	2,303	12,606	6,264	4,466	4,987	7,318	9,443	8,927
1,778,582	1,691,709	1,770,538	1,533,575	1,507,930	1,530,086	1,511,407	1,675,020	1,613,512	1,215,509	1,419,848	1,624,761	1,347,481	1,397,713
11,244,395	8,058,925	8,778,655	4,373,713	4,527,189	4,803,930	6,605,440	7,001,774	9,000,582	4,229,117	3,867,039	12,680,709	1,339,159	1,393,601
10,719,823	10,725,236	10,900,905	9,312,672	9,306,439	9,463,101	9,998,098	10,146,056	10,501,513	7,495,830	8,484,451	10,047,768	5,874,233	6,132,695
22,778,720	19,516,836	20,495,377	14,202,387	14,280,426	14,760,951	16,892,107	17,841,545	20,035,708	12,190,590	12,846,108	23,387,055	7,645,952	7,921,623
11,520,968	11,447,769	11,703,208	9,823,731	9,749,212	9,952,258	10,284,364	10,827,165	11,028,862	7,957,007	8,974,082	10,699,028	6,297,350	6,519,095
5,750,646	4,784,628	5,044,682	3,031,457	3,108,659	3,253,199	4,131,383	4,219,834	5,086,835	2,771,706	2,689,145	6,011,352	1,082,922	1,133,230
2,867,529	1,965,856	2,176,272	921,848	965,732	1,040,253	1,552,406	1,671,613	2,243,498	959,255	805,678	3,266,537	203,713	210,465
1,365,339	780,487	904,026	281,993	301,119	334,272	569,593	651,896	951,453	325,462	243,671	1,677,510	43,385	43,139
645,462	311,856	375,594	90,150	97,829	112,114	212,440	259,580	402,540	111,611	78,484	842,856	10,920	10,375
309,354	127,301	159,676	31,110	33,625	39,664	82,078	108,115	174,149	39,484	27,927	424,815	3,477	2,979
151,595	53,681	69,720	11,428	12,661	15,136	32,493	47,852	77,277	14,561	11,182	217,430	1,560	1,064
75,924	23,233	31,503	4,724	5,308	6,318	13,358	22,503	35,604	5,738	5,238	113,577	864	526
39,534	10,665	14,590	2,172	2,317	2,949	5,914	11,339	16,578	2,460	2,843	59,815	485	238
21,228	4,983	6,946	1,171	1,232	1,479	2,888	6,179	7,996	1,140	1,741	32,040	328	150
11,468	2,449	3,518	674	741	871	1,513	3,683	3,979	596	1,280	17,544	218	111
6,457	1,371	1,855	422	443	524	827	2,359	2,198	342	832	9,580	155	65
3,863	718	1,011	278	334	364	529	1,598	1,211	222	561	5,454	139	45
2,372	434	612	217	200	284	389	1,227	754	151	520	3,048	103	40
4,324	823	1,191	562	573	741	949	3,225	1,475	435	1,429	4,496	245	73
1,770	405	669	291	329	352	629	2,066	797	268	946	1,237	78	25
496	106	183	82	71	96	189	658	257	74	307	368	9	2
179	32	57	46	24	45	78	273	111	38	124	163	1	0
200	38	57	29	14	31	80	338	120	39	107	187	0	1
12	1	7	2	1	1	7	37	14	1	11	17	0	0
0	0	0	0	2	0	0	5	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
11,257,752	8,069,067	8,792,169	4,378,656	4,531,214	4,808,693	6,607,743	7,014,380	9,006,846	4,233,583	3,872,026	12,688,027	1,348,602	1,402,528

GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878	GM12878
RNAPII	RNAPII	RNAPII	RNAPII	RNAPII	RNAPII	RNAPII	RNAPII	RNAPII	RNAPII	RNAPII	RNAPII	RNAPII
SHG0234	SHG0235	SHG0238	SHG0239	SHG8034	SHG8096	SHG8097	SHG8100	SHG8101	SHG8112	SHG8116	SHG8130	SHG8131
hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38
0.21233489	0.09380037	0.03209397	0.03319454	0.04271081	0.01937799	0.01926378	0.02247902	0.02052824	0.02017425	0.01793076	0.08709192	0.02821182
