Tumor cell-specific bioluminescence platform to identify stroma-induced changes to anti-cancer drug activity

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SUPPLEMENTAL MATERIAL AND METHODS

Cells

Luciferase (luc)-expressing cells evaluated in this study included: the MM cell lines MM.1S-GFP/luc, MM.1R-GFP/luc KMS-18-GFP/Luc, KMS-34-mCherry-Luc, OPM-1-mCherry-Luc, OPM-2-GFP/luc, INA-6-mCherry-Luc; the leukemia cell lines K562-luc-neo, and KU812F-luc-neo; the breast cancer cell line MDA-MB-231met-luc-neo; the melanoma line A375-luc-neo; and the anaplastic thyroid carcinoma cell line FRO-luc-neo. Cell lines were generated by retroviral transduction with the pGC-*gfp/luc* vector (kind gift of C.G. Fathman, Stanford University) for MM.1S, MM.1R, KMS-18 and OPM-2 cells; and the MSCV-Luc-neo retroviral vector for KU812F, K562, MDA-MB-231met and A375 cells. FRO cells were transfected with the luciferase expression vector phCMV-FSR vector (Genlantis). INA-6, OPM-1 and KMS-34 cells were transduced with a lentiviral mCherry-luc vector. Further details on individual transduction protocols and selection of Luc$^+$ cells have been previously described [1]. For molecular profiling studies, INA-6, OPM-1 and KMS-34 cells transduced with a lentiviral GFP-vector were a kind gift of R. Carrasco (Dana-Farber Cancer Institute). Stromal cells evaluated in this study included the human immortalized bone marrow stromal cell lines HS-5 (American Type Culture Collection, ATCC) and the KM101, KM103, KM104, and KM105 cells, provided by YT Tai (Dana-Farber Cancer Institute) and previously described by Harigaya and Handa [2]. Patient stromal cells were isolated by culturing adherent cells from bone marrow aspirates for >14 d. Co-cultures of tumor cells with stromal cells were grown in RPMI1640 (Mediatech, Inc) for myeloma or leukemia cell lines) or DMEM (Mediatech, Inc.; for melanoma, breast cancer and thyroid cell lines) media supplemented with 10% FBS, 100 U ml^{-1} penicillin and 100 μg ml^{-1} streptomycin.

Reagents

Bortezomib (PS-341) was provided by Millennium Pharmaceuticals. Doxorubicin, dexamethasone, MTT, and Ara-C were purchased from Sigma-Aldrich (St. Louis, MO). Apo2.7

antibody was purchased from Beckman Coulter/Immunotech. Imatinib and Nilotinib were kindly provided by Novartis Pharma AG. 2-(4-morpholinoanilino)-6-cyclohexylaminopurine (reversine) was purchased from Cayman Chemical. Duration of treatment was 24 h for PS-341; 48 h for Doxo, AraC, imatinib, nilotinib, and 72 h for Dex and reversine, unless otherwise stated. IL-6 and IL-6R blocking antibodies were purchased from R & D Systems.

Cell survival assays

Viability of cells treated with reversine, alone or combined with other agents, was assessed by using 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrasodium bromide (MTT, Chemicon International) dye absorbance or CellTiterGlo (CTG; Promega). For MTT analysis, cells were pulsed with 1:10 the culture volume of 5 mg ml^{-1} MTT to each well for the last 4 h of culture, followed by 1.5-3 fold the culture volume of isopropanol containing 0.04 N HCl. Absorbance was measured at 570 and 630 nm using a spectrophotometer (Molecular Devices Corp., Sunnyvale CA). For CTG analysis, equal volume of reconstituted CTG reagent was added to cultures, incubated at 37ºC for 30 min, and luminescence read using a Luminoskan luminometer (Labsystems). Anti-IL-6 and IL-6 receptor neutralizing antibodies were used at 1 µg mL^{-1} (R&D Systems).

Flow cytometry-based drug sensitivity testing in tumor-stromal co-cultures

Tumor cell viability in the presence vs. absence of stromal cells was evaluated by flow cytometry. After incubation with drug or vehicle, MM.1S-GFP/luc MM cells were stained with Apo2.7 (BD Biosciences) to detect apoptotic cells. GFP^+ MM cells were gated to distinguish them from GFP^- stromal cells in the co-cultures. The ratio of Apo2.7-positive cells in the GFP^+ compartment of the drug-treated vs. vehicle control provided a quantified expression of viable MM cells in response to drug treatment, both in the context of drug treatment of MM cells alone and in the context of MM cell co-culture with BMSCs.

In vitro luciferase and kinase activity assays

For *in vitro* luciferase activity assay, luciferin substrate solution was prepared by dissolving firefly diluent (Sigma Aldrich) in ddH_2O supplemented with 100 nM Adenosine 5'Triphosphate (ATP, Sigma Aldrich). Serial dilutions of Reversine (Cayman Chemicals) and Resveratrol (Sigma Aldrich) were prepared in the luciferin solution. Firefly luciferase (Sigma Aldrich) was reconstituted in Glycine-Tris buffer supplemented with 10mM EDTA (Boston BioProducts) and 100 mM $MgSO_4$ (Sigma Aldrich). 1 µL of a 500 µg mL^{-1} stock of luciferase was seeded in each well of a 384-well optical bottom plate (Nunc). 50 µL of luciferin solution with a range of Reversine or Resveratrol concentrations were then added. Immediately after the addition of the substrate solution, luminescence was measure using a Luminoskan Ascent Luminometer with Ascent Software (Labsystems).

In vitro kinase activity was screened with 500 nM of reversine (in 1% DMSO) and ATP, using the Invitrogen Z'-LYTE™ kinase assay platform (Invitrogen). In summary, in the first reaction the kinase transfers the gamma-phosphate of ATP to a single tyrosine, serine or threonine residue in a synthetic FRET-peptide. In the secondary reaction, a site-specific protease recognizes and cleaves non-phosphorylated FRET-peptides. To calculate kinase activity, the ratio of donor emission to acceptor emission after excitation of the fluorophore at 400nm was compared.

Gene expression profiling and analyses

The transcriptional profile of MM cells co-cultured with stromal cells vs. when cultured alone was characterized by oligonucleotide microarray analysis, using the human U133 plus 2.0 Affymetrix GeneChip, according to previously described protocols for total RNA extraction and purification; cDNA synthesis; *in vitro* transcription reaction for production of biotin-labeled cRNA; hybridization of cRNA with U133plus2.0 Affymetrix gene chips; and scanning of image output files. Microarray data are available from the Gene Expression Omnibus database (http://www.ncbi.nlm.nih.gov/geo) under accession codes GSE# (pending). Analysis of gene expression datasets included filtering of upregulated or downregulated transcripts based on conventional criteria for statistical significance, as well as by hierarchical & functional clustering algorithms [5,7-9], and analysis of transcriptional signatures of pathway activation status. Specifically, for each experimental condition of our study, biotin-labeled cRNA was hybridized in duplicate U133 plus 2.0 Affymetrix chips. Scanned image output files were analyzed using DNA-Chip Analyzer (dChip) [10], including conversion to DCP files, normalization and modeling, and averaging of duplicate chips according to standard parameters recommended by the software. For each cell line, the gene expression profile in the presence of stomal cells was compared to the profile of the same cell line cultured in the absence of stromal cells, and filtering of upregulated or downregulated transcripts was based on conventional criteria for statistical significance incorporated in the software (e.g. >1.2 fold change and an absolute change in the signal of a probe by >100). Probes were then further filtered to identify those which have ≥2-fold change between a MM cell line co-cultured with BMSCs vs. the same cell line cultured alone and exhibit this change in at least 1 of the cell lines tested. Supervised hierarchical clustering of the dataset according to the list of transcripts significantly modulated in at least one cell line was then performed using dChip.

Functional clustering of transcripts modulated by tumor-stromal interaction: Transcripts modulated by ≥1.2 fold and by absolute signal change of ≥100 were further curated to identify clusters of genes with common functional roles. In particular, we sought to identify functional groups in which multiple transcripts may individually show even modest expression changes, but which collectively represent significant higher-order shifts in activity of key pathways responsible for phenotypic changes triggered by tumor-stromal interactions. The curation of the modulated transcripts into functional groups was performed based on: prior literature in the MM field and other tumor models; functional annotations present in the Ingenuity Pathway Analysis database (Ingenuity Systems Inc.) and dChip; as well as information provided by the unCHIP Cross-reference tool for microarray data (Children's Hospital Informatics Program, http://unchip.org:8080/). For this functional clustering analyses, we focused on diverse pathways implicated in tumor pathophysiology, including cytokine, growth factor and/or chemokine signaling; oncogenic transformation; resistance to apoptosis; Ras superfamily function; heat shock protein and chaperone function; ubiquitin/proteasome pathway; transcription factor networks; histone deacetylase and epigenetic regulation; cell cycle regulation; DNA repair and drug resistance; tumor cell interaction with the microenvironment, including adhesive interactions; ribosomal function; and/or mitochondrial genes. For each of these gene clusters and each cell line, the average value (+/- 95% confidence limit) of the difference in absolute expression signal in MM cells cultured in the presence vs. absence of BMSCs was calculated.

Pathway activation status analyses: Transcripts previously shown to reflect the activation state of pathways pertinent to tumor cell proliferation, survival drug resistance and other functional endpoints of tumor-stromal interactions were evaluated for differences in expression, for each of the indicated MM cell lines cultured in the presence vs. absence of BMSCs in vitro. As in the previously mentioned functional clustering analyses, the pathway activation status analyses sought to evaluate the effect triggered by tumor-stromal interactions on functional groups of multiple transcripts which individually may show only modest expression changes, but which collectively represent significant higher-order shifts in activity of key pathways responsible for phenotypic changes triggered by tumor-stromal interactions. Furthermore, this analysis allowed us to evaluate the activation state of known pathways in MM cell lines which respond to stromal co-culture in the absence of drug treatment with increased numbers of viable cells vs. those which do not. The activation status of signaling cascades are not only determined by the expression of individual members of the cascade, but also by translational regulation and post-translational modifications. Although these are not revealed by gene expression profiling, the overall activity of the pathway can be evaluated by the study of downstream target genes. For this analysis, we focused on a compendium of signatures previously determined to reflect the status of the ribosomal and proteasome pathways (as included in the Gene Set Enrichment Analysis (GSEA) database http://www.broad.mit.edu/GSEA and [11,12]); Akt activation signature derived as the human orthologs of probes upregulated in tumors of the MPAKT mouse model [13]; Ras activation signature derived as the human orthologs of probes upregulated in Ras-transformed mouse fibroblasts [14]; signature of NF-κB activated genes identified by Shaffer et al. [15] or a signature combining the NF-κB target genes identified by Shaffer et al. [15] and Keats et al [16]; signatures of self renewal implicated in normal and/or cancer stem cell biology, including myc [17,18], hTERT [19], Hedgehog [20], Notch [21] and a transcriptional signature of genes upregulated in undifferentiated human embryonic stem cells [22] (as included in the GSEA database); as well as the U133 plus 2.0 probes corresponding to the IRF4 target genes identified by Shaffer et al [23]. We also studied the transcriptional signature of genes downregulated by p53 function [24] (as identified with the use of Ingenuity PathwayAnalysis); a transcriptional signature previously reported to correlate with unfavorable clinical prognosis of MM patients [25]; a signature of genes overexpressed in angiogenic vs. non-angiogenic tumors, as identified by Hu et al. [26]; 3 previously validated gene signatures (as included n the GSEA database) shown to be upregulated under hypoxic condition [27-29]; and a transcriptional signature of HIF-1α target genes[30] (again from the GSEA database). The probes corresponding to each of these signatures were used to filter the dataset (either using the Ingenuity Pathway Analysis software or Microsoft Excel) and the outputs were processed to calculate the average value (+/- 95% confidence limit) of the difference in absolute expression signal in MM cells cultured in the presence vs. absence of BMSCs for each transcriptional signature and each cell line; as well as the average expression signal of all the genes of each signature (+/- 95% confidence limit) for each experimental condition of each cell line.

Transcriptional signature of stroma-responsive genes and relationship with clinical outcome. Gene expression data of stroma-responsive cell lines cultured in the presence or absence of stroma were normalized to the median probe intensity of the microarray with median brightness of the dataset using dChip. A transcriptional index of MM cell response to stroma was identified, based on transcripts upregulated (by >100% compared to control) and satisfying filtering criteria (absolute signal change of ≥100) in at least one of the cell lines tested. Common probes of that signature between the U133 plus 2.0 and the U133A microarray chips were utilized to filter the log2-transformed and median centered gene expression dataset of tumor cells from MM patients enrolled in a randomized phase III clinical trial comparing treatment with bortezomib vs. dexamethasone of relapsed/refractory MM [31,32]. After filtering based on the 1000 probes for non-immunogloblulin transcripts with the highest values of the 90th percentile of expression in the evaluable patients of this trial, the transcriptional index of stromal responsive genes was calculated as the average of the log2-transformed and median centered values for each probe of the signature. Patients were then classified as having high (top quartile of expression) vs. low (bottom 3 quartiles) expression of stroma-responsive genes and Kaplan-Meier survival analyses were performed for each arm of the randomized trial using SPSS 16.0. Concordant results were also obtained with alternative versions of the transcriptional index of stromal responsive genes (unpublished data).

SUPPLEMENTAL FIGURE LEGENDS

SUPPLEMENTAL FIGURE 1. Features of CS-BLI for the specific measurement of tumor viability in the presence or absence of accessory cells. (**a**) Luc+ MM.1S cells plated at increasing cell numbers had a linear correlation of viable MM cells both in the presence or absence of HS-5 stromal cells. (**b, c)** MTT viability assessment yielded results consistent in MM.1S parental cells and transduced cells expressing GFP/luc when treated with Doxo or PS-341 in the absence of stromal cells. (**d**) MM.1S-GFP/luc cells yielded consistent results when viability was measured by CellTiterGlo (CTG) or CS-BLI. Using flow cytometry, MM.1S-GFP/luc cells were exposed to Doxo in the presence and absence of GFP- stromal cells. (**e**) GFP$^+$ MM cells had fewer non-viable (Apo2.7$^+$) cells in the presence vs. absence of BMSCs.

SUPPLEMENTAL FIGURE 2. CS-BLI confirms that co-culture with BMSCs confers protection against specific anti-tumor agents in MM cells. (**a, c, e**) MM.1S-GFP/luc and (**b, d, f**) MM.1R-GFP/luc cells were plated in the presence or absence of HS-5 BMSCs (10,000 cells per well) and treated with (**a, b**) Dex, (**c, d**) Doxo or (**e, f**) the proteasome inhibitor bortezomib (PS-341). BMSCs confer to MM.1S cells protection against Dex and Doxo, but not PS-341. BMSCs have little effect on the Dex-resistant cell line, MM.1R, in response to Dex treatment, but confer protection against Doxo. In addition, BMSCs confer no protection to treatment of MM.1R cells with PS-341.

SUPPLEMENTAL FIGURE 3. BMSCs confer protection against various agents in leukemia cell lines. (**a, c, e, g**) Luc$^+$ KU812F and (**b, d, f, h**) K562 leukemia cells were plated in the presence or absence of HS-5 BMSCs (10,000 per well) and treated with (**a, b**) Ara-C, (**c, d**) imatinib, (**e, f**) Doxo or (**g, h**) nilotinib. BMSCs confer protection against AraC, Imatinib and nilotinib, but not Doxo in KU812F cells. For K562 cells, BMSCs confer protection against Ara-C, but not imatinib, Doxo or nilotinib.

SUPPLEMENTAL FIGURE 4. Co-culture with BMSCs can protect solid tumor cell lines against anti-cancer agents. (**a, b**) Luc$^+$ MDA-MB-231met, (**c, d**) A375 and (**e, f**) FRO cells were plated with or without HS-5 BMSCs (10,000 cells per well), treated the following day, and incubated for an additional 48 h. BMSCs confer modest protection against both (**a**) AraC and (**b**) Doxo in MDA-MB-231-met cells. BMSCs provided a considerable level of protection to (**c**) AraC, but not against (**d**) Doxo in A375 cells. Lastly, BMSCs confer no protection against (**e**) AraC, but confer modest protection against (**f**) Doxo in FRO cells.

SUPPLEMENTAL FIGURE 5. Co-culture with primary BMSCs from MM patients provides tumor cell protection against specific anti-cancer agents. MM.1S-GFP/luc were plated in the presence or absence of BMSCs isolated from two different MM patients (10,000 per well) and treated with (**a**) Dex, (**b**) Doxo or (**c**) PS-341. Both patient BMSC samples confer protection against Dex and Doxo, but not PS-341 in MM cells.

SUPPLEMENTAL FIGURE 6. Interaction of MM cells with BMSCs leads to distinct changes in transcriptional signatures indicative of the activation of key molecular pathways in tumor cell pathophysiology. Transcripts previously shown to reflect the activation state of the indicated pathways were evaluated for differences in expression in each MM cell line, in the presence vs. absence of BMSCs *in vitro*. For each transcriptional signature, the average value (+/- 95% confidence limit) of absolute expression signal in MM cells for each cell line and each experimental condition (i.e. culture in the presence vs. absence of BMSCs) is shown. Asterisks (*) denote statistically significant ($p<0.05$) change in value of a transcriptional signature in the presence vs. absence of BMSCs.

SUPPLEMENTAL FIGURE 7. In vitro luciferase and kinase activity assays of reversine. (**a**) *In vitro* luciferase activity was screened in the presence of reversine. Luciferase was reconstituted in Glycine-Tris buffer plus EDTA and MgSO4, with the addition of ATP and increasing concentrations of reversine or the positive control, resveratrol. Luminescence was detected immediately after the addition of the substrate (*n* = 4). Reversine (up to 100 μM) did not block luciferase activity. (**b**) Using the Z'-Lyte^{TM} kinase assay, select kinases were screened for activity in the presence of 500 nM reversine. Inhibition of activity was observed against a select subset of kinases, including Auroras, JAK2, and SRC, but not other kinases important for MM growth and survival, including AKT1, 2, 3, FGFR3, GSK3A or B.

SUPPLEMENTAL FIGURE 8. Imaging results over time for each reversine-treated and control mouse in the tumor experiment of MM.1S-GFP/luc cells injected i.v. vs s.c. (**a**) Imaging results are shown utilizing the IVIS Xenogen camera system following i.p. injection of luciferin substrate in *SCID-Beige* mice bearing diffuse lesion tumors. (**b**) Imaging results are shown utilizing the IVIS Xenogen camera system following i.p. injection of luciferin substrate in SCID-Beige mice bearing s.c. tumors. Graphical results for each model were analyzed using

Living Image software and displayed utilizing both high sensitivity settings as well as lower sensitivity settings to display tumors.

SUPPLEMENTAL TABLE LEGENDS

SUPPLEMENTAL TABLE 1. Examples of transcripts significantly modulated in tumor cells by their interaction with stroma. The ratio of change in expression in the presence compared to absence of stromal cells is presented for groups of transcripts related to diverse cell functions (cell signaling for proliferation/survival, resistance to apoptosis or drug treatments, DNA repair, heat shock protein and molecular chaperones, ubiquitin-proteasome pathway, histone regulation or chromatin remodeling, microenvironmental interactions and ribosomal function). The ratio of stroma-induced change in expression of each transcript is depicted for each cell line according to a color-coded scale.

SUPPLEMENTAL TABLE 2. Probes of a stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients. Individuals with MM in whom tumor cells have high averages levels of log2-median centered signal intensity values for these probes have adverse clinical outcome with Dex-treatment. Alternative versions of the transcriptional index of stromal responsive genes have also yielded concordant conclusions of association with clinical outcome.

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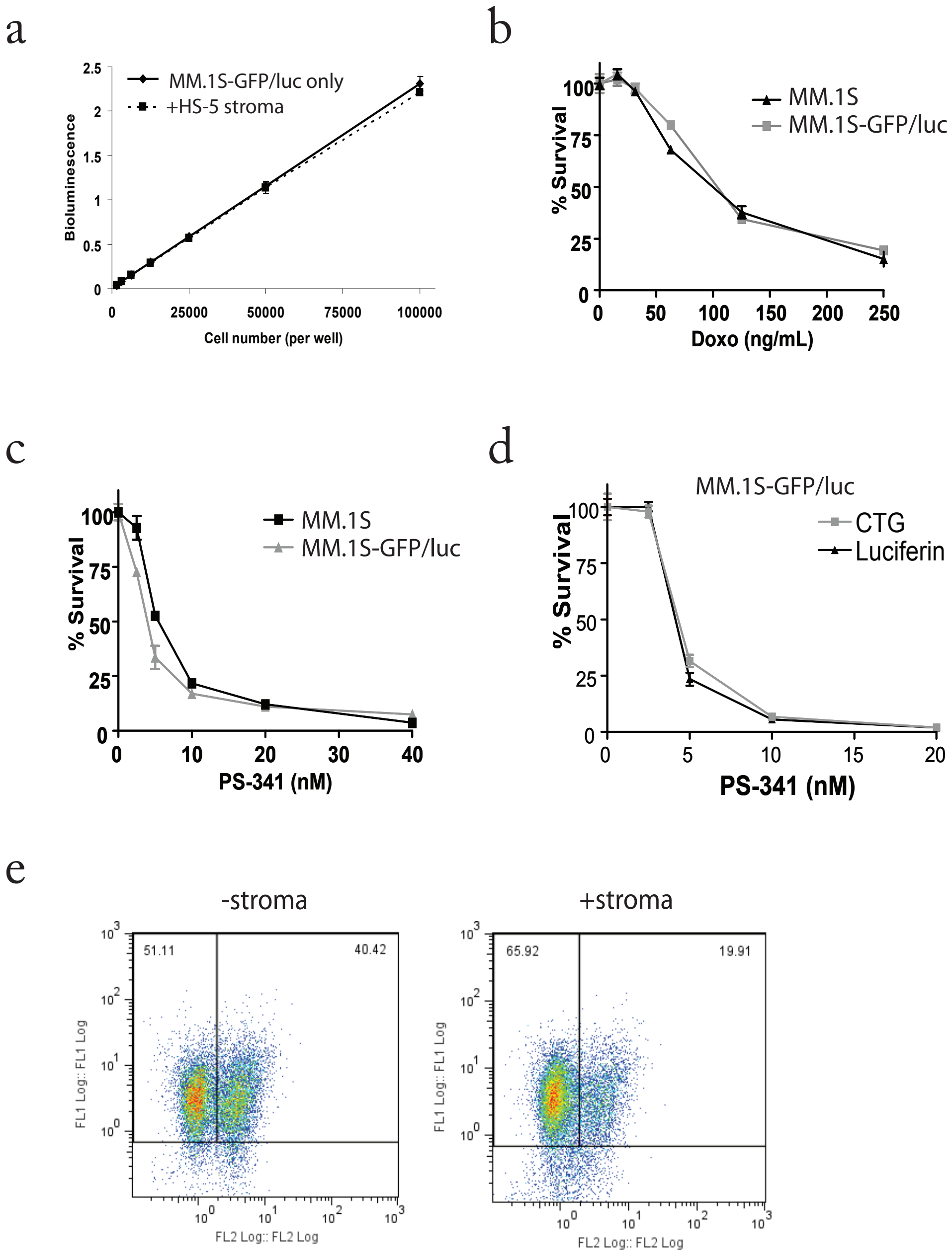
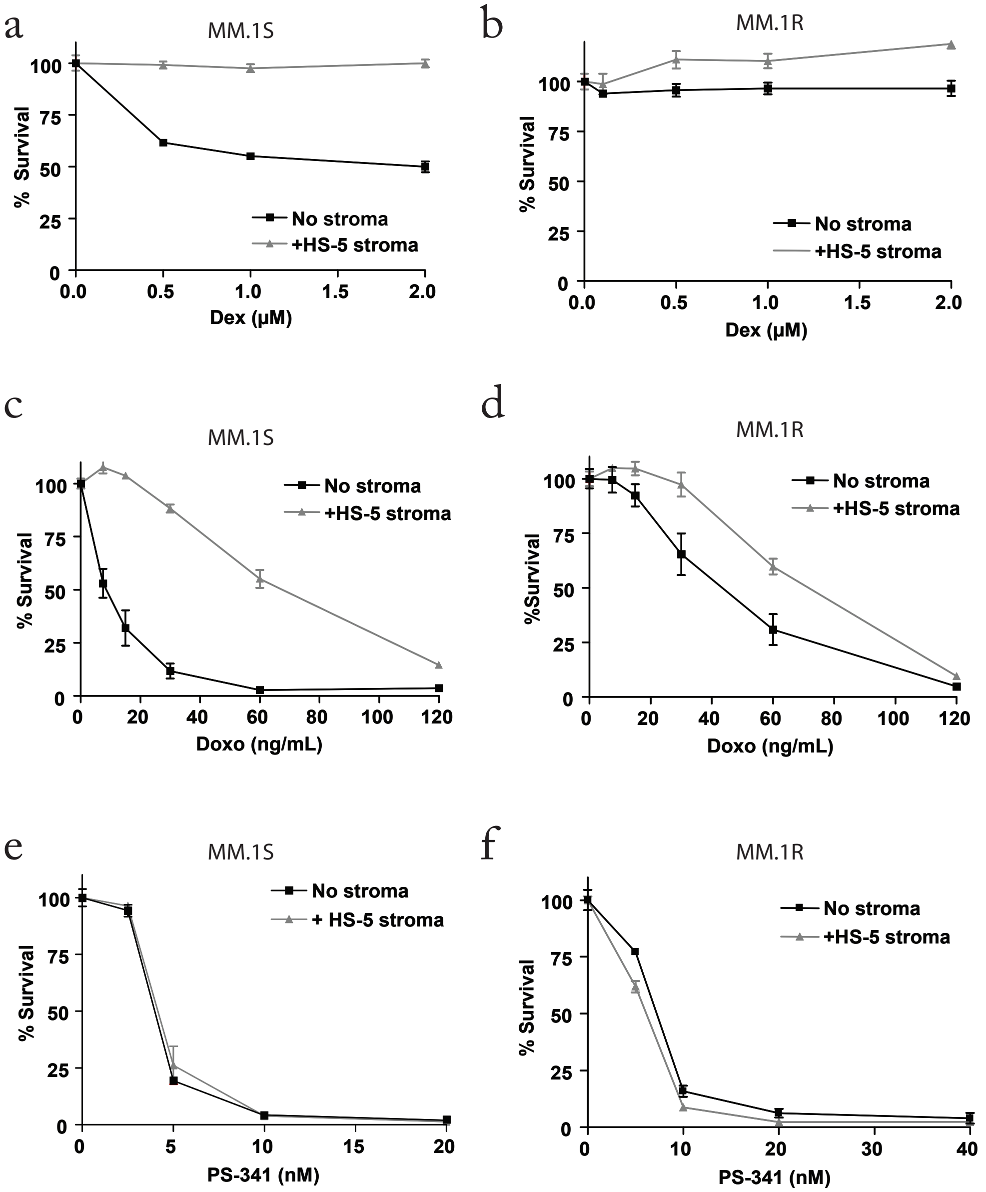
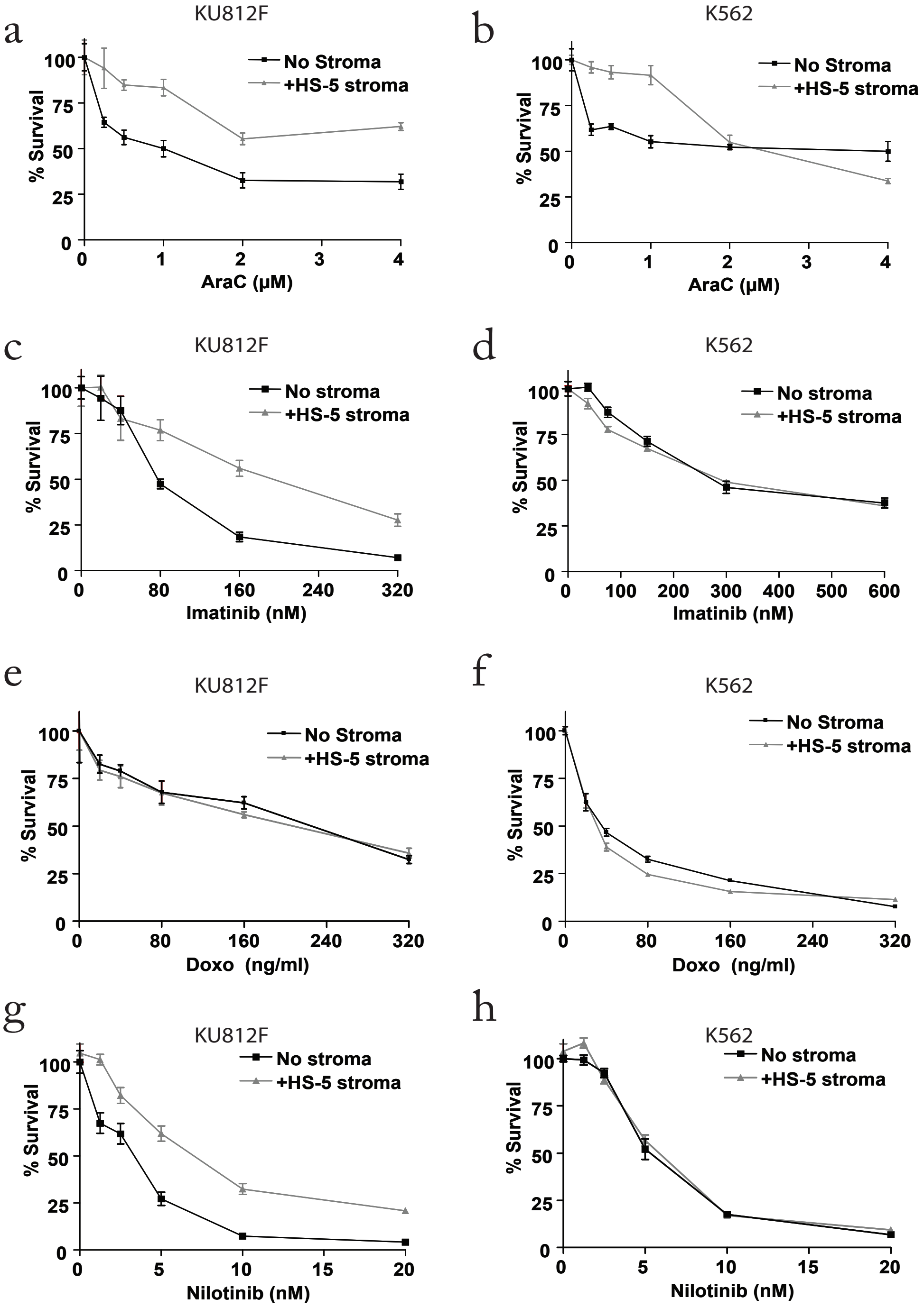


