Supporting Information

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Methods

Bioinformatic Analyses. For the analysis of conservation patterns in replication origins and in promoters, we retrieved 2991 transcripts corresponding to the set of 443 annotated known genes from the University of California, Santa Cruz (UCSC) ENCODE Website. The position of transcription start sites (TSS) was defined as the 5' end of those transcripts, and promoter regions were defined as the 1500 bp upstream of the TSS. Overlapping regions were grouped together. The final set includes 1035 promoter regions, with an average length of 1997 bp. Conserved regions (CRs) were retrieved from the UCSC ENCODE Website. These CRs correspond to the consensus of 3 methods and 3 different alignments from 28 different vertebrate species [Margulies EH, et al. (2007) Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Res 17(6):760-774]. We choose the moderate set, which provides CRs covering about 5% of the ENCODE regions [Margulies EH, et al. (2007) Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Res 17(6):760-774]. The conservation of sequences of interest (origins or promoters) was investigated by measuring the frequency of those regions that overlap with CRs. We tested the significance of the overlap by using a bootstrap of 1000 replicates of the same length of the origins or promoters randomly picked in the same ENCODE region

Amplification of SNS. First, we polydT tailed the 3' end of SNS with terminal transferase (New England Biolabs) as described by Liu, et al. Then, for second-strand synthesis and incorporation of the T7 promoter sequence, the tailing reaction product (20 μ l) was mixed with 1 µl 0.15 µM T7-A18B primer, 2.7 µl 10X NEB-2 buffer, and 1 µl 10 mM dNTPs (New England Biolabs). Samples were incubated at 94°C for 2 min, were ramped down at -C°/sec to 25°C, were held while T4 DNA polymerase (New England Biolabs) was added to a final concentration of 0.22 $U/\mu l$, and the volume was made up to 27 μl with H₂O. The sample was incubated at 37°C for 30 min, and the reaction was stopped by the addition of 5 μ l 0.5 M EDTA pH 8.0. Samples were purified with the MinElute Reaction Cleanup Kit (Qiagen), increasing the elution volume to 20 μ l. Finally, the MegaScript Kit (Ambion) was used for in vitro transcription of a concentrated 8- μ l sample as described in Liu, *et al.*, except that the NTP pool was optimized for RNA labeling. Two μ l of a mix consisting of 100 mM ATP, CTP, and GTP, 2 µl 50 mM aminoallyl-UTP (Fermentas) and 1 µl UTP 100 mM were added. The product was purified with the RNeasy Minikit (Qiagen), and RNA was quantified by Nanodrop and analyzed by BioAnalyser with Lab-on-a-chip total RNA nano biosizing assay (Agilent Technologies).



Fig. S1. Typical microarray profiles obtained for 3 ENCODE regions are shown. The normalized ratio profiles, obtained along three 500 kb regions showing (*A*) low density of origins, (*B*) middle density, and (*C*) high density are represented. Each red spot corresponds to 1 microarray oligonucleotide probe. Significant peaks selected for our study are indicated (black stars). Chromosome and coordinates are indicated below the graph.

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Fig. S2. Typical peaks found in Fig. S1 A-C. Numbers above the peaks refer to peak numbers of Fig. S1.

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Fig. S3. Validation of the sensitivity and the specificity of origin segment identification by SNS on chips. (*A*) Validation by quantitative PCR of positive and negative regions. Relative enrichments of 8 background regions, 29 peaks, and *c-myc* origin were analyzed by qPCR on 2 independent nonamplified preparations of SNS. Each quantification was repeated twice. Error bars indicate standard error of the mean. Enrichment found at the *c-myc* origin was defined arbitrarily as 100%. (*B*) Microarray profile obtained for the 5' part of the *HoxA* locus. The normalized ratio profile, obtained along the region spanning Chr7:26885000–26965000 with the ENCODE ChIP-on-chip microarray, is shown on the graph (red line). Five significant peaks were detected (black stars). Above the graph are shown the positions of *HoxA* genes. Chromosome coordinates are indicated on the graph described in *B*. (*C*) Validation of the profile obtained for the *HoxA* locus by quantitative PCR. The graph shows results obtained by qPCR with an independent nonamplified preparation of SNS with 32 primer pairs (black line) covering the chromosomal region shown in *A*. The average of 2 quantifications is shown.

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Chromosome	ENCODE begin	ENCODE end	N-domain border	Closest exp origin	Distance
chr7	89428339	90542763	89871000	89871631	631
chr7	115404471	117281897	115429000	115728548	299548
chr8	118882220	119382220	119195000	119250180	55180
chr11	63940888	64440888	64269000	64251467	17533
chr18	23719231	24219231	24011000	24011725	725
chr21	32668236	34364221	33066000	33143912	77912
chr21	32668236	34364221	33525000	33446859	78141

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Chromosome	ENCODE begin	ENCODE end	N-domain begin	N-domain end	Nb. origins
chr2	234273824	234773888	234060000	235644000	5
chr7	113527083	114527083	113331000	115429000	4
chr7	125672606	126835803	124166000	126880000	7
chr14	52947075	53447075	52702000	54042000	1
chr16	25780427	26280428	24943000	27477000	0

Fig. 54. Intersection between ENCODE regions and N-domains of replication computationally identified [Huvet M, *et al.* (2007) Human gene organization driven by the coordination of replication and transcription. *Genome Res* 17(9):1278–1285]. (A) Experimental validation of 2 computationally predicted origins. Six ENCODE regions contain 7 N-domain borders (i.e., putative replication origins). Positions of ENCODE regions borders, N-domain borders, closest experimental origin, and distance between each putative origin and its closest experimental origin are shown. Two of 7 are located less than 1 kb from our experimentally validated origins. We tested the significance of this overlap by using a bootstrap of 1000 replicates, of the same length of the origins, picked randomly in the same ENCODE regions. The probability that 2 computationally predicted origins fall by chance less than 1 kb from an experimentally characterized origin is only 10⁻⁴. (*B*) ENCODE regions included in N-domains contain 0 to 7 origins. Positions of ENCODE regions borders, N-domain borders, and number of origins found experimentally are shown.

