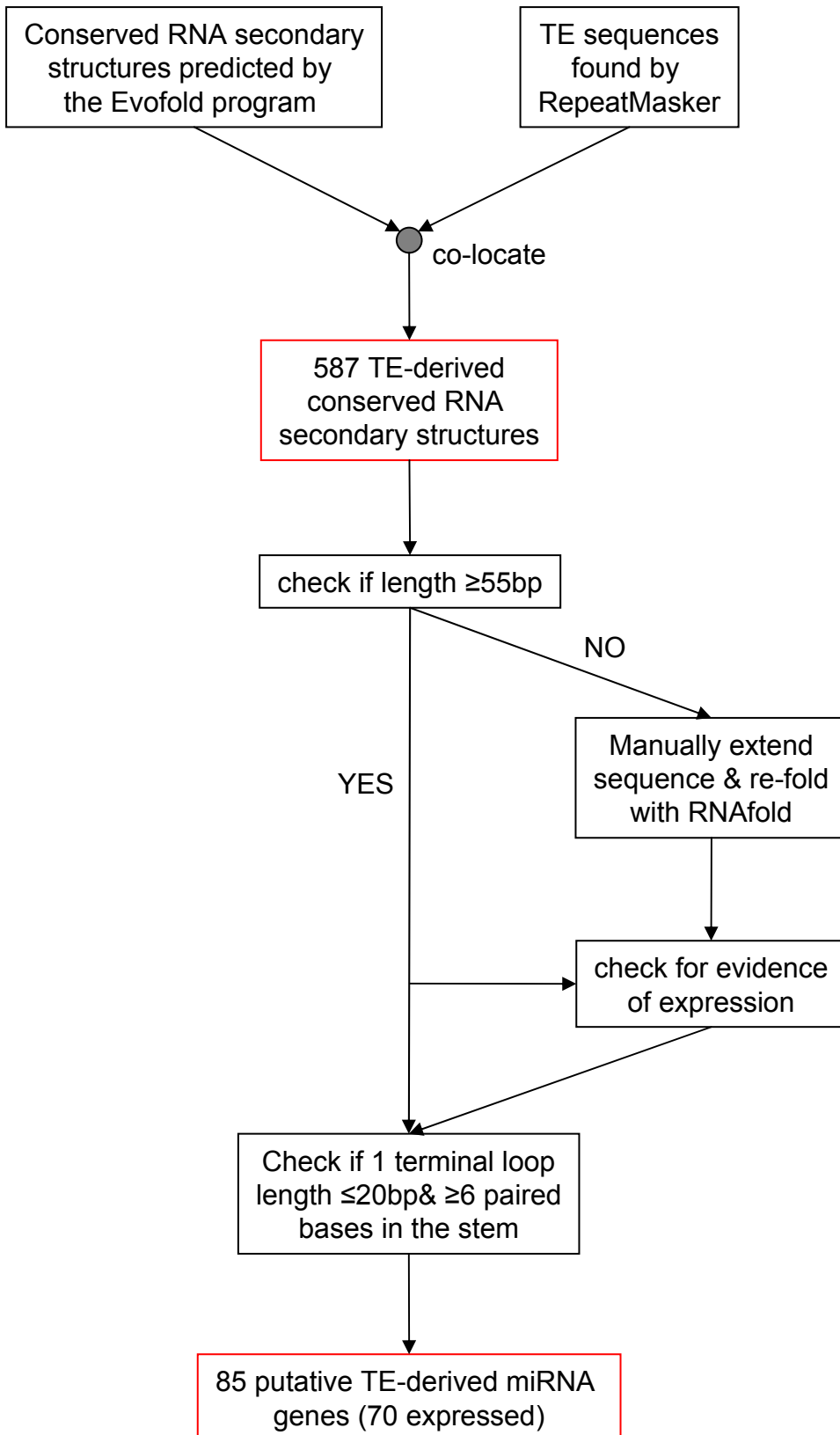


Supplementary FIGURE 1. Protocol for the *ab initio* prediction of human TE-derived miRNA genes.



>>> 9 hsa-mir-95 MI0000097 - 4 8057928 8058008 81 49:70, L2, L2 L2, L2 22/81(27.16) 77/81(95.06) 22/22(100.00)

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YY--XXX-
YY----- L2 (L2, LINE)
-----XXX- L2 (L2, LINE)

>>> 10 hsa-mir-575 MI0003582 - 4 83893514 83893607 94 61:79, MIR MIR 19/94(20.21) 58/94(61.70)
0/19(0.00)

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-----XXX
-----XXX MIR (MIR, SINE)

>>> 11 hsa-mir-576 MI0003583 + 4 110629303 110629400 98 16:38, L1MB7 L1 23/98(23.47) 98/98(100.00)
23/23(100.00)

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YY
YY L1MB7 (L1, LINE)

>>> 12 hsa-mir-578 MI0003585 + 4 166526844 166526939 96 61:81, L2 L2 21/96(21.88) 43/96(44.79)
21/21(100.00)

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-----XXX
-----XXX L2 (L2, LINE)

>>> 13 hsa-mir-579 MI0003586 - 5 32430241 32430338 98 61:83, MADE1, L1MB8 Mariner, L1 23/98(23.47)
98/98(100.00) 23/23(100.00)

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YY
YY-- MADE1 (Mariner, DNA)
-----YYYYY L1MB8 (L1, LINE)

>>> 19 hsa-mir-340 MI0000802 - 5 179374909 179375003 95 58:80, MARNA Mariner 23/95(24.21) 39/95(41.05)
0/23(0.00)

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-----YY-----

MARNA (Mariner, DNA)

>>> 20 hsa-mir-548a-1 MI0003593 + 6 18679994 18680090 97 61:82, MADE1 Mariner 22/97(22.68) 76/97(78.35)
22/22(100.00)

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-----YY-----

MADE1 (Mariner, DNA)

>>> 21 hsa-mir-587 MI0003595 + 6 107338693 107338788 96 16:36, MER115 Tip100 21/96(21.88) 96/96(100.00)
21/21(100.00)

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XX
XX

MER115 (Tip100, DNA)

>>> 22 hsa-mir-548b MI0003596 - 6 119431911 119432007 97 61:82, MADE1 Mariner 22/97(22.68) 81/97(83.51)
22/22(100.00)

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-----XX
-----XX

MADE1 (Mariner, DNA)

>>> 23 hsa-mir-588 MI0003597 + 6 126847470 126847552 83 16:36, L1MA3, L1MA3 L1, L1 21/83(25.30) 83/83(100.00)
21/21(100.00)

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XX
XX-----
XX

L1MA3 (L1, LINE)
L1MA3 (L1, LINE)

>>> 24 hsa-mir-548a-2 MI0003598 + 6 135601991 135602087 97 61:82, LTR16A1, MADE1, LTR16A1 ERVL, Mariner, ERVL
22/97(22.68) 97/97(100.00) 22/22(100.00)

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YY
YYYYYYYYYY-----
-----YY-----
-----YYYYYY

LTR16A1 (ERV, LTR)
MADE1 (Mariner, DNA)
LTR16A1 (ERV, LTR)

>>> 25 hsa-mir-591 MI0003603 - 7 95686910 95687004 95 16:35, MER5A MER1_type 20/95(21.05) 40/95(42.11)
0/20(0.00)

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XX
XX

MER5A (MER1_type, DNA)

>>> 26 hsa-mir-335 MI0000816 + 7 129923188 129923281 94 16:38, MIRb MIR 23/94(24.47) 2/94(2.13)
0/23(0.00)

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YY-----
YY-----

MIRb (MIR, SINE)

