Tumor evolution and progression in multifocal and paired non-invasive/invasive urothelial carcinoma

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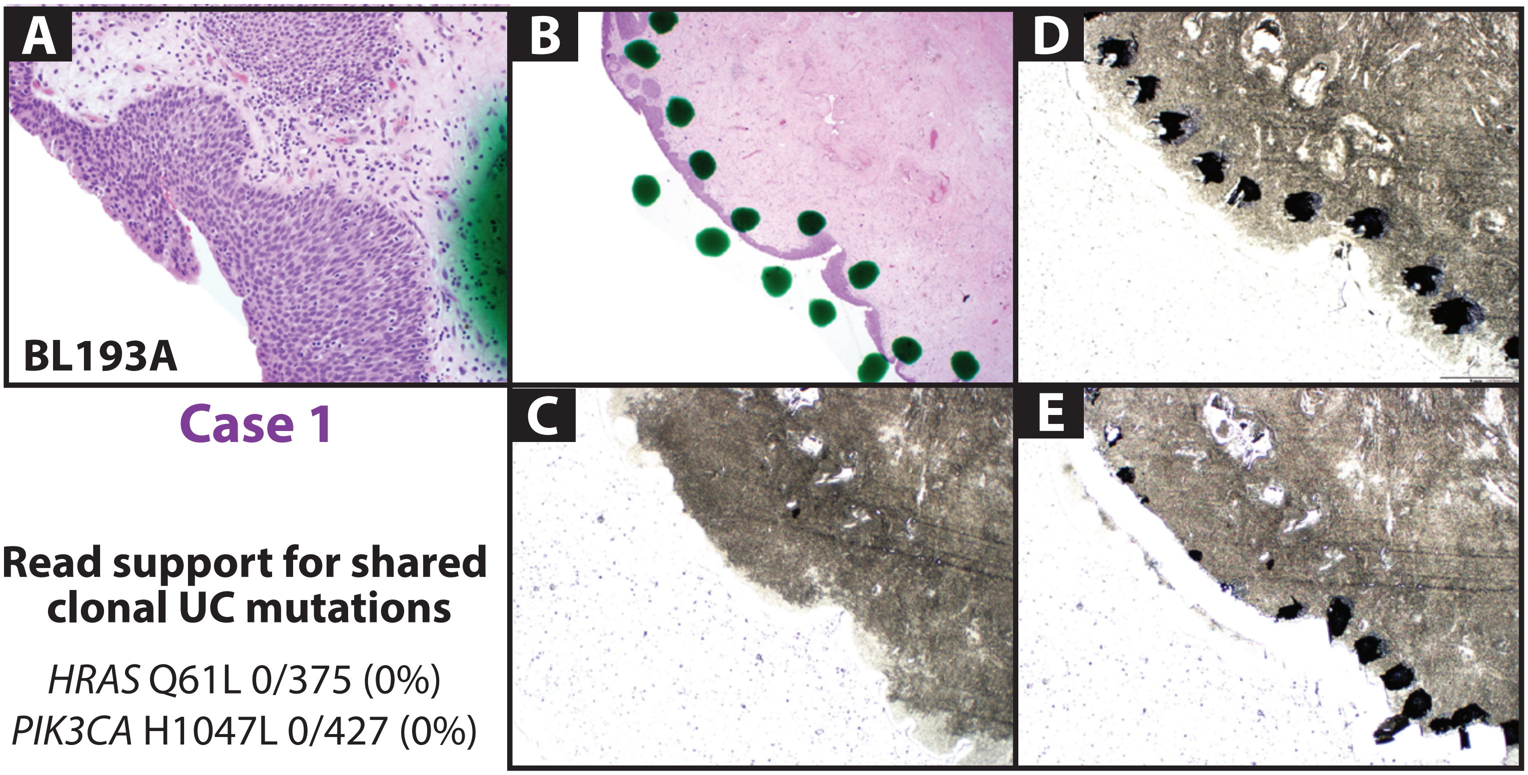
Supplementary Materials

