Supplementary Methods and Information:

Direct Solution Exome Capture and Sequencing and Mapping:

Exome design

Five (PD2125, PD2126, PD2144, PD2147, PD3441) of the matched clinical sample ccRCC pairs (normal + tumour) enrichment was performed using the Agilent SureSelect Human Exon Kit (Agilent, G3362) corresponding to the exons annotated within the CCDS database. For the remaining 2 clinical sample matched pairs (PD2126, PD3295), a custom in-house design was submitted and baits synthesized and supplied by Agilent (Agilent Technologies Inc, Santa Clara, CA, USA). The custom design included additional exonic regions over those present in CCDS and comprised a total of 288,654 unique exons from 46,275 transcripts of 20,921 Ensembl protein-coding genes, 33,621 transcripts of 13,772 manually annotated protein-coding genes, and 1635 miRNA genes (Coffey *et al*, manuscript in preparation). Baits for both exomes were provided in a single tube solution format.

Genomic library preparation

Genomic DNA (5ug) was fragmented by Adaptive Focused Acoustics on a Covaris E120 (Covaris Inc, Woburn, MA, USA) for 90 sec with a duty cycle of 20%, intensity of 5 and cycles per burst of 200. The fragmented DNA was purified using a Qiaquick PCR purification column (Qiagen, 28104) and quantified on a Bioanalyser using the Agilent DNA 1000 kit (Agilent, 5067-1504). The resulting DNA ranged in size from ~100-400bp, with a modal fragment size of ~250bp. Genomic libraries were prepared using the Illumina Paired End Sample Prep Kit kit following the manufacturer's instructions (Illumina, San Diego CA, USA). Adapter-ligated DNA was purified using AMPure beads (Agencourt BioSciences Corporation, Beverly, MA, USA) following the manufacturer's protocol, and eluted in 40ul of nuclease-free water. The prepared library was used directly in the subsequent enrichment procedure without prior size-selection or PCR amplification.

Exon enrichment

The genomic library (500ng) was mixed with 7.5ug human C_0t1 DNA, lyophilized in a speedvac for 30 min at 45^{o}C and rehydrated in 3.4ul of nuclease-free water. Enrichment of the genomic DNA was performed using the Agilent SureSelect kit with minor modifications to the manufacturer's protocol. Briefly, the genomic DNA library (3.4ul) was combined with 2.5ul of

Block reagent 1, 2.5ul of Block reagent 2 and 0.6ul of Block reagent 3 and transferred to a well of a microtitre plate. The sample was denatured by incubating the plate on a thermocycler at 95^{o}C for 5 min then snap-cooled on ice. A hybridization mix was prepared comprising 25ul of Hyb reagent 1, 1ul of Hyb reagent 2, 10ul of Hyb reagent 3 and 13ul of Hyb reagent 4. A 13ul aliqout of this mastermix was added to the denatured DNA, and the sample incubated at 95^{o}C for 5 min, then 65^{o}C for 5 min. In a separate microtitre plate, the baits were prepared by combining 5ul of SureSelect capture library with 1ul of nuclease free water and 1ul of RNAse block, and the plate incubated at 65^{o}C for 3 min. The pre-warmed DNA (22ul) was transferred to the pre-warmed bait mix and the solution incubated for 24h at 65^{o}C. Following hybridization, the captured DNA was isolated using streptavidin-coated magnetic Dynabeads, (Invitrogen, 653.05) and washed following the standard Agilent SureSelect protocol. The isolated DNA was purified using a Qiagen MinElute purification column, eluted in 15ul of elution buffer and PCR-amplified for 14 cycles as previously described[1].

Substitution variant calling:

Mapping of paired-end read data to the human genome (Build 37) was done using BWA[2] . An average of 5 gigabases of uniquely mapping and 3.7 gigabases of uniquely mapping reads on target were obtained per sample, with an average of 74% of all reads mapping on target. Sixty-percent of target bases had 20X or greater coverage and 50 percent had 40X or greater coverage.

CaVEMan (Cancer Variants through Expectation Maximisation), a bespoke Java application using a simple expectation maximisation algorithm implementation[3] was used to call single nucleotide substitutions. Through comparison of reads from both tumour and normal with the reference genome, CaVEMan calculates a probability for each possible genotype per base (given tumour and normal copy number). In order to provide more accurate estimates of sequence error rates within the algorithm, thus aid identification of true variants, variables such as base quality, read position, lane, and read orientation are incorporated into the calculations. Once CaVEMan was run, several post processing filters were applied in order to further increase the specificity of somatic mutation calls.

1. At least 1/3 of mutant alleles in tumour reads are of quality >= 25.
2. At least 1 mutant allele in a tumour read must fall in the middle third of the read, unless the tumour read depth is less than 10, when a mutant allele the first third is acceptable.
3. There is no more than 1 high quality (>= 20) mutant allele in a normal read.

Insertion/Deletion variant calling:

A modified version of Pindel[4] was used to call insertions and deletions. By modifying the input file generation process we were able to increase sensitivity and increase confidence in events detected by BWA which was used as the initial mapping tool. The accepted approach for generating input for Pindel is to provide all read pairs where one end is unmapped and the other is confidently mapped to the genome, an anchor read. We found that by including readpairs where both ends map to the genome but allowing for one of the pair to have mismatches, insertions or deletions we could greatly increase coverage over smaller events (in some cases both ends are used as an anchor, creating two input records). The majority of these small events are detected by the BWA mapping algorithm, however, this increases confidence that the events are worth investigating. A second modification to the input generation was included to help identify small events close to large scale deletions or repetitive regions. In regions such as these we would not be able to capture any of the smaller events that can be detected within a single end of a read that is confidently mapped but with some form of mismatch, insertion or deletion. In these cases we generated an artificial anchor co-ordinate so that Pindel can attempt a realignment of these reads. Software that can generate input files of this form can be obtained by contacting the authors.

Once Pindel was run several post processing filters were applied. We considered there to be 2 classes of event in our data, large events > 4 b.p. and small events <= 4 b.p. which are detectable by BWA (non-SW). For many of the filters the mapping depths within the BAM file are used to aid filtering of poor confidence calls.

For both classes the following filters were applied to the raw output:

1. Event must occur in tumour reads
2. >3 tumour reads must support call
3. <5% of calls must occur in wildtype
4. When no wildtype coverage in BAM, Pindel must not call event in wildtype

For small events these filters were applied:

1. Tumour with BAM depth of < 200 reads must have variant call in >=8% of reads
2. Tumour with BAM depth of >= 200 reads must have variant call in >=4% of reads
3. Wildtype BAM must have >5 reads spanning the region
4. Pindel calls in wildtype reads must be <= 5% of the wildtype BAM depth

5. If the tumour BAM depth > wildtype BAM depth, normalise the Pindel wildtype calls against this, discarding if new value is >= 5% reference
6. Apply poly nucleotide tract filter for events with repetitive region > 9 repeats
7. Wildtype BAM depth must be >=8% of tumour BAM depth
8. Tumour BAM bust have <8% BWA reference calls vs BWA variant calls.

Further, for large events no wildtype reads should be called as part of an event by Pindel and exome data results must annotate to coding regions of the genome. Novel germline variants (verified by PCR based capillary sequencing) not previously reported in dbSNP or found in other sequencing screens are given in Supplementary Table 7.

PBRM1 mutation screening.

The coding exons of *PBRM1* were sequenced via PCR-based capillary sequencing as previously described. Data were analysed semi-automated mutation detection followed by visual inspection of sequencing traces as previously described[5]. The primer sequences for *PBRM1* amplification and sequencing are given in Supplemental Table 8.

Missense mutation analyses

In order to evaluate the functional effects of the found missense mutations we fixed a scoring system using protein domain alignments from Pfam[6]. The gene PBRM1 contains three kinds of functional domains: six copies of the Bromo domain (Pfam entry PF00439), two copies of the BAH domain (PF01426) and one copy of the HMG-box domain (PF00505). For each domain, we have used the Pfam seed alignment to construct a HMM-profile[7] (http://hmmer.org). In the Pfam full alignments all reported observations of this domain are aligned to this HMM-profile. We have extended these full alignments by the (6/2/1) hits within PBRM1 to fix the coordinate system. We denote the counts of amino acid *a* in the alignment column *i* by $n_i(a)$ and compare this observation to a null distribution $p_0(a)$ (overall genomic frequencies of amino acids). Taking the log odds ratio of the amino acid frequencies within the alignment column and the null gives a so called position specific score [8].

$$s_i(a) = \log \frac{q_i(a)}{p_0(a)} = \log \frac{n_i(a) + p_0(a)}{(N_i + 1)p_0(a)} \quad (1)$$

where N_i is the total number of residues in the column. The above construct of the observed distribution uses pseudo-counts[8,9] proportional to p_0 to account for non-observed residues in the finite sample. The two extreme cases are columns that are highly conserved - where the most prevalent letter receives a large positive score and all others large negative ones - and columns that are highly variable and close to neutral - where all letters receive scores close to zero. For similar conservation based scoring schemes for disease related variation see e.g. the recent review[10] and in the context of cancer mutations[11,12]. For a given missense mutation (falling onto alignment column *i*), we can now record the score difference between the final and the initial residue :

$$\Delta s_i = s_i(a_{final}) - s_i(a_{initial}) \quad (2)$$

Out of the 9 missense mutations we could score 3 using the Pfam alignments (T232P □ s = −7.78, A597D □ s = −9.69, H1204P □ s = −2.76). In order to assess if these three somatic mutations differ significantly from random mutations we generated *in silico* all possible point events in PBRM1 (transcript ENST00000337303) that result in a missense mutation which falls onto our scoring system (i.e. mutational opportunity space). From this set we drew 10,000 sets of 3 mutations randomly and evaluated the mean score for each set - the resulting distribution is shown together with the somatic value in Figure 2 in the main paper. Somatic mutations are significantly different from the null set (p-value 0.01). More specifically, the somatic mutation set has a lower mean negative score (i.e. they are predicted to be more deleterious on average) than the null model - thus making them interesting candidates for follow up functional studies.

Confirmation of exon trapping by RT-PCR in mouse pancreatic tumours

Total RNA (1 μg) from tumors with transposon insertions in *Pbrm1* was reverse transcribed into single stranded cDNA using Reverse Transcriptase III (Invitrogen) and Random Hexamers (Invitrogen) following the manufacturer protocol. 1 μL of the resulting cDNA was used as a template in a first round of PCR using specific primers corresponding to exon 23 of *Pbrm1* (5'-TGGCTGAAGGTTGGTGATTG-3') and Carp-β-Actin Splice aceptor sequence (5'-TAAATTCCCGCGAATCCATC-3'). The product of this reaction was used as a template in a second round of nested PCR using specific primers corresponding to *Pbrm1* exon 24 (5'-TTGAGAAAGTATGGGTCCGAGA-3') and a second external primer corresponding to Carp-β-Actin Splice aceptor sequence (5'- CATACCGGCTACGTTGCTAA-3'). The resulting bands were capillary sequenced.

