Supporting Information

Materials and Methods

Antibodies. The rabbit anti-BAF180 polyclonal antibody raised against BAF180 residues 736-1475 was a gift from Ramon Parsons (31). A rat monoclonal antibody was created by the Dana-Farber Cancer Institute Antibody Core Facility after immunizing rats with a GST-BAF180 (1190-1430) fusion protein. Mouse anti-BRG1 antibody (sc-17796), goat anti-BAF155 (sc-9746), mouse anti-BAF200 (ARID2, sc-166117), mouse anti-BAF250a (sc-32761) and mouse anti-BAP1 (sc-28383) were purchased from Santa Cruz Biotechnology. Mouse anti-Vinculin monoclonal antibody (V9131) was from Sigma Aldrich. Mouse anti-BAF47 antibody (#612110) was from BD Biosciences. Rabbit anti-BRM antibody (#6889), mouse monoclonal anti-HA antibody (6E2) (HRP conjugate) and rabbit monoclonal anti-SETD2 antibody (#23486) were from Cell Signaling Technology.

Cell Culture. The sources of the cell lines used in this study and the media used to maintain them were described by us previously (26, 32). A704 was maintained in Eagle's Minimum Essential Medium (EMEM) supplemented with 2mM Glutamine, 1% Non Essential Amino Acids (NEAA), 1mM Sodium Pyruvate and 15% FBS.

Plasmids. pBabe-BAF180, which contains a wild-type BAF180, was from Dr. Ramon Parsons (31). The mutant BAF180Q1298* cDNA was generated by overlapping PCR using pBabe-BAF180 as the template. The BAF180 wild-type, Q1298*, Δ2BD and Δ6BD cDNAs were PCR amplified with primers that introduced a 5' AgeI site and a 3' ClaI site, digested with these two enzymes, and subcloned into pTRIPz-neo vector that was modified to contain AgeI and ClaI multiple cloning sites (a gift of Dr. Gang Lu) (the PCR primers were listed in Supplemental Table 3). A BRG1 cDNA with sgRNA-resistant synonomous mutations was generated by overlapping PCR using pBABE-BRG1 (a gift from Robert Kingston , Addgene plasmid # 1959) as a template and cloned into pDONR223. The cDNA was then shuttled into pLL3.7EF1a-PGK-Hygro-DEST using a Gateway Cloning Kit (#11791100, Invitrogen). All of the cDNAs described above were authenticated by DNA sequencing.

Generation of Lentiviruses: Lentiviruses were made using 293FT cells according to Broad Institute TRC protocol (http://portals.broadinstitute.org/gpp/public/resources/protocols). In brief, 293FT cells were maintained in DMEM supplemented with 10% FBS, 0.1 mM MEM non-essential amino acids, 6 mM L-glutamine, and 1 mM sodium pyruvate without any antibiotics. On day 0, $5x10^5$ cells in 2 ml of media per well were plated into 6-well plates. The next day the media was changed to fresh media and the cells were transfected with 0.5 μg of pspAX2, 0.05 μg of pMD2.G and 0.5 μg per well using Lipofectamine 2000 (Invitrogen) according to manufacturer's protocol. On day 2, the media was replaced with fresh media supplemented with 30% FBS. On day 3, the supernatants were collected and filtered through 0.45 μm filter membrane.

Preparation of Nuclear Extracts. Cells at 80% confluence were collected with a cell scraper and washed twice with ice cold PBS. After centrifugation at 1,000g for 3 min at 4 °C the cell pellets were resuspended in 5 pellet volumes of hypotonic buffer (10 mM Hepes, pH 7.5, 1.5 mM $MgCl_2$, 10 mM KCl, 1 mM EDTA, 1 mM EGTA, and 1 mM DTT) containing protease inhibitors (#11697498001, Roche) for 30 min and then disrupted by passing through a 22G needle 10 times. The suspensions were then centrifuged at 1,000g for 10 min at 4 °C. The pellets were resuspended in 2.5 pellet volumes of the same hypotonic buffer. 5M NaCl was added to a final concentration of 420 mM and then the suspensions were slowly rotated for 30 min at 4 °C. The lysates were then centrifuged at 100,000g for 1 hr at 4°C and the supernatants were collected.

BAF180 Mutation Identification. Total RNA was extracted using Trizol reagent (Invitrogen). cDNAs were synthesized using AffinityScript QPCR cDNA Synthesis Kit (#600559, Agilent Technologies). Overlapping BAF180 cDNA fragments were PCR amplified using a high fidelity thermostable DNA polymerase (One Taq; New England Biolabs) and sequenced using the Sanger method. See Supplemental Table 4 for primers.

BAF180 Homologous Recombination. The BAF180 homologous recombination template that introduced the N-terminal FLAG-HA epitope was created using Gibson assembly (Supplemental Figure 14). In brief, the CMV-TK-pA cassette (containing the negative selection marker) present in pAL119-TK (a gift from Dr. Maria Castro; Addgene plasmid # 21911) was recovered by PCR. The BAF180 exon containing the start ATG and surrounding intronic sequences were PCR amplified using genomic DNA extracted from 786-O using a 5' primer that introduced an N-terminal FLAG-HA tag. A cassette containing the positive selection marker in the reverse strand (PGK-puro-2A-EGFP-pA) was made by overlapping PCR. In one reaction the PGK-puro fragment in pLenti X1 Puro DEST (694-6)(a gift from Eric Campeau;Addgene plasmid # 17297) was PCR amplified with a 5' primer that introduced a loxP site at the 5' end. In the other reaction the 2A-EGFP-pA fragment in pSpCas9(BB)-2A-GFP (PX458; Addgene plasmid #48138) was amplified with a 3' primer that introduced a loxP site at the 3' end. Aliquots of these two PCR reactions were then mixed and reamplified with the outer primers. The cassettes were then assembled into a modified AAV vector (based on pAAV-MCS Promoterless Expression Vector from Cell Biolabs Inc, VPK-411) restricted with ClaI and XhoI. The U6 promoter and the sgRNA cloning site from Lenti-CRISPRv2.0 (Addgene) was recovered PCR and subcloned into pAAV-MCS into which was inserted a duplex oligonucleotide encoding a sgBAF180 (TTCTTCTCTTGGAACCCA). AAV viruses were generated according to a manufacturers protocol (Cell Biolabs Inc). 786-O cells were coinfected with these two AAV virus expressing either repair template or sgBAF180, and an adenvirus expressing Cas9 (1900, Vector Biolabs). Three days after infection puromycin was added. After an additional three days the surviving cells were subcloned into 96-well plates and cultured in the presence of ganciclovir (negative selection) and puromycin (positive selection) for two more weeks. The green clones (EGFP expressing) were expanded and tested for the presence of FLAG-HA tagged BAF180 by immunoblot analysis.

BAF180 Tandem Immunoprecipitation. For each experimental condition the cells from twenty 15 cm plates of confluent cells were pelleted and resuspended in 2.5 pellet volumes of FLAG lysis buffer (50 mM Tris, pH 8.0, 137 mM NaCl, 1 mM EDTA, 1% Triton X100, 10% glycerol, and 10 mM NaF). The final NaCl concentration was adjusted to 420 mM by adding 0.15 volumes of 5 M NaCl. The resuspended samples were gently rotated end over end for 30 mins at 4 °C, after which 3 volumes of FLAG lysis buffer was added to each sample. The lysates were ultracentrifuged at 100,000g for 1 hr at 4 °C. The supernatants were collected and their protein concentrations, measured using the Bradford Assay, were adjusted to 1 mg/ml by adding FLAG lysis buffer. 500 µl of Anti-FLAG M2 agarose (M8823, Sigma Aldrich), prewashed with FLAG lysis buffer, was added to the supernatants in 50 ml falcon tubes and incubated for 2 hrs at 4 °C. The agarose was washed 5 times with FLAG-lysis buffer and then eluted by incubating in 1.5 ml of FLAG Lysis buffer containing 0.2 mg/ml 3XFLAG peptide with rotation overnight at 4 °C. The supernatant containing the eluted proteins was then mixed with 30 µl pre-washed anti-HA agarose (SC-7392AC, Santa Cruz Biotechnology) for 4 hrs at 4 °C. The anti-HA agarose was then washed 5 times with FLAG-lysis buffer and then eluted by incubating in 60 µl of FLAG lysis buffer containing 0.2 mg/ml HA peptide (I2149, Sigma Aldrich) with rotation for 4 hrs at 4 °C. The eluted samples were either resolved by SDS-PAGE and silver stained or precipitated with trichloroacetic acid (TCA) and subjected to mass spectrometry analysis.

Glycerol Gradient Centrifugation. Nuclear extracts were prepared as described above (hereby referred to as S100). Glycerol gradient solutions were made in hypotonic lysis buffer adjusted to 420 mM NaCl. 200 µl of S100 was layered on top of a 10 ml 10-45% glycerol gradient in thin wall polypropylene tubes (from Beckman Coulter). The samples were centrifuged in SW41 rotor at 39,800 rpm for 18 hrs at 4 °C. 330 µl samples were progressively removed from the top and analyzed by SDS-PAGE.

Cell Proliferation Assays. 5 x 10^5 cells were plated in 10 cm tissue culture dish on day 0 with or without 1 µg/ml of doxycycline (DOX). Fresh media was changed every 3 days. When cells reached 80% confluency they were trypsinized, stained with trypan blue, and the number of viable cells was counted using a Countess automated cell counter (Invitrogen). 5% of the total number of viable cells was then replated into a new 10 cm plate and the same procedure was repeated for approximately 4 days, with most cell lines being counted 4-5 times during that period. The cell numbers at each time point for each cell line were normalized to the control cell line for that experiment.

CRISPR-Based Gene Editing. Oligonucleotides corresponding to the different sgRNAs were cloned into lentiCRISPRv2 vector (Addgene, plasmid #52961), which expresses Cas9 and contains an sgRNA cloning site. Lentivirus was generated using 293FT cells according to the Broad Institute TRC protocol. After lentivirus infection, the cells were grown in the presence of puromycin. Protein target knockdown was assessed after one or two weeks of puromycin selection. For UMRC2 single clone CRISPR, sgBAF180-3 was cloned into pX330-U6-Chimeric_BB-CBh-hSpCas9 (a gift from Feng Zhang, Addgene plasmid #42230) between BbsI sites. The plasmid was used to transiently tranfect UMRC2 using Lipofectamine LTX with Plus Reagent (15338100, ThermoFisher Scientific). 2 days after transfection the cells were split into 96-well plates for single clone selection. After another 2 weeks, the clones were screened by western blot to identify PBRM1 null cells. The sgRNA sequences used are listed in Supplemental Table 5.

RNA Interference. Duplex oligonucleotides corresponding to PBRM1 shRNAs were cloned into Tet-pLKO-puro (Addgene, plasmid #21915). A duplex oligonucleotide corresponding to the control shRNA was cloned into a modified Tet-pLKO-puro (Addgene, plasmid #21915) that contained 200 bp of stuffer DNA 3' of the shRNA multicloning site to distinguish it from the PBRM1 shRNA vectors in PCR assays. The shRNA sequences used are listed in Supplemental Table 5.

Nude Mice Subcutaneous Xenograft Assay. Renal carcinoma cells at 80% confluence were collected by trypsinization. After centrifugation at 300g for 3 min at room temperature the cells were washed twice with ice cold PBS and resuspended in ice cold PBS at a concentration of 10^7 cells/ml. Two million cells (200 µl) were injected subcutaneously into 5 week-old nude mice using a 29G needle and 0.3mL U-100 syringe (324702, Becton-Dickenson). Tumors were collected 40 to 60 days later.

Competitive Orthotopic Tumor Growth Assay. 2 x10^6 cells consisting of a 1:1 mixture of cells infected to inducibly express a PBRM1 shRNA or control shRNA were injected orthotopically into the renal parenchyma of 5 week-old NOD-SCID mice. The tumors were collected after two months, homogenized in Proteinase K Digestion Buffer (0.1M Tris-HCl, pH.8, 0.2 M NaCl, 5 mM EDTA, 0.4% SDS and 0.2 mg/ml proteinase K) and incubated at 55 °C overnight. Genomic DNA was recovered by phenol-chloroform extraction followed by precipitiation with isopropyl alcohol. The DNA pellets were washed with 70% ethanol, dried and resuspended in water. The shRNA coding regions from the two viruses were PCR amplified (see Supplemental Table 6 for primers), separated by agarose electrophoresis, detected with ethidium bromide. Band intensities were measured with Image Lab 5.1 software.

ChIP-Seq: A704 cells inducibly expressing either HA-BAF180 or infected with the empty vector were cultured in 15 cm plates and treated with 1 µg/ml of DOX for 9 days. Formaldehyde (F8775, Sigma) was added dropwise into the media to a final concentration of 1% after which the media was incubated at room temperature for 8 min. Glycine was then added to final concentration of 125 mM after which the media was incubated at room temperature for 5 min to quench the formaldehyde. The cells were removed by scraping, transferred to 50 ml conical tubes, and washed twice with ice cold PBS. The cell pellets (50 million cells per condition) were resuspended in 1.25 ml of ChIP-Seq Digestion Buffer (50 mM Tris-HCl, pH 8.0, 1 mM CaCl2, 0.2% Triton X-100) plus protease inhibitors and prewarmed in a 37°C water bath for 3min. 6.25 µl of micrococcal nuclease (MNase, M0247S, New England Biolabs) was then added to each sample and incubated at 37°C for 12 min. To stop the reaction, 150 µl of 0.5M EDTA was added into each sample, mixed well and spun down at 1,000g for 5 min at 4°C. The cell pellets were then resuspended in 1.25 ml of SDS ChIP Buffer (20 mM Tris-HCl, pH 8.1, 150 mM NaCl, 1% Triton X-100, 2 mM EDTA, 0.1% SDS) and aliquoted into 5 fresh eppendorf tubes (250 µl each). The cells were then sonicated using a Bioruptor (Diagenode) for 25 min and centrifuged at 18,000g for 15 min. The supernatants were collected and precleared by gentle rocking with 40 µl of protein G sepharose for 3hrs at 4°C. In parallel, anti-HA sepharose (#11815016001, Roche) was washed 4 times with SDS ChIP Buffer. The pre-cleared lysates were transferred to fresh eppendorf tubes and incubated with 30 µl of anti-HA agarose at 4°C overnight. The agarose was washed twice with 1 ml of SDS ChIP Buffer, with each wash consisting of gentle rocking for 10 min at room temperature. The agarose was then washed twice with Wash Buffer 1 (50 mM Hepes, pH 7.5, 300 mM NaCl, 1 mM EDTA, 1% Triton X-100, 0.1%

deoxycholate), with each wash consisting of gentle rocking for 10 min at room temperature, and then washed three times with Wash Buffer 2 (10 mM Tris-HCl, pH 8.1, 250 mM LiCl, 1 mM EDTA, 0.5% NP-40), again with gentle rocking for 10 min per wash at room temperature. The agarose was then washed once with TE Buffer plus 0.2% Triton X-100, washed once with TE Buffer, and then resuspended in 200 µl TE plus 3 µl 20% SDS and 10 µl of 20mg/ml Proteinase K. The resuspended agarose was incubated overnight at 65°C, after which it was spun down and the supernatant was collected. The agarose was then further eluted with 200 µl of TE Buffer plus 0.5M NaCl. The supernatant was collected, combined with the supernatant obtained after the overnight incubation in the presence of SDS and Proteinase K at 65°C, and extracted twice with Phenol/Chloroform/Isoamyl Alcohol. The final 300 µl samples were ethanol precipitated by adding 30 µl of 3M NaAC, pH 5.3, 3 µl of 15 mg/ml glycogen and 750 µl of cold ethanol and overnight incubation at -80 °C overnight. The DNA precipitates were collected by centrifugation at 18,000g for 10 min at 4°C, washed twice with 70% ethanol, air dried, and resuspended in 40 µl TE Buffer. The DNA samples were submitted to Dana-Farber Cancer Institute CCCB for deep sequencing.

MNase-Seq. A704 cells inducibly expressing either HA-BAF180 or infected with an empty vector were cultured in 10 cm plates and treated with 1 µg/ml of DOX for 9 days. The cells were collected by scraping and washed twice with ice cold PBS. The cell pellets (~2 million cells per sample) were resuspended in 200 µl of PBS plus 0.5% Triton X-100 and incubated on ice for 5 min. The nuclei were spun down and resuspended in 200 µl of ChIP-Seq Digestion Buffer containing 1 µl of MNase and incubated at 37°C for 12 min. The reactions were stopped by adding 300 µl of Stop Buffer (20 mM EDTA, 20 mM EGTA, 0.4% SDS, 0.5 mg/ml Proteinase K). The mixtures were then incubated overnight at 65°C and extracted twice with Phenol/Chloroform /Isoamyl alcohol. The aqueous phase (400 µl) was removed and the DNA precipitated by adding 40 µl 3M NaAc, pH5.3 and 1.2 ml cold ethanol. The DNA precipitates were spun down, washed twice with 70% ethanol, air dried, resuspended in 50 µl of TE buffer, and submitted to Dana-Farber Cancer Institute CCCB for deep sequencing.

RNA-seq. Cells were cultured in 6 cm plates to 80% confluence. The media was removed by aspiration and replaced with 1 ml of Trizol reagent (Life Technologies). After incubation for 5 min at room temperature, the Trizol was transferred to an eppendorf tube. 200 µl of Chloroform was then added to the Trizol and mixed thoroughly with shaking. After incubation for an additional 5 minutes at room temperature the mixtures were centrifuged at 12,000g for 10 min at 4°C. The supernatant was transferred to a fresh eppendorf tube containing 500 µl of isopropanol, mixed well, incubated for 10 min at room temperature, and then centrifuged at 12,000g for 10 min at 4°C. The RNA pellets were washed twice with 70% ethanol, air dried for 10 min, and resuspended in 60 µl of RNase-free water. A Turbo DNA-free Kit from Life Technologies was used according to manufacturer's protocol to eliminate residual genomic DNA. The RNA samples were submitted to Dana-Farber Cancer Institute core facility CCCB for RNA-seq analysis.

Q-PCR: The RNAs were extracted as described above for RNA Seq except that genomic DNA was removed by adding 1 Unit of DNase I (#18068015, Life Technologies) to 2 µg of RNA in a total volume of 10 µl followed by incubation for 15 min at room temperature. 1 µl of 25 mM EDTA was then added prior to heating the samples to 65°C for 10 min. AffinityScript QPCR cDNA Synthesis Kit (Agilent) was used for first strand cDNA synthesis according to manufacturer's protocol. Q-PCR was done using Light Cycler 480 Syber Green I master mixture (#04707516001, Roche Diagnostics) as described in Cho et al (26). All mRNA measurements were based on two independent samples and normalized against 18s rRNA. QPCR primers used are listed in Supplemental Table 7.

Computational analysis

The RNA-seq reads were mapped to the human reference genome (GRCh38) using TopHat2 (33). Read counts for each gene were then calculated using HTSeq (34). Differential analysis was performed using DESeq2 (35). The ChIP-seq reads were first mapped to human GRCh38 reference genome using Bowtie2(36) , and the peaks were identified using MACS2 (37). The MNase-seq reads were analyzed as previously described (38) Briefly, all sequenced reads were mapped back to the human reference genome (GRCh38) using Bowtie. Uniquely mapped reads with a maximum of two mismatches were kept for further analysis. To create nucleosome profiles, all mapped reads were extended to 147 bp in their 3' direction, and the middle 73 bp were piled up, as previously described (39).

The Gene Set Enrichment Analysis (GSEA) was performed using the "GSEAPreranked" module of the GenePattern server at Broad Institute* (https://genepattern.broadinstitute.org) (40). Genes are ranked by their differential expression statistics from DESeq2, and the default parameters in the GSEAPreranked module are used.