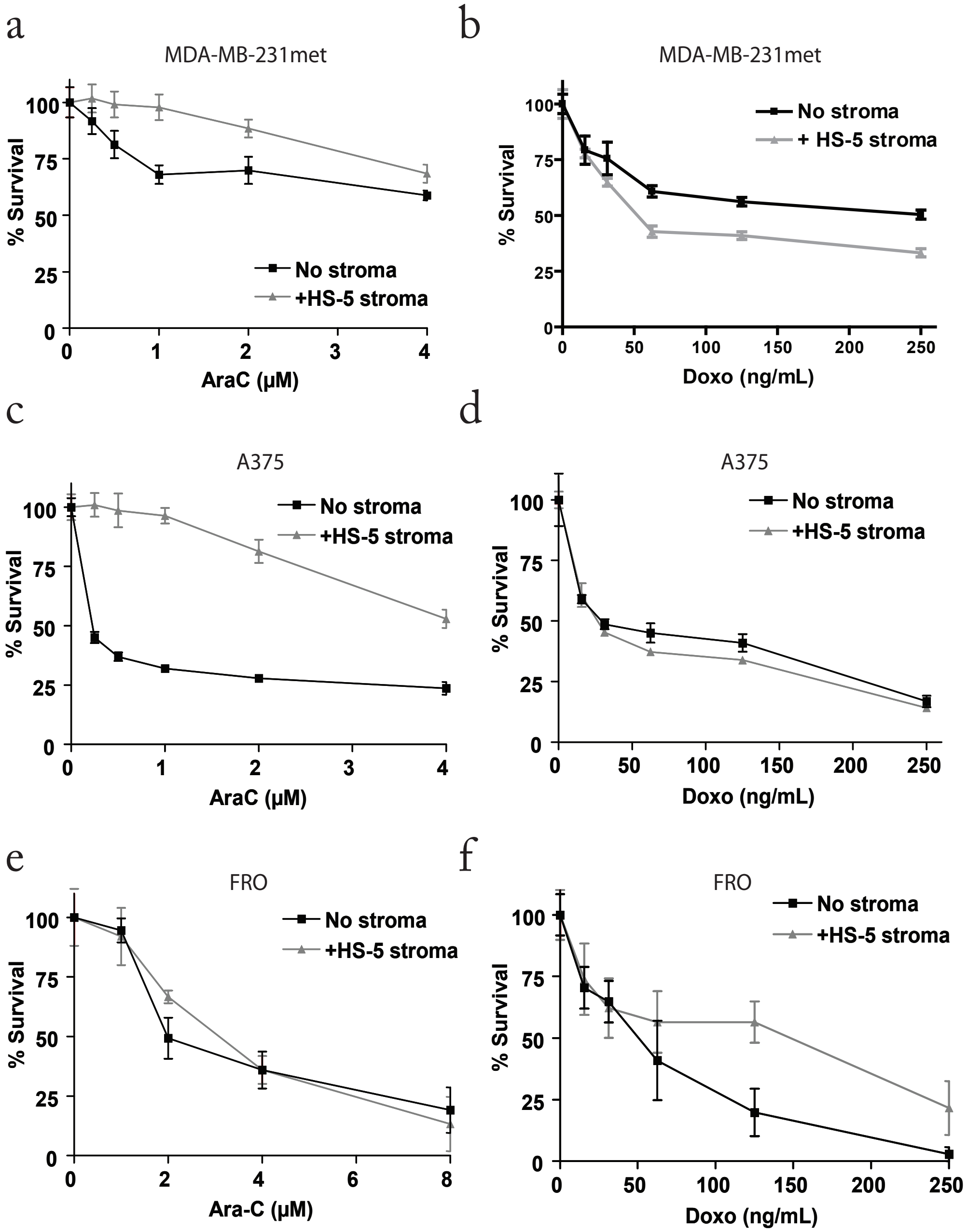
SUPPLEMENTAL FIGURE 1. Features of CS-BLI for the specific measurement of tumor viability in the presence or absence of accessory cells. (**a**) Luc+ MM.1S cells plated at increasing cell numbers had a linear correlation of viable MM cells both in the presence or absence of HS-5 stromal cells. (**b, c)** MTT viability assessment yielded results consistent in MM.1S parental cells and transduced cells expressing GFP/luc when treated with Doxo or PS-341 in the absence of stromal cells. (**d**) MM.1S-GFP/luc cells yielded consistent results when viability was measured by CellTiterGlo (CTG) or CS-BLI. Using flow cytometry, MM.1S-GFP/luc cells were exposed to Doxo in the presence and absence of GFP- stromal cells. (**e**) GFP$^+$ MM cells had fewer non-viable (Apo2.7$^+$) cells in the presence vs. absence of BMSCs.



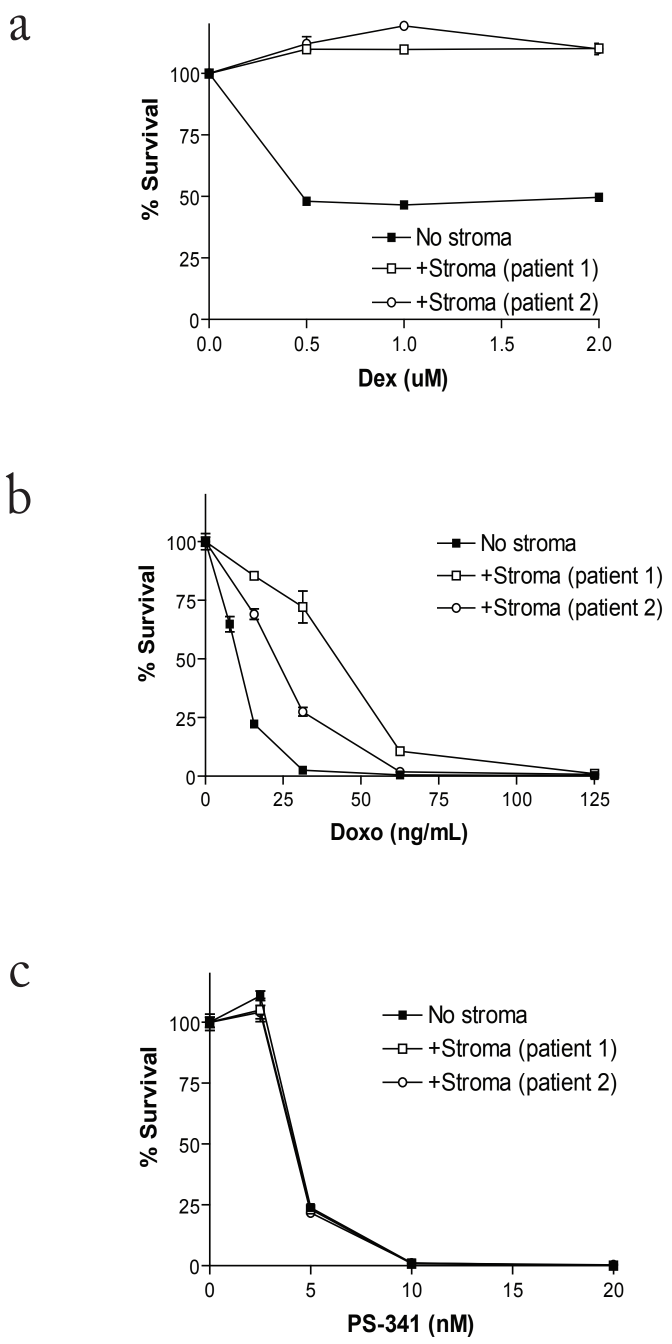
SUPPLEMENTAL FIGURE 2. CS-BLI confirms that co-culture with BMSCs confers protection against specific anti-tumor agents in MM cells. (**a, c, e**) MM.1S-GFP/luc and (**b, d, f**) MM.1R-GFP/luc cells were plated in the presence or absence of HS-5 BMSCs (10,000 cells per well) and treated with (**a, b**) Dex, (**c, d**) Doxo or (**e, f**) the proteasome inhibitor bortezomib (PS-341). BMSCs confer to MM.1S cells protection against Dex and Doxo, but not PS-341. BMSCs have little effect on the Dex-resistant cell line, MM.1R, in response to Dex treatment, but confer protection against Doxo. In addition, BMSCs confer no protection to treatment of MM.1R cells with PS-341.



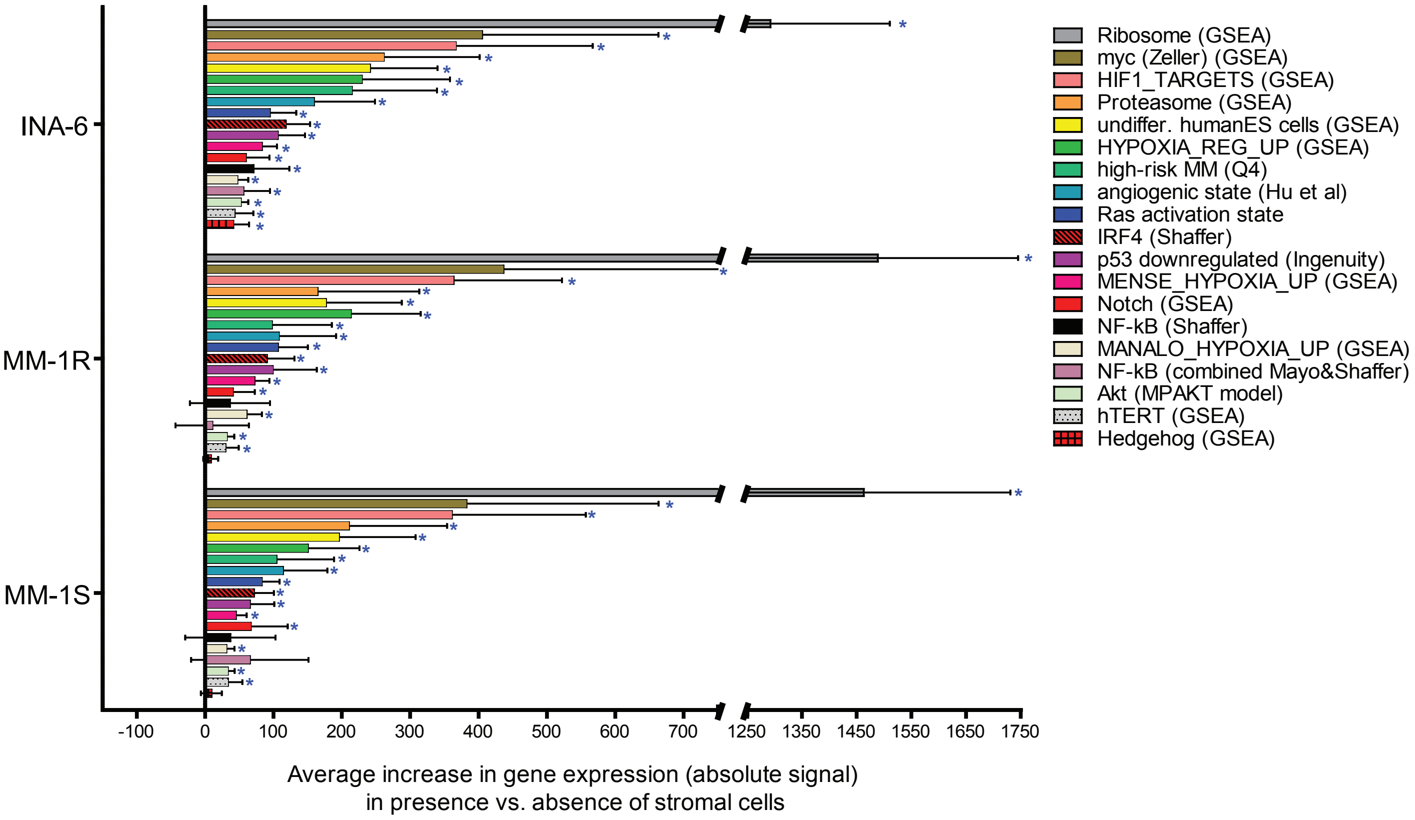
SUPPLEMENTAL FIGURE 3. BMSCs confer protection against various agents in leukemia cell lines. (**a, c, e, g**) Luc^{+} KU812F and (**b, d, f, h**) K562 leukemia cells were plated in the presence or absence of HS-5 BMSCs (10,000 per well) and treated with (**a, b**) Ara-C, (**c, d**) imatinib, (**e, f**) Doxo or (**g, h**) nilotinib. BMSCs confer protection against AraC, Imatinib and nilotinib, but not Doxo in KU812F cells. For K562 cells, BMSCs confer protection against Ara-C, but not imatinib, Doxo or nilotinib.



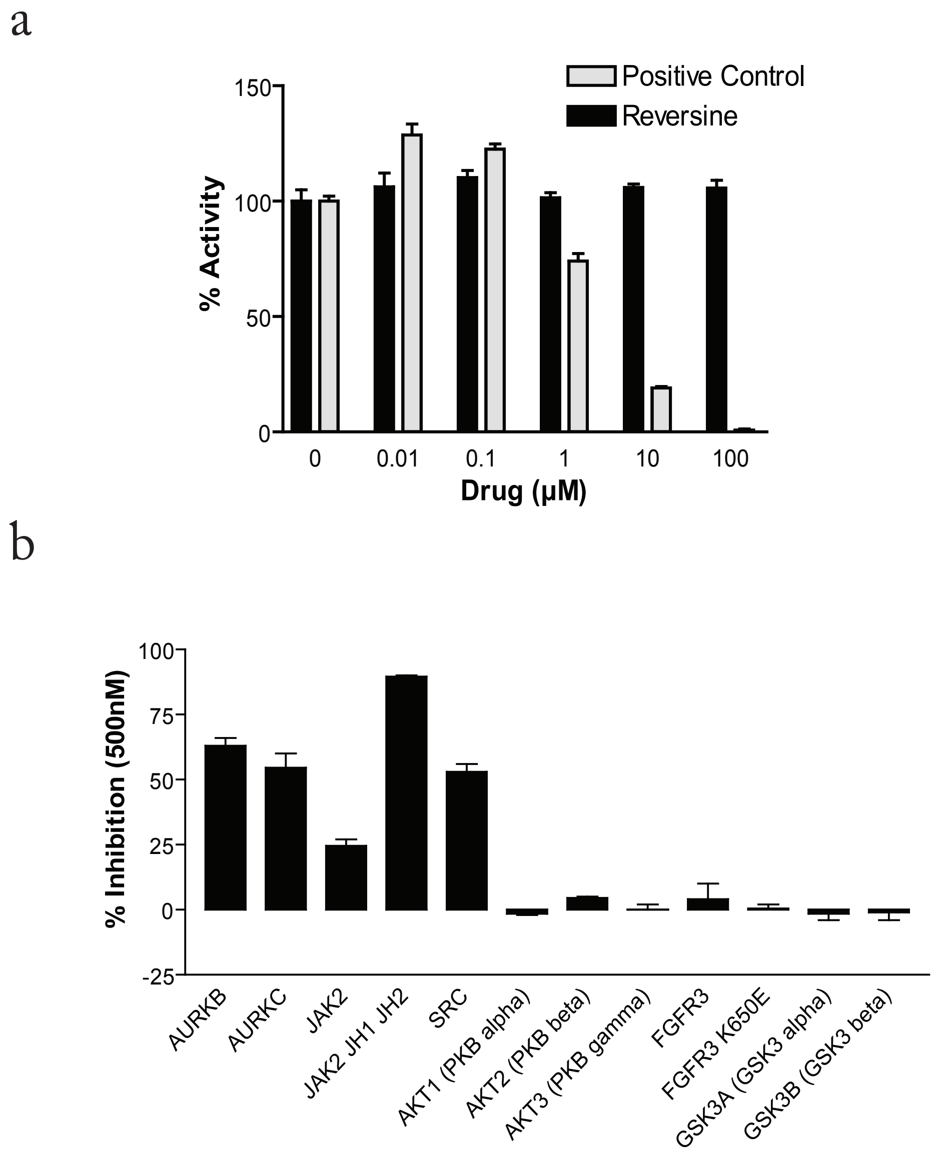
SUPPLEMENTAL FIGURE 4. Co-culture with BMSCs can protect solid tumor cell lines against anti-cancer agents. (**a**, **b**) Luc$^+$ MDA-MB-231met, (**c, d**) A375 and (**e**, **f**) FRO cells were plated with or without HS-5 BMSCs (10,000 cells per well), treated the following day, and incubated for an additional 48 h. BMSCs confer modest protection against both (**a**) AraC and (**b**) Doxo in MDA-MB-231-met cells. BMSCs provided a considerable level of protection to (**c**) AraC, but not against (**d**) Doxo in A375 cells. Lastly, BMSCs confer no protection against (**e**) AraC, but confer modest protection against (**f**) Doxo in FRO cells.



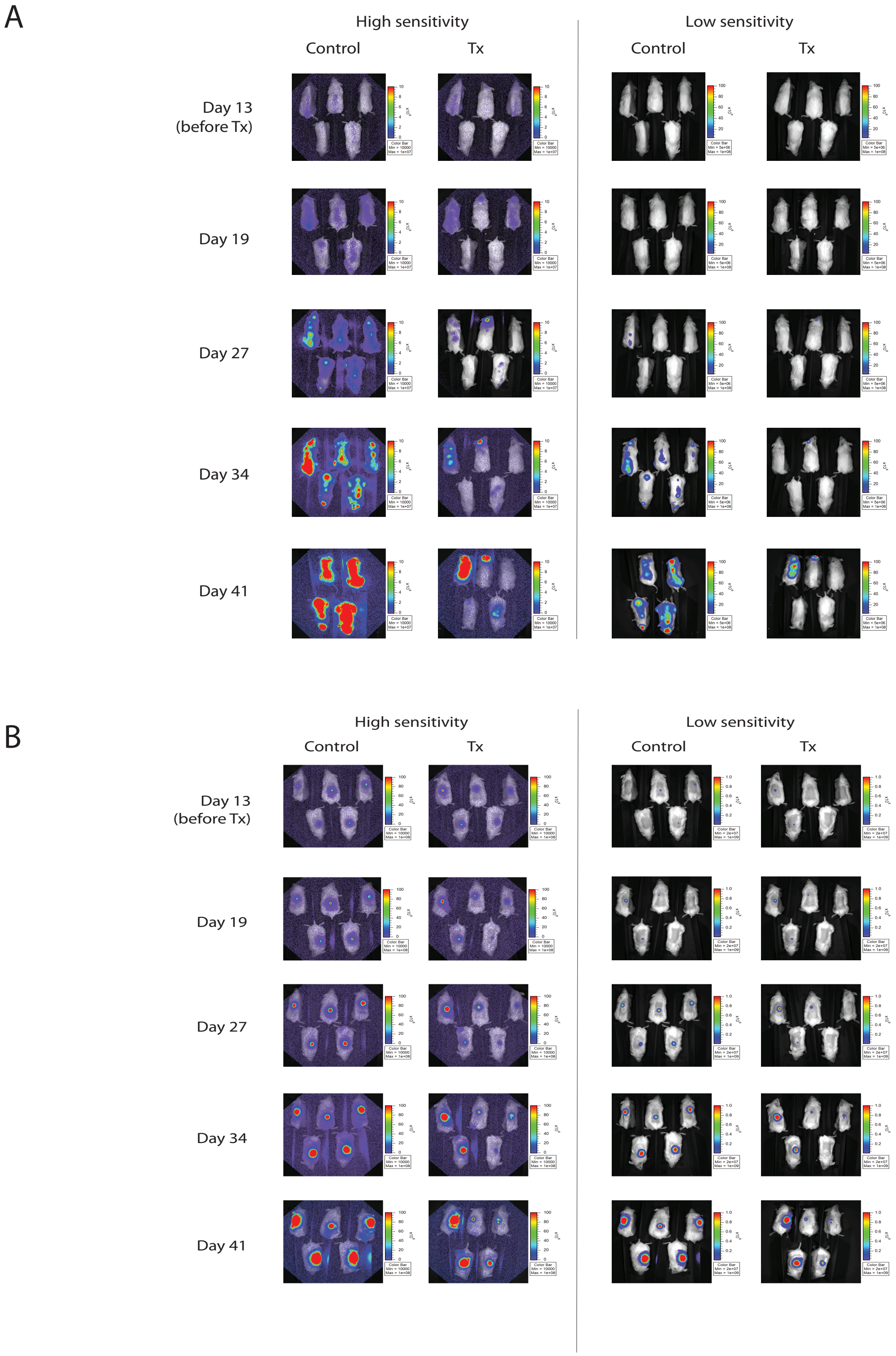
SUPPLEMENTAL FIGURE 5. Co-culture with primary BMSCs from MM patients provides tumor cell protection against specific anti-cancer agents. MM.1S-GFP/luc were plated in the presence or absence of BMSCs isolated from two different MM patients (10,000 per well) and treated with (**a**) Dex, (**b**) Doxo or (**c**) PS-341. Both patient BMSC samples confer protection against Dex and Doxo, but not PS-341 in MM cells.



SUPPLEMENTAL FIGURE 6. Interaction of MM cells with BMSCs leads to distinct changes in transcriptional signatures indicative of the activation of key molecular pathways in tumor cell pathophysiology. Transcripts previously shown to reflect the activation state of the indicated pathways were evaluated for differences in expression in each MM cell line, in the presence vs. absence of BMSCs *in vitro*. For each transcriptional signature, the average value (+/- 95% confidence limit) of absolute expression signal in MM cells for each cell line and each experimental condition (i.e. culture in the presence vs. absence of BMSCs) is shown.

