# SUPPORTING INFORMATION

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## SUPPLEMENTAL METHODS

### Antibody-Dependent Cell-Mediated Cytotoxicity assay

For Antibody-Dependent Cell-Mediated Cytotoxicity assay (ADCC), $10^6$ target cells were labelled with 125 μCi $^{51}$Cr by incubating for 1 h at 37°C. After washing, labeled cells were resuspended in regular culture medium. PBMC prepared by centrifugation on a Ficoll density gradient from healthy donors' veinous blood were used as effector cells. Briefly, $10^5$ target cells were mixed with PBMC at effector:target ratios of 50:1, 25:1 or 12.5:1, with 10 μg/ml of Rituximab or Herceptin (as control isotype). After 4-h incubation inhumidified atmosphere of 95% air and carbon dioxide, the $^{51}$Cr-release was determined in the formula 100x(E-S)/(T-S), where E is the cpm released in the presence of effector cells, T is the cpm released after target cells incubation with 1% saponin, and S is the cpm spontaneously released by target cells incubated with medium alone.

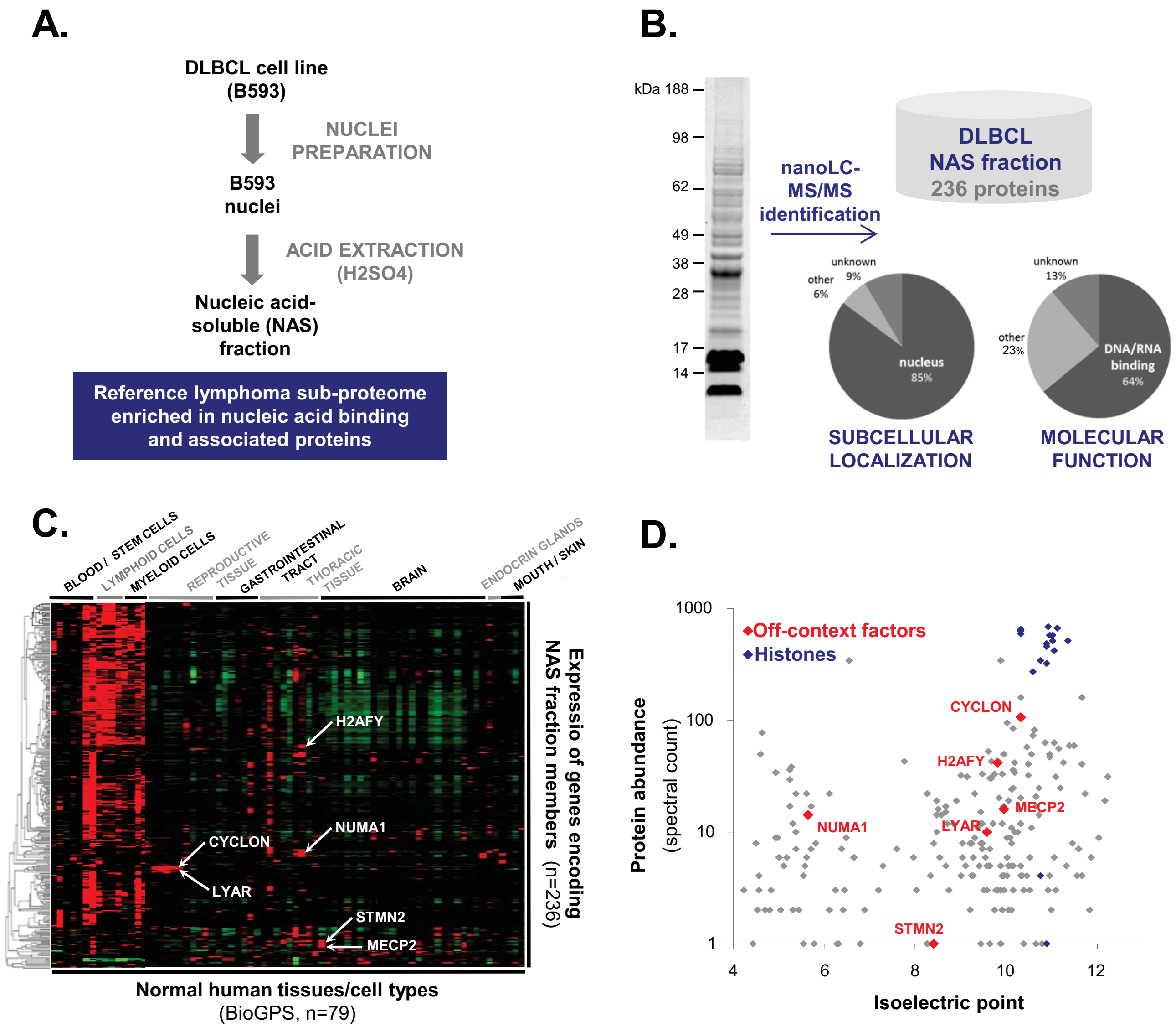
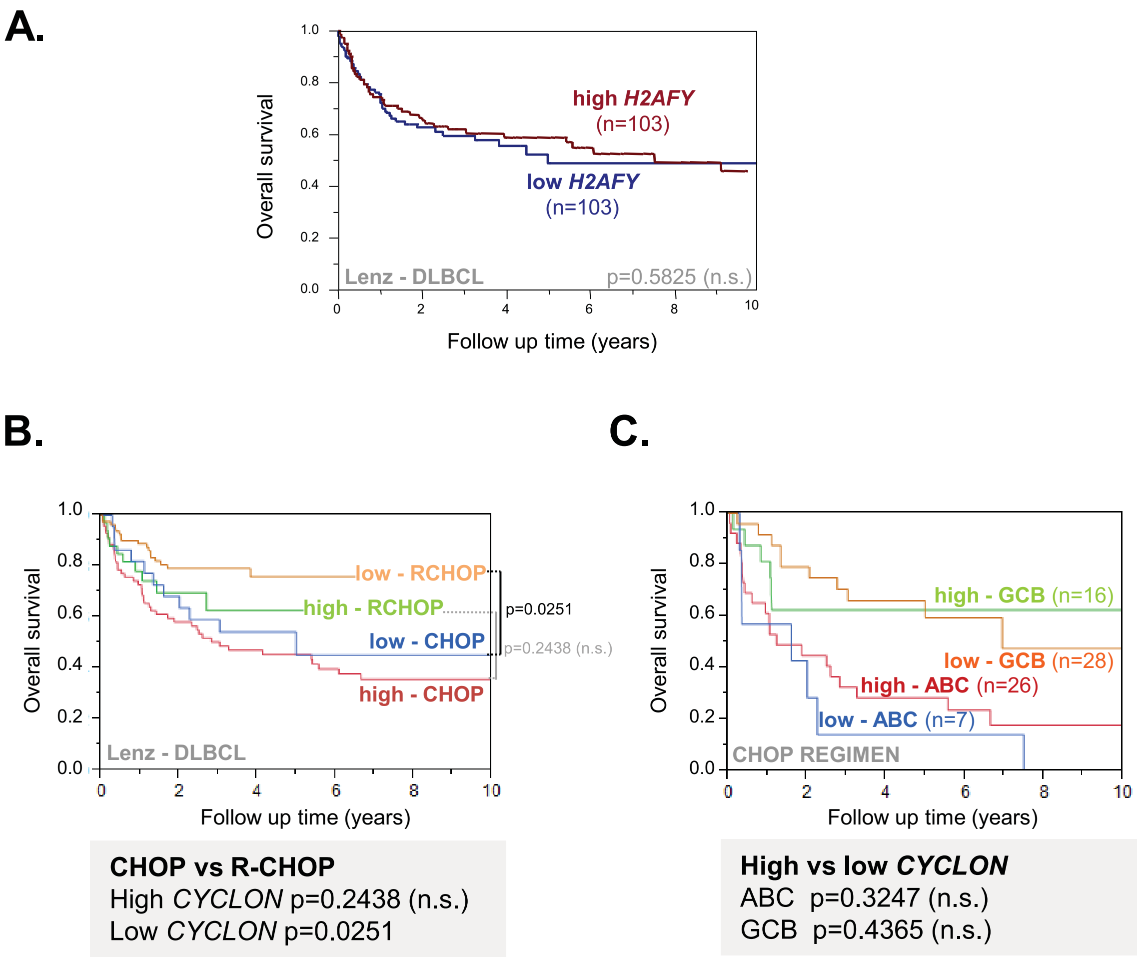


**Figure S1 - Proteomic analysis of a DLBCL nuclear acid soluble (NAS) fraction and identification of nuclear factors which show evidence of abnormal de-repression in lymphoma.**
**A.** Experimental strategy for B593 DLBCL cell line NAS fraction extraction, **B.** SDS-PAGE separation of NAS fraction proteins from the DLBCL cell line (left) and number, subcellular localization and molecular function of proteins identified by mass spectrometry from this fraction (right). **C.** Heat-map of physiological gene expression profiles (79 tissues comprising both lymphoid and non-lymphoid) for genes encoding the 236 factors identified by mass-spectrometry in the NAS fraction of B593 DLBCL cells (retrieved from BioGPS portal). "Off-context" factors are indicated (white arrows). **D.** Relative abundance (retrieved from spectral counts) and isoelectric point of all NAS fraction proteins including "off-context" factors (red) and core histones (blue).



**CHOP vs R-CHOP**
High *CYCLON* p=0.2438 (n.s.)
Low *CYCLON* p=0.0251

**High vs low *CYCLON***
ABC p=0.3247 (n.s.)
GCB p=0.4365 (n.s.)

**Figure S2 - Association of *H2AFY and CYCLON* levels with clinical outcome in DLBCL.**
Kaplan-Meier cumulative survival curves showing predicted survival in DLBCL patients from the Lenz (GEO GSE10846) study, as indicated. **A.** R-CHOP and CHOP-treated patients with high (above 3rd quartile) or low (below 1st quartile) *H2AFY* expression levels. **B.** R-CHOP or CHOP-treated patients with high (above 3rd quartile) or low (below 1st quartile) *CYCLON* expression levels. **C.** CHOP-treated patients with high (above 3rd quartile) or low (below 1st quartile) *CYCLON* expression levels according to DLBCL molecular subtype (ABC or GCB), p value from log-rank test ; n.s. : non significant.

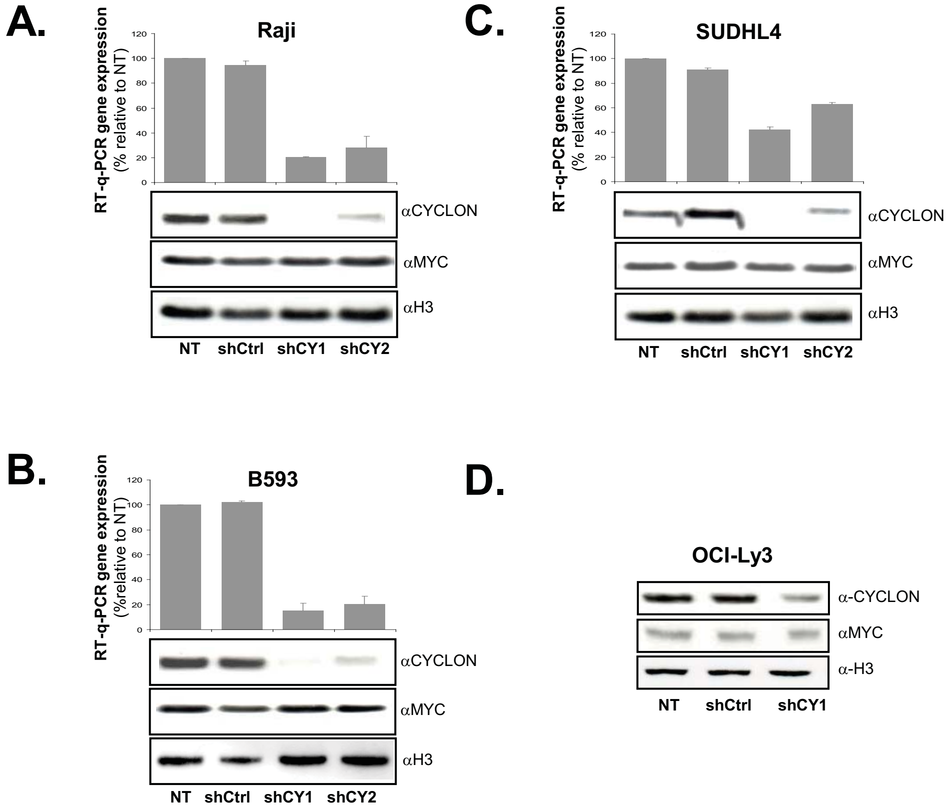


**Figure S3 - Establishment of CYCLON knock-down lymphoma cell lines.**
Expression analysis by RT-qPCR (*CYCLON*) and western blotting (CYCLON, MYC and histone H3, lower panels), as indicated, in Raji (**A**), B593 (**B**), SUDHL4 (**C**) and OCI-Ly3 (**D**) cell lines non transduced (NT), transduced with a non-targeting shRNA (shCtrl), or transduced with CYCLON-targeting shRNA (shCY1 = shCYCLON and CY2) ; n=3

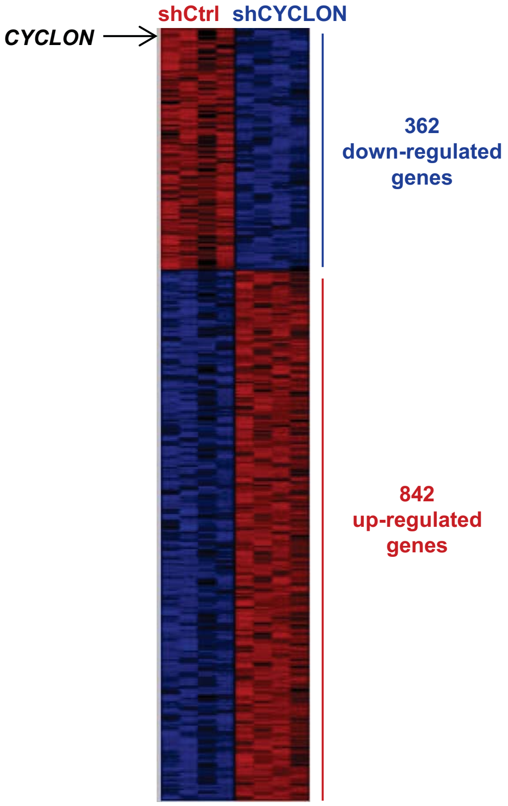


**Figure S4 - Differential expression of genes in CYCLON knock-down Raji lymphoma B cells.**
Heatmap showing differential expression of genes in shCtrl (n=4 biological replicates) or shCYCLON-treated (n=4 biological replicates) Raji B lymphoma cells (unpaired t-test with Benjamini Hochberg correction, corrected p value <0.05, fold change ≥1.2) ; see also Table S2.

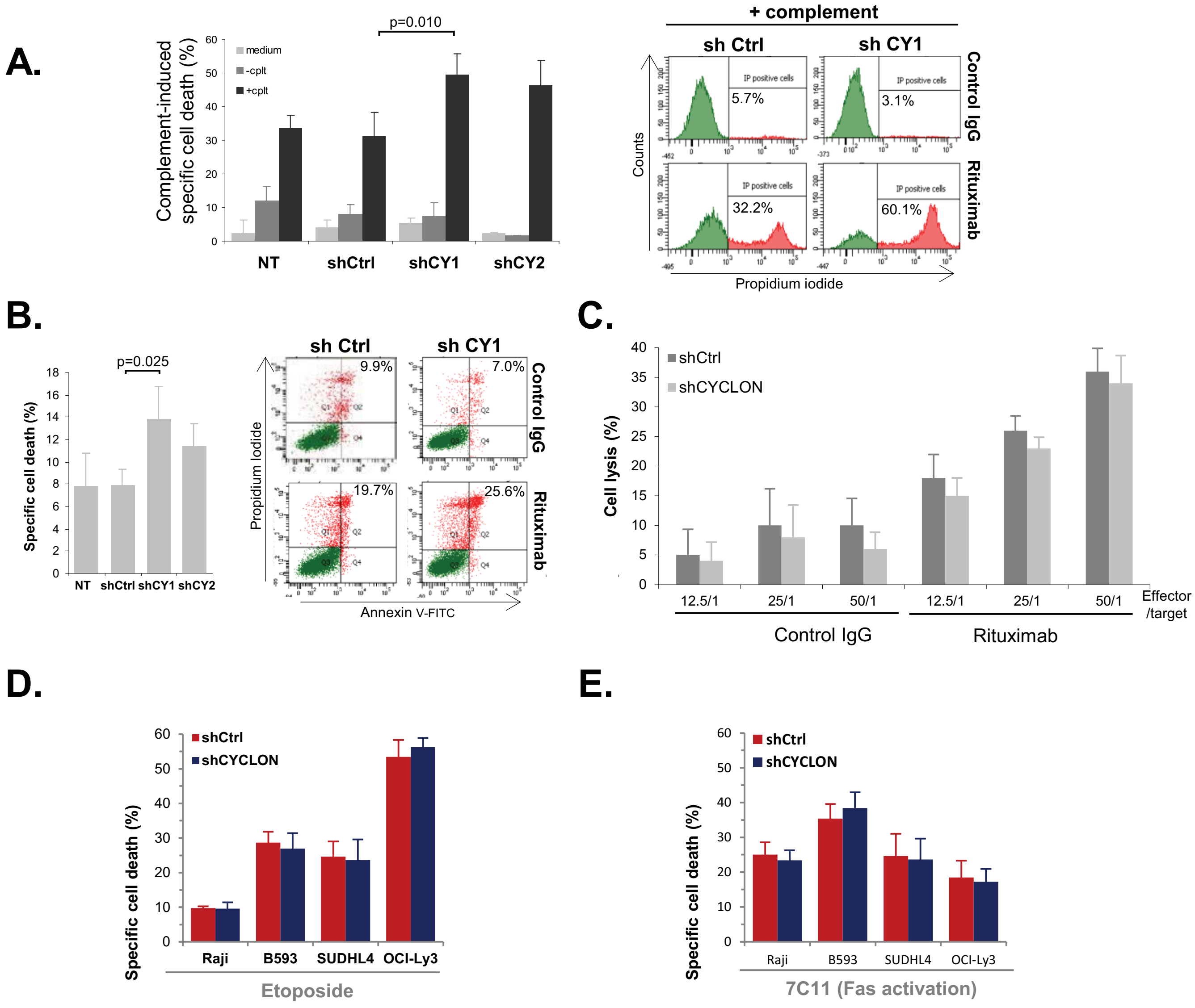


**Figure S5 - Evaluation of drug sensitivity in CYCLON knock-down B lymphoma cells.**
**A-C.** Evaluation of Raji sensitivity to Rituximab for non transduced cells (NT), cells transduced with a non-targeting shRNA (shCtrl), or cells transduced with two different CYCLON targeting shRNA (shCY1 and CY2), respectively. **A.** CDC assays after 1 µg/ml Rituximab or control IgG (Herceptin) treatment for 1h, in the presence or absence of human complement. Typical flow cytometry results using propidium iodide staining for shCtrl and shCY1 in Raji cells. **B.** Rituximab-induced apoptosis assays with 10 µg/ml Rituximab or control IgG (Herceptin) for 24h. Typical flow cytometry results using Annexin V / propidium iodide staining for shCtrl and shCY1 in Raji cells, p values are derived from a Wilcoxon test, n=8 for each cell line. **C.** ADCC $^{51}$Cr release assay in Raji cells: non transduced (NT), transduced with a non-targeting shRNA (shCtrl), or CYCLON-targeting shRNA (shCYCLON); treated with 10 µg/ml of Rituximab or Herceptin (as a control isotype); and with peripheral blood mononuclear cells (PBMC) at effector:target ratios of 50:1, 25:1 or 12.5:1 for 4h as described in Supplemental Methods section. **D-E.** Evaluation of etoposide (**D**) and Fas-dependant apoptosis (**E**) of Raji, B593, SUDHL4 and OCI-Ly3 cells transduced with a non-targeting shRNA (shCtrl) or with a CYCLON-targeting shRNA (shCYCLON), after a 24h treatment with 20 nM etoposide or DMSO and 1 µg/ml anti-FAS (7C11) or control IgG antibodies ; p values are derived from a Wilcoxon test, n=8 for each cell line.