The expression index measures the overall expression pattern of genes in a pathway in each sample, and was calculated using the previously published approaches (41, 42). Specifically, for all the genes in a pathway, the expression index of each sample is calculated as $\sum w_i x_i / |w_i|$, where x_i is the gene expression of signature gene i in that sample (measured as log2(FPKM)), and w_i is the weight of the gene i. We use pathway annotations in the MSigDB database of gene set enrichment analysis (GSEA) (43), and set $w_i = 1$ for genes that are in the same pathway. The expressions of genes in TCGA kidney cancer are extracted from the cBioPortal database (20).

Supplemental References:

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Supplemental Fig. 1. Identification of BAF180-Defective Clear Cell Renal Carcinoma Lines. Immunoblot analyses of the indicated cell lines with a rat anti-BAF180 antibody.

Supplemental Fig. 2. Failure of BAF180 to Suppress the Proliferation of Selected ccRCC Lines. (A and B) Rabbit polyclonal anti-BAF180 immunoblot analysis of SKRC20 (A), SLR24 (A), and RCC4 (B) cells infected to produce the indicated BAF180 variants (see Fig. 1C) in a DOX-inducible manner compared to 786-O cells. (C-E) Proliferation of ccRCC derivatives as in (A and B) grown in the presence or absence of DOX. For each line values were normalized to the untreated (no DOX) samples at each time point for that line.

Supplemental Fig. 3. Suppression of ccRCC Line Proliferation is Cell Line Specific. (A) Schematic of two component system used for DOX-inducible mRNA expression in panels that follow. (B and E) Rabbit polyclonal anti-BAF180 immunoblot analysis of SLR24 (B), A704 (B), and Caki-2 (E) cells infected to produce the indicated BAF180 variants (see Fig. 1C) in a DOX-inducible manner compared to 293FT cells. Note that the expression of the Q1298* variant was not completely suppressed in the absence of DOX in (E). (C, D, and F). Proliferation of ccRCC derivatives as in (B and E) grown in the presence or absence of DOX. For each line values were normalized to the untreated samples at each time point for that line.

Supplemental Fig. 4. Identification of Effective PBRM1 shRNAs. (A and C) Immunoblot analysis of 786-O cells infected with a lentivirus encoding the indicated shRNAs under the control of a DOX-inducible promoter. Where indicated cells were grown in the presence of DOX for 5 days (A) or 17 days (C). (B) Relative cell proliferation of cells as in (A). At each time point cell numbers were normalized to the values for the control shRNA cells at T=0 grown in the absence of DOX. (D). Bar graph showing decrease in cell growth of 786-O cells expressing DOX-inducible shRNAs as in (C) for 17 days. Values represent the difference in cell number (No DOX-DOX) normalized to the No DOX value for that line.

Supplemental Fig. 5. Failure of PBRM1 shRNA to Increase Proliferation of SN12C Cells. (A) Immunoblot analysis of SN12C infected with a lentivirus stably expressing a PBRM1 shRNA or control shRNA. (B) Cell proliferation of cells as in (A).

Supplemental Fig. 6. On-target Suppression of UMRC2 Cell Proliferation with PBRM1 shRNA. (A) Relative cell proliferation of UMRC2 cells as in Fig. 4A. For each cell line the value at each time point for the DOX-treated cells was normalized using the corresponding untreated cells. (B) Immunoblot (top panel) and relative cell proliferation (bottom panel) of UMRC2 cells infected with a lentivirus encoding a DOX-inducible PBRM1 shRNA (clone 131) and then superinfected with a lentivirus encoding an shRNA-resistant BAF180 cDNA. Cell proliferation data were representative of two independent experiments in which cells were or were not treated with DOX for 16 days. All the values were expressed relative to the EV cells grown in the absence of DOX.

Supplemental Fig. 7. CRISPR-Cas9 Mediated Inactivation of BAF180 Does Not Alter Proliferation of 786-O Cells. Proliferation of 786-O cells as in Fig. 4D. The number of viable cells was counted using a Countess automated cell counter. At each time point the values for the PBRM1 sgRNA cells were normalized to the value for the control sgRNA cells.

Supplemental Fig 8. Lack of Consistent Effects of BAF180 on p21. (A-C). Immunoblot analyses of A704 cells infected to produce the BAF180 in a DOX-inducible manner compared to empty vector cells (A) and 786-O cells infected to produce the indicated PBRM1 shRNAs (B and C) grown in the presence or absence of DOX as indicated.

Supplemental Fig. 9. BAF180 Does Not Grossly Alter Nucleosomal Positioning. (A and B) MNase signals of A704 cells infected to produce wild-type BAF180 (WT) or with the empty vector (EV)(A) and of UMRC2 parental cells compared to UMRC2 cells engineered to lack BAF180 using CRISPR/Cas9 (Clone4G2) (B). (C). Immunoblot analysis of the cells studied in (B).

Supplemental Fig. 10. Heatmap showing mRNAs that are activated (or suppressed) by BAF180, BRG1, and or BRM based on RNA-Seq of A704 cells as in (Fig. 5A)

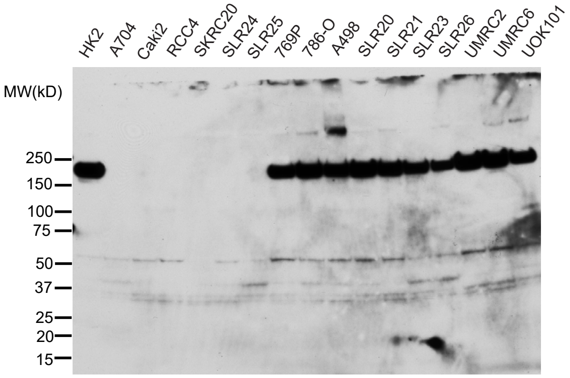
Supplemental Fig. 11. Modulation of HIF-target Gene Expression by BAF180. (A) Immunoblot analysis of A704 cells infected to produce BAF180WT in a DOX-inducible manner compared to A704 cells infected with the empty vector (EV) and 786-O cells that underwent CRISPR/Cas9-based gene editing with an sgRNA targeting *PBRM1*, *HIF2A*, or a control sgRNA (B). Levels of the indicated mRNAs, as determined by real-time PCR, in BAF180-proficient A704 (red bars) compared to their isogenic BAF180-defective counterparts (blue bars). (C). Gene Set Enrichment Analysis (GSEA) of differentially expressed mRNAs regulated by BAF180 in 786-O cells. (D-K). Anti-HA ChIP-Seq and RNA-Seq tracks for the indicated genes from A704 cells infected with a lentivirus encoding HA-tagged wild-type (WT) BAF180 or the empty vector (EV).

Supplemental Fig. 12. Prevalance of *VHL* and *PBRM1* Mutations in TCGA ccRCC Dataset.

Supplemental Fig. 13. Increased Sensitivity of A704 Cells to HIF2 Inhibitor. Proliferation of the indicated cell lines treated with the HIF2 inhibitor PT2399 relative to vehicle treated cells. For each cell line and at each time point the proliferation of the PT2399-treated cells was expressed relative to the corresponding DMSO-treated cells.

Supplemental Fig. 14. DNA sequence of the BAF180 FLAG-HA Knock-in homologous recombination template.

Fig. S1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RCC4
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75
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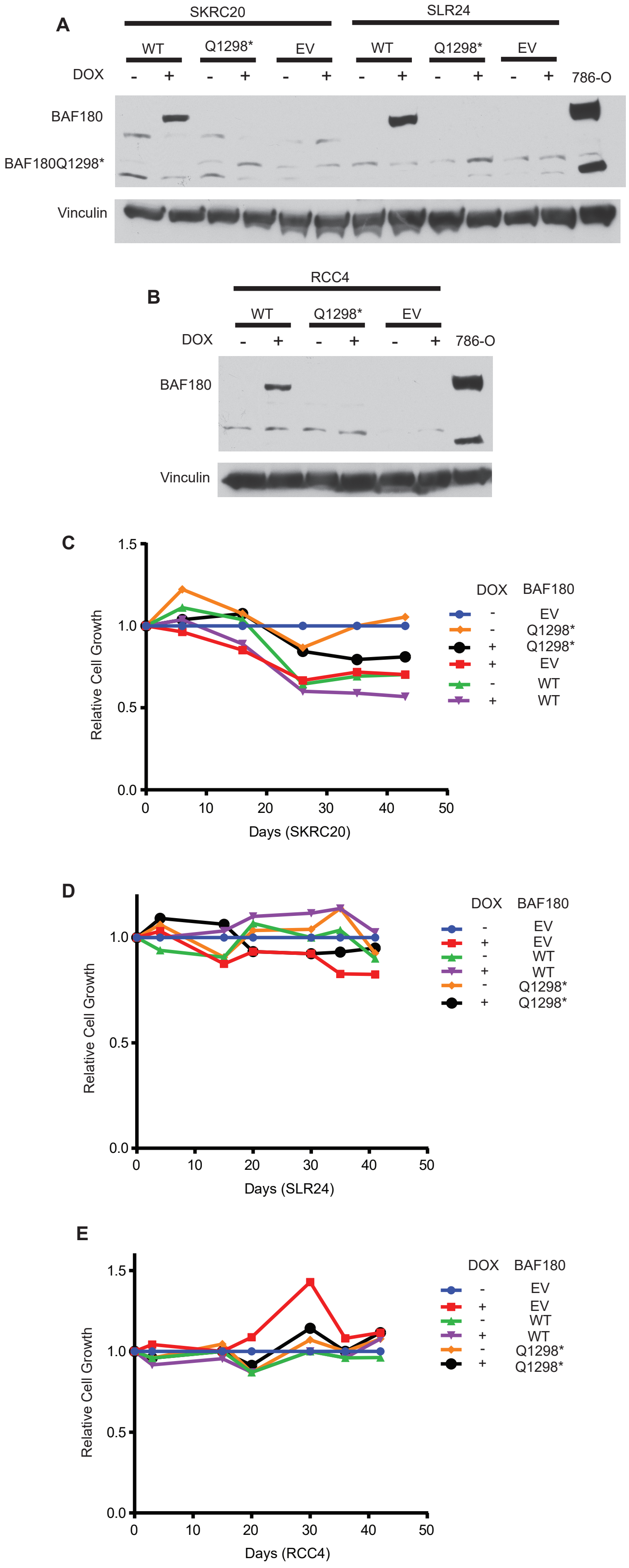
37
25
20
15

Fig. S2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SKRC20
SLR24
WT
Q1298*
EV
WT
Q1298*
EV
DOX
- + - + - + - + - + - +
786-O
BAF180
BAF180Q1298*
Vinculin
B
RCC4
WT
Q1298*
EV
DOX
- + - + - +
786-O
BAF180
Vinculin
C
Relative Cell Growth
1.5
1.0
0.5
0.0
0
10
20
30
40
50
Days (SKRC20)
DOX BAF180
- EV
- Q1298*
+ Q1298*
+ EV
- WT
+ WT
D
Relative Cell Growth
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0.5
0.0
0
10
20
30
40
50
Days (SLR24)
DOX BAF180
- EV
+ EV
- WT
+ WT
- Q1298*
+ Q1298*
E
Relative Cell Growth
1.5
1.0
0.5
0.0
0
10
20
30
40
50
Days (RCC4)
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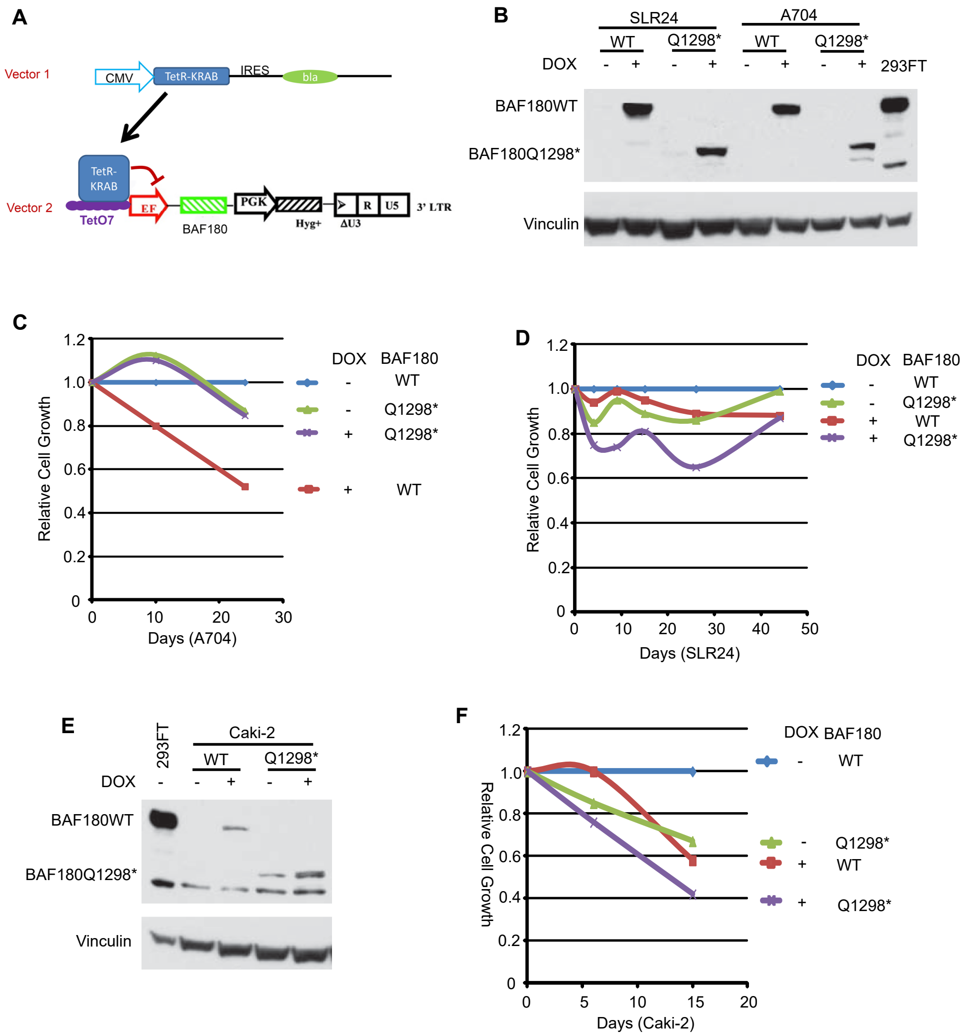
+ EV
- WT
+ WT
- Q1298*
+ Q1298*

Fig. S3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Vinculin
F
Relative Cell Growth
Days (Caki-2)
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- Q1298*
+ WT
+ Q1298*
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0.4
0.6
0.8
1.0
1.2
0
5
10
15
20
30
40
50

Fig. S4

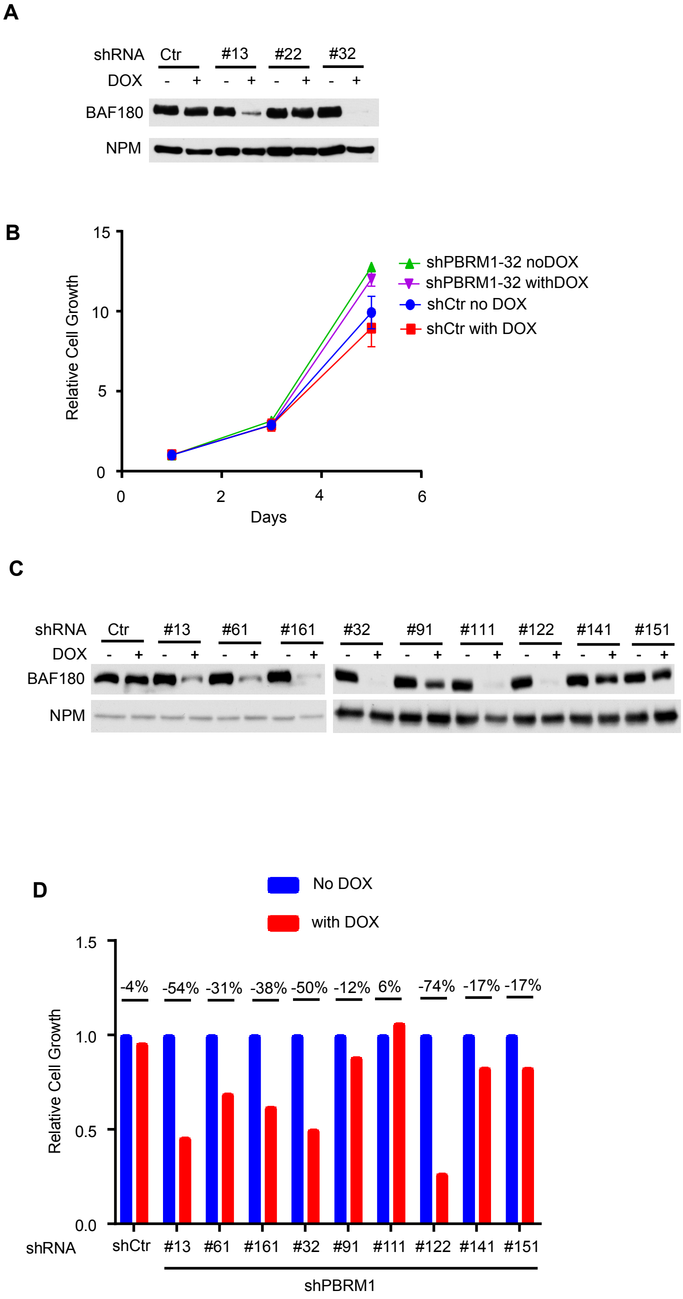

A
shRNA
Ctr
#13
#22
#32
DOX
- + - + - + - +
BAF180
NPM
B
Relative Cell Growth
15
10
5
0
0
2
4
6
Days
shPBRM1-32 noDOX
shPBRM1-32 withDOX
shCtr no DOX
shCtr with DOX
C
shRNA
Ctr
#13
#61
#161
#32
#91
#111
#122
#141
#151
DOX
- + - + - + - + - + - + - + - + - + - +
BAF180
NPM
D
No DOX
with DOX
Relative Cell Growth
1.5
1.0
0.5
0.0
-4%
-54%
-31%
-38%
-50%
-12%
6%
-74%
-17%
-17%
shRNA
shCtr
#13
#61
#161
#32
#91
#111
#122
#141
#151
shPBRM1

Fig. S5

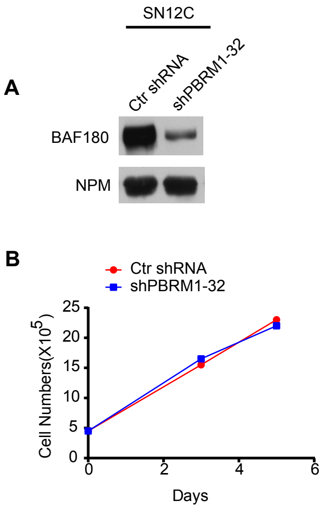

A
SN12C
Ctr shRNA
shPBRM1-32
BAF180
NPM
B
Ctr shRNA
shPBRM1-32
Cell Numbers(X10^5)
25
20
15
10
5
0
0
2
4
6
Days

Fig. S6

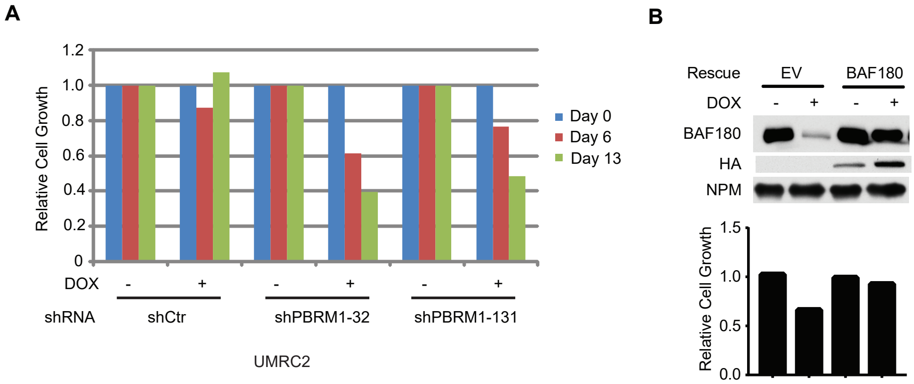

A
Relative Cell Growth
1.2
1.0
0.8
0.6
0.4
0.2
0
Day 0
Day 6
Day 13
DOX
-
+
-
+
-
+
shRNA
shCtr
shPBRM1-32
shPBRM1-131
UMRC2
B
Rescue
EV
BAF180
DOX
-
+
-
+
BAF180
HA
NPM
Relative Cell Growth
1.5
1.0
0.5
0.0