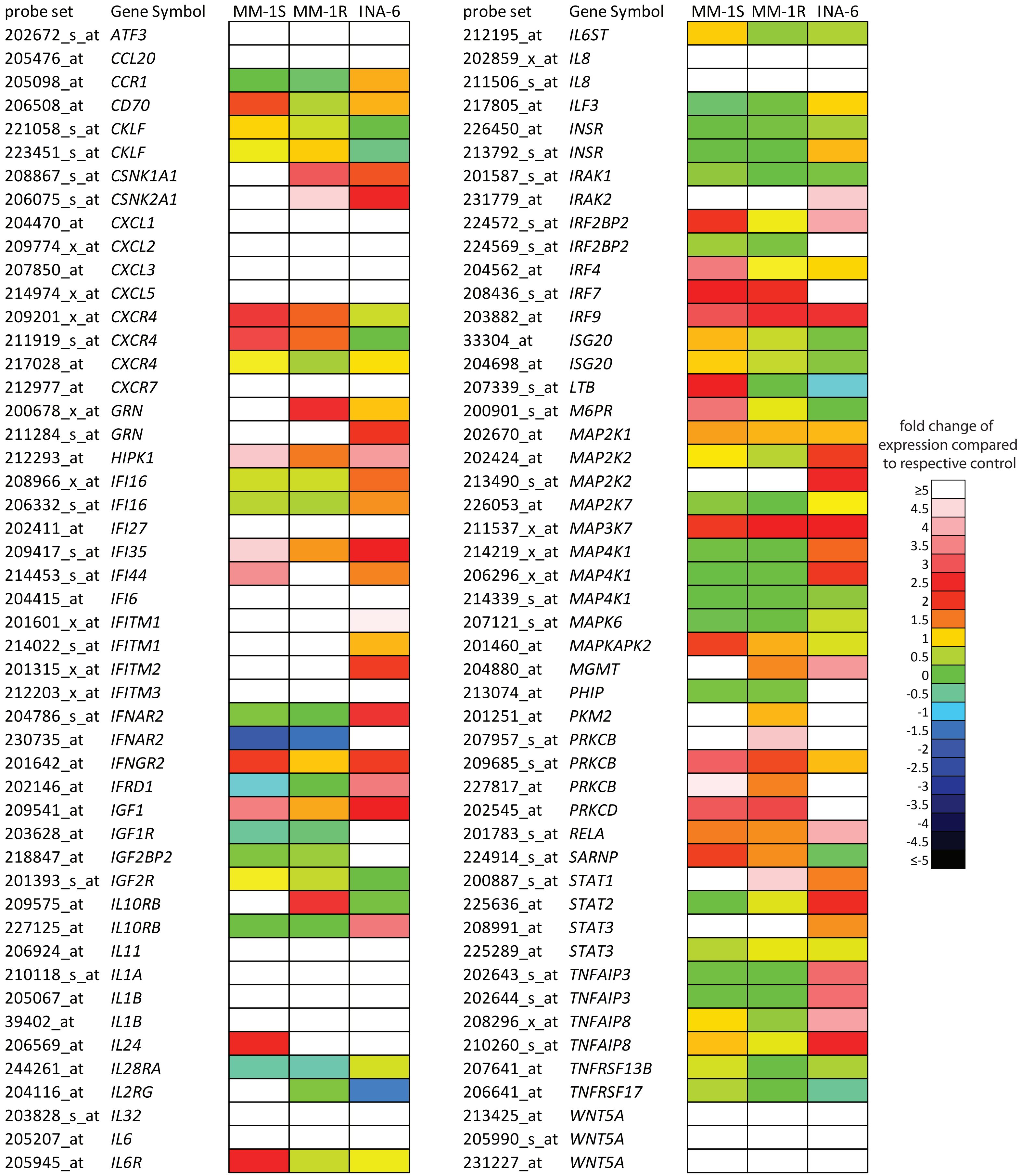


SUPPLEMENTAL FIGURE 7. In vitro luciferase and kinase activity assays of reversine. (**a**) *In vitro* luciferase activity was screened in the presence of reversine. Luciferase was reconstituted in Glycine-Tris buffer plus EDTA and MgSO4, with the addition of ATP and increasing concentrations of reversine or the positive control, resveratrol. Luminescence was detected immediately after the addition of the substrate (*n* = 4). Reversine (up to 100 µM) did not block luciferase activity. (**b**) Using the Z'-Lyte^{TM} kinase assay, select kinases were screened for activity in the presence of 500 nM reversine. Inhibition of activity was observed against a select subset of kinases, including Auroras, JAK2, and SRC, but not other kinases important for MM growth and survival, including AKT1, 2, 3, FGFR3, GSK3A or B.



SUPPLEMENTAL FIGURE 8. Imaging results over time for each reversine-treated and control mouse in the tumor experiment of MM.1S-GFP/luc cells injected i.v. vs s.c. (**a**) Imaging results are shown utilizing the IVIS Xenogen camera system following i.p. injection of luciferin substrate in *SCID-Beige* mice bearing diffuse lesion tumors. (**b**) Imaging results are shown utilizing the IVIS Xenogen camera system following i.p. injection of luciferin substrate in SCID-Beige mice bearing s.c. tumors. Graphical results for each model were analyzed using Living Image software and displayed utilizing both high sensitivity settings as well as lower sensitivity settings to display tumors.

Supplemental Table 1: Cell signaling transcripts

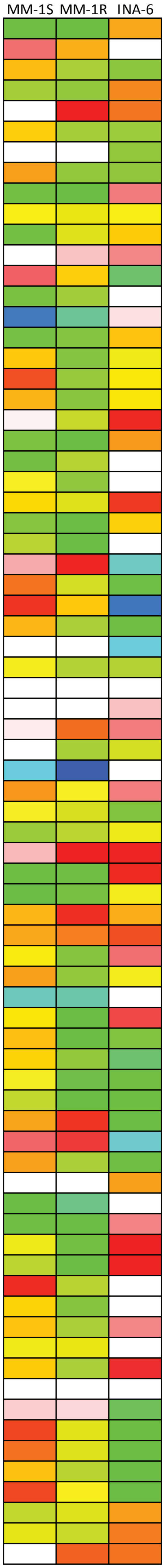


probe set	Gene Symbol	MM-1S	MM-1R	INA-6
202672_s_at	*ATF3*	⬜	⬜	⬜
205476_at	*CCL20*	⬜	⬜	⬜
205098_at	*CCR1*	🟩	🟩	🟧
206508_at	*CD70*	🟥	🟩	🟧
221058_s_at	*CKLF*	🟨	🟩	🟩
223451_s_at	*CKLF*	🟨	🟨	🟩
208867_s_at	*CSNK1A1*	⬜	🟥	🟥
206075_s_at	*CSNK2A1*	⬜	🟥	🟥
204470_at	*CXCL1*	⬜	⬜	⬜
209774_x_at	*CXCL2*	⬜	⬜	⬜
207850_at	*CXCL3*	⬜	⬜	⬜
214974_x_at	*CXCL5*	⬜	⬜	⬜
209201_x_at	*CXCR4*	🟥	🟧	🟩
211919_s_at	*CXCR4*	🟥	🟧	🟩
217028_at	*CXCR4*	🟨	🟩	🟨
212977_at	*CXCR7*	⬜	⬜	⬜
200678_x_at	*GRN*	⬜	🟥	🟨
211284_s_at	*GRN*	⬜	⬜	🟥
212293_at	*HIPK1*	🟥	🟧	🟥
208966_x_at	*IFI16*	🟩	🟩	🟧
206332_s_at	*IFI16*	🟩	🟩	🟧
202411_at	*IFI27*	⬜	⬜	⬜
209417_s_at	*IFI35*	🟥	🟧	🟥
214453_s_at	*IFI44*	🟥	⬜	🟧
204415_at	*IFI6*	⬜	⬜	⬜
201601_x_at	*IFITM1*	⬜	⬜	🟥
214022_s_at	*IFITM1*	⬜	⬜	🟧
201315_x_at	*IFITM2*	⬜	⬜	🟥
212203_x_at	*IFITM3*	⬜	⬜	⬜
204786_s_at	*IFNAR2*	🟩	🟩	🟥
230735_at	*IFNAR2*	🟦	🟦	⬜
201642_at	*IFNGR2*	🟥	🟨	🟥
202146_at	*IFRD1*	🟦	🟩	🟥
209541_at	*IGF1*	🟥	🟧	🟥
203628_at	*IGF1R*	🟩	🟩	⬜
218847_at	*IGF2BP2*	🟩	🟩	⬜
201393_s_at	*IGF2R*	🟨	🟩	🟩
209575_at	*IL10RB*	⬜	🟥	🟩
227125_at	*IL10RB*	🟩	🟩	🟥
206924_at	*IL11*	⬜	⬜	⬜
210118_s_at	*IL1A*	⬜	⬜	⬜
205067_at	*IL1B*	⬜	⬜	⬜
39402_at	*IL1B*	⬜	⬜	⬜
206569_at	*IL24*	🟥	⬜	⬜
244261_at	*IL28RA*	🟩	🟩	🟩
204116_at	*IL2RG*	⬜	🟩	🟦
203828_s_at	*IL32*	⬜	⬜	⬜
205207_at	*IL6*	⬜	⬜	⬜
205945_at	*IL6R*	🟥	🟩	🟨

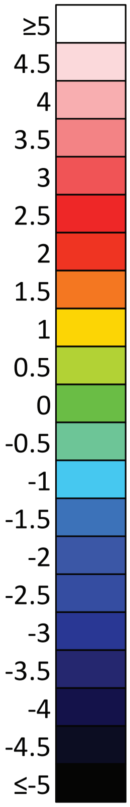
probe set	Gene Symbol	MM-1S	MM-1R	INA-6
212195_at	*IL6ST*	🟨	🟩	🟩
202859_x_at	*IL8*	⬜	⬜	⬜
211506_s_at	*IL8*	⬜	⬜	⬜
217805_at	*ILF3*	🟩	🟩	🟨
226450_at	*INSR*	🟩	🟩	🟩
213792_s_at	*INSR*	🟩	🟩	🟧
201587_s_at	*IRAK1*	🟩	🟩	🟩
231779_at	*IRAK2*	⬜	⬜	🟥
224572_s_at	*IRF2BP2*	🟥	🟨	🟥
224569_s_at	*IRF2BP2*	🟩	🟩	⬜
204562_at	*IRF4*	🟥	🟨	🟨
208436_s_at	*IRF7*	🟥	🟥	⬜
203882_at	*IRF9*	🟥	🟥	🟥
33304_at	*ISG20*	🟧	🟩	🟩
204698_at	*ISG20*	🟧	🟩	🟩
207339_s_at	*LTB*	🟥	🟩	🟦
200901_s_at	*M6PR*	🟥	🟨	🟩
202670_at	*MAP2K1*	🟧	🟧	🟧
202424_at	*MAP2K2*	🟨	🟩	🟥
213490_s_at	*MAP2K2*	⬜	⬜	🟥
226053_at	*MAP2K7*	🟩	🟩	🟨
211537_x_at	*MAP3K7*	🟥	🟥	🟥
214219_x_at	*MAP4K1*	🟩	🟩	🟧
206296_x_at	*MAP4K1*	🟩	🟩	🟥
214339_s_at	*MAP4K1*	🟩	🟩	🟩
207121_s_at	*MAPK6*	🟩	🟩	🟩
201460_at	*MAPKAPK2*	🟥	🟧	🟩
204880_at	*MGMT*	⬜	🟧	🟥
213074_at	*PHIP*	🟩	🟩	⬜
201251_at	*PKM2*	⬜	🟧	⬜
207957_s_at	*PRKCB*	⬜	🟥	⬜
209685_s_at	*PRKCB*	🟥	🟥	🟧
227817_at	*PRKCB*	🟥	🟧	⬜
202545_at	*PRKCD*	🟥	🟥	⬜
201783_s_at	*RELA*	🟧	🟧	🟥
224914_s_at	*SARNP*	🟥	🟧	🟩
200887_s_at	*STAT1*	⬜	🟥	🟧
225636_at	*STAT2*	🟩	🟨	🟥
208991_at	*STAT3*	⬜	⬜	🟧
225289_at	*STAT3*	🟩	🟨	🟨
202643_s_at	*TNFAIP3*	🟩	🟩	🟥
202644_s_at	*TNFAIP3*	🟩	🟩	🟥
208296_x_at	*TNFAIP8*	🟨	🟩	🟥
210260_s_at	*TNFAIP8*	🟧	🟨	🟥
207641_at	*TNFRSF13B*	🟩	🟩	🟩
206641_at	*TNFRSF17*	🟩	🟩	🟩
213425_at	*WNT5A*	⬜	⬜	⬜
205990_s_at	*WNT5A*	⬜	⬜	⬜
231227_at	*WNT5A*	⬜	⬜	⬜

Supplemental Table 1: Transcripts for putative oncoproteins

probe set	Gene Symbol
202123_s_at	*ABL1*
212607_at	*AKT3*
227546_x_at	*AURKAIP1*
218580_x_at	*AURKAIP1*
225552_x_at	*AURKAIP1*
209464_at	*AURKB*
206255_at	*BLK*
205504_at	*BTK*
227558_at	*CBX4*
212914_at	*CBX7*
202224_at	*CRK*
212180_at	*CRKL*
202329_at	*CSK*
208865_at	*CSNK1A1*
208774_at	*CSNK1D*
226858_at	*CSNK1E*
225756_at	*CSNK1E*
212072_s_at	*CSNK2A1*
201390_s_at	*CSNK2B*
200934_at	*DEK*
226281_at	*DNER*
218585_s_at	*DTL*
225415_at	*DTX3L*
201693_s_at	*EGR1*
227404_s_at	*EGR1*
224833_at	*ETS1*
210105_s_at	*FYN*
201514_s_at	*G3BP1*
208841_s_at	*G3BP2*
208840_s_at	*G3BP2*
217673_x_at	*GNAS*
214548_x_at	*GNAS*
211858_x_at	*GNAS*
200780_x_at	*GNAS*
212273_x_at	*GNAS*
200981_x_at	*GNAS*
211543_s_at	*GRK6*
222921_s_at	*HEY2*
225115_at	*HIPK2*
219028_at	*HIPK2*
225368_at	*HIPK2*
213763_at	*HIPK2*
205453_at	*HOXB2*
210045_at	*IDH2*
210046_s_at	*IDH2*
201234_at	*ILK*
201648_at	*JAK1*
227677_at	*JAK3*
201466_s_at	*JUN*
201464_x_at	*JUN*
201465_s_at	*JUN*
201473_at	*JUNB*
203752_s_at	*JUND*
204009_s_at	*KRAS*
214352_s_at	*KRAS*
209348_s_at	*MAF*
36711_at	*MAFF*
205193_at	*MAFF*
226206_at	*MAFK*
213189_at	*MINA*
213188_s_at	*MINA*
201710_at	*MYBL2*
202431_s_at	*MYC*
203360_s_at	*MYCBP*
200632_s_at	*NDRG1*
204641_at	*NEK2*
212530_at	*NEK7*
212377_s_at	*NOTCH2*
202443_x_at	*NOTCH2*
227067_x_at	*NOTCH2NL*
224985_at	*NRAS*
202647_s_at	*NRAS*
213070_at	*PIK3C2A*
203879_at	*PIK3CD*



probe set	Gene Symbol
1568629_s_at	*PIK3R2*
209193_at	*PIM1*
204269_at	*PIM2*
224739_at	*PIM3*
208640_at	*RAC1*
208641_s_at	*RAC1*
207419_s_at	*RAC2*
213603_s_at	*RAC2*
201244_s_at	*RAF1*
224880_at	*RALA*
214435_x_at	*RALA*
202100_at	*RALB*
200750_s_at	*RAN*
201713_s_at	*RANBP2*
213019_at	*RANBP6*
202582_s_at	*RANBP9*
218526_s_at	*RANGRF*
1555340_x_at	*RAP1A*
1555339_at	*RAP1A*
225585_at	*RAP2A*
213923_at	*RAP2B*
202677_at	*RASA1*
225562_at	*RASA3*
219752_at	*RASAL1*
223322_at	*RASSF5*
233463_at	*RASSF6*
1555780_a_a	*RHEB*
213404_s_at	*RHEB*
213409_s_at	*RHEB*
201453_x_at	*RHEB*
1555814_a_a	*RHOA*
200059_s_at	*RHOA*
212099_at	*RHOB*
200885_at	*RHOC*
219045_at	*RHOF*
203175_at	*RHOG*
236293_at	*RHOH*
212119_at	*RHOQ*
212117_at	*RHOQ*
212120_at	*RHOQ*
214449_s_at	*RHOQ*
218323_at	*RHOT1*
222148_s_at	*RHOT1*
210426_x_at	*RORA*
201628_s_at	*RRAGA*
221523_s_at	*RRAGD*
221524_s_at	*RRAGD*
213939_s_at	*RUFY3*
218737_at	*SBNO1*
210231_x_at	*SET*
213047_x_at	*SET*
200630_x_at	*SET*
40189_at	*SET*
201739_at	*SGK1*
207974_s_at	*SKP1*
200718_s_at	*SKP1*
215223_s_at	*SOD2*
210497_x_at	*SSX2*
216471_x_at	*SSX2*
210394_x_at	*SSX4 /// SSX4B*
211425_x_at	*SSX4 /// SSX4B*
212770_at	*TLE3*
228340_at	*TLE3*
212769_at	*TLE3*
204872_at	*TLE4*
212997_s_at	*TLK2*
213338_at	*TMEM158*
216520_s_at	*TPT1*
212869_x_at	*TPT1*
214327_x_at	*TPT1*
212284_x_at	*TPT1*
211943_x_at	*TPT1*
206219_s_at	*VAV1*
205126_at	*VRK2*
221998_s_at	*VRK3*



Supplemental Table 1: Transcripts for regulation of survival - apoptosis

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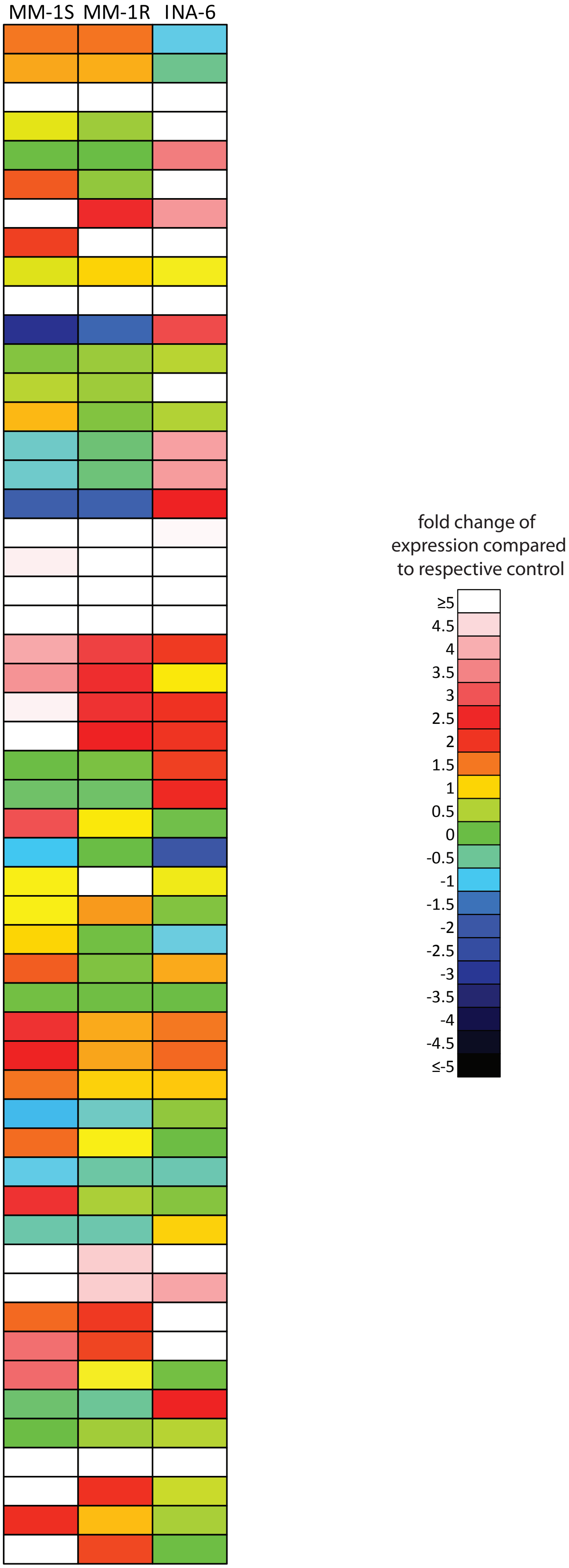
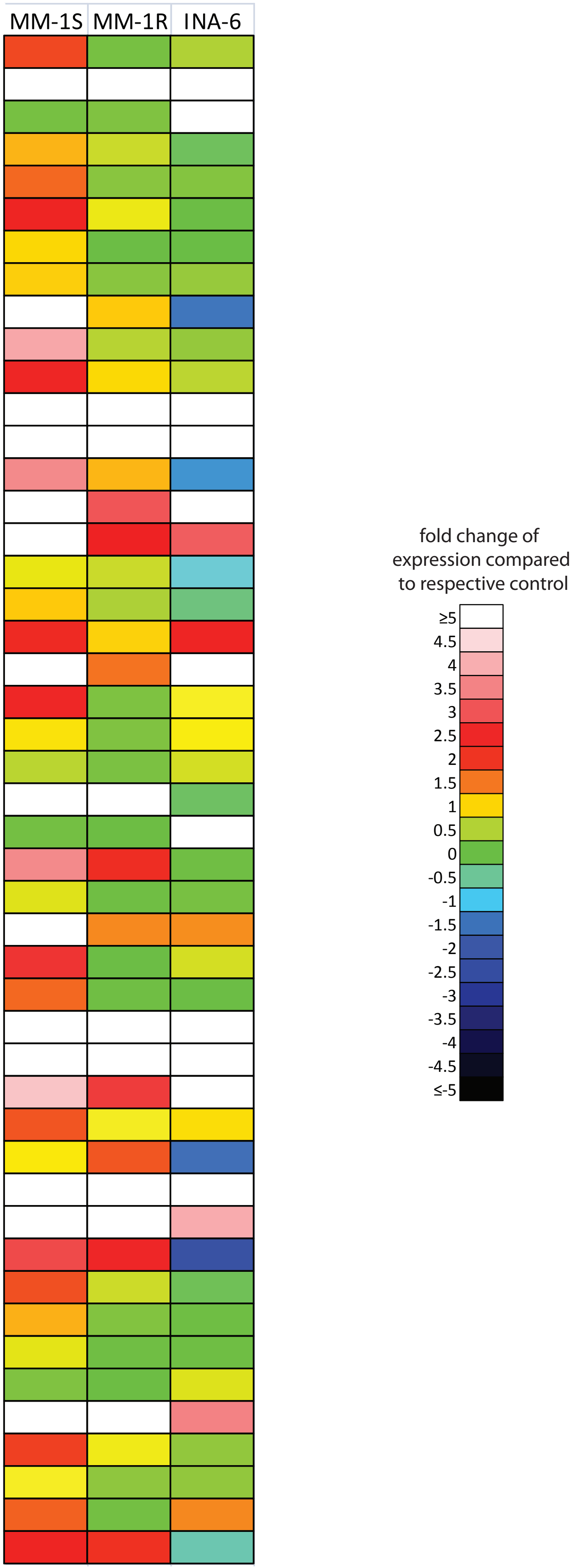
211475_s_at	*BAG1*
209406_at	*BAG2*
217911_s_at	*BAG3*
205263_at	*BCL10*
203685_at	*BCL2*
212312_at	*BCL2L1*
225606_at	*BCL2L11*
209311_at	*BCL2L2*
204908_s_at	*BCL3*
203140_at	*BCL6*
223915_at	*BCOR*
202076_at	*BIRC2*
210538_s_at	*BIRC3*
202095_s_at	*BIRC5*
224635_s_at	*BIRC6*
233093_s_at	*BIRC6*
242068_at	*BIRC6*
201848_s_at	*BNIP3*
201849_at	*BNIP3*
221478_at	*BNIP3L*
221479_s_at	*BNIP3L*
200921_s_at	*BTG1*
200920_s_at	*BTG1*
210563_x_at	*CFLAR*
210564_x_at	*CFLAR*
211316_x_at	*CFLAR*
221903_s_at	*CYLD*
200046_at	*DAD1*
205033_s_at	*DEFA1/DEFA1B/DEFA3*
224217_s_at	*FAF1*
218080_x_at	*FAF1*
220643_s_at	*FAIM*
221601_s_at	*FAIM3*
214114_x_at	*FASTK*
200797_s_at	*MCL1*
214057_at	*MCL1*
200798_x_at	*MCL1*
204861_s_at	*NAIP*
210907_s_at	*PDCD10*
212424_at	*PDCD11*
204025_s_at	*PDCD2*
213581_at	*PDCD2*
202731_at	*PDCD4*
202730_s_at	*PDCD4*
212593_s_at	*PDCD4*
212594_at	*PDCD4*
219275_at	*PDCD5*
1568763_s_at	*PDCD6*
217746_s_at	*PDCD6IP*
209339_at	*SIAH2*
212038_s_at	*VDAC1*
211662_s_at	*VDAC2*
208846_s_at	*VDAC3*