>>> 27 hsa-mir-548a-3 MI0003612 - 8 105565773 105565869 97 61:82, MLT1G1, MADE1, MLT1G1 MaLR, Mariner, MaLR
22/97(22.68) 97/97(100.00) 22/22(100.00)

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YYYYXX
YYYYY-----
-----XX
-----YYYYYYYYYYYYYY

MLT1G1 (MaLR, LTR)
MADE1 (Mariner, DNA)
MLT1G1 (MaLR, LTR)

>>> 28 hsa-mir-548d-1 MI0003668 - 8 124429455 124429551 97 61:82, MADE1 Mariner 22/97(22.68) 81/97(83.51)
22/22(100.00)

-----00000000000000000000-----
-----YY-----
-----YY-----

MADE1 (Mariner, DNA)

>>> 39 hsa-mir-606 MI0003619 + 10 76982222 76982317 96 61:81, L1MCc L1 21/96(21.88) 96/96(100.00)
21/21(100.00)

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YY

YY L1MCc (L1, LINE)

>>> 40 hsa-mir-607 MI0003620 - 10 98578416 98578511 96 61:81, MIR, MIR MIR, MIR 21/96(21.88)
96/96(100.00) 21/21(100.00)

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XX

XX- MIR (MIR, SINE)
-----YYY MIR (MIR, SINE)

>>> 41 hsa-mir-608 MI0003621 + 10 102724732 102724831 100 16:40, L2 L2 25/100(25.00) 7/100(7.00)
0/25(0.00)

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-----YYYYYYYY

-----YYYYYYYY L2 (L2, LINE)

>>> 42 hsa-mir-612 MI0003625 + 11 64968505 64968604 100 16:40, MIRb MIR 25/100(25.00) 9/100(9.00)
0/25(0.00)

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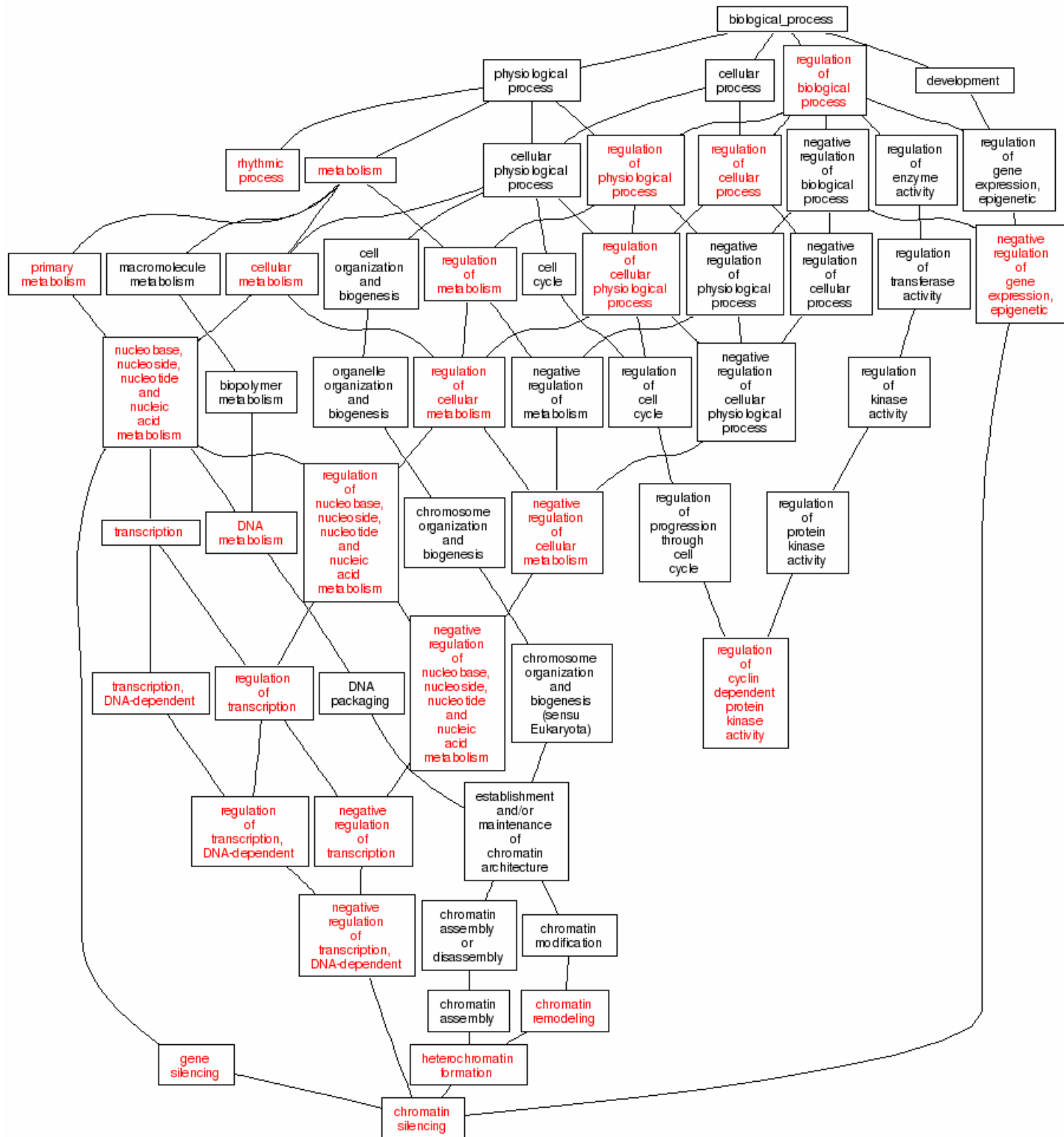
XXXXXXXXXX----- MIRb (MIR, SINE)

>>> 43 hsa-mir-326 MI0000808 - 11 74723784 74723878 95 60:79, Arthur1 Tip100 20/95(21.05) 12/95(12.63)
0/20(0.00)

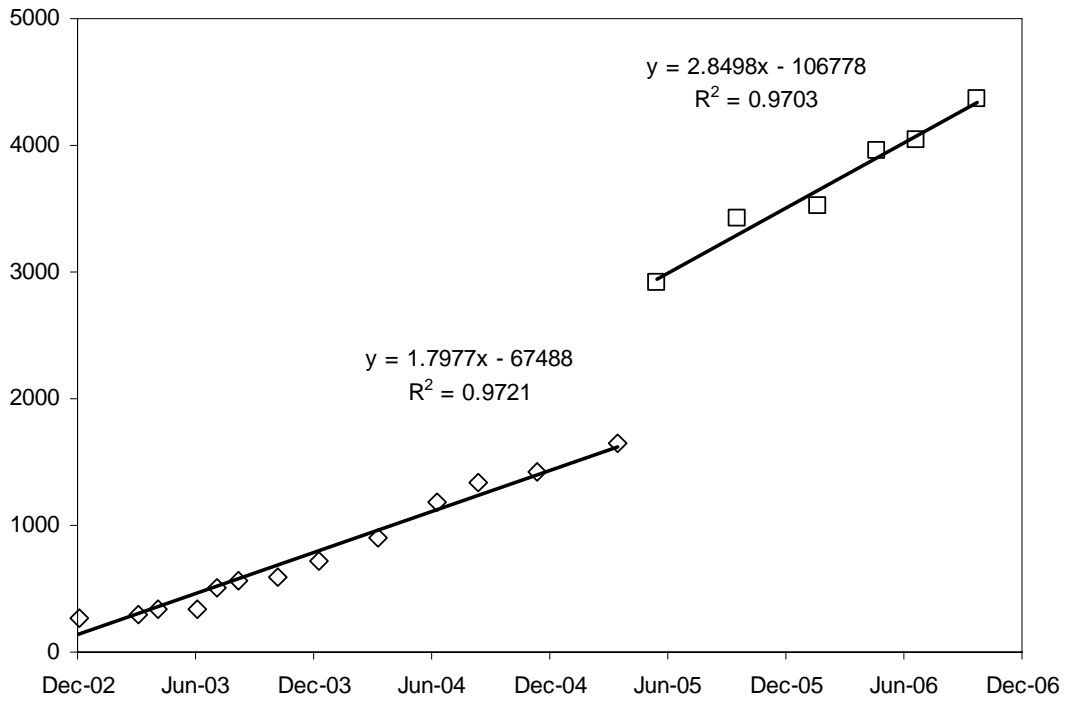
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XXXXXXXXXXXXXXXX----- Arthur1 (Tip100, DNA)

Supplementary FIGURE 3. **Gene Ontology (GO) biological process directed acyclic graph showing over-represented GO terms ($P < 0.01$; red) associated with mRNA targets of *hsa-mir-130b*. Targets were identified based on target site complementarity in 3' UTRs and miRNA-mRNA anti-correlated expression patterns.**



Supplementary FIGURE 4. **Rate of increase in the number of miRNA gene entries reported in miRBase.** The number of miRNA gene entries is plotted against the database release dates.



