Name	seq	Type
Insuline2a	ACAGGGGTGTGGGGACAGGGGTGTGGGG	1
12668310-PC12-16	AGAGTGGGGGGGATGTAGGTGGGTT	1
GUK1	AGCGGGAGAAGACGGGCTGGGAGGGCGC	1
29cn3	AGGGAAGAGAAAGGGGCCAGGGCCTGGGA	1
c-kit1-87-UP	AGGGAGGGCGCTGGGAGGAGGG	1
41cc1	AGGGATGGAACCGGGGAGGGCGGCGGGGGGGGGGGGGGGGT	1
TSG24	AGGGATTGGGATTGGGATTGGGTT	1
32B3(K-Ras)	AGGGCGGTGTGGGAAGAGGGAAGAGGGGGAGG	1
35B1(K-Ras)	AGGGCGGTGTGGGAAGAGGGAAGAGGGGGAGGCAG	1
CEB1	AGGGGGGAGGGAGGGTGG	1
26gtel4	AGGGGTTAGGGGTTAGGGGTTAGGGG	1
38	AGGGTCAGGGTCAGGGTCAGGG	1
Ceb25	AGGGTGGGTGTAAGTGTGGGTGGGT	1
22Ag	AGGGTTAGGGTTAGGGTTAGGG	1
18gtel2	AGGTTAGGTTAGGTTAGG	1
12668310-PC12-9	AGTGGGGGTAGGGGATAGGGTAGGC	1
21531729-CD16acMet-7	ATCACGTGGTGGGCAAATAACCGGTTGGGGTGGGTCGAGG	1
7542922-HIV-1-RT-3	CAGGCGTTAGGGAAGGGCGTCGAAAGCAGGGTGGG	1
14h3	CCCGGGACGGGGGCCGGCGGGCCACGGGCCC	1
16518777B-Ricin-2	CCGTAGGTTCGGGGCGGAGTGGTCCGGAAGGTGGCGTGG	1
16518777A-Ricin-1	CCGTAGGTTCGGGGTCGGAGTGGTCCGGAAGGTGGCGTGG	1
30cc3	CGGAGGGGTGGGGGAGGGGTGGGGGAGGGT	1
18617415-Tetracyclines-3	CGGGAGGGCGGGGTGTGGTATGTATTGAGCGTGGTCCGTG	1
c-kit2	CGGGCGGGCGCGAGGGAGGGGT	1
32cc9	CGGGGGGGGGGGGGGGGCGGGGGAGGGAGGC	1
MCM2	GAAGGGACACGGAGGGGCGGGCCAGAGGGTCC	1
21531729-CD16acMet-3	GAGCGGGGACGAACACATATGGGGAAGTGGCTTGGGGTGG	1
12668310-PC12-13	GAGGAGGGAGAATAGGGGTGGGTGG	1
21531729-CD16acMet-2	GAGTGCGTAATGGTACGATTTGGGAAGTGGCTTGGGGTGG	1
12954786-TTF1-2	GATACACGGGCGGAGGAGGTGGGGGGGGGTAGGTGGGTAT	1
20971648-rHuEPO-a-Ma-2	GATTGAAAGGTCTGTTTTTGGGGTTGGTTTGGGTCAATA	1
UTX	GCCGGGCGGGGAGGGGGGGTCA	1
14h2	GCCGGGGCGGCTCGGGACGGGGCCCGGGGAGCGTGGGTGGGACC	1
cellobiose-1	GCGGGGTTGGGCGGGTGGGTTCGCTGGGCAGGGGGCGAGTG	1
12h	GCTGGGCGAGGGGTGGGAGCAGACGGGCTG	1
12668310-PC12-10	GCTGGGGTGTTGGGTGTGGGGGTGA	1
PSMA2	GCTGGGTTGGGGCGGGGGGAGCGGGACG	1
18617415-Tetracyclines-2	GGAGGAACGGGTTCCAGTGTGGGGTCTATCGGGGCGTGCG	1
16518777B-Ricin-3	GGAGGCGCGATGTAGGTATGTGAGGGCGGCGCGGTGGGCG	1
CLN003	GGAGGGAAAAGTTATCAGGCTGGATGGTAGCTCGGTCGGGGTGGGTGGGTTGGCAAGTCT	1
c-kit*	GGCGAGGAGGGGCGTGGCCGGC	1

H-Bi-G4 GGGACGTAGTGGGGGGACGTAGTGGG 1
X3ACT GGGACTGGGACTGGGACTGGG 1
c-Kit1 GGGAGGGCGCTGGGAGGAGGG 1
A9A GGGAGGGTGTAAGTGTGGGAGGG 1
A9C GGGAGGGTGTAAGTGTGGGCGGG 1
A9T GGGAGGGTGTAAGTGTGGGTGGG 1