***PBRM1* knockdown and functional analyses**

Cell lines and Transfections

Cell lines tested including ACHN, 786-O, SN12C, U031 A704 Caki-1 and TK10 were cultured in complete medium supplemented with 10% FBS (v/v) under 37°C and 5% CO_2. PBRM1 or scrambled control siRNAs (Santa Cruz, CA) were transfected into renal cell lines using Lipofectamine 2000 (Invitrogen, CA) according to the manufacturer's conditions.

siRNA sequences, which detect all three PBRM1 splice forms corresponding to NM_018165, NM_018313 AND NM_181042, were as follows:

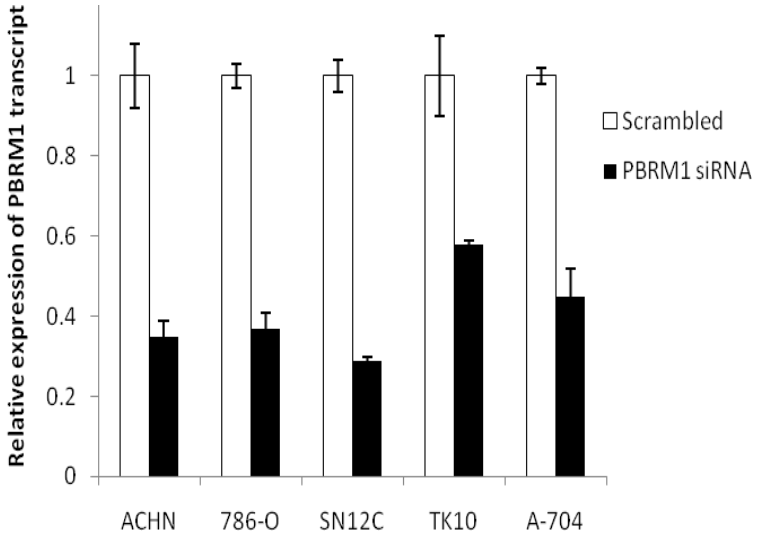
C CCAUAGUUGUAGCUACAAA

C GAAAGCAUCACUUCCUUUA

C GCACUCAGCUAUACCACAA

Real-time PCR

Total RNA was extracted from 48 hour post-transfected cells using TriPure (Roche, pIN). cDNA synthesis was carried out by using iScript™ cDNA Synthesis Kit (Bio-Rad, CA). Real-time PCR was performed to determine expression level of PBRM1 and β-actin by SsoFast EvaGreen Supermix using CFX96™ Real-Time PCR Detection System (Bio-Rad, CA). Primers used for amplification were: PBRM1-F (5'-GTGTGATGAACCAAGGAGTGGC-3'); PBRM1-R (5'-GATATGGAGGTGGTGCCTGCTG-3'); β-actin-F (5'-GATCAGCAAGCAGGAGTATGACG-3') and β-actin-R (5'-AAGGGTGTAACGCAACTAAGTCATAG-3'). Relative expression of PBRM1 was normalized with β-actin expression level.



Western blot analysis

Cellular proteins were extracted with phosphate buffered saline (PBS) containing 0.1% (v/v) Triton X-100 (Sigma, LA) in the presence of protease inhibitors. Proteins resolved by SDS-PAGE were electroblotted to a nitrocellulose membrane (Amersham, Buckinghamshire) and the membrane was incubated overnight at 4°C with blocking buffer (PBS containing 5% (w/v) skim milk and 0.05% (v/v) Tween-20). Primary and secondary antibody incubations were done in

blocking buffer. Anti-PBRM1 antibody was purchased from Bethyl Laboratories (TX) and anti-β-actin antibody was from Sigma (LA). The membranes were washed with PBS containing 0.05% (v/v) Tween-20 followed by analysis using the Supersignal Chemiluminescent kit (Pierce, IL) according to the manufacturer's recommendations.

Proliferation assay

After 48 hour transfection, 2×10^3 cells were plated per well in 96-well plate. Growth of PBRM1 siRNA- and scramble siRNA-transfected cells was determined using the colorimetric 3-(4,5-dimethylthiazol-2yl)-5-(3-carboxymethoxyphenyl)-(4-sulfophenyl)-2H-tetrazoluim assay according to the manufacturer's protocol (MTS; Promega, WI). The assay was performed in triplicate.

Migration assay

After 48 hour transfection, 2.0×10^5 cells in serum-free medium were seeded into the upper chamber of BioCoat inserts containing filters with 8 μm pores for migration assay (BD Pharmingen, CA). The lower chamber was filled with 10% (v/v) serum-containing medium as attractant. Cells that did not migrate through the filters after 22 hours post-incubation were removed with cotton swabs. Cells that traversed through the filter were fixed and stained by Diff-Quik Solution (Dade Behring, DE). After staining, cells were taken photos.

Soft Agar Assay

SN12C cells were cultured in a two-layer agar system to prevent their attachment to the plastic surface. After transfection, cells (4×10^4) were trypsinized to single-cell suspensions, resuspended in 0.4% agar (Sigma, LA), and added to a preset 1% bottom agar layer in six-well plates. The top agar cell layers were covered with culture medium. Cells were incubated in 5% CO_2 at 37°C for 14 days, and colonies were counted under ×2.5 object. Experiments were performed in triplicate.

PBRM1 knockdown expression phenotype analyses

Gene expression data generation and processing. RNA was isolated from 786-O, SN12C, and TK10 cells that were either transfected with scrambled siRNA or transfected with PBRM1

targeting siRNA. Single color gene expression data was generated using the HG-U133 Plus 2.0 chipset (Affymetrix, Santa Clara, CA) as described[13] and deposited in the Gene Expresson Omnibus (GEO22316). Gene expression analysis was performed using R/BioConductor version 2.0 software[14]. Summary expression values were computed using the RMA method as implemented in the *affy* package using updated probe set mappings (hgu133plus2hsentrezgcdf version 12) such that a single probe set is associated with each well measured gene[15,16] .

Gene expression analysis. Gene set enrichment analysis was performed using curated gene sets obtained from MSigDB (http://www.broadinstitute.org/gsea/msigdb/) and using additional curated gene sets obtained from the *PGSEA* package. Log-transformed relative expression values derived from comparision of targeted versus scrambled siRNA were computed for each cell line. For each cell line, gene sets that were significantly enriched in up-regulated genes were identified using the mean-rank method with permuation (n=10,000) as implimented in the *limma* package[17] . Gene sets that were significantly deregulated ($P < 0.05$) in all three cell lines were identified and sorted based on the lowest average p-value. Individual genes that were deregulated within specific genes sets were identified using a moderated t-statistic and significance values adjusted to control for multiple testing using the Benjamini & Hochberg approach as implimented in the *limma* package.

Gene expression data generated from renal cell carcinoma samples and non-diseased kidney samples were obtained from the Gene Expression Omnibus (GSE17895) as previously described[5] . The set of samples that displayed the hypoxic phenotype (*n*=90) were isolated and correlations between PBRM1 expression and other genes computed using Pearson's correlation.

1. Mamanova, L. et al. Target-enrichment strategies for next-generation sequencing. *Nat Meth* **7**, 111-118.

2. Li, H. & Durbin, R. Fast and accurate long-read alignment with Burrows-Wheeler transform. *Bioinformatics* **26**, 589-595 (2010).

3. Do, C.B. & Batzoglou, S. What is the expectation maximization algorithm? *Nat Biotech* **26**, 897-899 (2008).

4. Ye, K., Schulz, M.H., Long, Q., Apweiler, R. & Ning, Z. Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. *Bioinformatics* **25**, 2865-2871 (2009).

5. Dalgliesh, G.L. et al. Systematic sequencing of renal carcinoma reveals inactivation of histone modifying genes. *Nature* **463**, 360-363 (2010).

6. Finn, R.D. et al. The Pfam protein families database. *Nuc Acids Res* **38**, D211-222 (2010).

7. Eddy, S.R. Profile hidden Markov models. *Bioinformatics* **14**, 755-763 (1998).

8. Durbin, R., Eddy, S., Krogh, A. & Mitchison, G. *Biological sequence analysis: probabilistic models of proteins and nucleic acids*, (Cambridge University Press, Cambridge 1998).

9. Lawrence, C.E. et al. Detecting subtle sequence signals: a Gibbs sampling strategy for multiple alignment. *Science* **262**, 208-214 (1993).

10. Jordan, D.M., Ramensky, V.E. & Sunyaev, S.R. Human allelic variation: perspective from protein function, structure, and evolution. *Current Opinion in Structural Biology* **20**, 342-350.

11. Dixit, A. et al. Sequence and Structure Signatures of Cancer Mutation Hotspots in Protein Kinases. *PLoS ONE* **4**, e7485 (2009).

12. Yue, P. et al. Inferring the functional effects of mutation through clusters of mutations in homologous proteins. *Human Mutation* **31**, 264-271 (2010).

13. Yang, X.J. et al. A molecular classification of papillary renal cell carcinoma. *Cancer Res* **65**, 5628-37 (2005).

14. Gentleman, R.C. et al. Bioconductor: open software development for computational biology and bioinformatics. *Genome Biol* **5**, R80 (2004).

15. Dai, M. et al. Evolving gene/transcript definitions significantly alter the interpretation of GeneChip data. *Nuc Acids Res* **33**, e175 (2005).

16. Irizarry, R.A. et al. Exploration, normalization, and summaries of high density oligonucleotide array probe level data. *Biostatistics* **4**, 249-64 (2003).

17. Smyth, G.K. Linear models and empirical bayes methods for assessing differential expression in microarray experiments. *Stat Appl Genet Mol Biol* **3**, Article3 (2004).

Supplementary Table 1 - Clinical Samples in exome sequencing

Sample	Sex	Age	Grade	Histology	VHL mutation^	SETD2 mutation	UTX mutation
PD2125a	M	82	4	Clear Cell			
PD2126a	F	74	1	Clear Cell	c.236_241delGCAGTC; p.R79_P81>P	c.1801T>A; p.R601*	
PD2127a	F	59	4	Clear Cell			
PD2144a	F	63	4	Clear Cell	c.525delC; p.Y175*		
PD2147a	F	50	2	Clear Cell			c.4161_4162delTG; p.Y1387fs*1
PD3295a	M	62	4	Clear Cell			
PD3441a	M	69	1	Clear Cell	c.223_225delATC; p.F76_C77>C		

^ VHL mutations in PD2126a and PD3441a were not "re-discovered" in exome sequencing due to poor coverage of the highly GC-rich first exon.