Supplementary TABLE 1. **mRNAs anticorrelated with hsa-mir-130b and their associated GO terms.**

Name^a	GO^b	P-value^c
A4GNT	GO:0044237 cellular metabolism	0.0037
BACH2	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
BRPF1	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
CAPN10	GO:0044237 cellular metabolism	0.0037
CCNB1	GO:0050789 regulation of biological process	0.0017
CCRN4L	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
COX7A2L	GO:0044237 cellular metabolism	0.0037
EEF1B2	GO:0044237 cellular metabolism	0.0037
EPM2A	GO:0031323 regulation of cellular metabolism	0.0008
ERBB4	GO:0044237 cellular metabolism	0.0037
EREG	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
GADD45A	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
GALR1	GO:0050789 regulation of biological process	0.0017
GTF2H1	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
HOXD1	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
JARID2	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
KLF13	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
MAX	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
MBD4	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
MITF	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
MRPS30	GO:0044237 cellular metabolism	0.0037
MYB	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
NOX1	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
PITPNM2	GO:0008152 metabolism	0.0068
PPIG	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
PRKAA2	GO:0044237 cellular metabolism	0.0037
PRMT7	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
PSMA8	GO:0044237 cellular metabolism	0.0037
PTGER3	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
PTH	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05

RPS2	GO:0044237 cellular metabolism	0.0037
SIRT6	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
SIRT7	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
TGIF2	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
TP73L	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
UBE2W	GO:0044237 cellular metabolism	0.0037
VGLL2	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
WHSC1L1	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05
ZNF430	GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5.96E-05

^aGene name for the anticorrelated mRNA

^bOver-represented biological process GO term and description

^c*P*-value associated with that GO term

Supplementary TABLE 2. Conserved RNA secondary structures that co-locate with human TE sequences.

Name ^a	Coords ^b	TE ^c
6597_0_+_74	chr1:6483733-6483759(+)	Charlie8
15086_0_-_78	chr1:15041842-15041859(-)	HAL1
24981_0_+_74	chr1:23415863-23415881(+)	MIRb
25288_0_-_83	chr1:23621848-23621877(-)	MIRb
25923_0_+_48	chr1:24115467-24115495(+)	MIR3
30647_0_+_38	chr1:27752374-27752433(+)	MIRb
30820.5_0_-_68	chr1:27791805-27791823(-)	MIR3
38333_0_+_77	chr1:34707582-34707607(+)	Charlie7
43475_0_+_88	chr1:38294035-38294051(+)	L3
46777_0_+_71	chr1:40440123-40440153(+)	MER103
48001_0_+_47	chr1:41214471-41214487(+)	L2
48998_0_-_51	chr1:41888110-41888146(-)	L3
51113_0_+_73	chr1:43734410-43734424(+)	L1M5
58555_0_+_65	chr1:49094515-49094531(+)	L1ME4a
60187_0_+_106	chr1:50667381-50667396(+)	L1ME4a
72612_0_-_79	chr1:61379203-61379221(-)	L3
73590_0_-_75	chr1:61923623-61923650(-)	Charlie2
82264_0_-_68	chr1:71707409-71707427(-)	L3
85615_0_+_83	chr1:76474930-76474947(+)	MIRb
92562_0_-_56	chr1:83112753-83112791(-)	L2
108307_0_+_78	chr1:97287966-97287983(+)	L3b
112207_0_+_95	chr1:101216647-101216665(+)	MIR3
120809_0_+_79	chr1:111021701-111021719(+)	MIR
122080_0_-_62	chr1:112177611-112177631(-)	MIR
124780_0_-_66	chr1:114214379-114214407(-)	MIRb
132990_0_-_73	chr1:142748623-142748637(-)	MIR3
148967_0_+_106	chr1:157421181-157421197(+)	L2
149463_0_+_61	chr1:157999850-157999872(+)	L4
154215_0_+_65	chr1:162123173-162123189(+)	Tigger8
161465_0_+_90	chr1:169013965-169013984(+)	MER45A
177588_0_-_76	chr1:182715187-182715207(-)	MIRb
184070_0_-_57	chr1:192397663-192397683(-)	MER90
188643_0_+_89	chr1:198985820-198985838(+)	L2
190021_0_+_47	chr1:199883257-199883273(+)	MIRb
199932_0_-_79	chr1:206789414-206789432(-)	Charlie2
228731_0_+_62	chr1:242250135-242250150(+)	MER53
230542_0_-_67	chr1:244286075-244286098(-)	L1MB3
1190052_0_-_69	chr2:26795482-26795520(-)	L1ME4a
1194893_0_+_73	chr2:29846946-29846960(+)	HAL1
1201447_0_+_65	chr2:37374164-37374180(+)	L4
1208495_0_+_83	chr2:44171423-44171440(+)	LTR33
1208526_0_-_109	chr2:44198198-44198220(-)	MLT1J
1222791_0_+_110	chr2:59759711-59759730(+)	L1M5
1228152_0_-_94	chr2:64565601-64565616(-)	MIR3
1229575_0_+_76	chr2:65898157-65898173(+)	LTR33
1239485_0_+_80	chr2:75090614-75090638(+)	L1ME4a