VEGF GGGAGGGTTGGGGTGGG 1
A3A GGGAGGGTTTGGGAGGG 1
A3C GGGAGGGTTTGGGCGGG 1
A3T GGGAGGGTTTGGGTGGG 1
A6A GGGAGGGTTTTTTGGGAGGG 1
A6C GGGAGGGTTTTTTGGGCGGG 1
A6T GGGAGGGTTTTTTGGGTGGG 1
TSG4 GGGATTGGGATTGGGATTGGGTT 1
18617415-Tetracyclines-1 GGGCAGCGGTGGTGTGGCGGGATCTGGGGTTGTGCGGTGT
1
VAV1 GGGCAGGGAGGGAACTGGG 1
23c17d GGGCCTGTCAGGGTGGGCTAGGG 1
25c17d GGGCCTGTCAGGGTTTGGGTTTGGG 1
25c17b GGGCCTGTTGGGGTTTGGGTTTGGG 1
24c16a GGGCCTGTTGGGTTTGGGTTTGGG 1
25c17c GGGCCTTTCAGGGTTTGGGTTTGGG 1
BCL-2promoter GGGCGCGGGAGGAAGGGGGCGGG 1
BCL-2promoter-modified GGGCGCGGGAGGAATTGGGCGGG 1
25DDX GGGCGGGAUAGAGAGCGUGGGCGGG 1
C-Kit2GG GGGCGGGCGCGAGGGAGGGG 1
AKT1 GGGCGGGCGGCTCCGGGCGCGGG 1
B-raf GGGCGGGGAGGGGGAAGGGA 1
18617415-Tetracyclines-7 GGGCGGGGGTGCTGGGGGTGGAGTGCTGCGTGCTGCGG
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C9A GGGCGGGTGTAAGTGTGGGAGGG 1
C9C GGGCGGGTGTAAGTGTGGGCGGG 1
C9T GGGCGGGTGTAAGTGTGGGTGGG 1
C3A GGGCGGGTTTGGGAGGG 1
C3C GGGCGGGTTTGGGCGGG 1
C3T GGGCGGGTTTGGGTGGG 1
C6A GGGCGGGTTTTTTGGGAGGG 1
C6C GGGCGGGTTTTTTGGGCGGG 1
C6T GGGCGGGTTTTTTGGGTGGG 1
27KRas GGGCGGTGTGGGAAGAGGGAAGAGGGG 1
21CTA GGGCTAGGGCTAGGGCTAGGG 1
23c37d GGGCTAGGGTGGGCCTGTCAGGG 1
V-545195 GGGGAAAAAGGGGGGGGGGGGGGGGGGGG 1
IV-1242540 GGGGAGGGGAAGGGGAGGG 1
16518777A-Ricin-4 GGGGGAGGACGCGTAGTGGGGGGCCCATGGTTGTGTGG
1
15025912-NS5B-18 GGGGTAGGATAGGGTNTGGAAGGAGGTGCCCCGT 1
Gla26 GGGGTCTGGGTGCTGTGGGGTCTGGG 1
93del GGGGTGGGAGGAGGGT 1
XII-rDNA GGGGTTACCGCAAAATGGATAGATGGACCGGGGCACACCGGGTAGGGGTCCGGAGGG
1
Tet22 GGGGTTGGGGTTGGGGTTGGGG 1
0xy3,5/0xy28 GGGGTTTTGGGGTTTTGGGGTTTTGGGG 1
IX-356348 GGGTACGGTGGGTAATAAGGGAAGGTATCGGG 1

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25c17a   GGGTAGCATTGGGTTTGGGTTTGGG 1
Gia18    GGGTAGGGTAGGGTAGGG        1
X3TCA    GGGTCAGGGTCAGGGTCAGGG     1
X-106443 GGGTCCTCCAAGGGGTAAAACTTACATGGGATGGTGGGGTCACATGGG   1
23c27d   GGGTGGGCCTGTCAGGGCTAGGG   1
T30695(orT30923) GGGTGGGTGGGTGGGT 1
T95      GGGTGGGTGGGTGGGT 1
T9A      GGGTGGGTGTAAGTGTGGGAGGG   1
T9C      GGGTGGGTGTAAGTGTGGGCGGG   1
T9T      GGGTGGGTGTAAGTGTGGGTGGG   1
T3A      GGGTGGGTTTGGGAGGG         1
T3C      GGGTGGGTTTGGGCGGG         1
