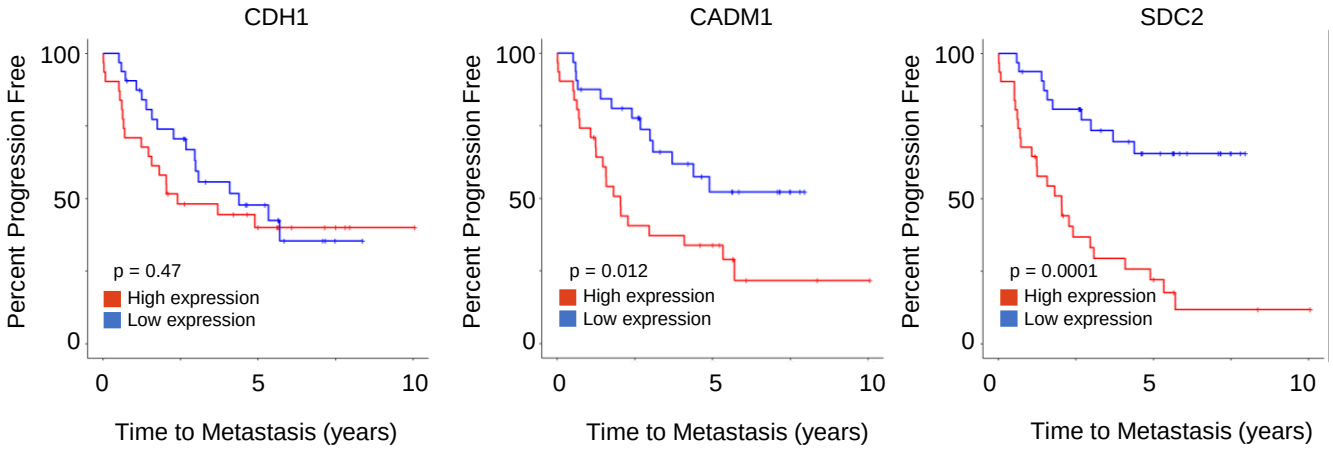
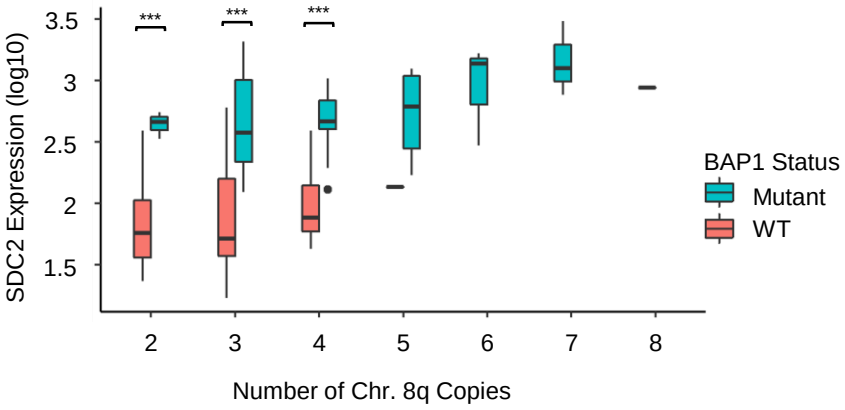
A