1239721_0_+_79	chr2:75407124-75407142(+)	MARNA
1239765_0_+_119	chr2:75520847-75520862(+)	L1MC
1243784_0_-_105	chr2:81417721-81417741(-)	MIRb
1245396_0_-_65	chr2:85055655-85055671(-)	MER58B
1247043_0_+_65	chr2:86563203-86563222(+)	L3
1250762_0_-_79	chr2:95726497-95726515(-)	L2
1257853_0_+_43	chr2:103875041-103875063(+)	MIRm
1258738_0_-_45	chr2:104657492-104657535(-)	L1ME4a
1265559_0_+_78	chr2:113813281-113813307(+)	L2
1280461_0_+_93	chr2:136964701-136964729(+)	Tigger8
1288189_0_+_138	chr2:145136397-145136417(+)	L1MC5
1304651_0_+_81	chr2:161680961-161680976(+)	MIRb
1307871_0_+_94	chr2:164440131-164440148(+)	L3b
1312547_0_+_65	chr2:169163008-169163024(+)	Kanga2_a
1318523_0_+_114	chr2:174053048-174053068(+)	L2
1319174_0_-_68	chr2:174641664-174641691(-)	L1MC4a
1320276_0_-_65	chr2:175480749-175480768(-)	L1ME4a
1344295_0_+_73	chr2:200120342-200120356(+)	MIRm
1346880_0_-_90	chr2:202119446-202119466(-)	L1MB8
1353436_0_-_43	chr2:206288743-206288763(-)	MIRb
1363676_0_-_76	chr2:215455658-215455686(-)	MARNA
1365045_0_+_67	chr2:216418189-216418209(+)	MLT1K
1371955_0_+_109	chr2:220595160-220595181(+)	Arthur1
1383146_0_-_65	chr2:232693947-232693963(-)	L2
1389370_0_-_70	chr2:240141186-240141212(-)	L1M5
1521839_0_+_74	chr3:10540626-10540652(+)	Charlie8
1525689_0_+_100	chr3:14249470-14249491(+)	L3
1530481_0_+_59	chr3:18526135-18526168(+)	L2
1542101_0_+_74	chr3:35354374-35354400(+)	L1ME3A
1558705_0_+_79	chr3:50643228-50643246(+)	MIRb
1572162_0_-_74	chr3:60630961-60630979(-)	L1M5
1584630_0_-_110	chr3:70684589-70684609(-)	L1ME3A
1590226_0_-_100	chr3:74756051-74756070(-)	MER45B
1593242_0_-_80	chr3:78065198-78065217(-)	MIRb
1595751_0_+_87	chr3:81453304-81453326(+)	MIRb
1605591_0_+_81	chr3:100984579-100984594(+)	L3b
1619386_0_-_86	chr3:115872816-115872837(-)	MER69A
1624711_0_+_126	chr3:120022139-120022157(+)	L1ME4a
1638166_0_-_65	chr3:133240374-133240390(-)	MLT1J
1651552_0_-_59	chr3:145681874-145681905(-)	L2
1664761_0_+_78	chr3:161388886-161388903(+)	MER3
1665104_0_-_61	chr3:161708071-161708106(-)	L2
1669125_0_+_65	chr3:169470145-169470170(+)	L1ME4a
1692753_0_+_65	chr3:194760060-194760076(+)	MIRb
1705626_0_-_63	chr4:12690588-12690606(-)	L2
1709742_0_-_82	chr4:17391442-17391474(-)	L2
1714124_0_-_124	chr4:23001557-23001573(-)	L2
1719629_0_+_105	chr4:27859462-27859480(+)	LTR33
1726312_0_-_63	chr4:39411734-39411760(-)	MIRb
1730972_0_-_56	chr4:46681709-46681733(-)	L1ME3B

1747758_0_-_63	chr4:74275595-74275629(-)	L1M5
1753586_0_-_83	chr4:81294838-81294860(-)	MIRb
1754111_0_+_88	chr4:81949213-81949228(+)	L3
1764240_0_-_76	chr4:95780967-95780983(-)	MIR3
1768888_0_-_54	chr4:101481090-101481113(-)	LTR33
1772239_0_+_73	chr4:106784430-106784444(+)	MIR3
1773181_0_+_100	chr4:108002087-108002108(+)	LTR68
1813460_0_-_96	chr4:158919215-158919239(-)	MER5A
1827139_0_+_83	chr4:181230274-181230297(+)	MLT1C
1827751_0_+_75	chr4:181988895-181988914(+)	MIRb
1829210_0_-_55	chr4:183054460-183054490(-)	MIR3
1830949_0_+_65	chr4:184054997-184055013(+)	MIRm
1842241_0_+_61	chr5:9629511-9629533(+)	Charlie2
1860397_0_+_94	chr5:38819321-38819337(+)	MIR3
1862891_0_+_55	chr5:42157514-42157542(+)	LTR16A1
1868925_0_+_75	chr5:53320758-53320785(+)	MIRb
1874290_0_-_110	chr5:59086690-59086709(-)	MER113
1876462_0_-_84	chr5:61101641-61101659(-)	MIRb
1900649_0_+_81	chr5:88600908-88600928(+)	MARNA
1904329_0_+_85	chr5:92449669-92449694(+)	L3
1912951_0_+_71	chr5:103360475-103360491(+)	MIRb
1919694_0_-_71	chr5:112530605-112530621(-)	L3b
1920501_0_+_72	chr5:113735156-113735173(+)	L2
1929047_0_+_75	chr5:124046980-124047023(+)	HAL1
1944753_0_+_72	chr5:139204106-139204134(+)	Charlie7
1944754_0_-_54	chr5:139204158-139204181(-)	Charlie7
1949916_0_-_74	chr5:141188281-141188299(-)	L1MC
1951254_0_-_65	chr5:142156112-142156128(-)	MIR3
1959488_0_-_87	chr5:149669722-149669736(-)	L2
1966281_0_+_83	chr5:156681824-156681841(+)	MIR3
1967253_0_+_52	chr5:157463563-157463620(+)	L1ME4a
1969951_0_+_79	chr5:159059780-159059812(+)	L4
1970767_0_+_67	chr5:159755119-159755139(+)	Charlie11
1973974_0_-_68	chr5:163838798-163838819(-)	L2
1980933_0_+_81	chr5:168747748-168747763(+)	Charlie1a
1987527_0_+_59	chr5:175727565-175727628(+)	L2
1988415_0_+_77	chr5:176255041-176255066(+)	MIRb
1874239_0_+_93	chr5:59035208-59035277(+)	L3
1999329_0_+_67	chr6:7450078-7450092(+)	MIR3
2006707_0_+_93	chr6:15110399-15110413(+)	MIRb
2012915_0_+_82	chr6:21665770-21665786(+)	Charlie8
2020947_0_+_75	chr6:31654313-31654336(+)	LTR42
2029187_0_+_46	chr6:37530191-37530227(+)	L3b
2029634_0_-_100	chr6:37784559-37784580(-)	L1ME4a
2032923_0_+_87	chr6:40857398-40857412(+)	L1ME4a
2037716_0_-_160	chr6:44077681-44077715(-)	MER53
2047183_0_+_78	chr6:54681376-54681393(+)	L2
2075048_0_-_91	chr6:94484941-94484963(-)	ERVL-E
2078828_0_-_111	chr6:99509678-99509696(-)	MIRb
2085959_0_+_73	chr6:107897109-107897123(+)	MER5B

