# Supplemental information.

## Supplemental methods.

**Cell Culture, Plasmids, and Transfections.** SCC25, Calu-3, and U937 were obtained from American Type Culture Collection (Manassas, VA). $P19^{INK4d}$ promoter sequences between –265 or –228 were cloned by PCR amplification with primers 5'-gaggtcccagagcagcc-3' or 5'-cagttaaaccagccttctttc-3', respectively, and 3' primer 5'-tagagaagaaggaccggttc-3', and cloned into PCR2.1 (Invitrogen, Burlington, ON, Canada), digested with BamH1 and Hind III and subcloned into pXP2 to make +ER8p19$^{INK4d}$/pXP2, and -ER8 p19$^{INK4d}$/pXP2. COS-7 cells were transfected in medium as described (Wang et al, 2004) with 100ng of pSG5/VDR or pSG5/RARβ, 300ng of +ER8-p19$^{INK4d}$/pXP2, -ER8-p19$^{INK4d}$/pXP2, and 100ng of internal control pCMV-βgal.

**RT/PCR and ChIP assays.** RT/PCRs and ChIP assays were performed as described (Wang *et al*, 2004). Cells were treated for 1h with 1μM RA or 4h with 100nM 1,25D$_3$ or vehicle. Immunoprecipitations were performed using normal rabbit IgG, anti-VDR (C-20), anti-RAR (M-454) or anti-RXR (ΔN 197) rabbit polyclonal antibodies (Santa Cruz Biotechnology, Santa Cruz, CA). PCRs were performed with primers: $p19^{INK4d}$ ER8 region (–427/–103), 5'-cctcggattgggtggtccag-3' and 5'-ctactgtgtagcggcaccgcg-3' and POLII binding site region (-264/+7), 5'-accggttgccacactctgac-3' and 5-tctgctctgagcctgcg-3'. For re-ChIPs, immunocomplexes were eluted by adding 200μl re-ChIP buffer (10mM DTT) for 30 min at room temperature with rotation. Supernatants were diluted 1:40 in ChIP dilution buffer, and re-ChIP was performed using anti-VDR, anti-RAR or anti-RXR antibodies, as indicated.

**Antibodies, Immunoprecipitation, and Immunoblotting.** Antibodies used were as follows: rabbit polyclonal p27$^{KIP1}$ (c-19), rabbit polyclonal Cdk4 (H-22), HRP-conjugated anti-mouse and anti-rabbit IgG (Santa Cruz Biotechnology, Santa Cruz, CA) and mouse monoclonal p19$^{INK4D}$ (US Biological, Swampscott MA). Immunoprecipitations and the immunoblotting were performed as described (Lin *et al*, 2003).

**EMSAs.** Assays were performed as described (Wang et al, 2004) with oligonucleotides containing the *p19$^{INK4d}$* (5'-gcccctgacctttctccctgggtcagttaa-3'), *mop* (5'-gatccgtacaaggttcacgaggttcacgtctta-3'), *cyp3A4* (5'-tagaatatgaactcaaaggaggtcagtgagtgg-3'), human *rarβ* (5-agcccgggtaggttcaccgaaagttcactcgca-3') elements, along with a mutant *defB2* DR3 (5'-gatcctgaagagaatggcagaatgtgagga-3').

**Cell cycle analysis.** SCC25 siRNA transfected cells were collected, washed in PBS and centrifuged at 1500 r.p.m , and each sample was resuspended in propidium iodide (PI) stain buffer (0.1% Triton X-100, 200 μg of DNase-free RNase A, 20 μg of PI) in PBS over night. After staining, samples were analyzed using a FACScan (BD Biosciences, Mississauga, ON, Canada) and analyzed using Cell Quest Software (BD Biosciences, Mississauga, ON, Canada). The trypan blue dye exclusion assay was performed as described (Sowa et al, 2003).

**Analysis of siRNA transfection efficiencies and analysis of U937 cell differentiation.** SCC25 cells were transfected with Oligofectamine (Invitrogen, Burlington, ON, Canada) under conditions recommended by the manufacturer (Dharmacon, Lafayette, CO) with vehicle (no siRNA) or with 100ng of negative control (cyclophilin) or Cy3 fluorescent-tagged cyclophilin siRNA (siGlo) as indicated. Media was changed after 24h and cells were harvested for FACS

analysis 48h after transfection. U937 cells were incubated with transfection medium (Lipofectin, Invitrogen, Burlington, ON, Canada) and 100nM of either siControl Cyclophilin B siRNA or siGlo (with Cy3) Cyclophilin B siRNA. After 24 h, cells were washed, harvested and analyzed by flow cytometry for Cy3 fluoresecence. FACS analysis of expression of monocytic marker CD11b in U937 cells cultured in the presence of vehicle or $1,25D_3$ (100nM) for 48h. Cells were untransfected (no transfection) or transfected with 100nM siRNAs directed against $p19^{ink4d}$ transcripts (si-p19) or scrambled siRNA control (siControl). Cells were incubated in the presence of Allophycocyanin (APC)-conjugated mouse anti-human monoclonal antibody CD 11b/Mac-1 (BD Biosciences, San Jose CA) prior to analysis by flow cytometry.

**Supplemental References.**

Lin R, Wang TT, Miller WH, White JH (2003) Inhibition of F-box protein $p45^{SKP2}$ expression and stabilization of cyclin-dependent kinase inhibitor $p27^{KIP1}$ in vitamin D analogue-treated cancer cells. *Endocrinology* **144**: 749-53.

Sowa H, Kaji H, Iu MF, Tsukamoto T, Sugimoto T, Chihara K (2003) Parathyroid hormone-Smad3 axis exerts anti-apoptotic action and augments anabolic action of transforming growth factor β in osteoblasts. *J Biol Chem* **278**: 52240-52.

Wang TT, Nestel F, Bourdeau V, Nagai Y, Wang Q, Wu J, Tavera-Mendoza L, Lin R, Hanrahan, JW, Mader S, White JH (2004) 1,25-dihydroxyvitamin D3 is a direct inducer of antimicrobial peptide gene expression. *J Immunol* **173**: 2909-12.