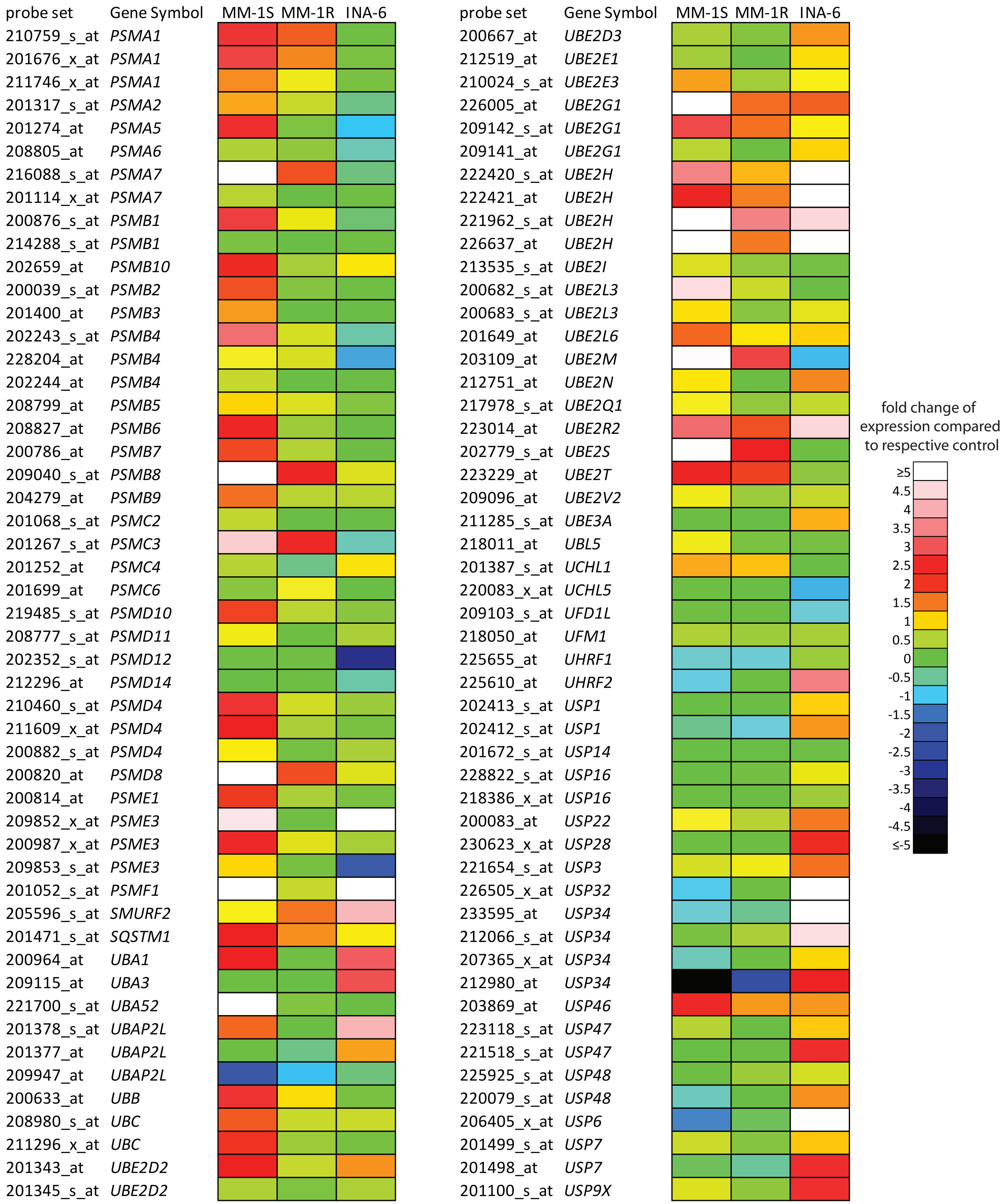


Supplemental Table 1: Transcripts for heat shock proteins - molecular chaperones

probe set	Gene Symbol
201491_at	*AHSA1*
226665_at	*AHSA2*
218168_s_at	*CABC1*
201947_s_at	*CCT2*
200910_at	*CCT3*
200877_at	*CCT4*
200812_at	*CCT7*
200873_s_at	*CCT8*
208791_at	*CLU*
208792_s_at	*CLU*
209157_at	*DNAJA2*
200664_s_at	*DNAJB1*
200666_s_at	*DNAJB1*
223054_at	*DNAJB11*
202500_at	*DNAJB2*
208810_at	*DNAJB6*
202842_s_at	*DNAJB9*
218409_s_at	*DNAJC1*
218976_at	*DNAJC12*
228622_s_at	*DNAJC4*
202416_at	*DNAJC7*
205545_x_at	*DNAJC8*
213088_s_at	*DNAJC9*
200942_s_at	*HSBP1*
209657_s_at	*HSF2*
210211_s_at	*HSP90AA1*
214328_s_at	*HSP90AA1*
214359_s_at	*HSP90AB1*
200064_at	*HSP90AB1*
1557910_at	*HSP90AB1*
200799_at	*HSPA1A*
200800_s_at	*HSPA1A/HSPA1B*
202581_at	*HSPA1A/HSPA1B*
211015_s_at	*HSPA4*
211936_at	*HSPA5*
213418_at	*HSPA6*
117_at	*HSPA6*
210338_s_at	*HSPA8*
208687_x_at	*HSPA8*
224187_x_at	*HSPA8*
221891_x_at	*HSPA8*
200691_s_at	*HSPA9*
201841_s_at	*HSPB1*
207132_x_at	*PFDN5*
210908_s_at	*PFDN5*
213330_s_at	*STIP1*
212009_s_at	*STIP1*



Supplemental Table 1: Transcripts for ubiquitin - proteasome pathway



probe set	Gene Symbol	MM-1S	MM-1R	INA-6
210759_s_at	*PSMA1*	🟥	🟧	🟩
201676_x_at	*PSMA1*	🟥	🟧	🟩
211746_x_at	*PSMA1*	🟧	🟨	🟩
201317_s_at	*PSMA2*	🟧	🟩	🟩
201274_at	*PSMA5*	🟥	🟩	🟦
208805_at	*PSMA6*	🟩	🟩	🟩
216088_s_at	*PSMA7*	⬜	🟥	🟩
201114_x_at	*PSMA7*	🟩	🟩	🟩
200876_s_at	*PSMB1*	🟥	🟨	🟩
214288_s_at	*PSMB1*	🟩	🟩	🟩
202659_at	*PSMB10*	🟥	🟩	🟨
200039_s_at	*PSMB2*	🟥	🟩	🟩
201400_at	*PSMB3*	🟧	🟩	🟩
202243_s_at	*PSMB4*	🟥	🟨	🟩
228204_at	*PSMB4*	🟨	🟨	🟦
202244_at	*PSMB4*	🟩	🟩	🟩
208799_at	*PSMB5*	🟨	🟨	🟩
208827_at	*PSMB6*	🟥	🟩	🟩
200786_at	*PSMB7*	🟥	🟩	🟩
209040_s_at	*PSMB8*	⬜	🟥	🟨
204279_at	*PSMB9*	🟧	🟩	🟩
201068_s_at	*PSMC2*	🟩	🟩	🟩
201267_s_at	*PSMC3*	🟥	🟥	🟩
201252_at	*PSMC4*	🟩	🟩	🟨
201699_at	*PSMC6*	🟩	🟨	🟩
219485_s_at	*PSMD10*	🟥	🟩	🟩
208777_s_at	*PSMD11*	🟨	🟩	🟩
202352_s_at	*PSMD12*	🟩	🟩	🟦
212296_at	*PSMD14*	🟩	🟩	🟩
210460_s_at	*PSMD4*	🟥	🟨	🟩
211609_x_at	*PSMD4*	🟥	🟩	🟩
200882_s_at	*PSMD4*	🟨	🟩	🟩
200820_at	*PSMD8*	⬜	🟥	🟨
200814_at	*PSME1*	🟥	🟩	🟩
209852_x_at	*PSME3*	🟥	🟩	⬜
200987_x_at	*PSME3*	🟥	🟨	🟩
209853_s_at	*PSME3*	🟨	🟩	🟦
201052_s_at	*PSMF1*	⬜	🟩	⬜
205596_s_at	*SMURF2*	🟨	🟧	🟥
201471_s_at	*SQSTM1*	🟥	🟧	🟨
200964_at	*UBA1*	🟥	🟩	🟥
209115_at	*UBA3*	🟩	🟩	🟥
221700_s_at	*UBA52*	⬜	🟩	🟩
201378_s_at	*UBAP2L*	🟧	🟩	🟥
201377_at	*UBAP2L*	🟩	🟩	🟧
209947_at	*UBAP2L*	🟦	🟦	🟩
200633_at	*UBB*	🟥	🟨	🟩
208980_s_at	*UBC*	🟥	🟩	🟩
211296_x_at	*UBC*	🟥	🟩	🟩
201343_at	*UBE2D2*	🟥	🟩	🟧
201345_s_at	*UBE2D2*	🟩	🟩	🟩

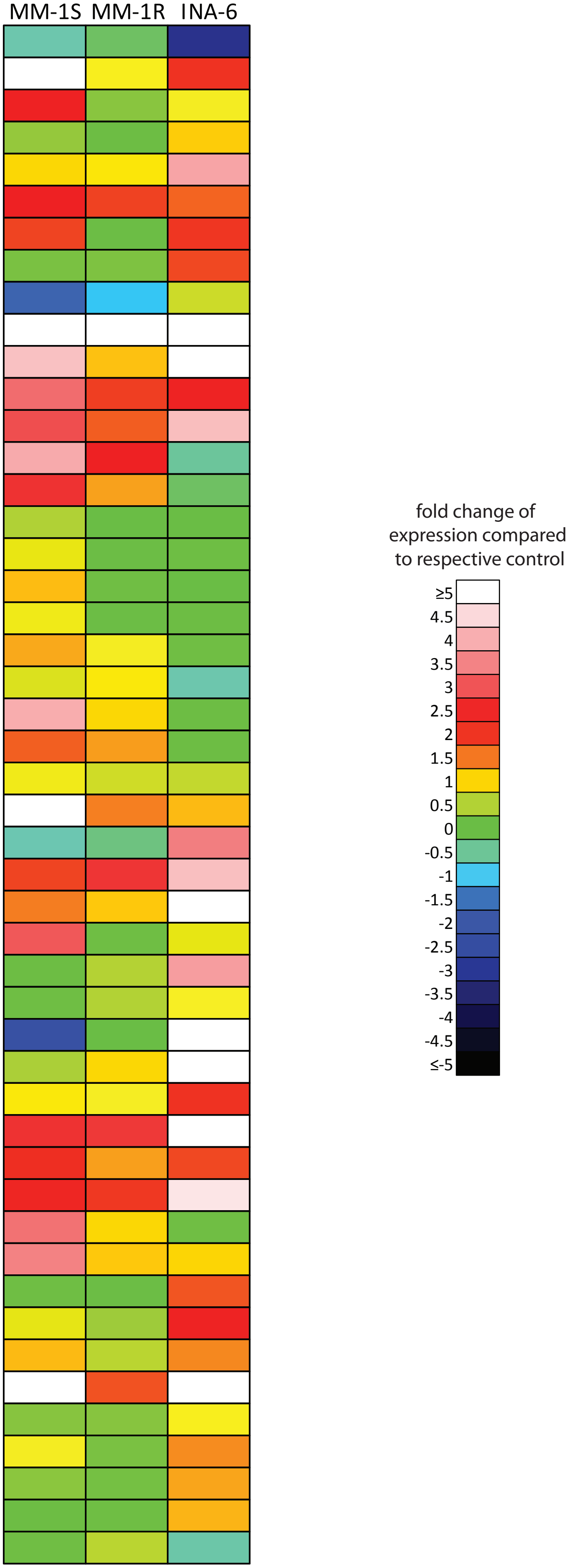
probe set	Gene Symbol	MM-1S	MM-1R	INA-6
200667_at	*UBE2D3*	🟩	🟩	🟧
212519_at	*UBE2E1*	🟩	🟩	🟨
210024_s_at	*UBE2E3*	🟧	🟩	🟨
226005_at	*UBE2G1*	⬜	🟧	🟧
209142_s_at	*UBE2G1*	🟥	🟧	🟨
209141_at	*UBE2G1*	🟩	🟩	🟨
222420_s_at	*UBE2H*	🟥	🟧	⬜
222421_at	*UBE2H*	🟥	🟧	⬜
221962_s_at	*UBE2H*	⬜	🟥	🟥
226637_at	*UBE2H*	⬜	🟧	⬜
213535_s_at	*UBE2I*	🟨	🟩	🟩
200682_s_at	*UBE2L3*	🟥	🟩	🟩
200683_s_at	*UBE2L3*	🟨	🟩	🟨
201649_at	*UBE2L6*	🟧	🟨	🟨
203109_at	*UBE2M*	⬜	🟥	🟦
212751_at	*UBE2N*	🟨	🟩	🟧
217978_s_at	*UBE2Q1*	🟨	🟩	🟩
223014_at	*UBE2R2*	🟥	🟥	🟥
202779_s_at	*UBE2S*	⬜	🟥	🟩
223229_at	*UBE2T*	🟥	🟥	🟩
209096_at	*UBE2V2*	🟨	🟩	🟩
211285_s_at	*UBE3A*	🟩	🟩	🟧
218011_at	*UBL5*	🟨	🟩	🟩
201387_s_at	*UCHL1*	🟧	🟧	🟩
220083_x_at	*UCHL5*	🟩	🟩	🟦
209103_s_at	*UFD1L*	🟩	🟩	🟦
218050_at	*UFM1*	🟩	🟩	🟩
225655_at	*UHRF1*	🟦	🟦	🟩
225610_at	*UHRF2*	🟦	🟩	🟥
202413_s_at	*USP1*	🟩	🟩	🟨
202412_s_at	*USP1*	🟩	🟦	🟧
201672_s_at	*USP14*	🟩	🟩	🟩
228822_s_at	*USP16*	🟩	🟩	🟨
218386_x_at	*USP16*	🟩	🟩	🟩
200083_at	*USP22*	🟨	🟩	🟧
230623_x_at	*USP28*	🟩	🟩	🟥
221654_s_at	*USP3*	🟨	🟨	🟧
226505_x_at	*USP32*	🟦	🟩	⬜
233595_at	*USP34*	🟦	🟩	⬜
212066_s_at	*USP34*	🟩	🟩	🟥
207365_x_at	*USP34*	🟦	🟩	🟨
212980_at	*USP34*	⬛	🟦	🟥
203869_at	*USP46*	🟥	🟧	🟧
223118_s_at	*USP47*	🟩	🟩	🟨
221518_s_at	*USP47*	🟩	🟩	🟥
225925_s_at	*USP48*	🟩	🟩	🟨
220079_s_at	*USP48*	🟦	🟩	🟧
206405_x_at	*USP6*	🟦	🟩	⬜
201499_s_at	*USP7*	🟨	🟩	🟨
201498_at	*USP7*	🟩	🟩	🟥
201100_s_at	*USP9X*	🟨	🟩	🟥

fold change of expression compared to respective control

≥5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
-2.5
-3
-3.5
-4
-4.5
≤-5

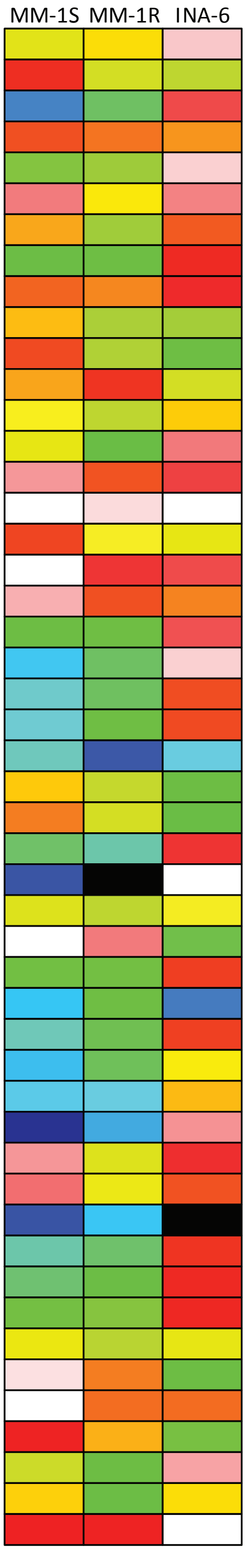
Supplemental Table 1: Transcripts for chromatin remodeling - histones

probe set	Gene Symbol
203975_s_at	*CHAF1A*
202121_s_at	*CHMP2A*
225119_at	*CHMP4B*
225498_at	*CHMP4B*
218085_at	*CHMP5*
219356_s_at	*CHMP5*
231764_at	*CHRAC1*
201697_s_at	*DNMT1*
220668_s_at	*DNMT3B*
208886_at	*H1F0*
204805_s_at	*H1FX*
224301_x_at	*H2AFJ*
225245_x_at	*H2AFJ*
200853_at	*H2AFZ*
213911_s_at	*H2AFZ*
200080_s_at	*H3F3A/H3F3B/LOC440926*
208755_x_at	*H3F3A/H3F3B/LOC440926*
211940_x_at	*H3F3A/H3F3B/LOC440926*
213828_x_at	*H3F3A/H3F3B/LOC440926*
209069_s_at	*H3F3B*
211997_x_at	*H3F3B*
211999_at	*H3F3B*
203138_at	*HAT1*
201209_at	*HDAC1*
223345_at	*HDAC8*
205659_at	*HDAC9*
202814_s_at	*HEXIM1*
238547_at	*HEXIM2*
209398_at	*HIST1H1C*
215071_s_at	*HIST1H2AC*
209806_at	*HIST1H2BK*
202708_s_at	*HIST2H2BE*
221582_at	*HIST3H2A*
202983_at	*HLTF*
212689_s_at	*KDM3A*
212495_at	*KDM4B*
209984_at	*KDM4C*
208742_s_at	*SAP18*
204900_x_at	*SAP30*
217707_x_at	*SMARCA2*
208794_s_at	*SMARCA4*
214728_x_at	*SMARCA4*
215714_s_at	*SMARCA4*
202303_x_at	*SMARCA5*
213859_x_at	*SMARCA5*
201074_at	*SMARCC1*
211988_at	*SMARCE1*
211989_at	*SMARCE1*

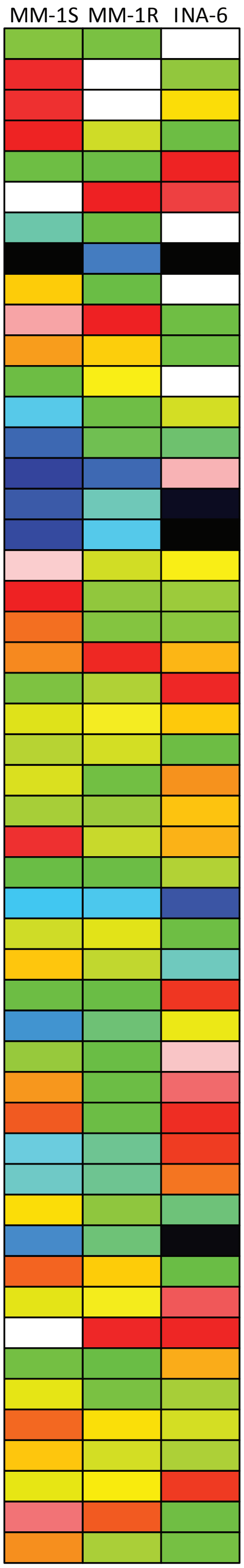


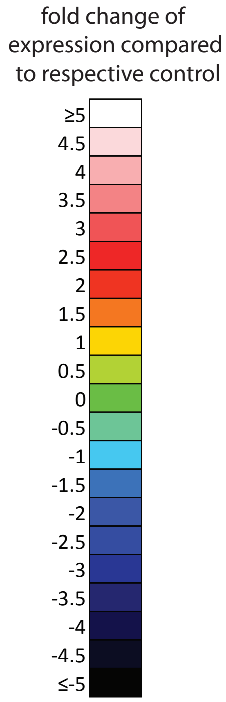
Supplemental Table 1: Transcripts for cell cycle regulation

probe set	Gene Symbol
231973_s_at	*ANAPC1*
226414_s_at	*ANAPC11*
226917_s_at	*ANAPC4*
201236_s_at	*BTG2*
209642_at	*BUB1*
201458_s_at	*BUB3*
209974_s_at	*BUB3*
214710_s_at	*CCNB1*
217988_at	*CCNB1IP1*
202705_at	*CCNB2*
201955_at	*CCNC*
208712_at	*CCND1*
201700_at	*CCND3*
204826_at	*CCNF*
208796_s_at	*CCNG1*
202769_at	*CCNG2*
204093_at	*CCNH*
208655_at	*CCNI*
208656_s_at	*CCNI*
225824_at	*CCNK*
220046_s_at	*CCNL1*
1555411_a_at	*CCNL1*
222999_s_at	*CCNL2*
206967_at	*CCNT1*
210559_s_at	*CDC2*
203214_x_at	*CDC2*
204695_at	*CDC25A*
1555772_a_at	*CDC25A*
201853_s_at	*CDC25B*
225422_at	*CDC26*
217880_at	*CDC27*
211289_x_at	*CDC2L1 /// CDC2L2*
212401_s_at	*CDC2L2*
232266_x_at	*CDC2L5*
207318_s_at	*CDC2L5*
214464_at	*CDC42BPA*
218157_x_at	*CDC42SE1*
229120_s_at	*CDC42SE1*
203968_s_at	*CDC6*
204510_at	*CDC7*
224428_s_at	*CDCA7*
204252_at	*CDK2*
201938_at	*CDK2AP1*
202246_s_at	*CDK4*
204247_s_at	*CDK5*
224847_at	*CDK6*
224851_at	*CDK6*
224848_at	*CDK6*
202284_s_at	*CDKN1A*



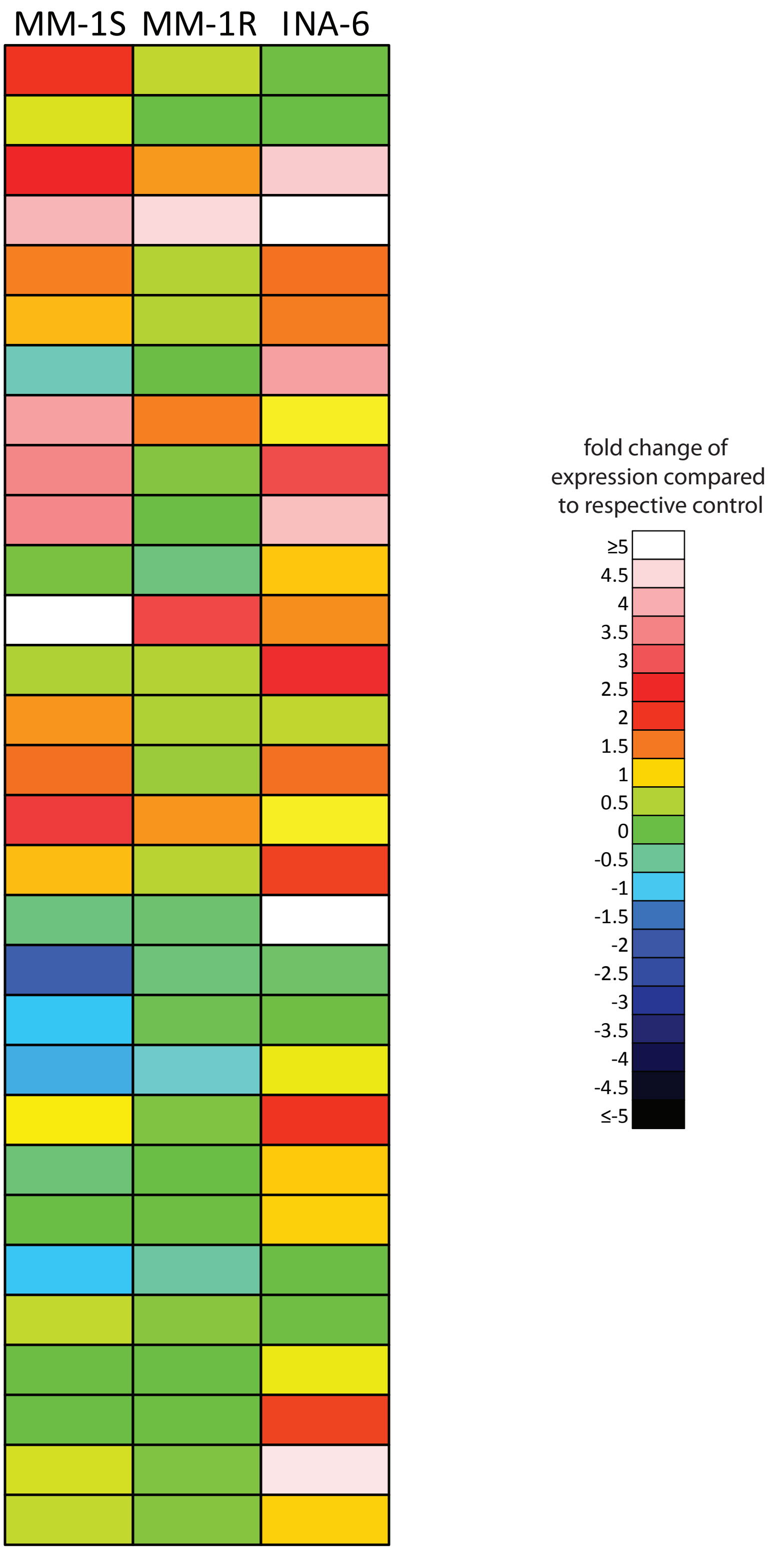
probe set	Gene Symbol
209112_at	*CDKN1B*
209644_x_at	*CDKN2A*
204159_at	*CDKN2C*
204962_s_at	*CENPA*
207828_s_at	*CENPF*
231772_x_at	*CENPH*
223513_at	*CENPJ*
242916_at	*CEP110*
204373_s_at	*CEP350*
201897_s_at	*CKS1B*
204170_s_at	*CKS2*
214683_s_at	*CLK1 /// PPIL3*
203229_s_at	*CLK2*
210346_s_at	*CLK4*
225697_at	*CRKRS*
220072_at	*CSPP1*
1554873_at	*CSPP1*
202533_s_at	*DHFR*
48808_at	*DHFR*
202532_s_at	*DHFR*
203725_at	*GADD45A*
207574_s_at	*GADD45B*
202177_at	*GAS6*
1598_g_at	*GAS6*
215075_s_at	*GRB2*
223049_at	*GRB2*
201912_s_at	*GSPT1*
215438_x_at	*GSPT1*
205070_at	*ING3*
201695_s_at	*NP*
221691_x_at	*NPM1*
223381_at	*NUF2*
218014_at	*NUP85*
226507_at	*PAK1*
208875_s_at	*PAK2*
208877_at	*PAK2*
214118_x_at	*PCM1*
214937_x_at	*PCM1*
201202_at	*PCNA*
203660_s_at	*PCNT*
217786_at	*PRMT5*
208021_s_at	*RFC1*
1053_at	*RFC2*
204127_at	*RFC3*
222154_s_at	*SPATS2L*
1554408_a_at	*TK1*
202338_at	*TK1*
202704_at	*TOB1*
1554696_s_at	*TYMS*
202589_at	*TYMS*