B

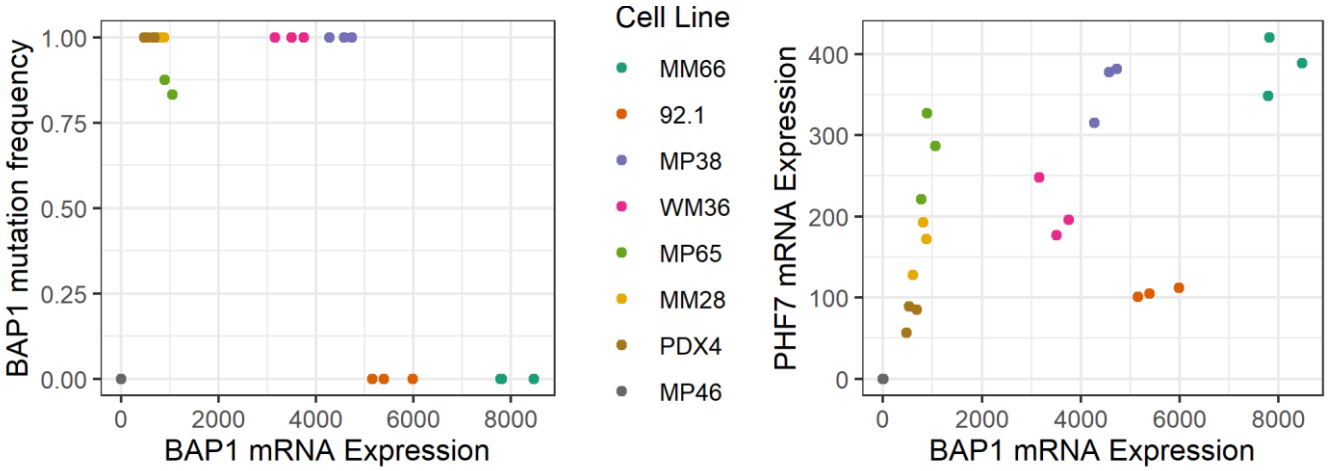
PFS Predictor	Hazard Ratio	95% LL	95% UL	p-value
SDC2 Expression (log10)	2.96	1.26	6.96	0.0128
Number of Chr. 8q Copies	1.35	0.98	1.85	0.0659

C

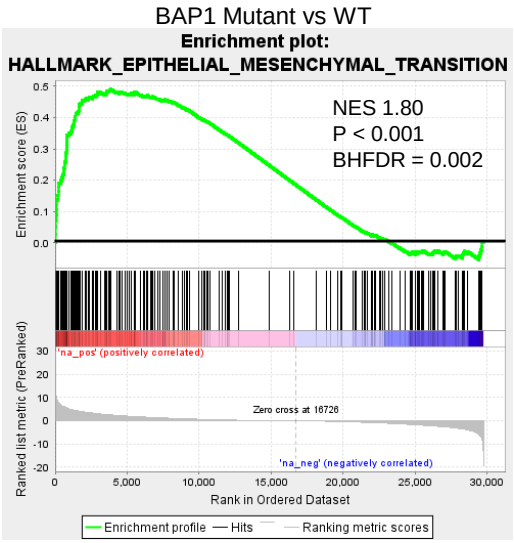


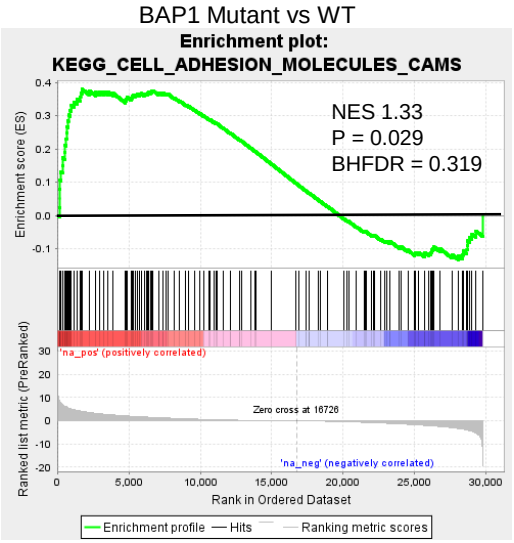
Supplementary Figure 1: Alternate data set shows increased expression *CADM1* and *SDC2* results in worse progression free survival. **(A)** Kaplan-Meier plots showing metastasis-free survival for patients stratified by median RNA expression of *CDH1* (left panel), *CADM1* (middle panel) and *SDC2* (right panel), in an independent cohort of 63 UM patients (80). **(B)** Table showing cox proportional hazards (PH) model analysis results for the association between progression-free survival, $\log_{10}$-transformed *SDC2* gene expression and chromosome 8q copy number alteration status for TCGA cohort. **(C)** Box plot showing $\log_{10}$-transformed expression of *SDC2* (y-axis) and the number of copies of chromosome 8q (x-axis). Samples are grouped based on *BAP1* mutation status. PFS, Progression Free Survival; *** p-value < 0.001