Supplementary Table 2 - Somatic mutations indentified in exome sequencing

Sample	Chromosome	Position	Gene	Annotated Transcript	WT base	Mut Base	Mutation Type	Protein Annotation	cDNA Annotation
PD2127a	16	20855285	AC004381.2	ENST00000261377	A	C	SYNONYMOUS	p.L552L	c.1656A>C
PD2127a	2	179449098	AC010680.2	ENST00000356127	C	A	MISSENSE	p.G19157V	c.57470G>T
PD2126a	15	51028374	AC012100.1	ENST00000261854	C	T	MISSENSE	p.E286K	c.856G>A
PD2147a	7	158529750	AC019084.2	ENST00000435514	C	T	SYNONYMOUS	p.V258V	c.774G>A
PD2147a	4	25677963	AC092436.2	ENST00000382051	G	C	SYNONYMOUS	p.L555L	c.1665G>C
PD2147a	17	43214437	ACBD4	ENST00000321854	T	-	FRAMESHIFT	p.F116fs*7	c.347DelT
PD2147a	5	80643677	ACOT12	ENST00000307624	A	T	MISSENSE	p.L190H	c.569T>A
PD2144a	2	148680563	ACVR2A	ENST00000241416	G	A	MISSENSE	p.A367T	c.1099G>A
PD2144a	2	9683393	ADAM17	ENST00000497134	G	C	NONSENSE	p.S40*	c.119G>C
PD2127a	2	100625295	AFF3	ENST00000409579	A	G	SYNONYMOUS	p.S76S	c.228T>C
PD2147a	5	132232053	AFF4	ENST00000378595	A	T	MISSENSE	p.S757T	c.2269T>A
PD2147a	10	45498936	AL353801.1	ENST00000298299	C	T	SYNONYMOUS	p.D40D	c.120C>T
PD2126a	12	45803231	ANO6	ENST00000441606	A	G	MISSENSE	p.M640V	c.1918A>G
PD2127a	11	55258787	AP001998.1	ENST00000314657	G	A	SYNONYMOUS	p.T23T	c.69G>A
PD2125a	19	45451775	APOC2	ENST00000252490	C	T	SYNONYMOUS	p.L14L	c.40C>T
PD2125a	13	111944635	ARHGEF7	ENST00000375737	A	G	MISSENSE	p.T612A	c.1834A>G
PD2126a	1	27094351	ARID1A	ENST00000457599	G	A	MISSENSE	p.R1020K	c.3059G>A
PD2127a	1	27106655	ARID1A	ENST00000457599	T	C	MISSENSE	p.L1872P	c.5615T>C
PD2127a	10	63850639	ARID5B	ENST00000279873	A	T	NONSENSE	p.K473*	c.1417A>T
PD2147a	17	42249629	ASB16	ENST00000293414	A	C	MISSENSE	p.T173P	c.517A>C
PD2127a	9	119976966	ASTN2	ENST00000373996	G	A	MISSENSE	p.A229V	c.686C>T
PD2127a	14	96794874	ATG2B	ENST00000359933	T	A	ESSENTIAL_SPLICE	p.---	c.-A>T
PD2126a	22	46085613	ATXN10	ENST00000252934	C	A	SYNONYMOUS	p.I46I	c.138C>A
PD3295a	1	171506448	BAT2D1	ENST00000367742	GTCACCGAACAGTTCTGA	-	N-FRAME DELETIO	p.P782_S787delPNSSES	c.2340delGTCACCGAACAGTTCTGA
PD2125a	6	31630173	BAT4	ENST00000375896	G	T	MISSENSE	p.T314N	c.941C>A
PD2127a	6	38142761	BTBD9	ENST00000419706	T	A	STOP_LOST	p.*583Y	c.1749A>A
PD2125a	10	124457732	C10orf120	ENST00000329446	C	G	SYNONYMOUS	p.R175R	c.525G>C
PD2147a	15	24922328	C15orf2	ENST00000329468	C	A	SYNONYMOUS	p.I438I	c.1314C>A

PD3295a	12	2702482	CACNA1C	ENST00000399595	C	G	MISSENSE	p.S878R	c.2634C>G
PD2126a	5	96077268	CAST	ENST00000395813	A	C	MISSENSE	p.K361T	c.1082A>C
PD2126a	3	49293582	CCDC36	ENST00000452691	ATAGAAA	-	FRAMESHIFT	p.I218fs*379	c.652delATAGAAA
PD2125a	5	43388447	CCL28	ENST00000361115	ctcacAT	-	SPLICE	p.I64fs*17	c.190delATgtgag
PD2147a	15	43483790	CCNDBP1	ENST00000407066	G	A	SYNONYMOUS	p.R259R	c.777G>A
PD2127a	9	137686950	COL5A1	ENST00000371817	C	T	MISSENSE	p.P908L	c.2723C>T
PD2127a	8	113358398	CSMD3	ENST00000455883	T	A	MISSENSE	p.S2020C	c.6058A>T
PD2125a	4	71114990	CSN3	ENST00000304954	C	A	SYNONYMOUS	p.P121P	c.363C>A
PD2127a	10	16882938	CUBN	ENST00000377833	T	C	MISSENSE	p.S3258G	c.9772A>G
PD2144a	2	158272284	CYTIP	ENST00000264192	G	A	MISSENSE	p.P329S	c.985C>T
PD2126a	5	39376176	DAB2	ENST00000339788	G	T	MISSENSE	p.L506M	c.1516C>A
PD2125a	X	23018596	DDX53	ENST00000327968	A	C	MISSENSE	p.N141T	c.422A>C
PD2127a	6	56471673	DST	ENST00000439203	T	C	MISSENSE	p.I2048V	c.6142A>G
PD3441a	17	7132566	DVL2	ENST00000005340	A	G	MISSENSE	p.I282T	c.845T>C
PD2127a	7	95657584	DYNC1I1	ENST00000359388	A	T	MISSENSE	p.H336L	c.1007A>T
PD3441a	22	36900169	EIF3D	ENST00000397224	T	A	MISSENSE	p.N342I	c.1025A>T
PD2147a	12	53416352	EIF4B	ENST00000430205	C	G	MISSENSE	p.P203R	c.608C>G
PD3295a	8	23297290	ENTPD4	ENST00000417069	T	C	MISSENSE	p.I333V	c.997A>G
PD2127a	5	10239283	FAM173B	ENST00000280330	A	G	SYNONYMOUS	p.L68L	c.202T>C
PD2125a	17	42979966	FAM187A	ENST00000357776	G	A	SYNONYMOUS	p.L170L	c.510G>A
PD2127a	5	127627328	FBN2	ENST00000262464	T	A	MISSENSE	p.E2062V	c.6185A>T
PD3441a	19	9922365	FBXL12	ENST00000247977	A	T	MISSENSE	p.L63H	c.188T>A
PD2147a	1	224345375	FBXO28	ENST00000366862	C	A	MISSENSE	p.P345H	c.1034C>A
PD2127a	5	108294968	FER	ENST00000438717	C	T	NONSENSE	p.Q526*	c.1576C>T
PD2125a	20	14306799	FLRT3	ENST00000378053	T	C	MISSENSE	p.I452V	c.1354A>G
PD2127a	19	3532607	FZR1	ENST00000395095	C	T	NONSENSE	p.Q401*	c.1201C>T
PD2147a	17	41053120	G6PC	ENST00000419123	A	G	MISSENSE	p.K78R	c.233A>G
PD2125a	2	17962775	GEN1	ENST00000381254	T	C	MISSENSE	p.C766R	c.2296T>C
PD2127a	12	57865610	GLI1	ENST00000228682	C	T	SYNONYMOUS	p.P1029P	c.3087C>T
PD2144a	17	42475605	GPATCH8	ENST00000335500	G	T	SYNONYMOUS	p.P1280P	c.3840C>A
PD2127a	19	34859538	GPI	ENST00000415930	C	T	SYNONYMOUS	p.I150I	c.450C>T
PD3441a	14	91701279	GPR68	ENST00000238699	T	C	MISSENSE	p.N49S	c.146A>G
PD2144a	X	2773196	GYG2	ENST00000381163	G	A	MISSENSE	p.G194R	c.580G>A

