

Table S3. Chromosome Replication Gene Elements on the Microarray

Agilent Probe	Gene Symbol	8CellA*	8 CellB*	Entrez Gene ID	Fibro-blasts*	iPS Cells*	hES01*	H9ES*	Geno mic Coord. in.	Gen- bank	TIGRI D	Ens- embl	UniGe ne
A_23_P37481	ATM	22.7	40.9	472	35.6	25.5	62.6	76.8	chr11:10NM_000	THC248	ENST00	Hs.36743	
A_23_P35916	ATM	534.0	758.1	472	591.8	317.8	57.2	56.8	chr11:10NM_000	THC248	ENST00	Hs.36743	
A_23_P13605	ATR	632.0	1663.1	545	1344.5	803.6	1134.2	1734.0	chr3:143NM_001	THC246	ENST00	Hs.27179	
A_23_P57379	CDC45L	16800.0	30050.3	8318	1492.5	5679.9	7069.8	6093.8	chr22:17NM_003	THC249	ENST00	Hs.47421	
A_23_P49972	CDC6	11900.0	5570.9	990	280.6	3164.9	6037.2	7307.9	chr17:35NM_001	THC2730974		Hs.40595	
A_23_P14880	CDC7	3240.0	11244.5	8317	312.6	2490.6	4035.3	3891.9	chr1:917NM_003	THC246	ENST0000037041		
A_23_P10465	CDC45	3665.3	6600.0	113130	1151.5	5837.3	10789.0	9934.7	chr11:64NM_080	THC246	ENST00	Hs.43488	
A_23_P37704	CDT1	15100.0	16244.2	81620	1716.4	11237.6	14306.3	17115.5	chr16:87NM_030	THC246	ENST00	Hs.12290	
A_24_P17637	CDT1	7670.0	6426.4	81620	395.1	2519.5	2619.3	3115.6	chr16:87NM_030	THC246	ENST00	Hs.12290	
A_24_P53519	CHAF1A	13300.0	16939.0	10036	1161.5	7100.4	13891.3	12107.3	chr19:43NM_005	THC2472537		Hs.79018	
A_23_P57306	CHAF1B	5360.0	6336.8	8208	784.7	2312.6	3859.7	4178.3	chr21:36NM_005	THC251	ENST00	Hs.75238	
A_24_P34770	CTCF	3510.0	3468.0	10664	543.6	1081.9	2383.9	2065.3	chr16:66NM_006	NP1472	ENST0000026401		
A_24_P35625	CTCF	381.0	339.8	10664	51.7	115.3	183.1	148.5	chr16:66NM_006	NP1472	ENST0000026401		
A_24_P38743	CTCF	556.0	1613.6	140690	2.5	6.2	7.6	19.7	chr20:55NM_080	THC247	ENST0000024391		
A_23_P25461	DBF4	1430.0	541.5	10926	244.7	1209.0	2353.1	2105.2	chr7:873NM_006	THC252	ENST00	Hs.48538	
A_24_P94335	DBF4	101.0	165.2	10926	21.8	33.5	45.3	35.4	chr7:873NM_006	THC246	ENST00	Hs.48538	
A_24_P36610	DNA2	701.0	359.4	1763	49.7	514.3	416.8	441.3	chr10:69NM_001	THC267	ENST00	Hs.53244	
A_23_P10385	DTL	3110.0	6902.3	51514	259.6	1726.0	3688.0	2832.8	chr1:210NM_016	THC246	ENST00	Hs.65647	
A_23_P32707	ESPL1	6873.7	4950.0	9700	476.2	2562.3	3371.8	3082.8	chr12:51NM_012	THC249	ENST00	Hs.15347	
A_32_P11900	ESPL1	367.0	313.0	9700	4.2	11.8	31.9	32.6	chr12:51NM_012	THC249	ENST00	Hs.15347	
A_24_P84898	FEN1	537.0	1380.3	2237	655.2	2045.0	3979.4	4471.7	chr11:61NM_004	THC246	ENST00	Hs.40906	
A_24_P73158	FEN1	577.0	1005.2	2237	516.5	1762.5	3067.2	3274.1	chr11:61NM_004	THC262	ENST00	Hs.40906	