Fig. S7

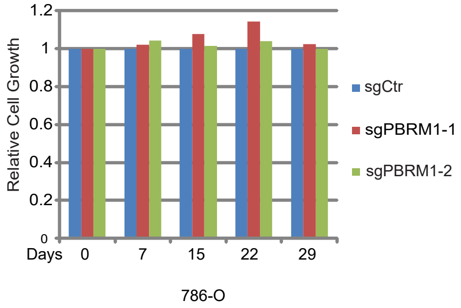

Relative Cell Growth
1.2
1
0.8
0.6
0.4
0.2
0
Days
0
7
15
22
29
786-O
sgCtr
sgPBRM1-1
sgPBRM1-2

Fig. S8

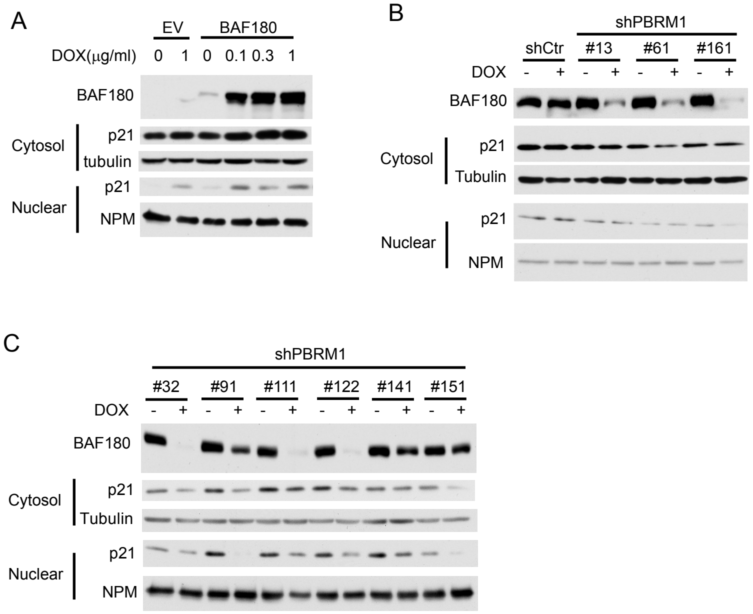

A
EV
BAF180
DOX(μg/ml) 0 1 0 0.1 0.3 1
BAF180
Cytosol
p21
tubulin
Nuclear
p21
NPM
B
shPBRM1
shCtr
#13
#61
#161
DOX - + - + - + - +
BAF180
Cytosol
p21
Tubulin
Nuclear
p21
NPM
C
shPBRM1
#32
#91
#111
#122
#141
#151
DOX - + - + - + - + - + - +
BAF180
Cytosol
p21
Tubulin
Nuclear
p21
NPM

Fig. S9

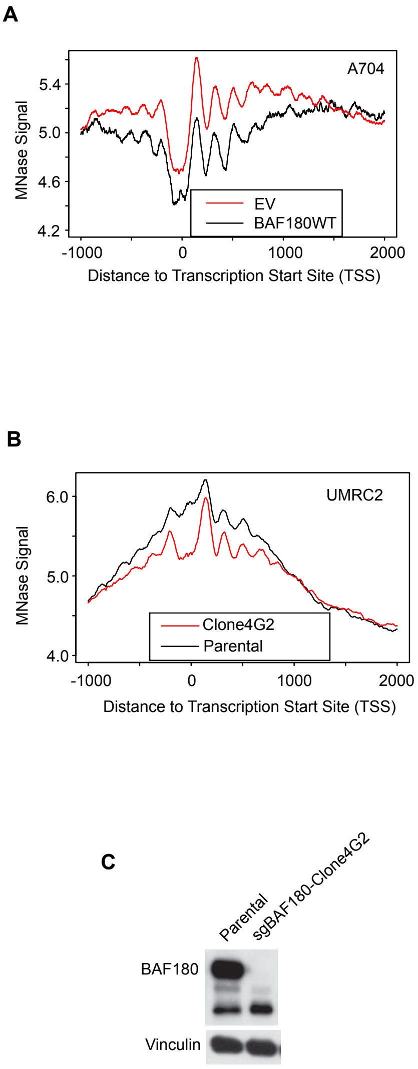

A
A704
MNase Signal
5.4
5.0
4.6
4.2
-1000
0
1000
2000
Distance to Transcription Start Site (TSS)
EV
BAF180WT
B
UMRC2
MNase Signal
6.0
5.0
4.0
-1000
0
1000
2000
Distance to Transcription Start Site (TSS)
Clone4G2
Parental
C
Parental
sgBAF180-Clone4G2
BAF180
Vinculin

Fig. S10

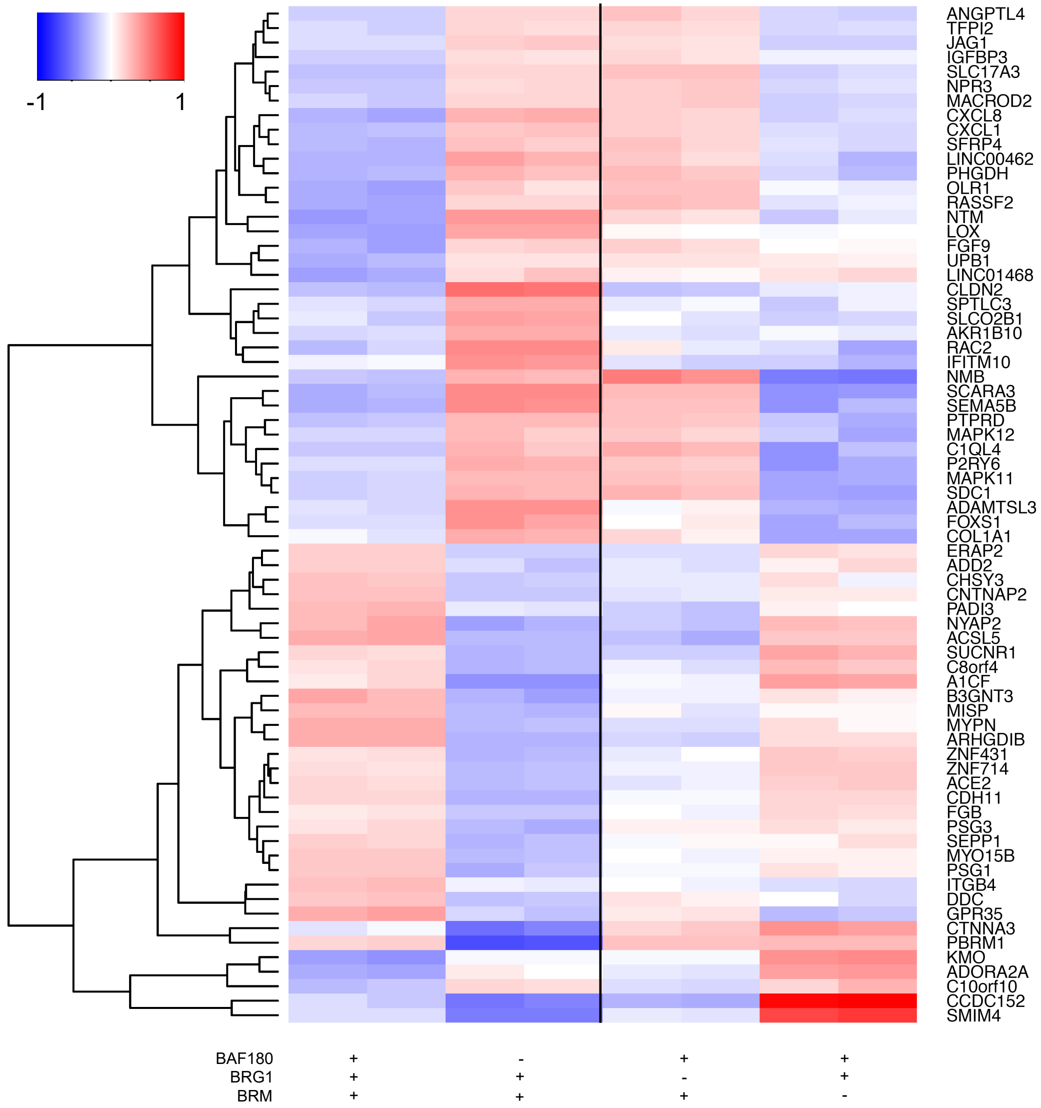

-1
1
ANGPTL4
TFPI2
JAG1
IGFBP3
SLC17A3
NPR3
MACROD2
CXCL8
CXCL1
SFRP4
LINC00462
PHGDH
OLR1
RASSF2
NTM
LOX
FGF9
UPB1
LINC01468
CLDN2
SPTLC3
SLCO2B1
AKR1B10
RAC2
IFITM10
NMB
SCARA3
SEMA5B
PTPRD
MAPK12
C1QL4
P2RY6
MAPK11
SDC1
ADAMTSL3
FOXS1
COL1A1
ERAP2
ADD2
CHSY3
CNTNAP2
PADI3
NYAP2
ACSL5
SUCNR1
C8orf4
A1CF
B3GNT3
MISP
MYPN
ARHGDIB
ZNF431
ZNF714
ACE2
CDH11
FGB
PSG3
SEPP1
MYO15B
PSG1
ITGB4
DDC
GPR35
CTNNA3
PBRM1
KMO
ADORA2A
C10orf10
CCDC152
SMIM4
BAF180 + - + +
BRG1 + + - +
BRM + + + -

Fig. S11

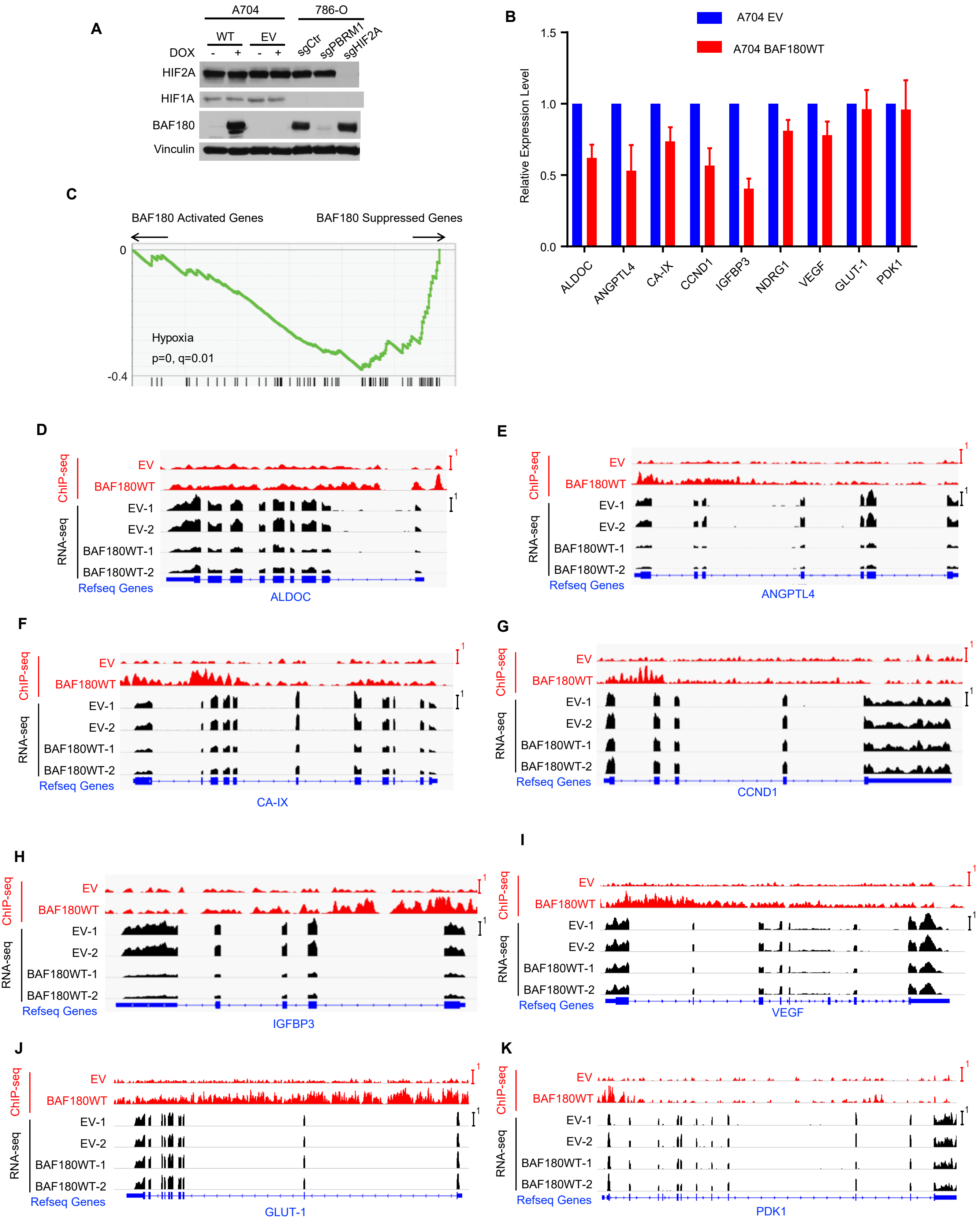

A
A704
786-O
WT
EV
DOX
- + - +
sgCtr
sgPBRM1
sgHIF2A
HIF2A
HIF1A
BAF180
Vinculin
B
A704 EV
A704 BAF180WT
Relative Expression Level
1.5
1.0
0.5
0.0
ALDOC
ANGPTL4
CA-IX
CCND1
IGFBP3
NDRG1
VEGF
GLUT-1
PDK1
C
BAF180 Activated Genes
BAF180 Suppressed Genes
0
-0.4
Hypoxia
p=0, q=0.01
D
ChIP-seq
EV
BAF180WT
RNA-seq
EV-1
EV-2
BAF180WT-1
BAF180WT-2
Refseq Genes
ALDOC
1
E
ANGPTL4
F
CA-IX
G
CCND1
H
IGFBP3
I
VEGF
J
GLUT-1
K
PDK1

Fig. S12

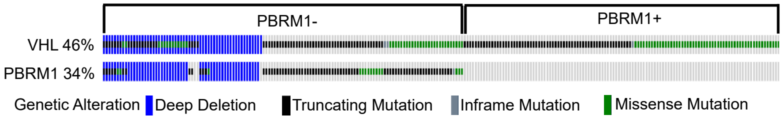
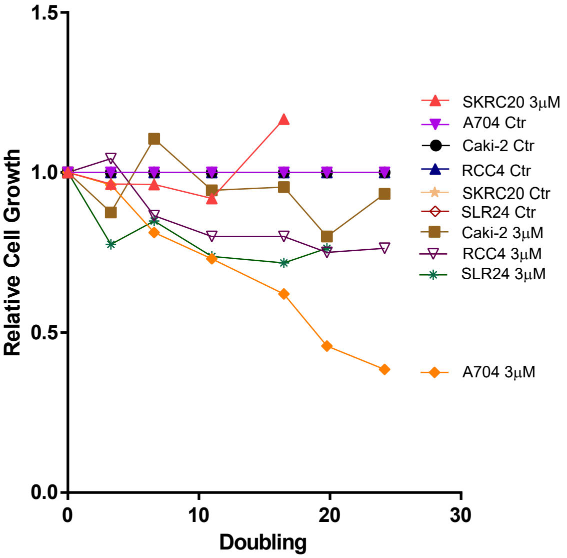

PBRM1-
PBRM1+
VHL 46%
PBRM1 34%
Genetic Alteration
Deep Deletion
Truncating Mutation
Inframe Mutation
Missense Mutation

Fig. S13



1.5
1.0
0.5
0.0
Relative Cell Growth
0
10
20
30
Doubling
SKRC20 3μM
A704 Ctr
Caki-2 Ctr
RCC4 Ctr
SKRC20 Ctr
SLR24 Ctr
Caki-2 3μM
RCC4 3μM
SLR24 3μM
A704 3μM

Fig. S14. DNA sequence of the BAF180 FLAG-HA Knock-in homologous recombination template:

CMV-TK-pA

BAF180 Intron

FLAG-HA

BAF180 Exon

loxP-PGK-puro-2A-EGFP-pA-loxP

AGCTTGCATGCCTGCAGGTCAATTCCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCC
TACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACA
TCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTnCAAGTCTCCACCCCATTGACGTCAAT
GGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATT
GACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGAAC
CGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATC
CAGCCTGGGGATCCCGACcATGGCTTCGTACCCCTGCCATCAACACGCGTCTGCGTTCGACCAGGC
TGCGCGTTCTCGCGGCCATAGCAACCGACGTACGGCGTTGCGCCCTCGCCGGCAGCAAGAAGCCA
CGGAAGTCCGCCTGGAGCAGAAAATGCCCACGCTACTGCGGGTTTATATAGACGGTCCTCACGGG
ATGGGGAAAACCACCACCACGCAACTGCTGGTGGCCCTGGGTTCGCGCGACGATATCGTCTACGT
ACCCGAGCCGATGACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCTACACCA
CACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGTAATGACAAGCGCC
CAGATAACAATGGGCATGCCTTATGCCGTGACCGACGCCGTTCTGGCTCCTCATATCGGGGGGA
GGCTGGGAGCTCACATGCCCCGCCCCCGGCCCTCACCCTCATCTTCGACCGCCATCCCATCGCCGC
CCTCCTGTGCTACCCGGCCGCGCGATACCTTATGGGCAGCATGACCCCCCAGGCCGTGCTGGCGTT
CGTGGCCCTCATCCCGCCGACCTTGCCCGGCACAAACATCGTGTTGGGGGCCCTTCCGGAGGACA
GACACATCGACCGCCTGGCCAAACGCCAGCGCCCCGGCGAGCGGCTTGACCTGGCTATGCTGGCC
GCGATTCGCCGCGTTTACGGGCTGCTTGCCAATACGGTGCGGTATCTGCAGGGCGGCGGGTCGTG
GCGGGAGGATTGGGGACAGCTTTCGGGGACGGCCGTGCCGCCCCAGGGTGCCGAGCCCCAGAGCA
ACGCGGGCCCACGACCCCATATCGGGGACACGTTATTTACCCTGTTTCGGGCCCCCGAGTTGCTG
GCCCCCAACGGCGACCTGTACAACGTGTTTGCCTGGGCCTTGGACGTCTTGGCCAAACGCCTCCG
TCCCATGCACGTCTTTATCCTGGATTACGACCAATCGCCCGCCGGCTGCCGGGACGCCCTGCTGCA
ACTTACCTCCGGGATGGTCCAGACCCACGTCACCACCCCCGGCTCCATACCGACGATCTGCGACCT
GGCGCGCACGTTTGCCCGGGAGATGGGGGAGGCTAACTGAGGATCCCACGTCACTATTGTATACT
CTATATTATACTCTATGTTATACTCTGTAATCCTACTCAATAAACGTGTCACGCCTGTGAAACCG
TACTAAGTCTCCCGTGTCTTCTTATCACCATCAGGTGACATCCTCGCCCAGGCTGTCAATCATGC
CGGTATCGATTCCAGTAGCACCGGCCCCACGCTGACAACCCACTCTTGCAGCGTTAGCAGCGCCCC
TCTTAACAAGCCGACCCCCACCAGCGTCGCGGTTACTAACACTCCTCTCCCCGACCTGCAGCCCAA
TCATTCAGTGGTTGCATTTCTTGTGTTGTAAATAGAGTTATAGTTAAAATTGTTATAGTTAAAT