# Primers used in this study.

## ChIP assays.

```
1.   DDIT              5'    5'-aaccaggaatgccaggtccg
                       3'    5'-taggctgctccgctgctc
     DDIT (2k)         5'    5'-acctgtgaagatccgtacctg
                       3'    5'-tgccttcctggagtcctctc


2.   p19               5'    5'-cctcggattgggtggctccag
                       3'    5'-ctactgtgtagcggcaccgcg
     p19 (2K)          5'    5'-accattctcctgcctcagcc
                       3'    5'-tgttggctagtctggtctcg

3.   Il10              5'    5'-ctcacttcctgattcttaggtttctac
                       3'    5'-gcattgagcttaagtagccatgga
     IL10-2K           5'    5'-aattgtgcccaggctgac
                       3'    5'-gacctatgggcttgggactt


4.   TYROPB            5'    5'-cctgcctccacagtctgc
                       3'    5'-atccacacgtcacacccacc
     TYROBP2K          5'    5'-actacaggtaggtgccacc
                       3'    5'-ggtggctcacgcctgtaat


5.   NFE2L2            5'    5'-ctgccagtattatctacttcacctgg
                       3'    5'-cgtgcctagaaaaaaattgaaggttacc
     NFE2L2K           5'    5'-aggatgatggctgacttcc
                       3'    5'-ggtgccatctttggaagct

6.   POLA2             5'    5'-tgctgatggtgggaaactgca
                       3'    5'-gcgtggtggcgagcacctgta

     POLA2-2K          5'    5'-actaggccaggcacagtg
                       3'    5'-gaccagcctggccaacat
```

## siRNAs

```
P19 siRNAs  (pool of 4)                p19 scrambled siRNAs (pool of 4)

5'-CAAUCCAUCUGGCAUUCAUU               5'-AUGAACGUGAAUUGCUCAAUU
  UUGUUAGGUAGACCGUAAGU -5'              UUUACUUGCACUUAACGAGUU-5'

5'-GUACCAGUCCAGUCCAUGAUU              5'-UAAGGCUAUGAAGAGAUACUU
  UUCAUGGUCAGGUCAGGUACU-5'             UUAUUCCGAUACUUCUCUAUG-5'

5'-GAUGUCAACGUGCCUGAUGUU             5'-AUGUAUUGGCCUGUAUUAGUU
  UUCUACAGUUGCACGGACUAC-5'             UUUACAUAACCGGACAUAAUC-5'

5'-UCUGGCAGCUGAAUCUGAUUU             5'-UAGCGACUAAACACAUCAAUU
  UUAGACCGUCGACUUAGACUA                UUAUCGCUGAUUUGUGUAGUU P-5'
```

## Promoter Primers

| **Gene** | | | **Name of primer** |
|---|---|---|---|
| P19INK4D | | | |
| 5' +ER8 | 5'-aagctt | tcaggaggcgccgaggt | CDKN2DD3P5' |
| -ER8 | 5'-aagctt | ggtccaccggttgcca | |
| 3' | 5'-ctcgag | tctgctctgagcctgcgc | CDKN2DD3P |
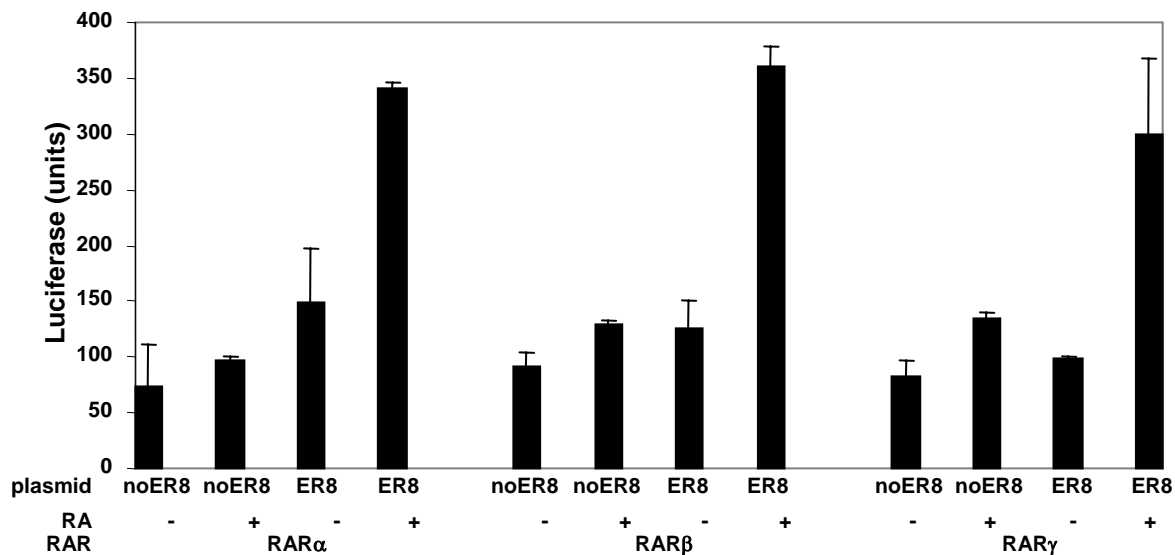
**Supplemental Fig. 1.**
Induction of p19INK4D promoter activity by RARs α, β or γ. Induction of reporter gene expression in COS-7 cells grown in 6-well plates transiently transfected with 1μg of proximal p19INK4D promoter-luciferase reporter plasmids either containing or lacking the ER8 motif, along with expression vectors for RARs α, β, or γ (300ng) as indicated. All-trans retinoic acid (+; 1μM) or DMSO (-) vehicle was added as indicated
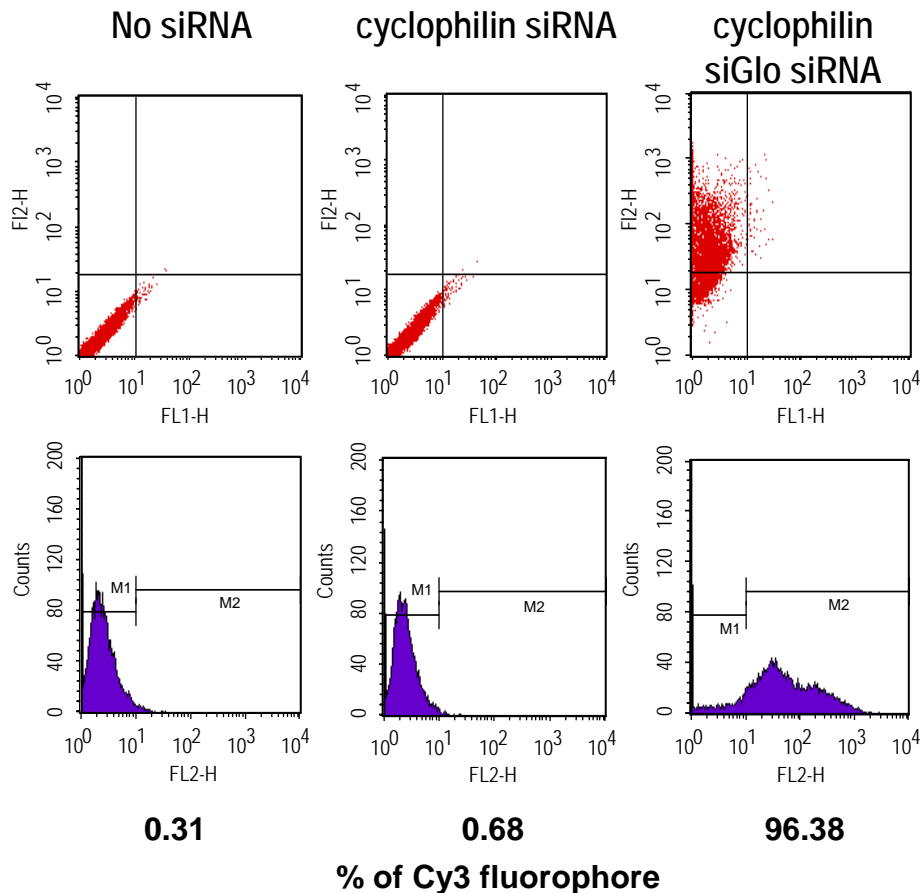
**Supplemental Fig. 2.**
FACS analysis of transfection efficiency of siRNA in SCC25 cells. Cells were transfected
under conditions recommended by the manufacturer (Dharmacon) with vehicle (no siRNA)
or with 100ng of negative control (cyclophilin) or Cy3 fluorescent-tagged cyclophilin
siRNA (siGlo) as indicated. Media was changed after 24h and cells were harvested for
FACS analysis 48h after transfection. Upper: dot plots showing two fluorescent parameters
(FL2-H, for Cy3, excitation wave length 575-600 nm; FL1-H, for excitation wave length
530 nm). Lower: Histograms of Cy3 fluorescence. M1/M2 is the negative/positive ratio of
Cy3 fluorescence. Bottom: percentage of cells with detectable Cy3 fluorescence. (See
supplemental information for details.)