A_23_P21085	GIN5	1240.0	488.9	9837	22.0	194.2	254.5	247.9	chr20:25NM_021	THC247	ENST00	Hs.65846	
A_23_P11824	GIN5	19700.0	44246.6	51659	962.9	5092.0	7692.9	7555.0	chr16:84NM_016	THC246	ENST00	Hs.43318	
A_23_P15213	GIN5	28800.0	13693.3	64785	793.3	1851.8	5057.2	4059.7	chr16:56NM_022	THC247	ENST00	Hs.47125	
A_24_P159323	GIN5	6500.0	1213.2	64785	28.7	79.4	249.0	203.3	chr16:56NM_022	THC247	ENST00	Hs.47125	
A_23_P13678	GIN5	5970.0	5842.8	84296	387.6	2093.4	215.4	228.0	chr8:415NM_032	THC251	ENST00	Hs.65699	
A_23_P13678	GIN5	2890.0	3265.3	84296	73.2	493.4	65.2	103.4	chr8:415NM_032	THC251	ENST00	Hs.65699	
A_23_P19712	GMNN	51400.0	73146.0	51053	2432.3	9467.7	19069.8	17944.0	chr6:245NM_015	THC246	ENST00	Hs.23489	
A_23_P15576	HMGB2	14300.0	12978.6	3148	5089.0	17683.3	20855.5	28723.1	chr4:174NM_002	THC250	ENST00	Hs.43495	
A_23_P17560	KIF3B	126.2	112.0	9371	103.8	51.8	79.1	58.1	chr20:30NM_004	THC249	ENST00	Hs.36967	
A_24_P94182	KIF3B	4334.1	2670.0	9371	2653.1	803.9	2029.2	1560.5	chr20:30NM_004	THC251	ENST00	Hs.36967	
A_24_P13437	KIF3B	934.4	549.0	9371	530.9	181.3	283.8	274.5	chr20:30NM_004	THC249	ENST00	Hs.36967	
A_23_P39116	LIG1	3990.0	5836.9	3978	1945.2	4917.8	9049.8	10107.2	chr19:53NM_000	THC247	ENST00	Hs.1770	
A_32_P8361	MAU2	1030.0	301.6	23383	615.6	345.2	582.3	580.5	chr19:19NM_015	THC256	ENST00	Hs.65493	
A_24_P41208	MCM10	1810.0	1551.2	55388	72.4	741.3	1742.3	1488.7	chr10:13NM_182	THC246	ENST00	Hs.19836	
A_23_P16147	MCM10	2530.0	2592.8	55388	142.1	1282.5	2134.4	1639.6	chr10:13NM_182	THC246	ENST00	Hs.19836	
A_32_P10363	MCM2	25100.0	22922.0	4171	1247.5	7281.9	12878.1	11172.0	chr3:125NM_004	THC252	ENST00	Hs.47748	
A_23_P7873	MCM3	35200.0	29352.1	4172	4883.5	29896.9	55418.9	61181.9	chr6:522NM_002	THC264	ENST00	Hs.17956	
A_23_P12074	MCM3AP	4440.0	4849.7	8888	3064.7	2497.3	4362.1	4622.8	chr21:46NM_003	THC258	ENST00	Hs.38903	
A_23_P37098	MCM4	6910.0	6266.4	4173	642.0	2393.8	2636.9	2019.8	chr8:490NM_005	THC254	ENST00	Hs.46018	
A_23_P13227	MCM5	13500.0	19491.4	4174	1894.6	11445.3	22196.8	15653.4	chr22:34NM_006	NP1157	ENST00	Hs.51758	
A_23_P90612	MCM6	6880.0	8071.1	4175	3671.3	22221.2	32512.0	25275.7	chr2:136NM_005	THC246	ENST00	Hs.44411	
A_23_P93690	MCM7	41700.0	43487.7	4176	8986.5	43438.3	57548.0	52957.8	chr7:995NM_182	NP8403	ENST00	Hs.43872	
A_23_P68547	MCM8	770.0	839.6	84515	352.8	1257.0	1513.7	1568.6	chr20:59NM_182	THC270	ENST00	Hs.63150	
A_24_P30555	MCM8	553.0	820.6	84515	158.3	626.9	838.5	872.3	chr20:59NM_182	THC249	ENST00	Hs.63150	