77,820,387	87,702,678	78,539,454	94,222,395	79,192,522	68,385,904	64,871,999	65,226,738	67,282,542	67,273,144	63,420,334	73,720,406	50,726,668
50,406,922	73,653,661	56,537,054	82,232,378	68,262,493	50,175,704	47,443,932	52,747,901	53,873,955	43,251,628	48,269,836	43,468,577	42,842,355
44,300,995	69,032,368	50,387,088	76,485,957	66,347,013	47,711,991	45,001,883	50,980,222	52,140,432	40,793,699	46,152,768	41,309,867	41,623,219
26,780,319	51,781,798	33,117,989	56,874,367	49,364,758	33,548,953	31,233,688	38,038,027	38,882,339	27,541,504	33,217,001	28,287,609	33,408,065
25,194,475	50,269,960	30,999,765	54,237,090	47,724,151	31,974,403	29,745,078	36,582,179	37,397,417	26,029,743	31,846,649	27,064,622	32,719,472
25,004,909	49,825,903	30,813,074	53,910,606	46,973,678	31,703,645	29,462,112	36,108,371	36,929,116	25,851,751	31,564,400	26,888,040	32,442,144
25,004,909	49,825,903	30,813,074	53,910,606	46,973,678	31,703,645	29,462,112	36,108,371	36,929,116	25,851,751	31,564,400	26,888,040	32,442,144
1,703,798	1,775,014	1,848,488	1,939,444	2,452,263	2,062,823	2,034,704	2,081,179	2,097,364	2,041,353	2,149,215	1,859,947	1,891,863
1,680,412	1,756,762	1,813,751	1,918,177	2,437,392	2,047,941	2,018,528	2,067,835	2,083,171	2,024,895	2,135,846	1,851,848	1,885,027
1,580,754	1,686,054	1,675,995	1,835,682	2,314,739	1,926,369	1,895,109	1,955,121	1,967,698	1,869,092	2,024,244	1,745,892	1,830,041
1,580,754	1,686,054	1,675,995	1,835,682	2,314,739	1,926,369	1,895,109	1,955,121	1,967,698	1,869,092	2,024,244	1,745,892	1,830,041
166,446	194,016	493,995	302,266	567,018	440,587	449,117	423,954	422,838	582,133	458,197	273,006	214,615
1,414,308	1,492,038	1,182,000	1,533,416	1,747,721	1,485,782	1,445,992	1,531,167	1,544,860	1,286,959	1,566,047	1,472,886	1,615,426
5,445	1,287	19,317	4,442	12,300	14,140	14,834	7,348	8,202	34,006	13,431	22,271	7,246
1,408,863	1,490,751	1,162,683	1,528,974	1,735,421	1,471,642	1,431,158	1,523,819	1,536,658	1,252,953	1,552,616	1,450,615	1,608,180
1,778,231	6,464,631	598,124	2,915,214	3,137,355	1,460,923	1,330,372	2,027,957	1,905,002	803,526	2,027,444	1,492,933	3,730,334
6,740,246	9,988,324	3,982,750	8,286,229	9,100,378	5,979,925	5,699,881	7,482,459	7,384,740	3,937,064	6,719,699	5,333,231	8,037,165
8,690,368	16,648,258	5,094,186	11,508,151	12,817,051	7,895,575	7,494,204	9,941,718	9,720,782	5,356,729	9,218,771	7,121,441	11,989,360
6,906,692	10,182,340	4,476,745	8,588,495	9,667,396	6,420,512	6,148,998	7,906,413	7,807,578	4,519,197	7,177,896	5,606,237	8,251,780
1,406,525	4,064,813	518,712	2,162,174	2,345,004	1,142,105	1,047,046	1,608,528	1,528,077	620,802	1,486,381	1,052,892	2,380,711
288,125	1,503,526	75,534	547,781	585,238	241,416	215,447	329,991	301,054	136,630	372,625	271,127	788,108
63,807	548,586	15,081	145,910	151,866	61,145	54,127	70,879	62,083	43,183	110,550	93,479	296,334
16,507	207,350	4,317	41,665	42,965	18,566	16,747	17,023	14,649	17,369	38,885	40,615	125,817
4,968	81,518	1,707	13,256	13,617	6,525	6,243	4,835	4,148	8,087	15,977	20,555	60,073
1,872	33,076	789	4,677	5,189	2,591	2,636	1,751	1,436	4,249	7,230	11,660	31,777