**A**



**B**
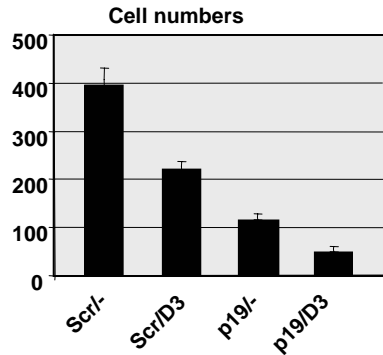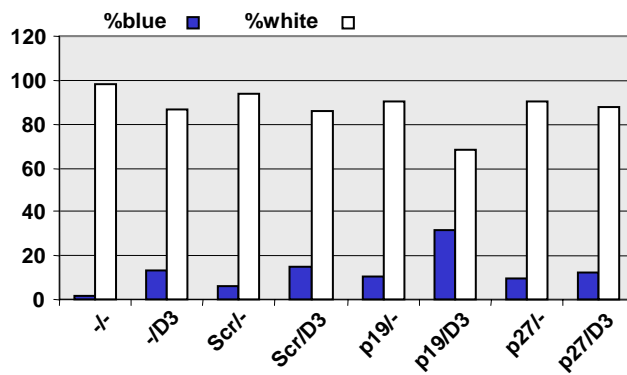


**Supplemental Fig. 3.**
Analysis of cell viability in the absence (-) or presence of $1,25D_3$ (D3) of SCC25 cells transfected with scrambled siRNA Scr/-; Scr/D3] or siRNAs directed against p19[INK4D] (p19/-; p19/D3) or p27[KIP1] [p27/-; p27/D3), as indicated. A. Cell numbers. B. Cell viability assessed by trypan blue exclusion assay.

**A**



**B**
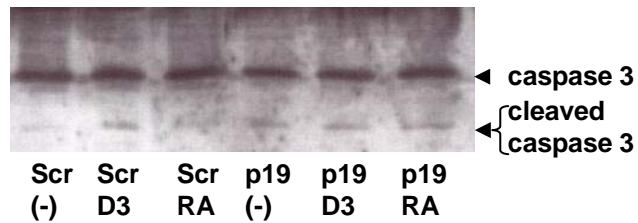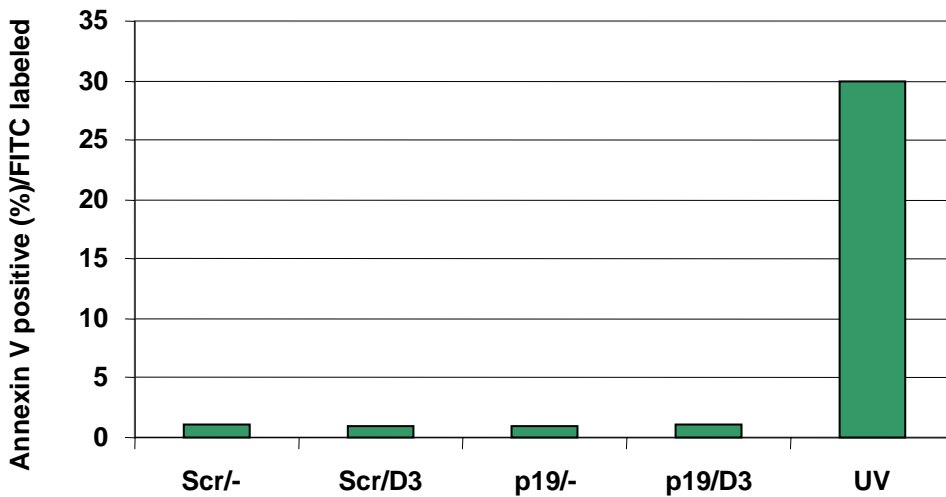


**Supplemental Fig. 4.** Knockdown of p19$^{INK4D}$ does not induce markers of apoptosis.
A. Western blot analysis of caspase 3 cleavage in extracts of SCC25 cells derived from
cells transfected with either scrambled (scr) siRNA or siRNA directed against p19$^{INK4D}$
(p19). Cells were treated with DMSO (-), 1,25D$_3$ (D3; 100nM) or retinoic acid (RA; 1µM),
as indicated for 48h. B. Analysis of annexin V binding by FACS analysis to SCC25 cells
transfected with either scrambled (scr) siRNA or siRNA directed against p19$^{INK4D}$ (p19).
Cells were treated with DMSO (-), 1,25D$_3$ (D3; 100nM), as indicated for 16h. Cells were
exposed to germicidal UV light for 30 min as a positive control for induction of apoptotic
cell death.