A_23_P15281	MYST2	7960.0	5670.7	11143	238.8	386.8	1783.4	1682.0	chr17:45NM_007	THC267	ENST00	Hs.21907	
A_23_P53646	NAP1L1	711.0	4997.7	4673	8495.3	19040.1	30576.1	35524.8	chr12:74NM_139	THC246	ENST00	Hs.52459	
A_32_P28365	NASP	28700.0	20957.0	4678	3023.4	23133.5	31292.0	38526.1	chr1:458NM_172	THC252	ENST00	Hs.31933	
A_23_P34800	NASP	8910.0	22424.1	4678	2095.6	17837.7	18067.2	23401.6	chr1:458NM_172	THC252	ENST00	Hs.31933	
A_24_P18038	NIPBL	986.0	640.3	25836	490.3	701.6	807.1	901.4	chr5:370NM_015	THC257	ENST00	Hs.48192	
A_23_P35768	NIPBL	861.0	1650.5	25836	109.9	147.6	456.1	423.8	chr5:370NM_015	THC249	ENST00	Hs.48192	
A_23_P21388	NIPBL	1140.0	2203.3	25836	1001.9	2942.3	1311.6	1399.2	chr5:371NM_133	THC253	ENST00	Hs.48192	
A_23_P20249	NOC3L	2140.0	1910.9	64318	1220.0	2280.4	3755.2	3120.1	chr10:96NM_022	THC246	ENST00	Hs.74899	

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A_23_P45799	ORC1L	2120.0	1893.3	4998	65.8	812.0	1497.4	1154.4	chr1:52f NM_004 THC246 ENST00 Hs.17908
A_23_P39616	ORC2L	2300.0	1474.4	4999	301.4	784.7	1452.0	1462.7	chr2:201 NM_006 THC246 ENST00 Hs.44487
A_23_P42045	ORC3L	1340.0	1066.3	23595	1387.9	2884.6	3871.4	4889.7	chr6:884 NM_181 THC249 ENST00 Hs.41022
A_32_P14161	ORC4L	18.8	37.9	5000	82.0	138.4	211.4	214.0	chr2:14f NM_002 THC246 ENST00 Hs.55836
A_23_P13114	ORC4L	2020.0	2826.2	5000	895.2	1850.5	2517.0	2487.9	chr2:14f NM_002 THC261 ENST00 Hs.55836
A_23_P31414	ORC5L	2840.0	10517.5	5001	1069.1	1523.8	2327.9	1832.9	chr7:10f NM_002 THC246 ENST00 Hs.43294
A_24_P39469	ORC5L	706.0	3025.4	5001	284.8	402.7	469.9	369.6	chr7:10f NM_181 THC248 ENST00 Hs.43294
A_23_P10034	ORC6L	4500.0	12931.8	23594	8675.3	17550.5	23162.2	23742.0	chr16:4f NM_014 THC257 ENST00 Hs.49760
A_23_P10034	ORC6L	3340.0	2760.4	23594	600.3	2511.0	3316.3	3596.6	chr16:4f NM_014 THC246 ENST00 Hs.49760
A_24_P94019	PAPD5	19.5	37.6	64282	304.2	176.1	381.9	394.1	chr16:4f NM_001 THC2492638 Hs.51434
A_23_P11833	PAPD5	2560.0	960.9	64282	268.3	190.2	223.8	507.9	chr16:4f NM_001 THC247 ENST00 Hs.51434
A_23_P28886	PCNA	56200.0	124480.5	5111	5176.2	12201.1	18463.2	18354.0	chr20:5f NM_002 THC256 ENST00 Hs.14743
A_24_P31350	PLK1	21214.0	64600.0	5347	1972.8	8069.1	15108.0	14765.4	chr16:2f NM_005 NP1455 ENST00 Hs.59204
A_23_P11817	PLK1	10466.5	22000.0	5347	1642.1	653.1	1266.3	1102.4	chr16:2f NM_005 THC250 ENST00 Hs.59204
A_23_P30254	PLK2	744.0	1460.0	10769	4352.8	1770.8	6164.6	1450.8	chr5:577 NM_006 THC258 ENST00 Hs.39815