788	13,925	423	1,935	2,292	1,171	1,221	781	657	2,432	3,633	7,306	18,283
442	6,291	278	884	1,179	643	657	414	374	1,523	1,970	4,664	11,104
226	2,975	185	476	668	312	371	282	223	990	1,191	3,192	7,195
123	1,575	106	251	434	194	231	162	132	606	741	2,287	4,770
93	839	91	180	277	123	139	134	76	460	478	1,641	3,374
56	473	57	109	196	73	82	98	73	311	301	1,206	2,361
32	275	33	77	151	48	69	52	39	192	204	957	1,676
81	511	84	178	299	91	118	204	100	504	448	2,301	3,989
27	137	42	84	208	47	59	115	60	165	207	1,093	1,631
2	33	2	15	45	8	10	36	12	23	35	178	259
2	5	0	2	17	5	2	14	9	4	12	38	77
0	10	0	2	10	0	1	6	2	2	7	13	39
0	0	0	0	0	0	0	0	0	0	0	0	2
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1,783,676	6,465,918	617,441	2,919,656	3,149,655	1,475,063	1,345,206	2,035,305	1,913,204	837,532	2,040,875	1,515,204	3,737,580

Library_ID	LHG0052H	LHG0051H	LHG0104V	LHG0051H_0104V	LHG0035N_0035V	LHH0118V	LHH0127V
Library_type	hiseq	hiseq	novaseq	pooled	pooled	novaseq	novaseq
Reference_genome	hg38	hg38	hg38	hg38	hg38	hg38	hg38
Cell_type	GM12878	GM12878	GM12878	GM12878	GM12878	HCT116	HCT116
Factor	**CTCF**	**SMC1A**	**RAD21**	**Cohesin**	**RNAPII**	**CTCF**	**CTCF**
Total_read_pairs	358,752,218	356152208	459,140,632	815,292,840	879,867,506	293,527,935	306,988,032
Read_pairs_with_linker	328,927,665	327803209	322,463,454	650,266,663	805,998,749	209,379,373	278,017,188
Fraction_read_pairs_with_lin	0.92	0.92	0.7	0.8	0.92	0.71	0.91
One_tag	91,116,895	92611052	121,729,821	214,340,873	305,223,593	67,711,510	90,202,553
PET	228,074,463	225677969	184,468,375	410,146,344	468,121,770	137,694,970	178,342,047
Uniquely_mapped_PET	179,600,076	179509164	147,434,776	326,943,940	359,389,378	101,683,183	139,475,184
Non-redundant_PET	106,110,023	112913401	67,917,076	180,798,216	58,636,573	14,691,093	58,699,205
Redundancy	0.41	0.37	0.54	0.45	0.84	0.86	0.58
Non-redundant_tag	362,869,381	362795441	379860551	736,311,882	269,106,487	86007544	214963074
Peak	28,992	19659	39,082	29,119	50,232	72,052	355,784
Self-ligation_PET	36,374,046	40192551	40,718,911	80,880,097	30,016,547	7,646,260	44,574,688
Inter-ligation_PET	69,735,977	72720850	27,198,165	99,918,119	28,620,026	7,044,833	14,124,517
Intra-chr_PET	53,879,279	57355817	24,463,289	81,818,234	22,888,857	5,371,336	12,558,160
Inter-chr_PET	15,856,698	15365033	2,734,876	18,099,885	5,731,169	1,673,497	1,566,357
ratio_of_intra/inter_PET	3.4	3.73	8.94	4.52	3.99	3.21	8.02
Singleton	54,239,711	57277746	20,413,204	72,885,936	19,742,331	5,489,032	11,124,088
Intra-chr_singleton	39,945,853	43361447	17,896,022	56,461,791	15,187,368	4,060,994	9,635,525
Inter-chr_singleton	14,293,858	13916299	2,517,182	16,424,145	4,554,963	1,428,038	1,488,563
PET_cluster	5,231,012	5487852	2,055,333	7,913,116	2,840,108	590,202	920,945
ratio_of_intra/inter_cluster	6.25	7.02	19.32	9.02	5.15	4.62	24.8
Intra-chr_PET_cluster	4,509,611	4803284	1,954,185	7,123,625	2,378,076	485,091	885,250
pets_number_2	3,328,184	3639546	1,401,063	5,104,152	1,581,827	358,928	608,866