Table S1. Origin segments

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ENCODE region	Chromosome	Beginning	End	Origin class
ENr231	chr1	147984909	147986846	
	chr1	148244302	148246331	
	chr1	148258507	148260234	
	chr1	148296747	148298101	
	chr1	148360133	148361364	
ENr112	chr2	51943931	51945315	Isolated
ENr121	chr2	118505924	118507071	
ENr331	chr2	220107251	220108794	
	chr2	220135657	220137337	
	chr2	220165844	220168917	
	chr2	220174966	220176411	
	chr2	220188829	220191429	
	chr2	220198477	220200657	Highly dense
	chr2	220201886	220203102	
	chr2	220228419	220230263	
	chr2	220242014	220245496	
	chr2	220250475	220251903	Highly dense
	chr2	220261756	220263177	riigiliy actise
	chr2	220336089	2202337258	
	chr2	220338833	220337250	
	chr2	220550055	220540250	
ENr121	chr2	220341427	220343128	Isolatod
ENITST	chr2	234480379	234467946	Isolateu
	chr2	234030307	224657028	Highly donco
	chr2	234000347	234007903	Fighty delise
	chr2	234071440	2340/2///	
EN-221	chiz	234740433	234741001	
ENIZZI	CIII 3	550/5201	550/45/0	Icolated
	CIII 5	55961546	55962651	Isolated
	CIII 3	50085416	50000517	
	chr5	56088066	56089478	
	chr5	56119168	56120680	
	chr5	56147525	56149060	
ENL: 002	chr5	56241199	56242625	
ENM002	cnr5	1315/1851	131573644	
	chr5	131620957	131622317	
	cnrs	131636239	131637448	
	cnr5	131/44261	131745522	
	cnrs	131801134	131802891	
	cnrs	131860038	131861573	
	chr5	132025755	132026955	
	chr5	132048184	132049426	
	chr5	132151529	132152659	
511 242	chr5	132248525	132250628	
ENr212	chr5	141950090	141951462	
	chr5	141999954	142001505	
	chr5	142078249	142081176	
	chr5	142176213	142178174	
	chr5	142199652	142201376	
	chr5	142236258	142237249	
	chr5	142259552	142261293	
	chr5	142361833	142363780	
ENr334	chr6	41518826	41520409	
	chr6	41543060	41544342	
	chr6	41544942	41546022	
	chr6	41578447	41579719	
	chr6	41585098	41586734	
	chr6	41599804	41601172	
	chr6	41622513	41624061	
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Table S1. Continued

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	Chromosomo	Paginning	End	Origin class
	Chromosome	Beginning	Ena	~~~~~~
	chr6	41719178	41720147	
	chr6	41854596	41855697	
	chr6	41856075	41857739	
ENr223	chr6	74011080	74012121	
	chr6	74108528	74110397	
	chr6	74160713	74161992	
EN 222	chr6	/428/525	/4288636	
ENr323	chr6	108385466	108386797	
	CNP6	10854/4/4	108548773	
	chr6	108552017	108555295	Isolated
ENIr222	chr6	132300844	132/01267	Isolated
ENIZZZ ENm010	chr7	26920770	26922694	isolateu
ENINGTO	chr7	26922861	26924734	Highly dense
	chr7	26926630	26928154	ringiny dense
	chr7	26941783	26943229	
	chr7	26943851	26945045	Highly dense
	chr7	26952545	26954275	
	chr7	26967119	26968225	
	chr7	26982812	26983987	
	chr7	27028731	27030030	
	chr7	27032062	27033765	
	chr7	27047481	27048910	
	chr7	27056729	27057891	
ENm013	chr7	89478648	89479835	
	chr7	89519250	89520459	
	chr7	89523106	89525040	
	chr7	89677540	89679141	Isolated
	chr7	89870257	89871631	Isolated
	chr7	90037675	90039130	
	chr/	90089748	90091313	
EN	chr/	90240841	90242057	Isolated
ENMUTZ	cnr/	114116472	1138/5052	Isolated
	chr7	11/318566	11/319629	Isolateu
	chr7	11/351397	11/352/60	
FNm001	chr7	115728548	115730087	
	chr7	115733502	115735495	Highly dense
	chr7	115739541	115741149	
	chr7	115758143	115759653	
	chr7	115760088	115761361	
	chr7	115792540	115794616	
	chr7	115932781	115934827	
	chr7	116029862	116032737	
	chr7	116096721	116098030	
	chr7	116187758	116189117	
	chr7	116301540	116302519	
	chr7	116398408	116400119	
	chr7	116413422	116414684	
	chr7	116425234	116426588	
	chr7	116556983	116558225	Isolated
	cnr/	116/1343/	116/15501	
	cnr/	1167208//	116900444	
	cnr/	117025106	117026260	Icolatad
ENm01/	chr7	11/022190	11/020309	isolated
EINITIU14	chr7	12614202 126142002	120080800	
	chr7	120112092	1267/882/	Isolated
	chr7	12658113/	126582/190	isolateu
	chr7	126501154	126502450	
	CIII7	120020307	120020033	