2096533_0_+_62	chr6:119656124-119656165(+)	L3
2171717_0_+_110	chr7:34814854-34814873(+)	HAL1b
2177366_0_-_111	chr7:41288277-41288304(-)	L1ME4a
2195049_0_+_117	chr7:73161289-73161306(+)	MIR3
2203727_0_+_62	chr7:83830368-83830388(+)	L3
2214152_0_-_57	chr7:95381816-95381836(-)	MIR
2215010_0_-_104	chr7:95921415-95921438(-)	L1ME3
2216137_0_+_72	chr7:97120781-97120805(+)	MIR3
2229371_0_+_67	chr7:110280027-110280041(+)	LTR40a
2234441_0_+_52	chr7:115222951-115222981(+)	L2
2246941_0_+_73	chr7:128849628-128849649(+)	L2
2247695_0_+_119	chr7:129521829-129521855(+)	L1ME4a
2247695_1_+_65	chr7:129521966-129521985(+)	L1ME4a
2251058_0_-_95	chr7:131926833-131926869(-)	Charlie7
2277373_0_+_89	chr8:9268418-9268435(+)	L1MD2
2278817_0_+_62	chr8:10784215-10784248(+)	MIRb
2285985_0_+_74	chr8:20987404-20987426(+)	L2
2286909_0_+_87	chr8:21794450-21794464(+)	MIRb
2293775_0_+_77	chr8:28190662-28190683(+)	L1MC4a
2296966_0_-_112	chr8:31652907-31652946(-)	MIRb
2299343_0_+_68	chr8:33896886-33896904(+)	L1MC4
2299747_0_+_76	chr8:34293119-34293135(+)	MIRb
2301209_0_+_94	chr8:35801853-35801870(+)	L3
2306450_0_-_70	chr8:41798076-41798095(-)	L2
2317552_0_-_83	chr8:64247707-64247729(-)	MIRb
2322741_0_+_67	chr8:69743160-69743177(+)	L3
2330830_0_-_81	chr8:78984234-78984259(-)	MER5B
2337143_0_+_72	chr8:89013976-89013993(+)	L2
2339739_0_+_72	chr8:92822152-92822176(+)	L3
2339740_0_-_87	chr8:92822207-92822229(-)	L3
2348773_0_+_51	chr8:102229956-102230022(+)	Charlie9
2356873_0_+_100	chr8:110789279-110789300(+)	L3
2363824_0_-_100	chr8:119852398-119852414(-)	L4
2369557_0_+_74	chr8:125994973-125994991(+)	MIRb
2373181_0_+_76	chr8:130158434-130158450(+)	L2
2376487_0_+_73	chr8:134299648-134299669(+)	MIRb
2378900_0_-_81	chr8:138418970-138418990(-)	MER91B
2380602_0_-_97	chr8:141811863-141811931(-)	L2
2389613_0_+_87	chr9:3936317-3936331(+)	L2
2393693_0_+_78	chr9:8804094-8804111(+)	L2
2394223_0_+_76	chr9:9267671-9267699(+)	L1M4
2401146_0_-_96	chr9:16787222-16787246(-)	MIR
2401571_0_+_67	chr9:17060609-17060626(+)	L1ME4a
2412879_0_+_68	chr9:29844233-29844254(+)	L3
2421368_0_-_79	chr9:37811135-37811158(-)	L1MC4a
2426661_0_+_64	chr9:70297285-70297306(+)	MER91A
2431307_1_+_89	chr9:75353184-75353201(+)	L4
2442499_0_+_85	chr9:88825569-88825595(+)	L4
2447361_0_+_94	chr9:97429994-97430011(+)	MLT1K
2452438_0_-_120	chr9:101754094-101754108(-)	L4

2452597_0_+_91	chr9:101776189-101776211(+)	L4
2452602_0_-_68	chr9:101776449-101776467(-)	L4
2455634_0_-_64	chr9:105918396-105918420(-)	MER5A
2468629_0_+_104	chr9:117452580-117452603(+)	L2
2472869_0_+_76	chr9:121613122-121613138(+)	L2
2479521_0_+_75	chr9:126607543-126607574(+)	L1ME4a
2500550_0_-_83	chrX:10899595-10899617(-)	L4
2507070_0_-_85	chrX:15944486-15944505(-)	L1ME4a
2509218_0_-_95	chrX:17351726-17351746(-)	MIRb
2513321_0_+_81	chrX:19783471-19783486(+)	MER58A
2514009_0_+_54	chrX:20163518-20163543(+)	L1ME4a
2514011_0_+_147	chrX:20164132-20164161(+)	L1ME4a
2514641_0_+_84	chrX:20436611-20436629(+)	L2
2519737_0_+_67	chrX:24557155-24557175(+)	L1ME4a
2527121_0_+_47	chrX:32060447-32060480(+)	MIRb
2537738_0_-_61	chrX:43454292-43454314(-)	MIRb
2557941_0_+_75	chrX:71069003-71069018(+)	L2
2571697_0_+_73	chrX:97698707-97698728(+)	Charlie1a
2573092_0_-_86	chrX:99503268-99503289(-)	MIR
2576468_0_-_59	chrX:102471559-102471585(-)	L1MC4a
2583739_0_+_63	chrX:108529599-108529617(+)	L2
2584535_0_+_91	chrX:109185224-109185300(+)	MER91C
2585968_0_-_86	chrX:110177627-110177654(-)	L2
2598315_0_+_62	chrX:123586235-123586255(+)	MIRb
2604008_0_-_88	chrX:129506265-129506281(-)	HAL1b
2604832_0_-_51	chrX:129994594-129994630(-)	L3
2607024_0_-_68	chrX:131689852-131689873(-)	L1MB5
2613374_0_-_71	chrX:135974107-135974123(-)	MIR
2613853_0_+_60	chrX:136377304-136377323(+)	L1MC4
2625375_0_+_86	chrX:152562536-152562556(+)	L2
241830_0_-_89	chr10:13315027-13315044(-)	MIR
246588_0_-_100	chr10:18657192-18657208(-)	MER5B
251147_0_+_94	chr10:24324839-24324855(+)	MIRb
276291_0_+_66	chr10:62836157-62836220(+)	L1M5
278579_0_+_157	chr10:64671753-64671775(+)	L2
279306_0_-_71	chr10:65568421-65568437(-)	MLT1L
292265_0_+_95	chr10:77784926-77784944(+)	L2
295318_0_-_86	chr10:80133480-80133500(-)	L3b
296055_0_+_79	chr10:80679702-80679720(+)	MIRb
299725_0_+_88	chr10:86569717-86569742(+)	L1ME4a
333376_0_-_70	chr10:115808231-115808257(-)	MER46C
334961_0_+_78	chr10:117579937-117579954(+)	L2
341781_0_+_89	chr10:123290268-123290285(+)	L3
361933_0_+_88	chr11:6635631-6635654(+)	Kanga2_a
368338_0_-_100	chr11:11787492-11787508(-)	L3
370306_0_-_88	chr11:13416460-13416476(-)	L3
377681_0_+_96	chr11:19331037-19331062(+)	L3
394814_0_-_79	chr11:40886992-40887015(-)	L2
395263_0_+_46	chr11:41605707-41605732(+)	FordPrefect_a
397099_0_+_71	chr11:43869396-43869412(+)	MIRb

408823_0_+_73	chr11:59187569-59187590(+)	MIR
425555_0_+_71	chr11:71985685-71985701(+)	MIR
438440_0_-_74	chr11:83316345-83316367(-)	L2
438439_0_+_83	chr11:83316376-83316398(+)	L2
440997_0_+_81	chr11:85937263-85937278(+)	L4
444101_0_+_100	chr11:91430989-91431005(+)	MIR
466625_0_+_110	chr11:116956700-116956719(+)	MIR
471849_0_+_90	chr11:119880617-119880636(+)	L3
486187_0_+_68	chr11:130861130-130861151(+)	MIRb
492576_0_-_95	chr12:2125422-2125443(-)	MIRb
498153_0_+_67	chr12:6658215-6658235(+)	MIRm
522947_0_+_70	chr12:40826566-40826585(+)	L2
533638.0_0_-_122	chr12:50492331-50492353(-)	MIRb
542148_0_-_83	chr12:55246557-55246574(-)	LTR37B
569483_0_+_39	chr12:87985382-87985425(+)	L2
570380_0_-_86	chr12:88718407-88718434(-)	MIRb
571837_0_+_78	chr12:90583073-90583090(+)	MER58B
578709_0_+_108	chr12:96992583-96992607(+)	L1ME3B
637241_0_+_66	chr13:52383235-52383263(+)	L3b
645204_0_-_94	chr13:62341135-62341150(-)	MIR
648567_0_+_59	chr13:67872860-67872891(+)	MIRb
650887_0_+_68	chr13:71623788-71623824(+)	L3b
654127_0_+_82	chr13:74685170-74685186(+)	MER5A
710673_0_+_58	chr14:49857372-49857390(+)	MIR
731341_0_+_70	chr14:67762102-67762121(+)	L3b
737958_0_-_62	chr14:72903436-72903456(-)	MIRb
740946_0_-_72	chr14:74763371-74763399(-)	L2
746350_0_-_81	chr14:78670822-78670842(-)	MIRm
766865_0_+_57	chr14:100584767-100584820(+)	MER5A1
775713_0_+_77	chr15:25703141-25703162(+)	L1MCc
783373_0_+_94	chr15:33592451-33592467(+)	L1ME4a
795825_0_+_111	chr15:41875416-41875434(+)	MIRb
804788_0_-_75	chr15:50144808-50144835(-)	L1M1
823849_0_+_52	chr15:65945171-65945195(+)	L1ME4a
830936_0_-_60	chr15:71924252-71924271(-)	L4
842223_0_+_71	chr15:81565655-81565678(+)	MIR3
844067_0_+_100	chr15:83150156-83150175(+)	L1ME4a
851769_0_+_126	chr15:89250081-89250099(+)	L4
854345_0_+_71	chr15:91631904-91631924(+)	MIRb
857021_0_+_68	chr15:94257983-94258001(+)	MIRb
858814_3_-_112	chr15:95403622-95403655(-)	L4
872420_0_-_70	chr16:6175415-6175434(-)	MIRb
896537_0_+_81	chr16:30749660-30749680(+)	MIR
904577_0_+_91	chr16:49653282-49653304(+)	MER99
905411_0_+_74	chr16:50290185-50290231(+)	L3
909177_0_+_82	chr16:53170182-53170198(+)	MIRb
914771_0_+_81	chr16:57783182-57783208(+)	MIRb
918945_0_+_64	chr16:63576155-63576179(+)	L1M5
924692_0_-_70	chr16:67025377-67025409(-)	L1ME4a
928869_0_+_74	chr16:70304015-70304037(+)	MIR3