T3T      GGGTGGGTTTGGGTGGG         1
T6A      GGGTGGGTTTTTTGGGAGGG      1
T6C      GGGTGGGTTTTTTGGGCGGG      1
T6T      GGGTGGGTTTTTTGGGTGGG      1
f191t    GGGTGGGTTTTTTTTTGGGTGGG   1
f1E1t    GGGTGGGTTTTTTTTTTTTTTTGGGTGGG     1
32T1H1   GGGTGGGTTTTTTTTTTTTTTTTTGGGTGGG  1
f1K1t    GGGTGGGTTTTTTTTTTTTTTTTTTTTGGGTGGG        1
38T1N1   GGGTGGGTTTTTTTTTTTTTTTTTTTTTTTTGGGTGGG    1
f1S1t    GGGTGGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGTGGG       1
12668310-PC12-23 GGGTGTGAGAGGTTGAGGGGGTTCG 1
12668310-PC12-7  GGGTGTGGGAGGTGATGGGGTAGGT 1
Scer21   GGGTGTGGGTGTGGGTGTGGG     1
27rap    GGGTGTGTGGGTGTGTGGGTGTGTGGG       1
Tom24    GGGTTAAGGGTTAAGGGTTAAGGG  1
Hum21    GGGTTAGGGTTAGGGTTAGGG     1
22gt     GGGTTAGGGTTAGGGTTAGGGT    1
24g      GGGTTAGGGTTAGGGTTAGGGTTA  1
45Ag     GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG      1
PlasC24  GGGTTCAGGGTTCAGGGTTCAGGG  1
19apt    GGGTTGGGTGTGGGTTGGG       1
19G2     GGGTTGGGTTAGGGTTGGG       1
20G1     GGGTTGGGTTTTGGGTTGGG      1
Ara24-1  GGGTTTAGGGTTTAGGGTTTAGGG  1
21sAAA   GGGTTTGGGAAAGGGTTTGGG     1
21sAAC   GGGTTTGGGAACGGGTTTGGG     1
21sAAT   GGGTTTGGGAATGGGTTTGGG     1
21sACA   GGGTTTGGGACAGGGTTTGGG     1
21sACC   GGGTTTGGGACCGGGTTTGGG     1
21sACT   GGGTTTGGGACTGGGTTTGGG     1
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21sAGC   GGGTTTGGGAGCGGGTTTGGG     1
21sAGT   GGGTTTGGGAGTGGGTTTGGG     1
21sATA   GGGTTTGGGATAGGGTTTGGG     1
21sATC   GGGTTTGGGATCGGGTTTGGG     1
21sATT   GGGTTTGGGATTGGGTTTGGG     1
21sCAA   GGGTTTGGGCAAGGGTTTGGG     1
21sCAC   GGGTTTGGGCACGGGTTTGGG     1
21sCAT   GGGTTTGGGCATGGGTTTGGG     1
21sCCA   GGGTTTGGGCCAGGGTTTGGG     1
21sCCC   GGGTTTGGGCCCGGGTTTGGG     1
21sCCT   GGGTTTGGGCCTGGGTTTGGG     1
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25c27d   GGGTTTGGGCCTGTCAGGGTTTGGG 1
25c27b   GGGTTTGGGCCTGTTGGGGTTTGGG 1
24c26a   GGGTTTGGGCCTGTTGGGTTTGGG  1
25c27c   GGGTTTGGGCCTTTCAGGGTTTGGG 1
21sCGA   GGGTTTGGGCGAGGGTTTGGG     1
21sCGC   GGGTTTGGGCGCGGGTTTGGG     1
21sCGT   GGGTTTGGGCGTGGGTTTGGG     1
21sCTA   GGGTTTGGGCTAGGGTTTGGG     1
21sCTC   GGGTTTGGGCTCGGGTTTGGG     1