A

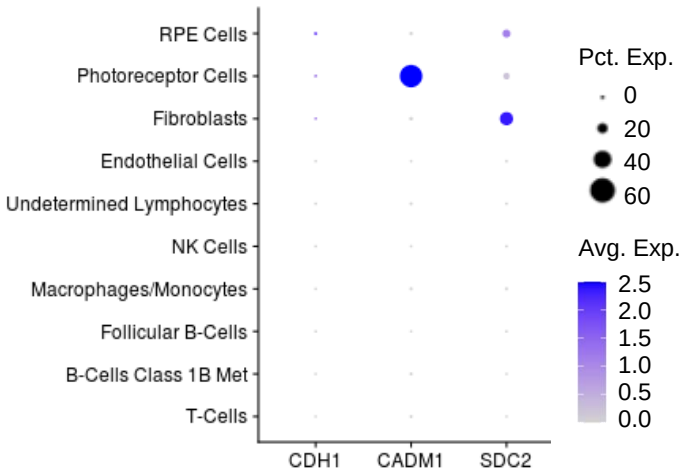

BAP1 mutation frequency
1.00
0.75
0.50
0.25
0.00
0
2000
4000
6000
8000
BAP1 mRNA Expression
Cell Line
MM66
92.1
MP38
WM36
MP65
MM28
PDX4
MP46
PHF7 mRNA Expression
400
300
200
100
0
0
2000
4000
6000
8000
BAP1 mRNA Expression

B

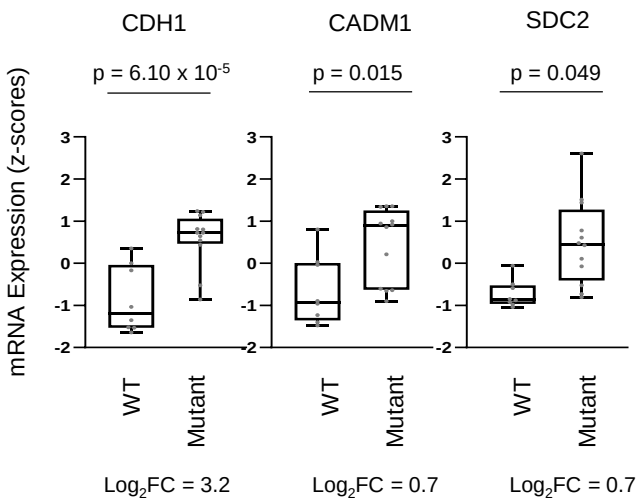

BAP1 Mutant vs WT
Enrichment plot:
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
NES 1.80
P < 0.001
BHFDR = 0.002
Enrichment score (ES)
'na_pos' (positively correlated)
Zero cross at 16726
'na_neg' (negatively correlated)
Ranked list metric (PreRanked)
Rank in Ordered Dataset
Enrichment profile
Hits
Ranking metric scores


BAP1 Mutant vs WT
Enrichment plot:
KEGG_CELL_ADHESION_MOLECULES_CAMS
NES 1.33
P = 0.029
BHFDR = 0.319
Enrichment score (ES)
'na_pos' (positively correlated)
Zero cross at 16726
'na_neg' (negatively correlated)
Ranked list metric (PreRanked)
Rank in Ordered Dataset
Enrichment profile
Hits
Ranking metric scores