929116_0_-_165	chr16:70444938-70444954(-)	MIR
933812_0_-_89	chr16:74025554-74025571(-)	Tigger2
976169_0+_86	chr17:24040248-24040268(+)	L1ME4a
989909_0+_100	chr17:34009010-34009024(+)	MIR3
993737_0+_67	chr17:36057125-36057139(+)	MIRb
1000039.8_0+_109	chr17:39468501-39468532(+)	L1MC4
1015457_0+_67	chr17:50377318-50377332(+)	MLT1C
1018093_0+_74	chr17:52576474-52576492(+)	MIR3
1027140_0_-_109	chr17:58956205-58956226(-)	MER5A
1029871_0+_79	chr17:60844235-60844253(+)	MIR
1044595_0+_71	chr17:73614287-73614307(+)	L1MDa
1054900_0_-_75	chr18:6426001-6426016(-)	L1M5
1062229_0+_73	chr18:18029737-18029751(+)	L1ME4a
1067853_0+_86	chr18:22989505-22989533(+)	L3
1072891_0+_61	chr18:29462119-29462141(+)	MIRb
1073425_0+_104	chr18:30062939-30062963(+)	L2
1076640_0_-_90	chr18:33541894-33541913(-)	L2
1077026_0_-_100	chr18:33875539-33875554(-)	MIRb
1077028_0_-_58	chr18:33875730-33875789(-)	MIRb
1079884_0_-_53	chr18:37167167-37167185(-)	L3
1083125_0+_82	chr18:41077120-41077141(+)	L2
1083586_0_-_71	chr18:41429464-41429484(-)	MIR
1084952_0_-_69	chr18:42863307-42863338(-)	L1ME4a
1085381_0+_105	chr18:43238379-43238399(+)	MIR
1085682_0_-_76	chr18:43568621-43568637(-)	MER113
1100012_0_-_81	chr18:59852148-59852168(-)	L3
1105949_0+_73	chr18:71397854-71397883(+)	L3b
1139206_0_-_87	chr19:37294434-37294456(-)	L2
1394080_0_-_52	chr20:2927811-2927835(-)	L1ME3B
1397189_0+_110	chr20:6163591-6163611(+)	L2
1401791_0+_119	chr20:10612937-10612952(+)	L2
1405784_0_-_100	chr20:14549750-14549770(-)	MIRb
1405783_1+_46	chr20:14549818-14549865(+)	MIRb
1412553_0+_87	chr20:20910851-20910873(+)	L1P4
1416308_0_-_95	chr20:29589818-29589838(-)	MIRb
1434998_0_-_100	chr20:44089910-44089928(-)	MIR
1435354_0_-_79	chr20:44235903-44235921(-)	MIR
1453725_0+_67	chr21:14966802-14966816(+)	MIR3
1466070_0_-_70	chr21:33853177-33853203(-)	L2
1489729_0+_59	chr22:28457760-28457800(+)	L1ME4a
1496941_0+_79	chr22:35289947-35289989(+)	L1MC4
1498291_0+_153	chr22:36325294-36325312(+)	L3b
1509614_0_-_55	chr22:48049650-48049680(-)	L1ME4a
3715_0+_61	chr1:3131597-3131629(+)	MER121
52664_0_-_50	chr1:44571346-44571464(-)	Eulor9A
52940_0_-_77	chr1:44674828-44674849(-)	MER121
67625_0+_68	chr1:57127369-57127387(+)	Eulor1
67626_0_-_76	chr1:57127400-57127465(-)	Eulor1
75315_0+_61	chr1:63495303-63495320(+)	UCON8
82063_0+_72	chr1:71463300-71463317(+)	MER133A

88341_0_+_95	chr1:79596295-79596315(+)	UCON15
88403_0_+_60	chr1:79660341-79660380(+)	UCON30
88624_0_-_75	chr1:80015139-80015158(-)	X6A_LINE
93362.2_0_-_68	chr1:83766400-83766418(-)	MER131
112743_0_+_87	chr1:101723969-101723998(+)	MER133A
130308_0_-_77	chr1:118651361-118651382(-)	MER121
130734_0_-_76	chr1:119254356-119254388(-)	MER121
154446_0_-_100	chr1:162492879-162492895(-)	UCON18
154818_0_-_64	chr1:162825371-162825437(-)	MER135
161005_0_+_64	chr1:168646670-168646694(+)	UCON26
187011_0_+_89	chr1:197245358-197245395(+)	MER121
188052_1_-_92	chr1:198460508-198460590(-)	Eulor3
198813_0_+_90	chr1:206237185-206237204(+)	MER136
204532_0_-_104	chr1:211522027-211522054(-)	UCON31
211312_0_-_76	chr1:217555499-217555519(-)	MER121
1171004_0_-_83	chr2:6568368-6568396(-)	MER121
1184389_0_+_73	chr2:22111720-22111741(+)	MER136
1221529_0_+_96	chr2:58895995-58896019(+)	X7C_LINE
1223513_0_+_97	chr2:60171167-60171200(+)	Eulor10
1231302_0_-_88	chr2:66979970-66979994(-)	Eulor3
1231553_0_+_75	chr2:67238894-67239028(+)	Eulor4
1241102_0_-_78	chr2:77353762-77353793(-)	MER123
1258257_0_+_85	chr2:104314401-104314489(+)	MER134
1258569_0_+_76	chr2:104524897-104524954(+)	Eulor1
1260469_0_+_45	chr2:107079289-107079332(+)	Eulor10
1260520_0_-_81	chr2:107258693-107258740(-)	UCON23
1285391_0_+_90	chr2:143702983-143703011(+)	MER136
1285391_1_+_129	chr2:143703042-143703075(+)	MER136
1285392_0_-_87	chr2:143703144-143703181(-)	MER136
1286513_0_+_57	chr2:144311903-144311946(+)	MER125
1288297_0_+_88	chr2:145186813-145186838(+)	Eulor4
1288651_0_+_86	chr2:145417357-145417378(+)	LmeSINE1b
1305099_0_+_74	chr2:161974382-161974408(+)	AmnSINE1_GG
1307386_0_-_85	chr2:164117565-164117584(-)	Eulor6D
1321435_0_+_100	chr2:176377724-176377743(+)	MER133A
1329277_0_+_76	chr2:181280870-181280886(+)	MER135
1343221_0_+_43	chr2:199281672-199281699(+)	X6A_LINE
1344357_0_+_95	chr2:200156156-200156174(+)	MER131
1344453_0_+_48	chr2:200237188-200237216(+)	MER121
1357076_0_-_85	chr2:208527969-208528001(-)	MER134
1361323_0_+_57	chr2:213067475-213067509(+)	Eulor5A
1372257_0_+_56	chr2:220785460-220785507(+)	UCON11
1373497_0_+_65	chr2:221709145-221709161(+)	MER121
1512259_0_+_84	chr3:886207-886231(+)	Eulor3
1529073_0_+_51	chr3:17512755-17512791(+)	UCON17
1537363_0_+_82	chr3:28861055-28861082(+)	Eulor4
1570585_0_+_100	chr3:59401515-59401529(+)	UCON17
1573547_0_+_44	chr3:61643441-61643518(+)	MER126
1573643_0_+_95	chr3:61718341-61718381(+)	MER134
1583919_0_+_136	chr3:70159597-70159621(+)	Eulor3