pets_number_3	653,815	669744	282,716	1,057,262	395,541	68,675	133,453
pets_number_4	215,205	209719	101,668	367,194	159,917	24,637	51,355
pets_number_5	95,704	90839	47,834	171,135	81,272	11,965	26,092
pets_number_6	51,669	48183	26,767	96,803	47,435	6,490	15,256
pets_number_7	32,366	29546	17,124	60,673	30,227	3,797	10,002
pets_number_8	21,928	20090	11,760	41,862	19,361	2,524	6,993
pets_number_9	15,747	14331	8,686	30,342	12,970	1,655	5,190
pets_number_10	12,021	10657	6,672	23,162	8,993	1,275	3,921
pets_number>10	82,972	70629	49,895	171,040	40,533	5,145	24,122
Inter-chr_PET_cluster	721,401	684568	101,148	789,491	462,032	105,111	35,695
pets_number_2	631,456	618023	89,814	710,643	338,328	86,076	31,230
pets_number_3	70,736	56398	8,625	65,653	68,613	11,466	3,275
pets_number_4	13,491	8181	1,956	10,365	25,405	3,897	788
pets_number_5	3,492	1498	528	2,083	12,313	1,662	254
pets_number_6	1,165	316	153	502	6,815	852	97
pets_number_7	447	92	39	140	4,210	464	19
pets_number_8	221	30	11	52	2,549	272	14
pets_number_9	169	7	6	12	1,541	146	5
pets_number_10	81	8	3	8	970	115	2
pets_number>10	143	15	13	33	1,288	161	11

intra_pets_number>2	1,181,427	1,163,738	553,122	2,019,473	796,249	126,163	276,384

LHH0118V_0	LHH0098V	LHH0128V	LHH0098V_0	LHH0139	LHH0139V	LHH0140	LHH0140V	LHH0139_01	LHH0146V	LHH0147V
pooled	novaseq	novaseq	pooled	qcseq	hiseq	qcseq	hiseq	pooled	novaseq	novaseq
hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38
HCT116-wt	HCT116	HCT116	HCT116-wt	HCT116-RAD2	HCT116-wt	HCT116-RAD2	HCT116-wt	HCT116-wt	HCT116-mAC	HCT116-mAC
CTCF	**RNAPII**	**RNAPII**	**RNAPII**	**RAD21**	**RAD21**	**RAD21**	**RAD21**	**RAD21**	**none-likehic**	**none-likehic**
600,515,967	517207217	316,087,217	833,294,434	48,523,665	90,562,053	42,973,485	110,921,989	292,981,192	360,397,636	372,697,334
487,396,561	451545618	272,698,811	724,244,429	40,331,721	75,028,257	36,548,964	93,886,130	245,795,072	332,763,506	328,476,305
0.81	0.87	0.86	0.87	0.83	0.83	0.85	0.85	0.84	0.92	0.88
157,914,063	173652631	78,399,895	252,052,526	11,591,968	21,789,368	10,344,168	26,846,543	70,572,047	102,735,699	88,151,514
316,037,017	270237912	184,446,325	454,684,237	27,411,989	51,330,793	25,034,264	64,739,897	168,516,943	221,734,530	231,282,572
241,158,367	177441741	148,915,219	326,356,960	23,001,256	43,118,396	20,973,285	54,221,758	141,314,695	175,237,861	185,042,954
73,213,214	38443824	44,042,591	82,471,851	6,705,673	8,345,186	7,585,990	10,991,359	21,572,799	106,924,059	110,480,076
0.7	0.78	0.7	0.75	0.71	0.81	0.64	0.8	0.85	0.39	0.4
297905125	189630121	164602051	351858151	25860590	33247217	27716144	42054236	85527138	355115179	359906998
117,603	598505	390,734	117,768	51,228	59,697	49,305	64,637	87,011	177,907	141,079
52,092,777	20140372	34,897,451	55,023,272	5,327,600	6,615,282	6,056,074	8,734,119	17,099,822	70,678,761	68,671,890
21,120,437	18303452	9,145,140	27,448,579	1,378,073	1,729,904	1,529,916	2,257,240	4,472,977	36,245,298	41,808,186
17,889,612	14357432	7,733,172	22,090,597	1,248,156	1,565,122	1,415,930	2,080,900	4,080,367	29,812,795	32,436,743