C

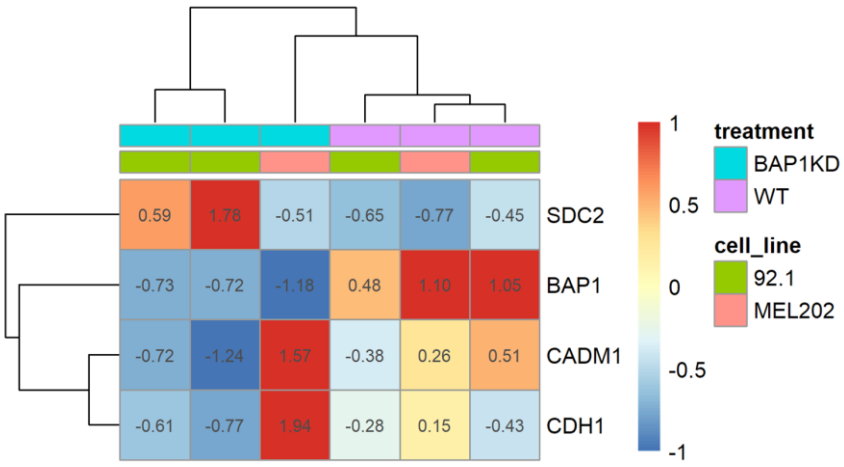

RPE Cells
Photoreceptor Cells
Fibroblasts
Endothelial Cells
Undetermined Lymphocytes
NK Cells
Macrophages/Monocytes
Follicular B-Cells
B-Cells Class 1B Met
T-Cells
CDH1
CADM1
SDC2
Pct. Exp.
0
20
40
60
Avg. Exp.
2.5
2.0
1.5
1.0
0.5
0.0