PD2144a	20	23345310	GZF1	ENST00000377051	C	T	MISSENSE	p.A97V	c.290C>T
PD2127a	7	18914186	HDAC9	ENST00000401921	C	A	MISSENSE	p.P880T	c.2638C>A
PD2147a	10	96352065	HELLS	ENST00000441434	A	G	MISSENSE	p.H568R	c.1703A>G
PD3441a	7	92848502	HEPACAM2	ENST00000394468	G	T	MISSENSE	p.F114L	c.342C>A
PD3441a	21	38269279	HLCS	ENST00000399120	C	T	SYNONYMOUS	p.E444E	c.1332G>A
PD2127a	5	149386186	HMGXB3	ENST00000261804	A	C	MISSENSE	p.K245N	c.735A>C
PD2126a	9	21077581	IFNB1	ENST00000380232	A	G	SYNONYMOUS	p.S96S	c.288T>C
PD3441a	7	112095838	IFRD1	ENST00000403825	C	A	MISSENSE	p.Q39K	c.115C>A
PD2126a	11	18745765	IGSF22	ENST00000412229	G	A	MISSENSE	p.R7W	c.19C>T
PD2125a	17	37922744	IKZF3	ENST00000351680	C	G	MISSENSE	p.E238Q	c.712G>C
PD2127a	14	75142441	KIAA0317	ENST00000356357	C	T	SYNONYMOUS	p.V347V	c.1041G>A
PD3441a	12	105519826	KIAA1033	ENST00000311317	T	A	SYNONYMOUS	p.S277S	c.831T>A
PD2126a	9	20990265	KIAA1797	ENST00000380249	T	A	SYNONYMOUS	p.L1716L	c.5148T>A
PD2147a	19	55333270	KIR3DL1	ENST00000358178	C	T	SYNONYMOUS	p.Y207Y	c.621C>T
PD2127a	X	117043963	KLHL13	ENST00000469946	A	T	MISSENSE	p.F172I	c.514T>A
PD3441a	17	39036504	KRT20	ENST00000167588	C	A	MISSENSE	p.G214C	c.640G>T
PD2125a	2	141986909	LRP1B	ENST00000389484	A	G	SYNONYMOUS	p.N231N	c.693T>C
PD2125a	2	170034344	LRP2	ENST00000263816	G	A	SYNONYMOUS	p.I3454I	c.10362C>T
PD2147a	2	170175275	LRP2	ENST00000263816	A	G	MISSENSE	p.C103R	c.307T>C
PD3295a	8	133650319	LRRC6	ENST00000250173	C	T	SYNONYMOUS	p.V97V	c.291G>A
PD3441a	12	40702385	LRRK2	ENST00000298910	A	T	MISSENSE	p.K1359I	c.4076A>T
PD3441a	X	140996490	MAGEC1	ENST00000285879	A	G	SYNONYMOUS	p.P1100P	c.3300A>G
PD3441a	5	112720811	MCC	ENST00000408903	A	G	MISSENSE	p.F90S	c.269T>C
PD3295a	2	207622089	MDH1B	ENST00000454776	G	T	MISSENSE	p.L48I	c.142C>A
PD3441a	6	131914220	MED23	ENST00000368068	A	T	SYNONYMOUS	p.T1108T	c.3324T>A
PD2126a	1	171751154	METTL13	ENST00000458517	A	G	MISSENSE	p.Y15C	c.44A>G
PD2144a	18	2567091	METTL4	ENST00000319888	G	A	MISSENSE	p.S42F	c.125C>T
PD3441a	7	141673326	MGAM	ENST00000333797	C	A	MISSENSE	p.C55F	c.164G>T
PD2147a	16	14339507	MKL2	ENST00000318282	A	G	MISSENSE	p.D401G	c.1202A>G
PD3441a	1	11174458	MTOR	ENST00000361445	A	G	MISSENSE	p.V2406A	c.7217T>C
PD2127a	1	11184559	MTOR	ENST00000361445	G	A	MISSENSE	p.L2220F	c.6658C>T
PD3441a	20	42331358	MYBL2	ENST00000396863	C	T	MISSENSE	p.P393S	c.1177C>T
PD2144a	17	10399827	MYH1	ENST00000226207	G	T	MISSENSE	p.Q1566K	c.4696C>A
PD2126a	17	10426866	MYH2	ENST00000245503	C	A	NONSENSE	p.E1807*	c.5419C>A

PD3295a	13	109777493	MYO16	ENST00000356711	T	A	MISSENSE	p.L1168H	c.3503T>A
PD2126a	6	76589831	MYO6	ENST00000369985	T	A	SYNONYMOUS	p.P760P	c.2280T>A
PD3295a	8	90958403	NBN	ENST00000265433	A	G	MISSENSE	p.Y679H	c.2035T>C
PD3441a	16	4519450	NMRAL1	ENST00000404295	G	T	SYNONYMOUS	p.S19S	c.57C>A
PD2126a	16	77759415	NUDT7	ENST00000268533	C	T	SYNONYMOUS	p.S41S	c.123C>T
PD2127a	X	70779127	OGT	ENST00000415630	T	C	MISSENSE	p.L412P	c.1235T>C
PD2144a	19	15198065	OR1I1	ENST00000209540	C	G	SYNONYMOUS	p.L63L	c.189C>G
PD2127a	1	248309179	OR2M5	ENST00000366476	C	A	MISSENSE	p.H244N	c.730C>A
PD2127a	17	3195189	OR3A1	ENST00000397187	G	A	NONSENSE	p.R236*	c.706G>A
PD2127a	17	3195190	OR3A1	ENST00000397187	C	T	SYNONYMOUS	p.L235L	c.705G>A
PD2127a	11	56409040	OR5AP2	ENST00000302981	A	-	FRAMESHIFT	p.N26fs*13	C.76delA
PD3441a	6	29323566	OR5V1	ENST00000377151	A	G	MISSENSE	p.L136P	c.407T>C
PD2147a	1	158687308	OR6K3	ENST00000368146	C	T	MISSENSE	p.V216M	c.646G>A
PD2126a	11	57798938	OR6Q1	ENST00000302622	T	A	MISSENSE	p.F172I	c.514T>A
PD3441a	3	125266296	OSBPL11	ENST00000393455	T	C	MISSENSE	p.S218G	c.652A>G
PD2147a	20	49366431	PARD6B	ENST00000371610	T	C	SYNONYMOUS	p.D175D	c.525T>C
PD3441a	3	52613158	PBRM1	ENST00000394830	C	A	NONSENSE	p.E1124*	c.3370C>A
PD2126a	3	52649441	PBRM1	ENST00000337303	-	T	FRAMESHIFT	p.K621fs*9	c.1862insT
PD2127a	3	52678768	PBRM1	ENST00000337303	T	-	FRAMESHIFT	p.K284fs*16	c.851delA
PD3295a	3	52613132	PBRM1	ENST00000337303	GC	-	FRAMESHIFT	p.W1157fs*23	c.3471_3472delGC
PD2126a	12	96692721	PCTK2	ENST00000261211	G	A	MISSENSE	p.T214I	c.641C>T
PD2126a	10	95422894	PDE6C	ENST00000371447	T	G	MISSENSE	p.I826S	c.2477T>G
PD2127a	10	75675107	PLAU	ENST00000446342	A	G	MISSENSE	p.T340A	c.1018A>G
PD2144a	17	37263687	PLXDC1	ENST00000444435	G	A	MISSENSE	p.D12V	c.35C>T
PD2127a	11	74329770	POLD3	ENST00000263681	G	T	MISSENSE	p.G194V	c.581G>T
PD2127a	11	74329772	POLD3	ENST00000263681	A	T	MISSENSE	p.M195L	c.583A>T
PD2127a	2	46313388	PRKCE	ENST00000306156	A	-	FRAMESHIFT	p.D493fs*33	c.1479delC
PD2125a	12	50027318	PRPF40B	ENST00000261897	G	A	MISSENSE	p.D162N	c.484G>A
PD3295a	14	73673169	PSEN1	ENST00000394164	A	G	MISSENSE	p.Y311C	c.932A>G
PD2144a	21	30342888	RNF160	ENST00000361371	C	T	SYNONYMOUS	p.T387T	c.1161G>A
PD2147a	22	39710171	RPL3	ENST00000401609	G	T	MISSENSE	p.L246M	c.736C>A
PD2127a	3	38768438	SCN10A	ENST00000449082	G	A	MISSENSE	p.R916W	c.2746C>T
PD2125a	7	83634829	SEMA3A	ENST00000265362	G	A	MISSENSE	p.P396S	c.1186C>T
PD2126a	3	47164325	SETD2	ENST00000409792	T	A	NONSENSE	p.R601*	c.1801T>A

PD3295a	6	146243853	SHPRH	ENST00000275233	A	T	MISSENSE	p.V1222D	c.3665T>A
PD3295a	19	51958879	SIGLEC8	ENST00000440804	C	G	MISSENSE	p.V282L	c.844G>C
PD2125a	1	95330381	SLC44A3	ENST00000446120	G	T	MISSENSE	p.G405W	c.1213G>T
PD2127a	4	72420907	SLC4A4	ENST00000340595	A	G	SYNONYMOUS	p.A871A	c.2613A>G
PD2127a	19	49813078	SLC6A16	ENST00000454748	C	T	MISSENSE	p.E236K	c.706G>A
PD2127a	X	70147450	SLC7A3	ENST00000374299	A	T	MISSENSE	p.M356K	c.1067T>A
PD2125a	2	40656752	SLC8A1	ENST00000408028	A	T	SYNONYMOUS	p.S223S	c.669T>A
PD2127a	17	1690187	SMYD4	ENST00000305513	C	G	MISSENSE	p.A601P	c.1801G>C
PD3441a	7	123593637	SPAM1	ENST00000413927	A	C	MISSENSE	p.K5Q	c.13A>C
PD3295a	10	70641830	STOX1	ENST00000399162	G	T	NONSENSE	p.E143*	c.427G>T
PD2144a	1	152081494	TCHH	ENST00000368804	C	G	MISSENSE	p.R1400P	c.4199G>C
PD2147a	14	96136875	TCL6	ENST00000357168	T	C	MISSENSE	p.S119P	c.355T>C
PD2127a	16	58011759	TEPP	ENST00000441824	C	T	SYNONYMOUS	p.G68G	c.204C>T
PD2125a	3	111782388	TMPRSS7	ENST00000443106	T	A	SYNONYMOUS	p.S476S	c.1428T>A
PD2127a	17	16855793	TNFRSF13B	ENST00000261652	G	T	MISSENSE	p.H56N	c.166C>A
PD2127a	8	59750765	TOX	ENST00000361421	C	T	MISSENSE	p.A267T	c.799G>A
PD2147a	14	81606140	TSHR	ENST00000298171	T	G	SYNONYMOUS	p.L270L	c.810T>G
PD2125a	19	49398324	TULP2	ENST00000221399	C	T	MISSENSE	p.V149I	c.445G>A
PD2147a	X	118979153	UPF3B	ENST00000276201	tactgt	-	SPLICE	p.---	c.---
PD3295a	1	216497008	USH2A	ENST00000366942	G	A	MISSENSE	p.T453I	c.1358C>T
PD2147a	X	44969479	UTX	ENST00000377967	TG	-	FRAMESHIFT	p.Y1387fs*1	c.4161_4162delTG
PD2144a	3	10191534	VHL	ENST00000256474	G	-	FRAMESHIFT	p.Y175*	c.525delC
PD3295a	3	113060702	WDR52	ENST00000393845	G	T	MISSENSE	p.T257N	c.770C>A
PD3441a	12	49373404	WNT1	ENST00000293549	G	T	SYNONYMOUS	p.L86L	c.258G>T
PD2127a	20	43530469	YWHAB	ENST00000353703	G	A	MISSENSE	p.V99I	c.295G>A
PD2127a	19	12460630	ZNF442	ENST00000420150	T	A	MISSENSE	p.H590L	c.1769A>T
PD3295a	19	32845488	ZNF507	ENST00000355898	C	T	SYNONYMOUS	p.S584S	c.1752C>T