3,230,825	3946020	1,411,968	5,357,982	129,917	164,782	113,986	176,340	392,610	6,432,503	9,371,443
5.54	3.64	5.48	4.12	9.61	9.5	12.42	11.8	10.39	4.63	3.46
15,771,334	15085865	7,766,436	22,053,300	1,167,944	1,351,801	1,345,956	1,792,701	3,282,048	31,965,122	37,613,583
12,864,812	11630363	6,454,446	17,286,529	1,048,582	1,210,361	1,239,282	1,640,644	2,953,267	25,735,750	28,607,251
2,906,522	3455502	1,311,990	4,766,771	119,362	141,440	106,674	152,057	328,781	6,229,372	9,006,332
1,617,543	1335842	506,966	2,024,843	78,635	141,066	70,779	176,097	413,910	1,699,287	1,721,093
10.46	5.11	10.42	6.69	15.86	13.1	20.55	15.97	14.65	16.46	8.82
1,476,339	1117059	462,584	1,761,433	73,972	131,060	67,495	165,719	387,454	1,601,936	1,545,821
999,042	889107	349,334	1,331,315	55,739	97,185	52,311	124,057	274,784	1,250,091	1,236,323
227,025	142431	63,563	245,926	10,140	18,636	8,945	23,394	58,207	215,147	194,839
89,437	43807	21,989	83,219	3,661	6,672	2,967	8,172	22,254	67,625	58,155
45,656	18485	9,938	37,137	1,618	3,122	1,251	3,920	10,995	28,242	23,620
27,210	8805	5,225	19,304	840	1,773	628	2,098	6,301	14,348	11,554
17,424	4724	3,016	11,074	525	1,061	389	1,280	3,848	8,127	6,518
12,246	2752	1,965	6,987	308	625	250	767	2,475	4,835	3,888
9,012	1668	1,382	4,793	234	417	145	479	1,778	3,279	2,621
6,896	1097	969	3,424	158	302	111	328	1,236	2,275	1,826
42,391	4183	5,203	18,254	749	1,267	498	1,224	5,576	7,967	6,477
141,204	218783	44,382	263,410	4,663	10,006	3,284	10,378	26,456	97,351	175,272
117,616	185576	37,140	222,896	3,842	8,046	2,765	8,334	20,637	90,766	163,464
14,795	22164	4,910	27,108	550	1,211	375	1,295	3,407	5,511	9,940
4,696	6386	1,464	7,866	180	402	96	396	1,179	810	1,438
1,923	2557	493	3,050	60	198	31	171	579	167	294
949	1107	207	1,321	22	85	9	93	314	51	74
492	525	96	621	6	36	5	36	148	15	26
288	238	29	272	2	15	1	29	79	5	10
152	112	18	130	0	3	0	12	51	6	4
120	61	13	73	0	4	1	6	26	4	3
173	57	12	73	1	6	1	6	36	16	19

477,297	227,952	113,250	430,118	18,233	33,875	15,184	41,662	112,670	351,845	309,498

LHH0157	LHH0172	LHH0157_01	LHH0158	LHH0173	LHH0158_01	LHH0170	LHH0159	LHH0159V	LHH0170_0159	LHH0171
novaseq	novaseq	pooled	novaseq	novaseq	pooled	novaseq	novaseq	novaseq	pooled	novaseq
hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38	hg38
HCT116-RAD2	HCT116-RAD2	HCT116-RAD2	HCT116-RAD2	HCT116-RAD2	HCT116-RAD2	HCT116-RAD2	HCT116-RAD2	HCT116-RAD2	HCT116-RAD21	HCT116-RAD2
CTCF	**CTCF**	**CTCF**	**CTCF**	**CTCF**	**CTCF**	**RNAPII**	**RNAPII**	**RNAPII**	**RNAPII**	**RNAPII**
366,508,457	569,205,831	935,714,288	401,699,562	460,564,094	862,263,656	557,061,917	343,180,214	483,901,014	1,384,143,145	565,251,115
339,696,732	527,351,506	867,048,238	371,666,476	425,780,166	797,446,642	517,998,624	320,331,706	453,410,923	1,291,741,253	523,472,548
0.93	0.93	0.93	0.93	0.92	0.92	0.93	0.93	0.94	0.93	0.93
107,052,736	175,480,282	282,533,018	115,962,944	142,223,489	258,186,433	197,218,539	107,125,259	152,138,436	456,482,234	193,704,777