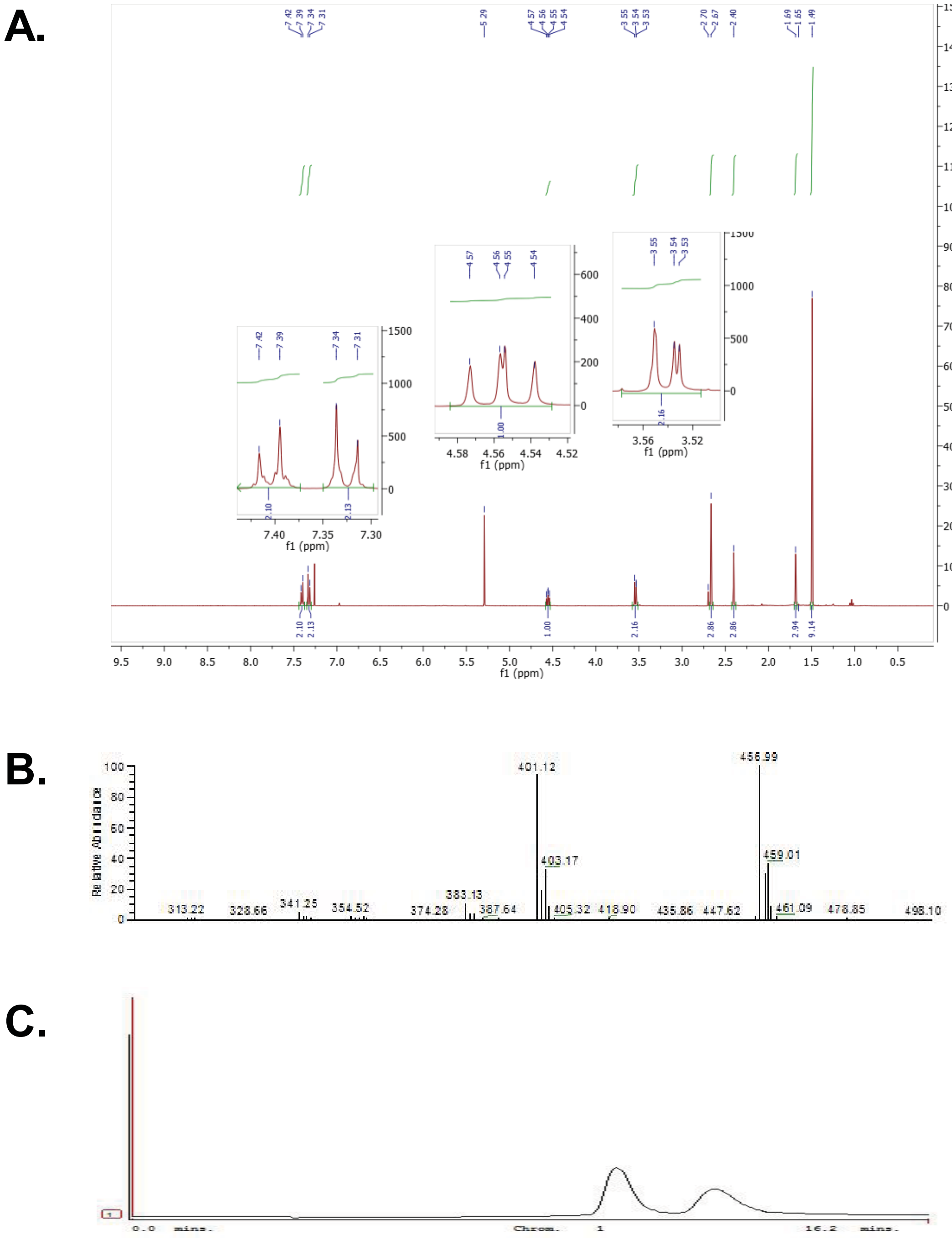


**Figure S6 - Characterization of JQ1 final compound**

**A.** $^1$H NMR spectra (CDCl3, 400MHz, 25°C): δ 7.39 (d, *J* = 8.5 Hz, 2H), 7.31 (d, *J* = 8.4 Hz, 2H), 4.55 (dd, $J^1$ = 6.5 Hz, $J^2$ = 8 Hz, 1H), 3.54 (dd, $J^1$ = 6.5 Hz, $J^2$ = 8 Hz, 2H), 2.67 (s, 3H), 2.40 (s, 3H), 1.69 (s,3H), 1.49 (s, 9H). Consistent with literature values: 1H NMR (600 MHz, CDCl3, 25 °C) δ 7.39 (d, *J* = 8.4 Hz, 2H), 7.31 (d, *J* = 8.4 Hz, 2H), 4.54 (t, *J* = 6.6 MHz, 1H), 3.54-3.52 (m, 2H), 2.66 (s, 3H), 2.39 (s, 3H), 1.67 (s, 3H), 1.48 (s, 9H). **B.** Low Resolution Mass Spectrometry (m/z) of final sample (+ESI). 456.99 [M+H], 401.12 fragmentation peak [M – tBu]. **C.** HPLC trace – analytical chiral column OD-H; *n*-hexane:2-propanol 85:15; (+)-JQ1 r.t.: 10 min, 55%, (-)-JQ1 r.t.: 12 min, 45%.

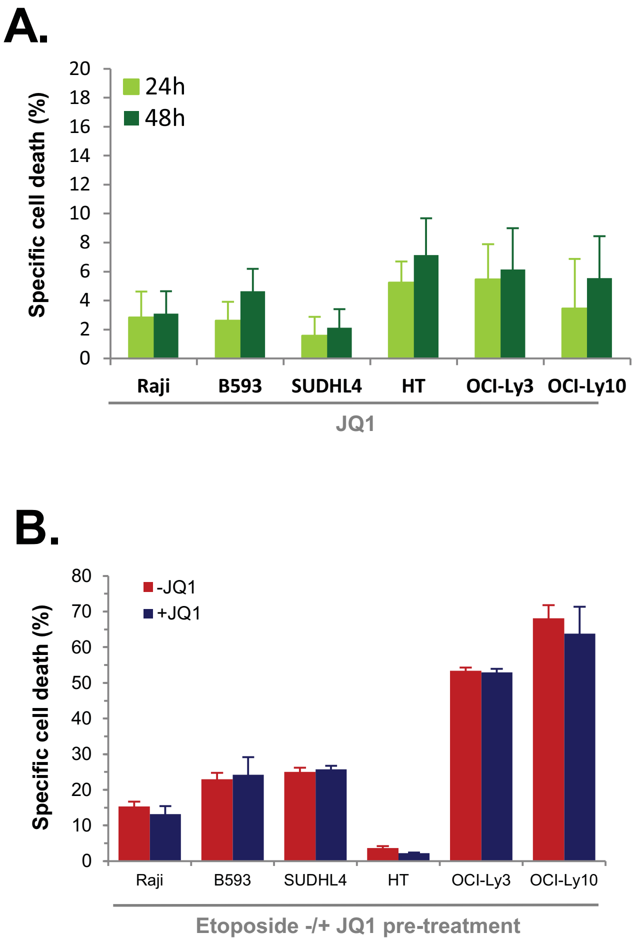


**Figure S7 – Cell death assays upon JQ1 and JQ1/etoposide treatment.**
**A.** Evaluation of specific cell death after a 24h or 48h treatment with 1 μM JQ1 or vehicle (DMSO), Specific cell death **=** [JQ1-DMSO)/(100-DMSO)]x100, n=4 for each cell line. **B**. Evaluation of specific cell death after a 24h pre-treatment with 1 μM JQ1 or vehicle (DMSO) followed by a 24h treatment with 20 μM etoposide or vehicle (DMSO), Specific cell death **=** [etoposide-DMSO)/(100-DMSO)]x100 ; n=4 for each cell line.