A_23_P51646	PLK3	1060.6	1630.0	1263	3087.8	1655.1	1513.2	941.8	chr1:45f NM_004 THC246 ENST00 Hs.63241
A_23_P15596	PLK4	322.8	213.0	10733	124.4	658.9	849.5	762.9	chr4:12f NM_014 THC246 ENST00 Hs.17205
A_24_P91292	PLK4	43.9	647.0	10733	6.6	49.0	43.1	41.4	chr4:12f NM_014 THC278 ENST00 Hs.17205
A_32_P1701	POLA1	1670.0	5224.9	5422	601.9	1969.1	3324.2	3315.9	chrX:24f NM_016 THC247 ENST00 Hs.56731
A_23_P16161	POLA2	440.0	616.5	23649	420.0	808.2	1811.0	1757.1	chr11:64 NM_002 THC246 ENST00 Hs.20189
A_32_P34552	POLB	423.0	2524.0	5423	96.3	208.8	283.8	393.7	chr8:42f NM_002 THC260 ENST00 Hs.65448
A_23_P50455	POLD1	3400.0	5889.0	5424	1475.3	7615.6	10505.3	9658.8	chr19:5f NM_002 NP1473 ENST00 Hs.27941
A_23_P50456	POLD1	2730.0	4124.0	5424	1180.6	5877.9	6574.4	6313.1	chr19:5f NM_002 NP1473 ENST00 Hs.27941
A_23_P71146	POLD2	382.0	1458.3	5425	791.0	862.5	1116.9	1192.5	chr7:441 NM_006 THC254 ENST00 Hs.30679
A_23_P12736	POLD4	1140.0	626.8	57804	15007.3	1812.8	3216.8	4271.1	chr11:6f NM_021 THC249 ENST00 Hs.52382
A_23_P36021	POLD4	169.0	5084.2	57804	4022.5	656.8	1244.6	1583.7	chr11:6f NM_021 THC259 ENST00 Hs.52382
A_23_P15935	POLE	200.0	224.2	5426	39.0	124.9	180.9	126.2	chr12:1f NM_006 THC246 ENST00 Hs.52487
A_32_P83416	POLE	20.9	2573.4	5426	31.8	82.6	149.8	127.3	chr12:1f AF1285f THC2641609 Hs.65768
A_24_P91838	POLE	190.0	2016.5	5426	14.3	7.6	18.5	14.0	chr12:1f AF1285f THC2774882 Hs.52487
A_23_P16309	POLE2	91.7	449.2	5427	152.8	1416.6	934.5	1192.8	chr14:4f NM_002 THC268 ENST00 Hs.16277
A_23_P13532	POLE3	48800.0	27104.9	54107	2688.0	2883.5	5205.7	4402.7	chr9:11f NM_017 THC251 ENST00 Hs.10811
A_23_P15423	POLE4	3130.0	3524.9	56655	11502.0	2090.6	2811.1	1653.5	chr2:75f NM_019 THC246 ENST00 Hs.46906
A_23_P38338	POLE4	2330.0	3071.4	56655	7709.3	1778.8	2077.5	1393.4	chr2:75f NM_019 NP1166 ENST00 Hs.46906
A_23_P3355	POLG	3960.0	2606.9	5428	1851.6	1296.6	1590.9	2059.1	chr15:87 NM_002 THC246 ENST00 Hs.65585
A_23_P26905	POLG2	2030.0	5164.3	11232	701.4	1796.0	1971.8	2962.5	chr17:5f NM_007 THC267 ENST00 Hs.43700
A_32_P69492	POLH	734.0	383.3	5429	353.5	57.0	95.6	60.7	chr6:43f AK0256f THC2492534 Hs.65546
A_23_P42271	POLH	26.5	44.5	5429	14.1	3.2	2.8	3.3	chr6:43f NM_006 THC246 ENST00 Hs.65546
A_23_P30689	POLI	420.0	440.7	11201	625.8	501.8	1462.8	2565.0	chr18:5f NM_007 THC260 ENST00 Hs.43853
A_23_P38645	POLK	51.5	47.6	51426	836.1	245.2	161.9	237.2	chr5:74f NM_016 THC246 ENST00 Hs.13575