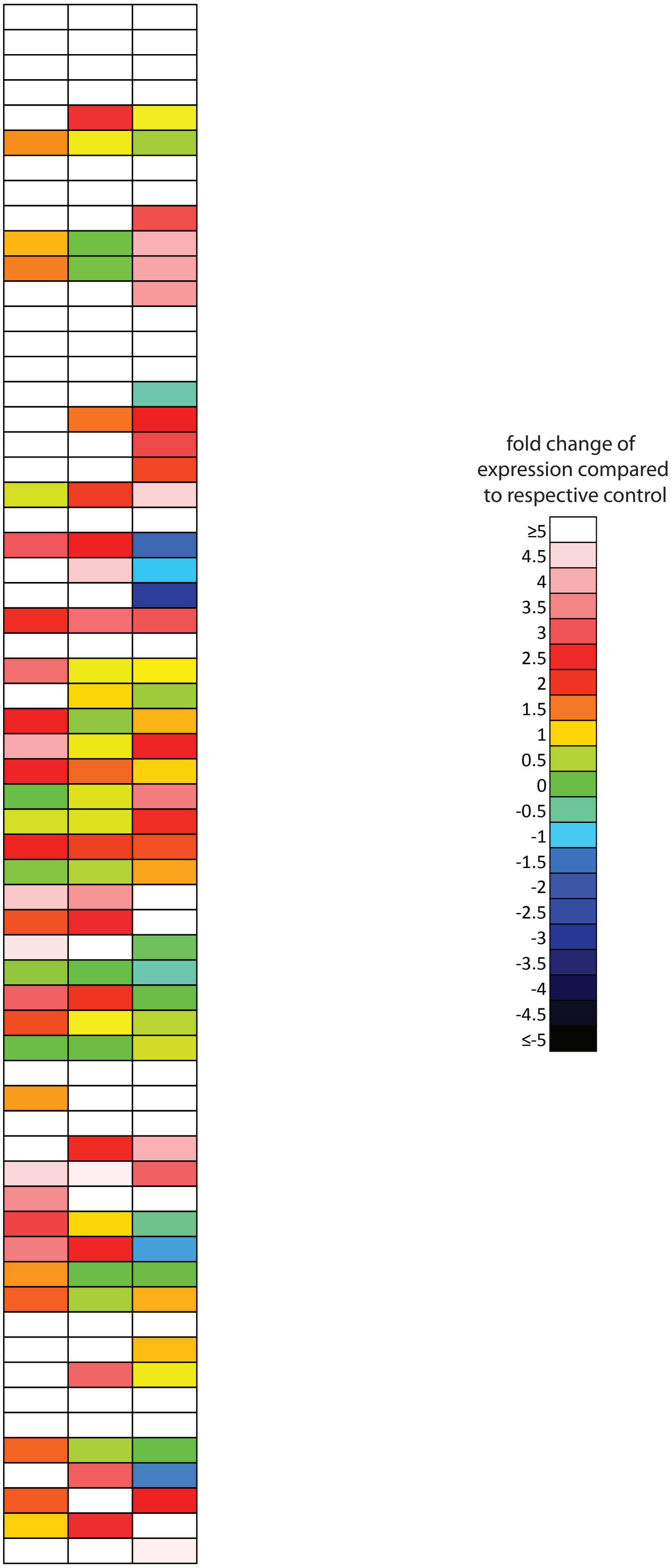

fold change of expression compared to respective control

Supplemental Table 1: Transcripts for DNA repair - drug resistance

probe set	Gene Symbol
223020_at	*CLPTM1L*
226935_s_at	*CLPTM1L*
203719_at	*ERCC1*
203720_s_at	*ERCC1*
202107_s_at	*MCM2*
201555_at	*MCM3*
212269_s_at	*MCM3AP*
212141_at	*MCM4*
222037_at	*MCM4*
201755_at	*MCM5*
216237_s_at	*MCM5*
210543_s_at	*PRKDC*
207405_s_at	*RAD17*
201039_s_at	*RAD23A*
201046_s_at	*RAD23A*
201222_s_at	*RAD23B*
201223_s_at	*RAD23B*
37793_r_at	*RAD51L3*
204558_at	*RAD54L*
204828_at	*RAD9A*
218598_at	*RINT1*
201589_at	*SMC1A*
201663_s_at	*SMC4*
201664_at	*SMC4*
212927_at	*SMC5*
202307_s_at	*TAP1*
225973_at	*TAP2*
225802_at	*TOP1MT*
201292_at	*TOP2A*
211987_at	*TOP2B*



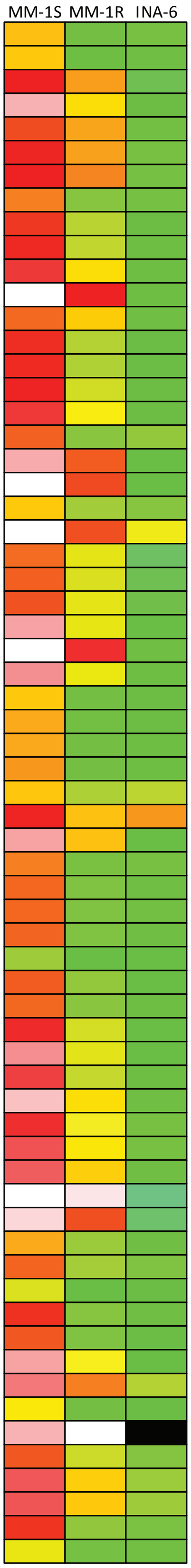
Supplemental Table 1: Transcripts related to microenvironmental interactions - hypoxia



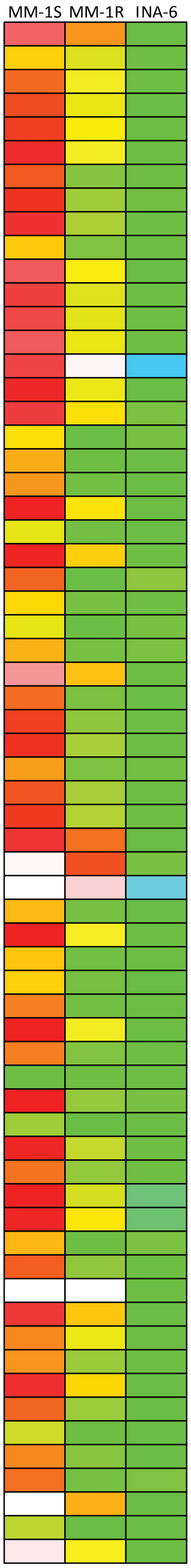
probe set	Gene Symbol	MM-1S	MM-1R	INA-6
221009_s_at	*ANGPTL4*	⬜	⬜	⬜
203963_at	*CA12*	⬜	⬜	⬜
214164_x_at	*CA12*	⬜	⬜	⬜
215867_x_at	*CA12*	⬜	⬜	⬜
203065_s_at	*CAV1*	⬜	🟥	🟨
212097_at	*CAV1*	🟧	🟨	🟩
202310_s_at	*COL1A1*	⬜	⬜	⬜
202403_s_at	*COL1A2*	⬜	⬜	⬜
202404_s_at	*COL1A2*	⬜	⬜	🟥
219625_s_at	*COL4A3BP*	🟧	🟩	🟥
223466_x_at	*COL4A3BP*	🟧	🟩	🟥
203325_s_at	*COL5A1*	⬜	⬜	🟥
213428_s_at	*COL6A1*	⬜	⬜	⬜
209156_s_at	*COL6A2*	⬜	⬜	⬜
201438_at	*COL6A3*	⬜	⬜	⬜
204136_at	*COL7A1*	⬜	⬜	🟦
201360_at	*CST3*	⬜	🟧	🟥
200838_at	*CTSB*	⬜	⬜	🟥
200839_s_at	*CTSB*	⬜	⬜	🟥
213275_x_at	*CTSB*	🟨	🟥	🟥
227961_at	*CTSB*	⬜	⬜	⬜
201487_at	*CTSC*	🟥	🟥	🟦
225646_at	*CTSC*	⬜	🟥	🟦
225647_s_at	*CTSC*	⬜	⬜	🟦
203657_s_at	*CTSF*	🟥	🟥	🟥
202087_s_at	*CTSL1*	⬜	⬜	⬜
209058_at	*EDF1*	🟥	🟨	🟨
209059_s_at	*EDF1*	⬜	🟨	🟩
210213_s_at	*EIF6*	🟥	🟩	🟧
202041_s_at	*FIBP*	🟥	🟨	🟥
210142_x_at	*FLOT1*	🟥	🟧	🟨
202304_at	*FNDC3A*	🟩	🟨	🟥
218618_s_at	*FNDC3B*	🟨	🟨	🟥
225032_at	*FNDC3B*	🟥	🟥	🟥
200989_at	*HIF1A*	🟩	🟩	🟧
1554452_a_at	*HIG2*	🟥	🟥	⬜
218507_at	*HIG2*	🟥	🟥	⬜
202637_s_at	*ICAM1*	🟥	⬜	🟩
213620_s_at	*ICAM2*	🟩	🟩	🟦
211945_s_at	*ITGB1*	🟥	🟥	🟩
203336_s_at	*ITGB1BP1*	🟥	🟨	🟩
205176_s_at	*ITGB3BP*	🟩	🟩	🟨
204475_at	*MMP1*	⬜	⬜	⬜
201069_at	*MMP2*	🟧	⬜	⬜
205828_at	*MMP3*	⬜	⬜	⬜
204479_at	*OSTF1*	⬜	🟥	🟥
207543_s_at	*P4HA1*	🟥	🟥	🟥
202733_at	*P4HA2*	🟥	⬜	⬜
200654_at	*P4HB*	🟥	🟨	🟦
200656_s_at	*P4HB*	🟥	🟥	🟦
200658_s_at	*PHB*	🟧	🟩	🟩
201600_at	*PHB2*	🟥	🟩	🟧
201860_s_at	*PLAT*	⬜	⬜	⬜
210845_s_at	*PLAUR*	⬜	⬜	🟧
200827_at	*PLOD1*	⬜	🟥	🟨
202619_s_at	*PLOD2*	⬜	⬜	⬜
202620_s_at	*PLOD2*	⬜	⬜	⬜
209879_at	*SELPLG*	🟥	🟩	🟩
209880_s_at	*SELPLG*	⬜	🟥	🟦
200931_s_at	*VCL*	🟥	⬜	🟥
210512_s_at	*VEGFA*	🟨	🟥	⬜
209946_at	*VEGFC*	⬜	⬜	🟥

Supplemental Table 1: Transcripts for ribosomal proteins

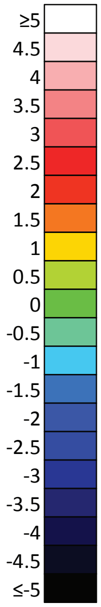
probe set	Gene Symbol
200725_x_at	*RPL10*
229563_s_at	*RPL10A*
200036_s_at	*RPL10A*
200010_at	*RPL11*
214271_x_at	*RPL12*
200088_x_at	*RPL12*
200809_x_at	*RPL12*
212933_x_at	*RPL13*
208929_x_at	*RPL13*
212734_x_at	*RPL13*
214351_x_at	*RPL13*
212191_x_at	*RPL13*
200715_x_at	*RPL13A*
212790_x_at	*RPL13A*
210646_x_at	*RPL13A*
200716_x_at	*RPL13A*
211942_x_at	*RPL13A /// RPL13AP5 /// RPL13AP6*
213588_x_at	*RPL14*
200074_s_at	*RPL14*
219138_at	*RPL14*
221475_s_at	*RPL15*
221476_s_at	*RPL15*
200038_s_at	*RPL17*
212537_x_at	*RPL17*
212270_x_at	*RPL17*
200022_at	*RPL18*
200869_at	*RPL18A /// RPL18AP3*
200029_at	*RPL19*
200012_x_at	*RPL21*
221775_x_at	*RPL22*
220960_x_at	*RPL22*
208768_x_at	*RPL22*
214042_s_at	*RPL22*
221726_at	*RPL22*
200888_s_at	*RPL23*
203012_x_at	*RPL23A*
208825_x_at	*RPL23A*
208834_x_at	*RPL23A*
213084_x_at	*RPL23A*
214143_x_at	*RPL24*
200013_at	*RPL24*
222229_x_at	*RPL26*
203034_s_at	*RPL27A*
200003_s_at	*RPL28*
213969_x_at	*RPL29*
200823_x_at	*RPL29*
212039_x_at	*RPL3*
211073_x_at	*RPL3*
201217_x_at	*RPL3*
211666_x_at	*RPL3*
200062_s_at	*RPL30*
200963_x_at	*RPL31*
200674_s_at	*RPL32*
200026_at	*RPL34*
200002_at	*RPL35*
219762_s_at	*RPL36*
201406_at	*RPL36A*
207585_s_at	*RPL36AL*
200092_s_at	*RPL37*
210115_at	*RPL39L*
200089_s_at	*RPL4*
201154_x_at	*RPL4*
211710_x_at	*RPL4*
201492_s_at	*RPL41*
213080_x_at	*RPL5*



probe set	Gene Symbol
200937_s_at	*RPL5*
200034_s_at	*RPL6*
212042_x_at	*RPL7*
200717_x_at	*RPL7*
217092_x_at	*RPL7*
234873_x_at	*RPL7A*
217740_x_at	*RPL7A*
224930_x_at	*RPL7A*
200936_at	*RPL8*
200032_s_at	*RPL9*
211972_x_at	*RPLP0*
208856_x_at	*RPLP0*
201033_x_at	*RPLP0*
211720_x_at	*RPLP0*
214167_s_at	*RPLP0 /// RPLP0P6*
200763_s_at	*RPLP1*
200909_s_at	*RPLP2*
200095_x_at	*RPS10*
200817_x_at	*RPS10*
211542_x_at	*RPS10*
213377_x_at	*RPS12*
200018_at	*RPS13*
208645_s_at	*RPS14*
200819_s_at	*RPS15*
200781_s_at	*RPS15A*
226131_s_at	*RPS16*
213890_x_at	*RPS16*
201258_at	*RPS16*
212578_x_at	*RPS17*
211487_x_at	*RPS17*
201665_x_at	*RPS17*
201049_s_at	*RPS18*
202649_x_at	*RPS19*
213414_s_at	*RPS19*
212433_x_at	*RPS2*
203107_x_at	*RPS2*
217466_x_at	*RPS2*
214003_x_at	*RPS20*
200949_x_at	*RPS20*
200926_at	*RPS23*
200091_s_at	*RPS25*
217753_s_at	*RPS26*
200741_s_at	*RPS27*
200017_at	*RPS27A*
222487_s_at	*RPS27L*
208904_s_at	*RPS28*
201094_at	*RPS29*
208692_at	*RPS3*
201257_x_at	*RPS3A*
212391_x_at	*RPS3A*
200099_s_at	*RPS3A*
213347_x_at	*RPS4X*
200933_x_at	*RPS4X*
201909_at	*RPS4Y1*
200024_at	*RPS5*
209134_s_at	*RPS6*
201254_x_at	*RPS6*
200081_s_at	*RPS6*
200082_s_at	*RPS7*
213941_x_at	*RPS7*
200858_s_at	*RPS8*
214317_x_at	*RPS9*
217747_s_at	*RPS9*
213801_x_at	*RPSA*
212018_s_at	*RSL1D1*



fold change of expression compared to respective control



Suppl. Table 2: A stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients

Probe set	Description	Gene
227404_s_at	EGR1	EGR1: Early growth response 1
201041_s_at	DUSP1	DUSP1: dual specificity phosphatase 1
225681_at	CTHRC1	CTHRC1: collagen triple helix repeat containing 1
200797_s_at	MCL1	MCL1: myeloid cell leukemia sequence 1 (BCL2-related)
208763_s_at	TSC22D3	TSC22D3: TSC22 domain family, member 3
224558_s_at	MALAT1	MALAT1: metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)
225912_at	TP53INP1	TP53INP1: tumor protein p53 inducible nuclear protein 1
224566_at	TncRNA	TncRNA: trophoblast-derived noncoding RNA
201464_x_at	JUN	JUN: v-jun sarcoma virus 17 oncogene homolog (avian)
214022_s_at	IFITM1	IFITM1: interferon induced transmembrane protein 1 (9-27)
209457_at	DUSP5	DUSP5: dual specificity phosphatase 5
201010_s_at	TXNIP	TXNIP: thioredoxin interacting protein
219371_s_at	KLF2	KLF2: Kruppel-like factor 2 (lung)
209189_at	FOS	FOS: v-fos FBJ murine osteosarcoma viral oncogene homolog
205483_s_at	ISG15	ISG15: ISG15 ubiquitin-like modifier
217983_s_at	RNASET2	RNASET2: ribonuclease T2
227189_at	CPNE5	CPNE5: copine V
202388_at	RGS2	RGS2: regulator of G-protein signalling 2, 24kDa
225032_at	FNDC3B	FNDC3B: fibronectin type III domain containing 3B
222975_s_at	CSDE1	CSDE1: cold shock domain containing E1, RNA-binding
224565_at	TncRNA	TncRNA: trophoblast-derived noncoding RNA
212099_at	RHOB	RHOB: ras homolog gene family, member B
208078_s_at	SNF1LK	SNF1LK: SNF1-like kinase /// SNF1-like kinase
207761_s_at	METTL7A	METTL7A: methyltransferase like 7A
216834_at	RGS1	RGS1: regulator of G-protein signalling 1
202081_at	IER2	IER2: immediate early response 2
217984_at	RNASET2	RNASET2: ribonuclease T2
201601_x_at	IFITM1	IFITM1: interferon induced transmembrane protein 1 (9-27)
204415_at	IFI6	IFI6: interferon, alpha-inducible protein 6
226982_at	ELL2	ELL2: elongation factor, RNA polymerase II, 2
239901_at	---	FLJ43663: Hypothetical protein FLJ43663
217783_s_at	YPEL5	YPEL5: yippee-like 5 (Drosophila)
224690_at	C20orf108	C20orf108: chromosome 20 open reading frame 108
202086_at	MX1	MX1: myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
225606_at	BCL2L11	BCL2L11: BCL2-like 11 (apoptosis facilitator)
200811_at	CIRBP	CIRBP: cold inducible RNA binding protein
201236_s_at	BTG2	BTG2: BTG family, member 2
222420_s_at	UBE2H	UBE2H: ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)
225390_s_at	KLF13	KLF13: Kruppel-like factor 13
200645_at	GABARAP	GABARAP: GABA(A) receptor-associated protein
224783_at	FAM100B	FAM100B: family with sequence similarity 100, member B
200921_s_at	BTG1	BTG1: B-cell translocation gene 1, anti-proliferative
223218_s_at	NFKBIZ	NFKBIZ: nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta
223649_s_at	SLC25A39	CGI-69: CGI-69 protein
200798_x_at	MCL1	MCL1: myeloid cell leukemia sequence 1 (BCL2-related)
226117_at	TIFA	TIFA: TRAF-interacting protein with a forkhead-associated domain
210592_s_at	SAT1	SAT1: spermidine/spermine N1-acetyltransferase 1
208961_s_at	KLF6	KLF6: Kruppel-like factor 6
226905_at	FAM101B	FAM101B: family with sequence similarity 101, member B
226835_s_at	C20orf199 /// TALDO1	TALDO1 /// C20orf199: transaldolase 1 /// chromosome 20 open reading frame 199
222528_s_at	SLC25A37	SLC25A37: solute carrier family 25, member 37
221726_at	RPL22	RPL22: ribosomal protein L22
226440_at	DUSP22	DUSP22: Dual specificity phosphatase 22
200887_s_at	STAT1	STAT1: signal transducer and activator of transcription 1, 91kDa
202084_s_at	SEC14L1	SEC14L1: SEC14-like 1 (S. cerevisiae)
203725_at	GADD45A	GADD45A: growth arrest and DNA-damage-inducible, alpha
210046_s_at	IDH2	IDH2: isocitrate dehydrogenase 2 (NADP+), mitochondrial
208656_s_at	CCNI	CCNI: cyclin I
217728_at	S100A6	S100A6: S100 calcium binding protein A6 (calcyclin)

Suppl. Table 2: A stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients

202411_at	IFI27	IFI27: interferon, alpha-inducible protein 27
200001_at	CAPNS1	CAPNS1: calpain, small subunit 1 /// calpain, small subunit 1
227558_at	CBX4	CBX4: chromobox homolog 4 (Pc class homolog, Drosophila)
223217_s_at	NFKBIZ	NFKBIZ: nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta
233571_x_at	C20orf149	C20orf149: chromosome 20 open reading frame 149
201531_at	ZFP36	ZFP36: zinc finger protein 36, C3H type, homolog (mouse)
210563_x_at	CFLAR	CFLAR: CASP8 and FADD-like apoptosis regulator
212956_at	TBC1D9	TBC1D9: TBC1 domain family, member 9 (with GRAM domain)
221479_s_at	BNIP3L	BNIP3L: BCL2/adenovirus E1B 19kDa interacting protein 3-like
217918_at	DYNLRB1	DYNLRB1: dynein, light chain, roadblock-type 1
206574_s_at	PTP4A3	PTP4A3: protein tyrosine phosphatase type IVA, member 3
227337_at	ANKRD37	ANKRD37: ankyrin repeat domain 37
204805_s_at	H1FX	H1FX: H1 histone family, member X
202201_at	BLVRB	BLVRB: biliverdin reductase B (flavin reductase (NADPH))
224967_at	UGCG	UGCG: UDP-glucose ceramide glucosyltransferase
230793_at	LRRC16	LRRC16: leucine rich repeat containing 16
224889_at	FOXO3	FOXO3A: forkhead box O3A
201315_x_at	IFITM2	IFITM2: interferon induced transmembrane protein 2 (1-8D)
226858_at	CSNK1E	CSNK1E: Casein kinase 1, epsilon
203097_s_at	RAPGEF2	RAPGEF2: Rap guanine nucleotide exchange factor (GEF) 2
202391_at	BASP1	BASP1: brain abundant, membrane attached signal protein 1
225012_at	HDLBP	HDLBP: high density lipoprotein binding protein (vigilin)
208655_at	CCNI	CCNI: Cyclin I
225245_x_at	H2AFJ	H2AFJ: H2A histone family, member J
244050_at	PTPLAD2	PTPLAD2: protein tyrosine phosphatase-like A domain containing 2
226702_at	LOC129607	LOC129607: hypothetical protein LOC129607
229963_at	BEX5	NGFRAP1L1: NGFRAP1-like 1
228415_at	---	gb:AA205444 /DB_XREF=gi:1803434 /DB_XREF=zq66c06.s1 /CLONE=IMAGE:646570 /FEA=EST /CNT=27 /TID=Hs.40368.2 /TIER=Stack /STK=21 /UG=Hs.40368 /LL=8905 /UG_GENE=AP1S2 /UG_TITLE=adaptor-related protein complex 1, sigma 2 subunit
209166_s_at	MAN2B1	MAN2B1: mannosidase, alpha, class 2B, member 1
224785_at	FAM100B	FAM100B: family with sequence similarity 100, member B
229450_at	IFIT3	gb:AI075407 /DB_XREF=gi:3399978 /DB_XREF=oz56e10.x1 /CLONE=IMAGE:1679370 /FEA=EST /CNT=14 /TID=Hs.296083.0 /TIER=Stack /STK=9 /UG=Hs.296083 /UG_TITLE=ESTs
226876_at	FAM101B	FAM101B: family with sequence similarity 101, member B
226025_at	ANKRD28	ANKRD28: ankyrin repeat domain 28
225415_at	DTX3L	DTX3L: deltex 3-like (Drosophila)
224301_x_at	H2AFJ	H2AFJ: H2A histone family, member J
228993_s_at	LOC92482	LOC92482: hypothetical protein LOC92482
228167_at	KLHL6	KLHL6: kelch-like 6 (Drosophila)
222472_at	AFTPH	AFTPH: aftiphilin
227621_at	---	WTAP: Wilms tumor 1 associated protein
202442_at	AP3S1	AP3S1: adaptor-related protein complex 3, sigma 1 subunit
212697_at	FAM134C	LOC162427: hypothetical protein LOC162427
202887_s_at	DDIT4	DDIT4: DNA-damage-inducible transcript 4
212203_x_at	IFITM3	IFITM3: interferon induced transmembrane protein 3 (1-8U)
200782_at	ANXA5	ANXA5: annexin A5
217917_s_at	DYNLRB1	DYNLRB1: dynein, light chain, roadblock-type 1
219888_at	SPAG4	SPAG4: sperm associated antigen 4
226146_at	---	CDNA clone IMAGE:5294560
227749_at	---	POU2F2: POU domain, class 2, transcription factor 2
201390_s_at	CSNK2B	CSNK2B: casein kinase 2, beta polypeptide
208771_s_at	LTA4H	LTA4H: leukotriene A4 hydrolase
200643_at	HDLBP	HDLBP: high density lipoprotein binding protein (vigilin)
212593_s_at	PDCD4	PDCD4: programmed cell death 4 (neoplastic transformation inhibitor)
224602_at	LOC401152	LOC401152: HCV F-transactivated protein 1
225282_at	SMAP1L	SMAP1L: stromal membrane-associated protein 1-like
231647_s_at	FCRL5	FCRL5: Fc receptor-like 5
200678_x_at	GRN	GRN: granulin
225058_at	GPR108	GPR108: G protein-coupled receptor 108