**A**

siControl          siGlo

% of Cy3          2.33          99.63

**B**
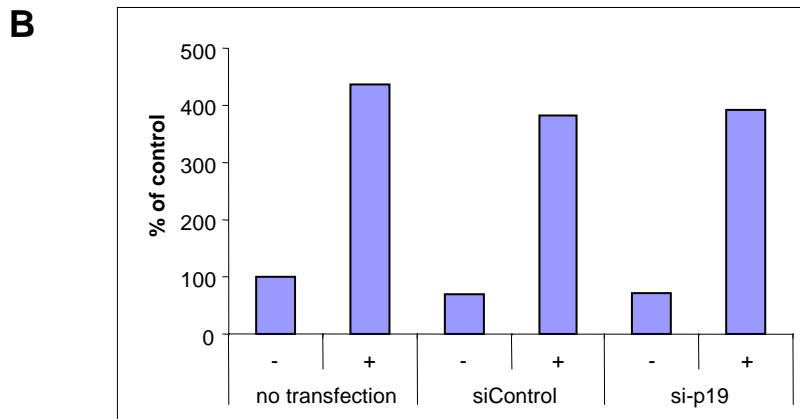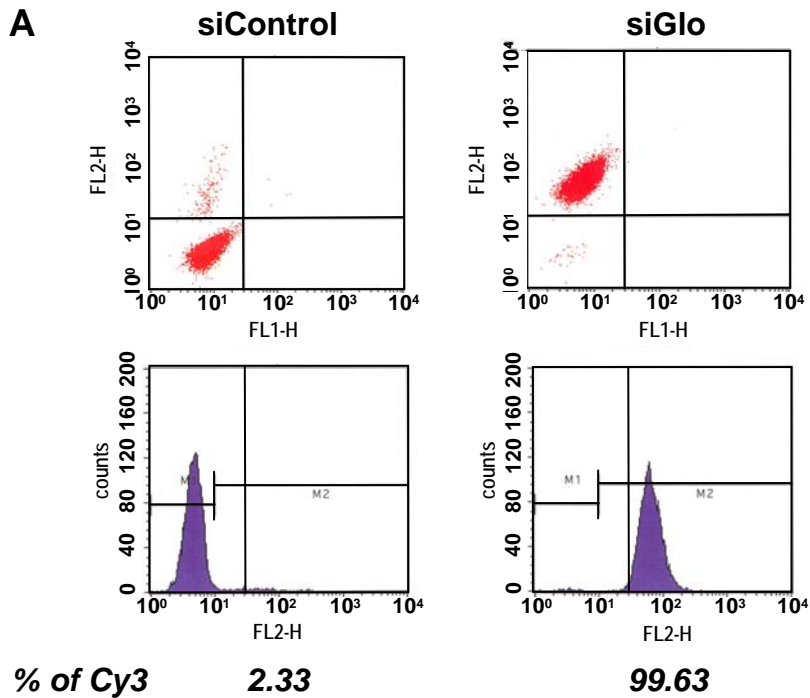
**Supplemental Fig. 5**
**A.** Transfection efficiency of U937 cells with siRNA. Cells were tranfected with either siControl Cyclophilin B siRNA or siGlo (with Cy3) Cyclophilin B siRNA and analyzed by flow cytometry for Cy3 fluoresecence 24h later. Upper: dot plots showing two fluorescent parameters (FL2-H, for Cy3, excitation wave length 575-600 nm; FL1-H, for excitation wave length 530 nm). Lower: Histograms of Cy3 fluorescence. M1/M2 is the negative/positive ratio of Cy3 fluorescence. **B.** Loss of $p19^{INK4D}$ does not affect $1,25D_3$-induced monocytic differentiation of U937 cells. FACS analysis of expression of monocytic marker CD11b in U937 cells cultured in the presence of vehicle or $1,25D_3$ (100nM) for 48h. Cells were incubated in the presence of Allophycocyanin (APC)-conjugated mouse anti-human monoclonal antibody CD 11b/Mac-1 (BD Biosciences, San Jose CA) prior to analysis by flow cytometry. (See supplemental information for details).

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| FLJ25976 | Chr14 | Normal | NT_026437.10 | TGACCTCATCTTCAGGTTCA | -1525 |
| PVALB | Chr22 | Complement | NT_011520.9 | TGAACTCTGGAGTGAGGTCA | -1504 |
| KIAA0408 | Chr6 | Complement | NT_025741.13 | TGACCTAGGACTACAGGTCA | -1486 |
| PTPN21 | Chr14 | Complement | NT_026437.10 | TGAACTCTATGAGGGGGTCA | -1433 |
| GK003 | Chr7 | Normal | NT_007819.14 | TGACCCTACTTCTTGGGTCA | -1420 |
| APOBEC1 | Chr12 | Complement | NT_009714.16 | TGAACCCTGGGTCAAGTTCA | -1379 |
| TXNRD1 | Chr12 | Normal | NT_019546.15 | TGACCCTGGTTCATGGGTCA | -1378 |
| GK003 | Chr7 | Normal | NT_079592.1 | TGACCCTACTTCTTGGGTCA | -1350 |
| LOC375980 | Chr11 | Normal | NT_009237.16 | TGACCCAAATATTTGGTTCA | -1324 |
| TRBV24OR9-2 | Chr9 | Normal | NT_008413.16 | TGAACCGCGAGAGGAGTTCA | -1314 |
| RPL27AP | Chr20 | Normal | NT_011362.8 | TGACCTCTGAGGCTAGGTCA | -1278 |
| TRIM3 | Chr11 | Complement | NT_009237.16 | TGACCTCTCCACAAGGTTCA | -1223 |
| MGC4415 | Chr10 | Normal | NT_030059.11 | TGACCTGGCTTGGTGGTTCA | -1195 |
| EPS8L2 | Chr11 | Normal | NT_035113.5 | TGACCCTGAGCTCTGGGTCA | -1184 |
| LOC157567 | Chr8 | Complement | NT_008046.14 | TGAACTCAGGTGAGAGTTCA | -1182 |
| LOC377863 | Chr23 | Normal | NT_011757.13 | TGAACCTCTGCCAGGGTTCA | -1176 |
| NFE2L2 | Chr2 | Complement | NT_005403.14 | TGAACTCTTATAAGGGTTCA | -1163 |
| CACH-1 | Chr5 | Complement | NT_006713.13 | TGACCTCTGCCATGAGGTCA | -1160 |
| PPP1R12A | Chr12 | Complement | NT_019546.15 | TGAACCACCTCTTGAGTTCA | -1128 |
| LIG3 | Chr17 | Normal | NT_010799.14 | TGAACCAAAGCCCTGGTTCA | -1126 |
| KCNA10 | Chr1 | Complement | NT_019273.16 | TGACCCCTTTTCTCAGTTCA | -1109 |
| IGLVIV-53 | Chr22 | Normal | NT_011520.9 | TGAACCACATTGACAGGTCA | -1095 |
| DKFZp451A175 | Chr6 | Complement | NT_025741.13 | TGAACTACTGGGTGGGTTCA | -1063 |
| KLK2 | Chr19 | Normal | NT_011109.15 | TGACCTAGGAGGGCAGGTCA | -1061 |
| LOC376356 | Chr16 | Complement | NT_024797.14 | TGACCCCCTGCAGTGGGTCA | -1049 |
| SLC38A5 | Chr23 | Complement | NT_011568.13 | TGAACCTGAATCCAGGTTCA | -1042 |
| FBXO7 | Chr22 | Normal | NT_011520.9 | TGACCTCTGGAGCTAGGTCA | -984 |
| GUCA1C | Chr3 | Complement | NT_005612.14 | TGAACTTAAGAACAGGGTCA | -811 |
| D2S448 | Chr2 | Normal | NT_022221.10 | TGACCTCCCTGGAGAGTTCA | -803 |
| KLK3 | Chr19 | Normal | NT_011109.15 | TGACCTGGGAGGGCAGGTCA | -716 |
| X102 | Chr15 | Complement | NT_026446.12 | TGACCTCCTGCCTAAGGTCA | -712 |
| RPL10P1 | Chr21 | Normal | NT_011512.9 | TGAACTTTCCAAAGGGTTCA | -654 |
| FLJ37300 | Chr17 | Normal | NT_010641.14 | TGACCTAGATTCTGGGTTCA | -627 |