A_24_P91986	POLK	26.5	45.9	51426	2.5	3.4	3.3	4.9	chr5:74f BC0149f THC2541636 Hs.13575
A_24_P30316	POLK	240.0	919.5	51426	222.6	60.8	46.6	77.5	chr5:74f NM_016 NP6497f ENST00 Hs.13575
A_23_P97889	POLL	880.0	2069.0	27343	406.4	440.5	726.6	704.8	chr10:1f NM_013 THC249 ENST00 Hs.52323
A_23_P39737	POLM	1160.0	2505.3	27434	1396.7	640.9	5722.5	7960.3	chr7:44f NM_013 NP6518f ENST00 Hs.59698
A_32_P41479	POLN	21.7	45.3	353497	4.4	3.5	3.3	8.0	chr4:21f NM_181 NP0792 ENST00 Hs.36845
A_23_P33399	POLQ	517.0	533.5	10721	70.5	839.6	1659.7	1040.5	chr3:122 AF0909f THC2485968
A_23_P21882	POLQ	1090.0	1507.4	10721	196.0	760.4	1011.2	1226.3	chr3:122 NM_199 NP3399f ENST00 Hs.24151
A_23_P18824	POLS	16400.0	31321.7	11044	1220.1	892.5	1047.8	1471.3	chr5:68f NM_006 THC246 ENST00 Hs.48154
A_23_P25019	PRIM1	298.0	492.3	5557	322.3	2984.1	3564.9	3633.5	chr12:5f NM_000 NP1207f ENST00 Hs.53433
A_23_P44139	PRIM2A	4140.0	4922.6	5558	963.4	1596.9	4463.7	3872.4	chr6:57f NM_000 THC2462617 Hs.65458
A_24_P28223	PRIM2A	253.0	878.7	5558	127.1	136.6	179.0	149.3	chr6:57f NM_000 THC260 ENST00 Hs.65458
A_23_P12833	PTMS	291000.0	83326.5	5763	5116.9	1659.1	8936.4	20535.0	chr12:67 NM_002 THC250 ENST00 Hs.50461
A_23_P7636	PTTG1	594610.3	564000.0	9232	15479.5	31030.4	41398.3	49470.2	chr5:15f NM_004 THC246 ENST00 Hs.35096
A_23_P10934	PTTG1IP	21191.4	21600.0	754	23739.2	7242.5	8773.3	8526.4	chr21:4f NM_004 NP4823 ENST00 Hs.47401
A_24_P39126	PTTG1IP	11788.1	7140.0	754	1471.9	405.9	684.7	671.6	chr21:4f NM_004 NP4823 ENST00 Hs.47401
A_23_P18579	PTTG2	267263.5	302000.0	10744	3151.4	5635.2	6024.5	6083.0	chr4:37f NM_006 THC260 ENST00 Hs.66880
A_23_P60016	PTTG3	29941.2	19300.0	26255	285.6	663.9	674.1	808.6	chr8:67f NR_002734 ENST00 Hs.64715
A_23_P20463	RAD21	16506.5	10400.0	5885	6386.3	10719.6	16061.2	16950.8	chr8:117 NM_006 THC246 ENST00 Hs.81848
A_23_P32669	RBBP4	16100.0	16477.4	5928	2107.1	5178.1	14881.5	12368.8	chr1:32f NM_005 THC248 ENST00 Hs.64765

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A_24_P91209	RBBP4	1160.0	2253.9	5928	54.6	94.7	225.7	191.9	chr1:329NM_005 NP0937 ENST00 Hs.64765
A_23_P11422	RBBP7	45200.0	88691.2	5931	14526.9	19694.1	14861.5	20247.0	chrX:167NM_002 THC249 ENST00 Hs.49575
A_23_P15025	RBM14	40200.0	25556.4	10432	2451.6	4587.1	10365.4	7512.6	chr11:66NM_006 THC246 ENST00 Hs.64883
A_23_P36496	RBMS1	805.0	38.7	5937	4118.9	1884.2	2555.7	1842.3	chr2:16C NM_016 THC246 ENST00 Hs.47041
A_32_P31577	RBMS1	22.0	58.3	5937	95.0	45.9	93.1	138.9	chr2:16C NM_002 THC259 ENST00 Hs.47041