**Table S1:** Protein list from LC-MS/MS analysis of B593 NAS fraction

| | Description | Uniprot accession | Uniprot primary accession | Gene name | Mascot score | Mass (kDa) | Protein coverage (%) | Peptides number (distinct) | Peptide number (redundant) = spectral count | pI | Molecular fonction[1] | Biological process[1] | Subcellular localisation[1] | Alternative localisation[1] |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | (P16401) Histone H1.5 (Histone H1a) | H15_HUMAN | P16401 | HIST1H1B,H1F5 | 1720.472416 | 22435 | 67.49 | 33 | 692 | 10.91 | DNA binding | chromatin organization | nucleus | |
| 2 | (P68431) Histone H3.1 (H3/a) (H3/b) (H3/c) (H3/d) ( | H31_HUMAN | P68431 | HIST1H3A,H3FA,HIST1H3B,H3F | 1089.92417 | 15263 | 63.77 | 26 | 668 | 11.13 | DNA binding | chromatin organization | nucleus | |
| 3 | (P62807) Histone H2B.a/g/h/k/l (H2B.1 A) (H2B/a) (I | H2B1C_HUMAN | P62807 | HIST1H2BC,H2BFL,HIST1H2BE | 769.7848129 | 13767 | 80.00 | 19 | 653 | 10.32 | DNA binding | chromatin organization | nucleus | |
| 4 | (O60814) Histone H2B K (HIRA-interacting protein 1 | H2B1K_HUMAN | O60814 | HIST1H2BK,H2BFT, HIRIP1 | 808.6248129 | 13751 | 81.60 | 19 | 650 | 10.32 | DNA binding | chromatin organization | nucleus | |
| 5 | (P33778) Histone H2B.f (H2B/f) (H2B.1) | H2B1B_HUMAN | P46778 | HIST1H2BB,H2BFF | 766.607904 | 13811 | 73.60 | 16 | 628 | 10.32 | DNA binding | chromatin organization | nucleus | |
| 6 | (P06899) Histone H2B.r (H2B/r) (H2B.1) | H2B1J_HUMAN | P06899 | HIST1H2BJ,H2BFR | 812.9548129 | 13765 | 80.00 | 18 | 628 | 10.32 | DNA binding | chromatin organization | nucleus | |
| 7 | (Q99880) Histone H2B.c (H2B/c) | H2B1L_HUMAN | Q99880 | HIST1H2BL,H2BFC | 813.2348129 | 13813 | 81.60 | 19 | 592 | 10.32 | DNA binding | chromatin organization | nucleus | |
| 8 | (P16403) Histone H1.2 (Histone H1d) | H12_HUMAN | P16403 | HIST1H1C,H1F2 | 1301.288741 | 21221 | 64.06 | 29 | 572 | 10.94 | DNA binding | chromatin organization | nucleus | |
| 9 | (P10412) Histone H1.4 (Histone H1b) | H14_HUMAN | P10412 | HIST1H1E,H1F4 | 1422.480694 | 21721 | 60.91 | 31 | 572 | 11.03 | DNA binding | chromatin organization | nucleus | |
| 10 | (P16402) Histone H1.3 (Histone H1c) | H13_HUMAN | P16402 | HIST1H1D,H1F3 | 1267.520599 | 22205 | 60.19 | 30 | 517 | 11.02 | DNA binding | chromatin organization | nucleus | |
| 11 | (P62805) Histone H4 | H4_HUMAN | P62805 | HIST1H4A,H4/A, H4FA,HIST1H4 | 1292.155271 | 11229 | 76.47 | 23 | 514 | 11.36 | DNA binding | chromatin organization | nucleus | |
| 12 | (P0C0S8) Histone H2A type 1 (H2A.1) | H2A1_HUMAN | P0C0S8 | HIST1H2AG,H2AFP,HIST1H2AI, | 487.1748129 | 13952 | 52.38 | 11 | 485 | 10.9 | DNA binding | chromatin organization | nucleus | |
| 13 | (P20671) Histone H2A type 1-D (H2A.3) | H2A1D_HUMAN | P07910 | HIST1H2AD,H2AFG, | 510.8348129 | 13968 | 52.38 | 12 | 453 | 10.9 | DNA binding | chromatin organization | nucleus | |
| 14 | (P28001) Histone H2A type 1-E (H2A.2) (H2A/m) | H2A1E_HUMAN | P04908 | HIST1H2AE,H2AFA, | 515.1648129 | 13996 | 51.97 | 11 | 416 | 11.05 | DNA binding | chromatin organization | nucleus | |
| 15 | (Q3MIH3) Ubiquitin and ribosomal protein L40, (Ubic | Q3MIH3_HUMAN | P0CG47 | UBA52,hCG_37048, | 264.6 | 14719 | 47.37 | 14 | 340 | 9.87 | stuctural component of ribosome | protein biosynthesis | nucleus | cytoplam |
| 16 | (P16104) Histone H2A.x (H2a/x) | H2AX_HUMAN | P16104 | H2AFX,H2AX, | 288.3338177 | 15004 | 22.54 | 10 | 336 | 10.74 | DNA binding | chromatin organization | nucleus | |
| 17 | (P62988) Ubiquitin | UBIQ_HUMAN | P62979 | RPS27A,UBA80, UBCEP1,UBA5 | 722.8069089 | 8560 | 87.01 | 13 | 336 | 6.56 | other, protein binding | protein targeting and degradation; signal transductio | cytoplasm | nucleus |
| 18 | (Q8IUE6) Histone H2A type 2-B | H2A2B_HUMAN | Q8IUE6 | HIST2H2AB | 290.147904 | 13856 | 35.43 | 9 | 320 | 10.88 | DNA binding | chromatin organization | nucleus | |
| 19 | (Q71UI9) Histone H2AV (H2A.F/Z) | H2AV_HUMAN | Q71UI9 | H2AFV,H2AV, | 283.6307266 | 13369 | 37.19 | 5 | 272 | 10.58 | DNA binding | chromatin organization | nucleus | |
| 20 | (P17096) High mobility group protein HMG-I/HMG-Y | HMGA1_HUMAN | P17096 | HMGA1,HMGIY, | 924.8134436 | 11538 | 73.58 | 18 | 159 | 10.31 | DNA binding | chromatin organization | nucleus | |
| 21 | (P26373) 60S ribosomal protein L13 (Breast basic c | RL13_HUMAN | P26373 | BBC1,OK/SW-cl.46, | 1086.065808 | 24115 | 58.90 | 24 | 158 | 11.65 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 22 | (Q9H6F5) Hypothetical protein FLJ22321 (Hypothet | CCD86_HUMAN | Q9H6F5 | CCDC86,CYCLON, | 1405.406729 | 40211 | 62.74 | 28 | 106 | 10.33 | unknown | unknown | nucleus | |
| 23 | (P05204) Nonhistone chromosomal protein HMG-17 | HMGN2_HUMAN | P05204 | HMGN2,HMG17, | 1148.86 | 9256 | 85.39 | 21 | 94 | 10 | DNA binding | chromatin organization ; transcription (+) | nucleus | |
| 24 | (O76021) Ribosomal L1 domain-containing protein 1 | RL1D1_HUMAN | O76021 | CATX11, CSIG, PBK1,L12, | 1509.316197 | 54939 | 44.89 | 31 | 83 | 10.13 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 25 | (P62424) 60S ribosomal protein L7a (Surfeit locus p | RL7A_HUMAN | P62424 | RPL7A,SURF-3, SURF3, | 913.1176355 | 29846 | 46.86 | 23 | 81 | 10.61 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 26 | (P06748) Nucleophosmin (NPM) (Nucleolar phospho | NPM_HUMAN | P06748 | NPM1,NPM, | 732.2565347 | 32555 | 36.61 | 19 | 78 | 4.64 | other, protein binding | chromatin organization ; apoptosis | nucleus | |
| 27 | (Q02878) 60S ribosomal protein L6 (TAX-responsiv | RL6_HUMAN | Q02878 | RPL6,TXREB1, | 1189.423943 | 32577 | 56.08 | 29 | 72 | 10.59 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 28 | (P62917) 60S ribosomal protein L8 | RL8_HUMAN | P62917 | RPL8 | 827.82 | 27876 | 36.33 | 17 | 63 | 11.04 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 29 | (P62753) 40S ribosomal protein S6 (Phosphoprotei | RS6_HUMAN | P62753 | RPS6,OK/SW-cl.2, | 989.9676355 | 28663 | 43.08 | 24 | 63 | 10.85 | stuctural component of ribosome | protein biosynthesis ; cell cycle | cytoplasm | nucleus |
| 30 | (P0CG48) Polyubiquitin-C | Q53G20_HUMAN | P0CG48 | UBC | 582.1067877 | 23630 | 37.38 | 14 | 60 | 11.4 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 31 | (P84098) 60S ribosomal protein L19 | RL19_HUMAN | P62750 | RPL19 | 466.6138177 | 23451 | 30.05 | 12 | 59 | 11.48 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 32 | (P62750) 60S ribosomal protein L23a | RL23A_HUMAN | P09429 | RPL23A | 629.4738177 | 17684 | 40.63 | 12 | 58 | 10.44 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 33 | (Q86V81) THO complex subunit 4 (Tho4) (Ally of AM | THOC4_HUMAN | Q86V81 | THOC4,ALY, BEF, | 470.987904 | 26741 | 25.40 | 10 | 56 | 11.15 | DNA binding | transcription | nucleus | |
| 34 | (P05114) Nonhistone chromosomal protein HMG-14 | HMGN1_HUMAN | P05114 | HMGN1,HMG14, | 1108.924439 | 10522 | 82.83 | 18 | 52 | 9.61 | DNA binding | chromatin organization | nucleus | |
| 35 | (Q8IXL5) Hypothetical protein HSPC111 (HBV pre-S | Q8IXL5_HUMAN | P50914 | CGI-117, HSPC111 | 679.3107266 | 21175 | 52.08 | 13 | 50 | 9.94 | unknown | unknown | nucleus | |
| 36 | (P50914) 60S ribosomal protein L14 (CAG-ISL 7) | RL14_HUMAN | P83731 | RPL14 | 176.0169089 | 23144 | 20.48 | 13 | 50 | 10.94 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 37 | (P19338) Nucleolin (Protein C23) | NUCL_HUMAN | Q15233 | NCL | 592.8361082 | 76437 | 16.57 | 15 | 50 | 4.6 | DNA/RNA/protein binding | chromatin organization | nucleus | |
| 38 | (P61254) 60S ribosomal protein L26 | RL26_HUMAN | P61254 | RPL26 | 720.040463 | 17248 | 43.59 | 16 | 49 | 10.55 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 39 | (Q6PK04) MGC16597 protein | Q6PK04_HUMAN | Q6PK04 | CCDC137,MGC16597 | 850.3399783 | 33211 | 51.83 | 21 | 47 | 10.94 | unknown | unknown | unknown | |
| 40 | (Q5SSJ5) HP1-BP74 | Q5SSJ5_HUMAN | Q5SSJ5 | HP1BP3,RP5-930J4.3-001, hC | 876.415276 | 61169 | 27.34 | 20 | 43 | 9.69 | DNA binding | chromatin organization | nucleus | |
| 41 | (P26583) High mobility group protein B2 (High mobil | HMGB2_HUMAN | P26583 | HMGB2,HMG2, | 997.0805731 | 23888 | 63.59 | 23 | 43 | 7.77 | DNA binding | chromatin organization ; DNA repair | nucleus | |
| 42 | (P83731) 60S ribosomal protein L24 (Ribosomal pro | RL24_HUMAN | P18124 | RPL24 | 542.3086307 | 17768 | 45.34 | 13 | 42 | 11.26 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 43 | (P22087) Fibrillarin (34 kDa nucleolar scleroderma a | FBRL_HUMAN | P60709 | FBL, FIB1, FLRN | 856.3209952 | 33763 | 49.37 | 15 | 42 | 10.18 | RNA binding | ribosome biogenesis | nucleus | |
| 44 | (O75367) Core histone macro-H2A.1 (Histone macr | H2AY_HUMAN | P22087 | H2AFY,MACROH2A1, | 1068.89089 | 39461 | 36.03 | 15 | 42 | 9.8 | DNA binding | chromatin organization | nucleus | |
| 45 | (P47914) 60S ribosomal protein L29 (Cell surface h | RL29_HUMAN | P47914 | RPL29 | 438.7 | 17610 | 38.13 | 10 | 41 | 11.66 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 46 | (P46778) 60S ribosomal protein L21 | RL21_HUMAN | Q9BXS6 | RPL21 | 682.2807266 | 18422 | 53.89 | 15 | 41 | 10.49 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 47 | (P60709) Actin, cytoplasmic 1 (Beta-actin) | ACTB_HUMAN | Q9Y3A2 | ACTB | 900.0676355 | 41710 | 36.68 | 15 | 38 | 5.29 | other, structural protein | cell structure | cytoplasm | nucleus |
| 48 | (P62701) 40S ribosomal protein S4, X isoform (Sing | RS4X_HUMAN | P62987 | RPS4X,CCG2, RPS4, SCAR, | 581.9807266 | 29448 | 36.70 | 13 | 36 | 10.16 | stuctural component of ribosome | protein biosynthesis ; cell cycle | cytoplasm | nucleus |
| 49 | (P10809) 60 kDa heat shock protein, mitochondrial | CH60_HUMAN | P10809 | HSPD1,HSP60, | 972.9414532 | 61016 | 27.44 | 20 | 36 | 5.24 | other, protein binding | protein folding | cytoplasm, mitochondria | nucleus |
| 50 | (P18621) 60S ribosomal protein L17 (L23) | RL17_HUMAN | P20671 | RPL17 | 454.88 | 21252 | 36.79 | 11 | 34 | 10.18 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 51 | (P07910) Heterogeneous nuclear ribonucleoproteins | HNRPC_HUMAN | P11142 | HNRNPC,HNRPC, | 637.3707266 | 33650 | 40.66 | 12 | 34 | 4.95 | RNA binding | RNA processing | nucleus | |
| 52 | (Q9BXS6) Liver nuclear protein | NUSAP_HUMAN | P19338 | NUSAP1,ANKT,BM-037, PRO03 | 744.8186307 | 49422 | 36.97 | 15 | 33 | 9.92 | DNA binding | cell proliferation, cell cycle (+) | nucleus | |
| 53 | (Q5VV70) Nucleolar and coiled-body phosphoprotei | Q5VV70_HUMAN | P33778 | NOLC1,RP11-302K17.5-001, h | 692.8032856 | 73560 | 19.16 | 16 | 33 | 9.46 | RNA binding | RNA processing | nucleus | |
| 54 | (P61247) 40S ribosomal protein S3a | RS3A_HUMAN | P61247 | RPS3A,MFTL, | 674.6062711 | 29795 | 49.63 | 16 | 33 | 9.75 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 55 | (O00479) High-mobility group nucleosome-binding d | HMGN4_HUMAN | O00479 | HMGN4,HMG17L3, NHC, | 168.46 | 9402 | 30.34 | 6 | 32 | 10.48 | DNA binding | chromatin organization ; transcription (+) | nucleus | |
| 56 | (Q15233) Non-POU domain-containing octamer-bind | NONO_HUMAN | O75367 | NONO, NRB54 | 122.8669089 | 54197 | 6.71 | 15 | 32 | 9.01 | DNA/RNA/protein binding | transcription ; recombinaison ; RNA splicing | nucleus | |
| 57 | (Q9Y3Y2) Protein C1orf77 | CA077_HUMAN | Q9Y3Y2 | C1orf77,HT031, PP7704, | 390.8369089 | 26380 | 29.29 | 8 | 31 | 12.24 | unknown | unknown | unknown | |
| 58 | (O75475) PC4 and SFRS1-interacting protein (Lens | PSIP1_HUMAN | Q9Y3C1 | PSIP1,DFS70, LEDGF, PSIP2, | 468.380463 | 60067 | 20.33 | 13 | 31 | 9.15 | DNA binding | transcription | nucleus | |
| 59 | (P36578) 60S ribosomal protein L4 (L1) | RL4_HUMAN | P36578 | RPL4,RPL1, | 642.3988992 | 47536 | 25.46 | 17 | 31 | 11.07 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 60 | (Q00059) Transcription factor A, mitochondrial prec | TFAM_HUMAN | Q00059 | TFAM,TCF6L2, | 311.8138177 | 29078 | 20.83 | 7 | 30 | 9.65 | DNA binding | transcription | mitochondria | nucleus |
| 61 | (P23396) 40S ribosomal protein S3 | RS3_HUMAN | P23396 | RPS3,OK/SW-cl.26, | 846.4969089 | 26671 | 61.32 | 16 | 30 | 9.68 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 62 | (P62736) Actin, aortic smooth muscle (Alpha-actin-2 | ACTA_HUMAN | P62736 | ACTSA, ACTVS,GIG46, | 236.73 | 41982 | 10.50 | 11 | 29 | 5.24 | other, structural protein | cell structure | cytoplasm | nucleus |
| 63 | (P14678) Small nuclear ribonucleoprotein-associate | RSMB_HUMAN | P14678 | SNRPB,COD, SNRPB1, | 329.11 | 24594 | 34.56 | 7 | 25 | 11.2 | RNA binding | RNA processing | nucleus | |
| 64 | (Q02543) 60S ribosomal protein L18a | RL18A_HUMAN | Q02543 | RPL18A | 274.54 | 20749 | 23.94 | 9 | 25 | 10.72 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 65 | (Q9Y3A2) Probable U3 small nucleolar RNA-associa | UTP11_HUMAN | Q3MIH3 | UTP11L,CGI-94, HDCMB12P, | 369.8729855 | 30428 | 26.81 | 14 | 25 | 10.16 | RNA binding | RNA processing | nucleus | cytoplasm |
| 66 | (Q6IB29) EBNA1BP2 protein (EBNA1 binding protei | Q6IB29_HUMAN | Q6IB29 | EBNA1BP2,RP5-1034F7.2-001, | 411.967904 | 34830 | 25.95 | 10 | 24 | 10.1 | RNA binding | ribosome biogenesis | nucleus | |
| 67 | (Q06830) Peroxiredoxin-1 (EC 1.11.1.15) (Thioredo | PRDX1_HUMAN | Q06830 | PRDX1,PAGA, PAGB, TDPX2, | 174.28 | 22096 | 22.50 | 6 | 22 | 8.27 | other, metabolic enzyme, deshydrogenase | cell metabolism | cytoplasm | nucleus |
| 68 | (Q07020) 60S ribosomal protein L18 | RL18_HUMAN | Q07020 | RPL18 | 344.8709952 | 21490 | 30.26 | 8 | 22 | 11.73 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 69 | (Q9ULW0) Targeting protein for Xklp2 (Restricted e | TPX2_HUMAN | Q9ULW0 | TPX2,C20orf1, C20orf2, DIL2, H | 287.6691993 | 85600 | 10.80 | 8 | 22 | 9.29 | other, protein binding | cell structure, cell cycle | nucleus | |
| 70 | (P82979) Nuclear protein Hcc-1 (Proliferation-assoc | HCC1_HUMAN | P82979 | HCC1,HSPC316, | 580.7229855 | 23525 | 47.42 | 11 | 22 | 6.12 | DNA binding | transcription, cell cycle (+) | nucleus | |
| 71 | (P11142) Heat shock cognate 71 kDa protein (Heat | HSP7C_HUMAN | P84098 | HSPA8,HSC70, HSP73, HSPA1 | 652.1348129 | 70854 | 19.10 | 12 | 22 | 5.37 | other, protein binding | protein folding | cytoplasm | nucleus |
| 72 | (P09429) High mobility group protein B1 (High mobil | HMGB1_HUMAN | O75475 | HMGB1,HMG1, | 561.2042808 | 24747 | 36.16 | 13 | 22 | 5.62 | DNA binding | chromatin organization ; apoptosis (-) | nucleus | |
| 73 | (P18124) 60S ribosomal protein L7 | RL7_HUMAN | P62701 | RPL7 | 419.0807266 | 29207 | 36.23 | 13 | 21 | 10.66 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 74 | (P62241) 40S ribosomal protein S8 | RS8_HUMAN | P62241 | RPS8,OK/SW-cl.83, | 313.7909952 | 24059 | 27.06 | 7 | 20 | 10.32 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 75 | (P09012) U1 small nuclear ribonucleoprotein A (U1 s | SNRPA_HUMAN | P09012 | SNRPA | 213.3753816 | 31128 | 22.70 | 10 | 20 | 9.83 | RNA binding | RNA processing | nucleus | |
| 76 | (P62861) 40S ribosomal protein S30 | RS30_HUMAN | P62861 | FAU | 149.4048129 | 6644 | 33.33 | 4 | 19 | 12.15 | stuctural component of ribosome | protein biosynthesis ; apoptosis (-) | cytoplasm | nucleus |
| 77 | (P38159) Heterogeneous nuclear ribonucleoprotein | HNRPG_HUMAN | P38159 | RBMX,HNRPG, RBMXP1, | 199.2119903 | 42306 | 13.80 | 5 | 19 | 10.06 | RNA binding | RNA processing | nucleus | |
| 78 | (P37802) Transgelin-2 (SM22-alpha homolog) | TAGL2_HUMAN | P37802 | TAGLN2,KIAA0120,CDABP0035 | 327.9469089 | 22246 | 33.66 | 7 | 19 | 8.45 | unknown | cell structure | cytoplasm | nucleus, plasma membrane |
| 79 | (P61604) 10 kDa heat shock protein, mitochondrial | CH10_HUMAN | P61604 | HSPE1 | 464.9209952 | 10794 | 61.22 | 9 | 19 | 8.91 | other, protein binding | protein folding | cytoplasm | mitochondria |
| 80 | (Q13185) Chromobox protein homolog 3 (Heterochr | CBX3_HUMAN | Q13185 | CBX3 | 296.3869089 | 20810 | 20.11 | 7 | 17 | 5.23 | other, protein binding | chromatin organization ; transcription (-) | nucleus | cytoplasm |
| 81 | (P46781) 40S ribosomal protein S9 | RS9_HUMAN | P46781 | RPS9 | 254.9469089 | 22447 | 29.90 | 7 | 17 | 10.66 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 82 | (P07195) L-lactate dehydrogenase B chain (EC 1.1 | LDHB_HUMAN | P07195 | LDHB | 481.44 | 36484 | 26.59 | 8 | 17 | 5.72 | other, metabolic enzyme, deshydrogenase | cell metabolism | cytoplasm | |
| 83 | (Q8NC51) Plasminogen activator inhibitor 1 RNA-bi | PAIRB_HUMAN | Q8NC51 | PAIRBP1,CGI-55, | 443.0238177 | 44938 | 21.81 | 10 | 17 | 8.66 | RNA/protein binding | translation | nucleus | |
| 84 | (Q6QHH9) Methyl CpG binding protein 2 isoform B | Q6QHH9_HUMAN | P30050 | CCDC137 | 494.5975299 | 53291 | 24.17 | 11 | 17 | 9.95 | DNA binding | transcription (-) | nucleus | |
| 85 | (P51608) Methyl-CpG-binding protein 2 (MeCP-2 pr | MECP2_HUMAN | P51608 | MECP2 | 365.7617218 | 52409 | 15.13 | 10 | 16 | 9.95 | DNA binding | transcription (-) | nucleus | |
| 86 | (O15347) High mobility group protein B3 (High mobil | HMGB3_HUMAN | O15347 | HMGB3,HMG2A, HMG4, | 328.267904 | 22834 | 27.54 | 8 | 16 | 8.5 | DNA binding | chromatin organization ; B cell differentiation (-) | nucleus | |
| 87 | (O95478) TGF-beta-inducible nuclear protein 1 (Hai | TIP1_HUMAN | O95478 | TINP1,HUSSY-29, | 304.7988992 | 30047 | 24.18 | 9 | 16 | 10.28 | unknown | unknown | nucleus | |
| 88 | (O15446) RNA polymerase I-associated factor PAF | PAF49_HUMAN | O15446 | CD3EAP,ASE1, CAST, PAF49, | 254.3439807 | 54951 | 17.03 | 7 | 15 | 8.66 | other, protein binding | transcription ; ribosme biogenesis | nucleus | |
| 89 | (P23246) Splicing factor, proline- and glutamine-rich | SFPQ_HUMAN | P23246 | SFPQ,PSF, | 259.7109952 | 76102 | 11.11 | 8 | 15 | 9.45 | RNA binding | RNA processing, transcription (-), DNA repair | nucleus | |
| 90 | (Q14980) Nuclear mitotic apparatus protein 1 (NuMA | NUMA1_HUMAN | Q14980 | NUMA1,NUMA, | 450.1716162 | 238130 | 5.27 | 10 | 14 | 5.63 | other, protein binding | cell cycle ; cell structure | nucleus | |
| 91 | (P62857) 40S ribosomal protein S28 | RS28_HUMAN | P62857 | RPS28 | 233.4009952 | 7836 | 57.75 | 5 | 14 | 10.7 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 92 | (P04406) Glyceraldehyde-3-phosphate dehydrogen | G3P_HUMAN | P04406 | GAPD,CDABP0047, OK/SW-cl.1 | 297.67 | 35899 | 26.99 | 7 | 14 | 8.58 | other, metabolic enzyme, deshydrogenase | cell metabolism | cytoplasm | nucleus |
| 93 | (P00338) L-lactate dehydrogenase A chain (EC 1.1 | LDHA_HUMAN | P00338 | LDHA,PIG19, | 327.75 | 36534 | 18.37 | 7 | 14 | 8.46 | other, metabolic enzyme, deshydrogenase | cell metabolism | cytoplasm | |
| 94 | (P61956) Small ubiquitin-related modifier 2 precurso | SUMO2_HUMAN | P61956 | SUMO2,SMT3B, SMT3H2, | 138.2609952 | 10864 | 28.57 | 3 | 12 | 5.32 | other, protein binding | protein targeting and degradation; signal transductio | nucleus | |
| 95 | (P08579) U2 small nuclear ribonucleoprotein B"" | RU2B_HUMAN | P08579 | SNRPB2 | 159.68 | 25470 | 14.72 | 5 | 12 | 9.72 | RNA binding | RNA processing | nucleus | |
| 96 | (P35659) Protein DEK | DEK_HUMAN | P35659 | DEK | 301.1722904 | 42648 | 14.99 | 7 | 12 | 8.69 | DNA/histone binding | chromatin organization ; transcription (-) | nucleus | |
| 97 | (P56182) NNP-1 protein (Novel nuclear protein 1) (N | NNP1_HUMAN | P56182 | RRP1, D21S2056E, NNP1, NOP | 346.097904 | 52807 | 16.04 | 7 | 12 | 9.39 | RNA binding | ribosome biogenesis | nucleus | |
| 98 | (Q14978) Nucleolar phosphoprotein p130 (Nucleola | NOLC1_HUMAN | Q14978 | NOLC1,KIAA0035, | 522.5022904 | 73677 | 16.74 | 7 | 12 | 9.46 | RNA binding | ribosome biogenesis | nucleus | |
| 99 | (Q6P6B4) Hypothetical protein C1orf131 | Q6P6B4_HUMAN | Q8NDD1 | C1orf131,DKFZp547B1713 | 333.5569089 | 32576 | 18.92 | 7 | 12 | 9.92 | unknown | unknown | unknown | |
| 100 | (Q13442) 28 kDa heat- and acid-stable phosphopro | HAP28_HUMAN | Q13442 | PDAP1,HASPP28, | 489.6313574 | 20618 | 47.59 | 9 | 12 | 8.84 | other, protein binding | signal transduction, cell cycle | cytoplam | nucleus |
| 101 | (P62280) 40S ribosomal protein S11 | RS11_HUMAN | P62280 | RPS11 | 397.2917218 | 18419 | 38.32 | 9 | 12 | 10.31 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 102 | (P30050) 60S ribosomal protein L12 | RL12_HUMAN | P18621 | RPL12 | 529.8609952 | 17808 | 56.52 | 11 | 12 | 9.48 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 103 | (P62899) 60S ribosomal protein L31 | RL31_HUMAN | P62899 | RPL31 | 143.47 | 14454 | 21.37 | 3 | 11 | 10.54 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 104 | (P62851) 40S ribosomal protein S25 | RS25_HUMAN | P62851 | RPS25 | 128.5 | 13734 | 20.97 | 3 | 11 | 10.12 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 105 | (O00422) Histone deacetylase complex subunit SAP | SAP18_HUMAN | O00422 | SAP18,GIG38, | 397.89 | 17550 | 37.11 | 8 | 11 | 9.38 | other, protein binding | chromatin organization | nucleus | |
| 106 | (Q9NX58) Cell growth-regulating nucleolar protein | LYAR_HUMAN | Q9NX58 | LYAR,PNAS-5, | 101.3509952 | 43588 | 7.32 | 4 | 10 | 9.57 | other, protein binding | cell cycle | nucleus | plasma membrane |
| 107 | (Q9NX24) H/ACA ribonucleoprotein complex subunit | NOLA2_HUMAN | Q9NX24 | NHP2,HSPC286, | 181.96 | 17190 | 16.67 | 3 | 10 | 8.48 | RNA binding | ribosome biogenesis | nucleus | |
| 108 | (Q96EU6) Hypothetical protein C6orf153 (OTTHUM | Q96EU6_HUMAN | Q96EU6 | C6orf153,HSPC253, | 249.6007266 | 29805 | 20.00 | 6 | 10 | 10.17 | unknown | unknown | unknown | |
| 109 | (P15880) 40S ribosomal protein S2 (S4) (LLRep3 p | RS2_HUMAN | P15880 | RPS2,RPS4, | 225.8369089 | 31305 | 14.44 | 6 | 10 | 10.25 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 110 | (P61978) Heterogeneous nuclear ribonucleoprotein | HNRPK_HUMAN | P61978 | HNRPK,HNRNPK, | 296.11 | 50944 | 14.90 | 7 | 10 | 5.39 | RNA binding | RNA processing ; signal transduction | nucleus | cytoplasm |
| 111 | (P62081) 40S ribosomal protein S7 | RS7_HUMAN | P62081 | RPS7 | 69.75099517 | 22113 | 11.44 | 4 | 9 | 10.09 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 112 | (Q9NR30) Nucleolar RNA helicase 2 (EC 3.6.1.-) (N | DDX21_HUMAN | Q9NR30 | DDX21 | 178.652717 | 87290 | 7.19 | 5 | 9 | 9.32 | RNA binding ; helicase | translation | nucleus | |
| 113 | (P01871) Ig mu chain C region | MUC_HUMAN | P01871 | IGHM | 212.42 | 49526 | 11.11 | 5 | 9 | 6.47 | other, protein binding | cell metabolism | secreted | |
| 114 | (Q9Y2S6) Coiled-coil domain-containing protein 72 | CCD72_HUMAN | Q9Y2S6 | CCDC72,HSPC016, HSPC330, | 209.58 | 7062 | 50.00 | 6 | 9 | 10 | unknown | unknown | unknown | |
| 115 | (P08238) Heat shock protein HSP 90-beta (HSP 84 | HS90B_HUMAN | P08238 | HSP90AB1,HSP90B, HSPC2, H | 258.9015638 | 83081 | 8.21 | 6 | 9 | 4.97 | other, protein binding | protein folding | cytoplasm | mitochondria |
| 116 | (P07900) Heat shock protein HSP 90-alpha (HSP 8 | HS90A_HUMAN | P07900 | HSP90AA1,HSP90A, HSPC1, H | 275.0715638 | 84476 | 7.69 | 7 | 9 | 4.94 | other, protein binding | protein folding | cytoplasm | nucleus |