Sample	Sex	Age	Grade	Histology
PD1580a	F	61	3	clear cell
PD1582a	F	47	2	clear cell
PD1590a	M	64	2	clear cell
PD1593a	M	59	4	clear cell
PD1753a	M	67	3	clear cell
PD1754a	F	42	3	clear cell
PD1759a	M	76	3	clear cell
PD1767a	F	80	2	clear cell
PD1769a	M	43	3	clear cell
PD2125a	M	82	4	clear cell
PD2126a	F	74	1	clear cell
PD2127a	F	59	4	clear cell
PD2129a	M	75	4	clear cell
PD2130a	F	67	2	clear cell
PD2131a	F	63	4	clear cell
PD2133a	M	52	3	clear cell
PD2134a	F	83	3	clear cell
PD2135a	M	73	4	clear cell
PD2136a	M	67	3	clear cell
PD2138a	M	74	4	clear cell
PD2139a	F	62	2	clear cell
PD2140a	M	48	3	clear cell
PD2142a	M	49	3	clear cell
PD2144a	F	63	4	clear cell
PD2145a	M	63	2	clear cell
PD2146a	M	64	3	clear cell
PD2147a	F	50	2	clear cell
PD2148a	F	77	2	clear cell
PD2149a	M	66	4	clear cell
PD2154a	F	64	4	clear cell
PD2155a	M	50	3	clear cell
PD2157a	M	32	2	clear cell
PD2160a	M	73	3	clear cell
PD2161a	F	42	2	clear cell
PD2163a	M	54	3	clear cell
PD2167a	M	59	2	clear cell
PD2168a	M	53	4	clear cell
PD2170a	M	60	4	clear cell
PD2172a	M	67	3	clear cell
PD2173a	F	83	1	clear cell
PD2174a	F	65	2	clear cell
PD2177a	M	49	2	clear cell
PD2180a	F	45	2	clear cell
PD2181a	F	71	2	clear cell
PD2183a	F	66	1	clear cell
PD2185a	F	71	1	clear cell
PD2186a	M	50	2	clear cell
PD2187a	F	49	2	clear cell
PD2190a	F	61	2	clear cell

PD2191a	M	68	3	clear cell
PD2192a	M	78	3	clear cell
PD2193a	M	61	3	clear cell
PD2194a	M	74	3	clear cell
PD2198a	M	70	3	clear cell
PD2199a	M	58	2	clear cell
PD2203a	F	60	2	clear cell
PD2207a	M	66	2	clear cell
PD2208a	F	65	2	clear cell
PD2209a	F	69	3	clear cell
PD2213a	M	60	4	clear cell
PD2217a	M	44	4	clear cell
PD2219a	M	47	2	clear cell
PD2222a	F	54	N/D	clear cell
PD3284a	M	56	3	clear cell
PD3285a	F	80	3	clear cell
PD3286a	F	71	4	clear cell
PD3287a	M	61	2	clear cell
PD3290a	F	58	2	clear cell
PD3292a	M	76	3	papillary
PD3293a	M	80	3	clear cell
PD3294a	F	60	3	clear cell
PD3295a	M	62	4	clear cell
PD3296a	M	72	3	clear cell
PD3306a	F	80	2-3	Clear Cell w/ minor granular component
PD3307a	F	64	4	clear cell
PD3308a	M	43	3	clear cell
PD3309a	M	67	4	clear cell
PD3312a	F	81	3	clear cell
PD3313a	F	48	2	clear cell
PD3314a	F	58	3	clear cell
PD3316a	M	44	3	clear cell
PD3317a	M	62	2	clear cell
PD3318a	M	74	2	papillary
PD3324a	M	51	3	clear cell
PD3332a	M	65	1-2	Papillary (Chromophil)
PD3334a	M	48	2	papillary
PD3336a	F	74	2	clear cell
PD3337a	F	71	2	clear cell
PD3340a	M	49	2	clear cell
PD3342a	M	65	3	clear cell
PD3343a	M	69	2	papillary 1
PD3348a	M	57	2	clear cell
PD3349a	F	56	3	clear cell
PD3350a	M	51	2	clear cell
PD3351a	M	65	3	clear cell
PD3355a	F	59	2	clear cell
PD3363a	F	72	2	clear cell
PD3364a	M	70	3	clear cell

PD3365a	F	54	3	chromophobe
PD3368a	M	54	3	clear cell
PD3371a	F	56	2	clear cell
PD3372a	F	67	4	clear cell/Sarcomatoid
PD3375a	F	57	2	clear cell
PD3376a	F	82	2	clear cell
PD3378a	F	52	3	clear cell
PD3379a	M	62	2	clear cell
PD3381a	M	66	3	clear cell
PD3382a	M	56	2	clear cell
PD3385a	M	71	4	clear cell
PD3388a	F	73	4	clear cell/sarcomatoid
PD3389a	M	48	3-4	clear cell
PD3390a	F	67	4	clear cell
PD3391a	M	54	2	clear cell
PD3392a	M	50	2	clear cell
PD3393a	F	54	3	clear cell
PD3394a	M	61	4	clear cell
PD3395a	M	74		Mucinous Tubular and Spindle Cell Carcinoma
PD3397a		47	1 (focally 2-3)	clear cell
PD3399a	F	58	1-2	clear cell
PD3400a	M	51	3	clear cell
PD3402a	M	53	2	clear cell
PD3403a	M	63	3	papillary
PD3404a	F	55	2	clear cell
PD3405a	M	55	4	clear cell
PD3408a	F	78	2	clear cell
PD3409a	M	69	2	clear cell
PD3410a	F	54	4	clear cell
PD3411a	F	58	3	clear cell
PD3413a	F	51	3	clear cell
PD3420a	M	58	2	clear cell
PD3421a	M	65	3	clear cell
PD3422a	M	68	1-2	clear cell
PD3423a	M	61	2	papillary 1
PD3424a	M	66	3	clear cell
PD3425a	M	48	3	clear cell
PD3426a	M	51	2	chromophobe
PD3427a	M	50	2	clear cell
PD3436a	M	38	2	clear cell
PD3437a	F	68	2	clear cell
PD3438a	M	51	3	clear cell
PD3439a	M	59	3	clear cell
PD3440a	M	70	2	clear cell
PD3441a	M	69	1	clear cell
PD3442a	M	73	2	Papillary w/ focal clear cell
PD3443a	F	48	4	clear cell
PD3446a	M	72	3	NOS
PD3449a	M	69	4	Clear Cell

PD3452a	M	68	3	Clear Cell
PD3453a	F	64	2	clear cell
PD3454a	M	70	3	clear cell
PD3455a	F	42	4	clear cell/Sarcomatoid
PD3456a	M	36	3	clear cell
PD3457a	M	39	2	clear cell
PD3458a	F	69	3	chromophobe
PD3459a	F	52	3 (focal areas of 4)	clear cell
PD3467a	F	72	2	clear cell
PD3468a	M	41	4	#N/A
PD3469a	F	85	3	clear cell
PD3470a	F	58	3	clear cell
PD3471a	F	57	2	clear cell
PD3472a	M	66	3	clear cell
PD3473a	F	73	2	clear cell
PD3474a	M	62	2	papillary 1
PD3475a	M	69	4	papillary
PD3476a	F	46	2	clear cell
PD3479a	M	76		oncocytoma
PD3481a	F	80	3	clear cell
PD3483a	M	67	2	clear cell
PD3484a	M	72	3	clear cell
PD3485a	M	69	4	clear cell
PD3486a	M	70	3	papillary
PD3487a	M	44	3	clear cell
PD3488a	F	69	2	clear cell
PD3489a	F	58	2	clear cell
PD3490a	F	59	2	clear cell
PD3491a	M	87	3	clear cell
PD3492a	M	42	4	clear cell
PD3493a	F	78	3	clear cell
PD3494a	M	42	2	clear cell
PD3495a	M	71	4	clear cell
PD3497a	M	63	4	clear cell
PD3499a	M	55	2	clear cell
PD3500a	M	49	3	clear cell
PD3501a	F	83	2	clear cell
PD3502a	M	84	4	chromophobe
PD3503a	M	60	4	clear cell
PD3504a	F	37	2	clear cell
PD3505a	M	54	2	clear cell
PD3506a	F	62	2	clear cell
PD3507a	M	57	2	clear cell
PD3508a	F	71	2	clear cell
PD3509a	M	58	4	clear cell
PD3510a	F	89	2	clear cell
PD3511a	F	58	2	clear cell
PD3512a	M	83	3	clear cell
PD3513a	M	69	3	clear cell
PD3514a	F	43	3	clear cell

PD3515a	M	80	2	clear cell
PD3516a	F	68	3	clear cell
PD3518a	M	74	2	chromophobe
PD3519a	F	85	3	NOS
PD3520a	M	64	2-3	clear cell
PD3521a	M	54	3	clear cell
PD3522a	M	64	3	clear cell
PD3523a	F	47	3	clear cell
PD3524a	M	66	3	clear cell
PD3525a	F	74	1	clear cell
PD3526a	M	59		papillary
PD3528a	F	50	2	clear cell
PD3529a	M	56	2	clear cell
PD3530a	M	69	3	clear cell
PD3532a	M	41	2	clear cell
PD3534a	M	55	2	clear cell
PD3536a	F	71	3	Clear Cell
PD3538a	M	73	3	clear cell
PD3539a	M	78	3	NOS
PD3540a	F	52	2	clear cell
PD3541a	M	61	2	clear cell
PD3542a	F	59	2	clear cell
PD3543a	M	55	2	clear cell
PD3544a	F	50	3	papillary
PD3545a	M	54	2	chromophobe
PD3546a	F	57	2	clear cell
PD3547a	F	63	2	papillary
PD3548a	M	66	2	clear cell
PD3550a	M	44	2	clear cell
PD3552a	M	54	2	clear cell
PD3554a	F	55	3	clear cell
PD3555a	F	66	1	clear cell
PD3556a	M	69	2	clear cell
PD3557a	F	49	1	clear cell
PD3558a	M	55	2	clear cell
PD3559a	F	74	2	clear cell
PD3560a	F	78	2	clear cell
PD3561a	M	72	3-4	clear cell
PD3562a	F	73		oncocytoma
PD3563a	M	57	3	clear cell
PD3564a	F	68	3	clear cell
PD3565a	M	65	3	clear cell
PD3566a	M	44	3	clear cell
PD3567a	M	75	high	Papillary Urothelial Carcinoma
PD3568a	F	52	N/D	Urothelial Carcinoma
PD3569a	F	N/D	3	clear cell
PD3570a	M	51	2	papillary
PD3571a	M	72	3	papillary 2
PD3572a	F	46	N/D	oncocytoma
PD3573a	M	65	2	clear cell