| EIF3S5P | Chr21 | Complement | NT_029490.3 | TGACCTCCTTTTTAGGTTCA | -550 |
|---|---|---|---|---|---|
| IFP38 | Chr13 | Complement | NT_078092.2 | TGACCTCCTTTTTAGGTTCA | -550 |
| FLJ32130 | Chr16 | Complement | NT_024812.10 | TGACCTTTGCCCCGAGGTCA | -548 |
| FLJ14345 | Chr19 | Complement | NT_011109.15 | TGAACCTGAGGAGGGGGTCA | -524 |
| MBD6 | Chr12 | Normal | NT_029419.10 | TGACCTGGGGAGGCGGGTCA | -501 |
| CDKN2D | Chr19 | Complement | NT_011295.10 | TGACCCAGGGAGAAAGGTCA | -245 |
| LOC375784 | Chr9 | Complement | NT_079538.1 | TGACCTACAGCACTGGGTCA | -159 |
| LOC375141 | Chr22 | Complement | NT_011520.9 | TGACCTTTGCGGGAAGGTCA | -88 |
| LGALS3 | Chr14 | Normal | NT_026437.10 | TGAACTAGTGGTGAGGTTCA | -77 |
| HSPC047 | Chr7 | Complement | NT_079596.1 | TGACCCCTGCCTCTGGGTCA | -71 |
| HSPC047 | Chr7 | Complement | NT_007933.13 | TGACCCCTGCCTCTGGGTCA | -1 |
| LOC375211 | Chr2 | Complement | NT_022184.13 | TGACCCGCCGCCCGAGGTCA | 18 |
| LOC377812 | Chr9 | Normal | NT_008470.16 | TGAACCCAATTTGCAGTTCA | 42 |
| LOC374897 | Chr19 | Complement | NT_011109.15 | TGACCTTCTCAATGGGGTCA | 96 |
| HSHIN1 | Chr4 | Complement | NT_016606.16 | TGAACTTCCCCCAAAGTTCA | 154 |
| SZFP41 | Chr19 | Complement | NT_011109.15 | TGAACTTTCAACTCAGGTCA | 391 |
| CETP | Chr16 | Normal | NT_010498.14 | TGACCTCGCCTTCAAGGTCA | 418 |
| MGC31963 | Chr1 | Complement | NT_079484.1 | TGACCCTGGTGGGCGGGTCA | 420 |
| LOC375129 | Chr22 | Complement | NT_011519.10 | TGACCTTTGTGGGAAGGTCA | 430 |
| LOC150236 | Chr22 | Complement | NT_011520.9 | TGACCTTCCCGCAAAGGTCA | 511 |
| FARSL | Chr19 | Complement | NT_011295.10 | TGACCCCCAAGGCTGGGTCA | 519 |
| LOC376464 | Chr18 | Normal | NT_025028.13 | TGACCCAACTTTATAGGTCA | 532 |
| ECGF1 | Chr22 | Complement | NT_011526.5 | TGACCTCCCAGTCGGGGTCA | 575 |
| GCGR | Chr17 | Normal | NT_079568.1 | TGACCCCGGCAAGCGGGTCA | 638 |
| IGHV2-10 | Chr14 | Complement | NT_026437.10 | TGAACCACTAACAGGGGTCA | 645 |
| CNIH | Chr14 | Complement | NT_026437.10 | TGAACTTGCATCAAAGTTCA | 708 |
| MRRF | Chr9 | Normal | NT_008470.16 | TGACCTCTTAGACTAGGTCA | 711 |
| LOC200810 | Chr3 | Complement | NT_005612.14 | TGAACCTATTTTCAAGGTCA | 811 |
| KIAA1462 | Chr10 | Complement | NT_008705.15 | TGAACTGTTCTTTTAGTTCA | 844 |
| KRTAP22-1 | Chr21 | Normal | NT_011512.9 | TGAACCTTTTATCAAGGTCA | 934 |
| LOC376523 | Chr19 | Complement | NT_011109.15 | TGAACCAACAAACAGGGTCA | 937 |
| LOC89944 | Chr11 | Normal | NT_033899.6 | TGACCCTATCTTTCAGGTCA | 990 |
| LOC375884 | Chr10 | Complement | NT_033985.6 | TGAACTCCTTTGACAGGTCA | 1002 |
| ZIBRA | Chr14 | Normal | NT_026437.10 | TGAACTATGGGCATAGTTCA | 1003 |
| GNA14 | Chr9 | Complement | NT_023935.16 | TGAACCCAAGATGTGGGTCA | 1006 |
| LOC284796 | Chr20 | Normal | NT_011387.8 | TGAACCCCACGTTGGGGTCA | 1026 |
| RPS6KA1 | Chr1 | Normal | NT_037485.3 | TGACCCCAGGGTCAAGGTCA | 1050 |
| ZNF265 | Chr1 | Complement | NT_032977.6 | TGAACTACTCCTTCAGGTCA | 1126 |
| LOC150174 | Chr22 | Normal | NT_011519.10 | TGAACCCCACGTTGGGGTCA | 1150 |
| LOC376821 | Chr22 | Normal | NT_011520.9 | TGAACCCCACGTTGGGGTCA | 1150 |
| POM121L4P | Chr22 | Normal | NT_011520.9 | TGAACCGCACATTGGGGTCA | 1150 |
| PPM1F | Chr22 | Complement | NT_011520.9 | TGAACTTGTGTAGAGGTTCA | 1167 |
| LOC150213 | Chr22 | Complement | NT_011520.9 | TGACCCCAACGTGGGGTTCA | 1169 |
| LOC343855 | Chr22 | Complement | NT_011520.9 | TGACCCCAACGTGGGGTTCA | 1169 |
| POM121L1 | Chr22 | Complement | NT_011520.9 | TGACCCCAACGTGGGGTTCA | 1169 |
| IGFALS | Chr16 | Complement | NT_037887.3 | TGAACTGAGGCTCGAGGTCA | 1216 |
| DUSP8 | Chr11 | Complement | NT_009237.16 | TGAACTTCCAGCTGGGGTCA | 1231 |
| FLJ32743 | Chr18 | Complement | NT_010966.13 | TGACCTCATGTAAGGGGTCA | 1237 |
| LOC376712 | Chr1 | Complement | NT_004559.11 | TGAACCCCAGAACAGGTTCA | 1244 |
| AGC1 | Chr15 | Normal | NT_010274.15 | TGAACTGTGACTTAGGGTCA | 1276 |
| SERPINA6 | Chr14 | Complement | NT_026437.10 | TGACCTCACTTAATGGGTCA | 1304 |
| DKFZP434P211 | Chr22 | Normal | NT_011520.9 | TGAACCCCACGTTGGGGTCA | 1327 |
| RRP41 | Chr8 | Normal | NT_023684.16 | TGAACTGTCAATATAGTTCA | 1360 |
| LOC118934 | Chr10 | Normal | NT_030059.11 | TGAACTGTAAGGACAGGTCA | 1389 |
| ABCA3 | Chr16 | Complement | NT_037887.3 | TGAACCCAGAGTTAAGTTCA | 1455 |
| LOC375496 | Chr6 | Normal | NT_007592.13 | TGAACCCCACGTCGGGGTCA | 1508 |
| BF | Chr6 | Normal | NT_007592.13 | TGACCTGTACCCCCAGGTCA | 1545 |
| CDC42EP1 | Chr22 | Normal | NT_011520.9 | TGACCTCCTTGCCCAGGTCA | 1546 |
| CANX | Chr5 | Normal | NT_077451.3 | TGAACTGTGTGTGGGGGTCA | 1565 |
| NARG2 | Chr15 | Complement | NT_010194.16 | TGACCCATCATACGAGGTCA | 1581 |
| LOC138198 | Chr9 | Normal | NT_023935.16 | TGAACCCACGCAGAAGGTCA | 1594 |
| LOC221270 | Chr6 | Complement | NT_025741.13 | TGAACTTGTTTATTAGTTCA | 1596 |
| TCF19 | Chr6 | Normal | NT_007592.13 | TGAACCTGGGAGGCGGGTCA | 1604 |
| LOC375234 | Chr2 | Normal | NT_034508.2 | TGACCCCATGATGGAGGTCA | 1612 |
| LOC375451 | Chr5 | Complement | NT_078019.1 | TGACCCCGACGTGGGGTTCA | 1645 |
| LOC375688 | Chr8 | Complement | NT_079526.1 | TGACCCCGACGTGGGGTTCA | 1645 |
| IL12B | Chr5 | Complement | NT_023133.11 | TGAACTGCACTTCAGGGTCA | 1683 |
| LOC128939 | Chr22 | Normal | NT_011516.5 | TGAACCCCAGGTATGGGTCA | 1766 |
| ZNF28 | Chr19 | Complement | NT_011109.15 | TGACCTTGAAAACAGGGTCA | 1803 |
| PIGF | Chr2 | Complement | NT_022184.13 | TGACCCCTAAAAATAGGTCA | 1815 |
| PEPP-2 | Chr23 | Normal | NT_077819.3 | TGAACTCGCAGTGCAGGTCA | 1827 |
| PLSCR2 | Chr3 | Complement | NT_005612.14 | TGACCTTTAGATTGAGGTCA | 1837 |
| LOC374292 | Chr1 | Normal | NT_021937.16 | TGACCCCTGAGCCTGGGTCA | 1863 |
| CS | Chr12 | Complement | NT_029419.10 | TGACCTACTTTTAAGGGTCA | 1908 |