AGAGTACGTGTTATAGTTAGAGTATGTCATATCACTAAAAGGTGATTAGTTTGAATTAACAGAA
GAGTTTCAAAGGATAGTTTGTACCTCTGTCTAGGTATAGCAAGTCTCATTAAGTGTTTTCCAGG
GATATGTCTTGTGGATCCTGTTTTAATGAATGGAGAACATTCATTTTCAGGGTTTTAATTTTAG
AGTACATCTAAAGTGCTAGAAGGTTAATTGTCCTCTGTCCCCTTACCTTTTTGCACTACTCATTT
GTCCTGGGCTCTGCTTCTTGCTCTTTTCCACATGATGGCCCACCTAGCAAATGATCATAATTGTA
AGGCACATAGAGAAGCAGATGAGGTGCTGACTCCAGAGGTGGATACCTTGGGGCCTCTGTACCCC
AGGCCTGCCTGACTGCCTCATGGGCTGAAGGCTTAATACCTTCAGCACACTAATGTACTGCTACA
TATAGGTTGGGAAACTCTAGGCCAAATTTGGAGCCAGAAGTTGAGTCATTCAAGATTGCTGATA
TACAAATGAATATGCTTTTGTTGAATTTGTCCCATCAAAATTGGAAGTATAGCATTCTGGTAAG
TGAAAGACTAAAACAAGGAAGTCCAGGGCTTAAAAAAAAAAAAAAACTTATAGCTAGTTAAACT
ACAACACGTTAAAATATCCTCCTAAGTGAGCCAGGAGTTTGGTAGCAGGTGTCCAGCTGAAGAC
TTGGTGACAGAGTCTATTTAAATGTAAGAACATGGCTGATTATTTCTTATAGAAGaagttggattcca
tgGACTACAAAGACGATGACGACAAGTACCCATACGATGTTCCAGATTACGCTggttccaagagaagaa
gagctacctccccttccagcagtgtcagcggggactttgatgatgggcaccattctgtgtcaacaccaggcccaagcaggaaaagg
aggagactttccaatcttccaactgtagatcctGTGAGTAACTTGGATTACATGGGGGACAACTTTATTATACA
AAGTTGTTGTCTGCTCTGACCCGACCATCataacttcgtataatgtatgctatacgaagttatccatagagcccaccgc
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gacaatgcgatgcaatttcctcattttattaggaaaggacagtgggagtggcaccttccagggtcaaggaaggcacgggggagggg
caaacaacagatggctggcaactagaaggcacagttaCTTGTACAGCTCGTCCATGCCGAGAGTGATCCCGGCG
GCGGTCACGAACTCCAGCAGGACCATGTGATCGCGCTTCTCGTTGGGGTCTTTGCTCAGGGCGGA
CTGGGTGCTCAGGTAGTGGTTGTCGGGCAGCAGCACGGGGCCGTCGCCGATGGGGGTGTTCTGCT
GGTAGTGGTCGGCGAGCTGCACGCTGCCGTCCTCGATGTTGTGGCGGATCTTGAAGTTCACCTTG
ATGCCGTTCTTCTGCTTGTCGGCCATGATATAGACGTTGTGGCTGTTGTAGTTGTACTCCAGCTT
GTGCCCCAGGATGTTGCCGTCCTCCTTGAAGTCGATGCCCTTCAGCTCGATGCGGTTCACCAGGG
TGTCGCCCTCGAACTTCACCTCGGCGCGGGTCTTGTAGTTGCCGTCGTCCTTGAAGAAGATGGTG
CGCTCCTGGACGTAGCCTTCGGGCATGGCGGACTTGAAGAAGTCGTGCTGCTTCATGTGGTCGGG
GTAGCGGCTGAAGCACTGCACGCCGTAGGTCAGGGTGGTCACGAGGGTGGGCCAGGGCACGGGCA
GCTTGCCGGTGGTGCAGATGAACTTCAGGGTCAGCTTGCCGTAGGTGGCATCGCCCTCGCCCTCG
CCGGACACGCTGAACTTGTGGCCGTTTACGTCGCCGTCCAGCTCGACCAGGATGGGCACCACCCC
GGTGAACAGCTCCTCGCCCTTGCTCACTGGGCCAGGATTCTCCTCGACGTCACCGCATGTTAGCA
GACTTCCTCTGCCCTCTCCACTGCCggcaccgggcttgcgggtcatgcaccaggtgcgcggtccttcgggcacctcgac
gtcggcggtgacggtgaagccgagccgctcgtagaaggggaggttgcggggcgcggaggtctccaggaaggcgggcaccccggc
gcgctcggccgcctccactccggggagcacgacggcgctgcccagacccttgccctggtggtcgggcgagacgccgacggtggcc
aggaaccacgcgggctccttgggccggtgcggcgccaggaggccttccatctgttgctgcgcggccagccgggaaccgctcaactc
ggccatgcgcgggccgatctcggcgaacaccgcccccgcttcgacgctctccggcgtggtccagaccgccaccgcggcgccgtcgt
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gatcgacggtgtggcgcgtggcggggtagtcggcgaacgcggcggcgagggtgcgtacggccctggggacgtcgtcgcgggtggc
gaggcgcaccgtgggcttgtactcggtCATGGTAAGCTTGGGCTGCAGGTCGAAAGGCCCGGAGATGAGGA
AGAGGAGAACAGCGCGGCAGACGTGCGCTTTTGAAGCGTGCAGAATGCCGGGCCTCCGGAGGACC

TTCGGGCGCCCGCCCCGCCCCTGAGCCCGCCCCTGAGCCCGCCCCCGGACCCACCCCTTCCCAGCCTCTGAGCCCAGAAAGCGAAGGAGCAAAGCTGCTATTGGCCGCTGCCCCAAAGGCCTACCCGCTTCCATTGCTCAGCGGTGCTGTCCATCTGCACGAGACTAGTGAGACGTGCTACTTCCATTTGTCACGTCCTGCACGACGCGAGCTGCGGGGCGGGGGGGAACTTCCTGACTAGGGGAGGAGTAGAAGGTGGCGCGAAGGGGCCACCAAAGAACGGAGCCGGTTGGCGCCTACCGGataacttcgtataatgtatgctatacgaagttatccttggatgccgtacgctgatCAACTTTGTATAGAAAAGTTGTCCCCGTTTCTGCCTGCTCTTCCCACAATTCCCCTATCTTCCCTTTAATGGTAAAATTGTTACGATGCAAGGCATCTCCACTTTTTTAAGATTCTCTTGATTAATAGTCTTTTCTTTTATGAACATTATGTATTCAGCTAAGTCTTAGAGTAATAGTGTGATCTTATGAATAATTTCAGTATGTTACATCATATATTAATTCAGCAAATAACTGTGTGACTATCATGTGACAAGCACTGTTCTCATGGTTGGGATATAGCCATGTGGGAAACAAGCCCATTTTTCACATGGAACTTAGATTCCAGGCGGGGGAAGTAGAATGTAAACAAGTAAACGAATAAAGAATAATGTATCCTTAGCTAGTAATAAGTGCTAAGAAGAAAATTTTGGGTGATTTGGGCTGTTTTGGCCTGAATTCGCTGGAAGAGAGTTCCAGACAGAACCAGTGCAGAGGGGTTGGGTCAGGGATGAGTTTGTGTGTCTTGGTTACAGAGCAGGGGATGGTCAGGAAGGAGAAGGAAACTGGCAAGCTCCACCCATTCAGAGTATGTAGGGCCCACACAAGCAATGTTTGGAGTTTAGATTTTATTCTCTGTGAAGTGATAAACCCTTCTGTCAGATGGCTTTAAGCAAGAGAGTGATAAACTGATTTAGTTTCAAAGAAGAAAACCCTTCAATTGGATGACTTTAAGCAAGAAAGTGATGAACTGATATAGTTTAGAAGACAAAATCACCAGGAGCATAAATCTGATGAAAGATACCAAAAAGTTAGTCAACTCAGTTGTTTGAAAGGAGACATATTGTCAGCATATTTCAGACTTTAGCATGTTTGGTAATATTGAGAGTCATCATTTTTCTTCTCTACTTGCCTTTTATTGAAGAGTAGAAAATAATTCTTATGTCTACACTGGCTTTCTGTTCACTTTTTTAGTGATTTTTTTCTCCTTTGCTAATGTGTAGATTGCCGTGTGCCATGAACTCTATAATACCATCCGAGACTATAAGGATGAACAGGGCAGACTTCTCTGTGAGCTCTTCATTAGGGCACCAAAGCGAAGGTGAGTTCGAAGC

Table S1. Proteins Identified by Mass Spectrometry in Different Cell Lines as Shown in Fig. 2

IP Mass Spec Proteins in 786-O

Unique	Total	reference	Gene Symbol	AVG
13	15	Q9Y2W1_TR150_HUMAN	THRAP3	2.5283
9	9	P11387_TOP1_HUMAN	TOP1	2.4151
8	8	P23246_SFPQ_HUMAN	SFPQ	3.2386
7	29	IGKC_MOUSE		2.8303
6	9	Q9NYF8_BCLF1_HUMAN	BCLAF1	3.0831
6	6	P11182_ODB2_HUMAN	DBT	2.7257
5	13	IGH1M_MOUSE	Ighg1	3.0134
5	7	IGHM_MOUSE	Igh-6	3.1822
5	5	Q6UWP8_SBSN_HUMAN	SBSN	3.8606
4	4	P04040_CATA_HUMAN	CAT	3.1957
4	4	Q6ZVX7_FBX50_HUMAN	NCCRP1	2.7568
3	5	Q8IX12_CCAR1_HUMAN	CCAR1	2.5355
3	4	P06748_NPM_HUMAN	NPM1	2.5492
3	3	HVM27_MOUSE		3.4837
3	3	P19338_NUCL_HUMAN	NCL	2.5834
3	3	P07355_ANXA2_HUMAN	ANXA2	2.5205
3	3	P68104_EF1A1_HUMAN	EEF1A1	2.4626
3	3	P10599_THIO_HUMAN	TXN	2.1513
2	6	KV2A7_MOUSE		2.9263
2	4	O14786_NRP1_HUMAN	NRP1	3.8512
2	3	P51991_ROA3_HUMAN	HNRNPA3	2.5589
2	3	O75223_GGCT_HUMAN	GGCT	2.1911
2	2	Q9HCY8_S10AE_HUMAN	S100A14	3.497
2	2	P62736_ACTA_HUMAN	ACTA2	3.0297
2	2	P62987_RL40_HUMAN	UBA52	2.9815
2	2	P62753_RS6_HUMAN	RPS6	2.9039
2	2	IGHG3_MOUSE		2.6884
2	2	Q02878_RL6_HUMAN	RPL6	2.6044
2	2	O75533_SF3B1_HUMAN	SF3B1	2.5284
2	2	Q00839_HNRPU_HUMAN	HNRNPU	2.4796
2	2	Q9NR30_DDX21_HUMAN	DDX21	2.4489
2	2	P62263_RS14_HUMAN	RPS14	2.3859
2	2	Q15233_NONO_HUMAN	NONO	2.343
2	2	P22626_ROA2_HUMAN	HNRNPA2B1	2.0091
2	2	P36578_RL4_HUMAN	RPL4	1.9971
2	2	Q7Z478_DHX29_HUMAN	DHX29	1.9621
2	2	Q13435_SF3B2_HUMAN	SF3B2	1.8396
1	30	P05067_A4_HUMAN	APP	3.2043
1	2	P05387_RLA2_HUMAN	RPLP2	4.0805
1	2	P05386_RLA1_HUMAN	RPLP1	4.032
1	2	Q15517_CDSN_HUMAN	CDSN	3.2628

1	2	P63173_RL38_HUMAN	RPL38	3.0967
1	2	Q96HS1_PGAM5_HUMAN	PGAM5	2.8005
1	2	SjGST_Schistosoma		2.149
1	2	P15311_EZRI_HUMAN	EZR	2.0666
1	2	Q7Z417_NUFP2_HUMAN	NUFIP2	1.9087
1	1	Q13867_BLMH_HUMAN	BLMH	5.0387
1	1	Q16610_ECM1_HUMAN	ECM1	3.792
1	1	P67809_YBOX1_HUMAN	YBX1	3.6917
1	1	Q9UH99_SUN2_HUMAN	SUN2	3.6246
1	1	P54792_DVLP1_HUMAN	DVL1P1	3.5738
1	1	P46821_MAP1B_HUMAN	MAP1B	3.4186
1	1	Q9H3D4_P63_HUMAN	TP63	3.261
1	1	P11142_HSP7C_HUMAN	HSPA8	3.2268
1	1	IgG1_bovine		3.0331
1	1	P47914_RL29_HUMAN	RPL29	3.0107
1	1	P19474_RO52_HUMAN	TRIM21	2.9487
1	1	Q07065_CKAP4_HUMAN	CKAP4	2.666
1	1	O60506_HNRPQ_HUMAN	SYNCRIP	2.6593
1	1	Q02539_H11_HUMAN	HIST1H1A	2.6295
1	1	P62917_RL8_HUMAN	RPL8	2.6261
1	1	Q86YP4_P66A_HUMAN	GATAD2A	2.6003
1	1	Q14839_CHD4_HUMAN	CHD4	2.5478
1	1	O95232_LC7L3_HUMAN	LUC7L3	2.5181
1	1	P39023_RL3_HUMAN	RPL3	2.3928
1	1	P07900_HS90A_HUMAN	HSP90AA1	2.392
1	1	Q9UNX3_RL26L_HUMAN	RPL26L1	2.3827
1	1	P16401_H15_HUMAN	HIST1H1B	2.3391
1	1	O75635_SPB7_HUMAN	SERPINB7	2.2902
1	1	P07437_TBB5_HUMAN	TUBB	2.2873
1	1	Q96P65_QRFPR_HUMAN	QRFPR	2.278
1	1	P23396_RS3_HUMAN	RPS3	2.2436
1	1	P35030_TRY3_HUMAN	PRSS3	2.2327
1	1	P28074_PSB5_HUMAN	PSMB5	2.1962
1	1	Q9GZS1_RPA49_HUMAN	POLR1E	2.1885
1	1	Q8IXB1_DJC10_HUMAN	DNAJC10	2.1825
1	1	Q15828_CYTM_HUMAN	CST6	2.165
1	1	P84103_SRSF3_HUMAN	SRSF3	2.1541
1	1	P02545_LMNA_HUMAN	LMNA	2.1278
1	1	Q14568_HS902_HUMAN	HSP90AA2	2.0943
1	1	P11279_LAMP1_HUMAN	LAMP1	2.0521
1	1	Q12906_ILF3_HUMAN	ILF3	2.0465
1	1	P32119_PRDX2_HUMAN	PRDX2	1.9705
1	1	Q6NVV1_R13P3_HUMAN	RPL13AP3	1.9644
1	1	P38646_GRP75_HUMAN	HSPA9	1.9023

IP Mass Spec Proteins in 786-O-BKI

Unique	Total	reference	Gene Symbol	AVG
92	503	Q86U86_PB1_HUMAN	PBRM1	2.8218
55	204	Q8TAQ2_SMRC2_HUMAN	SMARCC2	3.0684
51	176	P51531_SMCA2_HUMAN	SMARCA2	3.0112
49	163	Q92922_SMRC1_HUMAN	SMARCC1	3.206
46	169	Q68CP9_ARID2_HUMAN	ARID2	3.1321
42	53	P46013_KI67_HUMAN	MKI67	2.8771
35	82	P51532_SMCA4_HUMAN	SMARCA4	3.2409
34	49	P11388_TOP2A_HUMAN	TOP2A	2.9472
31	139	Q9NPI1_BRD7_HUMAN	BRD7	3.184
28	38	Q9NR30_DDX21_HUMAN	DDX21	2.9478
27	110	Q969G3_SMCE1_HUMAN	SMARCE1	2.8946
26	30	Q02880_TOP2B_HUMAN	TOP2B	3.0933
20	50	Q96GM5_SMRD1_HUMAN	SMARCD1	3.017
20	21	Q08211_DHX9_HUMAN	DHX9	2.8281
19	71	Q8WUB8_PHF10_HUMAN	PHF10	3.0336
18	24	P19338_NUCL_HUMAN	NCL	3.0049
16	36	Q92925_SMRD2_HUMAN	SMARCD2	2.8418
14	47	O96019_ACL6A_HUMAN	ACTL6A	2.782
14	15	P46087_NOP2_HUMAN	NOP2	2.9216
13	24	P52292_IMA1_HUMAN	KPNA2	3.1561
13	15	P18124_RL7_HUMAN	RPL7	2.5242
13	14	Q14676_MDC1_HUMAN	MDC1	3.4353
12	16	P11387_TOP1_HUMAN	TOP1	2.2997
11	28	Q12824_SNF5_HUMAN	SMARCB1	2.6286
11	21	P36578_RL4_HUMAN	RPL4	2.3317
11	20	Q13127_REST_HUMAN	REST	2.7965
11	20	P62701_RS4X_HUMAN	RPS4X	2.6156
11	14	Q6STE5_SMRD3_HUMAN	SMARCD3	3.2784
11	13	Q14669_TRIPC_HUMAN	TRIP12	3.2688
10	38	P39023_RL3_HUMAN	RPL3	2.7817
10	19	Q02878_RL6_HUMAN	RPL6	2.5274
10	14	Q9Y2W1_TR150_HUMAN	THRAP3	2.5016
10	13	P62424_RL7A_HUMAN	RPL7A	2.6929
10	11	Q07065_CKAP4_HUMAN	CKAP4	3.1995
10	10	O00567_NOP56_HUMAN	NOP56	2.5777
9	28	Q4VC05_BCL7A_HUMAN	BCL7A	3.0672
9	16	P15880_RS2_HUMAN	RPS2	2.3496
9	15	P46781_RS9_HUMAN	RPS9	2.4412
9	11	Q99575_POP1_HUMAN	POP1	3.2325
9	11	P22626_ROA2_HUMAN	HNRNPA2B1	3.0128
9	9	P38646_GRP75_HUMAN	HSPA9	3.5756
8	17	P23396_RS3_HUMAN	RPS3	2.5766
8	10	Q00839_HNRPU_HUMAN	HNRNPU	2.9276
8	9	P61247_RS3A_HUMAN	RPS3A	2.4322
8	8	P11021_GRP78_HUMAN	HSPA5	3.826

7	90	IGKC_MOUSE		2.912
7	17	P26373_RL13_HUMAN	RPL13	3.0663
7	17	P62736_ACTA_HUMAN	ACTA2	2.6544
7	10	P05387_RLA2_HUMAN	RPLP2	3.5922
7	10	P62917_RL8_HUMAN	RPL8	2.3188
7	8	Q9NVP1_DDX18_HUMAN	DDX18	2.6492
7	7	Q8IY81_SPB1_HUMAN	FTSJ3	3.3775
7	7	O60264_SMCA5_HUMAN	SMARCA5	2.9057
7	7	P11142_HSP7C_HUMAN	HSPA8	2.8269
6	16	P62241_RS8_HUMAN	RPS8	2.5103
6	15	IGH1M_MOUSE	Ighg1	2.7697
6	11	IGHM_MOUSE	Igh-6	2.9224
6	9	P06748_NPM_HUMAN	NPM1	3.1094
6	8	P52272_HNRPM_HUMAN	HNRNPM	2.9015
6	7	P67809_YBOX1_HUMAN	YBX1	3.8734
6	6	P35251_RFC1_HUMAN	RFC1	3.17
6	6	Q8IYB3_SRRM1_HUMAN	SRRM1	3.0596
6	6	Q9NW13_RBM28_HUMAN	RBM28	2.6255
6	6	P46778_RL21_HUMAN	RPL21	2.4685
6	6	P62750_RL23A_HUMAN	RPL23A	2.378
6	6	Q5SSJ5_HP1B3_HUMAN	HP1BP3	2.3297
5	14	P62753_RS6_HUMAN	RPS6	3.5774
5	12	Q96HS1_PGAM5_HUMAN	PGAM5	2.375
5	7	P61313_RL15_HUMAN	RPL15	2.5994
5	6	Q8NHW5_RLA0L_HUMAN	RPLP0P6	3.1625
5	6	P62269_RS18_HUMAN	RPS18	3.07
5	6	P62249_RS16_HUMAN	RPS16	2.5535
5	6	Q99848_EBP2_HUMAN	EBNA1BP2	2.4254
5	5	Q8TDN6_BRX1_HUMAN	BRIX1	3.2805
5	5	Q14839_CHD4_HUMAN	CHD4	3.1742
5	5	P23246_SFPQ_HUMAN	SFPQ	3.0783
5	5	Q9NUQ6_SPS2L_HUMAN	SPATS2L	3.0183
5	5	P46777_RL5_HUMAN	RPL5	2.8456
5	5	P62277_RS13_HUMAN	RPS13	2.6021
5	5	Q9BZE4_NOG1_HUMAN	GTPBP4	2.5921
5	5	Q9BQ39_DDX50_HUMAN	DDX50	2.3618
5	5	P18621_RL17_HUMAN	RPL17	2.1196
4	15	P60709_ACTB_HUMAN	ACTB	3.6641
4	12	P18077_RL35A_HUMAN	RPL35A	1.7926
4	10	Q8WUZ0_BCL7C_HUMAN	BCL7C	3.932
4	7	P51991_ROA3_HUMAN	HNRNPA3	3.1347
4	5	Q07020_RL18_HUMAN	RPL18	3.3983
4	5	Q14690_RRP5_HUMAN	PDCD11	2.7832
4	5	O60832_DKC1_HUMAN	DKC1	2.6739
4	5	P49207_RL34_HUMAN	RPL34	2.0639
4	5	P40429_RL13A_HUMAN	RPL13A	1.8756
4	4	Q12873_CHD3_HUMAN	CHD3	3.0535

