

RT-PCR primers

Gene	Primer1
<i>EGR1</i>	AACGACAGCAGTCCCATTACT
<i>EGR3</i>	AACTCTCTTACTCCGGCTCCTT
<i>NR4A1</i>	CTTCCTGGAGCTCTTCATCCTC
<i>NR4A2</i>	ATCTCTCCACAACCTCCACCAG
<i>RCAN1</i>	AGGGGAAAAGTATGAATTGCAC
<i>IGFBP3</i>	AGCTCCAGGAAATGCTAGTGAG
<i>MEF2C</i>	CATAACATGCCACCATCTGC
<i>GAPDH</i>	ATGACATCAAGAAGGTGGTG
<i>MYC</i>	TATCTGGAAGAAATTCGAGCTG
<i>DUSP5</i>	ATCCTTCCCTTCCTCTACCTG
<i>KDR</i>	TGAAGCTAGGTAAGCCTCTTG
<i>CD34</i>	ACTCCAGAGACAACCTTGAAGC
<i>HLX</i>	ACAACAACAGCAGCAGCAAC
<i>ETS1</i>	GAGATCCTGCAGAAAGAGGATG
<i>CJUN</i>	gaaggaggagcctcagacagt

EP300 SiRNA

Control SiRNA	CCACUACUGGAAUUCGGAAtt (sense)
ETS1 siRNA	CCGACGAGUGAUGGCACUGAA
cJUN siRNA	GCAGUAAGUGUUGAGCUCGGGCUG

DUSP5 3C Primers

probE	5'- /56-FAM/TT CAC AAC ACC C
DUSP5_E25f	GTTTCGCCTTTTATCCAGTGTC
DUSP5_E25c	TGGTCCGTGAGTGTTATCTGTC
DUSP5_E24c	TTCCCATCACCTTACATAAAAGAAA
DUSP5_E22c	GAAGGATCAATAAAGACCGGAAT
DUSP5_E21c	ACCCCGTCTCAACAAAAATAAAA
DUSP5_E15c	GATTGCTGAGAGCTACAGTCTGG
DUSP5_E14c	GCCTCAGCCTCCTGAGTAACTA
DUSP5_E13c	CAATCTCACCTCACACCTCAAG
DUSP5_E12c1	ACACACAGCAGACAGAAGGTACA
DUSP5_E11c	TTGCCTTAGCCTTCTGAGTAGC
DUSP5_E10c	TTTTTCTTCTGCATCACCAATAGA
DUSP5_E9c	AATGGAAGAGAAGCTTGGAAAAG
DUSP5_E8c	ATGTGAATCTACCCAGAGATGGA
DUSP5_E7c	GCATGACAAGTGACAAATGAAAA
DUSP5_E6c	AGCCTGGGTAACAGAGTGAGAC

KDR 3C Primers

ProbE_KDR	5'- /56-FAM/TT CCT GGA C/ZEN
KDR_E2F	ACTTGAAAAATTGTGCTCTCCAA
KDR_E2C	AGGGGGATATCATGGAATGTAGT
KDR_E3F	CACCCATTCTAGACTACCACTCA
KDR_E5F	TCAGCCACCAAGAACTTCTATTC
KDR_E6F	GGGGTGTGGATACAGTTATTGTT
KDR_E7F	ATTTGAGTTTTTTGCTCCCTATCC
KDR_E8F	ATCAATGCCAACAGAAAGAAATG
KDR_E9F	ACCCACAAATAAACCAGCAGAG
KDR_E10F	CTGGCTCCCAAGAATAAAACAC
KDR_E11F	GCACATGCATAAGAAGAAATGG
KDR_E12F	ACAAGCGTGTGAATAACAATGG
KDR_E13F	AGTGGAATCCCTGAATAGACCA
KDR_E14F	AAGGGTCAATTCACCAAGAAGA
KDR_E20F	TCCCAAGACTAAACCAGGAAGA
KDR_E21F	GGAGCTCTTCATGAGCAAAAAT
KDR_E23F	TCCTGTGGTTGCTCTAACAATCT
KDR_E24F	GTCTTCCTCAAAATAGCTACAGCA
KDR_E25F	AAGAGATGCTTCTGAAATGAGTCC
KDR_E26F	TAGGGAGGATTCCCTCTTTTTC