Figure S1: Macrodissection and sequencing of normal urothelium demonstrates lack of clonal founding mutations observed in multifocal tumors. Two areas of histologically normal urothelium (BL193A and BL193B) from Case 1 were macrodissected and subjected to targeted DNA based next generation sequencing (NGS) using a custom Ion Torrent Ampliseq panel targeting ~130 genes. This panel covers two shared clonal mutations present in all multifocal urothelial carcinoma (UC) tumor specimens identified herein (*HRAS* Q61L and *PIK3CA* H1047L). **A-E**. Blocks with normal urothelium (20x original magnification in **A**, **2**x in **B**) were cut, and unstained slides were visualized under a microscope (**C**), urothelium was identified (**D**) and macrodissected with confirmation of enrichment for urothelium (**E**). Original magnification 2x in **C-E** The read level support for the *HRAS* and *PIK3CA* mutations present in all tumor specimens is indicated. **F-J**. As in **A-E**, except for a second area of histologically normal urothelium from a separate block (BL193B).

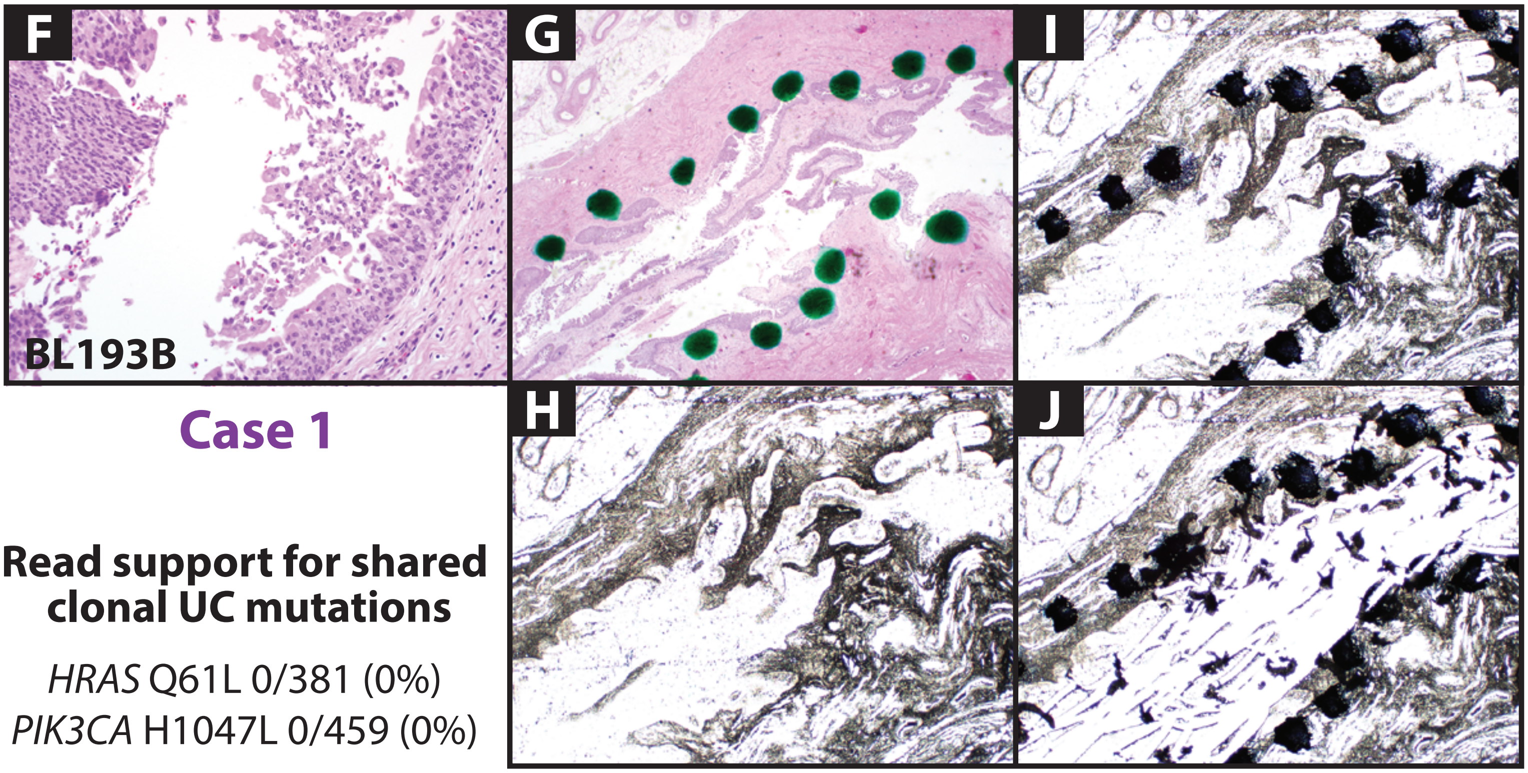
Figure S1



Case 1

Read support for shared clonal UC mutations

HRAS Q61L 0/375 (0%)
PIK3CA H1047L 0/427 (0%)



Case 1

Read support for shared clonal UC mutations

HRAS Q61L 0/381 (0%)
PIK3CA H1047L 0/459 (0%)

Table S1: DNA next generation sequencing statistics for urothelial carcinoma samples