1584125_0+_85	chr3:70282197-70282216(+)	MER121
1587903_0+_63	chr3:72770417-72770435(+)	MER121
1589951_0+_75	chr3:74512342-74512357(+)	MER129
1613192_0_-38	chr3:109671038-109671090(-)	MER127
1619194_0_-81	chr3:115772653-115772683(-)	UCON9
1620066_0_-64	chr3:116298434-116298458(-)	Eulor1
1631238_0_-62	chr3:125850420-125850440(-)	X7B_LINE
1644004_0_-55	chr3:138650699-138650738(-)	UCON4
1651767_0+_52	chr3:146074810-146074873(+)	Eulor3
1662217_0+_62	chr3:159045808-159045847(+)	MER121
1668216_0_-58	chr3:168436231-168436447(-)	MER126
1670278_0_-120	chr3:170405686-170405715(-)	MER131
1678363_0+_67	chr3:179445164-179445181(+)	X6B_LINE
1680024_0_-54	chr3:181521306-181521359(-)	UCON29
1688359_0+_58	chr3:189369310-189369328(+)	UCON7
1689205_1+_86	chr3:190161865-190161886(+)	UCON7
1705501_0+_62	chr4:12551247-12551267(+)	MER121
1705501_1+_80	chr4:12551274-12551293(+)	MER121
1706954_0_-78	chr4:14392438-14392473(-)	MER121
1710470_0_-75	chr4:18287096-18287119(-)	X6B_LINE
1713985_0+_114	chr4:22907781-22907802(+)	MER132
1713986_1_-100	chr4:22907805-22907826(-)	MER132
1714957_0+_71	chr4:23573735-23573758(+)	UCON2
1715903_0+_88	chr4:24017990-24018005(+)	UCON2
1743298_0_-89	chr4:67215793-67215838(-)	Eulor8
1743393_0+_92	chr4:67394199-67394235(+)	Eulor5B
1757379_0+_70	chr4:85466757-85466855(+)	MER134
1798767_0+_50	chr4:142921647-142921690(+)	UCON9
1802422_0_-75	chr4:147467073-147467100(-)	LF-SINE
1803203_0+_84	chr4:148224139-148224169(+)	X7C_LINE
1828955_0+_104	chr4:182906948-182906974(+)	Eulor6A
1829383_0+_100	chr4:183149701-183149718(+)	LF-SINE
1830405_0+_49	chr4:183690755-183690850(+)	MER135
1846135_0+_73	chr5:15474550-15474564(+)	MER121
1850975_0+_96	chr5:27214825-27214847(+)	Eulor3
1851065_0+_102	chr5:27505032-27505076(+)	Eulor4
1864187_0+_85	chr5:44037377-44037402(+)	MER121
1864730_0_-92	chr5:44649544-44649567(-)	MER121
1866169_0+_73	chr5:50392064-50392078(+)	MER127
1873731_0+_53	chr5:58495675-58495729(+)	UCON9
1876134_0_-86	chr5:60931589-60931609(-)	MER121
1890599_0+_79	chr5:77309961-77309998(+)	Eulor6B
1895055_0+_87	chr5:81671505-81671527(+)	MER121
1900625.5_0+_72	chr5:88585797-88585825(+)	MER121
1902777_0+_53	chr5:90643387-90643420(+)	AmnSINE1_GG
1903538_0_-79	chr5:91723955-91723983(-)	MER125
1913159_0+_89	chr5:103795810-103795856(+)	UCON31
1929440_0_-73	chr5:124269753-124269778(-)	Eulor5B
1930433_1+_82	chr5:125337043-125337092(+)	Eulor4
1955119_0+_44	chr5:145869978-145870018(+)	LF-SINE

1955395_0_+_81	chr5:146094979-146094999(+)	X5A_LINE
1975838_0_-_80	chr5:165688874-165688944(-)	Eulor5A
1979031_0_+_61	chr5:167506770-167506888(+)	Eulor9A
2000476_0_-_85	chr6:8499794-8499914(-)	Eulor6C
2001968_0_-_145	chr6:10178396-10178424(-)	MER131
2008557_0_+_81	chr6:16949073-16949103(+)	UCON26
2031067_0_+_44	chr6:39048083-39048162(+)	Eulor5A
2047829_0_+_41	chr6:55761992-55762018(+)	MER121
2066390_0_-_81	chr6:85075854-85075874(-)	MER121
2078773_0_+_88	chr6:99459607-99459623(+)	UCON9
2080615_0_+_60	chr6:101110199-101110218(+)	MER131
2103549_0_+_93	chr6:128809103-128809145(+)	UCON16
2110337_0_+_44	chr6:136398344-136398375(+)	UCON26
2114503.0_0_+_80	chr6:140364809-140364828(+)	MER121
2115069.5_0_+_82	chr6:141179709-141179763(+)	Eulor5B
2121113_0_+_55	chr6:148347371-148347399(+)	LF-SINE
2122492_0_-_129	chr6:149575272-149575305(-)	SacSINE1
2124929_0_+_75	chr6:152368090-152368109(+)	MER121
2127747_0_+_66	chr6:155834738-155834778(+)	UCON9
2129448_0_-_71	chr6:157252755-157252771(-)	X7B_LINE
2164946_0_-_47	chr7:28364896-28364929(-)	AmnSINE1_GG
2165103_0_+_104	chr7:28447122-28447144(+)	MER121
2177946_0_-_48	chr7:41927983-41928013(-)	MER121
2199161_0_+_76	chr7:78029611-78029627(+)	UCON25
2232211_0_+_45	chr7:113190696-113190791(+)	Eulor6B
2233748_0_-_181	chr7:114618868-114618893(-)	Eulor6B
2265159_0_+_85	chr7:146833245-146833271(+)	UCON4
2289857_0_+_81	chr8:24066738-24066758(+)	MER121
2298526_0_-_61	chr8:33038256-33038278(-)	MER121
2302531_0_+_170	chr8:37341837-37341883(+)	Eulor5B
2328941_0_+_120	chr8:76879838-76879852(+)	Eulor4
2330918_0_-_108	chr8:79081399-79081462(-)	Eulor3
2339767_0_+_82	chr8:92837069-92837101(+)	MER121
2339841_0_+_84	chr8:92935042-92935090(+)	MER121
2344217_0_+_65	chr8:97188471-97188580(+)	MER135
2354838_0_-_72	chr8:108773965-108774000(-)	UCON26
2379473_0_+_97	chr8:139630131-139630160(+)	Eulor1
2394293_0_+_95	chr9:9338370-9338389(+)	Eulor2A
2397055_0_+_80	chr9:13796837-13796866(+)	Eulor6A
2397055_1_+_73	chr9:13796922-13796943(+)	Eulor6A
2409235_0_+_142	chr9:25589526-25589549(+)	Eulor3
2431229_0_+_103	chr9:75174932-75174961(+)	Eulor6B
2439460_0_-_71	chr9:84169407-84169440(-)	Eulor10
2451401_0_+_100	chr9:101409466-101409483(+)	UCON27
2469220_0_-_74	chr9:118053225-118053243(-)	MER121
2469999_0_+_79	chr9:118715772-118715795(+)	UCON11
2521976_0_-_97	chrX:26365641-26365669(-)	MER131
2551760_0_-_64	chrX:65934376-65934400(-)	MER121
2572113_0_+_91	chrX:98425536-98425558(+)	MER124
2598753_0_+_171	chrX:123865376-123865447(+)	Eulor11