CD34 3C Primers

CD34_Probe	/56-FAM/CCCGGATAAGGGATACTCCA
CD34_E3F2 (ANC)	GGCATTTCCTGGATTTCAGATTTC
CD34_E3C2	ACTGGCTACAATGTGTGTTTGC
CD34_E4F	GTGGGAACCTGCCTGTAAAATC
CD34_E5F	CTTCCTCTGGGGAGGATTAGAT
CD34_E6F	AAAATCAGGCTTTGGAATCAGA
CD34_E11F	ATTTTCATTTCATTTTTCATCAGCA
CD34_E12F	AGCAGGTTTTCAATTAGGGTACTG
CD34_E13F	TTTGTTCCTGACAATAAGATGGA
CD34_E14F	AAGTTAAAGGTCCTATGCAAGCAG
CD34_E15F	AAATAAATGTGGGAAAAAGCAAAG
CD34_E20F	TTGAGCAGAAAGTAGAGTTGCTTG
CD34_E21F	CGGGTAGAGGAACCTCTGTCTG
CD34_E22F	TATCGTAGATCTGGCACAATGC

NR4A1 Primers

NR4A1_Probe	/56-FAM/CC TGG CAC ACA GCA AAC ACC
NR4A1_E1F	GCCTCAGTGTCTTCACCTAGAAA
NR4A1_E2F	CTAGGTGAGGAAGTCAGCCTGT
NR4A1_E3F	TTACAGGTTTCCCATGACAGTG

NR4A1_E4F	GGACTGAAGATAGCCTCTGTGG
NR4A1_E5F	GTGAGTGAGGATGACAGCAGTG
NR4A1_E6F	AATGTACAGGTTCTTGGGATGTG

VWF quantification primer (template loading control)

VWF_Q1	GCAGAACCATGAAACAAGAAGAC
VWF_Q1	CCCTGTTTCATAGGATACAAGCTG
VWF_Q2	ATGAAACTGGACCCCTATCTCTC
VWF_Q2	TAGGCCAATGTCCAGTACAGTTT

VWF control primer (internal ligation control)

VWF_Nprobe	5' - /56-FAM/TG TTT GGT TCA C
VWF_N2F	ACATATCGTCCCAGGATAGGACT
VWF_N3F	AGAAGTGAGTATCACAGCCATCC

Luciferase reporter primer

ID	primer1
Promoter-1	AGGTTCAAGCAATTCTCCTGTCT
Promoter-2	CTTTGGTATATTTCCGACCTGAC
Promoter-3	GGAATGGCCTCCTATAAACTTG
Promoter-4	GAGGGACAGAGAGAAGGAGGATA
Promoter-5	ACCACCACTCTCAAATAAAGCAC
Promoter-6	CAACTGTGGGATGTTCTCTTTCT
Promoter-7	ATTTTCCCTCCGAGAAAGGTT
Promoter-8	CCTCTTTTATCCGATGTTTTCCT
Promoter-9	GGTAGAGGTACAATCGGGGTAAC
Promoter-10	ATTTCCGTTCGTGGAGACTTG
Promoter-11	AATAGCATTTATTCCTGCCCTGT
Promoter-12	GCTGAATGGAGTCCTACACAAAC
Promoter-13	GGGAAGTTGAGAGAAAGTTTGGA
Promoter-14	AAGATGAGGGTCAGACCTGGAG
Promoter-15	TGGACAGTAGACAAAATGGAAAGA
Promoter-16	ATTTACAGAACAGAGCCTTCGTTT
Promoter-17	ACTGTGTAGAAAGAGGAGCAAAGG
Enhancer-1	AGACAGAATCTTGCTCTTGTTGC
Enhancer-2	GGCATTGCAGATGTGATTAATTT
Enhancer-3	CTTTTCCTTTTCGCAGACAATG
Enhancer-4	TCTGAGCATTTTTCCTATTGCAT
Enhancer-5	CCTGCCTGGCATTCTCTATATG
Enhancer-6	CACTTTCCATTTTGACAAACCA