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Table S1. Continued

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ENCODE region	Chromosome	Beginning	End	Origin class
ENr322	chr14	98486278	98487757	
	chr14	98696258	98697981	
	chr14	98724314	98725645	
	chr14	98767316	98769158	
	chr14	98771506	98772663	Highly dense
	chr14	98782269	08782573	riigiliy delise
	chr14	0000216	00000543	
	chr14	90000510	90009343	
	chr14	90001039	90003202	
EN 222	chr14	98956703	98958083	
ENr233	cnr15	41/35285	41/36157	
	CHT15	41850700	41852158	
	chr15	42013413	42014920	
ENm008	chr16	4/415	48530	
	chr16	128359	129221	
	chr16	144166	145603	
	chr16	154879	156172	
	chr16	176977	177951	
	chr16	265752	267214	
	chr16	271684	272766	
	chr16	343083	344285	
	chr16	353862	355393	
	chr16	371926	373475	
	chr16	391235	392389	
	chr16	458042	459289	
ENr313	chr16	60988052	60989443	Isolated
ENr213	chr18	24011725	24012891	
	chr18	24064501	24065770	
ENm007	chr19	59062973	59064186	
	chr19	59065358	59067169	
	chr19	59077897	59080362	
	chr19	59093470	59095647	
	chr19	59104275	59106633	
	chr19	59138068	59139337	
	chr19	59155330	59157173	
	chr19	59174913	59178718	
	chr19	59186590	59187790	
	chr19	59206956	59208156	
	chr19	59225201	59226338	
	chr19	59340003	59341368	
	chr19	59357776	59359107	
	chr19	59385445	59387234	
	chr19	59588883	59590167	
	chr19	59633614	59634656	
FNr333	chr20	33449379	33451062	
LINISSS	chr20	33520581	33521619	
	chr20	33593121	3359/722	
	chr20	33604647	33606279	
	chr20	33652073	3365/116	
	chr20	33667226	33668962	
	chr20	33763526	33764778	
ENIMOOF	chr21	22726476	20720127	
ENTITIOUS	chr21	22/204/0	22/2013/	
	CITZ I	22022022	32027210	
	chr21	32324033 221/2012	3232014U	Icolatad
		222145912	22216010	isolated
		33314649	33310910	
		33321658	33323457	
	chr21	333/1196	333/2523	
	chr21	33445752	33446859	
	chr21	33697620	33699322	
	chr21	33773906	33775426	
	chr21	33847294	33849173	
	chr21	33869514	33870830	
	chr21	33937141	33938736	

continued

Table S1. Continued

ENCODE region	Chromosome	Beginning	End	Origin class
ENr133	chr21	39299170	39300343	
	chr21	39377239	39378501	
	chr21	39607655	39608789	Isolated
ENm004	chr22	30314293	30315055	
	chr22	30336429	30337386	
	chr22	30349689	30350809	
	chr22	30802515	30804264	
	chr22	30843605	30844819	
	chr22	30896070	30897269	
	chr22	31030409	31031414	Isolated
	chr22	31156785	31158209	
	chr22	31195329	31197371	
	chr22	31366116	31367680	
	chr22	31437500	31439348	
	chr22	31530713	31531675	
	chr22	31545005	31546201	
ENr324	chrX	122559999	122561372	
	chrX	122590866	122592123	
	chrX	122624067	122625387	
	chrX	122660854	122662000	
	chrX	122719627	122720715	
	chrX	122820974	122822324	Isolated
	chrX	122959521	122961890	
ENm006	chrX	152662042	152663313	
	chrX	152689689	152691828	
	chrX	152704242	152705388	
	chrX	152721163	152722370	
	chrX	152757248	152758442	
	chrX	152816486	152818401	
	chrX	152883775	152885328	
	chrX	153070355	153071501	
	chrX	153081356	153082612	
	chrX	153123710	153124807	
	chrX	153130060	153131533	
	chrX	153181711	153184284	
	chrX	153236591	153237728	
	chrX	153249941	153251354	
	chrX	153327230	153328684	
	chrX	153338595	153339968	OriG6PD
	chrX	153818861	153819900	Isolated

Table	S2.	Short	ssDNA	segments	obtained	with	stringent	criteria

Chromosome	Beginning	End	
Chr1	148302434	148303315	
Chr11	4730926	4731822	
Chr11	63994433	63995679	
Chr14	98908400	98909476	
Chr2	234629711	234630595	
Chr21	34015696	34017159	
Chr5	56295243	56296211	
Chr7	113942120	113943850	
Chr8	119342198	119343366	