4	4	Q9UH99_SUN2_HUMAN	SUN2	2.9634
4	4	Q92841_DDX17_HUMAN	DDX17	2.9203
4	4	Q7Z2W4_ZCCHV_HUMAN	ZC3HAV1	2.8214
4	4	Q71U36_TBA1A_HUMAN	TUBA1A	2.7893
4	4	P62266_RS23_HUMAN	RPS23	2.7456
4	4	P17480_UBF1_HUMAN	UBTF	2.5288
4	4	Q9UNX3_RL26L_HUMAN	RPL26L1	2.4165
4	4	IGHG3_MOUSE		2.3987
4	4	Q9BQG0_MBB1A_HUMAN	MYBBP1A	2.3081
4	4	P62280_RS11_HUMAN	RPS11	1.8191
3	8	HVM27_MOUSE		3.3586
3	6	F8VXC8_F8VXC8_HUMAN	SMARCC2	3.1462
3	5	P46779_RL28_HUMAN	RPL28	1.9518
3	4	P31943_HNRH1_HUMAN	HNRNPH1	3.4635
3	4	Q12905_ILF2_HUMAN	ILF2	3.4294
3	4	P62847_RS24_HUMAN	RPS24	3.0842
3	4	P62913_RL11_HUMAN	RPL11	2.8795
3	4	Q12906_ILF3_HUMAN	ILF3	2.8626
3	4	Q86UE4_LYRIC_HUMAN	MTDH	2.5944
3	4	Q6NVV1_R13P3_HUMAN	RPL13AP3	2.2054
3	4	P46776_RL27A_HUMAN	RPL27A	2.0871
3	3	Q13435_SF3B2_HUMAN	SF3B2	3.5113
3	3	Q9Y383_LC7L2_HUMAN	LUC7L2	3.4097
3	3	P30050_RL12_HUMAN	RPL12	3.3471
3	3	Q13151_ROA0_HUMAN	HNRNPA0	3.2438
3	3	P39019_RS19_HUMAN	RPS19	3.2157
3	3	P32969_RL9_HUMAN	RPL9	3.1719
3	3	O43390_HNRPR_HUMAN	HNRNPR	3.1014
3	3	P16403_H12_HUMAN	HIST1H1C	3.0787
3	3	O95793_STAU1_HUMAN	STAU1	3.052
3	3	P16989_YBOX3_HUMAN	YBX3	3.0122
3	3	Q8NFW8_NEUA_HUMAN	CMAS	2.9737
3	3	P50914_RL14_HUMAN	RPL14	2.9341
3	3	P09651_ROA1_HUMAN	HNRNPA1	2.9194
3	3	P62906_RL10A_HUMAN	RPL10A	2.8643
3	3	P38159_RBMX_HUMAN	RBMX	2.8517
3	3	P07355_ANXA2_HUMAN	ANXA2	2.8415
3	3	O76021_RL1D1_HUMAN	RSL1D1	2.7124
3	3	O00505_IMA4_HUMAN	KPNA3	2.5326
3	3	O15523_DDX3Y_HUMAN	DDX3Y	2.4701
3	3	P62910_RL32_HUMAN	RPL32	2.3351
3	3	Q14684_RRP1B_HUMAN	RRP1B	2.3345
3	3	Q8N9T8_KRI1_HUMAN	KRI1	2.1844
2	29	P01605_KV113_HUMAN		2.2897
2	19	P05067_A4_HUMAN	APP	2.8712
2	16	P62263_RS14_HUMAN	RPS14	2.4346
2	9	P05386_RLA1_HUMAN	RPLP1	3.9504

2	8	P84098_RL19_HUMAN	RPL19	2.672
2	7	KV2A7_MOUSE		2.8615
2	7	P06312_KV401_HUMAN	IGKV4-1	2.6215
2	5	Q9BYX7_ACTBM_HUMAN	POTEKP	3.2365
2	4	Q86VM9_ZCH18_HUMAN	ZC3H18	3.0244
2	3	P05388_RLA0_HUMAN	RPLP0	3.7361
2	3	O95602_RPA1_HUMAN	POLR1A	3.3871
2	3	O00629_IMA3_HUMAN	KPNA4	3.2909
2	3	P22087_FBRL_HUMAN	FBL	3.2694
2	3	P61513_RL37A_HUMAN	RPL37A	3.1902
2	3	Q49A26_GLYR1_HUMAN	GLYR1	3.0821
2	3	P27635_RL10_HUMAN	RPL10	3.0543
2	3	Q86YP4_P66A_HUMAN	GATAD2A	2.8011
2	3	Q5JNZ5_RS26L_HUMAN	RPS26P11	2.4885
2	3	Q9Y3U8_RL36_HUMAN	RPL36	2.1392
2	3	Q9BU76_MMTA2_HUMAN	MMTAG2	2.12
2	3	P62851_RS25_HUMAN	RPS25	1.7435
2	2	Q6UWP8_SBSN_HUMAN	SBSN	4.3559
2	2	Q14692_BMS1_HUMAN	BMS1	4.0248
2	2	Q86V81_THOC4_HUMAN	ALYREF	4.0079
2	2	Q9Y2X3_NOP58_HUMAN	NOP58	3.9655
2	2	Q14498_RBM39_HUMAN	RBM39	3.931
2	2	P40938_RFC3_HUMAN	RFC3	3.8101
2	2	P16401_H15_HUMAN	HIST1H1B	3.4144
2	2	Q02539_H11_HUMAN	HIST1H1A	3.3074
2	2	P35637_FUS_HUMAN	FUS	3.2743
2	2	P47914_RL29_HUMAN	RPL29	3.1194
2	2	O75533_SF3B1_HUMAN	SF3B1	3.1017
2	2	Q5JTH9_RRP12_HUMAN	RRP12	3.0428
2	2	P35250_RFC2_HUMAN	RFC2	2.9804
2	2	P61978_HNRPK_HUMAN	HNRNPK	2.9687
2	2	P0CW22_RS17L_HUMAN	RPS17L	2.8971
2	2	Q9GZR7_DDX24_HUMAN	DDX24	2.8819
2	2	P52294_IMA5_HUMAN	KPNA1	2.8502
2	2	Q1ED39_KNOP1_HUMAN	KNOP1	2.7687
2	2	Q8TDD1_DDX54_HUMAN	DDX54	2.7645
2	2	Q9NP64_NO40_HUMAN	ZCCHC17	2.7279
2	2	P54652_HSP72_HUMAN	HSPA2	2.6813
2	2	P21333_FLNA_HUMAN	FLNA	2.672
2	2	P62987_RL40_HUMAN	UBA52	2.6333
2	2	P62081_RS7_HUMAN	RPS7	2.5949
2	2	O94776_MTA2_HUMAN	MTA2	2.5937
2	2	P62805_H4_HUMAN	HIST1H4A	2.5526
2	2	O43143_DHX15_HUMAN	DHX15	2.5251
2	2	Q96GQ7_DDX27_HUMAN	DDX27	2.49
2	2	P62244_RS15A_HUMAN	RPS15A	2.4091
2	2	Q9UIG0_BAZ1B_HUMAN	BAZ1B	2.4078

2	2	P62899_RL31_HUMAN	RPL31	2.3805
2	2	Q9UQ35_SRRM2_HUMAN	SRRM2	2.3455
2	2	Q13428_TCOF_HUMAN	TCOF1	2.3375
2	2	O15446_RPA34_HUMAN	CD3EAP	2.2507
2	2	Q969P6_TOP1M_HUMAN	TOP1MT	2.0773
2	2	Q02543_RL18A_HUMAN	RPL18A	2.0679
2	2	Q9GZS1_RPA49_HUMAN	POLR1E	2.0165
2	2	Q9NYF8_BCLF1_HUMAN	BCLAF1	1.9936
2	2	P62829_RL23_HUMAN	RPL23	1.74
2	2	P83881_RL36A_HUMAN	RPL36A	1.6151
2	2	Q9H6R4_NOL6_HUMAN	NOL6	1.5202
2	2	P68104_EF1A1_HUMAN	EEF1A1	1.4697
1	12	Q9C0D2_CE295_HUMAN	CEP295	1.6329
1	3	P46459_NSF_HUMAN	NSF	2.0605
1	2	O95232_LC7L3_HUMAN	LUC7L3	4.7504
1	2	P63173_RL38_HUMAN	RPL38	3.5375
1	2	P83731_RL24_HUMAN	RPL24	2.5144
1	2	SjGST_Schistosoma		2.1298
1	2	Q9GZU3_TM39B_HUMAN	TMEM39B	1.6444
1	2	Q8TB03_CX038_HUMAN	CXorf38	1.5089
1	1	Q9HCY8_S10AE_HUMAN	S100A14	4.8442
1	1	C9J053_C9J053_HUMAN	PBRM1	4.5572
1	1	P62995_TRA2B_HUMAN	TRA2B	4.4574
1	1	P05141_ADT2_HUMAN	SLC25A5	4.1286
1	1	P60866_RS20_HUMAN	RPS20	3.8495
1	1	Q9Y2R4_DDX52_HUMAN	DDX52	3.7688
1	1	Q9H7E9_CH033_HUMAN	C8orf33	3.7686
1	1	Q7Z2T5_TRM1L_HUMAN	TRMT1L	3.7216
1	1	G5E975_G5E975_HUMAN	SMARCB1	3.7005
1	1	O96028_NSD2_HUMAN	WHSC1	3.6673
1	1	P62857_RS28_HUMAN	RPS28	3.5628
1	1	P04908_H2A1B_HUMAN	HIST1H2AB	3.5358
1	1	Q9UKV3_ACINU_HUMAN	ACIN1	3.4542
1	1	O75223_GGCT_HUMAN	GGCT	3.4491
1	1	P63208_SKP1_HUMAN	SKP1	3.3835
1	1	O14786_NRP1_HUMAN	NRP1	3.336
1	1	P33778_H2B1B_HUMAN	HIST1H2BB	3.3221
1	1	P49411_EFTU_HUMAN	TUFM	3.322
1	1	Q13823_NOG2_HUMAN	GNL2	3.3198
1	1	Q15517_CDSN_HUMAN	CDSN	3.3051
1	1	Q9H4L4_SENP3_HUMAN	SENP3	3.292
1	1	P34931_HS71L_HUMAN	HSPA1L	3.2888
1	1	O60506_HNRPQ_HUMAN	SYNCRIP	3.2651
1	1	P12273_PIP_HUMAN	PIP	3.2564
1	1	Q9H3D4_P63_HUMAN	TP63	3.2364
1	1	Q9NQ39_RS10L_HUMAN	RPS10P5	3.2156
1	1	P62854_RS26_HUMAN	RPS26	3.2151

1	1	P62888_RL30_HUMAN	RPL30	3.1392
1	1	Q6ZVX7_FBX50_HUMAN	NCCRP1	3.1173
1	1	Q07021_C1QBP_HUMAN	C1QBP	3.1161
1	1	Q13885_TBB2A_HUMAN	TUBB2A	3.0862
1	1	P56182_RRP1_HUMAN	RRP1	2.9618
1	1	Q96KR1_ZFR_HUMAN	ZFR	2.9503
1	1	P61956_SUMO2_HUMAN	SUMO2	2.9451
1	1	B7ZW38_HNRC3_HUMAN	HNRNPCL3	2.8468
1	1	P42766_RL35_HUMAN	RPL35	2.8349
1	1	P78527_PRKDC_HUMAN	PRKDC	2.8326
1	1	P07437_TBB5_HUMAN	TUBB	2.8047
1	1	O94906_PRP6_HUMAN	PRPF6	2.7103
1	1	Q7Z478_DHX29_HUMAN	DHX29	2.6858
1	1	IgG1_bovine		2.673
1	1	P78362_SRPK2_HUMAN	SRPK2	2.6471
1	1	P46783_RS10_HUMAN	RPS10	2.6423
1	1	P53007_TXTP_HUMAN	SLC25A1	2.5907
1	1	Q9NRL2_BAZ1A_HUMAN	BAZ1A	2.5246
1	1	P23458_JAK1_HUMAN	JAK1	2.5221
1	1	Q58FF7_H90B3_HUMAN	HSP90AB3P	2.5
1	1	Q14444_CAPR1_HUMAN	CAPRIN1	2.4985
1	1	Q96L21_RL10L_HUMAN	RPL10L	2.467
1	1	P46821_MAP1B_HUMAN	MAP1B	2.466
1	1	Q08170_SRSF4_HUMAN	SRSF4	2.4522
1	1	F5H3T4_F5H3T4_HUMAN	SLC38A10	2.4521
1	1	P62861_RS30_HUMAN	FAU	2.3883
1	1	P12235_ADT1_HUMAN	SLC25A4	2.3848
1	1	Q16695_H31T_HUMAN	HIST3H3	2.3767
1	1	Q15431_SYCP1_HUMAN	SYCP1	2.3416
1	1	Q96T37_RBM15_HUMAN	RBM15	2.2946
1	1	P35268_RL22_HUMAN	RPL22	2.2816
1	1	P55769_NH2L1_HUMAN	NHP2L1	2.2511
1	1	Q15365_PCBP1_HUMAN	PCBP1	2.2449
1	1	Q9BRJ6_CG050_HUMAN	C7orf50	2.2328
1	1	P10599_THIO_HUMAN	TXN	2.1754
1	1	P02649_APOE_HUMAN	APOE	2.1676
1	1	Q96PK6_RBM14_HUMAN	RBM14	2.1096
1	1	P35249_RFC4_HUMAN	RFC4	2.0877
1	1	Q9UPR3_SMG5_HUMAN	SMG5	2.0652
1	1	Q96QV6_H2A1A_HUMAN	HIST1H2AA	2.0324
1	1	O75509_TNR21_HUMAN	TNFRSF21	2.0157
1	1	Q06830_PRDX1_HUMAN	PRDX1	1.9801
1	1	Q9BV38_WDR18_HUMAN	WDR18	1.9773
1	1	P02788_TRFL_HUMAN	LTF	1.9569
1	1	Q15233_NONO_HUMAN	NONO	1.9515
1	1	H0Y5B5_H0Y5B5_HUMAN	PBRM1	1.9238
1	1	Q9NVI7_ATD3A_HUMAN	ATAD3A	1.8753

1	1	Q969Q0_RL36L_HUMAN	RPL36AL	1.8661
1	1	Q13433_S39A6_HUMAN	SLC39A6	1.8595
1	1	O60293_ZC3H1_HUMAN	ZFC3H1	1.8351
1	1	P10809_CH60_HUMAN	HSPD1	1.8168
1	1	Q86V15_CASZ1_HUMAN	CASZ1	1.7977
1	1	P56537_IF6_HUMAN	EIF6	1.7887
1	1	Q9Y3C1_NOP16_HUMAN	NOP16	1.7582
1	1	P51589_CP2J2_HUMAN	CYP2J2	1.7391
1	1	Q9H307_PININ_HUMAN	PNN	1.6524
1	1	P12532_KCRU_HUMAN	CKMT1A	1.6148
1	1	Q9NT68_TEN2_HUMAN	TENM2	1.6017
1	1	F8WDE1_F8WDE1_HUMAN	IFNAR2	1.5519

IP Mass Spec Proteins in A704-BAF180WT

Unique	Total	reference	Gene Symbol	AVG
114	938	Q86U86_PB1_HUMAN	PBRM1	3.002
58	313	Q8TAQ2_SMRC2_HUMAN	SMARCC2	3.1503
55	279	Q68CP9_ARID2_HUMAN	ARID2	3.1938
54	231	P51531_SMCA2_HUMAN	SMARCA2	2.9201
43	146	P51532_SMCA4_HUMAN	SMARCA4	3.2281
35	144	Q92922_SMRC1_HUMAN	SMARCC1	3.1727
34	201	Q9NPI1_BRD7_HUMAN	BRD7	3.1539
33	116	Q969G3_SMCE1_HUMAN	SMARCE1	2.9025
26	102	Q96GM5_SMRD1_HUMAN	SMARCD1	2.9836
20	83	Q8WUB8_PHF10_HUMAN	PHF10	2.8649
20	61	Q92925_SMRD2_HUMAN	SMARCD2	2.9301
15	57	O96019_ACL6A_HUMAN	ACTL6A	2.8741
15	28	P52292_IMA1_HUMAN	KPNA2	2.9489
14	62	Q4VC05_BCL7A_HUMAN	BCL7A	3.1939
13	27	Q12824_SNF5_HUMAN	SMARCB1	2.7493
13	16	P11021_GRP78_HUMAN	HSPA5	3.4218
12	14	P38646_GRP75_HUMAN	HSPA9	3.2964
12	13	P14735_IDE_HUMAN	IDE	2.4613
12	12	Q9NR30_DDX21_HUMAN	DDX21	2.7774
11	16	P11142_HSP7C_HUMAN	HSPA8	3.1949
11	13	P42357_HUTH_HUMAN	HAL	2.971
10	15	P23396_RS3_HUMAN	RPS3	2.7027
9	122	IGKC_MOUSE		2.9941
9	12	Q71U36_TBA1A_HUMAN	TUBA1A	2.6814
9	11	P39060_COIA1_HUMAN	COL18A1	2.8145
9	10	P62701_RS4X_HUMAN	RPS4X	2.8156
9	9	Q9Y2W1_TR150_HUMAN	THRAP3	2.9591
8	11	Q00839_HNRPU_HUMAN	HNRNPU	2.9005
8	9	P15880_RS2_HUMAN	RPS2	2.6092
8	9	P46781_RS9_HUMAN	RPS9	2.236
8	8	P07355_ANXA2_HUMAN	ANXA2	3.3655
7	34	P62736_ACTA_HUMAN	ACTA2	2.6465
7	9	P06733_ENOA_HUMAN	ENO1	3.521
7	8	Q6UWP8_SBSN_HUMAN	SBSN	3.2117
7	8	Q13867_BLMH_HUMAN	BLMH	3.0144
7	8	Q06830_PRDX1_HUMAN	PRDX1	2.1114
7	8	P36578_RL4_HUMAN	RPL4	2.0889
7	7	P67809_YBOX1_HUMAN	YBX1	3.7665
7	7	Q02880_TOP2B_HUMAN	TOP2B	3.3014
7	7	Q07065_CKAP4_HUMAN	CKAP4	3.1132
7	7	Q08211_DHX9_HUMAN	DHX9	2.6771
7	7	P68104_EF1A1_HUMAN	EEF1A1	2.5
7	7	A8K2U0_A2ML1_HUMAN	A2ML1	2.2427
6	13	IGHM_MOUSE	Igh-6	3.3293
6	7	Q13127_REST_HUMAN	REST	2.8103