Enhancer-7	AAAAAGGGGAAC TTCATTATGG
Enhancer-8	TGAACCTTACAGTGCTCAATGAAT
Enhancer-9	CGAGATGGACAAATCAGATGAG
Enhancer-10	AGAGGTACTACAGCAAGCACACA
Enhancer-11	GGCAGAGAGTTTTTCCTCTGAA
Enhancer-12	TCACGCTCTTTAGTCCCTCAAT
Enhancer-13	GCCCTGAGTTTCTTGAGTTCTCT
Enhancer-14	GTCTTCAGGTTGAAAACGAGGAG
Enhancer-15	ATATGTTCCAGAGAGTGAACCACA
Enhancer-16	ATCCAGAACGAGAAGGAGACCAT
Enhancer-17	TCAGGGTATGTGTAGGTTTTGTTG
Enhancer-18	AAACTACAGTAGGGAGGGGACCT

eRNA

GENE	primer1
<i>NR4A1</i>	GGCCTCTCACTTCGTAAATCAC
<i>NR4A2</i>	TAGTTGCCAGCTAAGACAGCAG
<i>CD46</i>	TTGCCAGCTAAGACAGCAGTAA
<i>GEM</i>	ATAGATGAGTCACAGGGCCATT
<i>DUSP5</i>	CAGCAGAGGTGTTGCCTAAAAT
<i>HLX</i>	ATCCTCTCCCTTCAGAAGATCC
<i>KDR1</i>	ACAGTCAGGAGATCGAGACCAT
<i>KDR2</i>	AGCTGTGTTTGTTTTACGCAAG
<i>FGF12</i>	ACAGTTTGTTTGAGAGGAAGA
<i>ZSWIM2</i>	TTAGGTGAACCAACATCCCAGT
<i>CD34-1</i>	GGATGCCTAGGGAAGAGAAAGT
<i>NR4A2_adjacent_control</i>	ACAGGAAAAGGAAAAGGAGAGG
<i>CD34_adjacent_control</i>	AAGCAGTAAGAAGACGGTCCAC
<i>NR4A1_adjacent_control</i>	CAGCAGAGGTGTTGCCTAAAAT
<i>DUSP5_adjacent_control</i>	CTGCCTGAGTCACTTCCTCTTT
<i>GEM_adjacent_control</i>	ACCCAGAGCTTCAACAGTAAGC
<i>HLX_adjacent_control</i>	ACAACGTCCATGGTCTGCTAA
<i>KDR_adjacent_control</i>	GGCTTCAAGTCAGGTAGCAGTT
<i>FGF12_adjacent_control</i>	TCTTCTGCCTAGAGCTCTGCTT
<i>ZSWIM_adjacent_control</i>	TAGGAGAGACCAGAGCCAAGAC
<i>GAPDH</i>	ATGACATCAAGAAGGTGGTG

Dynamic H3K27ac primers

HLX_1	GCAGATGTGAATTGGACACAGT
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HLX_2	TGTTGCAATATGGAAGGAAACA
HLX_3	ATCCTCTCCCTTCAGAAGATCC
KDR_1	TTGACTCCCAGAGGAGTTTAGC
KDR_2	CCATATTTGAGAAACCAAGCTG
KDR_3	CACACCGGTTTGTTCATCATACT
NR4A1_1	GGCCTCTCACTTCGTAAATCAC
NR4A1_2	CATCAGACTAGGAGCCAGCTTT
NR4A1_3	AACTCTGAGTGCCTGCTGTGTA
NR4A2_1	CTTTCTCGGTGTGGCTCGTT
NR4A2_2	ACCTTAAGTTTCCCCCAGAtgt
NR4A2_3	CGGGAGAAGTTGAAGGTTGTAA
NOTCH1_1	GGTCTTTCTTCCCTTTCTGCTC
NOTCH1_2	CAGCTCTTTTGTCTGCAAATCTT
NOTCH1_3	AGGCTGTTTGGAGTGTGAAAAA
STAT1_1	GCTTTGGAGCCCTAGCTTTC
STAT1_2	TCTCTTTTACCCGCTTCACTTC
ETS1_Locus	TTCTATAAGCTTTTCCCCACCA
MEF2C_Locus	GCTCATTTTGAGTTTGGCATAAG