Table S3.	Short ssDNA	segments	obtained	with	less	stringen	t
criteria							

Table S3. Continued

Chromosome Beginning End Hrig Spage Chrin 147994346 14709511 Chrig Spage Chrin 148095157 Hab06595 Chrig Spage Chrin 14813526 14813524 Chrig Spage Chrin 14813526 14813524 Chrig Spage Chrin 148142044 14813288 Chrig Spage Chrin 148220348 148230128 Chrig Spage Chrin 14823083 148230128 Chrig Spage Chrin 14832044 14833017 14832181 Chrig Spage Chrin 148330817 14832183 Chrig Spage Spage Spage Spage Spage Spage Sp	criteria			Chromosome	Beginning
Chrl 14799446 147995114 Chrl 939276176 Chrl 148089197 14809135 Chrl 939226176 Chrl 148089197 148090135 Chrl 93922641 Chrl 14814004 148140794 Chrl 95903354 Chrl 148142044 14814282 Chrl 95903354 Chrl 148228183 148201282 Chrl 95903354 Chrl 148328782 148303125 Chrl 95961366 Chrl 148328782 14830135 Chrl 9596396 Chrl 148328782 14831035 Chrl 9596396 Chrl 148389782 14831035 Chrl 9596396 Chrl 148389782 148391035 Chrl 9596396 Chrl 148389782 148391035 Chrl 9596396 Chrl 1291849 2192573 Chr2 15960620 Chrl 1291849 2192573 Chr2 1838675 Chrl 23985914	Chromosome	Beginning	End	Chr19	59083008
chri 14800516 148006355 Chrin 5229726 Chri 14813525 14813624 Chrin 59392264 Chri 14813525 14813624 Chrin 59493347 Chri 148142040 148143288 Chrin 59493347 Chri 148142040 148143288 Chrin 59592518 Chri 148230434 14833282 Chrin 59592518 Chri 148230434 148332181 Chrin 59592518 Chri 1483308172 148332181 Chrin 59592518 Chri 1483308172 148332181 Chrin 59592568 Chri 1483308172 148332181 Chrin 59592568 Chri 1295783 S5228527 Chrin 5959268 Chri 1295783 2169257 S560080 Chri 1295783 2169257 S560807 Chri 1295783 S56649 Chri2 2285787 Chri 12958623 2295783 Chri	Chr1	147994346	147995114	Chr19	59207244
chri 140039197 140001135 chri 9 5933294 chri 14813326 14813624 chri 9 5933949 chri 148142044 14814288 chri 9 59503354 chri 144229583 1482382 chri 9 59503354 chri 144229583 14823287 chri 9 59503354 chri 144230741 14830215 chri 9 59613466 chri 14330817 14830215 chri 9 596566 chri 143330817 14830215 chri 9 5965266 chri 143330817 14830125 chri 9 5965266 chri 143330817 134824 chr2 5169297 chri 12167384 218223 chr2 118245142 chri 121738 chr2 118245142 118245142 chri 123965 4732277 chr2 224630670 chri 133331 513439 chr2 224630670 chr11 589598	Chr1	148045616	148046395	Chr19	59276176
Chri 148133236 14813624 Chri 9 55483497 Chri 14814004 14814774 Chri 9 55483497 Chri 14812044 148143288 Chri 9 55572518 Chri 14828583 148291397 Chri 9 55572518 Chri 148302434 14830315 Chri 9 55666309 Chri 148338817 148333181 Chri 9 55666309 Chri 148338817 148333181 Chri 9 55666309 Chri 148338817 148333181 Chri 9 55862668 Chri 1 148338972 14833015 Chri 9 55862668 Chri 1 2083511 2044406 Chri 2 51809073 Chri 1 2167384 2182739 Chri 2 21836678 Chri 1 2198493 2182739 Chri 2 226513360 Chri 1 533331 5144393 Chri 2 23481265 Chri 1 533531 51438 Chri 2 234630670 Chri 1 <td>Chr1</td> <td>148089197</td> <td>148090135</td> <td>Chr19</td> <td>59392364</td>	Chr1	148089197	148090135	Chr19	59392364
chr.1 14814004 14814074 Chr.19 55453354 Chr.1 1482420543 148282862 Chr.19 55553354 Chr.1 1482829533 148231287 Chr.19 55613466 Chr.1 148330817 148333181 Chr.19 5566309 Chr.1 148330817 148330315 Chr.19 559529 Chr.1 143330817 148387022 148301035 Chr.19 559529 Chr.1 143330817 204464 Chr.2 51609073 Chr.1 2.927528 55466448 Chr.2 51609073 Chr.1 2.93531 204864 Chr.2 51925613 Chr.11 2.936523 Chr.2 118445142 Chr.11 118445142 Chr.11 2.936523 Chr.2 2.24630678 Chr.2 2.24630670 Chr.11 5.935938 S5646644 Chr.2 2.244348126 Chr.11 5.995938 Chr.2 2.24630670 Chr.11 5.9395938 S59566677 Chr.2 2.24630670	Chr1	148135326	148136324	Chr19	59439949
chri 14814204 148143288 Chri 9 55372518 chri 148281719 14828262 Chri 9 55372518 chri 1482802434 14830135 Chri 9 5566369 chri 148320344 14830315 Chri 9 5566369 chri 14838077 148332181 Chri 9 59873818 Chri 0 5522632 Chri 9 5987381 5080737 Chri 0 55459529 5546646 Chri 2 5190620 Chri 1 205311 208446 Chri 2 5190620 Chri 1 2191849 218273 Chri 2 118106655 Chri 1 239331 513439 Chri 2 234384126 Chri 1 513339 513439 Chri 2 234384126 Chri 1 539383 556641 Chr 2 234384126 Chri 1 5393938 556641 Chr 2 2346574 Chri 1 5393914 Gh9272 Chr 2 23465745 Chri 1 569907	Chr1	148140049	148140794	Chr19	59483497
Chri 148281719 148282663 Chri9 55613466 Chri 148280583 148201837 Chri9 55613466 Chri1 14830817 14833103 Chri9 5966309 Chri1 148308172 14833103 Chri9 5966630 Chri1 148308172 14833103 Chri9 5966630 Chri1 2095513 2046484 Chri2 51926613 Chri1 2095511 2084466 Chri2 51925613 Chri1 2191849 2192739 Chri2 118245142 Chri1 2198623 2299533 Chri2 2188678 Chri1 5133331 5134393 Chri2 224638670 Chri1 5995938 55566644 Chri2 234630670 Chri1 5686767 S68222 Chri2 234630670 Chri1 6699406 6396757 Chri2 234630670 Chri1 6493158 Ghri30 33406227 Chri21 33265062 Chri1 <td>Chr1</td> <td>148142404</td> <td>148143288</td> <td>Chr19</td> <td>59503354</td>	Chr1	148142404	148143288	Chr19	59503354
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chri 144302434 14830315 chrl9 59565309 chri 14830817 14830315 chrl9 5956568 chri0 5522738 5526827 chrl9 5987347 chri1 203511 2084064 chr2 51906020 chr11 2033511 2084064 chr2 51906020 chr11 2167384 2166284 Chr2 51906020 chr11 2191849 218273 Chr2 11828678 chr11 470926 473227 Chr2 22481306 chr11 553538 5566841 Chr2 234875429 chr11 5687697 568922 Chr2 23466786 chr11 6399014 6399072 Chr2 23466786 chr11 649394206 64920212 Chr2 23466786 chr11 649394206 6492072 Chr2 23466786 chr11 64939420 64022128 Chr2 23466786 chr11 64193138 64190272	Chr1	148289583	148291287	Chr19	59613466
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Chr14 98908400 98909476 Chr21 39734404 Chr15 41546187 41547066 Chr22 30163672 Chr15 41705071 41705723 Chr22 30231331 Chr15 41705071 41705723 Chr22 30231331 Chr15 41711222 41711881 Chr22 30289137 Chr15 41716599 41717383 Chr22 30291389 Chr15 41727851 41728706 Chr22 30360511 Chr15 41835861 41836733 Chr22 30425554 Chr15 41947175 41948454 Chr22 30486758 Chr16 37951 38703 Chr22 30634326 Chr16 153019 153663 Chr22 30634326 Chr16 222700 223746 Chr22 30788719 Chr16 350344 351446 Chr22 31293476 Chr16 403327 404203 Chr22 31357188 Chr16 422121	Chr14	98906288	98907151	Chr21	39664436