225074_at	RAB2B	RAB2B: RAB2B, member RAS oncogene family
201832_s_at	USO1	PAK1 /// VDP: p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast) /// vesicle docking protein p115
226005_at	UBE2G1	UBE2G1: ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)
209606_at	PSCDBP	PSCDBP: pleckstrin homology, Sec7 and coiled-coil domains, binding protein /// pleckstrin homology, Sec7 and coiled-coil domains, binding protein
225929_s_at	RNF213	C17orf27: chromosome 17 open reading frame 27
208865_at	CSNK1A1	CSNK1A1: casein kinase 1, alpha 1
201285_at	MKRN1	MKRN1: makorin, ring finger protein, 1 /// makorin, ring finger protein, 1
208640_at	RAC1	RAC1: ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
222449_at	TMEPAI	TMEPAI: transmembrane, prostate androgen induced RNA
208308_s_at	GPI	GPI: glucose phosphate isomerase
208796_s_at	CCNG1	CCNG1: cyclin G1
200872_at	S100A10	S100A10: S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))
202364_at	MXI1	MXI1: MAX interactor 1 /// MAX interactor 1
227677_at	JAK3	JAK3: Janus kinase 3 (a protein tyrosine kinase, leukocyte)
227533_at	---	RALGPS2: Ral GEF with PH domain and SH3 binding motif 2
225576_at	C6orf72	C6orf72: chromosome 6 open reading frame 72
223014_at	UBE2R2	UBE2R2: ubiquitin-conjugating enzyme E2R 2
201527_at	ATP6V1F	ATP6V1F: ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F
214359_s_at	HSP90AB1	HSP90AB1: heat shock protein 90kDa alpha (cytosolic), class B member 1
201693_s_at	EGR1	EGR1: early growth response 1
224981_at	LOC124446	LOC124446: hypothetical protein BC017488
226779_at	---	CDNA FLJ37302 fis, clone BRAMY2016009
223179_at	YPEL3	YPEL3: yippee-like 3 (Drosophila)
224502_s_at	KIAA1191	KIAA1191: KIAA1191 /// KIAA1191
223318_s_at	ALKBH7	ALKBH7: alkB, alkylation repair homolog 7 (E. coli)
225265_at	RBMS1	RBMS1 /// C2orf12 /// LOC648293: RNA binding motif, single stranded interacting protein 1 /// chromosome 2 open reading frame 12 /// region containing chromosome 2 open reading frame 12; RNA binding motif, single stranded interacting protein 1
201360_at	CST3	CST3: cystatin C (amyloid angiopathy and cerebral hemorrhage)
231035_s_at	---	Transcribed locus
227067_x_at	NOTCH2NL	NOTCH2NL: Notch homolog 2 (Drosophila) N-terminal like
213281_at	JUN	JUN: V-jun sarcoma virus 17 oncogene homolog (avian)
228256_s_at	EPB41L4A	EPB41L4A: erythrocyte membrane protein band 4.1 like 4A
223436_s_at	TRPT1	TRPT1: tRNA phosphotransferase 1
201427_s_at	SEPP1	SEPP1: selenoprotein P, plasma, 1
225582_at	KIAA1754	KIAA1754: KIAA1754
233632_s_at	XRN1	XRN1: 5'-3' exoribonuclease 1
230405_at	LOC441108	RAD50: RAD50 homolog (S. cerevisiae)
225019_at	CAMK2D	CAMK2D: calcium/calmodulin-dependent protein kinase (CaM kinase) II delta
200760_s_at	ARL6IP5	ARL6IP5: ADP-ribosylation-like factor 6 interacting protein 5
225793_at	LIX1L	LIX1L: Lix1 homolog (mouse) like
226914_at	ARPC5L	ARPC5L: actin related protein 2/3 complex, subunit 5-like
203882_at	IRF9	ISGF3G: interferon-stimulated transcription factor 3, gamma 48kDa
212481_s_at	TPM4	TPM4: tropomyosin 4
201466_s_at	JUN	JUN: v-jun sarcoma virus 17 oncogene homolog (avian)
203455_s_at	SAT1	SAT1: spermidine/spermine N1-acetyltransferase 1
225898_at	WDR54	WDR54: WD repeat domain 54
235308_at	ZBTB20	ZBTB20: zinc finger and BTB domain containing 20
221704_s_at	VPS37B	VPS37B: vacuolar protein sorting 37 homolog B (S. cerevisiae) /// vacuolar protein sorting 37 homolog B (S. cerevisiae)
235061_at	PPM1K	PPM1K: protein phosphatase 1K (PP2C domain containing)
201669_s_at	MARCKS	MARCKS: myristoylated alanine-rich protein kinase C substrate
225183_at	C16orf72	C16orf72: chromosome 16 open reading frame 72
218678_at	NES	NES: nestin
200839_s_at	CTSB	CTSB: cathepsin B
224701_at	PARP14	PARP14: poly (ADP-ribose) polymerase family, member 14

Suppl. Table 2: A stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients

225373_at	C10orf54	C10orf54: chromosome 10 open reading frame 54
209357_at	CITED2	CITED2: Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
223754_at	MGC13057	MGC13057: hypothetical protein MGC13057
224643_at	PRRC1	PRRC1: proline-rich coiled-coil 1
210036_s_at	KCNH2	KCNH2: potassium voltage-gated channel, subfamily H (eag-related), member 2
208891_at	DUSP6	DUSP6: dual specificity phosphatase 6
200704_at	LITAF	LITAF: lipopolysaccharide-induced TNF factor
227279_at	TCEAL3	TCEAL3: transcription elongation factor A (SII)-like 3
212501_at	CEBPB	CEBPB: CCAAT/enhancer binding protein (C/EBP), beta
200621_at	CSRP1	CSRP1: cysteine and glycine-rich protein 1
208886_at	H1F0	H1F0: H1 histone family, member 0
209846_s_at	BTN3A2	BTN3A2: butyrophilin, subfamily 3, member A2
224949_at	YIPF5	YIPF5: Yip1 domain family, member 5
210470_x_at	NONO	NONO: non-POU domain containing, octamer-binding
200778_s_at	SEPT2	SEPT2: septin 2
201174_s_at	TERF2IP	TERF2IP: telomeric repeat binding factor 2, interacting protein
209786_at	HMGN4	HMGN4: high mobility group nucleosomal binding domain 4
225063_at	UBL7	UBL7: ubiquitin-like 7 (bone marrow stromal cell-derived)
224367_at	BEX2	BEX2: brain expressed X-linked 2 /// brain expressed X-linked 2
225897_at	MARCKS	Homo sapiens, clone IMAGE:5547644, mRNA
225522_at	AAK1	AAK1: AP2 associated kinase 1
226650_at	ZFAND2A	ZFAND2A: zinc finger, AN1-type domain 2A
243465_at	---	TMEM140: Transmembrane protein 140
222921_s_at	HEY2	HEY2: hairy/enhancer-of-split related with YRPW motif 2
224927_at	KIAA1949	KIAA1949: KIAA1949
225102_at	MGLL	MGLL: monoglyceride lipase
223135_s_at	BBX	BBX: bobby sox homolog (Drosophila)
214039_s_at	LAPTM4B	LAPTM4B: lysosomal associated protein transmembrane 4 beta
201642_at	IFNGR2	IFNGR2: interferon gamma receptor 2 (interferon gamma transducer 1)
202988_s_at	RGS1	RGS1: regulator of G-protein signalling 1
210142_x_at	FLOT1	FLOT1: flotillin 1
202284_s_at	CDKN1A	CDKN1A: cyclin-dependent kinase inhibitor 1A (p21, Cip1)
226007_at	ISCA2	HBLD1: HESB like domain containing 1
226456_at	C16orf75	C16orf75: chromosome 16 open reading frame 75
201029_s_at	CD99	CD99: CD99 molecule
224707_at	C5orf32	ORF1-FL49: putative nuclear protein ORF1-FL49
202336_s_at	PAM	PAM: peptidylglycine alpha-amidating monooxygenase
201678_s_at	C3orf37	C3orf37: chromosome 3 open reading frame 37
201885_s_at	CYB5R3	CYB5R3: cytochrome b5 reductase 3
231807_at	KIAA1217	KIAA1217: KIAA1217
225001_at	RAB3D	RAB3D: RAB3D, member RAS oncogene family
224759_s_at	C12orf23	C12orf23: chromosome 12 open reading frame 23
223046_at	EGLN1	EGLN1: egl nine homolog 1 (C. elegans)
225294_s_at	TRAPPC1	TRAPPC1: trafficking protein particle complex 1
202973_x_at	FAM13A1	FAM13A1: family with sequence similarity 13, member A1
223287_s_at	FOXP1	FOXP1: forkhead box P1
212185_x_at	MT2A	MT2A: metallothionein 2A
203445_s_at	CTDSP2	CTDSP2: CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2
225230_at	TMEM77	TMEM77: transmembrane protein 77
222421_at	UBE2H	UBE2H: ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)
209193_at	PIM1	PIM1: pim-1 oncogene /// pim-1 oncogene
223220_s_at	PARP9	PARP9: poly (ADP-ribose) polymerase family, member 9
224663_s_at	CFL2	CFL2: cofilin 2 (muscle)
226806_s_at	---	gb:AW022607 /DB_XREF=gi:5876137 /DB_XREF=df41c06.y1 /CLONE=IMAGE:2486002 /FEA=EST /CNT=49 /TID=Hs.12482.1 /TIER=Stack /STK=27 /UG=Hs.12482 /LL=8443 /UG_GENE=GNPAT /UG_TITLE=glyceronephosphate O-acyltransferase
201473_at	JUNB	JUNB: jun B proto-oncogene
225629_s_at	ZBTB4	ZBTB4: zinc finger and BTB domain containing 4
206896_s_at	GNG7	GNG7: guanine nucleotide binding protein (G protein), gamma 7

Suppl. Table 2: A stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients

227609_at	EPSTI1	EPSTI1: epithelial stromal interaction 1 (breast)
201176_s_at	ARCN1	ARCN1: archain 1
224918_x_at	MGST1	MGST1: microsomal glutathione S-transferase 1
226895_at	NFIC	NFIC: Nuclear factor I/C (CCAAT-binding transcription factor)
206174_s_at	PPP6C	PPP6C: protein phosphatase 6, catalytic subunit
209344_at	TPM4	TPM4: tropomyosin 4
202671_s_at	PDXK	PDXK: pyridoxal (pyridoxine, vitamin B6) kinase
200697_at	HK1	HK1: hexokinase 1
222743_s_at	C11orf71	C11orf71: chromosome 11 open reading frame 71
220147_s_at	FAM60A	FAM60A: family with sequence similarity 60, member A
201161_s_at	CSDA	CSDA: cold shock domain protein A
210401_at	P2RX1	P2RX1: purinergic receptor P2X, ligand-gated ion channel, 1
209034_at	PNRC1	PNRC1: proline-rich nuclear receptor coactivator 1
208991_at	STAT3	STAT3: signal transducer and activator of transcription 3 (acute-phase response factor)
207980_s_at	CITED2	CITED2: Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
223389_s_at	ZNF581	ZNF581: zinc finger protein 581
212041_at	ATP6V0D1	ATP6V0D1: ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1
202120_x_at	AP2S1	AP2S1: adaptor-related protein complex 2, sigma 1 subunit
219410_at	TMEM45A	TMEM45A: transmembrane protein 45A
217963_s_at	NGFRAP1	NGFRAP1: nerve growth factor receptor (TNFRSF16) associated protein 1
217047_s_at	FAM13A1	FAM13A1: family with sequence similarity 13, member A1
213836_s_at	WIPI1	WIPI1: WD repeat domain, phosphoinositide interacting 1
224793_s_at	TGFBR1	TGFBR1: transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)
228622_s_at	DNAJC4	DNAJC4: DnaJ (Hsp40) homolog, subfamily C, member 4
218450_at	HEBP1	HEBP1: heme binding protein 1
37028_at	PPP1R15A	PPP1R15A: protein phosphatase 1, regulatory (inhibitor) subunit 15A
200997_at	RBM4	RBM4 /// LOC650029: RNA binding motif protein 4 /// similar to RNA-binding protein 4 (RNA-binding motif protein 4) (Lark homolog) (Hlark) (RNA-binding motif protein 4a)
208892_s_at	DUSP6	DUSP6: dual specificity phosphatase 6
201251_at	PKM2	PKM2: pyruvate kinase, muscle
218097_s_at	CUEDC2	CUEDC2: CUE domain containing 2
217995_at	SQRDL	SQRDL: sulfide quinone reductase-like (yeast)
223234_at	MAD2L2	MAD2L2: MAD2 mitotic arrest deficient-like 2 (yeast)
224917_at	MIRN21	MIRN21: microRNA 21
202324_s_at	ACBD3	ACBD3: acyl-Coenzyme A binding domain containing 3
214057_at	MCL1	MCL1: Myeloid cell leukemia sequence 1 (BCL2-related)
200706_s_at	LITAF	LITAF: lipopolysaccharide-induced TNF factor
204285_s_at	PMAIP1	PMAIP1: phorbol-12-myristate-13-acetate-induced protein 1
224452_s_at	MGC12966	MGC12966: hypothetical protein LOC84792 /// hypothetical protein LOC84792
227479_at	KIAA1244	KIAA1244: KIAA1244
223269_at	POLR3GL	POLR3GL: polymerase (RNA) III (DNA directed) polypeptide G (32kD) like
225957_at	C5orf41	LOC153222: adult retina protein
218611_at	IER5	IER5: immediate early response 5
201841_s_at	HSPB1	HSPB1 /// MEIS3: heat shock 27kDa protein 1 /// Meis1, myeloid ecotropic viral integration site 1 homolog 3 (mouse)
226194_at	C13orf8	C13orf8: chromosome 13 open reading frame 8
234725_s_at	SEMA4B	SEMA4B: sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B
208436_s_at	IRF7	IRF7: interferon regulatory factor 7
202252_at	RAB13	RAB13: RAB13, member RAS oncogene family
223461_at	TBC1D7	TBC1D7: TBC1 domain family, member 7
222407_s_at	ZFP106	ZFP106: zinc finger protein 106 homolog (mouse)
200789_at	ECH1	ECH1: enoyl Coenzyme A hydratase 1, peroxisomal
201783_s_at	RELA	RELA: v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)
223206_s_at	NMRAL1	NMRAL1: NmrA-like family domain containing 1
201903_at	UQCRC1	UQCRC1: ubiquinol-cytochrome c reductase core protein I
225202_at	RHOBTB3	RHOBTB3: Rho-related BTB domain containing 3
209685_s_at	PRKCB1	PRKCB1: protein kinase C, beta 1

Suppl. Table 2: A stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients

224931_at	SLC41A3	SLC41A3: solute carrier family 41, member 3
223982_s_at	PNPLA8	PNPLA8: patatin-like phospholipase domain containing 8
229390_at	FAM26F	RP1-93H18.5: hypothetical protein LOC441168
226267_at	JDP2	JDP2: jun dimerization protein 2
221920_s_at	SLC25A37	SLC25A37: solute carrier family 25, member 37
212012_at	PXDN	PXDN: peroxidasin homolog (Drosophila)
225243_s_at	SLMAP	SLMAP: sarcolemma associated protein
202105_at	IGBP1	IGBP1: immunoglobulin (CD79A) binding protein 1
226094_at	PIK3C2A	PIK3C2A: phosphoinositide-3-kinase, class 2, alpha polypeptide
227817_at	PRKCB1	PRKCB1: Protein kinase C, beta 1
208908_s_at	CAST	CAST: calpastatin
227697_at	SOCS3	SOCS3: suppressor of cytokine signaling 3
209417_s_at	IFI35	IFI35: interferon-induced protein 35
228705_at	CAPN12	CAPN12: calpain 12
228284_at	TLE1	TLE1: Transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
213650_at	GOLGA8A /// GOLGA8	GOLGA8A /// GOLGA8B: golgi autoantigen, golgin subfamily a, 8A /// golgi autoantigen, golgin subfamily a, 8B
226726_at	MBOAT2	MBOAT2: membrane bound O-acyltransferase domain containing 2
208717_at	OXA1L	OXA1L: oxidase (cytochrome c) assembly 1-like
225941_at	EIF4E3	EIF4E3: eukaryotic translation initiation factor 4E member 3
228298_at	FAM113B	FAM113B: family with sequence similarity 113, member B
202672_s_at	ATF3	ATF3: activating transcription factor 3
219759_at	ERAP2	LRAP: leukocyte-derived arginine aminopeptidase
222826_at	PLDN	PLDN: pallidin homolog (mouse)
221748_s_at	TNS1	TNS1: tensin 1 /// tensin 1
218603_at	HECA	HECA: headcase homolog (Drosophila)
222993_at	MRPL37	MRPL37: mitochondrial ribosomal protein L37
225337_at	ABHD2	ABHD2: abhydrolase domain containing 2
201828_x_at	FAM127A	CXX1: CAAX box 1
215967_s_at	LY9	LY9: lymphocyte antigen 9
212724_at	RND3	RND3: Rho family GTPase 3
210978_s_at	TAGLN2	TAGLN2: transgelin 2
201811_x_at	SH3BP5	SH3BP5: SH3-domain binding protein 5 (BTK-associated)
201520_s_at	GRSF1	GRSF1: G-rich RNA sequence binding factor 1
224352_s_at	CFL2	CFL2: cofilin 2 (muscle) /// cofilin 2 (muscle)
218679_s_at	VPS28	VPS28: vacuolar protein sorting 28 homolog (S. cerevisiae)
226027_at	C9orf119	C9orf119: chromosome 9 open reading frame 119
205901_at	PNOC	PNOC: prepronociceptin
200613_at	AP2M1	AP2M1: adaptor-related protein complex 2, mu 1 subunit
217738_at	PBEF1	PBEF1 /// RP11-92J19.4: pre-B-cell colony enhancing factor 1 /// pre-B cell enhancing factor 1 pseudogene
227168_at	MIAT	FLJ25967: hypothetical gene supported by AK098833
205990_s_at	WNT5A	WNT5A: wingless-type MMTV integration site family, member 5A
220937_s_at	ST6GALNAC4	ST6GALNAC4: ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4
200993_at	IPO7	IPO7: importin 7
223311_s_at	MTA3	MTA3: metastasis associated 1 family, member 3
217900_at	IARS2	IARS2: isoleucine-tRNA synthetase 2, mitochondrial
202722_s_at	GFPT1	GFPT1: glutamine-fructose-6-phosphate transaminase 1
208967_s_at	AK2	AK2: adenylate kinase 2
202403_s_at	COL1A2	COL1A2: collagen, type I, alpha 2
201999_s_at	DYNLT1	DYNLT1: dynein, light chain, Tctex-type 1
201462_at	SCRN1	SCRN1: secernin 1
223226_x_at	SSBP4	SSBP4: single stranded DNA binding protein 4
227998_at	S100A16	S100A16: S100 calcium binding protein A16
230259_at	C10orf125	C10orf125: chromosome 10 open reading frame 125
200632_s_at	NDRG1	NDRG1: N-myc downstream regulated gene 1
202166_s_at	PPP1R2	PPP1R2: protein phosphatase 1, regulatory (inhibitor) subunit 2
212914_at	CBX7	CBX7: chromobox homolog 7
210817_s_at	CALCOCO2	CALCOCO2: calcium binding and coiled-coil domain 2

227414_at	RHBDD1	RHBDD1: rhomboid domain containing 1
221478_at	BNIP3L	BNIP3L: BCL2/adenovirus E1B 19kDa interacting protein 3-like /// BCL2/adenovirus E1B 19kDa interacting protein 3-like
200666_s_at	DNAJB1	DNAJB1: DnaJ (Hsp40) homolog, subfamily B, member 1
205000_at	DDX3Y	DDX3Y: DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
219147_s_at	C9orf95	C9orf95: chromosome 9 open reading frame 95
227325_at	LOC255783	LOC255783: hypothetical protein LOC255783
204881_s_at	UGCG	UGCG: UDP-glucose ceramide glucosyltransferase
214211_at	FTH1	FTH1: ferritin, heavy polypeptide 1
201628_s_at	RRAGA	RRAGA: Ras-related GTP binding A
220990_s_at	MIRN21 /// TMEM49	TMEM49 /// MIRN21: transmembrane protein 49 /// microRNA 21
204132_s_at	FOXO3	FOXO3A: forkhead box O3A
233933_s_at	OTUD5	OTUD5: OTU domain containing 5
222451_s_at	ZDHHC9	ZDHHC9: zinc finger, DHHC-type containing 9
202785_at	NDUFA7	NDUFA7: NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa
227641_at	FBXL16	FBXL16: F-box and leucine-rich repeat protein 16
218042_at	COPS4	COPS4: COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)
228427_at	FBXO16	FBXO16: F-box protein 16
212687_at	LIMS1	LIMS1: LIM and senescent cell antigen-like domains 1
205052_at	AUH	AUH: AU RNA binding protein/enoyl-Coenzyme A hydratase
223394_at	SERTAD1	SERTAD1: SERTA domain containing 1
218429_s_at	FLJ11286	FLJ11286: hypothetical protein FLJ11286
207196_s_at	TNIP1	TNIP1: TNFAIP3 interacting protein 1
209061_at	NCOA3	NCOA3: nuclear receptor coactivator 3
225080_at	MYO1C	MYO1C: Myosin IC
226134_s_at	---	Transcribed locus
218001_at	MRPS2	MRPS2: mitochondrial ribosomal protein S2
223290_at	PDXP	PDXP: pyridoxal (pyridoxine, vitamin B6) phosphatase
202083_s_at	SEC14L1	SEC14L1: SEC14-like 1 (S. cerevisiae)
226480_at	KIF2A	HSA9761: Dimethyladenosine transferase
222742_s_at	RABL5	RABL5: RAB, member RAS oncogene family-like 5
224884_at	AKAP13	AKAP13: A kinase (PRKA) anchor protein 13
226354_at	LACTB	LACTB: lactamase, beta
208698_s_at	NONO	NONO: non-POU domain containing, octamer-binding
212013_at	PXDN	PXDN: peroxidasin homolog (Drosophila)
211284_s_at	GRN	GRN: granulin
209581_at	HRASLS3	HRASLS3: HRAS-like suppressor 3
204752_x_at	PARP2	PARP2: poly (ADP-ribose) polymerase family, member 2
210564_x_at	CFLAR	CFLAR: CASP8 and FADD-like apoptosis regulator
222035_s_at	PAPOLA	PAPOLA: poly(A) polymerase alpha
202869_at	OAS1	OAS1: 2',5'-oligoadenylate synthetase 1, 40/46kDa
229164_s_at	ABTB1	ABTB1: ankyrin repeat and BTB (POZ) domain containing 1
201546_at	TRIP12	TRIP12: thyroid hormone receptor interactor 12
201425_at	ALDH2	ALDH2: aldehyde dehydrogenase 2 family (mitochondrial)
225842_at	PHLDA1	PHLDA1: pleckstrin homology-like domain, family A, member 1
203420_at	FAM8A1	FAM8A1: family with sequence similarity 8, member A1
238590_x_at	TMEM107	TMEM107: transmembrane protein 107
226331_at	---	ARTC1 mRNA, complete sequence
207198_s_at	LIMS1	LIMS1: LIM and senescent cell antigen-like domains 1
224953_at	YIPF5	YIPF5: Yip1 domain family, member 5
215333_x_at	GSTM1	GSTM1: glutathione S-transferase M1
224718_at	YY1	YY1: YY1 transcription factor
225940_at	EIF4E3	EIF4E3: eukaryotic translation initiation factor 4E member 3
211474_s_at	SERPINB6	SERPINB6: serpin peptidase inhibitor, clade B (ovalbumin), member 6
210844_x_at	CTNNA1	CTNNA1: catenin (cadherin-associated protein), alpha 1, 102kDa
203921_at	CHST2	CHST2: carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
223469_at	PGPEP1	PGPEP1: pyroglutamyl-peptidase I
202119_s_at	CPNE3	CPNE3: copine III
227020_at	YPEL2	YPEL2: yippee-like 2 (Drosophila)
200923_at	LGALS3BP	LGALS3BP: lectin, galactoside-binding, soluble, 3 binding protein