6	6	P02545_LMNA_HUMAN	LMNA	3.1354
6	6	P11388_TOP2A_HUMAN	TOP2A	2.8833
6	6	P62269_RS18_HUMAN	RPS18	2.5242
6	6	P49411_EFTU_HUMAN	TUFM	2.3847
6	6	P62917_RL8_HUMAN	RPL8	2.1468
5	26	P60709_ACTB_HUMAN	ACTB	3.5789
5	5	P29401_TKT_HUMAN	TKT	3.1324
5	5	O75342_LX12B_HUMAN	ALOX12B	2.8947
5	5	P54652_HSP72_HUMAN	HSPA2	2.816
5	5	P01876_IGHA1_HUMAN	IGHA1	2.6704
5	5	P62249_RS16_HUMAN	RPS16	2.5621
5	5	P32119_PRDX2_HUMAN	PRDX2	2.5319
5	5	P61247_RS3A_HUMAN	RPS3A	2.4999
5	5	Q02878_RL6_HUMAN	RPL6	2.1757
4	13	IGH1M_MOUSE	Ighg1	2.8568
4	8	P04280_PRP1_HUMAN	PRB1	3.3901
4	6	P39023_RL3_HUMAN	RPL3	2.3455
4	5	P04792_HSPB1_HUMAN	HSPB1	3.5519
4	5	P05387_RLA2_HUMAN	RPLP2	3.5184
4	5	P04406_G3P_HUMAN	GAPDH	3.3208
4	5	P06748_NPM_HUMAN	NPM1	2.5526
4	5	IGHG3_MOUSE		2.4964
4	4	Q13885_TBB2A_HUMAN	TUBB2A	4.1573
4	4	P62241_RS8_HUMAN	RPS8	3.2269
4	4	P12273_PIP_HUMAN	PIP	3.0537
4	4	Q8WVV4_POF1B_HUMAN	POF1B	2.9473
4	4	P62805_H4_HUMAN	HIST1H4A	2.932
4	4	Q6ZVX7_FBX50_HUMAN	NCCRP1	2.8894
4	4	P02788_TRFL_HUMAN	LTF	2.7881
4	4	Q96DA0_ZG16B_HUMAN	ZG16B	2.7797
4	4	O15523_DDX3Y_HUMAN	DDX3Y	2.6204
4	4	P62753_RS6_HUMAN	RPS6	2.5639
4	4	P25311_ZA2G_HUMAN	AZGP1	2.5457
4	4	P26373_RL13_HUMAN	RPL13	2.4908
4	4	P18124_RL7_HUMAN	RPL7	1.9952
3	11	Q8WUZ0_BCL7C_HUMAN	BCL7C	4.0083
3	6	P84098_RL19_HUMAN	RPL19	3.4902
3	5	P60174_TPIS_HUMAN	TPI1	2.613
3	4	P35579_MYH9_HUMAN	MYH9	3.2792
3	4	P30838_AL3A1_HUMAN	ALDH3A1	2.9645
3	4	Q86VM9_ZCH18_HUMAN	ZC3H18	2.7445
3	4	P10599_THIO_HUMAN	TXN	2.3319
3	3	P09211_GSTP1_HUMAN	GSTP1	4.1415
3	3	P52294_IMA5_HUMAN	KPNA1	4.0822
3	3	P16989_YBOX3_HUMAN	YBX3	4.0344
3	3	Q8NFW8_NEUA_HUMAN	CMAS	3.5635
3	3	P21333_FLNA_HUMAN	FLNA	3.4127

3	3	Q9HCY8_S10AE_HUMAN	S100A14	3.2753
3	3	P30050_RL12_HUMAN	RPL12	3.2739
3	3	Q9UH99_SUN2_HUMAN	SUN2	3.1274
3	3	P16403_H12_HUMAN	HIST1H1C	3.0986
3	3	P62987_RL40_HUMAN	UBA52	2.9578
3	3	P38159_RBMX_HUMAN	RBMX	2.9159
3	3	Q9UQ35_SRRM2_HUMAN	SRRM2	2.8869
3	3	Q07021_C1QBP_HUMAN	C1QBP	2.8433
3	3	P05141_ADT2_HUMAN	SLC25A5	2.8192
3	3	P78527_PRKDC_HUMAN	PRKDC	2.7877
3	3	Q09666_AHNK_HUMAN	AHNAK	2.7318
3	3	Q8IYB3_SRRM1_HUMAN	SRRM1	2.7248
3	3	P22626_ROA2_HUMAN	HNRNPA2B1	2.6328
3	3	Q49A26_GLYR1_HUMAN	GLYR1	2.5724
3	3	P19338_NUCL_HUMAN	NCL	2.4572
3	3	Q00577_PURA_HUMAN	PURA	2.3218
3	3	P62851_RS25_HUMAN	RPS25	2.2987
3	3	Q00325_MPCP_HUMAN	SLC25A3	2.2482
3	3	Q13428_TCOF_HUMAN	TCOF1	2.2197
3	3	P01024_CO3_HUMAN	C3	2.1243
3	3	Q96HS1_PGAM5_HUMAN	PGAM5	2.0701
2	51	P01605_KV113_HUMAN		2.3698
2	17	F8VXC8_F8VXC8_HUMAN	SMARCC2	3.655
2	13	P06312_KV401_HUMAN	IGKV4-1	2.5383
2	9	P46459_NSF_HUMAN	NSF	1.7771
2	7	P02814_SMR3B_HUMAN	SMR3B	2.8483
2	6	Q9BYX7_ACTBM_HUMAN	POTEKP	2.9206
2	3	P01834_IGKC_HUMAN	IGKC	4.5678
2	3	Q53RT3_APRV1_HUMAN	ASPRV1	2.9612
2	3	P60866_RS20_HUMAN	RPS20	2.8555
2	3	KV2A7_MOUSE		2.7996
2	2	Q86V81_THOC4_HUMAN	ALYREF	4.6914
2	2	P31943_HNRH1_HUMAN	HNRNPH1	4.4337
2	2	P05386_RLA1_HUMAN	RPLP1	4.0595
2	2	Q9BQ50_TREX2_HUMAN	TREX2	3.7998
2	2	P62424_RL7A_HUMAN	RPL7A	3.7699
2	2	P62913_RL11_HUMAN	RPL11	3.6791
2	2	Q07020_RL18_HUMAN	RPL18	3.5748
2	2	P04040_CATA_HUMAN	CAT	3.5722
2	2	P07900_HS90A_HUMAN	HSP90AA1	3.4237
2	2	O75223_GGCT_HUMAN	GGCT	3.4021
2	2	Q9UBG3_CRNN_HUMAN	CRNN	3.3538
2	2	Q02539_H11_HUMAN	HIST1H1A	3.3401
2	2	P30086_PEBP1_HUMAN	PEBP1	3.319
2	2	P62244_RS15A_HUMAN	RPS15A	3.3168
2	2	P12814_ACTN1_HUMAN	ACTN1	3.2889
2	2	P62847_RS24_HUMAN	RPS24	3.2493

2	2	Q9HC78_ZBT20_HUMAN	ZBTB20	3.2317
2	2	P52597_HNRPF_HUMAN	HNRNPF	3.2309
2	2	P23246_SFPQ_HUMAN	SFPQ	3.1382
2	2	P61978_HNRPK_HUMAN	HNRNPK	3.1322
2	2	B9A064_IGLL5_HUMAN	IGLL5	3.1154
2	2	P27635_RL10_HUMAN	RPL10	2.9959
2	2	P62266_RS23_HUMAN	RPS23	2.9894
2	2	P13639_EF2_HUMAN	EEF2	2.9697
2	2	Q9BQE9_BCL7B_HUMAN	BCL7B	2.9434
2	2	Q6NZI2_PTRF_HUMAN	PTRF	2.8703
2	2	P61626_LYSC_HUMAN	LYZ	2.8482
2	2	P51991_ROA3_HUMAN	HNRNPA3	2.8473
2	2	Q96EY7_PTCD3_HUMAN	PTCD3	2.8218
2	2	O43240_KLK10_HUMAN	KLK10	2.7772
2	2	Q9BRK5_CAB45_HUMAN	SDF4	2.7534
2	2	P00338_LDHA_HUMAN	LDHA	2.7478
2	2	P12235_ADT1_HUMAN	SLC25A4	2.7214
2	2	P62263_RS14_HUMAN	RPS14	2.6869
2	2	P19784_CSK22_HUMAN	CSNK2A2	2.6705
2	2	P46776_RL27A_HUMAN	RPL27A	2.6692
2	2	P01857_IGHG1_HUMAN	IGHG1	2.6322
2	2	O60506_HNRPQ_HUMAN	SYNCRIP	2.5473
2	2	P07437_TBB5_HUMAN	TUBB	2.5309
2	2	Q96FQ6_S10AG_HUMAN	S100A16	2.4674
2	2	Q9P0G3_KLK14_HUMAN	KLK14	2.1224
2	2	Q9HC84_MUC5B_HUMAN	MUC5B	2.072
2	2	P61353_RL27_HUMAN	RPL27	2.0108
2	2	P62280_RS11_HUMAN	RPS11	1.8923
2	2	P25398_RS12_HUMAN	RPS12	1.8809
2	2	P07910_HNRPC_HUMAN	HNRNPC	1.8188
2	2	Q13510_ASAH1_HUMAN	ASAH1	1.8182
2	2	Q5SSJ5_HP1B3_HUMAN	HP1BP3	1.7405
1	10	Q9C0D2_CE295_HUMAN	CEP295	1.6485
1	6	HVM27_MOUSE		3.9098
1	3	Q9NX55_HYPK_HUMAN	HYPK	1.9039
1	2	P04908_H2A1B_HUMAN	HIST1H2AB	3.1615
1	2	G5E975_G5E975_HUMAN	SMARCB1	2.9415
1	2	Q15517_CDSN_HUMAN	CDSN	2.7199
1	2	Q58FF7_H90B3_HUMAN	HSP90AB3P	2.6456
1	2	P15515_HIS1_HUMAN	HTN1	2.5564
1	2	Q13573_SNW1_HUMAN	SNW1	1.6607
1	2	P23435_CBLN1_HUMAN	CBLN1	1.6124
1	1	P05388_RLA0_HUMAN	RPLP0	5.1123
1	1	P35251_RFC1_HUMAN	RFC1	4.9426
1	1	Q9Y383_LC7L2_HUMAN	LUC7L2	4.6674
1	1	C9J053_C9J053_HUMAN	PBRM1	4.6129
1	1	O95232_LC7L3_HUMAN	LUC7L3	4.5736

1	1	P18510_IL1RA_HUMAN	IL1RN	4.5576
1	1	Ig1_sheep		4.5242
1	1	P01766_HV305_HUMAN		4.4503
1	1	P62995_TRA2B_HUMAN	TRA2B	4.4003
1	1	Q8WWA1_TMM40_HUMAN	TMEM40	4.3974
1	1	P56537_IF6_HUMAN	EIF6	4.3106
1	1	P69905_HBA_HUMAN	HBA1	4.21
1	1	C9J9L6_C9J9L6_HUMAN	PBRM1	4.0305
1	1	P12236_ADT3_HUMAN	SLC25A6	4.0119
1	1	Q9NUQ6_SPS2L_HUMAN	SPATS2L	3.9526
1	1	P52907_CAZA1_HUMAN	CAPZA1	3.897
1	1	P02647_APOA1_HUMAN	APOA1	3.8528
1	1	P62854_RS26_HUMAN	RPS26	3.8406
1	1	Q9UGM3_DMBT1_HUMAN	DMBT1	3.8341
1	1	P63173_RL38_HUMAN	RPL38	3.8245
1	1	Q9Y6N5_SQRD_HUMAN	SQRDL	3.8242
1	1	Q9UIG0_BAZ1B_HUMAN	BAZ1B	3.7595
1	1	P08107_HSP71_HUMAN	HSPA1A	3.6183
1	1	Q9HC07_TM165_HUMAN	TMEM165	3.543
1	1	O43390_HNRPR_HUMAN	HNRNPR	3.4413
1	1	P55072_TERA_HUMAN	VCP	3.4082
1	1	Q16610_ECM1_HUMAN	ECM1	3.316
1	1	Q8N9T8_KRI1_HUMAN	KRI1	3.3158
1	1	P61513_RL37A_HUMAN	RPL37A	3.3021
1	1	Q9UJ70_NAGK_HUMAN	NAGK	3.2997
1	1	P01871_IGHM_HUMAN	IGHM	3.2779
1	1	Q9NVP1_DDX18_HUMAN	DDX18	3.2671
1	1	P34931_HS71L_HUMAN	HSPA1L	3.2168
1	1	P10809_CH60_HUMAN	HSPD1	3.2026
1	1	P35250_RFC2_HUMAN	RFC2	3.1519
1	1	Q12906_ILF3_HUMAN	ILF3	3.1406
1	1	P68366_TBA4A_HUMAN	TUBA4A	3.0899
1	1	P62906_RL10A_HUMAN	RPL10A	3.0859
1	1	P62857_RS28_HUMAN	RPS28	3.0854
1	1	P0CW22_RS17L_HUMAN	RPS17L	3.0246
1	1	Q12905_ILF2_HUMAN	ILF2	2.987
1	1	Q9HCM4_E41L5_HUMAN	EPB41L5	2.9549
1	1	P39019_RS19_HUMAN	RPS19	2.952
1	1	Q7Z478_DHX29_HUMAN	DHX29	2.9293
1	1	Q5JNZ5_RS26L_HUMAN	RPS26P11	2.927
1	1	P46783_RS10_HUMAN	RPS10	2.918
1	1	Q9BQG0_MBB1A_HUMAN	MYBBP1A	2.8773
1	1	P11166_GTR1_HUMAN	SLC2A1	2.856
1	1	P23280_CAH6_HUMAN	CA6	2.8169
1	1	P28074_PSB5_HUMAN	PSMB5	2.8097
1	1	P68871_HBB_HUMAN	HBB	2.7957
1	1	P60900_PSA6_HUMAN	PSMA6	2.7903

1	1	P00441_SODC_HUMAN	SOD1	2.7778
1	1	Q9H3D4_P63_HUMAN	TP63	2.7654
1	1	P61956_SUMO2_HUMAN	SUMO2	2.7598
1	1	Q9Y2X3_NOP58_HUMAN	NOP58	2.7441
1	1	IgG1_bovine		2.7088
1	1	Q12873_CHD3_HUMAN	CHD3	2.7087
1	1	Q6NVV1_R13P3_HUMAN	RPL13AP3	2.6958
1	1	Q92665_RT31_HUMAN	MRPS31	2.6876
1	1	P53007_TXTP_HUMAN	SLC25A1	2.6448
1	1	P62861_RS30_HUMAN	FAU	2.6
1	1	Q96G03_PGM2_HUMAN	PGM2	2.5407
1	1	O60832_DKC1_HUMAN	DKC1	2.4914
1	1	P01591_IGJ_HUMAN	IGJ	2.4899
1	1	Q15365_PCBP1_HUMAN	PCBP1	2.4804
1	1	P62750_RL23A_HUMAN	RPL23A	2.4711
1	1	P49207_RL34_HUMAN	RPL34	2.4602
1	1	Q15293_RCN1_HUMAN	RCN1	2.404
1	1	O00629_IMA3_HUMAN	KPNA4	2.401
1	1	Q9NY12_GAR1_HUMAN	GAR1	2.3907
1	1	P11279_LAMP1_HUMAN	LAMP1	2.3598
1	1	Q6P4A8_PLBL1_HUMAN	PLBD1	2.3114
1	1	Q9NQ39_RS10L_HUMAN	RPS10P5	2.311
1	1	P31949_S10AB_HUMAN	S100A11	2.3058
1	1	Q9NP55_BPIA1_HUMAN	BPIFA1	2.3051
1	1	P58107_EPIPL_HUMAN	EPPK1	2.2795
1	1	P27482_CALL3_HUMAN	CALML3	2.2624
1	1	P20339_RAB5A_HUMAN	RAB5A	2.2611
1	1	O60684_IMA7_HUMAN	KPNA6	2.2588
1	1	O00505_IMA4_HUMAN	KPNA3	2.2561
1	1	A0FGR8_ESYT2_HUMAN	ESYT2	2.2232
1	1	Q9NS86_LANC2_HUMAN	LANCL2	2.2211
1	1	Q4FZB7_SV421_HUMAN	SUV420H1	2.2011
1	1	P18077_RL35A_HUMAN	RPL35A	2.1966
1	1	Q8TDL5_BPIB1_HUMAN	BPIFB1	2.1708
1	1	Q96QV6_H2A1A_HUMAN	HIST1H2AA	2.1674
1	1	P09038_FGF2_HUMAN	FGF2	2.1614
1	1	Q15828_CYTM_HUMAN	CST6	2.1497
1	1	P10323_ACRO_HUMAN	ACR	2.1368
1	1	Q02543_RL18A_HUMAN	RPL18A	2.1074
1	1	P45880_VDAC2_HUMAN	VDAC2	2.0231
1	1	P35249_RFC4_HUMAN	RFC4	2.0196
1	1	P62826_RAN_HUMAN	RAN	1.9512
1	1	P25789_PSA4_HUMAN	PSMA4	1.9413
1	1	P62829_RL23_HUMAN	RPL23	1.9269
1	1	Q96L21_RL10L_HUMAN	RPL10L	1.9215
1	1	P10643_CO7_HUMAN	C7	1.9164
1	1	Q9UPN3_MACF1_HUMAN	MACF1	1.8563

1	1	O00567_NOP56_HUMAN	NOP56	1.8477
1	1	Q8WWY3_PRP31_HUMAN	PRPF31	1.826
1	1	O95402_MED26_HUMAN	MED26	1.809
1	1	Q8WZ42_TITIN_HUMAN	TTN	1.7461
1	1	P50454_SERPH_HUMAN	SERPINH1	1.7399
1	1	O14556_G3PT_HUMAN	GAPDHS	1.6895
1	1	P01023_A2MG_HUMAN	A2M	1.6805
1	1	Q3KQU3_MA7D1_HUMAN	MAP7D1	1.6229
1	1	P83881_RL36A_HUMAN	RPL36A	1.5981
1	1	Q9UI42_CBPA4_HUMAN	CPA4	1.5802
1	1	P23588_IF4B_HUMAN	EIF4B	1.575
1	1	Q9NRD8_DUOX2_HUMAN	DUOX2	1.546
1	1	F8WCA4_F8WCA4_HUMAN	KLC4	1.5005