| 117 | (P00558) Phosphoglycerate kinase 1 (EC 2.7.2.3) ( | PGK1_HUMAN | P00558 | PGKA,MIG10, OK/SW-cl.110, | 199.63 | 44455 | 10.82 | 7 | 9 | 8.3 | other, metabolic enzyme, deshydrogenase | cell metabolism | cytoplasm | |
| 118 | (P46779) 60S ribosomal protein L28 | RL28_HUMAN | P46779 | RPL28 | 379.4007266 | 15607 | 45.39 | 9 | 9 | 12.02 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 119 | (P63173) 60S ribosomal protein L38 | RL38_HUMAN | P63173 | RPL38 | 145.64 | 8082 | 16.44 | 3 | 8 | 10.1 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 120 | (Q15717) ELAV-like protein 1 (Hu-antigen R) (HuR) | ELAV1_HUMAN | Q15717 | ELAVL1,HUR, | 203.11 | 36069 | 11.62 | 4 | 8 | 9.23 | RNA binding | translation | nucleus | cyoplasm |
| 121 | (P17066) Heat shock 70 kDa protein 6 (Heat shock | HSP76_HUMAN | P17066 | HSPA6,HSP70B', | 191.4009952 | 70984 | 6.51 | 4 | 8 | 5.81 | other, protein binding | protein folding | cytoplasm | nucleus |
| 122 | (Q9BRP8) Within bgcn homolog | Q9BRP8_HUMAN | Q9BRP8 | WIBG,PYM, | 278.6109952 | 22642 | 23.41 | 4 | 8 | 9.45 | unknown | unknown | nucleus | |
| 123 | (O60832) H/ACA ribonucleoprotein complex subunit | DKC1_HUMAN | O60832 | DKC1, NOLA4 | 137.0909952 | 57507 | 9.00 | 5 | 8 | 9.46 | RNA binding | ribosome biogenesis ; telomerase ; | nucleus | |
| 124 | (O75937) DnaJ homolog subfamily C member 8 (Sp | DNJC8_HUMAN | O75937 | SPF31,HSPC315, HSPC331, | 155.0819903 | 29823 | 12.92 | 5 | 8 | 9.04 | other, protein binding | protein folding | nucleus | |
| 125 | (O43516) Wiskott-Aldrich syndrome protein-interact | WASIP_HUMAN | O43516 | WIPF1,WASPIP, WIP, | 175.29 | 51243 | 12.04 | 5 | 8 | 11.47 | other, protein binding | cell structure | cytoplasm | nucleus |
| 126 | (P04075) Fructose-bisphosphate aldolase A (EC 4.1 | ALDOA_HUMAN | P04075 | ALDOA,ALDA, | 172.0669089 | 39264 | 12.64 | 6 | 8 | 8.39 | other, transporter | cell metabolism | cytoplasm | plasma membrane |
| 127 | (Q9UKM9) RNA-binding protein Raly (hnRNP associ | RALY_HUMAN | Q9UKM9 | RALY,HNRPCL2, P542, | 157.9869089 | 32444 | 15.65 | 6 | 8 | 9.2 | RNA binding | RNA processing | nucleus | |
| 128 | (Q9BQE6) MGC2477 protein | Q9BQE6_HUMAN | Q9BQE6 | C11orf48 | 454.27 | 18384 | 38.92 | 8 | 8 | 4.52 | unknown | unknown | unknown | |
| 129 | (Q14103) Heterogeneous nuclear ribonucleoprotein | HNRPD_HUMAN | Q14103 | HNRPD,AUF1, | 181.0938177 | 38410 | 9.74 | 3 | 7 | 7.61 | DNA/RNA binding | transcription, RNA splicing | nucleus | cytoplasm |
| 130 | (Q9Y3U8) 60S ribosomal protein L36 | RL36_HUMAN | Q9Y3U8 | RPL36 | 110.23 | 12115 | 18.18 | 3 | 7 | 11.59 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 131 | (P45973) Chromobox protein homolog 5 (Heterochr | CBX5_HUMAN | P45973 | CBX5,HP1A, | 140.6669089 | 22211 | 9.95 | 4 | 7 | 5.71 | other, protein binding | chromatin organization ; transcription (-) | nucleus | cytoplasm |
| 132 | (Q9Y3B9) CGI-115 protein | Q9Y3B9_HUMAN | Q9Y3B9 | CGI-115, KIAA0507, | 229.8009952 | 28955 | 18.25 | 4 | 7 | 5.39 | other, protein binding | translation | nucleus | |
| 133 | (P62888) 60S ribosomal protein L30 | RL30_HUMAN | P62888 | RPL30 | 151.4369089 | 12645 | 32.46 | 4 | 7 | 9.65 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 134 | (P46013) Antigen KI-67 | KI67_HUMAN | P46013 | MKI67 | 128.2458081 | 358526 | 1.10 | 5 | 7 | 9.49 | other, protein binding | cell cycle (+) | nucleus | |
| 135 | (P31948) Stress-induced-phosphoprotein 1 (STI1) ( | STIP1_HUMAN | P31948 | STIP1 | 173.6838177 | 62599 | 8.08 | 5 | 7 | 6.4 | other, protein binding | protein folding | cytoplasm | nucleus |
| 136 | (P84090) Enhancer of rudimentary homolog | ERH_HUMAN | P84090 | ERH | 101.9719903 | 12251 | 14.41 | 2 | 6 | 5.62 | unknown | unknown | unknown | |
| 137 | (Q12905) Interleukin enhancer-binding factor 2 (Nuc | ILF2_HUMAN | Q12905 | NF45,PRO3063, | 161.03 | 43035 | 7.93 | 3 | 6 | 5.19 | DNA/RNA binding | transcription | nucleus | |
| 138 | (P42766) 60S ribosomal protein L35 | RL35_HUMAN | P42766 | RPL35 | 93.46 | 14412 | 14.50 | 3 | 6 | 11.04 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 139 | (Q9H7B2) Brix domain-containing protein 1 | BXDC1_HUMAN | Q9H7B2 | BXDC1 | 90.88 | 35560 | 7.43 | 4 | 6 | 10 | RNA binding | ribosome biogenesis | nucleus | |
| 140 | (P11021) 78 kDa glucose-regulated protein precurs | GRP78_HUMAN | P11021 | HSPA5,GRP78, | 179.67 | 72288 | 6.09 | 4 | 6 | 5.01 | other, protein binding | protein folding ; apoptosis | endoplasmic reticulum | nucleus |
| 141 | (P14618) Pyruvate kinase isozymes M1/M2 (EC 2.7 | KPYM_HUMAN | P14618 | PKM2,PK2, PK3, PKM, | 86.7 | 57769 | 4.95 | 4 | 6 | 7.95 | other, metabolic enzyme, deshydrogenase | cell metabolism | cytoplasm | |
| 142 | (P40926) Malate dehydrogenase, mitochondrial pre | MDHM_HUMAN | P40926 | MDH2 | 135.92 | 35509 | 8.95 | 4 | 6 | 8.54 | other, metabolic enzyme, deshydrogenase | cell metabolism | cytoplasm | mitochondria |
| 143 | (Q9Y2X3) Nucleolar protein NOP5 (Nucleolar protei | NOP5_HUMAN | Q9Y2X3 | NOP5,HSPC120, | 129.95 | 59541 | 5.55 | 4 | 6 | 9.03 | RNA binding | ribosome biogenesis | nucleus | |
| 144 | (Q96CT7) Hypothetical protein LOC115098 | Q96CT7_HUMAN | Q96CT7 | CCDC124 | 160.7269089 | 25820 | 13.68 | 4 | 6 | 9.54 | unknown | unknown | unknown | |
| 145 | (Q01130) Splicing factor, arginine/serine-rich 2 (Spl | SFRS2_HUMAN | Q01130 | SFRS2 | 190.8909952 | 25330 | 17.83 | 4 | 6 | 11.86 | RNA binding | RNA processing, transcription (-) | nucleus | |
| 146 | (Q15365) Poly(rC)-binding protein 1 (Alpha-CP1) (hn | PCBP1_HUMAN | Q15365 | PCBP1 | 215.72 | 37474 | 11.76 | 5 | 6 | 6.66 | RNA binding | RNA processing | nucleus | |
| 147 | (P09651) Heterogeneous nuclear ribonucleoprotein | ROA1_HUMAN | P09651 | HNRNPA1,HNRPA1, | 178.77 | 38691 | 11.65 | 5 | 6 | 9.26 | RNA binding | RNA processing | nucleus | cytoplasm |
| 148 | (P62277) 40S ribosomal protein S13 | RS13_HUMAN | P62277 | RPS13 | 190.1609952 | 17081 | 28.39 | 5 | 6 | 10.53 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 149 | (P68104) Elongation factor 1-alpha 1 (EF-1-alpha-1 | EF1A1_HUMAN | P68104 | EEF1A1,EEF1A, EF1A, LENG7, | 99.46 | 50109 | 4.40 | 2 | 5 | 9.1 | other, protein binding | translation | cytoplasm | nucleus |
| 150 | (P62318) Small nuclear ribonucleoprotein Sm D3 (s | SMD3_HUMAN | P62318 | SNRPD3 | 110.7 | 13907 | 15.08 | 2 | 5 | 10.33 | RNA binding | RNA processing | nucleus | |
| 151 | (P17026) Zinc finger protein 22 (Zinc finger protein | ZNF22_HUMAN | P17026 | ZNF22,KOX15, KROX26, | 74.44 | 25899 | 7.23 | 2 | 5 | 10.06 | DNA binding | transcription | nucleus | |
| 152 | (Q8NEJ9) Protein C14orf120 | CN120_HUMAN | Q8NEJ9 | NGDN,C14orf120, | 123.05 | 35872 | 9.82 | 3 | 5 | 9.57 | other, protein binding | translation | nucleus | cytoplasm |
| 153 | (P20700) Lamin-B1 | LMNB1_HUMAN | P20700 | LMNB1,LMN2, LMNB, | 111.3669089 | 66237 | 5.15 | 3 | 5 | 5.11 | other, structural protein | cell structure | nucleus | |
| 154 | (Q53F64) Heterogeneous nuclear ribonucleoprotein | Q53F64_HUMAN | Q53F64 | | 250.9407266 | 35973 | 13.46 | 3 | 5 | 7.28 | RNA binding | RNA processing | nucleus | cytoplam |
| 155 | (P42696) RNA-binding protein 34 (RNA-binding moti | RBM34_HUMAN | P42696 | RBM34,KIAA0117, | 137.8869089 | 48535 | 7.03 | 3 | 5 | 10.11 | RNA binding | unknown | nucleus | |
| 156 | (P63220) 40S ribosomal protein S21 | RS21_HUMAN | P63220 | RPS21 | 171.32 | 9106 | 25.30 | 3 | 5 | 8.68 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 157 | (Q8WXX5) DnaJ homolog subfamily C member 9 (D | DNJC9_HUMAN | Q8WXX5 | DNAJC9 | 115.6884727 | 29891 | 11.81 | 4 | 5 | 5.58 | other, protein binding | protein folding | unknown | |
| 158 | (Q96BK5) Pin2-interacting protein X1 (TRF1-interac | PINX1_HUMAN | Q96BK5 | PINX1,LPTL, LPTS, | 157.3707266 | 37012 | 12.20 | 4 | 5 | 9.61 | DNA/RNA/protein binding | cell proliferation, cell cycle (+) | nucleus | |
| 159 | (Q9NPA8) E(Y)2 homolog (DC6 protein) (Enhancer | Q9NPA8_HUMAN | Q9NPA8 | ENY2,DC6, | 100.4669089 | 11521 | 25.00 | 4 | 5 | 9.39 | DNA/protein binding | transcription | unknown | |
| 160 | (P62913) 60S ribosomal protein L11 (CLL-associat | RL11_HUMAN | P62913 | RPL11 | 168.4394679 | 20109 | 20.88 | 4 | 5 | 9.64 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 161 | (Q15428) Splicing factor 3A subunit 2 (Spliceosome | SF3A2_HUMAN | Q15428 | SF3A2,SAP62, | 149.1309952 | 49224 | 8.50 | 4 | 5 | 9.65 | RNA binding | RNA processing | nucleus | |
| 162 | (P37108) Signal recognition particle 14 kDa protein | SRP14_HUMAN | P37108 | SRP14 | 195.5709952 | 14535 | 17.42 | 4 | 5 | 10.05 | RNA binding | translation (-) | cytoplasm | nucleus |
| 163 | (Q9Y2W1) Thyroid hormone receptor-associated pr | TR150_HUMAN | Q9Y2W1 | THRAP3,TRAP150, | 80.07690887 | 108601 | 2.23 | 4 | 5 | 10.16 | DNA binding | transcription (+) | nucleus | |
| 164 | (Q9H2V5) BR22 TTF-1 associated protein (Hypothe | Q9H2V5_HUMAN | Q9P031 | BR22, TAP26,HSPC128, | 245.2369089 | 28652 | 20.77 | 5 | 5 | 9.89 | unknown | unknown | unknown | |
| 165 | (P62910) 60S ribosomal protein L32 | RL32_HUMAN | P62910 | RPL32,PP9932, | 189.17 | 15719 | 30.99 | 5 | 5 | 11.32 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 166 | (P56537) Eukaryotic translation initiation factor 6 (e | IF6_HUMAN | P56537 | EIF3A, ITGB4BP,OK/SW-cl.27, | 128.77 | 26582 | 9.96 | 2 | 4 | 4.56 | other, protein binding | translation | cytoplasm | nucleus |
| 167 | (Q9UNZ5) Leydig cell tumor 10 kDa protein homolog | L10K_HUMAN | Q9UNZ5 | C19orf53,HSPC023, | 53.62690887 | 10570 | 8.33 | 2 | 4 | 11.55 | unknown | unknown | unknown | |
| 168 | (P62906) 60S ribosomal protein L10a (CSA-19) | RL10A_HUMAN | P62906 | RPL10A,NEDD6, | 67.2 | 24684 | 7.14 | 2 | 4 | 9.94 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 169 | (P40429) 60S ribosomal protein L13a (23 kDa highl | RL13A_HUMAN | P40429 | RPL13A | 92.57690887 | 23431 | 10.33 | 2 | 4 | 10.94 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 170 | (P32969) 60S ribosomal protein L9 | RL9_HUMAN | P32969 | RPL9,OK/SW-cl.103,RPL9P7, F | 93.26690887 | 21850 | 10.61 | 2 | 4 | 9.96 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 171 | (P39019) 40S ribosomal protein S19 | RS19_HUMAN | P39019 | RPS19 | 66.18690887 | 15919 | 13.19 | 2 | 4 | 10.31 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 172 | (Q8TDN6) Brix domain-containing protein 2 (Riboso | BXDC2_HUMAN | Q8TDN6 | BXDC2, BRIX | 145.5169089 | 41375 | 7.18 | 3 | 4 | 9.92 | RNA binding | ribosome biogenesis | nucleus | |
| 173 | (Q92522) Histone H1x | H1X_HUMAN | Q92522 | H1FX | 102.4384727 | 22474 | 13.24 | 3 | 4 | 10.76 | DNA binding | chromatin organization | nucleus | |
| 174 | (Q9UKD2) mRNA turnover protein 4 homolog | MRT4_HUMAN | Q9UKD2 | MRTO4, C1orf33, MRT4 | 71.26099517 | 27543 | 9.20 | 3 | 4 | 8.34 | RNA binding | ribosome biogenesis | nucleus | cytoplam |
| 175 | (Q9NPE3) H/ACA ribonucleoprotein complex subunit | NOLA3_HUMAN | Q9NPE3 | NOLA3,NOP10 | 345.2338177 | 7701 | 54.29 | 3 | 4 | 10.01 | RNA binding | ribosome biogenesis and telomere maintenance | nucleus | |
| 176 | (P09874) Poly [ADP-ribose] polymerase 1 (EC 2.4.2 | PARP1_HUMAN | P09874 | PARP1,ADPRT, PPOL, | 116.4269089 | 112881 | 3.70 | 3 | 4 | 8.99 | DNA binding ; transferase | transcription ; DNA repair | nucleus | |
| 177 | (Q9NWB6) CDNA FLJ10154 fis, clone HEMBA1003 | Q9NWB6_HUMAN | Q9NWB6 | ARGLU1 | 64.44690887 | 33197 | 4.98 | 3 | 4 | 10.35 | unknown | unknown | unknown | unknown |
| 178 | (Q9UI29) Adrenal gland protein AD-002 (HSPC148 p | Q9UI29_HUMAN | Q9P013 | C11orf5,AD-002, HSPC148, | 55.99790405 | 26608 | 9.96 | 3 | 4 | 5.55 | unknown | unknown | nucleus | |
| 179 | (P84101) Small EDRK-rich factor 2 (4F5rel) (h4F5re | SERF2_HUMAN | P84101 | SERF2,FAM2C, | 66.34 | 6896 | 30.65 | 3 | 4 | 10.44 | unknown | unknown | unknown | |
| 180 | (P84103) Splicing factor, arginine/serine-rich 3 (Pre | SFRS3_HUMAN | P84103 | SFRS3,SRP20, | 86.29 | 19318 | 11.43 | 3 | 4 | 11.64 | RNA binding | RNA processing ; cell cycle | nucleus | |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 181 | (P23284) Peptidyl-prolyl cis-trans isomerase B prec | PPIB_HUMAN | P23284 | PPIB,CYPB, | 180.37 | 22728 | 17.48 | 4 | 4 | 9.25 | other, metabolic enzyme, deshydrogenase | protein folding | ER, cytoplasm | nucleus |
| 182 | (Q9NW13) RNA-binding protein 28 (RNA-binding mo | RBM28_HUMAN | Q9NW13 | RBM28 | 75.29690887 | 85554 | 2.83 | 4 | 4 | 9.27 | RNA binding | ribosome biogenesis | nucleus |  |
| 183 | (P83916) Chromobox protein homolog 1 (Heterochr | CBX1_HUMAN | P83916 | CBX1,CBX, | 124.0769089 | 21405 | 8.25 | 1 | 3 | 4.85 | other, protein binding | chromatin organization ; transcription (-) | nucleus | cytoplasm |
| 184 | (Q6DKI1) Ribosomal protein L7-like 1 | RL7L_HUMAN | Q6DKI1 | RPL7L1 | 61.96099517 | 28643 | 3.85 | 1 | 3 | 10.51 | unknown | unknown | cytoplasm | nucleus |
| 185 | (P48047) ATP synthase O subunit, mitochondrial pr | ATPO_HUMAN | P48047 | ATP5O,ATPO, | 62.47 | 23263 | 9.48 | 2 | 3 | 9.81 | other, transporter | cell metabolism | mitochondria | cytoplasm |
| 186 | (Q9NSI2) Protein C21orf70 | CU070_HUMAN | Q9NSI2 | C21orf70,PRED56, | 103.27 | 25441 | 10.39 | 2 | 3 | 11.07 | unknown | unknown | unknown |  |
| 187 | (P16989) DNA-binding protein A (Cold shock domair | DBPA_HUMAN | P16989 | CSDA,DBPA, | 115.19 | 40066 | 10.22 | 2 | 3 | 9.77 | DNA binding | transcription (-) | nucleus | cytoplasm |
| 188 | (Q9BYG3) MKI67 FHA domain-interacting nucleolar | MK67I_HUMAN | Q9BYG3 | MKI67IP, NIFK, NOPP34 | 124.6409952 | 34201 | 7.74 | 2 | 3 | 9.88 | RNA binding | ribosome biogenesis | nucleus |  |
| 189 | (P55769) NHP2-like protein 1 (High mobility group-li | NHPX_HUMAN | P55769 | NHP2L1 | 110.1 | 14034 | 18.11 | 2 | 3 | 8.72 | RNA binding | ribosome biogenesis ; RNA splicing | nucleus |  |
| 190 | (Q9NY12) H/ACA ribonucleoprotein complex subunit | NOLA1_HUMAN | Q9NY12 | NOLA1,GAR1 | 105.05 | 22334 | 13.30 | 2 | 3 | 10.91 | RNA binding | ribosome biogenesis ; telomere maintenance | nucleus |  |
| 191 | (O43328) Testis-specific gene 118 protein | O43328_HUMAN | Q1ED39 | TSG118 | 94.24381774 | 21529 | 11.79 | 2 | 3 | 9.58 | unknown | unknown | nucleus |  |
| 192 | (O00233) 26S proteasome non-ATPase regulatory s | PSD9_HUMAN | O00233 | PSMD9 | 125.44 | 24638 | 9.87 | 2 | 3 | 6.46 | other, protein binding | protein targeting and degradation | cytoplasm | nucleus |
| 193 | (P62826) GTP-binding nuclear protein Ran (GTPase | RAN_HUMAN | P62826 | ARA24,OK/SW-cl.81, | 68.07099517 | 24277 | 10.00 | 2 | 3 | 7.2 | DNA/RNA/protein binding | chromatin organization | nucleus | cytoplam |
| 194 | (P60866) 40S ribosomal protein S20 | RS20_HUMAN | P60866 | RPS20 | 76.73 | 13364 | 19.01 | 2 | 3 | 9.95 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 195 | (Q01105) Protein SET (Phosphatase 2A inhibitor I2 | SET_HUMAN | Q01105 | SET | 117.2 | 33469 | 7.57 | 2 | 3 | 4.23 | other, protein binding | chromatin organization | nucleus | , cytoplasm, ER |
| 196 | (Q07955) Splicing factor, arginine/serine-rich 1 (pre | SFRS1_HUMAN | Q07955 | ASF, SF2, SF2P33,OK/SW-cl.3, | 69.49690887 | 27597 | 7.60 | 2 | 3 | 10.37 | RNA binding | RNA processing | nucleus | cytoplasm |
| 197 | (P40227) T-complex protein 1 subunit zeta (TCP-1-z | TCPZ_HUMAN | P40227 | CCT6A,CCT6, CCTZ, | 68.76690887 | 57857 | 3.62 | 2 | 3 | 6.25 | other, protein binding | protein folding | cytoplasm | nucleus |
| 198 | (Q9NVP1) ATP-dependent RNA helicase DDX18 (E | DDX18_HUMAN | Q9NVP1 | DDX18 | 83.29099517 | 75359 | 4.82 | 3 | 3 | 9.52 | RNA binding ; helicase | translation | nucleus |  |
| 199 | (Q92945) Far upstream element-binding protein 2 (F | FUBP2_HUMAN | Q92945 | KHSRP,FUBP2, | 133.14 | 72664 | 5.00 | 3 | 3 | 8.02 | DNA/RNA binding | transcription ; RNA processing | nucleus | cyoplasm |
| 200 | (Q13601) HIV-1 Rev-binding protein 2 (Rev-interact | HRB2_HUMAN | Q13601 | KRR1,HRB2, | 108.9458081 | 43507 | 5.82 | 3 | 3 | 9.78 | RNA binding | RNA processing | nucleus |  |
| 201 | (P12004) Proliferating cell nuclear antigen (PCNA) ( | PCNA_HUMAN | P12004 | PCNA | 218.18 | 28750 | 13.03 | 3 | 3 | 4.57 | DNA binding | cell proliferation, cell cycle, DNA repair, replication | nucleus |  |
| 202 | (P46783) 40S ribosomal protein S10 | RS10_HUMAN | P46783 | RPS10 | 142.4769089 | 18886 | 19.30 | 3 | 3 | 10.15 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 203 | (P07108) Acyl-CoA-binding protein (ACBP) (Diazepa | ACBP_HUMAN | P07108 | DBI | 92.94099517 | 9907 | 14.44 | 1 | 2 | 6.11 | other, metabolic enzyme, deshydrogenase | cell metabolism | cytoplasm | nucleus, mitochondria |
| 204 | (Q8NDC0) Protein C14orf32 | CN032_HUMAN | Q8NDC0 | C14orf32 | 75.13099517 | 24122 | 7.76 | 1 | 2 | 5.3 | unknown | unknown | nucleus |  |
| 205 | (O75607) Nucleoplasmin-3 | NPM3_HUMAN | O75607 | NPM3 | 88.73690887 | 19200 | 9.20 | 1 | 2 | 4.55 | other, protein binding | chromatin organization | nucleus |  |
| 206 | (Q86U42) Polyadenylate-binding protein 2 (Poly(A)-l | PABP2_HUMAN | Q86U42 | PABPN1,PAB2, PABP2, | 78.35690887 | 32598 | 5.41 | 1 | 2 | 5.04 | RNA binding | RNA processing | nucleus | cytoplasm |
| 207 | (Q6NX36) Hypothetical protein C1orf174 | Q6NX36_HUMAN | Q8IYL3 | C1orf174 | 96.96 | 26016 | 5.93 | 1 | 2 | 6.9 | unknown | unknown | unknown |  |
| 208 | (P46776) 60S ribosomal protein L27a | RL27A_HUMAN | P46776 | RPL27A | 119.94 | 16420 | 8.72 | 1 | 2 | 11 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 209 | (P62306) Small nuclear ribonucleoprotein F (snRNP | RUXF_HUMAN | P62306 | SNRPF,PBSCF, | 92.91 | 9719 | 14.77 | 1 | 2 | 4.7 | RNA binding | RNA processing | nucleus |  |
| 210 | (P62316) Small nuclear ribonucleoprotein Sm D2 (s | SMD2_HUMAN | P62316 | SNRPD2,SNRPD1, | 74.56099517 | 13518 | 13.11 | 1 | 2 | 9.92 | RNA binding | RNA processing | nucleus |  |
| 211 | (P61981) 14-3-3 protein gamma (Protein kinase C i | 1433G_HUMAN | P61981 | YWHAG | 65.57099517 | 28154 | 6.67 | 2 | 2 | 4.8 | other, protein binding | signal transduction ; apoptosis (-), cell cycle | cytoplasm | nucleus |
| 212 | (P13639) Elongation factor 2 (EF-2) | EF2_HUMAN | P13639 | EEF2,EF2, | 52.08 | 95146 | 2.31 | 2 | 2 | 6.42 | other, protein binding | translation | cytoplasm |  |
| 213 | (P38646) Stress-70 protein, mitochondrial precurso | GRP75_HUMAN | P38646 | HSPA9,GRP75, HSPA9B, | 69.4 | 73635 | 1.79 | 2 | 2 | 5.44 | other, protein binding | protein folding ; apoptosis (-) | cytoplasm, mitochondria | nucleus |
| 214 | (O15525) Transcription factor MafG (V-maf musculo | MAFG_HUMAN | O15525 | MAFG | 121.84 | 17839 | 13.58 | 2 | 2 | 10.04 | DNA/protein binding | transcription; cell cycle | nucleus |  |
| 215 | (O60675) Transcription factor MafK (Erythroid trans | MAFK_HUMAN | O60675 | MAFK | 79.07 | 17512 | 12.58 | 2 | 2 | 10.1 | DNA/protein binding | transcription | nucleus |  |
| 216 | (P26599) Polypyrimidine tract-binding protein 1 (PT | PTBP1_HUMAN | P26599 | PTBP1,PTB, | 67.78099517 | 57186 | 4.24 | 2 | 2 | 9.22 | RNA binding | RNA processing | nucleus |  |
| 217 | (P46782) 40S ribosomal protein S5 | RS5_HUMAN | P46782 | RPS5 | 63.41 | 22731 | 8.25 | 2 | 2 | 9.73 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 218 | (Q16629) Splicing factor, arginine/serine-rich 7 (Spl | SFRS7_HUMAN | Q16629 | SFRS7 | 83.51 | 27350 | 8.06 | 2 | 2 | 11.83 | RNA binding | RNA processing | nucleus |  |
| 219 | (Q93045) Stathmin-2 (SCG10 protein) (Superior ce | STMN2_HUMAN | Q93045 | STMN2,SCG10, SCGN10, | 109.3709952 | 20815 | 10.58 | 1 | 1 | 8.4 | other, protein binding | cell structure | cytoplasm |  |
| 220 | (Q96FF9) Sororin (Cell division cycle-associated pr | CDCA5_HUMAN | Q96FF9 | CDCA5 | 66.99 | 27583 | 5.60 | 1 | 1 | 9.65 | other, protein binding | chromatin organization ; cell cyle | nucleus | cytoplam (mitosis) |
| 221 | (P23528) Cofilin-1 (Cofilin, non-muscle isoform) (18 | COF1_HUMAN | P23528 | CFL1,CFL, | 75.86099517 | 18360 | 7.23 | 1 | 1 | 8.26 | other, protein binding | cell structure | cytoplasm | nucleus |
| 222 | (P14854) Cytochrome c oxidase subunit VIb isoforn | CX6B1_HUMAN | P14854 | COX6B1,COX6B, | 175.3609952 | 10055 | 26.37 | 1 | 1 | 6.79 | other, transporter | cell metabolism | mitochondria | nucleus, cytoplam |
| 223 | (P38919) Probable ATP-dependent RNA helicase D | DDX48_HUMAN | P38919 | EIF4A3,DDX48, KIAA0111, | 95.78481292 | 46710 | 5.90 | 1 | 1 | 6.33 | RNA binding ; helicase | translation | nucleus |  |
| 224 | (Q7Z6I8) Hypothetical protein C5orf24 | Q7Z6I8_HUMAN | Q7Z6I8 | C5orf24 | 80.91 | 20119 | 7.69 | 1 | 1 | 9.87 | unknown | unknown | unknown |  |
| 225 | (Q92646) H2A.k | Q92646_HUMAN | Q92646 | HIST1H2APS4,H2A/k, | 74.13 | 12646 | 8.77 | 1 | 1 | 10.9 | unknown | unknown | unknown |  |
| 226 | (Q96C57) Hypothetical protein C12orf43 | Q96C57_HUMAN | Q96C57 | C12orf43 | 71.84 | 28240 | 6.25 | 1 | 1 | 9.44 | unknown | unknown | unknown |  |
| 227 | (Q9BRT6) Hypothetical protein C12orf31 (CDNA FL | Q9BRT6_HUMAN | Q9BRT6 | C12orf31 | 128.33 | 15215 | 15.94 | 1 | 1 | 10.38 | unknown | unknown | unknown |  |
| 228 | (P05387) 60S acidic ribosomal protein P2 (NY-REN | RLA2_HUMAN | P05387 | RPLP2,D11S2243E, RPP2, | 74.07 | 11658 | 11.43 | 1 | 1 | 4.42 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 229 | (Q9Y2S0) DNA-directed RNA polymerase I subunit I | RPO1D_HUMAN | Q9Y2S0 | POLR1D | 65.38099517 | 15227 | 7.25 | 1 | 1 | 5.55 | DNA binding | transcription | nucleus |  |
| 230 | (P62847) 40S ribosomal protein S24 | RS24_HUMAN | P62847 | RPS24 | 60.78690887 | 15413 | 5.71 | 1 | 1 | 10.79 | stuctural component of ribosome | protein biosynthesis | cytoplasm | nucleus |
| 231 | (P49458) Signal recognition particle 9 kDa protein ( | SRP09_HUMAN | P49458 | SRP9 | 100.37 | 9974 | 17.78 | 1 | 1 | 8.28 | RNA binding | translation (-) | cytoplasm | nucleus |
| 232 | (P16949) Stathmin (Phosphoprotein p19) (pp19) (O | STMN1_HUMAN | P16949 | STMN1,LAP18, OP18, | 108.3238177 | 17161 | 12.82 | 1 | 1 | 5.77 | other, protein binding | cell structure | cytoplasm |  |
| 233 | (O75683) Surfeit locus protein 6 | SURF6_HUMAN | O75683 | SURF6,SURF-6 | 132.88 | 41426 | 8.24 | 1 | 1 | 10.65 | RNA binding | ribosome biogenesis | nucleus |  |
| 234 | (Q12931) Heat shock protein 75 kDa, mitochondrial | TRAP1_HUMAN | Q12931 | TRAP1,HSP75, | 84.27 | 80060 | 1.93 | 1 | 1 | 8.28 | other, protein binding | protein folding | mitochondria | cytoplasm |
| 235 | (P47985) Ubiquinol-cytochrome c reductase iron-su | UCRI_HUMAN | P47985 | UQCRFS1 | 135.5469089 | 29633 | 10.78 | 1 | 1 | 6.3 | other, metabolic enzyme, deshydrogenase | cell metabolism | mitochondria |  |
| 236 | (P67809) Nuclease sensitive element-binding protei | YBOX1_HUMAN | P67809 | YBX1,NSEP1, YB1, | 105.2 | 35772 | 5.85 | 1 | 1 | 9.87 | DNA/RNA binding | transcription, RNA processing, cell cycle | nucleus | cytoplasm |