A_23_P71558	RECQL4	2870.0	2447.7	9401	740.4	2429.5	3272.0	3598.1	chr8:145NM_004 THC260 ENST00 Hs.31442
A_24_P25632	REV1	959.0	681.2	51455	176.3	186.4	418.4	323.5	chr2:994NM_016 THC262 ENST00 Hs.44307
A_24_P29142	REV1	1440.0	3741.1	51455	220.5	241.3	324.7	356.8	chr2:993NM_016 THC246 ENST00 Hs.44307
A_24_P13680	RFC1	3480.0	1596.6	5981	989.9	2524.0	3720.8	3720.8	chr4:389NM_002 THC257 ENST00 Hs.50747
A_23_P18465	RFC1	1960.0	3378.1	5981	1150.1	1593.2	2589.1	2589.1	chr4:389NM_002 THC268 ENST00 Hs.50747
A_23_P15846	RFC1	23.5	44.0	5981	17.7	6.3	11.8	11.4	X75917 NP0941 ENST00 Hs.50747
A_23_P93823	RFC2	2420.0	762.3	5982	444.0	1482.7	1963.4	1953.0	chr7:732NM_181 THC253 ENST00 Hs.64706
A_23_P14193	RFC3	1410.0	4573.9	5983	168.5	926.2	1194.5	898.0	chr13:33NM_002 THC246 ENST00 Hs.11547
A_32_P19701	RFC3	4520.0	944.7	5983	17.7	130.6	131.8	240.2	chr13:33NM_181 THC2631246 Hs.11547
A_23_P18196	RFC4	6410.0	5200.3	5984	1602.5	8262.9	9538.3	11228.0	chr3:187NM_002 THC249 ENST00 Hs.51847
A_23_P95302	RFC5	1350.0	6969.3	5985	858.2	2464.0	2926.4	2962.5	chr12:11NM_181 THC246 ENST00 Hs.50698
A_23_P16482	RNASEH2A	2800.0	6865.0	10535	2758.1	5405.2	5663.9	6805.9	chr19:12NM_006 THC246 ENST00 Hs.53285
A_23_P25645	RPA3	22000.0	11640.7	6119	4932.8	9706.0	12794.2	15256.6	chr7:764NM_002 THC248 ENST00 Hs.48754
A_23_P25421	RPA4	222.0	52.5	29935	71.5	96.8	181.5	232.2	chrX:96(NM_013 THC248 ENST00 Hs.65934
A_23_P14429	SCC-112	37.6	540.0	23244	2351.0	2579.6	4854.8	4507.3	chr4:39502433-3 THC246 ENST00 Hs.33143
A_24_P18621	SCC-112	748.9	1010.0	23244	225.1	140.2	307.3	406.9	chr4:39576429-3 THC2474056 Hs.33143
A_24_P52004	SCC-112	9977.1	817.0	23244	830.9	911.0	1196.2	1217.1	chr4:395NM_033 THC246 ENST00 Hs.33143
A_23_P29723	SGOL1	76.6	318.0	151648	21.8	119.6	278.6	177.2	chr3:201NM_001 NP1472 ENST00 Hs.10515
A_24_P22597	SGOL1	868.4	2350.0	151648	80.3	417.6	891.3	915.7	chr3:201NM_001 NP1472 ENST00 Hs.10515
A_23_P41133	SGOL2	5782.9	5200.0	151246	385.1	1133.0	1270.4	1384.3	chr2:201NM_152 THC246 ENST00 Hs.65518
A_24_P94260	SMC1A	35.1	20.5	8243	420.0	301.2	787.6	1546.9	chrX:534NM_006 THC260 ENST00 Hs.21160
A_23_P21741	SMC1A	1934.5	2380.0	8243	1233.3	1391.4	2103.3	2464.5	chrX:534NM_006 THC246 ENST00 Hs.21160
A_23_P29330	SMC1B	39.2	21.0	27127	2.5	3.3	17.8	12.9	chr22:44NM_148 THC248 ENST00 Hs.33417
A_23_P60271	SMC2	1168.7	937.0	10592	316.3	635.5	800.7	756.1	chr9:105NM_006 THC277 ENST00 Hs.11902