D

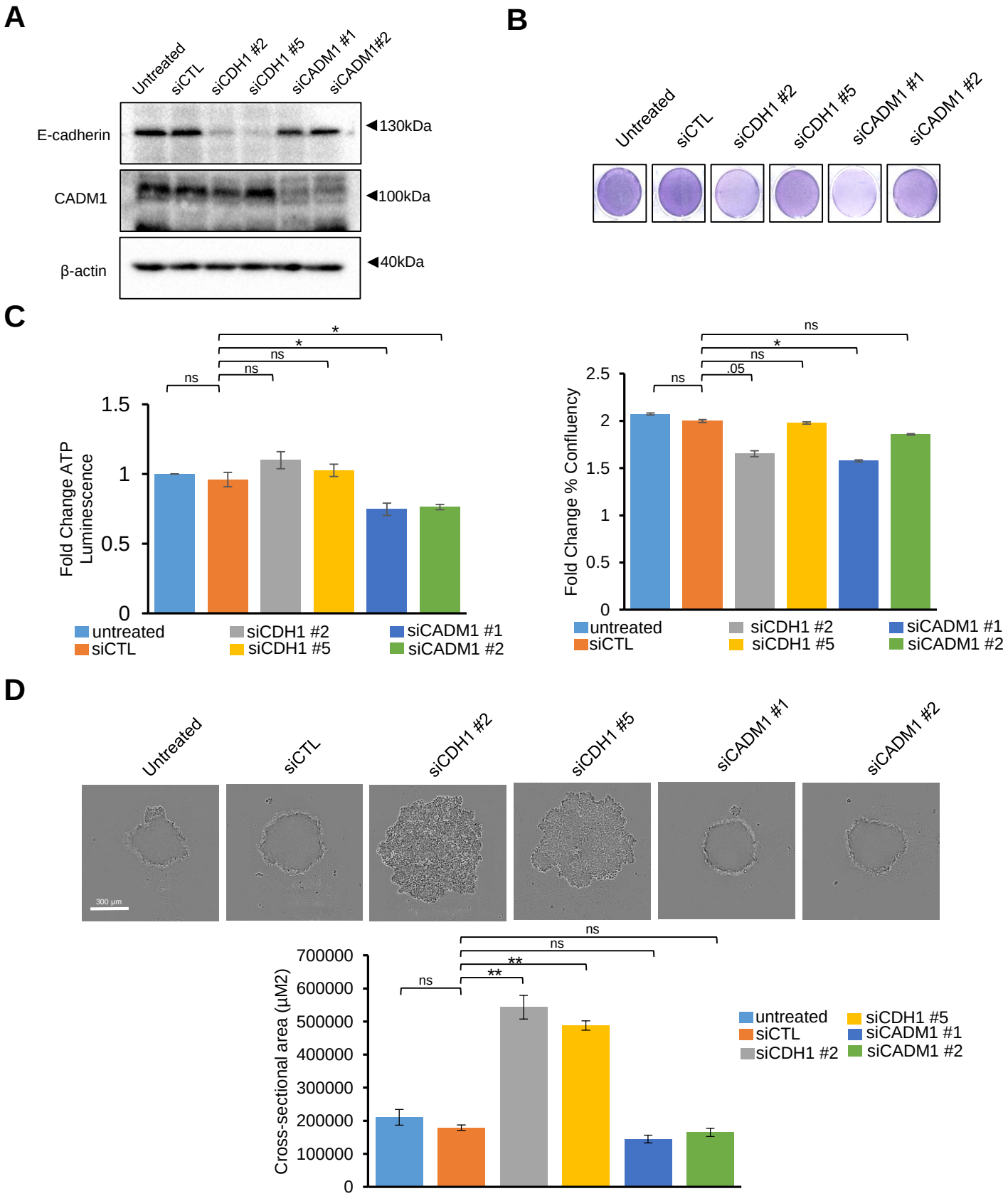

CDH1
CADM1
SDC2
p = 6.10 x 10-5
p = 0.015
p = 0.049
mRNA Expression (z-scores)
WT
Mutant
Log2FC = 3.2
Log2FC = 0.7
Log2FC = 0.7

Supplementary Figure 2: Cell adhesion molecule expression is enriched on cancer cells

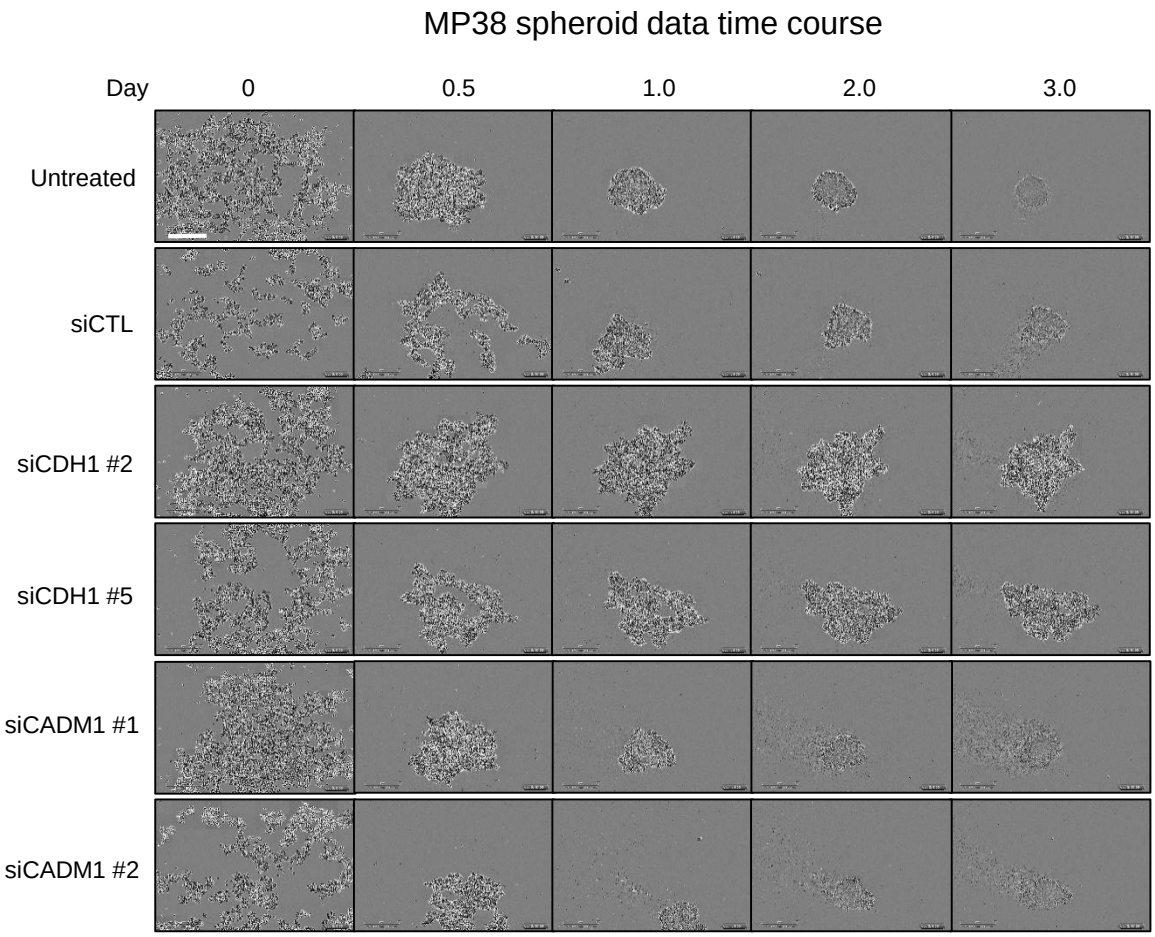
(A) Scatter plots showing *BAP1* mRNA expression compared to *BAP1* mutation frequency (left) or *PHF7* mRNA expression (right) for each cell line sample. **(B)** Enrichment plots of Hallmark EMT (left panel) and KEGG CAMs pathway (right panel) gene sets for *BAP1* mutant vs wild-type cell line RNA seq data. **(C)** Dot plots showing the average expression and percent of cells expressing *CDH1*, *CADM1* and *SDC2* in non-malignant cells from all *BAP1* wild-type and mutant UM tumor samples. **(D)** Box plots showing expression of *CDH1*, *CADM1* and *SDC2* in an independent cohort of BAP1 mutant and wild-type UM cell line samples.