21sCTT   GGGTTTGGGCTTGGGTTTGGG     1
21sTAA   GGGTTTGGGTAAGGGTTTGGG     1
21sTAC   GGGTTTGGGTACGGGTTTGGG     1
25c27a   GGGTTTGGGTAGCATTGGGTTTGGG 1
21sTAT   GGGTTTGGGTATGGGTTTGGG     1
21sTCA   GGGTTTGGGTCAGGGTTTGGG     1
21sTCC   GGGTTTGGGTCCGGGTTTGGG     1
21sTCT   GGGTTTGGGTCTGGGTTTGGG     1
21sTGA   GGGTTTGGGTGAGGGTTTGGG     1
21sTGC   GGGTTTGGGTGCGGGTTTGGG     1
19T313   GGGTTTGGGTGGGTTTGGG       1
21sTGT   GGGTTTGGGTGTGGGTTTGGG     1
21sTTA   GGGTTTGGGTTAGGGTTTGGG     1
21sTTC   GGGTTTGGGTTCGGGTTTGGG     1
20T323   GGGTTTGGGTTGGGTTTGGG      1
25c37d   GGGTTTGGGTTTGGGCCTGTCAGGG 1
24c36a   GGGTTTGGGTTTGGGCCTGTTGGG  1
25c37b   GGGTTTGGGTTTGGGCCTGTTGGGG 1
25c37c   GGGTTTGGGTTTGGGCCTTTCAGGG 1
Par21    GGGTTTGGGTTTGGGTTTGGG     1
22T343   GGGTTTGGGTTTTGGGTTTGGG    1
23T353   GGGTTTGGGTTTTTGGGTTTGGG   1
24T363   GGGTTTGGGTTTTTTGGGTTTGGG  1
25T373   GGGTTTGGGTTTTTTTGGGTTTGGG 1
f393t    GGGTTTGGGTTTTTTTTTGGGTTTGGG       1
f3E3t    GGGTTTGGGTTTTTTTTTTTTTTTGGGTTTGGG 1
f3K3t    GGGTTTGGGTTTTTTTTTTTTTTTTTTTTTGGGTTTGGG    1
f3S3t    GGGTTTGGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGTTTGGG   1
Chla27   GGGTTTTAGGGTTTTAGGGTTTTAGGG       1
Bom17    GGTTAGGTTAGGTTAGG         1
12668310-PC12-17 GGTTGGATGTAAGGTTGGAGGGGGG 1
TBA      GGTTGGTGTGGTTGG  1
15G1     GGTTGGTTAGGTTGG  1
15GT     GGTTGGTTTGGTTGG  1
16G1     GGTTGGTTTTGGTTGG 1
21531729-CD16acMet-11    GTAGGTGGGGGACTGGGGACGGGTATGGGCACACGGTAT
1
cellobiose-3     GTCAAGGTGGGTGGGTGGGGTTGGTTGTTGTTTTGA      1
PS2,M    GTGGGTAGGGCGGGTTGG        1
T30177(orI100-15)         GTGGTGGGTGGGTGGGT         1
27CB3    TAAGGGTGGGTGTAAGTGTGGGTGGGT       1
29CB3    TAAGGGTGGGTGTAAGTGTGGGTGGGTGT     1
cellobiose-2     TAGCGGGTGTGGTGGGTGGGGGAGGCATGGTTTTTGGTAA  1
25TAG    TAGGGTTAGGGTTAGGGTTAGGGATT        1
12668310-PC12-4  TATGGGGGTGGGTCAGGTTTCGGTA 1
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NFKB2 TCAGGGTGGGGGCCCCGAGGGCTGGGGCCG 1
21704505-FADGDH-1 TCCGGGGGGCTGGGCAGGGGGGTAACTTTC 1
14744035-HIV-1NucleocapsidProtein-4
TCGAGGGGTGTGCAAGGCGGGTCAACGGGCCTTATTTGGTGCTTAGGTA 1
12668310-PC12-2 TGAGGGTCTAGGGTGGTGGGGTGGA 1
c-Myc TGAGGGTGGGTAGGGTGGGTAA 1