Chr15 41546187 41547066 Chr22 30163672 Chr15 41705071 41705723 Chr22 30231331 Chr15 41711222 41711881 Chr22 30289137 Chr15 41716599 41717383 Chr22 30291389 Chr15 41727851 41728706 Chr22 30360511 Chr15 41835861 41836733 Chr22 30425554 Chr15 41947175 41948454 Chr22 30486758 Chr16 37951 38703 Chr22 30509856 Chr16 153019 153663 Chr22 30788719 Chr16 222700 223746 Chr22 30788719 Chr16 339942 240852 Chr22 31047522 Chr16 350344 351446 Chr22 31250037 Chr16 403327 404203 Chr22 31357188 Chr16 420121 422871 Chr22 31357188 Chr16 25980622 25981932 Chr22 31609686 Chr16 26075229 26076	Chr14	98908400	98909476	Chr21	39734404
Chr154170507141705723Chr2230231331Chr154171122241711881Chr2230289137Chr154171659941717383Chr2230291389Chr154172785141728706Chr2230360511Chr154183586141836733Chr2230425554Chr154194717541948454Chr2230486758Chr163795138703Chr2230634326Chr16153019153663Chr2230634326Chr16222700223746Chr2230788719Chr16350344351446Chr2231047522Chr16350344351446Chr2231250037Chr16403327404203Chr2231293476Chr16422121422871Chr223157188Chr162598062225981932Chr2231609686Chr162607522926076594Chr4118641431Chr166111135361112457Chr4119048139Chr18240390172404002Chr555965960Chr18549773159498624Chr555965960	Chr15	41546187	41547066	Chr22	30163672
Chr15 41711222 41711881 Chr22 30289137 Chr15 41716599 41717383 Chr22 30291389 Chr15 41727851 41728706 Chr22 30360511 Chr15 41835861 41836733 Chr22 30425554 Chr15 41947175 41948454 Chr22 30486758 Chr16 37951 38703 Chr22 30509856 Chr16 153019 153663 Chr22 30634326 Chr16 222700 223746 Chr22 30788719 Chr16 239942 240852 Chr22 31047522 Chr16 350344 351446 Chr22 31250037 Chr16 403327 404203 Chr22 31357188 Chr16 422121 422871 Chr22 31357188 Chr16 25980622 25981932 Chr22 31609686 Chr16 26075229 26076594 Chr4 118641431 Chr16 61111353 61112457 Chr4 119048139 Chr18 29497731 24040	Chr15	41705071	41705723	Chr22	30231331
Chr154171659941717383Chr2230291389Chr154172785141728706Chr2230360511Chr154183586141836733Chr2230425554Chr154194717541948454Chr2230486758Chr163795138703Chr2230634326Chr16153019153663Chr2230788719Chr16222700223746Chr2230788719Chr16239942240852Chr2231047522Chr16350344351446Chr2231250037Chr16403327404203Chr2231293476Chr162598062225981932Chr2231609686Chr162607522926076594Chr4118641431Chr166111135361112457Chr4119048139Chr182403901724040002Chr555965960Chr185949773159498624Chr556161424	Chr15	41711222	41711881	Chr22	30289137
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Chr15 41947175 41948454 Chr22 30486758 Chr16 37951 38703 Chr22 30509856 Chr16 153019 153663 Chr22 30634326 Chr16 222700 223746 Chr22 30788719 Chr16 239942 240852 Chr22 31047522 Chr16 350344 351446 Chr22 31047522 Chr16 350344 351446 Chr22 31250037 Chr16 403327 404203 Chr22 31293476 Chr16 422121 422871 Chr22 31357188 Chr16 25980622 25981932 Chr22 31609686 Chr16 26075229 26076594 Chr4 118641431 Chr16 61111353 61112457 Chr4 119048139 Chr18 24039017 24040002 Chr5 55965960 Chr18 59497731 59498624 Chr5 56161424	Chr15	41835861	41836733	Chr22	30425554
Chrif 37951 38703 Chriz 30509856 Chrif 153019 153663 Chriz 30509856 Chrif 153019 153663 Chriz 30634326 Chrif 222700 223746 Chriz 30788719 Chrif 239942 240852 Chriz 31047522 Chrif 350344 351446 Chriz 31250037 Chrif 350344 351446 Chriz 31293476 Chrif 403327 404203 Chriz 31293476 Chrif 422121 422871 Chriz 31357188 Chrif 25980622 25981932 Chriz 31609686 Chrif 26075229 26076594 Chrid 118641431 Chrif 61111353 61112457 Chrid 119048139 Chrif 24039017 24040002 Chris 55965960 Chrif 59497731 59498624 Chris 56161424	Chr15	41947175	41948454	Chr22	30486758
Chr16 153019 153663 Chr22 30634326 Chr16 222700 223746 Chr22 30788719 Chr16 239942 240852 Chr22 31047522 Chr16 350344 351446 Chr22 31250037 Chr16 403327 404203 Chr22 31293476 Chr16 422121 422871 Chr22 31357188 Chr16 25980622 25981932 Chr22 31609686 Chr16 26075229 26076594 Chr4 118641431 Chr16 61111353 61112457 Chr4 119048139 Chr18 24039017 24040002 Chr5 55965960 Chr18 59497731 59498624 Chr5 56161424	Chr16	37951	38703	Chr22	30509856
Chr16 222700 223746 Chr22 30788719 Chr16 239942 240852 Chr22 31047522 Chr16 350344 351446 Chr22 31250037 Chr16 403327 404203 Chr22 31293476 Chr16 422121 422871 Chr22 31357188 Chr16 25980622 25981932 Chr22 31609686 Chr16 26075229 26076594 Chr4 118641431 Chr16 61111353 61112457 Chr4 119048139 Chr18 24039017 24040002 Chr5 55965960 Chr18 59497731 59498624 Chr5 56161424	Chr16	153019	153663	Chr22	30634326
Chrif 239942 240852 Chr22 31047522 Chr16 350344 351446 Chr22 31250037 Chr16 403327 404203 Chr22 31293476 Chr16 403327 404203 Chr22 31357188 Chr16 422121 422871 Chr22 31609686 Chr16 25980622 25981932 Chr22 31609686 Chr16 26075229 26076594 Chr4 118641431 Chr16 61111353 61112457 Chr4 119048139 Chr18 24039017 24040002 Chr5 55965960 Chr18 59497731 59498624 Chr5 56161424	Chr16	222700	223746	Chr22	30788719
Chrif 350344 351446 Chr22 31250037 Chr16 403327 404203 Chr22 31293476 Chr16 422121 422871 Chr22 31357188 Chr16 25980622 25981932 Chr22 31609686 Chr16 26075229 26076594 Chr4 118641431 Chr16 61111353 61112457 Chr4 119048139 Chr18 24039017 24040002 Chr5 55965960 Chr18 59497731 59498624 Chr5 56161424	Chr16	239942	240852	Chr22	31047522
Chrif 403327 404203 Chrif 51250057 Chrif 403327 404203 Chrif 31293476 Chrif 422121 422871 Chrif 31357188 Chrif 25980622 25981932 Chrif 31609686 Chrif 26075229 26076594 Chrif 118641431 Chrif 61111353 61112457 Chrif 119048139 Chrif 24039017 24040002 Chrif 55965960 Chrifs 59497731 59498624 Chrif 56161424	Chr16	350344	351446	Chr22	31250037
Chr16 422121 422871 Chr22 31357188 Chr16 25980622 25981932 Chr22 31609686 Chr16 26075229 26076594 Chr4 118641431 Chr16 61111353 61112457 Chr4 119048139 Chr18 24039017 24040002 Chr5 55965960 Chr18 59497731 59498624 Chr5 56161424	Chr16	403327	404203	Chr22	31293476
Chr16 25980622 25981932 Chr22 31609686 Chr16 26075229 26076594 Chr4 118641431 Chr16 61111353 61112457 Chr4 119048139 Chr18 24039017 24040002 Chr5 55965960 Chr18 59497731 59498624 Chr5 56161424	Chr16	422121	422871	Chr22	31357188
Chr16 26075229 26076594 Chr4 118641431 Chr16 61111353 61112457 Chr4 119048139 Chr18 24039017 24040002 Chr5 55965960 Chr18 59497731 59498624 Chr5 56161424	Chr16	25980622	25981932	Chr22	31609686
Chr16 61111353 61112457 Chr4 119048139 Chr18 24039017 24040002 Chr5 55965960 Chr18 59497731 59498624 Chr5 56161424	Chr16	26075229	26076594	Chr4	118641431
Chr18 24039017 24040002 Chr5 55965960 Chr18 59497731 59498624 Chr5 56161424	Chr16	61111353	61112457	Chr4	119048139
Chr18 59497731 59498624 Chr5 56161424	Chr18	24039017	24040002	Chr5	55965960
	Chr18	59497731	59498624	Chr5	56161424
		55 157 , 51	55 750024		