A_23_P13863	SMC3	7604.4	11100.0	9126	2889.8	8123.2	7686.9	6922.5	chr10:11NM_005 THC246 ENST00 Hs.24485
A_23_P32764	SMC4	43.4	20.0	10051	2.7	35.5	71.3	68.8	chr3:161AK00221 THC2575207 Hs.58992
A_23_P91900	SMC4	4202.2	4070.0	10051	1399.6	2667.8	3645.2	4083.5	chr3:161NM_005 THC247 ENST00 Hs.58992
A_23_P34961	SMC5	172.8	22.1	23137	1070.1	917.4	1480.5	1772.1	chr9:721AB01111 THC256 ENST00 Hs.53418
A_32_P12660	SMC5	42.4	23.0	23137	80.3	62.5	95.4	92.9	chr9:721AB01111 THC254 ENST00 Hs.53418
A_23_P14652	SMC5	237.3	2910.0	23137	240.3	413.5	236.7	269.6	chr9:721NM_015 THC247 ENST00 Hs.53418
A_23_P20996	SMC6	1031.7	1200.0	79677	690.4	1834.1	2193.5	2812.2	chr2:177NM_024 THC261 ENST00 Hs.52672
A_23_P38879	SMCR5	73824.0	36400.0	140771	502.4	14702.4	27702.5	25979.5	chr17:17AF4674 THC2489161 Hs.35264
A_23_P50137	SMCR7	34.9	34.3	125170	741.5	423.3	612.5	701.4	chr17:18NM_139 THC246 ENST00 Hs.65555
A_23_P10954	SMCR7L	475.2	1100.0	54471	969.1	772.2	1263.0	1437.5	chr22:38NM_019 THC246 ENST00 Hs.14867
A_24_P33348	SMCR7L	1312.7	1340.0	54471	1136.5	1125.9	1749.0	1689.1	chr22:38NM_019 THC246 ENST00 Hs.14867
A_23_P10313	SMCR7L	3812.1	4220.0	54471	2714.1	2396.0	4207.2	4397.9	chr22:38NM_019 THC246 ENST00 Hs.14867
A_23_P30012	SMCR8	937.2	324.0	140775	70.5	41.0	162.8	218.4	chr17:18NM_144 THC247 ENST00 Hs.66633
A_23_P31536	SSBP1	2310.0	2639.2	6742	3835.9	5627.6	8357.1	11069.3	chr7:141NM_003 THC251 ENST00 Hs.49039
A_24_P91313	SSBP1	22.6	42.5	6742	2.8	14.1	31.7	19.5	chr7:141BC008402 Hs.49039
A_23_P36076	SSRP1	9120.0	8806.8	6749	15857.4	27573.1	39123.3	40748.5	chr11:56NM_003 THC253 ENST00 Hs.52368
A_23_P35736	STAG1	963.8	552.0	10274	249.0	200.2	339.9	216.7	chr3:137NM_005 THC248 ENST00 Hs.41258
A_24_P66125	STAG2	37.6	248.0	10735	1591.3	2386.1	4899.4	4562.0	chrX:12(NM_006 THC278 ENST00 Hs.49671
A_23_P33856	STAG2	280.7	1810.0	10735	967.0	2067.3	2452.6	2131.7	chrX:12(NM_006 THC269 ENST00 Hs.49671
A_23_P14565	STAG3	110926.9	50200.0	10734	138.4	1080.9	1077.4	717.1	chr7:996NM_012 THC247 ENST00 Hs.59228
A_32_P45894	STAG3L1	8572.0	5370.0	54441	2356.6	3907.4	7634.5	6061.3	chr7:74834197-7 THC247 ENST00 Hs.63231
A_23_P93818	STAG3L1	3479.1	1160.0	54441	336.7	479.3	153.1	279.4	chr7:74857450-7 THC2479732 Hs.63231
A_24_P37496	STAG3L1	18581.8	11500.0	54441	115.9	132.7	314.0	262.3	chr7:74834647-7 THC247 ENST00 Hs.63231
A_32_P17074	STAG3L3	24701.3	54500.0	442578	493.7	908.9	690.0	522.0	chr7:74829201-7 THC251 ENST00 Hs.54907
A_24_P19243	TERF1	24.3	38.1	7013	300.5	7320.2	13585.4	17547.5	chr8:741NM_017 THC2476661 Hs.44270