PD3574a	M	38	3	clear cell
PD3575a	F	62	N/D	inflammatory myofibroblastic tumor
PD3576a	M	69	2	papillary
PD3577a	F	53	3	chromophobe
PD3578a	M	67	2-3	clear cell
PD3581a	M	66	3	clear cell
PD3582a	M	56	2	clear cell
PD3587a	M	N/D	2	clear cell
PD3588a	F	77	1	clear cell
PD3589a	M	91	3	clear cell
PD3590a	M	43	3	papillary 2
PD3591a	M	79	high	Urothelial Carcinoma
PD3592a	F	49	2	clear cell
PD3594a	M	44	2	clear cell
PD3596a	M	54	3	Clear Cell
PD3597a	M	60	2	clear cell
PD3598a	M	70	3	clear cell

Supplementary Table 4 - PBRM1 somatic mutations

Sample	Chr	Position	WT allele	Mut Allele	Annotated Trascript	Protein annotation	cDNA annotation	Type
PD1580a	3	52662980	T	-	ENST00000337303	p.N458fs*17	c.1373delA	INDEL
PD1590a	3	52712590	AT	-	ENST00000337303	p.Y54fs*1	c.162_163delTA	INDEL
PD1754a	3	52712583	GAT	-	ENST00000337303	p.I57del	c.169_171delATC	INFRAME DEL
PD1759a	3	52620608	T	A	ENST00000337303	p.K1074*	c.3220A>T	NONSENSE
PD1767a	3	52702550	GCTGG	A	ENST00000337303	p.Q117fs*56	c.348_352>T	INDEL
PD2127a	3	52643913	T	A	ENST00000337303	p.K661N	c.1983A>T	MISSENSE
PD2129a	3	52643561	G	A	ENST00000337303	p.Q779*	c.2335C>T	NONSENSE
PD2130a	3	52696193	C	-	ENST00000337303	p.D162fs*12	c.484delG	INDEL
PD2131a	3	52620701	TTAAAGTA	-	ENST00000337303	p.Y1043fs*9	c.3127_3134delTACTTTAA	INDEL
PD2135a	3	52597493	G	A	ENST00000337303	p.Q1298*	c.3892C>T	NONSENSE
PD2140a	3	52637682	T	-	ENST00000337303	p.E878fs*37	c.2634delA	INDEL
PD2145a	3	52651277	C	T	ENST00000337303	p.?	Exon 14 +1 G>A	ESSENTIAL_SPLICE
PD2146a	3	52678784	T	-	ENST00000337303	p.I279fs*4	c.835delA	INDEL
PD2154a	3	52712548	AG	-	ENST00000337303	p.C69fs*1	c.204_205delCT	INDEL
PD2155a	3	52668646	T	A	ENST00000337303	p.K425*	c.1273A>T	NONSENSE
PD2163a	3	52678763	C	A	ENST00000337303	p.E286*	c.856G>T	NONSENSE
PD2170a	3	52595987	G	C	ENST00000337303	p.?	Exon 25 -3 C>G	INTRONIC
PD2172a	3	52584514	G	C	ENST00000337303	p.S1500*	c.4499C>G	NONSENSE
PD2174a	3	52651306	G	T	ENST00000337303	p.A597D	c.1790C>A	MISSENSE
PD2181a	3	52597493	G	A	ENST00000337303	p.Q1298*	c.3892C>T	NONSENSE
PD2183a	3	52621485	ATGTTTC	-	ENST00000337303	p.E1003fs*9	c.3007_3013delGAAACAT	INDEL
PD2186a	3	52610623	TTCTTTTTTGTAGAACAT	-	ENST00000337303	p.M1209_E1214delMFYKKE	c.3625_3642delATGTTCTACAAAAAAGAA	INFRAME DEL
PD2186a	3	52610637	T	G	ENST00000337303	p.H1204P	c.3611A>C	MISSENSE
PD2190a	3	52643742	TGG	-	ENST00000337303	p.Y718_Q719>*	c.2154_2156delCCA	INDEL
PD2192a	3	52651294	TCAT	AT	ENST00000337303	p.N601fs*8	c.1802_1805>TA	INDEL
PD2193a	3	52696194	A	-	ENST00000337303	p.D161fs*13	c.483delT	INDEL
PD2194a	3	52643755	A	-	ENST00000337303	p.M714fs*17	c.2141delT	INDEL
PD2199a	3	52595782	C	A	ENST00000337303	p.?	Exon 25 +1 G>T	ESSENTIAL_SPLICE
PD2203a	3	52663050	T	-	ENST00000337303	p.T435fs*3	c.1303delA	INDEL
PD2207a	3	52661375	T	-	ENST00000337303	p.E486fs*14	c.1455delA	INDEL
PD2208a	3	52668757	G	A	ENST00000337303	p.Q388*	c.1162C>T	NONSENSE
PD2209a	3	52702591	T	-	ENST00000337303	p.M103fs*10	c.307delA	INDEL

PD2217a	3	52678784	T	-	ENST00000337303	p.I279fs*4	c.835delA	INDEL
PD2219a	3	52651332	T	-	ENST00000337303	p.D589fs*2	c.1764delA	INDEL
PD2222a	3	52685831	A	C	ENST00000337303	p.?	Exon 6 -5 T>G	INTRONIC
PD2222a	3	52643941	G	C	ENST00000337303	p.S652*	c.1955C>G	NONSENSE
PD3284a	3	52643959	GATTTTTTGGAGAAATGC	-	ENST00000337303	p.G646fs*4	c.1937_1955delGCATTTCTCCTAAAAAATC	INDEL
PD3290a	3	52643915	T	A	ENST00000337303	p.K661*	c.1981A>T	NONSENSE
PD3293a	3	52643770	-	T	ENST00000337303	p.R710fs*13	c.2126_2127insA	INDEL
PD3296a	3	52610615	G	T	ENST00000337303	p.Y1211*	c.3633C>A	NONSENSE
PD3308a	3	52595884	TGGGCCTTAATCA	-	ENST00000337303	p.V1396fs*32	c.4187_4199delTGATTAAGGCCCA	INDEL
PD3309a	3	52692216	A	-	ENST00000337303	p.V215fs*9	c.644delT	INDEL
PD3312a	3	52685827	C	T	ENST00000337303	p.?	Exon 6 -1 G>A	ESSENTIAL_SPLICE
PD3313a	3	52610715	CTTGGGGAGGAAAATATAA	-	ENST00000337303	p.?	Exon 22 -1 del(TTATATATTTTCCTCCCCAAG)	ESSENTIAL_SPLICE
PD3314a	3	52643772	TT	-	ENST00000337303	p.K708fs*14	c.2124_2125delAA	INDEL
PD3317a	3	52651527	C	A	ENST00000337303	p.M523I	c.1569G>T	MISSENSE
PD3336a	3	52584493	A	T	ENST00000337303	p.I1507N	c.4520T>A	MISSENSE
PD3337a	3	52651476	T	G	ENST00000337303	p.R540S	c.1620A>C	MISSENSE
PD3340a	3	52643966	TGCCACTCTT	-	ENST00000337303	p.K644fs*9	c.1930_1939delAAGAGTGGCA	INDEL
PD3349a	3	52712520	CTTCG	-	ENST00000337303	p.R78fs*7	c.232_236delCGAAG	INDEL
PD3355a	3	52649473	C	G	ENST00000337303	p.?	Exon 15 -1 G>C	ESSENTIAL_SPLICE
PD3363a	3	52712514	ACCTTCGCT	-	ENST00000337303	p.?	Exon 2 +2 del(AGCGAAGgt)	ESSENTIAL_SPLICE
PD3371a	3	52623178	ACATGGT	-	ENST00000337303	p.Y958fs*54	c.2873_2879delACCATGT	INDEL
PD3372a	3	52668733	A	-	ENST00000337303	p.C396fs*8	c.1186delT	INDEL
PD3375a	3	52643656	GCATCTT	-	ENST00000337303	p.K747fs*26	c.2240_2246delAAGATGC	INDEL
PD3379a	3	52610695	G	A	ENST00000337303	p.R1185*	c.3553C>T	NONSENSE
PD3382a	3	52643912	AG	-	ENST00000337303	p.L662fs*2	c.1984_1985delCT	INDEL
PD3385a	3	52597493	G	A	ENST00000337303	p.Q1298*	c.3892C>T	NONSENSE
PD3391a	3	52643874	A	C	ENST00000337303	p.D674E	c.2022T>G	MISSENSE
PD3400a	3	52702535	TG	-	ENST00000337303	p.N121fs*7	c.363_364delCA	INDEL
PD3402a	3	52702591	T	-	ENST00000337303	p.M103fs*10	c.307delA	INDEL
PD3411a	3	52702511	T	A	ENST00000337303	p.?	Exon 3 +3 A>T	INTRONIC
PD3413a	3	52643561	G	A	ENST00000337303	p.Q779*	c.2335C>T	NONSENSE
PD3422a	3	52589246	T	-	ENST00000337303	p.K1232fs*37	c.3695delA	INDEL
PD3437a	3	52668807	AGTGATGCTTTCTGCTTCTG	-	ENST00000337303	p.S371fs*14	c.1112_1131delCAGAAGCAGAAAGCATCACT	INDEL