[1]Retrieved from Uniprot

**Variable modifications allowed for Mascot searches :**
acetyl-lysine
dimethyl-lysine
methyl-lysine
serine and threonine phosphorylation
protein N-acetylation
peptide N-terminal acetylation
methionine oxidation
methionine sulphone
cysteic acid

**Table S2**: Genes significantly modulated between Raji shCtrl and Raji shCYCLON cell lines

# Notes : Created from Advanced Analysis operation: significance Analysis.
#Entitylist : 3465r_ShcyclonvsShCtrl_FC>= 1.2
#Interpretation : Group_ShcyclonvsShCtrl
#corrected p-value cut-off:0.05
#Selected Test : T Test unpaired
#p-value computation: Asymptotic
#Multiple Testing Correction: Benjamini-Hochberg
# Technology : Affymetrix.GeneChip.HG-U133_Plus_2

| Probe Set ID | Regulation | Gene Symbol | FC |
|---|---|---|---|
| 1554747_a_at | up | SEPT2 | 1.3452525 |
| 210348_at | up | SEPT4 | 1.2318484 |
| 201308_s_at | up | SEPT11 | 1.5969949 |
| 202852_s_at | up | AAGAB | 1.3515162 |
| 202170_s_at | up | AASDHPPT | 1.2595851 |
| 1555039_a_at | up | ABCC4 | 1.5179213 |
| 213805_at | up | ABHD5 | 1.2745662 |
| 221679_s_at | up | ABHD6 | 1.2033099 |
| 210461_s_at | up | ABLIM1 | 1.3266736 |
| 242081_at | down | ACAP1 | -1.2228346 |
| 234312_s_at | up | ACSS2 | 1.210379 |
| 200727_s_at | up | ACTR2 | 1.6853753 |
| 208223_s_at | up | ACVR1B | 1.2258034 |
| 207422_at | down | ADAM20 | -1.2314298 |
| 244463_at | down | ADAM23 | -1.2529302 |
| 241446_at | down | ADAM28 | -1.2574718 |
| 1555326_a_at | up | ADAM9 | 1.2373784 |
| 229004_at | down | ADAMTS15 | -1.215619 |
| 228911_at | down | ADAMTS7 | -1.2000039 |
| 222117_s_at | up | ADCK2 | 1.2364966 |
| 239530_at | down | ADD2 | -1.2626154 |
| 211491_at | up | ADRA1A | 1.2238052 |
| 210957_s_at | up | AFF2 | 1.2449454 |
| 205734_s_at | up | AFF3 | 1.2646971 |
| 1565034_s_at | up | AFF3 /// MLL | 1.2641628 |
| 213926_s_at | up | AGFG1 | 1.8158666 |
| 207293_s_at | up | AGTR2 | 1.2052976 |
| 243793_at | down | AHDC1 | -1.2500672 |
| 208325_s_at | up | AKAP13 | 1.2306771 |
| 241978_at | up | AKR1A1 | 1.347034 |
| 203809_s_at | down | AKT2 | -1.209167 |
| 203609_s_at | up | ALDH5A1 | 1.3379878 |
| 204290_s_at | up | ALDH6A1 | 1.2529459 |
| 211618_s_at | down | ALPI | -1.227935 |
| 1553219_a_at | up | AMMECR1 | 1.5873324 |
| 206121_at | down | AMPD1 | -1.2286934 |
| 239651_at | up | ANAPC5 | 1.4114015 |
| 205389_s_at | down | ANK1 | -1.2072151 |
| 207950_s_at | up | ANK3 | 1.2679877 |
| 219868_s_at | up | ANKFY1 | 1.2791767 |
| 233292_s_at | up | ANKHD1 /// ANKHD1-EIF4EBP3 | 1.4842196 |
| 226663_at | up | ANKRD10 | 1.4403979 |
| 216563_at | down | ANKRD12 | -1.2450268 |
| 231423_s_at | up | ANKRD16 | 1.2168254 |
| 236421_at | up | ANKRD45 | 1.2065878 |
| 219496_at | down | ANKRD57 | -1.2382185 |
| 229128_s_at | down | ANP32E | -1.2317584 |
| 208816_x_at | up | ANXA2P2 | 1.2402707 |
| 204894_s_at | down | AOC3 | -1.2256814 |
| 230413_s_at | up | AP1S2 | 1.4901165 |

| | | | |
|---|---|---|---|
| 1555733_s_at | up | AP1S3 | 1.4179875 |
| 223237_x_at | down | AP2A1 | -1.2146109 |
| 219994_at | up | APBB1IP | 1.2727188 |
| 202631_s_at | up | APPBP2 | 1.2402741 |
| 214483_s_at | up | ARFIP1 | 1.2043763 |
| 228477_at | up | ARGLU1 | 1.7832876 |
| 202547_s_at | up | ARHGEF7 | 1.2464342 |
| 210649_s_at | down | ARID1A | -1.2068951 |
| 225184_at | up | ARID1B | 1.2046044 |
| 231016_s_at | up | ARNT | 1.4634826 |
| 208736_at | up | ARPC3 | 1.6490312 |
| 207284_s_at | down | ASPH | -1.2005804 |
| 219918_s_at | down | ASPM | -1.2408969 |
| 218659_at | down | ASXL2 | -1.230501 |
| 1558807_at | up | ATAD2B | 1.2740762 |
| 208442_s_at | up | ATM | 1.4249728 |
| 209186_at | down | ATP2A2 | -1.2545114 |
| 207521_s_at | up | ATP2A3 | 1.2174581 |
| 217603_at | up | ATP6V0A2 | 1.250147 |
| 214149_s_at | up | ATP6V0E1 | 1.5006995 |
| 212384_at | up | ATP6V1G2 /// BAT1 | 1.3440068 |
| 1569773_at | up | ATP8A1 | 1.4654691 |
| 214594_x_at | down | ATP8B1 | -1.257413 |
| 211022_s_at | up | ATRX | 1.6874208 |
| 212113_at | up | ATXN7L3B | 1.5715481 |
| 227905_s_at | down | AZI2 | -1.2240304 |
| 219326_s_at | up | B3GNT2 | 1.3589712 |
| 210535_at | down | B9D1 | -1.2588447 |
| 222780_s_at | down | BAALC | -1.2152404 |
| 210125_s_at | down | BANF1 | -1.2180156 |
| 214201_x_at | down | BAT2 | -1.2025415 |
| 230618_s_at | up | BAT2L2 | 1.5455139 |
| 227896_at | down | BCCIP | -1.2400014 |
| 1557258_a_at | up | BCL10 | 1.2613658 |
| 203684_s_at | up | BCL2 | 1.3407803 |
| 224227_s_at | up | BDP1 | 1.3714335 |
| 220451_s_at | down | BIRC7 | -1.2500215 |
| 226853_at | down | BMP2K | -1.2142243 |
| 210523_at | down | BMPR1B | -1.3424524 |
| 210214_s_at | up | BMPR2 | 1.344528 |
| 204930_s_at | up | BNIP1 | 1.2533311 |
| 235009_at | up | BOD1L | 1.7748537 |
| 232698_at | up | BPIL1 | 1.237938 |
| 41512_at | down | BRAP | -1.2698414 |
| 222737_s_at | down | BRD7 | -1.2065537 |
| 206787_at | down | BRDT | -1.21183 |
| 218954_s_at | down | BRF2 | -1.2064899 |
| 240362_at | up | BRP44L | 1.3525517 |
| 1553252_a_at | up | BRWD3 | 1.3571057 |
| 201235_s_at | up | BTG2 | 1.3849775 |
| 215509_s_at | up | BUB1 | 1.3521194 |
| 209182_s_at | up | C10orf10 | 1.2326845 |
| 229399_at | up | C10orf118 | 1.6101971 |
| 227136_s_at | down | C10orf46 | -1.2587973 |
| 239998_at | up | C10orf53 | 1.2944402 |
| 227099_s_at | down | C11orf96 | -1.2407529 |
| 227152_at | up | C12orf35 | 1.4074843 |
| 229778_at | up | C12orf39 | 1.2305417 |
| 226349_at | down | C12orf45 | -1.2465434 |
| 227928_at | down | C12orf48 | -1.2019851 |
| 236853_at | down | C13orf16 | -1.2512114 |