212,107,094	342,780,972	554,888,066	232,472,432	275,740,089	508,212,521	316,451,293	192,719,614	269,464,891	778,635,798	323,895,885
171,149,739	272,626,140	443,775,879	187,436,945	220,538,751	407,975,696	247,521,404	152,353,109	213,103,487	612,978,000	255,007,981
43,952,826	78,684,532	122,544,001	46,417,943	51,541,251	97,870,444	34,436,532	36,654,383	39,516,824	80,322,705	51,158,533
0.74	0.71	0.72	0.75	0.77	0.76	0.86	0.76	0.81	0.87	0.8
162587502	292882828	449256959	172911962	203452802	371635392	161925339	146107485	161556435	350483376	220694073
110,176	127,600	131,371	106,552	122,255	127,824	109,499	108,411	112,496	129,576	122,089
26,184,726	41,874,843	67,966,716	30,300,253	29,878,151	60,089,841	21,048,717	23,672,339	25,521,178	50,582,246	33,260,249
17,768,100	36,809,689	54,577,285	16,117,690	21,663,100	37,780,603	13,387,815	12,982,044	13,995,646	29,740,459	17,898,284
14,623,852	26,969,581	41,593,019	11,722,636	14,413,758	26,136,274	9,377,270	10,254,888	11,040,356	22,232,867	11,803,079
3,144,248	9,840,108	12,984,266	4,395,054	7,249,342	11,644,329	4,010,545	2,727,156	2,955,290	7,507,592	6,095,205
4.65	2.74	3.2	2.67	1.99	2.24	2.34	3.76	3.74	2.96	1.94
13,028,489	29,912,273	40,805,430	12,732,023	18,289,936	30,050,380	10,487,081	10,006,862	10,745,264	21,057,467	15,085,696
10,266,628	20,861,230	28,997,270	8,876,478	11,802,614	19,712,597	7,101,928	7,670,360	8,213,675	14,921,577	9,694,807
2,761,861	9,051,043	11,808,160	3,855,545	6,487,322	10,337,783	3,385,153	2,336,502	2,531,589	6,135,890	5,390,889
1,526,800	2,348,011	4,063,337	1,214,251	1,328,864	2,659,834	1,054,709	1,079,685	1,130,837	2,845,881	1,104,285
7.93	5.74	6.8	4.08	2.97	3.62	3.17	5.3	5.37	4.14	2.67
1,355,830	1,999,617	3,542,226	975,006	993,955	2,083,725	801,892	908,331	953,336	2,291,727	803,627
939,893	1,419,871	2,393,958	701,185	748,694	1,485,805	571,362	674,246	678,869	1,574,241	607,243
205,317	296,536	548,079	140,485	137,258	303,202	117,299	129,304	144,179	355,364	110,076
79,815	110,861	216,026	52,970	48,897	114,356	46,394	45,721	55,700	141,451	39,463
39,519	53,730	108,662	25,907	22,476	55,774	23,271	21,328	26,657	71,848	18,680
22,387	30,405	63,309	14,353	11,974	31,008	13,472	11,246	14,680	41,900	9,815
14,351	19,054	40,717	9,012	6,860	19,295	8,361	6,538	8,746	26,420	5,441
9,649	12,916	27,975	6,055	4,258	13,071	5,556	3,993	5,237	17,439	3,289
6,754	9,102	20,376	4,220	2,874	9,262	3,703	2,672	3,510	11,951	2,036
5,274	6,780	15,349	3,169	1,938	6,997	2,614	1,848	2,409	8,495	1,444
32,871	40,362	107,775	17,650	8,726	44,955	9,860	11,435	13,349	42,618	6,140
170,970	348,394	521,111	239,245	334,909	576,109	252,817	171,354	177,501	554,154	300,658
144,115	292,172	437,460	199,792	277,398	478,560	194,951	141,177	138,782	424,615	241,669
18,596	36,346	55,287	26,454	37,378	64,177	31,704	19,950	23,105	71,833	35,975
5,104	11,409	16,646	7,952	11,918	20,014	11,978	5,994	8,442	26,757	12,341
1,924	4,504	6,485	2,990	4,626	7,656	5,856	2,421	3,636	13,133	5,427
745	2,057	2,817	1,244	2,036	3,309	3,214	1,023	1,748	7,130	2,687