PD3438a	3	52582134	-	A	ENST00000337303	p.L1565fs*>19	c.4694_4695insT	INDEL
PD3457a	3	52623136	T	-	ENST00000337303	p.N972fs*42	c.2915delA	INDEL
PD3467a	3	52649441	A	T	ENST00000337303	p.L617*	c.1850T>A	NONSENSE
PD3469a	3	52620607	TT	-	ENST00000337303	p.K1074fs*32	c.3221_3222delAA	INDEL
PD3470a	3	52649469	A	-	ENST00000337303	p.Y608fs*34	c.1822delT	INDEL
PD3472a	3	52637691	A	-	ENST00000337303	p.R876fs*39	c.2625delT	INDEL
PD3476a	3	52696289	TATTCAGGAGAATC	-	ENST00000337303	p.D130fs*1	c.388_401delGATTCTCCTGAATA	INDEL
PD3487a	3	52620611	T	-	ENST00000337303	p.I1073fs*86	c.3217delA	INDEL
PD3490a	3	52712586	-	T	ENST00000337303	p.T56fs*6	c.166_167insA	INDEL
PD3492a	3	52677318	G	T	ENST00000337303	p.S314*	c.941C>A	NONSENSE
PD3501a	3	52649430	T	C	ENST00000337303	p.K621E	c.1861A>G	MISSENSE
PD3506a	3	52712614	C	-	ENST00000337303	p.?	Exon 2 -1 del(G)	ESSENTIAL_SPLICE
PD3511a	3	52623085	TTAC	-	ENST00000337303	p.?	Exon 18 +1 del(GTAA)	ESSENTIAL_SPLICE
PD3524a	3	52663053	T	A	ENST00000337303	p.?	Exon 12 -2 A>T	ESSENTIAL_SPLICE
PD3529a	3	52685778	T	G	ENST00000337303	p.T232P	c.694A>C	MISSENSE
PD3536a	3	52584541	G	-	ENST00000337303	p.P1491fs*14	c.4472delC	INDEL
PD3538a	3	52610715	C	A	ENST00000337303	p.?	Exon 22 -1 G>T	ESSENTIAL_SPLICE
PD3540a	3	52643510	C	-	ENST00000337303	p.E796fs*9	c.2386delG	INDEL
PD3541a	3	52613210	T	-	ENST00000337303	p.E1132fs*27	c.3393delA	INDEL
PD3543a	3	52582239	T	-	ENST00000337303	p.D1530fs*17	c.4589delA	INDEL
PD3548a	3	52682460	T	C	ENST00000337303	p.?	Exon 7 -2 A>G	ESSENTIAL_SPLICE
PD3550a	3	52663035	G	A	ENST00000337303	p.Q440*	c.1318C>T	NONSENSE
PD3554a	3	52597340	G	-	ENST00000337303	p.L1349fs*35	c.4045delC	INDEL
PD3555a	3	52702645	-	A	ENST00000337303	p.Y85fs*2	c.253_254insT	INDEL
PD3556a	3	52696272	GTTTGCAAGCGGCT	-	ENST00000337303	p.K135fs*11	c.405_418delAGCCGCTTGCAAAC	INDEL
PD3559a	3	52643974	TTTTCATTTTTTAGGAGAAATGCCACTCTTCCTACCTA	-	ENST00000337303	p.?	Exon 16 -3 del(tagGTAGGAAGAGTGGCATTTCTCCTAAAAAATCAAAA)	ESSENTIAL_SPLICE
PD3563a	3	52589125	T	-	ENST00000337303	p.G1273fs*2	c.3816delA	INDEL
PD3573a	3	52712587	A	-	ENST00000337303	p.N55fs*40	c.165delT	INDEL
PD3582a	3	52668716	C	-	ENST00000337303	p.Q402fs*2	c.1203delG	INDEL
PD3587a	3	52651439	T	A	ENST00000337303	p.K553*	c.1657A>T	NONSENSE
PD3588a	3	52613142	TCAT	-	ENST00000337303	p.N1154fs*4	c.3461_3464delATGA	INDEL
PD3596a	3	52610766	T	-	ENST00000337303	p.E1214fs*4	c.3639delA	NONSENSE

Sample	Tissue	Histology	Zygosity	CHr	Position	WT allele	Mut Allele	Annotated Transcript	cDNA Annotation	Protein Annotation	Type
NCI-H1793	Lung	Adenocarcinoma	Heterozygous	3	52692313	T	A	ENST00000337303	c.547A>T	p.K183*	NONSENSE
OC-314	Ovary	Serous micropapillary carcinoma	Heterozygous	3	52678727	G	A	ENST00000337303	c.892C>T	p.R298*	NONSENSE
PANC-10-05	Pancreas	Ductal carcinoma	Homozygous	3	52651496	G	A	ENST00000337303	c.1600C>T	p.R534*	NONSENSE
ESS-1	Endometrium	Carcinosarcoma-malignant mesodermal mixed tumour	Heterozygous	3	52643768	G	A	ENST00000337303	c.2128C>T	p.R710*	NONSENSE
HCC2998	Large intestine, colon	Adenocarcinoma	Heterozygous	3	52643768	G	A	ENST00000337303	c.2128C>T	p.R710*	NONSENSE
ACHN	Kidney	Renal cell carcinoma	Heterozygous	3	52620674	G	A	ENST00000337303	c.3154C>T	p.R1052*	NONSENSE
NCI-H226	Lung	Squamous cell carcinoma	Homozygous	3	52584768	G	A	ENST00000337303	c.4354C>T	p.Q1452*	NONSENSE
TALL-1	Haematopoietic and lymphoid tissue	Lymphoid neoplasm, acute lymphoblastic T cell leukaemia	Heterozygous	3	52584629	G	A	ENST00000337303	c.4384C>T	p.Q1462*	NONSENSE
CW-2	Large intestine, colon	Carcinoma	Heterozygous	3	52678784	T	-	ENST00000337303	c.835delA	p.I279fs*4	INDEL
NCI-SNU-1	Stomach	Carcinoma	Heterozygous	3	52678784	T	-	ENST00000337303	c.835delA	p.I279fs*4	INDEL
A704	Kidney	Renal cell carcinoma	Homozygous	3	52651383	-	AA	ENST00000337303	c.1713_1714insTT	p.E572fs*16	INDEL
NCI-H2196	Lung	Small cell carcinoma	Homozygous	3	52637580	T	-	ENST00000337303	c.2736delA	p.E913fs*2	INDEL
TGBC24TKB	Biliary tract, bile duct	Carcinoma	Homozygous	3	52613114	-	A	ENST00000337303	c.3489_3490insT	p.V1164fs*17	INDEL
SUP-T1	Haematopoietic and lymphoid tissue	Lymphoid neoplasm, acute lymphoblastic T cell leukaemia	Heterozygous	3	52597340	G	-	ENST00000337303	c.4045delC	p.L1349fs*35	INDEL
HCC2998	Large intestine, colon	Adenocarcinoma	Heterozygous	3	52582255	A	C	ENST00000337303	Exon 28 -4 T>G	p.?	INTRONIC
NCI-H378	Lung	Small cell carcinoma	Homozygous	3	52623082	C	T	ENST00000337303	Exon 17 +4 G>A	p.?	INTRONIC
NCI-H650	Lung	Bronchioloalveolar adenocarcinoma	Heterozygous	3	52712607	C	G	ENST00000337303	c.145G>C	p.V49L	MISSENSE
8-MG-BA	Central nervous system, frontal lobe	Glioma, astrocytoma Grade IV, glioblastoma multiforme	Homozygous	3	52712586	T	C	ENST00000337303	c.166A>G	p.T56A	MISSENSE
SW1417	Large intestine, colon	Adenocarcinoma	Homozygous	3	52712556	T	C	ENST00000337303	c.196A>G	p.R66G	MISSENSE
647-V	Urinary tract, bladder	Transitional cell carcinoma	Heterozygous	3	52702630	G	C	ENST00000337303	c.268C>G	p.Q90E	MISSENSE
A4-Fuk	Skin	Malignant melanoma	Heterozygous	3	52696246	T	A	ENST00000337303	c.431A>T	p.Y144F	MISSENSE
A4-Fuk	Skin	Malignant melanoma	Heterozygous	3	52696198	T	G	ENST00000337303	c.479A>C	p.E160A	MISSENSE
SNG-M	Endometrium	Adenocarcinoma	Heterozygous	3	52692256	G	A	ENST00000337303	c.604C>T	p.R202C	MISSENSE
CCRF-CEM	Haematopoietic and lymphoid tissue	Haematopoietic neoplasm, acute lymphoblastic leukaemia	Heterozygous	3	52692244	C	T	ENST00000337303	c.616G>A	p.E206K	MISSENSE
CTV-1	Haematopoietic and lymphoid tissue	Haematopoietic neoplasm, acute myeloid leukaemia, M5	Heterozygous	3	52685795	T	C	ENST00000337303	c.677A>G	p.E226G	MISSENSE
MDA-MB-231	Breast	Carcinoma	Heterozygous	3	52685790	T	C	ENST00000337303	c.682A>G	p.I228V	MISSENSE
OS-RC-2	Kidney	Renal cell carcinoma	Homozygous	3	52685774	A	G	ENST00000337303	c.698T>C	p.I233T	MISSENSE
OVCAR-5	Ovary	Carcinoma	Heterozygous	3	52682407	C	T	ENST00000337303	c.766G>A	p.A256T	MISSENSE
IGR-1	Skin	Malignant melanoma	Homozygous	3	52676038	C	G	ENST00000337303	c.1019G>C	p.G340A	MISSENSE
A388	NS	Carcinoma	Heterozygous	3	52643864	G	A	ENST00000337303	c.2032C>T	p.R678C	MISSENSE
LC4-1	Haematopoietic and lymphoid tissue	Haematopoietic neoplasm, acute lymphoblastic leukaemia	Heterozygous	3	52637638	T	C	ENST00000337303	c.2678A>G	p.Y893C	MISSENSE

SBC-1	Lung	Small cell carcinoma	Homozygous	3	52637638	T	C	ENST00000337303	c.2678A>G	p.Y893C	MISSENSE
SNU-449	Liver	Hepatocellular carcinoma	Heterozygous	3	52637638	T	C	ENST00000337303	c.2678A>G	p.Y893C	MISSENSE
NCI-H446	Lung	Small cell carcinoma	Heterozygous	3	52637633	T	A	ENST00000337303	c.2683A>T	p.T895S	MISSENSE
ZR-75-30	Breast	Ductal carcinoma	Heterozygous	3	52637552	C	G	ENST00000337303	c.2764G>C	p.E922Q	MISSENSE
HCC2998	Large intestine, colon	Adenocarcinoma	Heterozygous	3	52637543	T	G	ENST00000337303	c.2773A>C	p.K925Q	MISSENSE
BONNA-12	Haematopoietic and lymphoid tissue	Lymphoid neoplasm, hairy cell leukaemia	Heterozygous	3	52620536	C	A	ENST00000337303	c.3292G>T	p.A1098S	MISSENSE
RS4-11	Haematopoietic and lymphoid tissue	Haematopoietic neoplasm, acute leukaemia	Heterozygous	3	52620469	C	T	ENST00000337303	c.3359G>A	p.R1120Q	MISSENSE
BFTC-909	Kidney	Carcinoma	Heterozygous	3	52613074	C	T	ENST00000337303	c.3529G>A	p.G1177S	MISSENSE
MDA-MB-415	Breast	Carcinoma	Homozygous	3	52589082	C	G	ENST00000337303	c.3859G>C	p.E1287Q	MISSENSE
Calu-3	Lung	Adenocarcinoma	Heterozygous	3	52595830	C	T	ENST00000337303	c.4241G>A	p.G1414E	MISSENSE
NCI-SNU-1	Stomach	Carcinoma	Heterozygous	3	52588842	C	A	ENST00000356770	c.4246G>T	p.G1416C	MISSENSE
HEC-1	Endometrium	Adenocarcinoma	Heterozygous	3	52584763	C	A	ENST00000337303	c.4359G>T	p.Q1453H	MISSENSE
EVSA-T	Breast	Carcinoma	Heterozygous	3	52582210	G	A	ENST00000337303	c.4618C>T	p.R1540C	MISSENSE
RKO	Large intestine, colon	Carcinoma	Heterozygous	3	52620593	GG	TA	ENST00000337303	c.3235_3236CC>TA	p.P1079>Y	INDEL
HCE-T	Upper aerodigestive tract, sinonasal and nasal cavity, sinus	Squamous cell carcinoma	Heterozygous	3	52613207	TCT	-	ENST00000337303	c.3396_3398delAGA	p.E1132_D1133>D	SILENT