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|---|---|---|---|---|---|
| LOC134357 | Chr5 | Complement | NT_006713.13 | TGAACTCAAAGAGAGGGTCA | 1976 |
| LOC376306 | Chr16 | Complement | NT_010393.14 | TGACCCAACAGGCAGGGTCA | 1977 |
| BCRL4 | Chr22 | Normal | NT_011520.9 | TGACCTTCCCGCAAAGGTCA | 2001 |
| CDH16 | Chr16 | Complement | NT_010498.14 | TGACCTCATGTGACAGGTCA | 2025 |
| NMP200 | Chr11 | Complement | NT_033903.6 | TGACCTCCTTTTTGGGTTCA | 2028 |
| POU2F2 | Chr19 | Complement | NT_011109.15 | TGACCTCTGAACCCAGTTCA | 2061 |
| SNW1 | Chr14 | Complement | NT_026437.10 | TGACCTCATCTTCAGGTTCA | 2129 |
| LOC149950 | Chr20 | Normal | NT_028392.4 | TGACCTCTCAGGTTGGGTCA | 2184 |
| C6orf141 | Chr6 | Normal | NT_007592.13 | TGACCCTTACTTAGGGGTCA | 2197 |
| KIAA0937 | Chr11 | Normal | NT_033903.6 | TGACCTGCCTTTCCAGGTCA | 2294 |
| FLJ33817 | Chr17 | Normal | NT_010718.14 | TGACCCCACCCCCTAGGTCA | 2313 |
| LOC375496 | Chr6 | Normal | NT_007592.13 | TGAACCCCACGTCGGGGTCA | 2325 |
| VCIP135 | Chr8 | Complement | NT_008183.17 | TGACCTTGATCACAAGGTCA | 2328 |
| HTR6 | Chr1 | Normal | NT_004610.16 | TGAACTCCTGATCGAGGTCA | 2348 |
| GRIP1 | Chr12 | Complement | NT_029419.10 | TGACCCTAAAAGAAAGGTCA | 2376 |
| C11orf5 | Chr11 | Complement | NT_033903.6 | TGACCTTGACCACCGGTTCA | 2418 |
| LOC377203 | Chr4 | Complement | NT_016354.16 | TGACCCTATGCCTCAGGTCA | 2440 |
| SSX9 | Chr23 | Complement | NT_011568.13 | TGACCTGCCACGGTGGTTCA | 2500 |
| MGC2749 | Chr19 | Normal | NT_011295.10 | TGAACTCCCTAGGAGGGTCA | 2614 |
| DKFZP566B183 | Chr12 | Normal | NT_009714.16 | TGAACTGTTAAATAAGGTCA | 2632 |
| NALP8 | Chr19 | Normal | NT_011109.15 | TGACCTCCTAGCCGAGGTCA | 2695 |
| KRTHA5 | Chr17 | Complement | NT_010755.14 | TGACCTTGTCAGCAAGGTCA | 2709 |
| LOC345643 | Chr5 | Complement | NT_006431.13 | TGACCTAGGCCTCTGGGTCA | 2718 |
| KRTHA5 | Chr17 | Complement | NT_010755.14 | TGACCTTGTCAGCAAGGTCA | 2747 |
| C20orf187 | Chr20 | Normal | NT_011387.8 | TGACCCATCACATGAGGTCA | 2780 |
| SDC1 | Chr2 | Complement | NT_015926.13 | TGAACTTTCAGAGAGGGTCA | 2837 |
| ABCB9 | Chr12 | Complement | NT_009755.16 | TGACCCACAGAGTTGGGTCA | 2934 |
| DNPEP | Chr2 | Complement | NT_005403.14 | TGACCTCTTCCTGTGGGTCA | 2983 |
| BITE | Chr3 | Complement | NT_005612.14 | TGACCTTATGTGACAGGTCA | 3046 |
| E4F1 | Chr16 | Normal | NT_037887.3 | TGACCTTGAACTTCAGGTCA | 3102 |
| HNRPK | Chr9 | Complement | NT_023935.16 | TGACCTGTAGTGGCGGTTCA | 3127 |
| LOC375177 | Chr22 | Complement | NT_011526.5 | TGACCTCCCAGTCGGGGTCA | 3129 |
| CMKLR1 | Chr12 | Complement | NT_019546.15 | TGACCTGGGGTGCTGGTTCA | 3137 |
| KIAA1102 | Chr4 | Normal | NT_006238.10 | TGAACTGTCTGCGGGGTTCA | 3139 |
| LOC375496 | Chr6 | Normal | NT_007592.13 | TGAACCCCACGTCGGGGTCA | 3145 |
| SNCB | Chr5 | Complement | NT_023133.11 | TGAACTGACATTCAAGTTCA | 3175 |
| CERK | Chr22 | Complement | NT_011523.9 | TGACCTGCCCAACGAGGTCA | 3293 |
| LOC340581 | Chr23 | Normal | NT_011786.14 | TGACCTTCAGGCCTAGGTCA | 3306 |
| FLJ13273 | Chr4 | Normal | NT_016354.16 | TGAACTAAAGTTTCAGTTCA | 3345 |
| LOC340371 | Chr8 | Complement | NT_023684.16 | TGACCCCCACAAGGGGGTCA | 3348 |
| FLJ20249 | Chr1 | Complement | NT_079484.1 | TGAACTCCTTGGCAGGGTCA | 3362 |
| LOC375171 | Chr22 | Normal | NT_011520.9 | TGACCTGACCCCTAAGGTCA | 3377 |
| LOC375691 | Chr9 | Complement | NT_008413.16 | TGAACTGTATACCGAGGTCA | 3378 |
| TM7SF2 | Chr11 | Normal | NT_033903.6 | TGACCTTGACCACCGGTTCA | 3378 |
| VEGFB | Chr11 | Normal | NT_033903.6 | TGACCTTTGCAAAAGGTTCA | 3398 |
| ECM2 | Chr9 | Complement | NT_008476.14 | TGAACTGATCTTCCAGTTCA | 3403 |
| FLJ20403 | Chr1 | Normal | NT_004686.16 | TGACCTTGTTTTTGAGGTCA | 3410 |
| PAP | Chr2 | Complement | NT_022184.13 | TGACCTGGAGCCTGGGGTCA | 3497 |
| FLJ12439 | Chr1 | Complement | NT_032977.6 | TGAACCAAGGAGGAGGGTCA | 3499 |
| CASP8AP2 | Chr6 | Normal | NT_007299.12 | TGAACTTCAAGAAGAGGTCA | 3504 |
| LOC284227 | Chr18 | Complement | NT_010859.13 | TGAACTGGGGCAGGGGTTCA | 3613 |
| ACADVL | Chr17 | Normal | NT_010718.14 | TGACCTGACAAGCTAGGTCA | 3621 |
| KIAA1018 | Chr15 | Normal | NT_010194.16 | TGAACCATCATGACAGGTCA | 3652 |
| MGC22805 | Chr10 | Complement | NT_030059.11 | TGACCCATCACATGAGGTCA | 3662 |
| FLJ23231 | Chr1 | Normal | NT_079482.1 | TGACCTATTGTGGCAGGTCA | 3667 |
| LOC222103 | Chr7 | Normal | NT_007819.14 | TGACCTGGGCTTGTGGGTCA | 3732 |
| LOC219983 | Chr11 | Normal | NT_033903.6 | TGAACTCAGTTGAGAGGTCA | 3743 |
| IGLV10-54 | Chr22 | Normal | NT_011520.9 | TGAACCACATTGACAGGTCA | 3752 |
| MMP8 | Chr11 | Complement | NT_033899.6 | TGACCTAAGAAGTAAGGTCA | 3755 |
| HNRPM | Chr19 | Normal | NT_077812.2 | TGAACCGCTTCCCGGGTTCA | 3791 |
| LOC378255 | Chr7 | Normal | NT_079592.1 | TGACCTGGGCTTGTGGGTCA | 3801 |
| LOC376599 | Chr1 | Complement | NT_032977.6 | TGACCTATGAGGTTAGGTCA | 3858 |
| SPHK2 | Chr19 | Normal | NT_011109.15 | TGAACCAGGCAGGCGGTTCA | 3871 |
| LOC158352 | Chr9 | Complement | NT_008413.16 | TGACCCCATTTTCTGGGTCA | 3887 |
| LOC376661 | Chr1 | Complement | NT_079484.1 | TGACCCTGGTGGGCGGGTCA | 3951 |
| GSCL | Chr22 | Complement | NT_011519.10 | TGACCTAGTTCGGGAGGTCA | 3957 |
| LOC147740 | Chr19 | Normal | NT_011295.10 | TGACCTAGCCTCAGGGGTCA | 4012 |
| ANGPT4 | Chr20 | Complement | NT_011387.8 | TGACCCCACATCAAAGGTCA | 4034 |
| LOC377880 | Chr23 | Complement | NT_011568.13 | TGAACTAGGAGAACAGTTCA | 4041 |
| TCTEL1 | Chr6 | Complement | NT_007422.12 | TGAACTCCCTGGGTGGGTCA | 4056 |
| TRBV7-1 | Chr7 | Normal | NT_007914.13 | TGACCCCTTCTTGAAGGTCA | 4058 |
| LOC128939 | Chr22 | Normal | NT_011516.5 | TGAACTAACACCCGGGTTCA | 4063 |
| BCKDK | Chr16 | Normal | NT_024812.10 | TGACCTGTTATTAAAGTTCA | 4134 |
| PLA2G3 | Chr22 | Complement | NT_011520.9 | TGAACCAGTTGCCAAGGTCA | 4160 |