continued

Table S3. Continued

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Table S3. Continued

Chromosome	Beginning	End	Chromosome	Beginning	End
Chr5	56171809	56172754	Chr7	116002734	116004180
Chr5	56208147	56209379	chr7	116132825	116133894
Chr5	56236890	56237768	chr7	116135955	116137015
Chr5	56295243	56296506	chr7	116245091	116246603
Chr5	5636//99	56365537	chr7	116311106	116240003
ChrE	121214176	121215/52	chr7	116422524	116/3205/
Chir	131314170	121212422	chii7	110422324	110423034
Chirs	131044222	121700020	cnr7	110490219	11049/040
Chr5	131099969	131700628	cnr7	116701391	116/02429
Chr5	131702693	131703924	chr/	116847362	116848419
Chr5	131802295	1318034/4	chr/	116955478	116956689
Chr5	131892636	131893495	chr/	1256/2412	1256/3548
Chr5	131913615	131914617	chr7	125807943	125809366
Chr5	132114174	132115910	chr7	126008548	126009702
Chr5	132254248	132256381	chr7	126265980	126267374
Chr5	141991892	141992845	chr7	126346777	126347886
Chr5	141993970	141995100	chr7	126506435	126507581
Chr5	142040787	142042049	chr7	126717000	126717843
Chr5	142185785	142187051	chr7	126834944	126836060
Chr5	142220482	142221627	chr8	118960993	118962255
Chr5	142221926	142223095	chr8	119342198	119343366
Chr5	142253507	142254382	chr9	128794755	128795677
Chr6	41726681	41727816	chr9	128889564	128890443
Chr6	73822868	73823527	chr9	128905126	128905983
Chr6	73989145	73990245	chr9	129045889	129047000
Chr6	74046066	74046823	chr9	129062567	129063520
Chr6	74062625	74063645	chr9	129147873	129148778
Chr6	74138721	74139633	chr9	129233993	129234857
Chr6	74183965	74184846	chrX	122588818	122589783
Chr6	108387574	108388843	chrX	122667010	122668072
Chr6	108717698	108718445	chrX	122676289	122677051
Chr6	108767902	108768561	chrX	122683688	122684576
Chr6	108793554	108795119	chrX	122695881	122696740
Chr6	108808699	108809553	chrX	122711978	122030710
Chr6	132218230	132219270	chrX	122720689	122712037
Chr6	132249013	132250194	chrX	122761887	122762813
Chr6	132253995	132254881	chrX	122951811	122953043
Chr6	132319891	132321035	chrX	152866215	152867053
Chr6	132499510	132500169	chrX	153121076	152007099
Chr6	132594660	132596133	chrX	153159894	153160838
Chr7	26845300	26846496	chrX	153253186	153254338
Chr7	26898781	26899853	chrX	153267146	153268206
Chr7	26991346	26992642		155267110	155200200
Chr7	27008654	27010066			
Chr7	27112598	27010000			
Chr7	89573220	89574867			
Chr7	89757217	89758860			
Chr7	89812125	89812997			
Chr7	89870878	89872152			
Chr7	89940627	89941532			
Chr7	89984545	89986083			
Chr7	89986664	89987856			
Chr7	90042445	90043667			
Chr7	113551814	113552673			
Chr7	113718301	113719513			
Chr7	113860170	113861500			
Chr7	113866891	113868270			
Chr7	113942120	113944150			
Chr7	114076222	114077176			
Chr7	114378598	114379603			
Chr7	114442905	114444855			
Chr7	115/02631	115/10/020			
Chr7	115819967	115820830			
Chr7	115939797	115941370			
		continued			