Pu24T TGAGGGTGGTGAGGGTGGGGAAGG 1
12668310-PC12-3 TGATGGATGTGGGGATGCGGGGGCG 1
PRO1 TGGCCTGGGCGGGACTGGG 1
12954786-TTF1-3 TGGCTAGTGGGTAAGGGGCGGGAGGGTGACAGGGCGATCC 1
39cn1 TGGGCAGGGGAGACACTGGGATCTGAGGGTCTGGGT 1
27cn2 TGGGCCAAGGGCAGAGAAGGGCTGGGA 1
29cn4 TGGGCCGTGTGGGCAGAGGGCACATGGGC 1
52cc6 TGGGCGGGGGAGGGAGGGAGGGAGGGGGTTGAGGGTGGGGATGCCAAGGGGT
1
Pu27 TGGGGAGGGTGGGGAGGGTGGGGAAGG 1
29cc2 TGGGGGATGGGGTTGGAATGGGGGCGGGA 1
23cc4 TGGGGGCGGGGAGGGAAGGGGGT 1
35cc8 TGGGGGGAGGGGCGGAGGGGTGGGGTCGCGCGGGT 1
16518777A-Ricin-3 TGGGGGTCGGGATACGGTCAGTGGTGGTGAGTGGTAACGG
1
(TG5T)4 TGGGGGTTGGGGGTTGGGGGTTGGGGGT 1
32cc7 TGGGGTGGGGGTGGAAAGGGGGTGGGGGTGGT 1
29cc5 TGGGGTGGGGGTGGGGGTGGTGGTGGGGC 1
(TG4T)4 TGGGGTTGGGGTTGGGGTTGGGGT 1
12668310-PC12-15 TGGGTAGGTTCGAGGGGTGGGTGTG 1
25CD3 TGGGTGGGTTTAATTTTGGGTGGGA 1
33CB1 TGGGTGTAAGTGTGGGTGGGTGTAATTGTGGGT 1
12668310-PC12-1 TGGTTGGGGATAGAGGTGGGTGTTT 1
15984861-NeuropeptideY-12 TGTGAAGGGGGGTACATGACGGGGACTGGCCGGACTACAG
1
14h1 TGTGGGGTAGGGGGAGGGGGGAGGGATA 1
20h TGTGGGGTCGGGGGAGGGGGGAGGGATA 1
T30177-T TGTGGTGGGTGGGTGGGT 1
12954786-TTF1-5 TTGGGGTGGGAGGGCGGGTTAACAAAGATAGCGCAACAGG 1
T95-2T TTGGGTGGGTGGGTGGGT 1
24TTG TTGGGTTAGGGTTAGGGTTAGGGA 1
T30177-TT(orTB-1) TTGTGGTGGGTGGGTGGGT 1
26gsc TTTGTGGGTGTGGGTGTGGGTGTGGG 1
G4CT-pallidum GGGGCTGGGGCTGGGGCTGGGG 1
GAG AGCGGGGGAGAAUUAGAUAAAUGGGAAAAAAUUCGGUUAAGGCCAGGGGGAAA
1
Cppt1 TTTTAAAAGAAAAGGGGGGATTGGGGGGTACAGTGCAGGGG 1
Cppt2 TTTTAAAAGAAGGGGAGGAATAGGGGATATGA 1
Promoter GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGTGGCCTGGGCGGGACTGGGGAGTGG
1
Nef8528 GAGGAGGAGGTGGGT 1
Nef8547 GGTCTTAAAGGTACCTGAGGTCTGACTGG 1
Nef8624 GGGGGGACTGGAAGGG 1
HPV3 GGGCTTGGGTGGGCGCTTGGG 1
HPV9 GGGAGTGGGAGCGGGAACGGGAACGGGACTGGGA 1
HPV9-1 CGGGAACGGGAACGGGACTGGGA 1
HPV9-2 GTGGGAGCGGGAACGGGAACGGGA 1
HPV9-324 CCGGGAGTGGGAGCGGGAACGGGA 1

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HPV255   GGGAGCGGGACTGGGACCGGGACCGGGACCGGG 1
HPV25-1  GGGAGCGGGACTGGGACCGGGACCGGGA      1
HPV25-2  GGGAGCGGGACTGGGACCGGGA    1
HPV25-3  GGGACTGGGACCGGGACCGGGA    1
HPV32    GGGAGTATGGGTAACGGGGGGGG   1
HPV42    GGGACTATGGGTAACGGGGGGG    1
HPV52    GGGTAGGGCAGGGGACACAGGGTAGGG       1