A_32_P22069	TERF1	25.6	44.8	7013	377.5	8546.6	14233.0	17778.0	chr8:741NM_017 THC2466177 Hs.44270
A_23_P21614	TERF1	3210.0	1157.5	7013	967.1	23070.1	32005.9	35230.4	chr8:741NM_017 THC247 ENST00 Hs.44270
A_24_P50458	TERF1	5120.0	2376.1	7013	1017.1	18204.1	39549.7	46803.6	chr8:741NM_017 THC252 ENST00 Hs.44270
A_23_P41720	TERF2	1440.0	1124.9	7014	196.1	46.8	119.9	178.9	chr16:67NM_005 THC267 ENST00 Hs.63335

Table S3. Chromosome Replication Gene Elements on the Microarray

A_23_P53276	TIMELESS	2300.0	2425.1	8914	2115.4	8048.2	13880.9	15808.7	NM_003920
A_24_P23100	TIMELESS	29.7	330.0	8914	17.1	60.2	65.5	86.3	NM_003920
A_23_P99930	TIPIN	6889.1	8740.0	54962	1060.3	3315.3	4979.8	4512.0	NM_017858
A_23_P30550	TOP1	6770.0	3053.8	7150	1480.7	2296.3	2815.8	2441.2	chr20:39 NM_003 NP1175 ENST00 Hs.59213
A_23_P11883	TOP2A	2190.0	2450.2	7153	1424.6	3327.9	4347.5	4711.0	chr17:35 NM_001 THC246 ENST00 Hs.15634
A_23_P15939	TOPBP1	660.0	51.6	11073	174.0	320.7	525.1	555.4	NM_007 THC246 ENST0000026081
A_24_P37142	TREX1	373.0	582.9	11277	107.3	215.0	595.1	476.9	chr3:484 NM_032 NP1208 ENST00 Hs.65556
A_23_P50177	TREX1	313.0	464.0	11277	87.1	179.8	324.5	344.0	chr3:484 NM_032 THC248 ENST00 Hs.65556
A_23_P21887	TREX1	95.0	396.1	11277	624.8	81.2	142.7	118.6	chr3:484 NM_016 THC276 ENST00 Hs.65556
A_23_P13720	UBE1	15200.0	11935.7	7317	2135.5	4629.9	2629.9	3240.6	chrX:46 NM_003 THC253 ENST00 Hs.53327
A_24_P23737	UBE1	10800.0	7018.1	7317	839.0	1050.5	966.4	1291.7	chrX:46 NM_003 THC253 ENST00 Hs.53327
A_32_P17490	WAPAL	3088.5	1240.0	23063	2335.0	3872.6	6266.0	6330.8	chr10:8 NM_015 THC246 ENST00 Hs.20309
A_23_P34218	WAPAL	3920.8	2150.0	23063	352.3	520.1	1050.8	1010.3	chr10:8 NM_015 THC249 ENST00 Hs.20309
A_32_P14860	WDHD1	37.0	20.1	11169	10.7	106.1	261.0	376.1	chr14:54 AY5175: THC2605693 Hs.38599
A_23_P25873	WDHD1	1006.8	3590.0	11169	656.3	3351.7	3325.9	3676.1	chr14:54 NM_007 THC246 ENST00 Hs.38599
A_23_P12094	XRCC6	10700.0	6175.2	2547	5248.1	9922.2	18435.6	19714.5	chr22:4C NM_001 THC258 ENST00 Hs.29249
A_23_P12094	XRCC6	62000.0	58976.4	2547	45856.4	72367.3	118464.2	117077.6	chr22:4C NM_001 THC249 ENST00 Hs.29249
A_23_P53363	XRCC6BP1	901.0	194.9	91419	982.8	1038.0	882.1	1062.2	chr12:5 NM_033 THC260 ENST00 Hs.61188
A_24_P92740	XRCC6BP1	203.0	445.9	91419	9.8	10.6	32.8	25.6	chr12:5 BC0338 THC2484094 Hs.61188

*Values are normalized fluorescence units (FUs); fibroblasts and iPS from(13); hES cells from (12).