|  |  |  |  |
|---|---|---|---|
| 231859_at | up | C14orf132 | 1.2126943 |
| 237640_at | up | C14orf138 | 1.3045775 |
| 224798_s_at | up | C15orf17 | 1.2529098 |
| 221300_at | down | C15orf2 | -1.2586917 |
| 231338_at | up | C15orf55 | 1.2323191 |
| 225088_at | up | C16orf63 | 1.4222207 |
| 213815_x_at | down | C19orf29 | -1.221676 |
| 232730_at | down | C19orf44 | -1.2715486 |
| 212574_x_at | up | C19orf6 | 1.6493751 |
| 219439_at | down | C1GALT1 | -1.2167912 |
| 238365_s_at | up | C1orf228 | 1.2860056 |
| 223459_s_at | down | C1orf56 | -1.2008423 |
| 222301_at | up | C1orf61 | 1.2541444 |
| 202953_at | up | C1QB | 1.2004935 |
| 205575_at | up | C1QL1 | 1.2549008 |
| 223499_at | up | C1QTNF5 /// MFRP | 1.2410158 |
| 232619_at | down | C20orf134 | -1.2012147 |
| 234002_at | down | C20orf135 | -1.2864715 |
| 231991_at | up | C20orf160 | 1.220118 |
| 1559252_a_at | down | C20orf29 | -1.2932229 |
| 227867_at | up | C2orf89 | 1.2594761 |
| 225279_s_at | up | C3orf17 | 1.310732 |
| 224273_at | down | C3orf20 | -1.2145138 |
| 1569374_at | up | C3orf62 | 1.4442676 |
| 1562832_at | down | C3orf65 | -1.3066753 |
| 1554192_s_at | up | C4orf23 | 1.2053691 |
| 1552660_a_at | up | C5orf22 | 1.7116319 |
| 229443_at | up | C6orf125 | 1.2189027 |
| 213875_x_at | up | C6orf62 | 1.6402713 |
| 224988_at | up | C6orf89 | 1.2278509 |
| 1564658_at | down | C7orf52 | -1.2618679 |
| 219455_at | up | C7orf63 | 1.2178006 |
| 241781_at | up | C9orf41 | 1.4025706 |
| 224311_s_at | up | CAB39 | 1.6028811 |
| 210691_s_at | down | CACYBP | -1.2209071 |
| 215259_s_at | up | CADM4 | 1.2313446 |
| 243084_at | down | CALD1 | -1.220924 |
| 214845_s_at | up | CALU | 1.3490969 |
| 1552768_at | up | CAMKK1 | 1.2035276 |
| 208853_s_at | up | CANX | 1.2782067 |
| 202966_at | down | CAPN6 | -1.228815 |
| 200722_s_at | up | CAPRIN1 | 1.261952 |
| 212512_s_at | down | CARM1 | -1.2410667 |
| 240983_s_at | up | CARS | 1.2952435 |
| 207620_s_at | up | CASK | 1.2381201 |
| 211140_s_at | up | CASP2 | 1.2327163 |
| 207686_s_at | up | CASP8 | 1.274467 |
| 211922_s_at | up | CAT | 1.2101026 |
| 226085_at | down | CBX5 | -1.3132952 |
| 226539_s_at | up | CCDC42B | 1.513871 |
| 223815_at | up | CCDC45 | 1.2056692 |
| 231657_s_at | up | CCDC74B | 1.2446398 |
| 203119_at | down | CCDC86 | -1.5212156 |
| 219387_at | up | CCDC88A | 1.4102992 |
| 205392_s_at | up | CCL14 /// CCL14-CCL15 | 1.2726742 |
| 213226_at | down | CCNA2 | -1.2112991 |
| 214710_s_at | down | CCNB1 | -1.2857515 |
| 211814_s_at | up | CCNE2 | 1.4793905 |
| 206337_at | up | CCR7 | 1.2161129 |
| 220351_at | down | CCRL1 | -1.3955326 |
| 220671_at | up | CCRN4L | 1.2673248 |

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|---|---|---|---|
| 210436_at | up | CCT8 | 1.3461922 |
| 208653_s_at | up | CD164 | 1.274331 |
| 209582_s_at | up | CD200 | 1.3509473 |
| 205264_at | down | CD3EAP | -1.2416427 |
| 205153_s_at | up | CD40 | 1.2441132 |
| 207549_x_at | up | CD46 | 1.5851563 |
| 1555746_at | down | CD79B | -1.3073603 |
| 204440_at | up | CD83 | 1.2129368 |
| 211192_s_at | up | CD84 | 1.6923444 |
| 202870_s_at | down | CDC20 | -1.2372586 |
| 205167_s_at | down | CDC25C | -1.2311934 |
| 235787_at | down | CDC37L1 | -1.235508 |
| 203377_s_at | up | CDC40 | 1.2268724 |
| 209287_s_at | up | CDC42EP3 | 1.2792972 |
| 218063_s_at | up | CDC42EP4 | 1.2054125 |
| 223674_s_at | up | CDC42SE1 | 1.4024023 |
| 209055_s_at | up | CDC5L | 1.2400482 |
| 218399_s_at | down | CDCA4 | -1.2088729 |
| 201130_s_at | up | CDH1 | 1.2587872 |
| 207172_s_at | down | CDH11 | -1.204747 |
| 231534_at | up | CDK1 | 1.3227781 |
| 207319_s_at | up | CDK13 | 1.516393 |
| 206474_at | up | CDK17 | 1.2785498 |
| 211804_s_at | up | CDK2 | 1.3398486 |
| 207188_at | up | CDK3 | 1.2244807 |
| 207143_at | up | CDK6 | 1.2442181 |
| 1553112_s_at | up | CDK8 | 1.2156193 |
| 236023_at | up | CDK9 | 1.2284026 |
| 209714_s_at | down | CDKN3 | -1.2462797 |
| 213548_s_at | up | CDV3 | 1.6756972 |
| 204113_at | up | CELF1 | 1.3241057 |
| 210821_x_at | down | CENPA | -1.2390207 |
| 205046_at | down | CENPE | -1.2900797 |
| 220885_s_at | up | CENPJ | 1.3188705 |
| 228559_at | down | CENPN | -1.2548182 |
| 1554606_at | up | CEP120 | 1.3448977 |
| 221683_s_at | up | CEP290 | 1.2106994 |
| 213957_s_at | up | CEP350 | 1.2438337 |
| 238154_at | down | CEP70 | -1.2000693 |
| 207645_s_at | up | CHD1L | 1.3562883 |
| 1555463_a_at | up | CHD6 | 1.2927212 |
| 220630_s_at | up | CHIA | 1.2619979 |
| 211358_s_at | down | CIZ1 | -1.2203966 |
| 229610_at | up | CKAP2L | 1.2619487 |
| 206164_at | down | CLCA2 | -1.3078173 |
| 205149_s_at | up | CLCN4 | 1.3501853 |
| 232128_s_at | down | CLCN5 | -1.2090104 |
| 221328_at | up | CLDN17 | 1.3624657 |
| 201559_s_at | up | CLIC4 | 1.2409272 |
| 201768_s_at | up | CLINT1 | 1.2812784 |
| 1558924_s_at | up | CLIP1 | 1.6365954 |
| 211136_s_at | up | CLPTM1 | 1.2145925 |
| 229777_at | down | CLRN3 | -1.2053759 |
| 1553120_at | up | CLSPN | 1.2195165 |
| 205518_s_at | down | CMAH | -1.2105225 |
| 224991_at | down | CMIP | -1.2962687 |
| 224998_at | down | CMTM4 | -1.2570964 |
| 203239_s_at | down | CNOT3 | -1.2588922 |
| 223465_at | up | COL4A3BP | 1.4276825 |
| 229600_s_at | down | CPD | -1.2248484 |
| 224828_at | up | CPEB4 | 1.6389138 |

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|---|---|---|---|
| 241706_at | down | CPNE8 | -1.2941418 |
| 206184_at | up | CRKL | 1.2209756 |
| 1554464_a_at | up | CRTAP | 1.2234758 |
| 207531_at | down | CRYGC | -1.27568 |
| 1568620_at | up | CSAD | 1.2058828 |
| 1570169_at | up | CSMD2 | 1.2031901 |
| 240228_at | up | CSMD3 | 1.2381549 |
| 208867_s_at | up | CSNK1A1 | 1.2152762 |
| 222015_at | up | CSNK1E | 1.2865859 |
| 212075_s_at | up | CSNK2A1 | 1.2449902 |
| 1555106_a_at | up | CTDSPL2 | 1.2179205 |
| 202213_s_at | up | CUL4B | 1.2547195 |
| 220724_at | down | CWH43 | -1.2131425 |
| 212977_at | up | CXCR7 | 1.3204342 |
| 235442_at | up | CXorf56 | 1.4556006 |
| 1431_at | up | CYP2E1 | 1.2867599 |
| 207786_at | up | CYP2R1 | 1.2100302 |
| 216607_s_at | up | CYP51A1 | 1.3477283 |
| 202879_s_at | up | CYTH1 | 1.2249681 |
| 1554335_at | up | CYTH4 | 1.2090207 |
| 219837_s_at | up | CYTL1 | 1.2000073 |
| 203890_s_at | up | DAPK3 | 1.7849464 |
| 236707_at | up | DAPP1 | 1.2138002 |
| 205369_x_at | up | DBT | 1.2331996 |
| 216389_s_at | up | DCAF11 | 1.3267969 |
| 221851_at | down | DCAF15 | -1.2154462 |
| 239187_at | up | DCAF16 | 1.2104834 |
| 231921_at | down | DCAF17 | -1.2542593 |
| 1554558_at | down | DCAF5 | -1.2519573 |
| 221224_s_at | up | DCAKD | 1.2103885 |
| 235258_at | down | DCP2 | -1.2283409 |
| 205338_s_at | down | DCT | -1.2673953 |
| 208675_s_at | up | DDOST | 1.3880887 |
| 210749_x_at | up | DDR1 | 1.2399544 |
| 213998_s_at | up | DDX17 | 1.4270669 |
| 212514_x_at | up | DDX3X | 1.4152759 |
| 1559954_s_at | up | DDX42 | 1.5512836 |
| 234347_s_at | up | DENR | 1.260583 |
| 226980_at | down | DEPDC1B | -1.2741364 |
| 203695_s_at | up | DFNA5 | 1.239448 |
| 202099_s_at | up | DGCR2 | 1.2059903 |
| 1566038_at | up | DGCR7 | 1.2371081 |
| 234728_s_at | up | DHX35 | 1.4181397 |
| 216870_x_at | down | DLEU2 | -1.2148956 |
| 215629_s_at | down | DLEU2 /// DLEU2L | -1.2359343 |
| 1561617_at | down | DNAH6 | -1.2059814 |
| 203810_at | down | DNAJB4 | -1.2782338 |
| 1555360_a_at | up | DNAJC11 | 1.2229487 |
| 1554451_s_at | up | DNAJC14 | 1.203102 |
| 223505_s_at | up | DNAJC27 | 1.2841597 |
| 232240_at | up | DNHD1 | 1.2583019 |
| 234942_s_at | down | DNTTIP1 | -1.2394392 |
| 222004_s_at | up | DOCK6 | 1.2252464 |
| 239027_at | up | DOCK8 | 1.3660889 |
| 219452_at | up | DPEP2 | 1.2691046 |
| 226721_at | down | DPY19L4 | -1.2199434 |
| 1554536_at | up | DPYD | 1.3013089 |
| 205493_s_at | up | DPYSL4 | 1.2052408 |
| 203258_at | down | DRAP1 | -1.2713146 |
| 204455_at | down | DST | -1.2563896 |
| 230402_at | down | DUSP15 | -1.2101262 |

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|---|---|---|---|
| 204794_at | up | DUSP2 | 1.2044349 |
| 226440_at | up | DUSP22 | 1.3387105 |
| 208892_s_at | down | DUSP6 | -1.2646854 |
| 229115_at | up | DYNC1H1 | 1.308681 |
| 203692_s_at | up | E2F3 | 1.2034937 |
| 233850_s_at | down | EBF4 | -1.2579534 |
| 219424_at | up | EBI3 | 1.2312487 |
| 230659_at | down | EDEM1 | -1.2852004 |
| 219833_s_at | down | EFHC1 | -1.226724 |
| 227283_at | down | EFR3B | -1.2550792 |
| 1565484_x_at | down | EGFR | -1.2807788 |
| 222314_x_at | down | EGOT | -1.2756013 |
| 205249_at | up | EGR2 | 1.2305626 |
| 209037_s_at | up | EHD1 | 1.2235167 |
| 222576_s_at | up | EIF2C1 | 1.6433426 |
| 205321_at | up | EIF2S3 | 1.2300643 |
| 1555996_s_at | up | EIF4A2 | 1.5830824 |
| 211937_at | up | EIF4B | 1.254732 |
| 1554310_a_at | up | EIF4G3 | 1.2433524 |
| 220363_s_at | up | ELMO2 | 1.235109 |
| 204398_s_at | up | EML2 | 1.5175923 |
| 220386_s_at | up | EML4 | 1.2657421 |
| 237691_x_at | up | ENO3 | 1.2202686 |
| 204142_at | down | ENOSF1 | -1.202513 |
| 205066_s_at | up | ENPP1 | 1.2224588 |
| 220153_at | up | ENTPD7 | 1.2953317 |
| 217254_s_at | down | EPO | -1.2142091 |
| 209962_at | down | EPOR | -1.3258492 |
| 200841_s_at | up | EPRS | 1.5490665 |
| 210385_s_at | up | ERAP1 | 1.301499 |
| 217611_at | up | ERICH1 | 1.2212138 |
| 202444_s_at | up | ERLIN1 | 1.6385611 |
| 1555830_s_at | up | ESYT2 | 1.265215 |
| 226432_at | up | ETNK1 | 1.2364532 |
| 211825_s_at | up | EWSR1 /// FLI1 | 1.3454281 |
| 218748_s_at | up | EXOC5 | 1.5498394 |
| 1553947_at | up | EXOSC6 | 1.3065883 |
| 214734_at | down | EXPH5 | -1.2002375 |
| 214608_s_at | up | EYA1 | 1.2200563 |
| 211310_at | up | EZH1 | 1.5040091 |
| 208621_s_at | up | EZR | 1.7633995 |
| 207810_at | down | F13B | -1.2223849 |
| 222511_x_at | up | FAF1 | 1.8919816 |
| 212106_at | up | FAF2 | 1.2984308 |
| 1557128_at | up | FAM111B | 1.2446389 |
| 1555947_at | down | FAM120A | -1.4169422 |
| 1552882_a_at | down | FAM123B | -1.2533257 |
| 230519_at | up | FAM124A | 1.2670133 |
| 231874_at | up | FAM126B | 1.3884314 |
| 227828_s_at | up | FAM176A | 1.2805197 |
| 1554132_a_at | up | FAM190B | 1.4590812 |
| 232217_at | down | FAM26E | -1.2108623 |
| 1554165_at | down | FAM53B | -1.2080717 |
| 235030_at | up | FAM55C | 1.3563026 |
| 1559950_at | down | FAM66C /// FAM66D | -1.4033489 |
| 216897_s_at | up | FAM76A | 1.3062598 |
| 1553749_at | down | FAM76B | -1.2745601 |
| 241481_at | down | FAM81A | -1.2045404 |
| 238741_at | down | FAM83A | -1.2098011 |
| 1557217_a_at | up | FANCB | 1.2661111 |
| 1554277_s_at | up | FANCM | 1.3058311 |

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|---|---|---|---|
| 215068_s_at | down | FBXL18 | -1.33131 |
| 1553500_at | down | FBXL21 | -1.2053086 |
| 226970_at | down | FBXO33 | -1.3342328 |
| 1559094_at | up | FBXO9 | 1.2685993 |
| 209456_s_at | up | FBXW11 | 1.4762064 |
| 218831_s_at | up | FCGRT | 1.2031544 |
| 1553196_a_at | up | FCRL3 | 1.3161232 |
| 229989_at | up | FDXACB1 | 1.2486943 |
| 222245_s_at | up | FER1L4 | 1.2021043 |
| 210973_s_at | up | FGFR1 | 1.2479326 |
| 223263_s_at | up | FGFR1OP2 | 1.2579206 |
| 219718_at | up | FGGY | 1.2104558 |
| 226769_at | up | FIBIN | 1.2131882 |
| 76897_s_at | up | FKBP15 | 1.5776329 |
| 204560_at | up | FKBP5 | 1.4996216 |
| 224288_x_at | up | FKSG49 | 1.3765793 |
| 227302_s_at | up | FLII /// LLGL1 | 1.201744 |
| 205511_at | up | FLJ10038 | 1.4245838 |
| 224073_at | up | FLJ20464 | 1.2149084 |
| 1553145_at | up | FLJ39653 | 1.4630386 |
| 1557372_at | up | FLJ41757 | 1.2652222 |
| 211299_s_at | up | FLOT2 | 1.2812767 |
| 219316_s_at | up | FLVCR2 | 1.2433511 |
| 232249_at | up | FMNL3 | 1.3272188 |
| 235101_at | up | FNBP4 | 1.2754292 |
| 242029_at | up | FNDC3B | 1.3083805 |
| 1555247_a_at | up | FNIP1 /// RAPGEF6 | 1.2547759 |
| 228463_at | down | FOXA3 | -1.2123741 |
| 208006_at | up | FOXI1 | 1.208199 |
| 217310_s_at | up | FOXJ3 | 1.3377043 |
| 218031_s_at | up | FOXN3 | 1.2644747 |
| 210655_s_at | up | FOXO3 /// FOXO3B | 1.3594829 |
| 1563687_a_at | up | FRYL | 1.2577755 |
| 223985_at | up | FSD1L | 1.2842823 |
| 223120_at | up | FUCA2 | 1.2420087 |
| 204452_s_at | up | FZD1 | 1.2272542 |
| 210220_at | up | FZD2 | 1.2654998 |
| 223254_s_at | up | G2E3 | 1.2814575 |
| 242422_at | up | G3BP1 | 1.6025373 |
| 214987_at | up | GAB1 | 1.2537209 |
| 203146_s_at | up | GABBR1 | 1.2307272 |
| 211679_x_at | up | GABBR2 | 1.2047298 |
| 232708_at | up | GALT | 1.2353748 |
| 217445_s_at | up | GART | 1.4258344 |
| 205848_at | up | GAS2 | 1.2561656 |
| 207704_s_at | up | GAS7 | 1.212802 |
| 214711_at | up | GATC | 1.2177708 |
| 1555125_at | up | GCFC1 | 1.4320351 |
| 221279_at | up | GDAP1 | 1.450111 |
| 229868_s_at | down | GDF15 | -1.287701 |
| 221576_at | up | GDF15 | 1.2748805 |
| 1555606_a_at | down | GDPD1 | -1.200385 |
| 231918_s_at | up | GFM2 | 1.2053763 |
| 1554670_at | up | GGA1 | 1.3941542 |
| 214190_x_at | up | GGA2 | 1.3312801 |
| 236583_at | down | GIMAP1 | -1.2174828 |
| 1553058_at | up | GIPC3 | 1.241221 |
| 207387_s_at | up | GK | 1.2935873 |
| 215966_x_at | up | GK3P | 1.2335669 |
| 219933_at | down | GLRX2 | -1.2033429 |
| 223079_s_at | up | GLS | 1.2266082 |