2615332_2_-_77	chrX:137769424-137769462(-)	Eulor5A
236504_0_-_113	chr10:7164642-7164680(-)	MER134
256849_0_+_114	chr10:31429075-31429102(+)	MER131
276892.3_0_-_76	chr10:63322047-63322080(-)	Eulor9A
276891.4_0_+_88	chr10:63322163-63322186(+)	Eulor9A
285555_0_+_63	chr10:72980870-72980944(+)	MER125
292625_0_+_200	chr10:78081072-78081104(+)	Eulor3
292626_0_-_70	chr10:78081151-78081173(-)	Eulor3
295479_0_+_56	chr10:80319880-80319927(+)	MER125
318452_0_-_79	chr10:103288332-103288350(-)	AmnSINE1_GG, AmnSINE1_HS
327752_0_-_82	chr10:111678355-111678382(-)	MER121
330818_0_-_148	chr10:114305414-114305436(-)	MER134
335779_0_+_54	chr10:118027456-118027512(+)	Eulor6D
337561_0_+_69	chr10:119614151-119614186(+)	MER121
338610_0_-_64	chr10:120269645-120269680(-)	Eulor2A
369668_0_-_112	chr11:12893042-12893058(-)	UCON31
373787_0_+_88	chr11:16322974-16322989(+)	MER131
487071_1_+_53	chr11:131453807-131453846(+)	MER121
487071_2_+_103	chr11:131453921-131453949(+)	MER121
512063_0_+_83	chr12:23491193-23491210(+)	LF-SINE
513095_0_+_110	chr12:24372647-24372676(+)	UCON15
516227_0_+_65	chr12:27866363-27866396(+)	AmnSINE1_HS
551096_0_-_85	chr12:64538090-64538148(-)	Eulor5A
596281_0_+_59	chr12:114732788-114732836(+)	MER121
596947_0_+_93	chr12:115505370-115505426(+)	MER123
622745_0_+_100	chr13:35243065-35243085(+)	MER131
645738_0_-_105	chr13:63899169-63899187(-)	UCON7
645910_0_-_48	chr13:64241844-64241876(-)	MER131
646225_0_+_88	chr13:65068325-65068348(+)	Eulor6B
647102_0_-_48	chr13:66105298-66105320(-)	LF-SINE
648333_0_+_100	chr13:67341863-67341891(+)	Eulor5B
649736_0_-_74	chr13:70683133-70683151(-)	UCON15
651061_0_+_58	chr13:71771123-71771160(+)	Eulor8
651179.1_0_+_60	chr13:71904255-71904296(+)	Eulor6B
653822_0_-_62	chr13:74296760-74296798(-)	Eulor5A
677411_0_+_89	chr13:106457940-106457957(+)	UCON9
677411_1_+_76	chr13:106457967-106457999(+)	UCON9
677411_2_+_85	chr13:106458051-106458083(+)	UCON9
677677_0_+_73	chr13:106991355-106991369(+)	MER123
692404_0_-_138	chr14:28918314-28918337(-)	MER133B
693415_0_+_104	chr14:29848578-29848603(+)	Eulor6A
697653_0_+_69	chr14:33093444-33093479(+)	UCON11
700890_0_-_65	chr14:35855217-35855366(-)	Eulor6A
714186_0_-_107	chr14:53128581-53128608(-)	MER121
751714_0_-_85	chr14:84779620-84779653(-)	UCON30
753005_0_+_40	chr14:86595882-86595921(+)	UCON30
783832_0_-_73	chr15:33865137-33865158(-)	MER133A
785532_1_-_63	chr15:34979215-34979241(-)	MER121
785532_0_-_103	chr15:34979391-34979424(-)	MER121

786420_0_-_57	chr15:35436668-35436697(-)	MER133A
787092_0_-_65	chr15:35993736-35993832(-)	Eulor5A
798275_0_+_115	chr15:43865498-43865524(+)	X7C_LINE
821528_0_-_96	chr15:64357134-64357156(-)	UCON3
853348_0_-_69	chr15:90707731-90707784(-)	UCON7
861597_0_+_94	chr15:98233883-98233900(+)	Eulor1
872174_0_-_78	chr16:5965366-5965388(-)	Eulor3
881780_0_-_82	chr16:17002623-17002644(-)	Eulor6A
905560_0_-_64	chr16:50405915-50405939(-)	MER121
905867_0_+_68	chr16:50695398-50695444(+)	MER121
917018_0_-_100	chr16:60639392-60639413(-)	MER121
920401_0_+_83	chr16:64684847-64684892(+)	Eulor10
931567_0_+_51	chr16:72032498-72032534(+)	MER135
984571_0_+_105	chr17:30189303-30189321(+)	MER123
1015325_0_+_70	chr17:50225698-50225730(+)	Eulor8
1024163_0_+_84	chr17:56744693-56744735(+)	UCON8
1036020_0_-_69	chr17:66781338-66781363(-)	MER121
1038462_1_-_124	chr17:68911481-68911497(-)	UCON7
1066259_0_+_153	chr18:21498030-21498080(+)	Eulor8
1068544_0_-_89	chr18:23659572-23659590(-)	Eulor2A
1083195_0_+_73	chr18:41146705-41146745(+)	UCON21
1084969_0_+_97	chr18:42888291-42888326(+)	MER123
1091966_0_-_67	chr18:51316122-51316169(-)	MER125
1092513_0_+_129	chr18:51746153-51746176(+)	MER121
1105916_0_-_78	chr18:71369451-71369514(-)	UCON11
1106836_0_-_55	chr18:72345054-72345073(-)	Eulor9C
1107891_0_+_101	chr18:74472718-74472919(+)	MER123
1136689_2_+_91	chr19:35356712-35356733(+)	Eulor5B
1136695_0_+_93	chr19:35387180-35387194(+)	UCON28
1137640_0_-_88	chr19:35962919-35962951(-)	MER121
1137668_1_-_133	chr19:35986024-35986041(-)	UCON18
1137917_0_+_156	chr19:36199466-36199483(+)	Eulor1
1138452_0_-_84	chr19:36589246-36589288(-)	Eulor10
1139164_0_-_65	chr19:37257771-37257787(-)	UCON18
1427009_0_+_75	chr20:37524951-37524982(+)	MER121
1427160_0_-_120	chr20:37678080-37678099(-)	MER125
1427182_0_-_100	chr20:37689430-37689447(-)	MER125
1431929_0_+_129	chr20:41294085-41294112(+)	MER128
1443968_0_-_61	chr20:53838763-53838824(-)	UCON29
1462483_0_+_84	chr21:29777827-29777864(+)	MER127
1463946_0_-_55	chr21:31573085-31573124(-)	Eulor10
1504557_0_+_88	chr22:41047017-41047040(+)	Eulor9A

^aName of the EvoFold locus from the hg18 UCSC Genome Browser annotation

^bGenome coordinates and strand of the EvoFold locus

^cName of the co-located TE