Suppl. Table 2: A stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients

209383_at	DDIT3	DDIT3: DNA-damage-inducible transcript 3
203411_s_at	LMNA	LMNA: lamin A/C
235134_at	---	CDNA FLJ30156 fis, clone BRACE2000487
205903_s_at	KCNN3	KCNN3: potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3
222500_at	PPIL1	PPIL1: peptidylprolyl isomerase (cyclophilin)-like 1
226682_at	LOC283666	LOC283666: hypothetical protein LOC283666
212473_s_at	MICAL2	MICAL2: microtubule associated monoxygenase, calponin and LIM domain containing 2
225433_at	GTF2A1	GTF2A1: General transcription factor IIA, 1, 19/37kDa
207266_x_at	RBMS1	RBMS1 /// LOC648293: RNA binding motif, single stranded interacting protein 1 /// region containing chromosome 2 open reading frame 12; RNA binding motif, single stranded interacting protein 1
219270_at	CHAC1	CHAC1: ChaC, cation transport regulator-like 1 (E. coli)
202014_at	PPP1R15A	PPP1R15A: protein phosphatase 1, regulatory (inhibitor) subunit 15A
202074_s_at	OPTN	OPTN: optineurin
205081_at	CRIP1	CRIP1 /// GALK2: cysteine-rich protein 1 (intestinal) /// galactokinase 2
209102_s_at	HBP1	HBP1: HMG-box transcription factor 1
207170_s_at	LETMD1	LETMD1: LETM1 domain containing 1
204141_at	TUBB2A	TUBB2A: tubulin, beta 2A
217873_at	CAB39	CAB39: calcium binding protein 39
201050_at	PLD3	PLD3: phospholipase D family, member 3
217202_s_at	GLUL	GLUL: glutamate-ammonia ligase (glutamine synthetase)
203020_at	RABGAP1L	RABGAP1L: RAB GTPase activating protein 1-like
201810_s_at	SH3BP5	SH3BP5: SH3-domain binding protein 5 (BTK-associated)
224857_s_at	POLR1D	POLR1D: polymerase (RNA) I polypeptide D, 16kDa
224812_at	HIBADH	HIBADH: 3-hydroxyisobutyrate dehydrogenase
200868_s_at	ZNF313	ZNF313: zinc finger protein 313
211928_at	DYNC1H1	DYNC1H1: dynein, cytoplasmic 1, heavy chain 1
221985_at	KLHL24	KLHL24: kelch-like 24 (Drosophila)
202145_at	LY6E	LY6E: lymphocyte antigen 6 complex, locus E
227584_at	NAV1	NAV1: Neuron navigator 1
228483_s_at	TAF9B	TAF9B: TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa
64486_at	CORO1B	CORO1B: coronin, actin binding protein, 1B
224772_at	NAV1	NAV1: neuron navigator 1
202545_at	PRKCD	PRKCD: protein kinase C, delta
236150_at	LOC123688	LOC123688: similar to RIKEN cDNA C630028N24 gene
200799_at	HSPA1A	HSPA1A: heat shock 70kDa protein 1A
223114_at	COQ5	COQ5: coenzyme Q5 homolog, methyltransferase (S. cerevisiae)
234111_at	ZNF81	CDNA: FLJ23063 fis, clone LNG04745
227200_at	---	gb:AI871408 /DB_XREF=gi:5545457 /DB_XREF=wl81g09.x1 /CLONE=IMAGE:2431360 /FEA=EST /CNT=28 /TID=Hs.105636.0 /TIER=Stack /STK=19 /UG=Hs.105636 /UG_TITLE=ESTs
201384_s_at	LOC727732 /// NBR1	NBR1 /// LOC653347: neighbor of BRCA1 gene 1 /// similar to neighbor of BRCA1 gene 1
236655_at	TPD52	TPD52: tumor protein D52
205467_at	CASP10	CASP10: caspase 10, apoptosis-related cysteine peptidase
225024_at	C20orf77	C20orf77: chromosome 20 open reading frame 77
225743_at	RPUSD3	RPUSD3: RNA pseudouridylate synthase domain containing 3
200771_at	LAMC1	LAMC1: laminin, gamma 1 (formerly LAMB2)
201729_s_at	KIAA0100	KIAA0100: KIAA0100
223125_s_at	C1orf21	C1orf21: chromosome 1 open reading frame 21
207571_x_at	C1orf38	C1orf38: chromosome 1 open reading frame 38
229969_at	---	gb:AV723931 /DB_XREF=gi:10827818 /DB_XREF=AV723931 /CLONE=HTBAQD04 /FEA=EST /CNT=13 /TID=Hs.26904.0 /TIER=Stack /STK=9 /UG=Hs.26904 /UG_TITLE=ESTs
223028_s_at	SNX9	SNX9: sorting nexin 9
203999_at	---	gb:AV731490 /DB_XREF=gi:10840911 /DB_XREF=AV731490 /CLONE=HTFAZD04 /FEA=FLmRNA /CNT=104 /TID=Hs.154679.0 /TIER=Stack /STK=16 /UG=Hs.154679 /LL=6857 /UG_GENE=SYT1 /UG_TITLE=synaptotagmin I /FL=gb:M55047.1 gb:NM_005639.1
200695_at	PPP2R1A	PPP2R1A: protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform
219356_s_at	CHMP5	CHMP5: chromatin modifying protein 5

226347_at	---	gb:AI754928 /DB_XREF=gi:5133192 /DB_XREF=cr32g12.x1 /CLONE=HBMSC_cr32g12 /FEA=mRNA /CNT=59 /TID=Hs.268231.0 /TIER=Stack /STK=12 /UG=Hs.268231 /UG_TITLE=Homo sapiens cDNA: FLJ23111 fis, clone LNG07835
229269_x_at	LOC646044 /// SSBP4	SSBP4: single stranded DNA binding protein 4
209868_s_at	RBMS1	RBMS1 /// LOC648293: RNA binding motif, single stranded interacting protein 1 /// region containing chromosome 2 open reading frame 12; RNA binding motif, single stranded interacting protein 1
211458_s_at	GABARAPL1 /// GABA	GABARAPL1 /// GABARAPL3: GABA(A) receptor-associated protein like 1 /// GABA(A) receptors associated protein like 3
221962_s_at	UBE2H	UBE2H: ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)
203657_s_at	CTSF	CTSF: cathepsin F
225167_at	FRMD4A	FRMD4A: FERM domain containing 4A
235716_at	---	Transcribed locus
209391_at	DPM2	DPM2: dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit
202429_s_at	PPP3CA	PPP3CA: protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)
215772_x_at	SUCLG2	SUCLG2: succinate-CoA ligase, GDP-forming, beta subunit
207738_s_at	NCKAP1	NCKAP1: NCK-associated protein 1
224975_at	NFIA	NFIA: nuclear factor I/A
212459_x_at	SUCLG2	SUCLG2: succinate-CoA ligase, GDP-forming, beta subunit
215773_x_at	PARP2	PARP2: poly (ADP-ribose) polymerase family, member 2
200744_s_at	GNB1	GNB1: guanine nucleotide binding protein (G protein), beta polypeptide 1
217988_at	CCNB1IP1	CCNB1IP1: cyclin B1 interacting protein 1
238547_at	HEXIM2	HEXIM2: hexamthylene bis-acetamide inducible 2
209385_s_at	PROSC	PROSC: proline synthetase co-transcribed homolog (bacterial)
223130_s_at	MYLIP	MYLIP: myosin regulatory light chain interacting protein
201059_at	CTTN	CTTN: cortactin
215565_at	DTNB	DTNB: dystrobrevin, beta
200622_x_at	CALM3	CALM3: calmodulin 3 (phosphorylase kinase, delta)
214453_s_at	IFI44	IFI44: interferon-induced protein 44
225803_at	FBXO32	FBXO32: F-box protein 32
219525_at	SLC47A1	FLJ10847: hypothetical protein FLJ10847
200883_at	UQCRC2	UQCRC2: ubiquinol-cytochrome c reductase core protein II
202731_at	PDCD4	PDCD4: programmed cell death 4 (neoplastic transformation inhibitor)
210561_s_at	WSB1	WSB1: WD repeat and SOCS box-containing 1
222557_at	STMN3	STMN3: stathmin-like 3
221087_s_at	APOL3	APOL3: apolipoprotein L, 3
209183_s_at	C10orf10	C10orf10: chromosome 10 open reading frame 10
200838_at	CTSB	CTSB: cathepsin B
227080_at	ZNF697	ZNF697: zinc finger protein 697
221808_at	RAB9A	RAB9A: RAB9A, member RAS oncogene family
226433_at	RNF157	RNF157: ring finger protein 157
202581_at	HSPA1B	HSPA1B: heat shock 70kDa protein 1B
218241_at	GOLGA5	GOLGA5: golgi autoantigen, golgin subfamily a, 5
204985_s_at	TRAPPC6A	TRAPPC6A: trafficking protein particle complex 6A
228763_at	CHMP4A /// MDP-1	CHMP4A /// MDP-1: chromatin modifying protein 4A /// magnesium-dependent phosphatase 1
226398_s_at	C10orf4	C10orf4: chromosome 10 open reading frame 4
222555_s_at	MRPL44	MRPL44: mitochondrial ribosomal protein L44
227567_at	AMZ2	AMZ2: Archaemetzincins-2
203524_s_at	MPST	MPST: mercaptopyruvate sulfurtransferase
208074_s_at	AP2S1	AP2S1: adaptor-related protein complex 2, sigma 1 subunit
209481_at	SNRK	SNRK: SNF related kinase
207543_s_at	P4HA1	P4HA1: procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I
204972_at	OAS2	OAS2: 2'-5'-oligoadenylate synthetase 2, 69/71kDa
224671_at	MRPL10	MRPL10: mitochondrial ribosomal protein L10
223176_at	KCTD20	KCTD20: potassium channel tetramerisation domain containing 20
212974_at	DENND3	DENND3: DENN/MADD domain containing 3

Suppl. Table 2: A stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients

220987_s_at	C11orf17 /// NUAK2	C11orf17 /// NUAK2: chromosome 11 open reading frame 17 /// chromosome 11 open reading frame 17 /// NUAK family, SNF1-like kinase, 2 /// NUAK family, SNF1-like kinase, 2
239824_s_at	TMEM107	TMEM107: transmembrane protein 107
201220_x_at	CTBP2	CTBP2: C-terminal binding protein 2
201950_x_at	CAPZB	CAPZB: capping protein (actin filament) muscle Z-line, beta
209762_x_at	SP110	SP110: SP110 nuclear body protein
225997_at	MOBKL1A	MOBKL1A: MOB1, Mps One Binder kinase activator-like 1A (yeast)
224728_at	ATPAF1	ATPAF1: ATP synthase mitochondrial F1 complex assembly factor 1
226665_at	AHSA2	AHSA2: AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)
208626_s_at	VAT1	VAT1: vesicle amine transport protein 1 homolog (T californica)
200730_s_at	PTP4A1	PTP4A1: protein tyrosine phosphatase type IVA, member 1
204794_at	DUSP2	DUSP2: dual specificity phosphatase 2
201877_s_at	PPP2R5C	PPP2R5C: protein phosphatase 2, regulatory subunit B (B56), gamma isoform
215535_s_at	AGPAT1	AGPAT1: 1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)
201234_at	ILK	ILK: integrin-linked kinase
202670_at	MAP2K1	MAP2K1: mitogen-activated protein kinase kinase 1
225613_at	MAST4	MAST4: microtubule associated serine/threonine kinase family member 4
233841_s_at	SUDS3	SUDS3: suppressor of defective silencing 3 homolog (S. cerevisiae)
221269_s_at	SH3BGRL3	SH3BGRL3: SH3 domain binding glutamic acid-rich protein like 3 /// SH3 domain binding glutamic acid-rich protein like 3
203825_at	BRD3	BRD3: bromodomain containing 3
201482_at	QSOX1	QSCN6: quiescin Q6
214129_at	LOC727942	PDE4DIP /// LOC642549: phosphodiesterase 4D interacting protein (myomegalin) /// similar to phosphodiesterase 4D interacting protein isoform 2
1729_at	TRADD	TRADD: TNFRSF1A-associated via death domain
202863_at	SP100	SP100: SP100 nuclear antigen
225524_at	ANTXR2	ANTXR2: anthrax toxin receptor 2
205790_at	SKAP1	SCAP1: src family associated phosphoprotein 1
202096_s_at	TSPO	TSPO: translocator protein (18kDa)
209122_at	ADFP	ADFP: adipose differentiation-related protein
218773_s_at	MSRB2	MSRB2: methionine sulfoxide reductase B2
221868_at	PAIP2B	KIAA1155: KIAA1155 protein
200664_s_at	DNAJB1	DNAJB1: DnaJ (Hsp40) homolog, subfamily B, member 1
210512_s_at	VEGFA	VEGF: vascular endothelial growth factor
223437_at	PPARA	PPARA: peroxisome proliferative activated receptor, alpha
221486_at	ENSA	ENSA: endosulfine alpha
202020_s_at	LANCL1	LANCL1: LanC lantibiotic synthetase component C-like 1 (bacterial)
211456_x_at	MT1P2	LOC645745 /// LOC650610: metallothionein 1H-like protein /// hypothetical protein LOC650610
225768_at	NR1D2	NR1D2: nuclear receptor subfamily 1, group D, member 2
204081_at	NRGN	NRGN: neurogranin (protein kinase C substrate, RC3)
204319_s_at	RGS10	RGS10: regulator of G-protein signalling 10
225892_at	IREB2	IREB2: Iron-responsive element binding protein 2
203719_at	ERCC1	ERCC1: excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)
205512_s_at	AIFM1	PDCD8: programmed cell death 8 (apoptosis-inducing factor)
212594_at	PDCD4	PDCD4: programmed cell death 4 (neoplastic transformation inhibitor)
231202_at	ALDH1L2	ALDH1L2: aldehyde dehydrogenase 1 family, member L2
221918_at	PCTK2	PCTK2: PCTAIRE protein kinase 2
223072_s_at	WBP1	WBP1: WW domain binding protein 1
202331_at	BCKDHA	BCKDHA: Branched chain keto acid dehydrogenase E1, alpha polypeptide
206918_s_at	CPNE1	CPNE1: copine I
209536_s_at	EHD4	EHD4: EH-domain containing 4
204745_x_at	MT1G	MT1G: metallothionein 1G
209339_at	SIAH2	SIAH2: seven in absentia homolog 2 (Drosophila) /// seven in absentia homolog 2 (Drosophila)
209004_s_at	FBXL5	FBXL5: F-box and leucine-rich repeat protein 5
211926_s_at	MYH9	MYH9: myosin, heavy polypeptide 9, non-muscle
230027_s_at	MRPL43	MRPL43: mitochondrial ribosomal protein L43

Suppl. Table 2: A stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients

203905_at	PARN	PARN: poly(A)-specific ribonuclease (deadenylation nuclease)
210045_at	IDH2	IDH2: isocitrate dehydrogenase 2 (NADP+), mitochondrial
224807_at	GRAMD1A	GRAMD1A: GRAM domain containing 1A
203349_s_at	ETV5	ETV5: ets variant gene 5 (ets-related molecule)
202564_x_at	ARL2	ARL2: ADP-ribosylation factor-like 2
212509_s_at	MXRA7	MXRA7: matrix-remodelling associated 7
201781_s_at	AIP	AIP: aryl hydrocarbon receptor interacting protein
223479_s_at	CHCHD5	CHCHD5: coiled-coil-helix-coiled-coil-helix domain containing 5
210052_s_at	TPX2	TPX2: TPX2, microtubule-associated, homolog (Xenopus laevis)
223196_s_at	SESN2	SESN2: sestrin 2
217764_s_at	RAB31	RAB31: RAB31, member RAS oncogene family
227058_at	C13orf33	C13orf33: chromosome 13 open reading frame 33
206200_s_at	ANXA11	ANXA11: annexin A11
229739_s_at	FAM116B	FAM116B: family with sequence similarity 116, member B
204961_s_at	NCF1 /// NCF1B /// N	NCF1 /// LOC653361 /// LOC653840: neutrophil cytosolic factor 1, (chronic granulomatous disease, autosomal 1)
240991_at	---	NDRG1: N-myc downstream regulated gene 1
202729_s_at	LTBP1	LTBP1: latent transforming growth factor beta binding protein 1
202003_s_at	ACAA2	ACAA2: acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)
200878_at	EPAS1	EPAS1: endothelial PAS domain protein 1
203907_s_at	IQSEC1	IQSEC1: IQ motif and Sec7 domain 1
226715_at	FOXK1	FOXK1: forkhead box K1
204621_s_at	NR4A2	NR4A2: nuclear receptor subfamily 4, group A, member 2
203674_at	HELZ	HELZ: helicase with zinc finger
226637_at	UBE2H	UBE2H: Ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)
226381_at	PS1TP4	PS1TP4: HBV preS1-transactivated protein 4
226517_at	BCAT1	BCAT1: branched chain aminotransferase 1, cytosolic
202060_at	CTR9	CTR9: Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)
209539_at	ARHGEF6	ARHGEF6: Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
203232_s_at	ATXN1	ATXN1: ataxin 1
235518_at	SLC8A1	SLC8A1: solute carrier family 8 (sodium/calcium exchanger), member 1
213198_at	ACVR1B	ACVR1B: activin A receptor, type IB
208893_s_at	DUSP6	DUSP6: dual specificity phosphatase 6
201570_at	SAMM50	SAMM50: sorting and assembly machinery component 50 homolog (S. cerevisiae)
203885_at	RAB21	RAB21: RAB21, member RAS oncogene family
204070_at	RARRES3	RARRES3: retinoic acid receptor responder (tazarotene induced) 3
209191_at	TUBB6	TUBB6: tubulin, beta 6
215088_s_at	SDHC	SDHC: succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa
225689_at	C3orf39	C3orf39: chromosome 3 open reading frame 39
208890_s_at	PLXNB2	PLXNB2: plexin B2
225224_at	C20orf112	C20orf112: chromosome 20 open reading frame 112
212689_s_at	JMJD1A	JMJD1A: jumonji domain containing 1A
224535_s_at	MRP63	MRP63: mitochondrial ribosomal protein 63 /// mitochondrial ribosomal protein 63
202658_at	PEX11B	PEX11B: peroxisomal biogenesis factor 11B
226275_at	MXD1	MXD1: MAX dimerization protein 1
204173_at	MYL6B	MYL6B: myosin, light polypeptide 6B, alkali, smooth muscle and non-muscle
203568_s_at	TRIM38	TRIM38: tripartite motif-containing 38
203311_s_at	ARF6	ARF6: ADP-ribosylation factor 6
200765_x_at	CTNNA1	CTNNA1: catenin (cadherin-associated protein), alpha 1, 102kDa
227864_s_at	FAM125A	FAM125A: family with sequence similarity 125, member A
230090_at	---	LOC646739: hypothetical protein LOC646739
209194_at	CETN2	CETN2: centrin, EF-hand protein, 2
202446_s_at	PLSCR1	PLSCR1: phospholipid scramblase 1
201921_at	GNG10 /// LOC55289	GNG10 /// LOC552891 /// LOC653503: guanine nucleotide binding protein (G protein), gamma 10 /// hypothetical protein LOC552891 /// GNG10 pseudogene
212818_s_at	ASB1	ASB1: ankyrin repeat and SOCS box-containing 1
207983_s_at	STAG2	STAG2: stromal antigen 2
203720_s_at	ERCC1	ERCC1: excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)

Suppl. Table 2: A stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients

232762_at	KIAA1217	KIAA1217: KIAA1217
209447_at	SYNE1	SYNE1: spectrin repeat containing, nuclear envelope 1
220330_s_at	SAMSN1	SAMSN1: SAM domain, SH3 domain and nuclear localisation signals, 1
202122_s_at	M6PRBP1	M6PRBP1: mannose-6-phosphate receptor binding protein 1
203476_at	TPBG	TPBG: trophoblast glycoprotein
225611_at	MAST4	gb:AI922968 /DB_XREF=gi:5659018 /DB_XREF=wn66h03.x1 /CLONE=IMAGE:2450453 /FEA=EST /CNT=76 /TID=Hs.110341.0 /TIER=Stack /STK=10 /UG=Hs.110341 /UG_TITLE=ESTs, Weakly similar to unknown (M.musculus)
223276_at	MST150	MST150: MSTP150
201365_at	OAZ2	OAZ2: ornithine decarboxylase antizyme 2
230212_at	LOC729345	gb:AW027076 /DB_XREF=gi:5885832 /DB_XREF=wt71g11.x1 /CLONE=IMAGE:2512964 /FEA=EST /CNT=9 /TID=Hs.189114.0 /TIER=Stack /STK=8 /UG=Hs.189114 /UG_TITLE=ESTs
226989_at	RGMB	RGMB: RGM domain family, member B
225855_at	EPB41L5	EPB41L5: erythrocyte membrane protein band 4.1 like 5
204034_at	ETHE1	ETHE1: ethylmalonic encephalopathy 1
226697_at	FAM114A1	LOC92689: hypothetical protein BC001096
215714_s_at	SMARCA4	SMARCA4: SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
205207_at	IL6	IL6: interleukin 6 (interferon, beta 2)
231769_at	FBXO6	FBXO6: F-box protein 6
235696_at	---	CDNA clone IMAGE:4837650
224819_at	TCEAL8	TCEAL8: transcription elongation factor A (SII)-like 8
206118_at	STAT4	STAT4: signal transducer and activator of transcription 4
203912_s_at	DNASE1L1	DNASE1L1: deoxyribonuclease I-like 1
226301_at	C6orf192	C6orf192: chromosome 6 open reading frame 192
226562_at	ZSCAN29	ZNF690: zinc finger protein 690
200931_s_at	VCL	VCL: vinculin
202758_s_at	RFXANK	RFXANK: regulatory factor X-associated ankyrin-containing protein
205902_at	KCNN3	KCNN3: potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3
217990_at	GMPR2	GMPR2: guanosine monophosphate reductase 2
228499_at	PFKFB4	PFKFB4: 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4
227961_at	CTSB	CTSB: cathepsin B
209662_at	CETN3	CETN3: centrin, EF-hand protein, 3 (CDC31 homolog, yeast)
219175_s_at	SLC41A3	SLC41A3: solute carrier family 41, member 3
209984_at	JMJD2C	JMJD2C: jumonji domain containing 2C
229771_at	TMEM41A	TMEM41A: Transmembrane protein 41A
202030_at	BCKDK	BCKDK: branched chain ketoacid dehydrogenase kinase
214736_s_at	ADD1	ADD1: adducin 1 (alpha)
214449_s_at	RHOQ	RHOQ: ras homolog gene family, member Q
205042_at	GNE	GNE: glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase
202733_at	P4HA2	P4HA2: procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II
229828_at	---	gb:AL044007 /DB_XREF=gi:5432235 /DB_XREF=DKFZp434I2028_s1 /CLONE=DKFZp434I2028 /FEA=EST /CNT=13 /TID=Hs.95663.0 /TIER=Stack /STK=10 /UG=Hs.95663 /UG_TITLE=ESTs
200675_at	CD81	CD81: CD81 molecule
208854_s_at	STK24	STK24: serine/threonine kinase 24 (STE20 homolog, yeast)
228728_at	C7orf58	FLJ21986: hypothetical protein FLJ21986
225872_at	SLC35F5	SLC35F5: solute carrier family 35, member F5
226855_at	---	PDP2: Pyruvate dehydrogenase phosphatase isoenzyme 2
202777_at	SHOC2	SHOC2: soc-2 suppressor of clear homolog (C. elegans)
227182_at	SUSD3	SUSD3: sushi domain containing 3
200665_s_at	SPARC	SPARC: secreted protein, acidic, cysteine-rich (osteonectin) /// secreted protein, acidic, cysteine-rich (osteonectin)
212051_at	WIPF2	WIRE: WIRE protein
225604_s_at	C9orf19	C9orf19: chromosome 9 open reading frame 19
202934_at	HK2	HK2: hexokinase 2
201416_at	SOX4	SOX4: SRY (sex determining region Y)-box 4
224790_at	DDEF1	DDEF1: development and differentiation enhancing factor 1
221998_s_at	VRK3	VRK3: vaccinia related kinase 3

Suppl. Table 2: A stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients

230619_at	ARNT	ARNT: aryl hydrocarbon receptor nuclear translocator
210479_s_at	RORA	RORA: RAR-related orphan receptor A
223395_at	ABI3BP	ABI3BP: ABI gene family, member 3 (NESH) binding protein
213455_at	FAM114A1	LOC92689: hypothetical protein BC001096
231956_at	KIAA1618	KIAA1618: KIAA1618
226568_at	FAM102B	FAM102B: family with sequence similarity 102, member B
224823_at	MYLK	MYLK: myosin, light polypeptide kinase
239045_at	---	ERN1: Endoplasmic reticulum to nucleus signalling 1
212544_at	ZNHIT3	ZNHIT3: zinc finger, HIT type 3
202623_at	EAPP	C14orf11: chromosome 14 open reading frame 11
212547_at	FLJ35348	FLJ35348: FLJ35348
208631_s_at	HADHA	HADHA: hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit
217909_s_at	MLX	MLX: MAX-like protein X
221731_x_at	VCAN	CSPG2: chondroitin sulfate proteoglycan 2 (versican)
227123_at	RAB3B	RAB3B: RAB3B, member RAS oncogene family
226038_at	LONRF1	LONRF1: LON peptidase N-terminal domain and ring finger 1
209137_s_at	USP10	USP10: ubiquitin specific peptidase 10
225710_at	GNB4	CDNA FLJ34013 fis, clone FCBBF2002111
227941_at	LOC339803	LOC339803: hypothetical protein LOC339803
224710_at	RAB34	RAB34: RAB34, member RAS oncogene family
244025_at	---	gb:BF590917 /DB_XREF=gi:11683241 /DB_XREF=7h46a08.x1 /CLONE=IMAGE:3318998 /FEA=EST /CNT=6 /TID=Hs.224432.0 /TIER=ConsEnd /STK=3 /UG=Hs.224432 /UG_TITLE=ESTs
202224_at	CRK	CRK: v-crk sarcoma virus CT10 oncogene homolog (avian)
211318_s_at	RAE1	RAE1: RAE1 RNA export 1 homolog (S. pombe)
242866_x_at	---	POU2F2: POU domain, class 2, transcription factor 2
218286_s_at	RNF7	RNF7: ring finger protein 7
210543_s_at	PRKDC	PRKDC: protein kinase, DNA-activated, catalytic polypeptide
224657_at	ERRFI1	ERRFI1: ERBB receptor feedback inhibitor 1
223614_at	C8orf57	C8orf57: chromosome 8 open reading frame 57
214437_s_at	SHMT2	SHMT2: serine hydroxymethyltransferase 2 (mitochondrial)
202942_at	ETFB	ETFB: electron-transfer-flavoprotein, beta polypeptide
223263_s_at	FGFR1OP2	FGFR1OP2: FGFR1 oncogene partner 2
200604_s_at	PRKAR1A	PRKAR1A: protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)
235256_s_at	GALM	GALM: galactose mutarotase (aldose 1-epimerase)
232616_at	LOC199725	LOC199725: hypothetical protein LOC199725
212484_at	FAM89B	FAM89B: family with sequence similarity 89, member B
217975_at	WBP5	WBP5: WW domain binding protein 5
204748_at	PTGS2	PTGS2: prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
223382_s_at	ZNRF1	ZNRF1: zinc and ring finger 1
212206_s_at	H2AFV	H2AFV: H2A histone family, member V
225378_at	VPS37A	VPS37A: vacuolar protein sorting 37 homolog A (S. cerevisiae)
208581_x_at	MT1X	MT1X: metallothionein 1X
223625_at	FAM126A	DRCTNNB1A: down-regulated by Ctnnb1, a
225228_at	TMEM77	TMEM77: transmembrane protein 77
214439_x_at	BIN1	BIN1: bridging integrator 1
212632_at	STX7	STX7: Syntaxin 7
227955_s_at	---	CDNA: FLJ22256 fis, clone HRC02860
208029_s_at	LAPTM4B	LAPTM4B: lysosomal associated protein transmembrane 4 beta /// lysosomal associated protein transmembrane 4 beta
203091_at	FUBP1	FUBP1: far upstream element (FUSE) binding protein 1
218300_at	C16orf53	C16orf53: chromosome 16 open reading frame 53
210524_x_at	---	gb:AF078844.1 /DB_XREF=gi:6683748 /FEA=FLmRNA /CNT=6 /TID=Hs.8765.1 /TIER=FL /STK=0 /UG=Hs.8765 /LL=11325 /UG_GENE=RNAHP /DEF=Homo sapiens hqp0376 protein mRNA, complete cds. /PROD=hqp0376 protein /FL=gb:AF078844.1
202123_s_at	ABL1	ABL1: v-abl Abelson murine leukemia viral oncogene homolog 1
200764_s_at	CTNNA1	CTNNA1: catenin (cadherin-associated protein), alpha 1, 102kDa
229628_s_at	KIAA1529	KIAA1529: KIAA1529