Table S4. Primer pairs used for quantitative PCR analysis

Gene name	Forward primer sequence validation origins	Reverse primer sequence	Amplicon position
HOX1	CTCACAGGCCAAAGCAAGAC	GACTCATAGCCTTTCCAGCAGTT	chr7:26885610 + 26885716
HOX2	AGGCAGAGGGTCACCAAAGT	TGGATGGGGCTGTAAAAGAA	chr7:26903050 + 26903167
HOX3	CCTTTGGGGAGGAAGGAAGT	CCTCCCAGGCCTCTTTATTG	chr7:26905203 + 26905336
HOX4	CCTGACCACATGAGAAAGAACA	GGAGGTAACAGCCCAATGAA	chr7:26908895 + 26908996
HOX5	GGATGAACGAAAACAGCACAA	CTGCTCAGAGTGGAACCAGAA	chr7:26909048 + 26909162
HOX6	TGCTTACATGCTGCGTTTTCT	GGGTGTGTCACTGGGTTGTT	chr7:26912201 + 26912325
HOX7	TGTTTAGGCCAGCTCCACAG	CGCCTTTAACCAGCAATGAG	chr7:26913785 + 26913892
HOX8	GATGTTTGCTTCCGGGTTCT	CAAGATGCGCTCAGTCTCAA	chr7:26916918 + 26917054
HOX9	CCTCCTGACGCGATAACAGA	CGGACCAACTAACGCCTAAA	chr7:26919343 + 26919468
HOX10	CGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ATGGGACCCCACACATACAG	chr7:26920935 + 26921042
HOX11	TTGACCAGCGAATGCATAGA	ATCGCCGCATGAAGTACAAA	chr7:26921252 + 26921384
HOX12		AGGCCAAAGGGACCAGTAAA	chr/:26921/65 + 26921894
HUXI3			cnr7:26922986 + 26923111
HOX14		AAGCGACACCCCAAGTTICT	cnr/:26923838 + 26923976
HUXIS		GAGCCAAATGACCCCCATAC	cnr7:20924034 + 20924752
			chr7.2692/452 + 2692/569
	GAAGCTGGCATTTCGAGGTAG		$chr7.26926276 \pm 26926403$
	GETAGETGGGGAACCTTGAC		chr7.26923265 + 26923450
HOX20		GECAGECAGECAGTAAGAATG	$chr7.26932813 \pm 26932933$
HOX21	GGGACTGGCGACAATTICTT	GCCCCAAACAAACCACTACA	chr7.2693/981 + 26935125
HOX22	GCCCGTCCTGTGGTATCTCT	AGTTCGGGCTTGGGTTTTCT	$chr7.26937166 \pm 26937289$
HOX23	AGGATTIGAGGGGCCAGTAG	CTTTGCTAGGGCAACCATAAGA	chr7.26939273 + 26939372
HOX24	GCTCAAGAGCCTTCCTACTCTTT	CTTGGATTCTGACGGCTCAC	chr7:26941141 + 26941266
HOX25	CCCAGAACCCCGAAATAGAA	TTGCGTGAACTTGGTGTCAG	chr7:26942438 + 26942570
HOX26	TTTGAGCCACAGACAGAAATCA	TGCTAGGGAGAGATATTGGTTCA	chr7:26945479 + 26945591
HOX27	TGCAACAGCAATCACCACAG	TTTTCCAAACACTGCCTTCA	chr7:26947488 + 26947632
HOX28	AAGCGGGTGAATTGACTGTG	CAGTTCACTGCCGGGTTAAGT	chr7:26949397 + 26949502
HOX29	CACACGTAGCCTGCAAAAGA	CGTGGGGCCATTAAAGTAAG	chr7:26953036 + 26953155
HOX30	CTCCCCTTCCAACGTCTAA	GAGCTCTCCTTGCCGTTCTC	chr7:26955662 + 26955788
HOX31	AGTCGGAGGGTTCTCCTTGA	GCTTCCATTATCGCCCTCATT	chr7:26957425 + 26957568
HOX32	CAAGAATAGGCACCCCAGAC	CCCCCTTGGAGAGAAACTGA	chr7:26963059 + 26963189
ori c-myc	ACCAAGACCCCTTTAACTCAAGA	CCTCGTCGCAGTAGAAATACG	chr8:128819623 + 128819772
bg c-myc	CAAGAATCGGACGTGAAGG	ATCATTCCAGGAATCCTCTGG	chr8:128824963 + 128825100
ori1	GAGCACCGAAGTCCAGAAAA	ATAAGAAAAGGCGGCTCCTG	chr1:148259102 + 148259251
ori2	TCCCTACATGCTCAGTCCTTG	CTGCCCAAGCAACTTAAAGC	chr2:51944348 + 51944496
ori3	TCTCACAGCTTGTGCAGTCC	GCTGTTTCCCCACAAAACAC	chr2:220542305 + 220542448
ori4	CTCGGTAACGCCTGTCAAAG	CTTAGCAGTGCAGTTCGCATT	chr5:56148279 + 56148418
ori5	GCTTAGAGGCCACCTGAGTG	TGACACAGCTGACCCAGAAA	chr5:131744565 + 131744712
ori6	AGGICIICIGGGGACICAGC	CGGCTTGAGAGAAGGAAACA	chr5:131801531 + 1318016/0
ori/	GGIGIGIGIACICCACCCAGA		chr5:142200469 + 142200613
oria			cnr6:74108946 + 74109095
orijo			cnr/.896/8094 + 896/8238
ori11			(119.120955059 + 120954011)
ori12	GTGTTGTTTTTGAACACTGAGATGA		$chr12.38938112 \pm 38938588$
ori13	CLATGGGGTAGCGTGTGTGT	GCTGGCTAGAAGTGCTTT	chr13.112395841 + 112395992
ori14	GGTAAGAGGCAGAGCTGAGGT		chr14.98696782 + 98696929
ori15	GGCTGCTTGTGTTTAGGGACT	GCTTCCCCGAGTTTTCTAGG	chr16:372517 + 372673
ori16	TCCGCGGTAGGGAATCTAAT	TGCGTCCTTAGTTTGCTGTG	chr18:24012244 + 24012394
ori17	TGTTCTTTCCTTCGCCAATC	GGAAAATGGAGGCCCAGA	chr20:33450169 + 33450310
ori18	GGAATTGGTCACCTGGACTG	CCCATCCCGTATTGCCTAA	chr21:32826113 + 32826266
ori19	AGGCATTGTCTGGCACCTAC	TGACCCTCTCTGCCTGTTTC	chr7:27032892 + 27033022
ori20	GGTAGGTGAGTGAGGGAGCA	CAAGTGATCTGTCCACCTTGG	chrX:122560373 + 122560522
ori21	CCGTCAATTGGCGAGATTT	ATTCCGCCCACTAAACCAGT	chrX:152884205 + 152884345
ori22	CTCCTTTCCTTGGAGACAGTTG	CGGTATCACAGTGTAGCTGGTG	chr16:177353 + 177494
ori23	ACTCTGAGGGGTTTGGGAAC	ATCCCTGAGAGAGCCCAGAT	chr19:59340510 + 59340662
ori24	ATTATCCCCTCTGCCTCTGC	TGGTTGCGAAACTCACCAT	chr22:31531161 + 31531301
ori25	AGACAAGGGGTTCAGCTCTGT	CCTCTATTCCTCACCCTTCCA	chr6:41856863 + 41857016
ori26	TCTGCCAGTGTTGGGATACA	TGGCGCGTCCAAAATACTAC	chr7:26967360 + 26967481
ori27	GTTAGAAGTGGCTGGGGACA	CTGGCACAGGCTTGAATCTC	chrX:153328123 + 153328269
ori28	CCCTACCCTGCTCCAATC	CTGGGAATGGCACCTAGACA	chr9:128930543 + 128930651
ori29	GCTGCGGCCTTGTTTAAGT	GCAAAGCAGTTTCCATCACA	chr1:148245477 + 148245597