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|---|---|---|---|---|---|
| SSTK-IP | Chr1 | Normal | NT_079484.1 | TGACCCTACTTTAAGGGTCA | 4196 |
| FNTB | Chr14 | Normal | NT_026437.10 | TGAACCATTGGCATGGTTCA | 4251 |
| FLJ14721 | Chr12 | Normal | NT_009775.14 | TGACCTTCCCCTCCAGGTCA | 4259 |
| IAN4L1 | Chr7 | Normal | NT_007914.13 | TGACCCCCGGCAGTGGGTCA | 4262 |
| IAN4L1 | Chr7 | Normal | NT_079596.1 | TGACCCCCGGCAGTGGGTCA | 4332 |
| VPS4A | Chr16 | Normal | NT_010498.14 | TGACCTGAGATATTAGGTCA | 4349 |
| OR4H6P | Chr15 | Normal | NT_077631.1 | TGAACTTCAGTGGGAGGTCA | 4371 |
| MGC35179 | Chr17 | Normal | NT_010718.14 | TGACCCCCACGGACAGGTCA | 4398 |
| CARS | Chr11 | Complement | NT_009237.16 | TGACCTTGCAGTTCAGTTCA | 4479 |
| FLJ12076 | Chr16 | Normal | NT_010498.14 | TGACCTGACCTAGGGGTTCA | 4480 |
| LOC378072 | Chr7 | Normal | NT_079592.1 | TGAACTTGTCAGAGAGGTCA | 4509 |
| TCF3 | Chr19 | Complement | NT_011255.14 | TGACCCGCTCATCCAGGTCA | 4513 |
| SLC28A1 | Chr15 | Normal | NT_010274.15 | TGAACTTGAAAGTAGGGTCA | 4572 |
| LOC375614 | Chr7 | Normal | NT_007933.13 | TGACCTAGATAGAAAGGTCA | 4610 |
| LANCL2 | Chr7 | Normal | NT_033968.5 | TGAACTTGTCAGAGAGGTCA | 4625 |
| CLMN | Chr14 | Complement | NT_026437.10 | TGACCTCGCACAACAGGTCA | 4645 |
| CDC14B | Chr9 | Complement | NT_008470.16 | TGAACTAGCAGTATAGTTCA | 4646 |
| MFN2 | Chr1 | Normal | NT_021937.16 | TGAACTCAAAGAGGGGGTCA | 4654 |
| LOC378171 | Chr7 | Normal | NT_079596.1 | TGACCTAGATAGAAAGGTCA | 4683 |
| LANCL2 | Chr7 | Normal | NT_079592.1 | TGAACTTGTCAGAGAGGTCA | 4702 |
| BTN2A1 | Chr6 | Normal | NT_007592.13 | TGAACTAGACAGAAGGGTCA | 4742 |
| UBASH3A | Chr21 | Normal | NT_030188.3 | TGAACTCCTATGTTGGGTCA | 4786 |
| JAZF1 | Chr7 | Complement | NT_079592.1 | TGACCTTCATCTCGAGTTCA | 4894 |
| TOP3B2 | Chr22 | Complement | NT_011520.9 | TGAACCACATTGACAGGTCA | 4940 |
| JAZF1 | Chr7 | Complement | NT_007819.14 | TGACCTTCATCTCGAGTTCA | 4963 |
| VIP32 | Chr10 | Complement | NT_030059.11 | TGACCTTTGTACCTGGGTCA | 4974 |