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Unique	Total	reference	Gene Symbol	AVG
99	1042	Q86U86_PB1_HUMAN	PBRM1	2.9729
13	17	Q9Y2W1_TR150_HUMAN	THRAP3	2.8972
8	12	P52292_IMA1_HUMAN	KPNA2	3.4165
7	7	P01876_IGHA1_HUMAN	IGHA1	2.5164
6	6	Q8TAQ2_SMRC2_HUMAN	SMARCC2	3.5866
6	6	P51532_SMCA4_HUMAN	SMARCA4	3.2815
6	6	P62701_RS4X_HUMAN	RPS4X	2.832
6	6	P19338_NUCL_HUMAN	NCL	2.6391
6	6	Q02878_RL6_HUMAN	RPL6	2.2105
5	7	P23396_RS3_HUMAN	RPS3	2.6145
5	6	P36578_RL4_HUMAN	RPL4	2.4664
5	6	P38646_GRP75_HUMAN	HSPA9	2.454
5	6	P39060_COIA1_HUMAN	COL18A1	2.4456
5	6	P46781_RS9_HUMAN	RPS9	2.1682
5	5	Q07065_CKAP4_HUMAN	CKAP4	3.1687
5	5	P07355_ANXA2_HUMAN	ANXA2	3.1385
5	5	P11021_GRP78_HUMAN	HSPA5	3.039
5	5	P11388_TOP2A_HUMAN	TOP2A	2.7557
5	5	Q06830_PRDX1_HUMAN	PRDX1	2.139
4	6	P62736_ACTA_HUMAN	ACTA2	2.1609
4	5	P62241_RS8_HUMAN	RPS8	3.1699
4	4	Q71U36_TBA1A_HUMAN	TUBA1A	3.383
4	4	P51531_SMCA2_HUMAN	SMARCA2	2.7549
4	4	Q13127_REST_HUMAN	REST	2.4654
4	4	P10599_THIO_HUMAN	TXN	2.3697
4	4	P61247_RS3A_HUMAN	RPS3A	2.0085
3	5	P67809_YBOX1_HUMAN	YBX1	3.564
3	5	IGH1M_MOUSE	Ighg1	2.9087
3	4	P05387_RLA2_HUMAN	RPLP2	4.1584
3	4	P60709_ACTB_HUMAN	ACTB	2.9888
3	3	Q00839_HNRPU_HUMAN	HNRNPU	3.6047
3	3	Q02880_TOP2B_HUMAN	TOP2B	3.3567
3	3	Q13885_TBB2A_HUMAN	TUBB2A	3.2027
3	3	P11142_HSP7C_HUMAN	HSPA8	3.1345
3	3	P62987_RL40_HUMAN	UBA52	3.1056
3	3	Q8IYB3_SRRM1_HUMAN	SRRM1	3.0899
3	3	P68104_EF1A1_HUMAN	EEF1A1	2.9476
3	3	Q8NFW8_NEUA_HUMAN	CMAS	2.7513
3	3	P62805_H4_HUMAN	HIST1H4A	2.6471
3	3	P16403_H12_HUMAN	HIST1H1C	2.6153
3	3	Q8WUB8_PHF10_HUMAN	PHF10	2.5444
3	3	P22626_ROA2_HUMAN	HNRNPA2B1	2.4298
3	3	P15880_RS2_HUMAN	RPS2	2.3963
3	3	P39023_RL3_HUMAN	RPL3	2.3254
2	34	IGKC_MOUSE		2.9853

2	3	P05386_RLA1_HUMAN	RPLP1	3.9106
2	3	Q9NPI1_BRD7_HUMAN	BRD7	3.346
2	3	O14786_NRP1_HUMAN	NRP1	3.0854
2	3	P06748_NPM_HUMAN	NPM1	2.9906
2	3	Q96HS1_PGAM5_HUMAN	PGAM5	2.8347
2	3	P06733_ENOA_HUMAN	ENO1	2.6059
2	3	SjGST_Schistosoma		2.224
2	2	Q9NYF8_BCLF1_HUMAN	BCLAF1	4.1768
2	2	P84098_RL19_HUMAN	RPL19	3.8286
2	2	IGHM_MOUSE	Igh-6	3.7405
2	2	P04406_G3P_HUMAN	GAPDH	3.4099
2	2	Q9Y383_LC7L2_HUMAN	LUC7L2	3.3286
2	2	P62424_RL7A_HUMAN	RPL7A	3.0881
2	2	P62266_RS23_HUMAN	RPS23	3.079
2	2	P60866_RS20_HUMAN	RPS20	2.7606
2	2	P18124_RL7_HUMAN	RPL7	2.7582
2	2	P23246_SFPQ_HUMAN	SFPQ	2.6521
2	2	P62847_RS24_HUMAN	RPS24	2.6351
2	2	P62249_RS16_HUMAN	RPS16	2.6215
2	2	Q9UQ35_SRRM2_HUMAN	SRRM2	2.5888
2	2	P30050_RL12_HUMAN	RPL12	2.5856
2	2	Q09666_AHNK_HUMAN	AHNAK	2.5636
2	2	P61978_HNRPK_HUMAN	HNRNPK	2.5497
2	2	P62899_RL31_HUMAN	RPL31	2.5265
2	2	P62913_RL11_HUMAN	RPL11	2.5153
2	2	P50454_SERPH_HUMAN	SERPINH1	2.4506
2	2	P62917_RL8_HUMAN	RPL8	2.4363
2	2	P62269_RS18_HUMAN	RPS18	2.336
2	2	P12235_ADT1_HUMAN	SLC25A4	2.1915
2	2	P21333_FLNA_HUMAN	FLNA	2.1645
2	2	O15523_DDX3Y_HUMAN	DDX3Y	2.1584
2	2	Q68CP9_ARID2_HUMAN	ARID2	2.124
2	2	P62807_H2B1C_HUMAN	HIST1H2BC	2.0373
2	2	P62753_RS6_HUMAN	RPS6	1.9912
2	2	Q16695_H31T_HUMAN	HIST3H3	1.988
2	2	P62277_RS13_HUMAN	RPS13	1.8614
2	2	P18077_RL35A_HUMAN	RPL35A	1.8451
2	2	Q8NHW5_RLA0L_HUMAN	RPLP0P6	1.6679
1	3	Q15517_CDSN_HUMAN	CDSN	2.923
1	3	P06312_KV401_HUMAN	IGKV4-1	2.3488
1	2	Q6UWP8_SBSN_HUMAN	SBSN	4.2839
1	2	C9J9L6_C9J9L6_HUMAN	PBRM1	3.9229
1	2	Q13428_TCOF_HUMAN	TCOF1	3.4206
1	2	Q8WWY3_PRP31_HUMAN	PRPF31	2.1078
1	1	P16989_YBOX3_HUMAN	YBX3	5.2926
1	1	C9J053_C9J053_HUMAN	PBRM1	4.5582
1	1	P62244_RS15A_HUMAN	RPS15A	4.4839

1	1	P51991_ROA3_HUMAN	HNRNPA3	4.4457
1	1	Q969G3_SMCE1_HUMAN	SMARCE1	4.2794
1	1	P31943_HNRH1_HUMAN	HNRNPH1	4.0928
1	1	P62995_TRA2B_HUMAN	TRA2B	3.8904
1	1	P63173_RL38_HUMAN	RPL38	3.8371
1	1	P47914_RL29_HUMAN	RPL29	3.82
1	1	Q9H3D4_P63_HUMAN	TP63	3.7412
1	1	O75223_GGCT_HUMAN	GGCT	3.6906
1	1	Q9NR30_DDX21_HUMAN	DDX21	3.6743
1	1	KV2A7_MOUSE		3.6711
1	1	P84103_SRSF3_HUMAN	SRSF3	3.5306
1	1	Q96GM5_SMRD1_HUMAN	SMARCD1	3.4259
1	1	Q49A26_GLYR1_HUMAN	GLYR1	3.4218
1	1	P26373_RL13_HUMAN	RPL13	3.3437
1	1	P39019_RS19_HUMAN	RPS19	3.3313
1	1	P01834_IGKC_HUMAN	IGKC	3.2874
1	1	B9A064_IGLL5_HUMAN	IGLL5	3.2297
1	1	Q16610_ECM1_HUMAN	ECM1	3.1057
1	1	Q86VM9_ZCH18_HUMAN	ZC3H18	3.0476
1	1	Q02539_H11_HUMAN	HIST1H1A	2.9988
1	1	P62263_RS14_HUMAN	RPS14	2.9956
1	1	P68871_HBB_HUMAN	HBB	2.9203
1	1	P49411_EFTU_HUMAN	TUFM	2.9056
1	1	Q9UGM3_DMBT1_HUMAN	DMBT1	2.882
1	1	P38159_RBMX_HUMAN	RBMX	2.8125
1	1	P34931_HS71L_HUMAN	HSPA1L	2.7962
1	1	Q9BRK5_CAB45_HUMAN	SDF4	2.7824
1	1	Q16629_SRSF7_HUMAN	SRSF7	2.7036
1	1	Q6NVV1_R13P3_HUMAN	RPL13AP3	2.6938
1	1	Q9BUJ2_HNRL1_HUMAN	HNRNPUL1	2.6667
1	1	Q5JNZ5_RS26L_HUMAN	RPS26P11	2.63
1	1	Q12873_CHD3_HUMAN	CHD3	2.6253
1	1	Q9UNX3_RL26L_HUMAN	RPL26L1	2.5585
1	1	Q14669_TRIPC_HUMAN	TRIP12	2.5463
1	1	P62861_RS30_HUMAN	FAU	2.5453
1	1	Q9NVP1_DDX18_HUMAN	DDX18	2.5412
1	1	P27816_MAP4_HUMAN	MAP4	2.5059
1	1	P04908_H2A1B_HUMAN	HIST1H2AB	2.4913
1	1	IgG1_bovine		2.4897
1	1	P46776_RL27A_HUMAN	RPL27A	2.4707
1	1	P33778_H2B1B_HUMAN	HIST1H2BB	2.4598
1	1	P18462_1A25_HUMAN	HLA-A	2.4539
1	1	P25705_ATPA_HUMAN	ATP5A1	2.4181
1	1	Q12824_SNF5_HUMAN	SMARCB1	2.3934
1	1	P34741_SDC2_HUMAN	SDC2	2.38
1	1	P46779_RL28_HUMAN	RPL28	2.3627
1	1	Q7Z478_DHX29_HUMAN	DHX29	2.3226

1	1	F8WAF8_F8WAF8_HUMAN	ZNF140	2.2549
1	1	P01591_IGJ_HUMAN	IGJ	2.2382
1	1	Q96A08_H2B1A_HUMAN	HIST1H2BA	2.1926
1	1	Q13867_BLMH_HUMAN	BLMH	2.1497
1	1	P83731_RL24_HUMAN	RPL24	2.1043
1	1	P04083_ANXA1_HUMAN	ANXA1	2.0597
1	1	P42166_LAP2A_HUMAN	TMPO	2.0452
1	1	P11387_TOP1_HUMAN	TOP1	2.0421
1	1	Q8N9T8_KRI1_HUMAN	KRI1	2.0396
1	1	Q9HAZ2_PRD16_HUMAN	PRDM16	2.0266
1	1	Q92922_SMRC1_HUMAN	SMARCC1	2.0221
1	1	O75342_LX12B_HUMAN	ALOX12B	2.0145
1	1	Q6UB35_C1TM_HUMAN	MTHFD1L	1.9464
1	1	Q5T750_XP32_HUMAN	XP32	1.9364
1	1	Q6ZR08_DYH12_HUMAN	DNAH12	1.9005
1	1	Q99848_EBP2_HUMAN	EBNA1BP2	1.8687
1	1	Q13576_IQGA2_HUMAN	IQGAP2	1.8548
1	1	P61353_RL27_HUMAN	RPL27	1.8505
1	1	P07910_HNRPC_HUMAN	HNRNPC	1.8132
1	1	Q6ZVX7_FBX50_HUMAN	NCCRP1	1.7839
1	1	P15090_FABP4_HUMAN	FABP4	1.7451
1	1	P05141_ADT2_HUMAN	SLC25A5	1.7353
1	1	Q08211_DHX9_HUMAN	DHX9	1.6497
1	1	Q8N9T2_CX042_HUMAN	NKAPP1	1.6068
1	1	J3QKQ5_J3QKQ5_HUMAN	KPNB1	1.6049
1	1	P23435_CBLN1_HUMAN	CBLN1	1.5782
1	1	P20936_RASA1_HUMAN	RASA1	1.5638

IP Mass Spec Proteins in A704-EV

Unique	Total	reference	Gene Symbol	AVG
13	13	Q6UWP8_SBSN_HUMAN	SBSN	2.6916
10	13	P07355_ANXA2_HUMAN	ANXA2	3.2264
8	99	IGKC_MOUSE		2.9804
8	10	P32119_PRDX2_HUMAN	PRDX2	2.4571
8	9	P04040_CATA_HUMAN	CAT	3.5058
8	8	P42357_HUTH_HUMAN	HAL	2.4756
7	12	P04406_G3P_HUMAN	GAPDH	3.3877
5	11	IGH1M_MOUSE	Ighg1	2.8707
5	9	IGHM_MOUSE	Igh-6	3.0703
5	6	Q15517_CDSN_HUMAN	CDSN	3.114
5	6	P11021_GRP78_HUMAN	HSPA5	3.1097
5	6	P14618_KPYM_HUMAN	PKM	2.9457
5	5	P58107_EPIPL_HUMAN	EPPK1	3.5169
5	5	P00491_PNPH_HUMAN	PNP	2.7839
5	5	Q13867_BLMH_HUMAN	BLMH	2.682
5	5	Q06830_PRDX1_HUMAN	PRDX1	2.0912
4	5	P06733_ENOA_HUMAN	ENO1	3.2822
4	5	P60709_ACTB_HUMAN	ACTB	2.6573
4	4	Q6ZVX7_FBX50_HUMAN	NCCRP1	2.7473
4	4	P25311_ZA2G_HUMAN	AZGP1	2.1972
3	4	P04792_HSPB1_HUMAN	HSPB1	3.7547
3	4	IGHG3_MOUSE		2.5006
3	3	Q8WVV4_POF1B_HUMAN	POF1B	3.4149
3	3	P29401_TKT_HUMAN	TKT	3.4118
3	3	P49189_AL9A1_HUMAN	ALDH9A1	3.3805
3	3	O75223_GGCT_HUMAN	GGCT	2.8089
3	3	P28074_PSB5_HUMAN	PSMB5	2.7691
3	3	Q16610_ECM1_HUMAN	ECM1	2.504
3	3	P07900_HS90A_HUMAN	HSP90AA1	2.3078
3	3	Q8IW75_SPA12_HUMAN	SERPINA12	2.0838
2	36	P01605_KV113_HUMAN		2.3031
2	11	P06312_KV401_HUMAN	IGKV4-1	2.424
2	4	HVM27_MOUSE		4.0637
2	2	P62736_ACTA_HUMAN	ACTA2	3.8117
2	2	P62987_RL40_HUMAN	UBA52	3.4239
2	2	P06396_GELS_HUMAN	GSN	3.4012
2	2	Q8TAA3_PSA7L_HUMAN	PSMA8	3.2329
2	2	P30086_PEBP1_HUMAN	PEBP1	3.1103
2	2	P50395_GDIB_HUMAN	GDI2	2.8586
2	2	P18206_VINC_HUMAN	VCL	2.6098
2	2	P35606_COPB2_HUMAN	COPB2	2.5594
2	2	Q01469_FABP5_HUMAN	FABP5	2.3925
2	2	P10599_THIO_HUMAN	TXN	2.2415
2	2	P12081_SYHC_HUMAN	HARS	1.9821
2	2	Q6E0U4_DMKN_HUMAN	DMKN	1.9511

2	2	Q15149_PLEC_HUMAN	PLEC	1.9349
1	3	P04280_PRP1_HUMAN	PRB1	3.3567
1	2	O60303_K0556_HUMAN	KIAA0556	1.7346
1	2	O14556_G3PT_HUMAN	GAPDHS	1.5681
1	2	Q14149_MORC3_HUMAN	MORC3	1.5587
1	1	O14786_NRP1_HUMAN	NRP1	5.0292
1	1	P49721_PSB2_HUMAN	PSMB2	4.2161
1	1	Q9HCY8_S10AE_HUMAN	S100A14	4.2003
1	1	O95865_DDAH2_HUMAN	DDAH2	4.1597
1	1	Q9UJ70_NAGK_HUMAN	NAGK	3.8591
1	1	P25786_PSA1_HUMAN	PSMA1	3.6051
1	1	P35579_MYH9_HUMAN	MYH9	3.5501
1	1	KV2A7_MOUSE		3.4544
1	1	P53634_CATC_HUMAN	CTSC	3.3835
1	1	P49720_PSB3_HUMAN	PSMB3	3.3203
1	1	P25787_PSA2_HUMAN	PSMA2	3.2832
1	1	P35030_TRY3_HUMAN	PRSS3	3.2588
1	1	P47756_CAPZB_HUMAN	CAPZB	3.1515
1	1	P60900_PSA6_HUMAN	PSMA6	3.1501
1	1	Q9H3D4_P63_HUMAN	TP63	2.8942
1	1	Q9BVK6_TMED9_HUMAN	TMED9	2.8237
1	1	Q9BZG9_LYNX1_HUMAN	LYNX1	2.8174
1	1	P27482_CALL3_HUMAN	CALML3	2.7771
1	1	P12273_PIP_HUMAN	PIP	2.7529
1	1	P02545_LMNA_HUMAN	LMNA	2.7521
1	1	P34931_HS71L_HUMAN	HSPA1L	2.7275
1	1	P54652_HSP72_HUMAN	HSPA2	2.7214
1	1	P11279_LAMP1_HUMAN	LAMP1	2.7212
1	1	Q6XQN6_PNCB_HUMAN	NAPRT	2.6954
1	1	P30740_ILEU_HUMAN	SERPINB1	2.6498
1	1	P55786_PSA_HUMAN	NPEPPS	2.6314
1	1	Q12873_CHD3_HUMAN	CHD3	2.6312
1	1	Q96DR8_MUCL1_HUMAN	MUCL1	2.5991
1	1	P01024_CO3_HUMAN	C3	2.577
1	1	P04083_ANXA1_HUMAN	ANXA1	2.5197
1	1	P13639_EF2_HUMAN	EEF2	2.4787
1	1	P01876_IGHA1_HUMAN	IGHA1	2.4774
1	1	Q96G03_PGM2_HUMAN	PGM2	2.3648
1	1	Q3ZCW2_LEGL_HUMAN	LGALSL	2.3254
1	1	Q92665_RT31_HUMAN	MRPS31	2.266
1	1	Q9NZH8_IL36G_HUMAN	IL36G	2.2618
1	1	P35237_SPB6_HUMAN	SERPINB6	2.2569
1	1	Q7Z478_DHX29_HUMAN	DHX29	2.2255
1	1	Q58FF7_H90B3_HUMAN	HSP90AB3P	2.1973
1	1	O95969_SG1D2_HUMAN	SCGB1D2	2.1883
1	1	P06753_TPM3_HUMAN	TPM3	2.1281
1	1	Q15828_CYTM_HUMAN	CST6	2.1188

1	1	P20618_PSB1_HUMAN	PSMB1	2.0593
1	1	A6NCQ8_A6NCQ8_HUMAN	FCER1G	2.0023
1	1	P25789_PSA4_HUMAN	PSMA4	1.9396
1	1	Q53RT3_APRV1_HUMAN	ASPRV1	1.9331
1	1	Q7Z6R9_AP2D_HUMAN	TFAP2D	1.9216
1	1	B9A064_IGLL5_HUMAN	IGLL5	1.8643
1	1	O95140_MFN2_HUMAN	MFN2	1.8383
1	1	Q8N9T2_CX042_HUMAN	NKAPP1	1.6922
1	1	Q9Y6L6_SO1B1_HUMAN	SLCO1B1	1.6807
1	1	P01023_A2MG_HUMAN	A2M	1.6465
1	1	P23435_CBLN1_HUMAN	CBLN1	1.6266
1	1	Q5QJ74_TBCEL_HUMAN	TBCEL	1.5361

Table S2. Genes Regulated by BAF180/BRG1 Complex but not BAF180/BRM Complex.