Supplementary Figure 3: Changes in cell adhesion molecules gene expression due to BAP1 knockdown. A heatmap showing expression of *BAP1*, *CDH1*, *CADM1*, and *SDC2* in *BAP1* knockdown and wild-type cell line samples.


A
Untreated
siCTL
siCDH1 #2
siCDH1 #5
siCADM1 #1
siCADM1#2
E-cadherin
CADM1
β-actin
130kDa
100kDa
40kDa
B
Untreated
siCTL
siCDH1 #2
siCDH1 #5
siCADM1 #1
siCADM1 #2
C
Fold Change ATP Luminescence
ns
*
Fold Change % Confluency
.05
untreated
siCTL
siCDH1 #2
siCDH1 #5
siCADM1 #1
siCADM1 #2
D
300 µm
Cross-sectional area (µM2)
**
700000
600000
500000
400000
300000
200000
100000
0

Supplementary Figure 4: Functional effects of *CDH1* and *CADM1* knockdown on MM28 cell line (A) Western blot analysis was used to confirm E-cadherin and CADM1 expression levels with either control, *CDH1*, or *CADM1* siRNAs in MM28 cells. **(A)** Effect of si*CDH1* and si*CADM1* on MP38 cell growth was analyzed using the IncuCyte Live Cell Analysis Imaging System. Scale bars represent 300 μm. Fold change was calculated as % confluency compared to day 0, *p < 0.05 as determined by t-test, and error bars are ±SEM. **(C)** Effect of si*CDH1* and si*CADM1* on cell viability as measured by ATP luminescence (Cell Titer Glo) after 72 hours in low attachment condition in MM28 cell line, *p <0.05 as determined by t-test, and error bars are ±SEM. **(D)** Effect of si*CDH1* and si*CADM1* on spheroid size and cluster formation after being cultured on low attachment conditions for 72 hours. Representative images from the IncuCyte Live Cell Analysis Imaging System of MM28 spheroids are from three independent biological replicates. Scale bars represent 300 μm. Quantitation of spheroid size was determined by ImageJ, *p <0.05 and **p <0.01 as determined by t-test, and error bars are ±SEM.



Supplementary Figure 5: Knockdown of CDH1 effected cluster formation over three days. Effect of si*CDH1* and si*CADM1* on spheroid size and cluster formation after being cultured on low attachment conditions for 72 hours. MP38 3D cluster formation was analyzed over time through the IncuCyte Live Cell Analysis Imaging System. Scale bars represent 300 µm.