ETS1 and c-JUN Chip primers

MEF2C_Locus	CCTCCTTCCCTCCTACAAATCT
KDR_Locus	CACAAAGGTCACTTGTGGTGAT
NR4A1_Locus	GGACCCCTCTTAACTCATTTCC
ETS1_Locus	GAAAGTCCGTCTGATTCTCCAC

p300 and mediator primers

GENE	primer1
NR4A1	CTAGTGACGTAGCGGCTTCC
NR4A2	AAAATAGCAGCAACTCCAGCTC
CD46	GAATGCTGCTGGATGATGACTA
PRKAR1B	CTCAGGCCCTGGTAAGAGAAAGA
RHO	ATCTGCACAGTTCATCACACCT
NR4A1_1	CCTCACCTGAGAACCAGCTC
DUSP5	GCTCACTTTCCACACTGACCT
MYC	CAAGGGAGAGTGAATGAGGAAG
HLX	AGCTGCTAGTCAAAGCCAGTTT
KDR	TCCCTATCAATAACGCCAGAAC
CD34_1	TGAACAAAGCACAATGCTTCTC
KDR_1	TTGCTACAGTCATTCAGCTGGT
ZSWIM2	AGATATTGCACTTGCGAGCAT
HLX_1	GCACAAATATTGAAAGGGGAAG
CD34_2	GGGTGGTCATTTATTTGTGTGA
CD34-3	AGGGCTAGGAAAGAAAGGAGAA

<i>STAT1</i>	AAACCGAAAAGCGAAAGTTAGA
<i>NOTCH1</i>	CAGCTCTTTTGTCTGCAAATCTT
<i>SUFU</i>	TCCCTCCTTATCTCAGTCTTGG
<i>EPHB3</i>	CTGTTCTATCAAGCCAGCTCCT
<i>STAB1</i>	GCAGGATGTTTCTGACTCACAT
<i>EGFL7</i>	GGTGGGAGTTTTCCCAGAAAC

CHIP-seq and RNA-seq 3' primer

Index_1	CAAGCAGAAGACGGCATAACGAGATCGTC
Index_2	CAAGCAGAAGACGGCATAACGAGATACAT
Index_3	CAAGCAGAAGACGGCATAACGAGATGCCI
Index_4	CAAGCAGAAGACGGCATAACGAGATTGGI
Index_5	CAAGCAGAAGACGGCATAACGAGATCACT
Index_6	CAAGCAGAAGACGGCATAACGAGATATTG
Index_7	CAAGCAGAAGACGGCATAACGAGATGATC
Index_8	CAAGCAGAAGACGGCATAACGAGATTCAA
Index_9	CAAGCAGAAGACGGCATAACGAGATCTGA
Index_10	CAAGCAGAAGACGGCATAACGAGATAAGC
Index_11	CAAGCAGAAGACGGCATAACGAGATGTAC
Index_12	CAAGCAGAAGACGGCATAACGAGATTACA

3' adaptor sequence of DHS_seq red letters are mutiplex barcode)

DHS 3' adaptor

DHS_linker2_index1	p-AGTACATCGGTTTCGTATGCCGTCTTCTGC
DHS_linker2_index1	CAAGCAGAAGACGGCATAACGAACCGATGT
DHS_linker2_index2	p-AGTTGGTCA GTTCGTATGCCGTCTTCTGC
DHS_linker2_index2	CAAGCAGAAGACGGCATAACGAAC TGACCA
DHS_linker3_index3	p-AGTATTGGCGTTCGTATGCCGTCTTCTGC
DHS_linker3_index3	CAAGCAGAAGACGGCATAACGAACGCCAAT