Genes Downregulated by BAF180/BRG1, but not BAF180/BRM---214 genes

Ensemble ID	symbol	entrezgene
ENSG00000006210	CX3CL1	6376
ENSG00000024422	EHD2	30846
ENSG00000029153	ARNTL2	56938
ENSG00000039560	RAI14	26064
ENSG00000052126	PLEKHA5	54477
ENSG00000052802	MSMO1	6307
ENSG00000061918	GUCY1B3	2983
ENSG00000068697	LAPTM4A	9741
ENSG00000072274	TFRC	7037
ENSG00000074410	CA12	771
ENSG00000075218	GTSE1	51512
ENSG00000075234	TTC38	55020
ENSG00000075275	CELSR1	9620
ENSG00000075618	FSCN1	6624
ENSG00000082438	COBLL1	22837
ENSG00000082684	SEMA5B	54437
ENSG00000082898	XPO1	7514
ENSG00000085662	AKR1B1	231
ENSG00000088812	ATRN	8455
ENSG00000088832	FKBP1A	2280
ENSG00000088930	XRN2	22803
ENSG00000089006	SNX5	27131
ENSG00000089063	TMEM230	29058
ENSG00000090006	LTBP4	8425
ENSG00000090530	P3H2	55214
ENSG00000092621	PHGDH	26227
ENSG00000093000	NUP50	10762
ENSG00000095637	SORBS1	10580
ENSG00000099194	SCD	6319
ENSG00000099942	CRKL	1399
ENSG00000099999	RNF215	200312
ENSG00000100028	SNRPD3	6634
ENSG00000100030	MAPK1	5594
ENSG00000100060	MFNG	4242
ENSG00000100065	CARD10	29775
ENSG00000100097	LGALS1	3956
ENSG00000100201	DDX17	10521
ENSG00000100241	SBF1	6305
ENSG00000100263	RHBDD3	25807

ENSG00000100297	MCM5	4174
ENSG00000100320	RBFOX2	23543
ENSG00000100330	MTMR3	8897
ENSG00000100342	APOL1	8542
ENSG00000100345	MYH9	4627
ENSG00000100403	ZC3H7B	23264
ENSG00000101003	GINS1	9837
ENSG00000101224	CDC25B	994
ENSG00000101266	CSNK2A1	1457
ENSG00000101290	CDS2	8760
ENSG00000101384	JAG1	182
ENSG00000101474	APMAP	57136
ENSG00000102038	SMARCA1	6594
ENSG00000102678	FGF9	2254
ENSG00000105048	TNNT1	7138
ENSG00000105825	TFPI2	7980
ENSG00000105854	PON2	5445
ENSG00000105875	WDR91	29062
ENSG00000106080	FKBP14	55033
ENSG00000106415	GLCCI1	113263
ENSG00000106483	SFRP4	6424
ENSG00000107798	LIPA	3988
ENSG00000108821	COL1A1	1277
ENSG00000109814	UGDH	7358
ENSG00000109846	CRYAB	1410
ENSG00000111799	COL12A1	1303
ENSG00000112902	SEMA5A	9037
ENSG00000112972	HMGCS1	3157
ENSG00000113389	NPR3	4883
ENSG00000113924	HGD	3081
ENSG00000115419	GLS	2744
ENSG00000115884	SDC1	6382
ENSG00000116016	EPAS1	2034
ENSG00000116133	DHCR24	1718
ENSG00000116962	NID1	4811
ENSG00000117020	AKT3	10000
ENSG00000117114	ADGRL2	23266
ENSG00000117298	ECE1	1889
ENSG00000118515	SGK1	6446
ENSG00000118762	PKD2	5311
ENSG00000118971	CCND2	894
ENSG00000119969	HELLS	3070
ENSG00000121039	RDH10	157506

ENSG00000121858	TNFSF10	8743
ENSG00000122591	FAM126A	84668
ENSG00000123384	LRP1	4035
ENSG00000124564	SLC17A3	10786
ENSG00000124766	SOX4	6659
ENSG00000125398	SOX9	6662
ENSG00000125726	CD70	970
ENSG00000125730	C3	718
ENSG00000125826	RBCK1	10616
ENSG00000125848	FLRT3	23767
ENSG00000125864	BFSP1	631
ENSG00000125868	DSTN	11034
ENSG00000125871	MGME1	92667
ENSG00000125875	TBC1D20	128637
ENSG00000125885	MCM8	84515
ENSG00000125968	ID1	3397
ENSG00000127863	TNFRSF19	55504
ENSG00000127920	GNG11	2791
ENSG00000127990	SGCE	8910
ENSG00000128245	YWHAH	7533
ENSG00000128274	A4GALT	53947
ENSG00000128342	LIF	3976
ENSG00000130638	ATXN10	25814
ENSG00000132646	PCNA	5111
ENSG00000132669	RIN2	54453
ENSG00000133401	PDZD2	23037
ENSG00000133466	C1QTNF6	114904
ENSG00000134215	VAV3	10451
ENSG00000135457	TFCP2	7024
ENSG00000135862	LAMC1	3915
ENSG00000136156	ITM2B	9445
ENSG00000136244	IL6	3569
ENSG00000136295	TTYH3	80727
ENSG00000136378	ADAMTS7	11173
ENSG00000137273	FOXF2	2295
ENSG00000137478	FCHSD2	9873
ENSG00000138942	RNF185	91445
ENSG00000142102	ATHL1	80162
ENSG00000143742	SRP9	6726
ENSG00000144354	CDCA7	83879
ENSG00000145555	MYO10	4651
ENSG00000145604	SKP2	6502
ENSG00000148672	GLUD1	2746

ENSG00000152527	PLEKHH2	130271
ENSG00000152578	GRIA4	2893
ENSG00000153707	PTPRD	5789
ENSG00000153902	LGI4	163175
ENSG00000154269	ENPP3	5169
ENSG00000155629	PIK3AP1	118788
ENSG00000156113	KCNMA1	3778
ENSG00000157514	TSC22D3	1831
ENSG00000157851	DPYSL5	56896
ENSG00000159403	C1R	715
ENSG00000160285	LSS	4047
ENSG00000162496	DHRS3	9249
ENSG00000162745	OLFML2B	25903
ENSG00000162878	PKDCC	91461
ENSG00000163347	CLDN1	9076
ENSG00000163739	CXCL1	2919
ENSG00000164211	STARD4	134429
ENSG00000164237	CMBL	134147
ENSG00000164366	CCDC127	133957
ENSG00000164830	OXR1	55074
ENSG00000165092	ALDH1A1	216
ENSG00000165685	TMEM52B	120939
ENSG00000166681	NGFRAP1	27018
ENSG00000166897	ELFN2	114794
ENSG00000167191	GPRC5B	51704
ENSG00000167693	NXN	64359
ENSG00000167772	ANGPTL4	51129
ENSG00000167996	FTH1	2495
ENSG00000168077	SCARA3	51435
ENSG00000168385	2-Sep	4735
ENSG00000168672	FAM84B	157638
ENSG00000169435	RASSF6	166824
ENSG00000169439	SDC2	6383
ENSG00000169604	ANTXR1	84168
ENSG00000170915	PAQR8	85315
ENSG00000171631	P2RY6	5031
ENSG00000171867	PRNP	5621
ENSG00000172264	MACROD2	140733
ENSG00000172380	GNG12	55970
ENSG00000172893	DHCR7	1717
ENSG00000173391	OLR1	4973
ENSG00000177508	IRX3	79191
ENSG00000178234	GALNT11	63917

ENSG00000178803	ADORA2A-AS	646023
ENSG00000179456	ZBTB18	10472
ENSG00000179750	APOBEC3B	9582
ENSG00000181019	NQO1	1728
ENSG00000182272	B4GALNT4	338707
ENSG00000182326	C1S	716
ENSG00000182667	NTM	50863
ENSG00000182944	EWSR1	2130
ENSG00000183049	CAMK1D	57118
ENSG00000183421	RIPK4	54101
ENSG00000183696	UPP1	7378
ENSG00000183741	CBX6	23466
ENSG00000184117	NIPSNAP1	8508
ENSG00000184164	CRELD2	79174
ENSG00000185033	SEMA4B	10509
ENSG00000185340	GAS2L1	10634
ENSG00000185386	MAPK11	5600
ENSG00000185499	MUC1	4582
ENSG00000185630	PBX1	5087
ENSG00000185651	UBE2L3	7332
ENSG00000185950	IRS2	8660
ENSG00000186575	NF2	4771
ENSG00000186897	C1QL4	338761
ENSG00000187244	BCAM	4059
ENSG00000188064	WNT7B	7477
ENSG00000188130	MAPK12	6300
ENSG00000188153	COL4A5	1287
ENSG00000188636	LDOC1L	84247
ENSG00000196411	EPHB4	2050
ENSG00000196562	SULF2	55959
ENSG00000196576	PLXNB2	23654
ENSG00000197696	NMB	4828
ENSG00000198053	SIRPA	140885
ENSG00000198792	TMEM184B	25829
ENSG00000198911	SREBF2	6721
ENSG00000198959	TGM2	7052
ENSG00000215193	PEX26	55670
ENSG00000221890	NPTXR	23467
ENSG00000225431	LOC10192823	101928233
ENSG00000237517	DGCR5	26220
ENSG00000240694	PNMA2	10687
ENSG00000241878	PISD	23761
ENSG00000242265	PEG10	23089

ENSG00000243156	MICAL3	57553
ENSG00000244509	APOBEC3C	27350
ENSG00000261115	TMEM178B	100507421

Genes Upregulated by BAF180/BRG1, but not BAF180/BRM---136 genes

Ensemble ID	symbol	entrezgene
ENSG00000004961	HCCS	3052
ENSG00000039123	SKIV2L2	23517
ENSG00000040275	SPDL1	54908
ENSG00000044446	PHKA2	5256
ENSG00000044524	EPHA3	2042
ENSG00000064042	LIMCH1	22998
ENSG00000064763	FAR2	55711
ENSG00000067167	TRAM1	23471
ENSG00000069869	NEDD4	4734
ENSG00000075340	ADD2	119
ENSG00000079819	EPB41L2	2037
ENSG00000081923	ATP8B1	5205
ENSG00000086712	TXLNG	55787
ENSG00000089486	CDIP1	29965
ENSG00000091490	SEL1L3	23231
ENSG00000092841	MYL6	4637
ENSG00000101849	TBL1X	6907
ENSG00000102054	RBBP7	5931
ENSG00000102172	SMS	6611
ENSG00000106105	GARS	2617
ENSG00000106688	SLC1A1	6505
ENSG00000110048	OSBP	5007
ENSG00000112499	SLC22A2	6582
ENSG00000112983	BRD8	10902
ENSG00000112984	KIF20A	10112
ENSG00000113013	HSPA9	3313
ENSG00000113141	IK	3550
ENSG00000113163	COL4A3BP	10087
ENSG00000113282	CLINT1	9685
ENSG00000113312	TTC1	7265
ENSG00000113369	ARRDC3	57561
ENSG00000113441	LNPEP	4012
ENSG00000113575	PPP2CA	5515
ENSG00000113580	NR3C1	2908
ENSG00000118620	ZNF430	80264
ENSG00000118640	VAMP8	8673
ENSG00000120314	WDR55	54853
ENSG00000120549	KIAA1217	56243
ENSG00000120725	SIL1	64374
ENSG00000121281	ADCY7	113
ENSG00000127022	CANX	821

ENSG00000129625	REEP5	7905
ENSG00000129680	MAP7D3	79649
ENSG00000129824	RPS4Y1	6192
ENSG00000130021	PUDP	8226
ENSG00000130234	ACE2	59272
ENSG00000131507	NDFIP1	80762
ENSG00000132561	MATN2	4147
ENSG00000134138	MEIS2	4212
ENSG00000134352	IL6ST	3572
ENSG00000134480	CCNH	902
ENSG00000134516	DOCK2	1794
ENSG00000135318	NT5E	4907
ENSG00000138675	FGF5	2250
ENSG00000140416	TPM1	7168
ENSG00000140937	CDH11	1009
ENSG00000141562	NARF	26502
ENSG00000143367	TUFT1	7286
ENSG00000144218	AFF3	3899
ENSG00000144460	NYAP2	57624
ENSG00000145217	SLC26A1	10861
ENSG00000145703	IQGAP2	10788
ENSG00000145730	PAM	5066
ENSG00000145741	BTF3	689
ENSG00000145819	ARHGAP26	23092
ENSG00000145907	G3BP1	10146
ENSG00000145916	RMND5B	64777
ENSG00000146007	ZMAT2	153527
ENSG00000147642	SYBU	55638
ENSG00000148677	ANKRD1	27063
ENSG00000149380	P4HA3	283208
ENSG00000149591	TAGLN	6876
ENSG00000150687	PRSS23	11098
ENSG00000152348	ATG10	83734
ENSG00000152409	JMY	133746
ENSG00000153015	CWC27	10283
ENSG00000153113	CAST	831
ENSG00000157625	TAB3	257397
ENSG00000157992	KRTCAP3	200634
ENSG00000160352	ZNF714	148206
ENSG00000160613	PCSK7	9159
ENSG00000161010	C5orf45	51149
ENSG00000162004	CCDC78	124093
ENSG00000164209	SLC25A46	91137

ENSG00000164244	PRRC1	133619
ENSG00000164292	RHOBTB3	22836
ENSG00000164307	ERAP1	51752
ENSG00000164308	ERAP2	64167
ENSG00000164346	NSA2	10412
ENSG00000164347	GFM2	84340
ENSG00000164402	8-Sep	23176
ENSG00000164465	DCBLD1	285761
ENSG00000164587	RPS14	6208
ENSG00000164609	SLU7	10569
ENSG00000166411	IDH3A	3419
ENSG00000167306	MYO5B	4645
ENSG00000169567	HINT1	3094
ENSG00000170421	KRT8	3856
ENSG00000170445	HARS	3035
ENSG00000170606	HSPA4	3308
ENSG00000171310	CHST11	50515
ENSG00000171564	FGB	2244
ENSG00000172927	MYEOV	26579
ENSG00000173597	SULT1B1	27284
ENSG00000173674	EIF1AX	1964
ENSG00000174469	CNTNAP2	26047
ENSG00000175602	CCDC85B	11007
ENSG00000176907	C8orf4	56892
ENSG00000177189	RPS6KA3	6197
ENSG00000178913	TAF7	6879
ENSG00000178922	HYI	81888
ENSG00000179023	KLHDC7A	127707
ENSG00000179715	PCED1B	91523
ENSG00000179869	ABCA13	154664
ENSG00000179913	B3GNT3	10331
ENSG00000180448	HMHA1	23526
ENSG00000181163	NPM1	4869
ENSG00000182557	SPNS3	201305
ENSG00000188158	NHS	4810
ENSG00000189143	CLDN4	1364
ENSG00000196705	ZNF431	170959
ENSG00000197142	ACSL5	51703
ENSG00000198108	CHSY3	337876
ENSG00000198198	SZT2	23334
ENSG00000198380	GFPT1	2673
ENSG00000198478	SH3BGRL2	83699
ENSG00000198677	TTC37	9652

ENSG00000198829	SUCNR1	56670
ENSG00000198865	CCDC152	100129792
ENSG00000198874	TYW1	55253
ENSG00000213347	MXD3	83463
ENSG00000214944	ARHGEF28	64283
ENSG00000224057	EGFR-AS1	100507500
ENSG00000225206	MIR137HG	400765
ENSG00000248445	SEMA6A-AS1	101927233
ENSG00000266751	MIR3661	100500905

Table S3

BAF180Q1298stopF	5'-CTTCAGAAAACCAATTGTTCCTTAGAAGGAGCCATCACCTTTGCTGG-3'
BAF180Q1298stopR	5'-CCAGCAAAGGTGATGGCTCCTTCTAAGGAACAATTGGTTTTCTGAAG-3'
BAF180AgeIF	5'-GGATATGACCGGTATGGGTTCCAAGAGAAGAAGAGCTACC-3'
BAF180ClaIR	5'-GGCGGATCGATTTAAACATTTTCTAGGTTGTATGCTTG-3'
BAF180delta2BDF	5'-GGATATGACCGGTATGGTTTCAAATCCTTTTTATCAGCTTTATGAC-3'
BAF180delta6BDF	5'-GGATATGACCGGTATGGGAGAGATTCTTCTTTCACCGGCAC-3'
BRG1sg2mutF	5'-ATGCATGAGAAGGGCATGTCGGACGATCCCAGGTACAACCAGATGAAAGGAATGGGGATG-3'
BRG1sg2mutR	5'-CATCCCCATTCCTTTCATCTGGTTGTACCTGGGATCGTCCGACATGCCCTTCTCATGCAT-3'
BRG1attB1F	5'-GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGTCCACTCCAGACCCACCCCTGGG-3'
BRG1attB2R	5'-GGGGACCACTTTGTACAAGAAAGCTGGGTCAGTCTTCTTCGCTGCCACTTCCTG-3'

Table S4

BAF180F23	5'-CTACCTCCCCTTCCAGCAGTGTC-3'
BAF180F495	5'-TGGGCAAGACAATCAGGGCACAG-3'
BAF180F1089	5'-TGCACGCTATGAAGAGGGAGAG-3'
BAF180F1468	5'-AGAGACGATATCGAGGACGGAG-3'
BAF180F2027	5'-GGGGTCGCCGCCTCAGTG-3'
BAF180F2499	5'-CTACCGTCGGCTTGATTTATTTC-3'
BAF180F3232	5'-ATGCCCATCAGCTCAGTCAGG-3'
BAF180F3784	5'-AATGAGAGCGACAAGCAGATGAAG-3'
BAF180F4552	5'-CCTCCACCCCACCATCTTCC-3'

Table S5

shCtr	5'-ccggCAACAAGATGAAGAGCACCAActcgagTTGGTGCTCTTCATCTTGTTGttttt-3'
shPBRM1-13	5'-ccggCCATAGTTGTAGCTACAAAttcaagagaTTTGTAGCTACAACTATGGttttt-3'
shPBRM1-32	5'-ccggGCACTCAGCTATACCACAAaactcgagttTTGTGGTATAGCTGAGTGCttttt-3'
shPBRM1-61	5'-ccggGGACAGATTCAGAAATATAaactcgagttTATATTTCTGAATCTGTCCttttt-3'
shPBRM1-161	5'-ccggCCGTGTGCCATGAACTCTATAttcaagagaTATAGAGTTCATGGCACACGGttttt-3'
shPBRM1-91	5'-ccggCAGAAGACTTTGTGACCTAaactcgagttTAGGTCACAAAGTCTTCTGttttt-3'
shPBRM1-111	5'-ccggGCGACAAGCAGATGAAGAAaactcgagttTTCTTCATCTGCTTGTCGCttttt-3'
shPBRM1-122	5'-ccggGTTAGAAGGTGGAGATGATaactcgagttATCATCTCCACCTTCTAACttttt-3'
shPBRM1-141	5'-ccggCCATCTACAAGCGAGTTCTAAttcaagagaTTAGAACTCGCTTGTAGATGGttttt-3'
shPBRM1-151	5'-ccggCGCTACCGTCGGCTTGATTTAttcaagagaTAAATCAAGCCGACGGTAGCGttttt-3'
sgCtr	5'-CTTCCGCGGCCCGTTCAA-3'
sgPBRM1-1	5'-CGAGGAGATCTATATCTT-3'
sgPBRM1-2	5'-CATCCTTATAGTCTCGGA-3'
sgPBRM1-3	5'-TGCCAGGAGAGACGATATCG-3'
sgBRG1-1	5'-GCCGAGGAGTTCCGCCCA-3'
sgBRG1-2	5'-TTCATCTGGTTGTAGCGC-3'
sgBRM-1	5'-CATGCTGTGGACGGAACC-3'
sgBRM-2	5'-GGACCCCATCGTCGGCAT-3'

Table S6

pLKOteton8332F	5'-GGACCCGACAGGCCCGAAGGAATAG-3'
pLKOteton127R	5'-CGCTGCGAACGGACGTGAAGAATGTGC-3'

Table S7

Genes	Forward	Reverse
ALDOC	5'-TGCTGATGACCGTGTGAAAAA-3'	5'-CGGACGAAGGGAACACCAT-3'
ANGPTL4	5'-GGCTCAGTGGACTTCAACCG-3'	5'-CCGTGATGCTATGCACCTTCT-3'
CA-IX	5'-GGGTGTCATCTGGACTGTGTT-3'	5'-CTTCTGTGCTGCCTTCTCATC-3'
CCND1	5'-CCGTCCATGCGGAAGATC-3'	5'-ATGGCCAGCGGGAAGAC-3'
IGFBP3	5'-AGAGCACAGATACCCAGAACT-3'	5'-GGTGATTCAGTGTGTCTTCCATT-3'
NDRG1	5'-CTCCTGCAAGAGTTTGATGTCC-3'	5'-TCATGCCGATGTCATGGTAGG-3'
VEGF	5'-CGAAACCATGAACTTTCTGC-3'	5'-CCTGAGTGGGCACACACTCC-3'
GLUT-1	5’-ATCGTGGCCATCTTTGGCTTTGTG-3'	5'-CTGGAAGCACATGCCCACAATGAA-3'
PDK1	5'-GGATTGCCCATATCACGTCTTT-3'	5'-TCCCGTAACCCTCTAGGGAATA-4'