Table S4. Continued

Gene name	Forward primer sequence validation origins	Reverse primer sequence	Amplicon position
background1	AGGGCTGAGCCATAATTCTTCT	CTGCAATGCACTCACAACAAC	chr2:51629857 + 51630010
background2	GGCAAGGGAAGGGGTAACT	ATTCCCACTCATTGCTCAGG	chr4:118920576 + 118920719
background3	CACTGTCAAAAGTCTGTGAAGCTATT	AGGCCAAACGTTTTTCTCTTG	chr6:132581326 + 132581470
background4	TAGGCGCAGCTTGTAGGACT	CAGGATTTGGGACAACTTGG	chr11:4898934 + 4899089
background5	CTTGCACAATGCCTCACTCA	GAAAACACCAGCCACCAGAA	chr7:89922194 + 89922313
background6	GATGCTGAGGGGTTTCACAA	TGCAAGCCACTTTCGGTTAG	chr7:116505991 + 116506123
background7	TGACATACAACCCAACCAGAAC	GGAATGAGATGGACAGCAAATC	chr7:26880046 + 26880177
background8	CTTTGAAGGAAATCCCAGTTGTC	CCGGCTTCCCACTGTAGTTATT	chr7:27109288 + 27109393
Highly dense origin	ns		
T1	GGCTTGGAGTTTCAACAGGA	CGCAGGTACGAGTCACAACA	chr7:115734636 + 115734791
T2	GGTGAGATTGGGGGTTTTGT	TGTCCCAGTTGTTCCCAGTC	chr2:234664712 + 234664826
Т3	CAGTGAAATGGGATGCTCTG	CTGTCTTCCCTGTGGGTGAG	chr7:26927452 + 26927569
T4	CCTGCCCTTTGGTAGGTCTC	CAGCTCATCTGGCAACACAG	chr2:220197823 + 220197951
T5	TGGTTGGCTGGCTACACTCT	CGCGTCTACCTCCTGATGAC	chr14:98783632 + 98783755
Т6	AGCACCTCTGTCTGCCTCAA	CCTTCCCCTCTGCGTAGTTC	chr9:128864132 + 128864273
Τ7	CCTGGAATGTAGGCTGTGTGA	CCCACTCTAGCACCCCAACT	chr11:64339669 + 64339802
Т8	CCTTCTCCATCTGTGCTGCT	CTGTGAGCCCTTCAAATTGC	chr13:112428887 + 112429038
Isolated origins			
Т9	TCGTGGCGTCATTCTGTGTA	CTTAAAGACGTGCTCCACTGC	chrX:153819393 + 153819546
T10	AGCGAGATTTGGGTGTTCAG	CAACAGCCCCTGAGCTCTATT	chr7:89871198 + 89871332
T11	AGCGTGCAATGTGAGGAAAC	GGAGAGAAGCGAAGCAATGA	chr7:116557558 + 116557666
T12	GGGAAGGAAATGCAAGACAA	AATTTGGCTGCTTAGCATGG	chr7:126268071 + 126268212
ENCODE regions w	/ithout origins		
T13	CCTCATTGTAGAAGTATGTCCT	GGTGTAATTACTCAGTGGACT	chr11:5280585—5280735
T14	AGAAAAAGGAGCTTCCAGTCG	TGTGGGTGCAATTGAACTGT	chr4:118853686 + 118853826
T15	AGTGGAACAGCCAGGTGTGA	TGATCTTTTCTCGGGGTGTG	chr10:55415286 + 55415418
T16	CTGCCTTGTGCAGTGTGAAG	CGCTGAGCCAGGATTTATGT	chr18:59660223 + 59660371
T17	ACCACCATCTGGGGAAAAAC	GTTGGGAACTTGCCCTCTTC	chr11:116160417 + 116160536
T18	CACGCAGACACTGTCAAAGAA	GGAGAGGGGGAAATACTGGA	chr16:26054593 + 26054749
T19	CTGGACAGGAATCCAGGAAA	CCTTGATTGGTACCCACACC	chr16:25955735 + 25955892