HPV52-122        GGGCAGGGGACACAGGGTAGGG    1
HPV52-223        GGGTAGGGCAGGGGACACAGGGT   1
HPV-5729 GGGAAAGGGTACCTCGAGGGGCCGCGGGG     1
HPV-5823 GGGCAGGGTAGGGCAATTTAGGG   1
HT       GGGTTAGGGTTAGGGTTAGGG     1
A        GGATGGGGTGGGGAGG 1
Ac       AGATGGAGTGGAGAGG 1
B        GGGGGATGCGGGGG   1
Bc       AGGAGATGCAGGAG   1
C        GGAGGGTGGATGG    1
Cc       AGAGGGTAGATGG    1
d(G4C2)4 GGGGCCGGGGCCGGGGCCGGGGC   1
CatG4    TGGGTAGGGCGGGTTGGGAAA     1
J19-TT   TTGGGTGGGTGGGTGGGT        1
AGRO100  GGTGGTGGTGGTTGTGGTGGTGGTGG        1
CSBIIWT  GAAGCGGGGGAGGGGGGGUUUGGUGGAAAU    1
G4TERT1  GGGGTGAAAGGGGCCCTGGGCTTGGG        1
G4TERT2  GGGGGCCTTGGGGCTCGGCAGGGGTGAAAGGGG 1
VNTR6-1  GGGGTAGGTGGGGATCTGTGGGATTGG       1
GTERT-060        AGGGGAGGGGCTGGGAGGGC      1
GTERT-110        AGGGGTCGGGTCGGGGCGGGGT    1
G3T6     GGGTTTTTTGGGTTTTTTGGGTTTTTTGGG    1
G4T6     GGGGTTTTTTGGGGTTTTTTGGGGTTTTTTGGG 1
G4T5     GGGGTTTTTGGGGTTTTTGGGGTTTTTGGG    1
SMG3T6   TCACAGGGTTTTTTGGGTTTTTTGGGTTTTTTGGGACAA    1
SMG4T6   TCACAGGGGTTTTTTGGGGTTTTTTGGGGTTTTTTGGGGACAA        1
SMG4T5   TCACAGGGGTTTTTGGGGTTTTTGGGGTTTTTGGGGACAA   1
CanG1    TGGGTGGGACTATTGGGACGGGT   1
CanG2    TGGGTGGGACTATTGGGACAGGGC  1
CanG3    TGGGGCTGGGGTTACGGGGCCAGTGGGGT     1
LysG1    TGGGACCATTGAGGGTGGGAAATTGGACAATGGGGA       1
LysG3    CGGGGTCCGAGGGGATTCCTAAGGGGGTTCTGGGGA       1
LysG4    CGGGCGGGTGGGTTGGCCGAAGGGT 1
LysG5    CGGGCGGGTGGGTTGGCCGAGGGT  1
LysG6    CGGGCTCACGGGTGGGTATGGGC   1
CDC25G4-1        AGGGCGGGACTGAGGGCGGGGC    1
CDC25G4-2        CGGGGTGGGCGGGGGGCGAGGGA   1
URA3G1   CGGGGTGGTGGGCCCAGGGATTGTTAGCGGGT  1
URA3G2   AGGGACATGGGTGGGAGGGA      1
GTERT-051        AGGGCGGGGCCGCGGAAAGGAAGGGGAGGGGC  1
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GTERT-076        TGGGAGGGCCCGGAGGGGGCTGGGC 1
GTERT-082        AGGGCCCGGAGGGGGCTGGGCCGGGGA       1
GTERT-089        AGGGGGCTGGGCCGGGGACCCGGGA 1
GTERT-105        CGGGAGGGGTCGGGACGGGGC     1
CSBII-295-296mut GAAGCGGGGGAGGGGGGGUUUGGUAAAAAU    0
24R      CGCGGAAAGGAAGGGGAGGGGCTG  0
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X3CGC    GGGCGCGGGCGCGGGCGCGGG     0