DHS-seq 5' adaptor

DHS_linker1	Bio-ACAGGTTTCAGAGTTCTACAGTCCGAC
DHS_linker1	GTCGGACTGTAGAACTCTGAAC-Amm

DHS_seq sequence primer

CCACCGACAGGTTTCAGAGTTCTACAGTCCGAC

primer2

GCTGCTGTGGAAACAGGTAGTC
TGAGGCTAATGATGTTGTCCTG
GCCAGGATACTGTCAATCCAGT
GCGATTGCTTAAAGGAGAAGAG
TCCTGGTCTGGATAATTTTGG
CTGTCTTTAGCATGCCCTTTCT
CGTGTGTTGTGGGTATCTCG
CATAACAGGAAATGAGCTTG
ACTCTGGTTCACCATGTCTCCT
GCTTCTTGAAAGTGGGAGCTAA
TCACTGTGTGTTGCTCCTTCT
TTTCACTTCTCTGATGCCTGAA
GGTCAATTCCAAATTTGAGGTC
GGAGCGTCTGATAGGACTCTGT
aaggttttcacttttctccag

UUCCGAAUCCAGUAGUGGat (antisense From ABI (S4696)

From Qiagen (1027280)

GGCUGCUCACUACCGUGACUU

From Qiagen SI00074263

CAGCCCGAGCUAACACUUAUCUGCUA

From IDT (HSC.RNAI.N002228.12.2)

'TC ACA TGG TGA GGG /36-TAMSp/ -3 '

↓/A TCT CTG TGT ATG TTC CAC CA/3IABkFQ/ -3'

↓TCCTGCA/36-TAMSp/

↓CAA TAA A/3BHQ_1/

'AA AGC CAC TTC AAA CCA /36-TAMSp/ -3'

primer2	Chromatin	start	end
GGAGCCACAGCTTGTCTTTTAT	chr20	30,191,351	30,193,086
TTAAGGTGGTCACGTAGGTTTC	chr2	157,189,294	157,190,940
AGATTCCGCTCTTGCTACATTC	chr2	191,512,190	191,513,841
GACTAGCACTGCAAAGAGAGGAG	chr1	156,083,293	156,086,003
ATAAGGCCAAATATGGGTGTTTC	chr10	112,255,625	112,257,616
AAGGTAGTCCCACCTTCTTCATCC	chr4	74,965,007	74,966,306
GTCATTGCGTGAACACTTTTACA	chr2	191,514,093	191,515,253
GAAAGAGGAGAAGCAGAGGAAGT	chr1	183,439,982	183,441,508
GACAGATGCTTTCCACTTTCAAC	chr5	64,777,712	64,779,293
GTACTCGGTCTGATGATTTGCTT	chr21	27,107,955	27,108,977
ACATTCCATTTTGTTGTTTCCAG	chr4	73,934,239	73,936,421
TAAAATCATCCACAAGGGAAGAA	chr6	132,272,486	132,274,463
ATCTGGGTACAGAGTGAGAGTGG	chr7	100,425,257	100,427,497
AGCAGTGAAGTGTTTCAGAGTGG	chr9	139,556,506	139,558,801
CCAAGTAACTCACCACCTACCTG	chr1	159,747,587	159,750,889
CTACTTGACGGTAGGGAGAACATT	chr14	75,593,049	75,594,799
AACGCAATGATATTTACAGGGATT	chr4	126,235,379	126,237,536
CCCCGTCTTACCAACTACTTTCT	chr3	184,176,526	184,178,236
TTTGTGGGCCTTTATCTACTCAA	chr10	112,219,031	112,220,987
CTTTTCTACTCGCGCAGAGCGT	chr2	157,190,064	157,191,847
GAGAAGTCTCCCAAAGTGAGGA	chr1	208,021,194	208,022,734
TGTACATCCATGTGTCCATTCA	chr7	649,650	651,519
AAAACAGGGCAAGGTGAATAA	chr1	113,247,041	113,248,383