Suppl. Table 2: A stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients

226978_at	PPARA	PPARA: peroxisome proliferative activated receptor, alpha
212136_at	ATP2B4	ATP2B4: ATPase, Ca++ transporting, plasma membrane 4
228832_at	FLJ20021	FLJ20021: hypothetical LOC90024
200615_s_at	AP2B1	AP2B1: adaptor-related protein complex 2, beta 1 subunit
210986_s_at	TPM1	TPM1: tropomyosin 1 (alpha)
212573_at	ENDOD1	ENDOD1: endonuclease domain containing 1
223443_s_at	FLJ32065	FLJ32065: hypothetical protein FLJ32065
228189_at	BAG4	BAG4: BCL2-associated athanogene 4
236126_at	ACVR2B	Transcribed locus
216705_s_at	ADA	ADA: adenosine deaminase
210296_s_at	PXMP3	PXMP3: peroxisomal membrane protein 3, 35kDa (Zellweger syndrome)
238996_x_at	ALDOA	ALDOA: aldolase A, fructose-bisphosphate
217691_x_at	SLC16A3	SLC16A3: solute carrier family 16, member 3 (monocarboxylic acid transporter 4)
228670_at	TEP1	TEP1: telomerase-associated protein 1
210554_s_at	CTBP2	CTBP2: C-terminal binding protein 2
213629_x_at	MT1F	MT1F: metallothionein 1F (functional)
36711_at	MAFF	MAFF: v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)
213357_at	GTF2H5	GTF2H5: general transcription factor IIH, polypeptide 5
219878_s_at	KLF13	KLF13: Kruppel-like factor 13
202615_at	GNAQ	GNAQ: Guanine nucleotide binding protein (G protein), q polypeptide
209541_at	IGF1	IGF1: insulin-like growth factor 1 (somatomedin C)
232902_s_at	RARS2	RARSL: arginyl-tRNA synthetase-like
227728_at	---	CDNA FLJ42306 fis, clone TRACH2001646
225955_at	LOC653506 /// METRN	MED25 /// METRNL /// LOC653506: mediator of RNA polymerase II transcription, subunit 25 homolog (S. cerevisiae) /// meteorin, glial cell differentiation regulator-like /// similar to meteorin, glial cell differentiation regulator-like
239317_at	CEACAM21	gb:BG484601 /DB_XREF=gi:13416880 /DB_XREF=602505772F1 /CLONE=IMAGE:4619369 /FEA=EST /CNT=8 /TID=Hs.282899.0 /TIER=ConsEnd /STK=0 /UG=Hs.282899 /UG_TITLE=ESTs
228452_at	C17orf39	C17orf39: chromosome 17 open reading frame 39
212875_s_at	C2CD2	C21orf25: chromosome 21 open reading frame 25
228297_at	CNN3	CNN3: Calponin 3, acidic
224476_s_at	MESP1	MESP1: mesoderm posterior 1 homolog (mouse) /// mesoderm posterior 1 homolog (mouse)
203277_at	DFFA	DFFA: DNA fragmentation factor, 45kDa, alpha polypeptide
218260_at	DDA1	C19orf58: chromosome 19 open reading frame 58
202129_s_at	RIOK3	RIOK3: RIO kinase 3 (yeast) /// RIO kinase 3 (yeast)
91703_at	EHBP1L1	MGC15523 /// EHBP1L1: hypothetical protein MGC15523 /// EH domain binding protein 1-like 1
203338_at	PPP2R5E	PPP2R5E: protein phosphatase 2, regulatory subunit B (B56), epsilon isoform
232095_at	SRGAP2P1	SRGAP2: SLIT-ROBO Rho GTPase activating protein 2
227089_at	HBP1	Transcribed locus
218976_at	DNAJC12	DNAJC12: DnaJ (Hsp40) homolog, subfamily C, member 12
216733_s_at	GATM	GATM: glycine amidinotransferase (L-arginine:glycine amidinotransferase)
203814_s_at	NQO2	NQO2: NAD(P)H dehydrogenase, quinone 2
231772_x_at	CENPH	CENPH: centromere protein H
201417_at	SOX4	SOX4: SRY (sex determining region Y)-box 4
202371_at	TCEAL4	TCEAL4: transcription elongation factor A (SII)-like 4
220052_s_at	TINF2	TINF2: TERF1 (TRF1)-interacting nuclear factor 2
226621_at	---	gb:AI133452 /DB_XREF=gi:6360768 /DB_XREF=HA2061 /FEA=EST /CNT=48 /TID=Hs.75431.3 /TIER=Stack /STK=29 /UG=Hs.75431 /LL=2266 /UG_GENE=FGG /UG_TITLE=fibrinogen, gamma polypeptide
204194_at	BACH1	BACH1: BTB and CNC homology 1, basic leucine zipper transcription factor 1
201624_at	DARS	DARS: aspartyl-tRNA synthetase
210426_x_at	RORA	RORA: RAR-related orphan receptor A
202501_at	MAPRE2	MAPRE2: microtubule-associated protein, RP/EB family, member 2
229553_at	PGM2L1	PGM2L1: phosphoglucomutase 2-like 1
225930_at	NKIRAS1	NKIRAS1: NFKB inhibitor interacting Ras-like 1
222572_at	PPM2C	PPM2C: protein phosphatase 2C, magnesium-dependent, catalytic subunit
223221_at	SCO1	SCO1: SCO cytochrome oxidase deficient homolog 1 (yeast)
231166_at	GPR155	GPR155: G protein-coupled receptor 155

Suppl. Table 2: A stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients

216602_s_at	FARSA	FARSLA: phenylalanine-tRNA synthetase-like, alpha subunit
227792_at	LOC162073	LOC162073: Hypothetical protein LOC162073
218149_s_at	ZNF395	ZNF395: zinc finger protein 395
204384_at	GOLGA2	GOLGA2: golgi autoantigen, golgin subfamily a, 2
201881_s_at	ARIH1	ARIH1: ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)
202978_s_at	CREBZF	ZF: HCF-binding transcription factor Zhangfei
241367_at	FLJ35767	FLJ35767: FLJ35767 protein
225812_at	LOC619208	LOC619208: hypothetical protein LOC619208
223392_s_at	TSHZ3	TSHZ3: teashirt family zinc finger 3
212495_at	JMJD2B	JMJD2B: jumonji domain containing 2B
212472_at	MICAL2	MICAL2: microtubule associated monoxygenase, calponin and LIM domain containing 2
227452_at	---	LOC146795: Hypothetical protein LOC146795
206075_s_at	CSNK2A1	CSNK2A1: casein kinase 2, alpha 1 polypeptide
217875_s_at	TMEPAI	TMEPAI: transmembrane, prostate androgen induced RNA
221755_at	EHBP1L1	EHBP1L1: EH domain binding protein 1-like 1
227718_at	PURB	PURB: purine-rich element binding protein B
228678_at	FAM116B	CYP2U1 /// FAM116B: cytochrome P450, family 2, subfamily U, polypeptide 1 /// family with sequence similarity 116, member B
225766_s_at	TNPO1	TNPO1: Transportin 1
212315_s_at	NUP210	NUP210: nucleoporin 210kDa
231227_at	---	Transcribed locus, strongly similar to NP_003383.2 wingless-type MMTV integration site family, member 5A precursor; WNT-5A protein precursor [Homo sapiens]
225446_at	BRWD1	BRWD1: bromodomain and WD repeat domain containing 1
201971_s_at	ATP6V1A	ATP6V1A: ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A
217952_x_at	PHF3	PHF3: PHD finger protein 3
221986_s_at	KLHL24	KLHL24: kelch-like 24 (Drosophila)
50374_at	C17orf90	LOC339229: hypothetical protein LOC339229
202587_s_at	AK1	AK1: adenylate kinase 1
228280_at	ZC3HAV1L	ZC3HAV1L: zinc finger CCCH-type, antiviral 1-like
203823_at	RGS3	RGS3: regulator of G-protein signalling 3
221666_s_at	PYCARD	PYCARD: PYD and CARD domain containing
224911_s_at	DCBLD2	DCBLD2: discoidin, CUB and LCCL domain containing 2
221778_at	JHDM1D	KIAA1718: KIAA1718 protein
225436_at	FAM108C1	LOC58489: hypothetical protein from EUROIMAGE 588495
218487_at	ALAD	ALAD: aminolevulinate, delta-, dehydratase
214835_s_at	SUCLG2	SUCLG2: succinate-CoA ligase, GDP-forming, beta subunit
210105_s_at	FYN	FYN: FYN oncogene related to SRC, FGR, YES
232145_at	LOC388969	LOC388969: hypothetical LOC388969
204114_at	NID2	NID2: nidogen 2 (osteonidogen)
217782_s_at	GPS1	GPS1: G protein pathway suppressor 1
212293_at	HIPK1	HIPK1: homeodomain interacting protein kinase 1
212246_at	MCFD2	MCFD2: multiple coagulation factor deficiency 2
202996_at	POLD4	POLD4: polymerase (DNA-directed), delta 4
202100_at	RALB	RALB: v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)
204115_at	GNG11	GNG11: guanine nucleotide binding protein (G protein), gamma 11
212418_at	ELF1	ELF1: E74-like factor 1 (ets domain transcription factor)
201132_at	HNRPH2	HNRPH2: heterogeneous nuclear ribonucleoprotein H2 (H')
221498_at	SNX27	SNX27: sorting nexin family member 27
212646_at	RFTN1	RAFTLIN: raft-linking protein
219336_s_at	ASCC1	ASCC1: activating signal cointegrator 1 complex subunit 1
204479_at	OSTF1	OSTF1: osteoclast stimulating factor 1
210387_at	HIST1H2BG	HIST1H2BG: histone 1, H2bg
211543_s_at	GRK6	GRK6: G protein-coupled receptor kinase 6
202386_s_at	KIAA0430	KIAA0430: KIAA0430
225189_s_at	RAPH1	RAPH1: Ras association (RalGDS/AF-6) and pleckstrin homology domains 1
244509_at	GPR155	GPR155: G protein-coupled receptor 155
201170_s_at	BHLHB2	BHLHB2: basic helix-loop-helix domain containing, class B, 2
227868_at	LOC154761	LOC154761: hypothetical protein LOC154761
200885_at	RHOC	RHOC: ras homolog gene family, member C
224968_at	CCDC104	CCDC104: coiled-coil domain containing 104

Suppl. Table 2: A stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients

218507_at	HIG2	HIG2: hypoxia-inducible protein 2
204326_x_at	MT1X	MT1X: metallothionein 1X
217925_s_at	C6orf106	C6orf106: chromosome 6 open reading frame 106
200991_s_at	SNX17	SNX17: sorting nexin 17
208782_at	FSTL1	FSTL1: follistatin-like 1
216336_x_at	MT1M	MT1M: metallothionein 1M
212859_x_at	MT1E	MT1E: metallothionein 1E (functional)
202667_s_at	SLC39A7	SLC39A7: solute carrier family 39 (zinc transporter), member 7
212690_at	DDHD2	DDHD2: DDHD domain containing 2
202113_s_at	SNX2	SNX2: sorting nexin 2
228343_at	POU2F2	POU2F2: POU domain, class 2, transcription factor 2
232024_at	GIMAP2	GIMAP2: GTPase, IMAP family member 2
222662_at	PPP1R3B	LOC286044: hypothetical protein LOC286044
209817_at	PPP3CB	PPP3CB: protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)
219188_s_at	MACROD1	LRP16: LRP16 protein
217886_at	EPS15	EPS15: epidermal growth factor receptor pathway substrate 15
202087_s_at	CTSL1	CTSL: cathepsin L
217996_at	PHLDA1	PHLDA1: pleckstrin homology-like domain, family A, member 1
205067_at	IL1B	IL1B: interleukin 1, beta
231779_at	IRAK2	IRAK2: interleukin-1 receptor-associated kinase 2
207957_s_at	PRKCB1	PRKCB1: Protein kinase C, beta 1
218277_s_at	DHX40	DHX40: DEAH (Asp-Glu-Ala-His) box polypeptide 40
204238_s_at	C6orf108	C6orf108: chromosome 6 open reading frame 108
223019_at	FAM129B	C9orf88: chromosome 9 open reading frame 88
202732_at	PKIG	PKIG: protein kinase (cAMP-dependent, catalytic) inhibitor gamma
205214_at	STK17B	STK17B: serine/threonine kinase 17b (apoptosis-inducing)
202730_s_at	PDCD4	PDCD4: programmed cell death 4 (neoplastic transformation inhibitor)
210517_s_at	AKAP12	AKAP12: A kinase (PRKA) anchor protein (gravin) 12
217892_s_at	LIMA1	LIMA1: LIM domain and actin binding 1
212453_at	KIAA1279	KIAA1279: KIAA1279
203973_s_at	CEBPD	CEBPD: CCAAT/enhancer binding protein (C/EBP), delta
203588_s_at	TFDP2	TFDP2: transcription factor Dp-2 (E2F dimerization partner 2)
208867_s_at	CSNK1A1	CSNK1A1: casein kinase 1, alpha 1
200927_s_at	RAB14	RAB14: RAB14, member RAS oncogene family
218616_at	INTS12	INTS12: integrator complex subunit 12
219390_at	FKBP14	FKBP14: FK506 binding protein 14, 22 kDa
205441_at	OCEL1	OCEL1: occludin/ELL domain containing 1
202761_s_at	SYNE2	SYNE2: spectrin repeat containing, nuclear envelope 2
211537_x_at	MAP3K7	MAP3K7: mitogen-activated protein kinase kinase kinase 7
225665_at	ZAK	ZAK: sterile alpha motif and leucine zipper containing kinase AZK
214620_x_at	PAM	PAM: peptidylglycine alpha-amidating monooxygenase
224583_at	COTL1	COTL1: coactosin-like 1 (Dictyostelium)
219926_at	POPDC3	POPDC3: popeye domain containing 3
217730_at	TMBIM1	TMBIM1: transmembrane BAX inhibitor motif containing 1
235067_at	MKLN1	MKLN1: muskelin 1, intracellular mediator containing kelch motifs
218504_at	FAHD2A	FAHD2A: fumarylacetoacetate hydrolase domain containing 2A
204875_s_at	GMDS	GMDS: GDP-mannose 4,6-dehydratase
201824_at	RNF14	RNF14: ring finger protein 14
214083_at	PPP2R5C	PPP2R5C: Protein phosphatase 2, regulatory subunit B (B56), gamma isoform
229850_at	FVT1	Full length insert cDNA clone YX81F03
201212_at	LGMN	LGMN: legumain
221911_at	ETV1	ETV1: ets variant gene 1
201455_s_at	NPEPPS	NPEPPS: aminopeptidase puromycin sensitive
218999_at	TMEM140	TMEM140: transmembrane protein 140
226952_at	EAF1	EAF1: ELL associated factor 1
202814_s_at	HEXIM1	HEXIM1: hexamethylene bis-acetamide inducible 1
203060_s_at	PAPSS2	PAPSS2: 3'-phosphoadenosine 5'-phosphosulfate synthase 2
235567_at	LOC283666	LOC283666: Hypothetical protein LOC283666
203853_s_at	GAB2	GAB2: GRB2-associated binding protein 2

Suppl. Table 2: A stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients

203665_at	HMOX1	HMOX1: heme oxygenase (decycling) 1
221482_s_at	ARPP-19	ARPP-19: cyclic AMP phosphoprotein, 19 kD
217763_s_at	RAB31	RAB31: RAB31, member RAS oncogene family
217841_s_at	PPME1	PPME1: protein phosphatase methylesterase 1
203955_at	KIAA0649	KIAA0649: KIAA0649
226158_at	KLHL24	KLHL24: kelch-like 24 (Drosophila)
209118_s_at	TUBA1A	TUBA3: tubulin, alpha 3
228573_at	---	Full-length cDNA clone CS0DD001YA12 of Neuroblastoma Cot 50-normalized of Homo sapiens (human)
213944_x_at	GNA11	NCLN: Nicalin homolog (zebrafish)
200867_at	ZNF313	ZNF313: zinc finger protein 313
213418_at	HSPA6	HSPA6: heat shock 70kDa protein 6 (HSP70B')
235006_at	CDKN2AIPNL	MGC13017: similar to RIKEN cDNA A430101B06 gene
236104_at	---	CDNA FLJ35303 fis, clone PROST2009571
213388_at	LOC727942	PDE4DIP: phosphodiesterase 4D interacting protein (myomegalin)
205552_s_at	OAS1	OAS1: 2',5'-oligoadenylate synthetase 1, 40/46kDa
229287_at	PCNX	Full-length cDNA clone CS0DK010YA20 of HeLa cells Cot 25-normalized of Homo sapiens (human)
220199_s_at	C1orf80	C1orf80: chromosome 1 open reading frame 80
204880_at	MGMT	MGMT: O-6-methylguanine-DNA methyltransferase
222111_at	---	CDNA clone IMAGE:4794011
226725_at	SLFN5	Transcribed locus
225623_at	KIAA1737	KIAA1737: KIAA1737
209394_at	ASMTL	ASMTL: acetylserotonin O-methyltransferase-like
201185_at	HTRA1	HTRA1: HtrA serine peptidase 1
212642_s_at	HIVEP2	HIVEP2: human immunodeficiency virus type I enhancer binding protein 2
203871_at	SENP3	SENP3: SUMO1/sentrin/SMT3 specific peptidase 3
210845_s_at	PLAUR	PLAUR: plasminogen activator, urokinase receptor
219235_s_at	PHACTR4	PHACTR4: phosphatase and actin regulator 4
229264_at	LOC642441 /// LOC73	LOC642441: hypothetical protein LOC642441
204004_at	PAWR	PAWR: PRKC, apoptosis, WT1, regulator
226249_at	SNX30	SNX30: sorting nexin family member 30
212169_at	FKBP9	FKBP9: FK506 binding protein 9, 63 kDa
210299_s_at	FHL1	FHL1: four and a half LIM domains 1
226022_at	SASH1	SASH1: SAM and SH3 domain containing 1
203333_at	KIFAP3	KIFAP3: kinesin-associated protein 3
225045_at	CCDC88A	KIAA1212: KIAA1212
202976_s_at	RHOBTB3	RHOBTB3: Rho-related BTB domain containing 3
201408_at	PPP1CB	PPP1CB: protein phosphatase 1, catalytic subunit, beta isoform
230416_at	---	Transcribed locus
200800_s_at	HSPA1A /// HSPA1B	HSPA1A /// HSPA1B: heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B
214958_s_at	TMC6	TMC6: transmembrane channel-like 6
218506_x_at	N-PAC	N-PAC: cytokine-like nuclear factor n-pac
204867_at	GCHFR	GCHFR: GTP cyclohydrolase I feedback regulator
219045_at	RHOF	RHOF: ras homolog gene family, member F (in filopodia)
212458_at	SPRED2	SPRED2: sprouty-related, EVH1 domain containing 2
202856_s_at	SLC16A3	SLC16A3: solute carrier family 16, member 3 (monocarboxylic acid transporter 4)
244741_s_at	MGC9913	gb:BE855713 /DB_XREF=gi:10368199 /DB_XREF=7g08d09.x1 /CLONE=IMAGE:3305873 /FEA=EST /CNT=6 /TID=Hs.23133.1 /TIER=ConsEnd /STK=2 /UG=Hs.23133 /UG_TITLE=ESTs, Weakly similar to A33569 alcohol sulfotransferase (R.norvegicus)
219628_at	ZMAT3	ZMAT3: zinc finger, matrin type 3
226270_at	EXOC2	EXOC2: exocyst complex component 2
202225_at	---	CDNA FLJ38130 fis, clone D6OST2000464
221882_s_at	TMEM8	TMEM8: transmembrane protein 8 (five membrane-spanning domains)
227136_s_at	C10orf46	C10orf46: Chromosome 10 open reading frame 46
204247_s_at	CDK5	CDK5: cyclin-dependent kinase 5
213256_at	MARCH3	MARCH3: membrane-associated ring finger (C3HC4) 3
216442_x_at	FN1	FN1: fibronectin 1
213490_s_at	MAP2K2	MAP2K2: mitogen-activated protein kinase kinase 2
224733_at	CMTM3	CMTM3: CKLF-like MARVEL transmembrane domain containing 3

203348_s_at	ETV5	ETV5: ets variant gene 5 (ets-related molecule)
221563_at	DUSP10	DUSP10: dual specificity phosphatase 10
36554_at	ASMTL	ASMTL: acetylserotonin O-methyltransferase-like
209206_at	SEC22B	SEC22B: SEC22 vesicle trafficking protein homolog B (S. cerevisiae)
214844_s_at	DOK5	DOK5: docking protein 5
218849_s_at	PPP1R13L	PPP1R13L: protein phosphatase 1, regulatory (inhibitor) subunit 13 like
205193_at	MAFF	MAFF: v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)
217762_s_at	RAB31	RAB31: RAB31, member RAS oncogene family
202748_at	GBP2	GBP2: guanylate binding protein 2, interferon-inducible /// guanylate binding protein 2, interferon-inducible
243278_at	FOXP2	FOXP2: Forkhead box P2
203879_at	PIK3CD	PIK3CD: phosphoinositide-3-kinase, catalytic, delta polypeptide /// phosphoinositide-3-kinase, catalytic, delta polypeptide
204212_at	ACOT8	ACOT8: acyl-CoA thioesterase 8
213045_at	MAST3	MAST3: microtubule associated serine/threonine kinase 3
212348_s_at	AOF2	AOF2: amine oxidase (flavin containing) domain 2
235428_at	---	LOC642405: Hypothetical protein LOC642405
202806_at	DBN1	DBN1: drebrin 1
203935_at	ACVR1	ACVR1: activin A receptor, type I
206472_s_at	TLE3	TLE3: transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)
202500_at	DNAJB2	DNAJB2: DnaJ (Hsp40) homolog, subfamily B, member 2
227943_at	---	gb:AI798680 /DB_XREF=gi:5364152 /DB_XREF=we91d01.x1 /CLONE=IMAGE:2348449 /FEA=EST /CNT=31 /TID=Hs.25933.0 /TIER=Stack /STK=19 /UG=Hs.25933 /UG_TITLE=ESTs
205633_s_at	ALAS1	ALAS1: aminolevulinate, delta-, synthase 1
201075_s_at	SMARCC1	SMARCC1: SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
225774_at	RSPRY1	RSPRY1: ring finger and SPRY domain containing 1
209566_at	INSIG2	INSIG2: insulin induced gene 2
201760_s_at	WSB2	WSB2: WD repeat and SOCS box-containing 2
212233_at	MAP1B	3'UTR of hypothetical protein (ORF1)
222065_s_at	FLII	FLII: flightless I homolog (Drosophila)
217549_at	---	Transcribed locus, strongly similar to NP_848718.1 mitochondrial ribosomal protein L50 [Mus musculus]
218368_s_at	TNFRSF12A	TNFRSF12A: tumor necrosis factor receptor superfamily, member 12A
237203_at	---	Homo sapiens, clone IMAGE:4214313, mRNA
207630_s_at	CREM	CREM: cAMP responsive element modulator
211979_at	GPR107	GPR107: G protein-coupled receptor 107
201017_at	EIF1AX	EIF1AX: eukaryotic translation initiation factor 1A, X-linked
206580_s_at	EFEMP2	EFEMP2: EGF-containing fibulin-like extracellular matrix protein 2
221752_at	SSH1	SSH1: Slingshot homolog 1 (Drosophila)
202262_x_at	DDAH2	DDAH2: dimethylarginine dimethylaminohydrolase 2
212253_x_at	DST	DST: dystonin
214264_s_at	C14orf143	C14orf143: chromosome 14 open reading frame 143
209085_x_at	RFC1	RFC1: replication factor C (activator 1) 1, 145kDa
209538_at	ZNF32	ZNF32: zinc finger protein 32
217821_s_at	WBP11	WBP11: WW domain binding protein 11
218645_at	ZNF277	ZNF277: zinc finger protein 277
219060_at	C8orf32	C8orf32: chromosome 8 open reading frame 32
213397_x_at	RNASE4	RNASE4: ribonuclease, RNase A family, 4
201261_x_at	BGN	BGN: biglycan
209409_at	GRB10	GRB10: growth factor receptor-bound protein 10
218582_at	MARCH5	MARCH5: membrane-associated ring finger (C3HC4) 5
225946_at	RASSF8	RASSF8: Ras association (RalGDS/AF-6) domain family 8
226695_at	PRRX1	PRRX1: paired related homeobox 1
209365_s_at	ECM1	ECM1: extracellular matrix protein 1
208869_s_at	GABARAPL1	GABARAPL1: GABA(A) receptor-associated protein like 1
202472_at	MPI	MPI: mannose phosphate isomerase
204824_at	ENDOG	ENDOG: endonuclease G
201932_at	LRRC41	LRRC41: leucine rich repeat containing 41
204809_at	CLPX	CLPX: ClpX caseinolytic peptidase X homolog (E. coli)

Suppl. Table 2: A stroma-induced transcriptional signature associated with adverse clinical outcome in Dex-treated myeloma patients

217901_at	DSG2	DSG2: Desmoglein 2
205453_at	HOXB2	HOXB2: homeobox B2
201798_s_at	FER1L3	FER1L3: fer-1-like 3, myoferlin (C. elegans)
223345_at	HDAC8	HDAC8: histone deacetylase 8
209311_at	BCL2L2	BCL2L2: BCL2-like 2
221547_at	PRPF18	PRPF18: PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)