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|---|---|---|---|
| 215794_x_at | up | GLUD2 | 1.309881 |
| 1554712_a_at | down | GLYATL2 | -1.2565421 |
| 222115_x_at | up | GLYR1 | 1.2689847 |
| 200744_s_at | up | GNB1 | 1.2560008 |
| 46947_at | up | GNL3L | 1.2525293 |
| 211522_s_at | down | GNRHR | -1.2125251 |
| 208797_s_at | up | GOLGA8A | 1.4147563 |
| 204324_s_at | up | GOLIM4 | 1.3684632 |
| 239159_at | up | GOSR2 | 1.2846826 |
| 212487_at | up | GPATCH8 | 1.2186728 |
| 202756_s_at | up | GPC1 | 1.2246386 |
| 232195_at | down | GPR158 | -1.2056496 |
| 244617_at | down | GPR26 | -1.3236516 |
| 228313_at | down | GPRC5B | -1.2442926 |
| 206620_at | up | GRAP | 1.2719648 |
| 233171_at | down | GRIN3A | -1.2056001 |
| 215766_at | up | GSTA1 | 1.3533078 |
| 238585_at | up | GTDC1 | 1.2703116 |
| 210620_s_at | up | GTF3C2 | 1.2934701 |
| 204318_s_at | down | GTSE1 | -1.318172 |
| 1555568_at | up | GUSBL1 | 1.4084787 |
| 221892_at | up | H6PD | 1.230185 |
| 209819_at | down | HABP4 | -1.2562569 |
| 218602_s_at | down | HAUS6 | -1.2056735 |
| 240602_at | up | HBS1L | 1.2289792 |
| 1554478_a_at | up | HEATR3 | 1.204536 |
| 1557100_s_at | up | HECTD1 | 1.4062873 |
| 219319_at | down | HIF3A | -1.206478 |
| 226537_at | up | HINT3 | 1.2206274 |
| 205425_at | up | HIP1 | 1.3270811 |
| 217427_s_at | up | HIRA | 1.4724717 |
| 207982_at | up | HIST1H1T | 1.2245693 |
| 215071_s_at | up | HIST1H2AC | 1.2059689 |
| 214516_at | down | HIST1H4B | -1.2549939 |
| 1560485_at | up | HIVEP1 | 1.2035419 |
| 221978_at | up | HLA-F | 1.2324376 |
| 205822_s_at | up | HMGCS1 | 1.7307211 |
| 201055_s_at | up | HNRNPA0 | 1.2105442 |
| 213470_s_at | up | HNRNPH1 | 1.3795176 |
| 209675_s_at | down | HNRNPUL1 | -1.2262769 |
| 219976_at | down | HOOK1 | -1.2269777 |
| 213150_at | up | HOXA10 | 1.2043763 |
| 231121_at | down | HPS3 | -1.239754 |
| 231705_at | up | HRSP12 | 1.3997586 |
| 211220_s_at | up | HSF2 | 1.2357876 |
| 1557910_at | up | HSP90AB1 | 1.560843 |
| 216450_x_at | up | HSP90B1 | 1.2380035 |
| 211016_x_at | up | HSPA4 | 1.5372337 |
| 215485_s_at | up | ICAM1 | 1.2222471 |
| 1552837_at | down | ICK | -1.2683991 |
| 209293_x_at | up | ID4 | 1.2500161 |
| 208965_s_at | up | IFI16 | 1.2847668 |
| 1555464_at | up | IFIH1 | 1.555285 |
| 216494_at | up | IGF2BP3 | 1.2441297 |
| 213674_x_at | up | IGHD | 1.209107 |
| 216901_s_at | up | IKZF1 | 1.6100539 |
| 221092_at | up | IKZF3 | 1.9275341 |
| 207433_at | up | IL10 | 1.2236744 |
| 204773_at | up | IL11RA | 1.2118208 |
| 228685_at | down | IL17RA | -1.2246972 |
| 224283_x_at | down | IL18BP | -1.2907579 |

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|---|---|---|---|
| 208200_at | down | IL1A | -1.3095239 |
| 204863_s_at | up | IL6ST | 1.2395563 |
| 208930_s_at | up | ILF3 | 1.3399829 |
| 219769_at | up | INCENP | 1.479723 |
| 213544_at | down | ING2 | -1.3011824 |
| 242293_at | up | ING3 | 1.2958503 |
| 243070_at | up | INO80D | 1.3911563 |
| 208364_at | up | INPP4A | 1.2509352 |
| 1554757_a_at | up | INPP5A | 1.2216833 |
| 213643_s_at | up | INPP5B | 1.2094048 |
| 201625_s_at | up | INSIG1 | 1.2569327 |
| 229633_at | down | INTS10 | -1.2230217 |
| 228946_at | down | INTU | -1.2113076 |
| 215130_s_at | up | IQCK | 1.2329689 |
| 238725_at | up | IRF1 | 1.2011575 |
| 224571_at | up | IRF2BP2 | 1.2547354 |
| 235182_at | down | ISM1 | -1.2516865 |
| 209743_s_at | up | ITCH | 1.2091734 |
| 1553530_a_at | up | ITGB1 | 1.2460012 |
| 1555349_a_at | up | ITGB2 | 1.3044101 |
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| 206364_at | down | KIF14 | -1.3524646 |
| 218755_at | down | KIF20A | -1.2435501 |
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| 205447_s_at | up | MAP3K12 | 1.2999891 |
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| 208534_s_at | up | RASA4 /// RASA4P | 1.2383194 |
| 1554999_at | up | RASGEF1B | 1.4152662 |
| 244526_at | up | RASGRP3 | 1.3843083 |
| 49306_at | up | RASSF4 | 1.2583784 |
| 1554834_a_at | up | RASSF5 | 1.7692351 |
| 229147_at | down | RASSF6 | -1.2008153 |
| 220680_at | down | RAVER2 | -1.2555538 |
| 244872_at | up | RBBP4 | 1.2970577 |
| 205296_at | down | RBL1 | -1.2286828 |
| 212332_at | up | RBL2 | 1.3096447 |
| 1555639_a_at | up | RBM14 | 1.2185898 |
| 212030_at | up | RBM25 | 1.2497025 |
| 227355_at | up | RBM26 | 1.2677643 |
| 243295_at | up | RBM27 | 1.2368121 |
| 229540_at | up | RBPJ | 1.3988622 |
| 238421_at | up | RC3H2 | 1.3498273 |
| 215253_s_at | up | RCAN1 | 1.3321257 |
| 215747_s_at | up | RCC1 | 1.2344323 |
| 231290_at | up | RCCD1 | 1.2373477 |
| 1552378_s_at | up | RDH10 | 1.2376839 |
| 217042_at | up | RDH11 | 1.2581693 |
| 228815_s_at | down | REPIN1 | -1.2646469 |
| 203696_s_at | down | RFC2 | -1.200967 |
| 218430_s_at | up | RFX7 | 1.2080417 |
| 208492_at | up | RFXAP | 1.2934612 |
| 232053_x_at | up | RHBDD2 | 1.3001236 |
| 1554586_a_at | up | RHOBTB2 | 1.2027346 |
| 225202_at | down | RHOBTB3 | -1.2068317 |
| 1552734_at | up | RICTOR | 1.290041 |
| 241820_at | up | RIF1 | 1.5660197 |
| 226164_x_at | up | RIMKLB | 1.218177 |
| 227644_at | down | RIMS4 | -1.2290297 |
| 202129_s_at | up | RIOK3 | 1.3536125 |
| 239843_at | up | RIT1 | 1.4179438 |
| 241343_at | up | RNASEH1 | 1.3129164 |
| 1568665_at | up | RNF103 | 1.240279 |
| 221430_s_at | up | RNF146 | 1.2100194 |
| 213038_at | down | RNF19B | -1.28376 |
| 244591_x_at | down | RNF207 | -1.2251945 |
| 221194_s_at | up | RNFT1 | 1.2375506 |
| 211849_s_at | up | RNGTT | 1.2514795 |
| 226975_at | up | RNPC3 | 1.2758292 |
| 235854_x_at | up | ROCK1 | 1.2846856 |
| 227849_at | down | RP9 | -1.3087299 |
| 1555202_a_at | up | RPRD1A | 1.2812835 |
| 1566720_at | up | RPS10P7 | 1.2844806 |
| 241241_at | up | RPS14 | 1.202032 |
| 218909_at | down | RPS6KC1 | -1.2025446 |
| 201203_s_at | up | RRBP1 | 1.3286365 |
| 230952_at | down | RRN3P2 | -1.2034118 |
| 214764_at | down | RRP15 | -1.2728981 |
| 1554012_at | down | RSPO2 | -1.2520705 |

| | | | |
|---|---|---|---|
| 216976_s_at | up | RYK | 1.2388287 |
| 1553411_s_at | down | SALL3 | -1.2206621 |
| 233001_at | up | SAMD10 | 1.3059096 |
| 1569599_at | up | SAMSN1 | 1.3768791 |
| 210790_s_at | up | SAR1A | 1.2145623 |
| 234536_at | down | SARDH | -1.2055428 |
| 231895_at | down | SASS6 | -1.2071501 |
| 213435_at | down | SATB2 | -1.2463737 |
| 206667_s_at | up | SCAMP1 | 1.818395 |
| 201646_at | up | SCARB2 | 1.3623428 |
| 239454_at | down | SCARF2 | -1.2787607 |
| 217600_at | up | SCUBE3 | 1.2554878 |
| 214166_at | up | SDHB | 1.3223996 |
| 237598_at | down | SEC1 | -1.3342972 |
| 224470_at | up | SEC22C | 1.3926569 |
| 216392_s_at | up | SEC23IP | 1.2186832 |
| 209889_at | up | SEC31B | 1.2235045 |
| 222385_x_at | up | SEC61A1 | 1.2277613 |
| 208942_s_at | down | SEC62 | -1.2364924 |
| 230265_at | up | SEL1L | 2.1871579 |
| 223610_at | up | SEMA5B | 1.2528108 |
| 223449_at | up | SEMA6A | 1.2717769 |
| 1552812_a_at | up | SENP1 | 1.4154449 |
| 1569974_x_at | down | SEPT7P2 | -1.2163311 |
| 212268_at | up | SERPINB1 | 1.2601981 |
| 210172_at | up | SF1 | 1.6793821 |
| 202036_s_at | down | SFRP1 | -1.2926308 |
| 202773_s_at | up | SFSWAP | 1.3958496 |
| 214354_x_at | up | SFTPB | 1.3084375 |
| 220008_at | up | SGK269 | 1.2009856 |
| 235425_at | down | SGOL2 | -1.2952648 |
| 227923_at | up | SHANK3 | 1.2362424 |
| 219493_at | down | SHCBP1 | -1.3287972 |
| 1552806_a_at | up | SIGLEC10 /// SIGLEC12 | 1.2042744 |
| 1552911_at | up | SIGLEC11 | 1.2368029 |
| 208078_s_at | down | SIK1 | -1.2145748 |
| 238006_at | down | SIN3A | -1.2486405 |
| 242129_at | up | SIN3B | 1.2242844 |
| 228347_at | down | SIX1 | -1.205419 |
| 217640_x_at | down | SKA1 | -1.2202777 |
| 203626_s_at | up | SKP2 | 1.3183829 |
| 224854_s_at | up | SLAIN2 | 1.4008476 |
| 234306_s_at | up | SLAMF7 | 1.3527923 |
| 220740_s_at | up | SLC12A6 | 1.2041407 |
| 225043_at | up | SLC15A4 | 1.3279849 |
| 1557918_s_at | up | SLC16A1 | 1.3504031 |
| 202856_s_at | up | SLC16A3 | 1.2586629 |
| 206599_at | down | SLC16A5 | -1.2317543 |
| 206396_at | up | SLC1A1 | 1.2255124 |
| 237741_at | up | SLC25A36 | 1.3550351 |
| 218136_s_at | up | SLC25A37 | 1.3462328 |
| 231187_at | down | SLC28A1 | -1.2183646 |
| 204429_s_at | up | SLC2A5 | 1.3449061 |
| 239596_at | up | SLC30A7 | 1.2320589 |
| 207439_s_at | up | SLC35A2 | 1.3793849 |
| 238347_at | down | SLC38A10 | -1.2498363 |
| 220413_at | up | SLC39A2 | 1.2097262 |
| 1556551_s_at | up | SLC39A6 | 1.324786 |
| 216504_s_at | up | SLC39A8 | 1.4625964 |
| 243894_at | up | SLC41A2 | 1.2238272 |
| 210692_s_at | up | SLC43A3 | 1.2657751 |

|  |  |  |  |
|---|---|---|---|
| 213167_s_at | up | SLC5A3 | 1.3581944 |
| 214860_at | up | SLC9A7 | 1.3646177 |
| 1553315_at | up | SLFNL1 | 1.3791132 |
| 224149_x_at | up | SLMAP | 1.4679229 |
| 222441_x_at | up | SLMO2 | 1.2856749 |
| 213565_s_at | down | SMAD6 | -1.2128699 |
| 212257_s_at | up | SMARCA2 | 1.5270525 |
| 217656_at | up | SMARCA4 | 1.2888131 |
| 1558747_at | up | SMCHD1 | 1.418564 |
| 238434_at | up | SMCR8 | 1.2463514 |
| 201793_x_at | up | SMG7 | 1.3407514 |
| 205309_at | up | SMPDL3B | 1.4094319 |
| 209427_at | down | SMTN | -1.2547399 |
| 209131_s_at | up | SNAP23 | 1.5971612 |
| 1566403_at | up | SNORA68 | 1.2123123 |
| 226438_at | down | SNTB1 | -1.2145936 |
| 220140_s_at | up | SNX11 | 1.2068441 |
| 229045_at | up | SNX20 | 1.22107 |
| 201085_s_at | up | SON | 1.4134407 |
| 217576_x_at | up | SOS2 | 1.2219704 |
| 204432_at | down | SOX12 | -1.2580765 |
| 1553685_s_at | up | SP1 | 2.0792925 |
| 239743_at | down | SP8 | -1.2185072 |
| 219888_at | up | SPAG4 | 1.2389477 |
| 229075_at | down | SPATA5 | -1.20239 |
| 214403_x_at | down | SPDEF | -1.288168 |
| 216119_s_at | down | SPEF1 | -1.2985827 |
| 201996_s_at | up | SPEN | 1.3673474 |
| 219257_s_at | up | SPHK1 | 1.207213 |
| 244439_at | up | SPRED1 | 1.2163281 |
| 208539_x_at | down | SPRR2B | -1.261287 |
| 232082_x_at | down | SPRR3 | -1.3679508 |
| 224144_at | down | SPTBN4 | -1.2943119 |
| 202278_s_at | up | SPTLC1 | 1.2286109 |
| 1557352_at | up | SQLE | 1.5077261 |
| 244804_at | up | SQSTM1 | 1.220337 |
| 1553581_s_at | down | SREK1IP1 | -1.2559975 |
| 1568957_x_at | up | SRGAP2P1 | 1.2570063 |
| 202199_s_at | up | SRPK1 | 1.2542448 |
| 216639_at | down | SRPX2 | -1.2295233 |
| 208610_s_at | up | SRRM2 | 1.2696333 |
| 201742_x_at | up | SRSF1 | 1.3683664 |
| 213742_at | down | SRSF11 | -1.2527901 |
| 212266_s_at | up | SRSF5 | 1.2475252 |
| 223635_s_at | down | SSBP3 | -1.2413251 |
| 200890_s_at | up | SSR1 | 1.2888123 |
| 217790_s_at | up | SSR3 | 1.2095879 |
| 214555_at | down | SSTR5 | -1.3298289 |
| 214971_s_at | up | ST6GAL1 | 1.4594728 |
| 207524_at | up | ST7 | 1.2825435 |
| 209622_at | up | STK16 | 1.2114447 |
| 215505_s_at | up | STRN3 | 1.60572 |
| 203768_s_at | up | STS | 1.2445357 |
| 226655_at | up | STX17 | 1.3695139 |
| 230691_at | up | STX1B | 1.2003728 |
| 235180_at | up | STYX | 1.267792 |
| 237784_at | up | SUB1 | 1.5253067 |
| 207601_at | up | SULT1B1 | 1.2181348 |
| 240200_at | up | SULT1C2 | 1.2146759 |
| 233827_s_at | up | SUPT16H | 1.4232175 |
| 216271_x_at | up | SYDE1 | 1.3616 |

| | | | |
|---|---|---|---|
| 242774_at | up | SYNE2 | 2.3912773 |
| 215860_at | down | SYT12 | -1.2480085 |
| 205966_at | up | TAF13 | 1.3606119 |
| 202840_at | up | TAF15 | 1.355117 |
| 1553528_a_at | down | TAF5 | -1.2176661 |
| 221618_s_at | up | TAF9B | 1.7934484 |
| 242388_x_at | up | TAGAP | 1.211516 |
| 1555565_s_at | up | TAPBP | 1.3154305 |
| 1564883_a_at | down | TAS1R1 | -1.213903 |
| 234042_at | up | TAS2R45 | 1.2266921 |
| 213913_s_at | down | TBC1D30 | -1.2710199 |
| 222634_s_at | up | TBL1XR1 | 1.319699 |
| 1553132_a_at | down | TC2N | -1.220804 |
| 226388_at | up | TCEA3 | 1.2056544 |
| 202371_at | down | TCEAL4 | -1.2451591 |
| 1553635_s_at | down | TCTEX1D1 | -1.261144 |
| 202719_s_at | up | TES | 1.209044 |
| 221035_s_at | up | TEX14 | 1.2990773 |
| 205688_at | down | TFAP4 | -1.2406025 |
| 215863_at | down | TFR2 | -1.3023049 |
| 233983_at | up | TGM6 | 1.2137678 |
| 203833_s_at | up | TGOLN2 | 1.4449682 |
| 235653_s_at | up | THAP6 | 1.2576196 |
| 209419_at | up | THOC5 | 1.5055614 |
| 222439_s_at | up | THRAP3 | 1.4155089 |
| 229758_at | down | TIGD5 | -1.2184504 |
| 235765_at | up | TLE4 | 1.3426694 |
| 220639_at | down | TM4SF20 | -1.239756 |
| 204426_at | up | TMED2 | 1.3311411 |
| 224496_s_at | up | TMEM107 | 1.4161645 |
| 1564067_x_at | down | TMEM151B | -1.3088908 |
| 213272_s_at | up | TMEM159 | 1.4152834 |
| 228671_at | down | TMEM201 | -1.255594 |
| 226647_at | up | TMEM25 | 1.2335995 |
| 232591_s_at | up | TMEM30A | 1.2167075 |
| 222736_s_at | up | TMEM38B | 1.4124749 |
| 219462_at | up | TMEM53 | 1.2220973 |
| 226083_at | down | TMEM70 | -1.3651098 |
| 242103_at | up | TMEM86A | 1.2434255 |
| 225412_at | up | TMEM87B | 1.2428396 |
| 232941_at | down | TMPRSS6 | -1.3270667 |
| 208097_s_at | up | TMX1 | 1.6823621 |
| 202510_s_at | up | TNFAIP2 | 1.2287173 |
| 222562_s_at | up | TNKS2 | 1.684256 |
| 210585_s_at | up | TNPO2 | 1.3838719 |
| 234734_s_at | down | TNRC6A | -1.2421542 |
| 228998_at | up | TNRC6B | 1.2436055 |
| 208900_s_at | up | TOP1 | 1.2583352 |
| 216100_s_at | up | TOR1AIP1 | 1.4923571 |
| 201683_x_at | up | TOX4 | 1.3020196 |
| 1569098_s_at | up | TP53BP1 | 1.2252831 |
| 211194_s_at | up | TP63 | 1.5798955 |
| 231978_at | up | TPCN2 | 1.2877588 |
| 238065_at | down | TPM3 | -1.3146789 |
| 218876_at | down | TPPP3 | -1.2144017 |
| 215220_s_at | up | TPR | 1.789101 |
| 213575_at | up | TRA2A | 1.4068787 |
| 201399_s_at | up | TRAM1 | 1.4255743 |
| 234440_at | down | TRDV3 | -1.2984595 |
| 219937_at | down | TRHDE | -1.2900738 |
| 202479_s_at | up | TRIB2 | 1.2289041 |