TCAATCTGCTTCTGTGTAAGCAA	chr5	88,122,839	88,125,470
GGATAATGGCTTTGGCAAAAAT	chr5	88,109,533	88,111,464
TCTACTGGAAAAAGCCTGCAAT	chr1	208,065,681	208,066,946
AGCTGATTTCTAGGAGCAGGAAT	chr4	123,703,795	123,705,439
AGAGATTGAAGTCAGGGCTTTG	chr1	221,046,701	221,048,386
ATTTCTTCACCACCAGGATGAT	chr4	56,049,877	56,051,577
TATGGGTAGACCTCTCTGAATGG	chr3	184,165,943	184,167,746
AGAGAGATGCCACCTGGGCTAT	chr3	52,524,077	52,525,914
GCTCAGTTAATTTGGCATTAAAGGT	chr2	191,843,260	191,845,571
CTTCTCAACTCATGCCACCTACTA	chr12	53,343,075	53,344,509
TTTGTTGCTGTTGTTGTTCTTTTT	chr1	59,358,474	59,360,404
TTTTCAATGGGTGACTTTTTCTG	chr1	16,471,458	16,473,663

pirmer2	Chromatin	start	end
GGCTCTTAAAAATCCTCTGCAA	chr12	52,427,090	52,427,428
TCTCCCTTTGCTAGTGGAAGTC	chr1	208,021,887	208,022,198
TCTCCCTTTGCTAGTGGAAGTC	chr1	208,021,958	208,022,373
GCAGCTCAAGCAGTTAGGATTT	chr8	95,254,708	95,255,039
CAAAGATGGAAGTGGAGAAAGG	chr10	112,220,152	112,220,710
AAACCTTCTTCCCTGTGAGACA	chr1	221,047,754	221,048,182
TCCCAAGTAGCTGGGACTACAG	chr4	55,808,552	55,809,005
GGCCATTTCATTCATTCATTTT	chr4	56,050,177	56,050,523
GTAAGTGGCTCCAGATCACACA	chr3	192,675,060	192,675,457
GGCAAACAAGAATAACAAGAGAAAA	chr2	188,167,718	188,168,140
CCACCTTGGTCCTACTCAGAAC	chr1	208,096,369	208,096,832
CAACTGTGTGCTTCCAAATGAT	chr2	158,038,851	158,039,395
GTCGCCTTTCATCCTTTACAGAC	chr1	208,136,348	208,136,842
CAAAGATGGAAGTGGAGAAAGG	chr12	52,457,424	52,458,015
TGACAATGGTTGAGGAATCAAG	chr10	11,220,724	112,207,747
TCTCCATCTCTTGACCTTGTGA	chr8	95,070,852	95,071,402
CATTATTTCTTGCTGGCTTTTC	chr1	221,017,385	221,017,737
GGAGAAGGAGCCAGGATTACTT	chr4	56,038,552	56,038,990
AAACTGTGGGACTCTTGATGGT	chr3	192,675,007	192,675,418
TCCTTTTGCTGTGATACTTGGA	chr2	188,164,078	188,164,523
CATACCAGGAAATGAGCTTG			

ACACACTTCCCTGTCCTGAAAT	chr1	221,046,966	221,047,263
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ACCTGCTGGACCATCTCTACAT	chr1	221,047,400	221,047,830
AAACCTTCTTCCCTGTGAGACA	chr1	221,047,821	221,048,140
TTTATGGCCTCTCATTTGTCCCT	chr4	55,779,302	55,779,551
GACAATGGGACACACAAGAAAA	chr4	55,779,575	55,779,818
TATAGAAGCCAAGGTGCAGAGG	chr4	55,779,862	55,780,129
GGCTCTTAAAAATCCTCTGCAA	chr12	52,427,057	52,427,468
GCAGATAGGAAAGGTGAGGAGA	chr12	52,428,017	52,428,428
AGATGGTGGAAGAAGCAGTCTC	chr12	52,428,759	52,429,133
CTGCAGATTAGGGTTGAGCAG	chr2	157,189,385	157,189,790
ACCGAGCTCATGCTAATATGCT	chr2	157,189,732	157,190,072
AGGACACTTTTCAGCTCTCTGG	chr2	157,190,048	157,190,729
CAATCTCGTGGTTTTGTGCTC	chr9	139,424,129	139,424,442
GAGCCAGAGGAGGAAACCTG	chr9	139,424,496	139,424,809
CTCCAACCTCAAGAGGTTTGTCC	chr9	139,424,954	139,425,319
CCTCTCAATCCCAGTCCTTCT	chr2	191,884,926	191,885,322
ACGCCTATAGAAACTGCCAGAC	chr2	191,885,331	191,885,674
AGGAGGAGGAGGAGGACTGTT	chr11	128391486	128391859
ATGTGTCACTCAAGGGAAC TTGT	chr5	88122749	88123129