CSBII-305-306mut GAAGCGGGGGAGGGAAGGUUUGGUGGAAAU    0
CSBII-312-313mut GAAGCGGAAGAGGGGGGGUUUGGUGGAAAU    0
TB-1-2-3-4       TTGTGTGTGTGTGTGGGTGGGT    0
CGG12    CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG       0
TB-1-4-7-8       TTGTGGTGGTGTGGGTGTGTGT    0
TB-1-3-5-7       TTGTGGTGTGGTGTGGTGTGGT    0
TB-2-3-5-8       TTGGTGTGTGGTGGTGTGGTGT    0
TB-1-2-3-4-5     TTGTGTGTGTGTGTGTGGTGGGT   0
TB-1-2-3-4-5-6   TTGTGTGTGTGTGTGTGTGTGGGT  0
Spom20   GGTTACGGTTACGGTTACGG      0
Cgi26    GGTGTACTGGTGTACTGGTGTACTGG        0
Spom23   GGTTACAGGTTACAGGTTACAGG   0
12954786-TTF1-4  TTATGGGGATGAAAGTGGTTGTTCGGGTTCGCCACTTCCAC  0
dx12(a)  GCGTGAGTTCGG     0
TB-1-2-3-4-5-6-7-8       TTGTGTGTGTGTGTGTGTGTGTGTG 0
19GA     AGAGAGAGAGAGAGAGAGA       0
miniTAR  CCAGAUUUGAGCCUGGGAGCUGUCUGG       0
psL1     GAGAGAGAGAGAGAGTTTTTATTAAATATA    0
psL2     GAGAGAGAGAGAGAGAAAAATAATTTATAT    0
RNAI     GGCACCGUUGGUAGCGGUGCC     0
19AT(a)  ACGTCGATTATAGACGAGC       0
Dx       TATAGCTATAA-linker-TATAGCTATA     0
CAG12    CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG       0
CTG12    CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG       0
ds10     CGCAATTGCG       0
ds12-CG  CGTTTTAAAACG     0
ds12-GC  GCTTTTAAAAGC     0
ds14     CGCGAAATTTCGCG   0
ds15-h   CGCGAAGCATTCGCG  0
ds26     CAATCGGATCGAATTCGATCCGATTG        0
dslac    GAATTGTGAGCGCTCACAATTC    0
GCdx     GCGCGCGCTTTTGCGCGCGC      0
PS1c(a)  TTTTTTTTTTATTAAAATTTATAA  0
PS1c(b)  AAAAAAAAAATAATTTTAAATATT  0
T30      TTTTTTTTTTTTTTTTTTTTTTTTTTTTT    0
AB16     AAATTTAATTAAATTT 0
AE16     TTTTTTTTAAAAAAAA 0
AG16     AATATATATATATATT 0
CTG5     CTGCTGCTGCTGCTG  0
CTG7     CTGCTGCTGCTGCTGCTGCTG     0
24Y      CAGCCCCTCCCCTTCCTTTCCGCG  0
CCG9     CCGCCGCCGCCGCCGCCGCCGCCGCCG       0
CCG10    CCGCCGCCGCCGCCGCCGCCGCCGCCGCCG    0
CCG15    CCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCG      0
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CCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCG
0
26PyTC   CTCCTCTCTTCCCTTCTTCTCTCCTC        0
22PyTC3  CCTCTCTCTCCTTCCTCTCTCT   0
JVITS    GAGAGAGAAACCCCTTTCTCTCTCTTTTCTCTCTCTTT    0