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|---|---|---|---|
| 210995_s_at | up | TRIM23 | 1.2798948 |
| 225868_at | down | TRIM47 | -1.2430952 |
| 1568594_s_at | up | TRIM52 | 1.208695 |
| 235476_at | up | TRIM59 | 1.3533504 |
| 208178_x_at | up | TRIO | 1.2142777 |
| 1568596_a_at | down | TROAP | -1.2470404 |
| 210438_x_at | down | TROVE2 | -1.2332542 |
| 208589_at | down | TRPC7 | -1.2523592 |
| 234351_x_at | up | TRPS1 | 1.3097113 |
| 222855_s_at | up | TRPV2 | 1.2624544 |
| 214908_s_at | up | TRRAP | 1.3985238 |
| 235447_at | up | TRUB1 | 1.2014401 |
| 208763_s_at | up | TSC22D3 | 1.3510768 |
| 227610_at | up | TSPAN11 | 1.2390826 |
| 242595_at | down | TSSK4 | -1.2497983 |
| 1569472_s_at | up | TTC3 | 2.0169203 |
| 208099_x_at | down | TTLL5 | -1.22137 |
| 228883_at | up | TUB | 1.2046323 |
| 215739_s_at | up | TUBGCP3 | 1.230523 |
| 214007_s_at | up | TWF1 | 1.4828343 |
| 219969_at | up | TXLNG | 1.2185957 |
| 201008_s_at | up | TXNIP | 1.474721 |
| 202954_at | down | UBE2C | -1.2116129 |
| 209041_s_at | up | UBE2G2 | 1.2502512 |
| 217799_x_at | up | UBE2H | 1.2914091 |
| 225179_at | up | UBE2K | 1.3215816 |
| 212404_s_at | up | UBE3B | 1.2354816 |
| 202316_x_at | up | UBE4B | 1.431709 |
| 243916_x_at | down | UBLCP1 | -1.3228263 |
| 209088_s_at | up | UBN1 | 1.2053555 |
| 212008_at | up | UBXN4 | 1.3866497 |
| 217100_s_at | up | UBXN7 | 1.2896739 |
| 221765_at | up | UGCG | 1.588019 |
| 1552656_s_at | up | UHMK1 | 1.444792 |
| 202707_at | up | UMPS | 1.2337593 |
| 225869_s_at | up | UNC93B1 | 1.2116233 |
| 208947_s_at | up | UPF1 | 1.3120805 |
| 202412_s_at | up | USP1 | 1.2643702 |
| 209136_s_at | up | USP10 | 1.2028841 |
| 1552678_a_at | up | USP28 | 1.2405721 |
| 212065_s_at | up | USP34 | 1.4104941 |
| 224979_s_at | down | USP36 | -1.2450577 |
| 226729_at | down | USP37 | -1.2221959 |
| 244133_at | up | USP49 | 1.2217152 |
| 242242_at | up | USP6 | 1.2613249 |
| 238561_s_at | up | UTP23 | 1.3668115 |
| 218169_at | down | VAC14 | -1.2132423 |
| 226029_at | down | VANGL2 | -1.2071311 |
| 202549_at | up | VAPB | 1.2119246 |
| 208844_at | down | VDAC3 | -1.3201733 |
| 235237_at | up | VMA21 | 1.295458 |
| 1558549_s_at | down | VNN1 | -1.2886419 |
| 231585_at | down | VPS13A | -1.2454926 |
| 1553852_at | down | VPS13B | -1.2053165 |
| 232386_at | up | VPS13C | 1.3182617 |
| 244400_at | down | VPS33A | -1.2361475 |
| 222387_s_at | up | VPS35 | 1.5461305 |
| 219679_s_at | up | WAC | 1.468996 |
| 224563_at | up | WASF2 | 1.3752091 |
| 205809_s_at | up | WASL | 1.3241796 |
| 203597_s_at | down | WBP4 | -1.2457443 |

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|---|---|---|---|
| 1554410_a_at | up | WBSCR16 | 1.3194683 |
| 228326_at | up | WDR27 | 1.2001189 |
| 209216_at | down | WDR45 | -1.2053094 |
| 228295_at | up | WDR59 | 1.3030602 |
| 1570033_at | down | WIPI2 | -1.2018325 |
| 211993_at | up | WNK1 | 1.3538823 |
| 229547_s_at | down | WNK2 | -1.2346348 |
| 201295_s_at | up | WSB1 | 1.5458132 |
| 1560274_at | up | WTAP | 1.4658818 |
| 218110_at | down | XAB2 | -1.2017821 |
| 1555785_a_at | up | XRN1 | 1.2922058 |
| 231550_at | up | XYLT2 | 1.2105894 |
| 200641_s_at | up | YWHAZ | 1.275037 |
| 243648_at | up | ZBED6 | 1.7465087 |
| 226284_at | down | ZBTB2 | -1.2484276 |
| 1554973_a_at | up | ZBTB26 | 1.3215235 |
| 223953_s_at | up | ZBTB37 | 1.2880547 |
| 230754_at | down | ZBTB38 | -1.2643255 |
| 229691_at | down | ZBTB42 | -1.273353 |
| 213303_x_at | down | ZBTB7A | -1.2313094 |
| 205787_x_at | up | ZC3H11A | 1.2317656 |
| 226897_s_at | up | ZC3H7A | 1.4115872 |
| 1556967_at | up | ZDHHC14 | 1.5948302 |
| 212758_s_at | up | ZEB1 | 1.2435546 |
| 234455_at | down | ZFP1 | -1.2003193 |
| 224631_at | up | ZFP91 | 1.3623356 |
| 203730_s_at | up | ZKSCAN5 | 1.2241715 |
| 1555609_a_at | up | ZMAT3 | 1.728943 |
| 232508_at | down | ZMIZ1 | -1.202388 |
| 210282_at | up | ZMYM2 | 1.4444937 |
| 243814_at | up | ZMYND8 | 1.218426 |
| 1567032_s_at | up | ZNF160 | 1.2833675 |
| 1558184_s_at | down | ZNF17 | -1.2054374 |
| 207164_s_at | up | ZNF238 | 1.3226553 |
| 228185_at | up | ZNF25 | 1.20233 |
| 241720_at | up | ZNF326 | 1.2385306 |
| 220117_at | down | ZNF385D | -1.2603899 |
| 232117_at | down | ZNF471 | -1.2525529 |
| 228138_at | up | ZNF498 | 1.2042183 |
| 1558995_at | up | ZNF547 | 1.3093116 |
| 1556187_at | up | ZNF555 | 1.3690343 |
| 228305_at | up | ZNF565 | 1.2549423 |
| 212620_at | up | ZNF609 | 1.2321737 |
| 227045_at | down | ZNF614 | -1.3506169 |
| 1554249_a_at | up | ZNF638 | 1.2135195 |
| 235179_at | up | ZNF641 | 1.2808677 |
| 1554726_at | up | ZNF655 | 1.573 |
| 222760_at | down | ZNF703 | -1.2891688 |
| 235079_at | down | ZNF704 | -1.2210963 |
| 238606_at | down | ZNF747 | -1.2295533 |
| 239441_at | down | ZNF780A | -1.2400992 |
| 227101_at | up | ZNF800 | 1.5563715 |
| 228130_at | up | ZSCAN30 | 1.386811 |
| 217592_at | up | ZSWIM1 | 1.2098714 |
| 227918_s_at | up | ZYG11B | 1.322702 |

**Table S3:** GSEA "Aggressive multiple myeloma" signature

| PROBE | GENE SYMBOL | GENE_TITLE | RANK IN GENE LIST | RANK METRIC SCORE | RUNNING ES | CORE ENRICHMENT |
|---|---|---|---|---|---|---|
| KIF14 | *KIF14* | kinesin family member 14 | 3 | 0.751 | 0.0594 | Yes |
| CCNB1 | *CCNB1* | cyclin B1 | 5 | 0.727 | 0.1171 | Yes |
| DEPDC1B | *DEPDC1B* | DEP domain containing 1B | 20 | 0.652 | 0.1681 | Yes |
| ASPM | *ASPM* | asp (abnormal spindle) homolog, microcephaly associated (Drosophila) | 97 | 0.544 | 0.2075 | Yes |
| UBE2C | *UBE2C* | ubiquitin-conjugating enzyme E2C | 119 | 0.521 | 0.2478 | Yes |
| NEK2 | *NEK2* | NIMA (never in mitosis gene a)-related kinase 2 | 328 | 0.432 | 0.2720 | Yes |
| C18ORF24 | *C18ORF24* | chromosome 18 open reading frame 24 | 340 | 0.430 | 0.3055 | Yes |
| FOXM1 | *FOXM1* | forkhead box M1 | 501 | 0.394 | 0.3290 | Yes |
| SLC19A1 | *SLC19A1* | solute carrier family 19 (folate transporter), member 1 | 547 | 0.386 | 0.3575 | Yes |
| MAGEA3 | *MAGEA3* | melanoma antigen family A, 3 | 675 | 0.370 | 0.3806 | Yes |
| SPBC25 | *SPBC25* | spindle pole body component 25 homolog (S. cerevisiae) | 762 | 0.359 | 0.4049 | Yes |
| AURKA | *AURKA* | aurora kinase A | 794 | 0.356 | 0.4317 | Yes |
| CDCA1 | *CDCA1* | cell division cycle associated 1 | 861 | 0.348 | 0.4561 | Yes |
| BIRC5 | *BIRC5* | baculoviral IAP repeat-containing 5 (survivin) | 1039 | 0.330 | 0.4737 | Yes |
| TTK | *TTK* | TTK protein kinase | 1061 | 0.328 | 0.4987 | Yes |
| TOP2A | *TOP2A* | topoisomerase (DNA) II alpha 170kDa | 1262 | 0.312 | 0.5137 | Yes |
| DLG7 | *DLG7* | discs, large homolog 7 (Drosophila) | 1304 | 0.309 | 0.5362 | Yes |
| UBE2T | *UBE2T* | ubiquitin-conjugating enzyme E2T (putative) | 1437 | 0.300 | 0.5536 | Yes |
| LOC652689/FAM72A | *not available* |  | 1813 | 0.276 | 0.5573 | Yes |
| ZWILCH | *ZWILCH* | Zwilch, kinetochore associated, homolog (Drosophila) | 2068 | 0.261 | 0.5656 | Yes |
| GAGE1/GAGE2 | *not available* |  | 2088 | 0.260 | 0.5853 | Yes |
| MAGEA1 | *MAGEA1* | melanoma antigen family A, 1 (directs expression of antigen MZ2-E) | 2155 | 0.257 | 0.6025 | Yes |
| BUB1B | *BUB1B* | BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast) | 2341 | 0.249 | 0.6132 | Yes |
| SPBC24 | *SPBC24* | spindle pole body component 24 homolog (S. cerevisiae) | 2596 | 0.237 | 0.6196 | Yes |
| MAGEA6 | *MAGEA6* | melanoma antigen family A, 6 | 3708 | 0.194 | 0.5810 | Yes |
| E2F8 | *E2F8* | E2F transcription factor 8 | 3781 | 0.191 | 0.5926 | Yes |
| DCC1 | *not available* |  | 3913 | 0.187 | 0.6011 | Yes |
| MCM10 | *MCM10* | MCM10 minichromosome maintenance deficient 10 (S. cerevisiae) | 3995 | 0.185 | 0.6119 | Yes |
| CCDC34 | *CCDC34* | coiled-coil domain containing 34 | 4039 | 0.184 | 0.6244 | Yes |
| TRIP13 | *TRIP13* | thyroid hormone receptor interactor 13 | 4150 | 0.181 | 0.6333 | Yes |
| RFC4 | *RFC4* | replication factor C (activator 1) 4, 37kDa | 4317 | 0.176 | 0.6392 | Yes |
| PRC1 | *PRC1* | protein regulator of cytokinesis 1 | 4353 | 0.175 | 0.6513 | Yes |
| TYMS | *TYMS* | thymidylate synthetase | 4523 | 0.170 | 0.6566 | Yes |
| TPX2 | *TPX2* | TPX2, microtubule-associated, homolog (Xenopus laevis) | 5070 | 0.154 | 0.6422 | Yes |
| KIAA1794 | *KIAA1794* | KIAA1794 | 5203 | 0.150 | 0.6477 | Yes |
| CDC2 | *CDC2* | cell division cycle 2, G1 to S and G2 to M | 5245 | 0.149 | 0.6575 | Yes |

**Table S4:** GSEA **"**CD40 dependant B cell" signature

| PROBE | GENE SYMBOL | GENE_TITLE | RANK IN GENE LIST | RANK METRIC SCORE | RUNNING ES | CORE ENRICHMENT |
|---|---|---|---|---|---|---|
| NFKB2 | *NFKB2* | nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) | 20573 | -0.743 | 0.0016 | Yes |
| NCKAP1L | *NCKAP1L* | NCK-associated protein 1-like | 20563 | -0.706 | -0.0373 | Yes |
| TNFAIP2 | *TNFAIP2* | tumor necrosis factor, alpha-induced protein 2 | 20470 | -0.517 | -0.0702 | Yes |
| CD40 | *CD40* | CD40 molecule, TNF receptor superfamily member 5 | 20467 | -0.515 | -0.0975 | Yes |
| CCR7 | *CCR7* | chemokine (C-C motif) receptor 7 | 20438 | -0.495 | -0.1233 | Yes |
| CD83 | *CD83* | CD83 molecule | 20429 | -0.490 | -0.1491 | Yes |
| DUSP2 | *DUSP2* | dual specificity phosphatase 2 | 20415 | -0.481 | -0.1744 | Yes |
| HTR3A | *HTR3A* | 5-hydroxytryptamine (serotonin) receptor 3A | 20267 | -0.423 | -0.1927 | Yes |
| SLAMF1 | *SLAMF1* | signaling lymphocytic activation molecule family member 1 | 20177 | -0.395 | -0.2108 | Yes |
| HLA-DQB1 | *HLA-DQB1* | major histocompatibility complex, class II, DQ beta 1 | 19998 | -0.363 | -0.2230 | Yes |
| TNFAIP8 | *TNFAIP8* | tumor necrosis factor, alpha-induced protein 8 | 19949 | -0.355 | -0.2398 | Yes |
| TRIP10 | *TRIP10* | thyroid hormone receptor interactor 10 | 19874 | -0.343 | -0.2550 | Yes |
| BCL2 | *BCL2* | B-cell CLL/lymphoma 2 | 19667 | -0.316 | -0.2632 | Yes |
| PHACTR1 | *PHACTR1* | phosphatase and actin regulator 1 | 19586 | -0.307 | -0.2760 | Yes |
| FAIM3 | *FAIM3* | Fas apoptotic inhibitory molecule 3 | 19526 | -0.298 | -0.2893 | Yes |
| MAP3K8 | *MAP3K8* | mitogen-activated protein kinase kinase kinase 8 | 19506 | -0.296 | -0.3042 | Yes |
| STAT5A | *STAT5A* | signal transducer and activator of transcription 5A | 19496 | -0.295 | -0.3194 | Yes |
| NFKBIA | *NFKBIA* | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha | 19468 | -0.292 | -0.3337 | Yes |
| DDIT4 | *DDIT4* | DNA-damage-inducible transcript 4 | 19443 | -0.290 | -0.3480 | Yes |
| CFLAR | *CFLAR* | CASP8 and FADD-like apoptosis regulator | 19434 | -0.289 | -0.3630 | Yes |
| CR2 | *CR2* | complement component (3d/Epstein Barr virus) receptor 2 | 19401 | -0.286 | -0.3768 | Yes |
| CCL4 | *CCL4* | chemokine (C-C motif) ligand 4 | 19304 | -0.278 | -0.3872 | Yes |
| EBI2 | *EBI2* | Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor) | 19233 | -0.270 | -0.3985 | Yes |
| UNC119 | *UNC119* | unc-119 homolog (C. elegans) | 19195 | -0.267 | -0.4109 | Yes |
| TNFAIP3 | *TNFAIP3* | tumor necrosis factor, alpha-induced protein 3 | 18909 | -0.244 | -0.4112 | Yes |
| LRRC32 | *LRRC32* | leucine rich repeat containing 32 | 18894 | -0.243 | -0.4234 | Yes |
| ZFP36L1 | *ZFP36L1* | zinc finger protein 36, C3H type-like 1 | 18764 | -0.235 | -0.4300 | Yes |
| ICAM1 | *ICAM1* | intercellular adhesion molecule 1 (CD54), human rhinovirus receptor | 18745 | -0.233 | -0.4416 | Yes |
| KRT7 | *KRT7* | keratin 7 | 18666 | -0.228 | -0.4501 | Yes |
| NEF3 | *NEF3* | neurofilament 3 (150kDa medium) | 18243 | -0.204 | -0.4416 | Yes |
| MEF2C | *MEF2C* | MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) | 18204 | -0.201 | -0.4505 | Yes |
| TRAF1 | *TRAF1* | TNF receptor-associated factor 1 | 17831 | -0.182 | -0.4430 | Yes |
| PLEK | *PLEK* | pleckstrin | 17794 | -0.180 | -0.4509 | Yes |
| LYN | *LYN* | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog | 17576 | -0.170 | -0.4498 | Yes |
| NFKBIE | *NFKBIE* | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon | 17522 | -0.168 | -0.4563 | Yes |
| RAC2 | *RAC2* | ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) | 17513 | -0.168 | -0.4648 | Yes |
| SYNGR2 | *SYNGR2* | synaptogyrin 2 | 17446 | -0.165 | -0.4704 | Yes |
| TNF | *TNF* | tumor necrosis factor (TNF superfamily, member 2) | 17428 | -0.165 | -0.4783 | Yes |
| HLA-DRB1 /// | *HLA-DRB1* | Major histocompatibility complex, class II, DR beta 1 | 17296 | -0.158 | -0.4807 | Yes |
| BLR1 | *BLR1* | Burkitt lymphoma receptor 1, GTP binding protein (chemokine (C-X-C motif) receptor 5) | 17189 | -0.154 | -0.4839 | Yes |
| ARID5B | *ARID5B* | AT rich interactive domain 5B (MRF1-like) | 17158 | -0.153 | -0.4905 | Yes |
| GADD45B | *GADD45B* | growth arrest and DNA-damage-inducible, beta | 16998 | -0.146 | -0.4908 | Yes |
| PIK3CD | *PIK3CD* | phosphoinositide-3-kinase, catalytic, delta polypeptide | 16885 | -0.141 | -0.4931 | Yes |
| HLA-F | *HLA-F* | major histocompatibility complex, class I, F | 16880 | -0.141 | -0.5004 | Yes |
| TMC6 | *TMC6* | transmembrane channel-like 6 | 16866 | -0.141 | -0.5072 | Yes |

**Table S5:** Oligonucleotides used for this study

### sh cloning

| Duplex name | Oligo Name | Sequence 5' to 3' |
|---|---|---|
| shCY1 = shCYCLON | Cyclonsh2F | CGTGTACCGGTCCGTCCAAGAAGTTGAATAAAGCTCGAGCTTTATTCAACTTCTTGGACGTTTTTGAATTCCGTCGT |
| | Cyclonsh2R | ACGACGGAATTCAAAAACGTCCAAGAAGTTGAATAAAGCTCGAGCTTTATTCAACTTCTTGGACGGACCGGTACACG |
| shCY2 | Cyclonsh3F | CGTGTACCGGTCCCCAGATGCTTCAGGACAAGCCTCGAGGCTTGTCCTGAAGCATCTGGGTTTTTGAATTCCGTCGT |
| | Cyclonsh3R | ACGACGGAATTCAAAAACCCAGATGCTTCAGGACAAGCCTCGAGGCTTGTCCTGAAGCATCTGGGGACCGGTACACG |
| shCtrl | CtrlshF | CGTGTACCGGTCCCTAAGGTTAAGTCGCCCTCGCTCGAGCGAGGGCGACTTAACCTTAGGTTTTTGAATTCCGTCGT |
| | CtrlshR | ACGACGGAATTCAAAAACCTAAGGTTAAGTCGCCCTCGCTCGAGCGAGGGCGACTTAACCTTAGGGACCGGTACACG |

### q-PCR

| Oligo Name | Sequence 5' to 3' |
|---|---|
| CyclonF | AGCGAAAAGGTTCTTCATCC |
| CyclonR | TTCCTCTCCTGTCGTTCCTT |