TTTATTGTTCTGTTGCTGAC	chr5	88122976	88123344
ACAGTGTGTGAGTTGTGGAACC	chr4	55779876	55780287
CCAGGATTCCATTACCTCACC	chr12	52426681	52427072
CACGTCCTGTGTGTCAGTCTTT	chr11	128392441	128392822

pirmer2	Chromatin	start	end
GACGGCTTCCAGATTTTTCTC	chr12	52,426,922	52,427,218
GTTTCCGACTGCCTGAAAATAG	chr2	157,191,106	157,191,571
CACACCCAAGGTTACATCCTCT	chr1	208,021,522	208,021,939
CTTCTTGACCTTGGGTGAAGTT	chr7	650,474	650,889
AGCCTTGACTTCATCTCAGCTC	chr1	113,247,542	113,247,867
CCTCATCAATGGGGCTAAAAAT	chr12	52,426,769	52,427,177
GTAGGTCCCCAACTCTTCCTTC	chr10	112,219,902	112,220,261
TCACCCTACAGAGCCACAGAAT	chr8	129,061,463	129,061,773
ACCTGCTGGACCATCTCTACAT	chr1	221,047,504	221,047,824
TGAGTCCTACAGCTCACAGGAA	chr4	55,808,115	55,808,556
TCTCATGAACAAAATGGTGAGG	chr1	208,066,210	208,066,553
GGAACCTCTGTGTTTCCAAAAGG	chr4	56,050,502	56,050,848
GTGAATCACATCCTGGTCTTCA	chr2	188,167,352	188,167,646
TCTCAAAATAGAAGCGGCCTTA	chr1	221,049,974	221,050,353
AGCTATTCTTAGCCGAGGTGTG	chr1	208,095,976	208,096,281
TCTGCTGTAAAAGAGGATGCAG	chr1	208,096,993	208,097,279

GAGAAACCGTTGGGAGGAAG	chr2	191,885,035	191,885,416
GAGCCAGAGGAGGAAACCTG	chr9	139,424,561	139,424,886
CAAAAGACTTCCTTTCCCTTCC	chr10	104,359,525	104,359,899
TTCCATACAGCATTGTTTCCAA	chr3	184,166,631	184,167,011
CCACACAGGAAAGAATCATGG	chr3	52,525,006	52,525,292
GACCGCAGTCTCAGTCACAG	chr9	139,508,787	139,509,147

;ATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
 ?CGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
 ?AAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
 ?CAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
 ?GTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
 ;GCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
 ?TGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
 AGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
 ATCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
 ?TAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
 ;CCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
 AAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT

.TTG
 ACTNN
 .TTG
 ACTNN
 .TTG
 ACTNN

cluster

H1

H1

H1

H1

H1

H1

H1

H1

H4-12

H4-12

H4-12

H4-12

H0

H0

H0

H0

H0

H1

H1

H1

H1

H1

H1

H4-12
H4-12
H4-12
H4-12
H4-12
H4-12
H0
H0
H0
H0
H0
H0

cluster

H1
H1
H1
H1
H1
H4-12
H4-12
H4-12
H4-12
H4-12
H4-12
H1
H1
H1
H1
H1
H4-12
H4-12
H4-12
H4-12

Cluster

H1

H1

H1

H1

H1

H1

H1

H1

H4-12

H4-12

H4-12

H4-12

H4-12

H4-12

H4-12

H4-12

H0
H0
H0
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