dx12(b)  CCGAACTCACGC     0
AC9      ACACACACACACACACAC        0
18AC18   ACACACACACACACACACACACACACACACACAC       0
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RNAII    CGGGUCGCUACCAACGACCCG     0
R06      UCAACACGGUCCCAGACGUGUUGA  0
T1RY+    CACTCCCTATCAGTGATAGAGAGAGAGAAAAAAAGAGAAGATCTGAGCTCGGTACCCT
0
19AT(b)  TGCAGCTAATATCTGCTCG       0
d(C4G2)4 GGCCCCGGCCCCGGCCCCGGCCCC  0
27sc     GTATTACTTGCTTTTAACGTACGAATG       0
27sg     CATTCGTACGTTAAAAGCAAGTAATAC       0
G3R      CCCCCTAAAAGAAAAAAGAAAAGACCTCGA    0
G3Y      TCGAGGTCTTTTCTTTTTTCTTTTAGGGGG    0
G3TC18   TTTTCTTTTTTCTTTTCT        0
40RT     CATTCGTACGTTAGGAGTAAAAGGAGGATGCAAGTAATAC   0
40RTT    CATTCGTACGTTAGGAGTAAAAGTAGGATGCAAGTAATAC   0
40YA     GTATTACTTGCATCCTCCTTTTACTCCTAACGTACGAATG   0
40YAA    GTATTACTTGCATCCTACTTTTACTCCTAACGTACGAATG   0
27dx     TAACCCTAACCCTAAGGGTTAGGGTTA       0
21mix    CTCACAACTCACACTCACACCC    0
21CT     TAACCTAACTAACCCTAATAAA    0
17ACA    TACACAAACAAAGGAGA         0
17AAA    TACACAAAAAAAGGAGA         0
17TGT    TCTCCTTTGTTTGTGTA         0
23G13    TGGGGCAGGACGGGTGCCCGGGT   0
TAD1     GGCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGCC
0
TAD2     GTCGCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGCGGC
0
21ACJ    CGCTCACAAACAAAGGGAGCG     0
17TGJ    CGCTCTTTGTTTGAGCG         0
17TTJ    CGCTCTTTTTTTGAGCG         0
22Agm4   ATGGTTAGTGTTAGGTTTAGTG    0
22Agm3   ATGGTTAGTGTTAGGTTTAGGG    0
22Agm2   AGGGTTAGTGTTAGGTTTAGGG    0
hp1      TATATACGTACTGTGTTTTCACAGTACGTATATA         0
hp2      TATATACGTACGGTGTTTTCACCGTACGTATATA         0
hpctrl   TATATATGTACTGTGTTTTCACAGTACATATATA         0
ura3ct1  CGGTGTGGTGGGCCCAGGTATTGTTAGCGGTT  0
ura3ct2  AGAGACATGGGTGGAAGAGA      0
A46gm8   ATGGTTAGTGTTAGGTTTAGTGTTATGGTTAGTGTTAGTG   0
45LG2T   CATTCGTACGTTGTGTTAGGGTTAGGGTTAGTGAGCAAGTAATAC      0
27SGT    CATTCGTACGTTTTTAGCAAGTAATAC       0
G4TERT1mu        AGGATGAAAGGAGCCCTGAGCTTGGG        0
G4TERT2mu        GAGAGCCTTGAAGCTCGGCAGGAGTGAAAGGGG         0
VNTR6-1mu        AGGATAGGTGAAGATCTGTGGGATTGG       0
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