278	1,012	1,296	461	891	1,368	1,963	443	902	4,180	1,305
116	448	571	217	377	600	1,202	200	454	2,511	629
53	217	273	89	161	251	727	72	218	1,593	321
23	115	139	28	65	94	481	45	113	977	151
16	114	137	18	59	80	741	29	101	1,425	153

415,937	579,746	1,148,268	273,821	245,261	597,920	230,530	234,085	274,467	717,486	196,384

LHH0160	LHH0160V	LHH0171_0160_	LHES0007H	LHK0009H_0	LHH0123_01	LHM0011_0011H_0014_0014H
novaseq	novaseq	pooled	hiseq	pooled	pooled	pooled
hg38	hg38	hg38	hg38	hg38	hg38	hg38
HCT116-RAD	HCT116-RAD	HCT116-RAD21-	H1	K562	HepG2	MCF7
RNAPII	**RNAPII**	**RNAPII**	**RNAPII**	**RNAPII**	**RNAPII**	**RNAPII**
363,275,787	533,711,372	1,462,238,274	302061532	914,524,429	743,739,702	716,354,301
342,116,735	503,748,354	1,369,337,637	269758389	739,766,316	622,275,298	643,504,683
0.94	0.94	0.94	0.89	0.81	0.84	0.9
125,284,102	184,849,728	503,838,607	57451567	201,703,349	200,525,038	178,125,576
194,175,452	282,276,316	800,347,653	210129518	519,892,314	374,836,539	444,009,576
150,912,198	219,341,332	625,261,511	171470262	391,929,409	295,625,450	348,697,395
38,995,470	42,335,354	99,886,632	74426727	156,295,365	65,026,411	154,826,157
0.74	0.81	0.84	0.57	0.6	0.78	0.56
162250996	181560853	429169409	234348256	582615618	276774478	529025826
104,830	107,036	128,211	28333	21,757	48,741	20,673
28,505,332	30,964,279	68,778,048	42233786	84,392,579	48,372,785	87,161,316
10,490,138	11,371,075	31,108,584	32192941	71,902,786	16,653,626	67,664,841
7,335,665	7,938,284	20,986,880	26596494	44,670,542	13,101,973	51,270,878
3,154,473	3,432,791	10,121,704	5596447	27,232,244	3,551,653	16,393,963
2.33	2.31	2.07	4.75	1.64	3.69	3.13
8,330,886	8,944,532	23,954,192	25130789	53,688,182	10,525,832	41,130,149
5,600,175	5,992,254	15,370,358	20114319	31,207,039	7,425,655	29,048,919
2,730,711	2,952,278	8,583,834	5016470	22,481,143	3,100,177	12,081,230
788,470	848,627	2,468,116	2542710	6,657,361	1,363,984	8,765,510
3.22	3.21	2.87	8.39	2.15	6.48	3.77
601,727	646,960	1,830,733	2271974	4,546,668	1,181,743	6,928,170
447,022	460,321	1,296,916	1740365	3,259,054	715,177	4,747,398
83,730	95,704	272,754	316246	749,303	190,897	1,251,428
29,782	37,706	105,231	98702	248,839	85,424	434,829
13,881	18,228	52,271	41074	106,124	47,751	184,866
7,387	9,904	29,352	20724	53,767	29,959	92,042
4,446	5,976	18,010	11989	31,609	20,048	52,045
2,868	3,820	11,678	7962	19,486	14,150	32,134
1,971	2,580	7,834	5618	13,416	10,507	21,810
1,473	1,848	5,566	4046	9,735	8,000	15,658
9,167	10,873	31,121	25248	55,335	59,830	95,960
186,743	201,667	637,383	36947	2,110,693	182,241	1,837,340
154,715	157,999	498,278	270736	1,725,833	139,794	1,429,651
21,426	26,041	80,906	240706	292,527	22,645	291,013
6,288	9,494	28,921	23648	65,042	9,261	76,835
2,514	4,259	13,457	4828	17,418	4,635	24,538
1,059	2,044	7,092	1200	5,539	2,540	8,711
416	969	3,906	260	2,111	1,414	3,375
181	422	2,094	71	940	826	1,443
70	215	1,190	15	459	479	598
32	110	678	5	216	282	319
42	114	861	1	608	365	857
154,705	186,639	533,817	531,609	1,287,614	466,566	2,180,772