Supplemental Table X. Deregulated Gene Sets in PBRM1 Knockdown Cellines

Gene Set Description[a,b]	Significance of enrichment		
	786-O	SN12C	TK10
CHROMOSOME_INSTABILITY - PMID: 16921376	0.0001	0.0001	0.0001
ZHAN_MM_CD138_PR_VS_REST	0.0002	0.0004	0.0001
IDX_TSA_UP_CLUSTER3	0.0001	0.0022	0.0001
SERUM_FIBROBLAST_CELLCYCLE	0.0001	0.0301	0.0002
DOX_RESIST_GASTRIC_UP	0.0001	0.0332	0.0003
P21_P53_ANY_DN	0.0054	0.0032	0.0001
CROONQUIST_IL6_STARVE_UP	0.0058	0.0078	0.0001
CROONQUIST_IL6_RAS_DN	0.0025	0.0322	0.0001
DNA_REPLICATION_REACTOME	0.0060	0.0418	0.0002
ADIP_DIFF_CLUSTER4	0.0038	0.0083	0.0016
GAY_YY1_DN	0.0011	0.0297	0.0028
HSA00240_PYRIMIDINE_METABOLISM	0.0015	0.0038	0.0189
LEE_TCELLS3_UP	0.0377	0.0161	0.0002
OLDAGE_DN	0.0001	0.0287	0.0460
PYRIMIDINE_METABOLISM	0.0012	0.0153	0.0196
IGF_VS_PDGF_DN	0.0016	0.0267	0.0295
GOLDRATH_CELLCYCLE	0.0087	0.0262	0.0096
P21_ANY_DN	0.0160	0.0173	0.0098
P21_P53_MIDDLE_DN	0.0043	0.0249	0.0412
GERY_CEBP_TARGETS	0.0085	0.0190	0.0382

[a]Pathways were obtained from the MSigDB with the exception of the CHROMOSOME_INSTABILITY gene set that was obtained from the BioConductor PGSEA package

[b]Comparisons between PBRM1 targeting and scrambled siRNA

Sample	Chromosome	Position	WT base	Mut Base	Gene	Annotated Transcript	Type	Protein Annotation	cDNA Annotation
PD2125a	1	145075775	G	A	PDE4DIP	ENST00000369359	MISSENSE	p.P30S	c.88C>T
PD2125a	4	190904395	T	C	AF146191.1	ENST00000248151	SILENT	p.A196A	c.588A>G
PD2126a	1	17083888	C	T	MSTP9	ENST00000455405	MISSENSE	p.G663S	c.1987G>A
PD2126a	11	76954792	G	T	GDPD4	ENST00000376217	MISSENSE	p.N396K	c.1188C>A
PD2127a	2	108479275	A	G	RGPD4	ENST00000408999	SILENT	p.P781P	c.2343A>G
PD2127a	3	62459846	A	T	CADPS	ENST00000478408	ESSENTIAL_SPLICE	p.---	c.-T>A
PD2127a	6	31238942	G	T	HLA-C	ENST00000423188	MISSENSE	p.A176E	c.527C>A
PD2127a	7	102196401	T	G	POLR2J3	ENST00000432940	MISSENSE	p.M145R	c.434T>G
PD2127a	9	43891510	A	C	CNTNAP3B	ENST00000377561	SILENT	p.T900T	c.2699A>C
PD2127a	16	66679	T	C	WASH4P	ENST00000326592	SILENT	p.P260P	c.780A>G
PD2144a	1	16973996	A	G	RP5-1182A14.1	ENST00000334429	MISSENSE	p.I97V	c.289A>G
PD2144a	9	33385235	T	G	AQP7	ENST00000379507	MISSENSE	p.Y265S	c.794A>C
PD2144a	21	14983063	G	C	POTED	ENST00000299443	MISSENSE	p.E172Q	c.514G>C
PD2147a	4	79792166	C	G	BMP2K	ENST00000389010	MISSENSE	p.H487Q	c.1461C>G
PD2147a	5	140563853	T	C	PCDHB16	ENST00000361016	SILENT	p.T573T	c.1719T>C
PD2147a	9	33386167	G	C	AQP7	ENST00000447660	MISSENSE	p.Q13E	c.37C>G
PD2147a	9	67968287	G	T	ANKRD20A3	ENST00000377477	MISSENSE	p.A616S	c.1846G>T
PD2147a	9	67968295	C	T	ANKRD20A3	ENST00000377477	SILENT	p.S618S	c.1854C>T
PD2147a	11	66444273	T	A	RBM4B	ENST00000310046	MISSENSE	p.E93V	c.278A>T
PD2147a	17	45219620	G	A	CDC27	ENST00000066544	SILENT	p.A451A	c.1353C>T
PD3295a	3	75718298	C	T	RP11-413E6.1	ENST00000420018	MISSENSE	p.R100C	c.298C>T
PD3295a	10	51225281	C	G	AGAP8	ENST00000425119	MISSENSE	p.Q567H	c.1701G>C
PD3295a	17	20254267	T	G	AC008088.2	ENST00000444742	MISSENSE	p.S578A	c.1732T>G
PD3441a	15	20362850	T	C	AC126603.2	ENST00000442923	MISSENSE	p.Y38H	c.112T>C
PD3441a	15	75982275	T	C	CSPG4	ENST00000308508	SILENT	p.A377A	c.1131A>G
PD3441a	17	14095383	T	A	COX10	ENST00000261643	MISSENSE	p.L258H	c.773T>A
PD3441a	17	16068340	C	T	NCOR1	ENST00000417028	MISSENSE	p.E50K	c.148G>A

PBRM1 primer sequences

STS	Forward Primer	Reverse Primer
stCE03-616895	AAACAAGGAAGTCCAGGGC	AAAAAGTGGAGATGCCTTGC
stCE03-616896	TTGGAAGCGGGATTTGGA	GGCACACGTTGTCCAGGAT
stCE03-616897	TTTGTCTGCAGGTTATATTTCACT	GTTTCAAGCAGGACTTTGTGTAG
stCE03-616898	CCCTCTAGATCTGAGTTGCCTG	ATCCTTCTTGCTCGTTCCAA
stCE03-616899	CCCAAATGTGACTTTGCTGA	AAGAGATTTTCAATTTTGTCTTCCTC
stCE03-616900	AAGTATCTTTTCATGTGTTTAATGGG	AAAAAGCACAAATACCTACCGA
stCE03-616901	CCATATGGACAACAGGTGAGC	AAACATGCAAAGAAACTCCAAAC
stCE03-616902	GAAATGTGCCTGGAAATATTCTG	TTGAAATAGCTTATTAAAAGTGTCCG
stCE03-616903	AAGTAAGCTTCAAAGTCCATGAAA	TAAAAATCATATGAATGTCCAGTCTC
stCE03-616905	GTTGCTGTTTTGAATTAGCTCTACA	CAACATCTTCCTTTTGAACTTACTTT
stCE03-616906	ATGGTTCTGATATAATAAATGTGCTG	TATAATCAGAAATGTCGGTAACCA
stCE03-616907	TACCTTAATGTAATGGTGCTTTTGC	TAATATTACTGCTGAGGGTGGGG
stCE03-616908	TTTTGTCATGCAGGCTTTTG	ATGTAGTAGTCATTTTCATCTGGGTC
stCE03-616909	CATGCAGTACTAAGGGTGCTTTATT	CTCTGCCATGTGTGCTGTG
stCE03-616910	TGACTTTACATGTTGTTCATATGTGT	AACTAACCTTGAATACTTGAGAGCC
stCE03-616911	GATTGATGGTGTATTTCCTAATTTTG	CAGAGTTCCTAATTTTGTAAACATCG
stCE03-616912	AAACTCTTTCCATGCTGCCT	TCATGGCACTGACAAAATCTG
stCE03-616913	GTTCAGCTTTTGTTTGGTTGG	TTCCTGTTTGGCTAAGGTTTTG
stCE03-616914	ACTCAGTTGTTTGAAAGGAGACA	AAAAAGCTTCACTACAGCTTGATTA
stCE03-616915	TGAAGATAGATATTTTGGAAGCTTGT	AGACATTTTCTTAAACCTACCTCATTC
stCE03-616916	AGTTGGGGGCATTAAGCTGT	CAGCAAATATAAAGGCATTAAGGG
stCE03-616917	TGCTTATAACTTCCAGCATGGTT	CTATAAGTACCCCTCTCCCGC
stCE03-616918	GGTTAAACCATCCAAAAAGGA	GGAACGTTTATCTTTATAATGTACTGC
stCE03-616919	CAAACTTCGGAAAGATACTCTTCA	TTCCATCTCATTGCGTCTACTC
stCE03-616920	GCATGTTGCAAATGGAATTAAA	TGTGACACTTGCCCAATAGGT
stCE03-616921	GTGTTCCTGGCTTCTGAAAAA	TCACAGCCCTCATCTCACTG
stCE03-616922	TTAAGTACAGAGATAAACTAAGGAGGC	GTTTTAAACCAGGATCTGCTAAGT
stCE03-616923	CAGGACTTTTGTTAAAACCTGC	CAGAAAAATCAGCAATCTCTTCTT
stCE03-616924	TTGGAATGTAGGTTTATAATGATGC	CTGTCCAGTTGGAACTGCTG
stCE03-616925	CCACAAAGATTCAAGGGCAG	TAATGCTGTTGGACTCCGC
stCE03-616926	GTACCAGGTCCTCTGGTCACT	AATAAACCATTTGACAACAGATTCTC
stCE03-616995	TTGAGCAGTTAACCAAATGTAATGT	TTTTGGAGAAATTTGCAGGG
stCE03-616996	GTAACTATGACCACAGTTTACTCCTTT	TGACAGGATATAAACCAGAACCA
stCE03-616997	AAGAAAAGTCTGCTTTCGTTTCTTAC	GTGTCACTTCAAATTTATGCTAAAGG
stCE03-616998	ATATTTAGTTCAATCTGGAAGGTTGT	GGTAATGAACAGTTAAAATTTGAGG