| Gene | Chrom. | ER8 Sequence | Position | Protein |
|-------|--------|--------------|----------|---------|
| *krt13* | Chr17 | TGAACCCGAGAAGGGGGTCA | -3339 | keratin 13 |
| *ddit3* | Chr12 | TGACCTGGGGAGGCGGGTCA | -1830 | DNA-damage-ind. transcript 3; CHOP, CEBPZ, CHOP10, GADD153 |
| *il10* | Chr1 | TGACCTATGGATCAGGGTCA | -1702 | interleukin 10 |
| *runx1/aml1* | Chr21 | TGAACCCCAAACCAGGTTCA | -1662 | runt-related transcription factor 1; acute myeloid leukemia 1 oncogene |
| *tyrobp/dap12* | Chr19 | TGACCTGACTCAGGGGTTCA | -1580 | TYRO protein tyrsine kinase binding protein/DNAX-activation protein 12 |
| *txnrd1* | Chr12 | TGACCCTGGTTCATGGGTCA | -1378 | thioredoxin reductase 1 D3 reg on Affy chips |
| *nfe2l2* | Chr2 | TGAACTCTTATAAGGGTTCA | -1163 | nuclear factor (erythroid-derived 2)-like 2; a.k.a. NRF2 |
| *cdkn2d* | Chr19 | TGACCCAGGGAGAAAGGTCA | -245 | p19ink4d CDK inhibitor |
| *cetp* | Chr16 | TGACCTCGCCTTCAAGGTCA | 418 | cholesteryl ester transfer protein |
| *e4f1* | Chr16 | TGACCTTGAACTTCAGGTCA | 3102 | interacts with tumor suppressors, blocks cell cycle |

*Tavera-Mendoza et al, Supplemental Table 2.*