Sample	Case	Type	Estimated Tumor content	DNA isolated	Sequencer	Panel	Number of mapped reads	Percent reads on target[1]	Average base coverage depth	Uniformity of base coverage	Target base coverage at 1x	Target base coverage at 20x	Target base coverage at 100x	Variant Calls
BL193	1	Benign Kidney	0%	1.83ug	PGM	CCP	6,162,548	99%	380	90%	99%	96%	87%	1080
BL191	1	pTa	70%	1.98ug	PGM	CCP	6,077,217	99%	377	92%	99%	96%	89%	1088
BL192	1	pTa	70%	1.07ug	PGM	CCP	4,483,190	99%	280	90%	99%	95%	82%	1136
BL194	1	pTa	70%	1.74ug	PGM	CCP	3,593,322	87%	179	89%	99%	94%	66%	1190
BL195	1	pTa	70%	1.58ug	PGM	CCP	5,731,464	99%	359	80%	98%	89%	76%	1079
BL196	1	pTa	70%	2.47ug	PGM	CCP	3,570,567	95%	212	89%	99%	95%	72%	1103
BL190	1	> pTa	70%	1.22ug	PGM	CCP	5,403,796	99%	342	91%	99%	96%	86%	1288
BL300	2	pTa	75%	1.16ug	Proton	CCP	33,863,024	99%	2102	89%	100%	98%	96%	1199
BL301	2	> pTa	40%	2.31ug	Proton	CCP	5,441,489	99%	328	87%	99%	94%	81%	1058
BL303mn	3	Benign Urothelium	0%	0.40ug	Proton	CCP	5,758,432	99%	346	86%	99%	95%	80%	1068
BL302	3	pTa	75%	3.35ug	Proton	CCP	7,505,325	99%	456	89%	99%	96%	88%	1158
BL303	3	> pTa	75%	1.35ug	Proton	CCP	6,595,021	99%	407	89%	99%	96%	87%	1096
BL305	4	pTa	80%	1.22ug	Proton	CCP	2,764,767	99%	163	82%	98%	88%	51%	807
BL306	4	> pTa	70%	3.88ug	Proton	CCP	3,708,029	99%	224	87%	99%	93%	70%	911

For each sample, the Case and whether the sample represented benign tissue, pTa or > pTa urothelial carcinoma is indicated. For Case 1, each sample was sequenced on a single Ion Torrent 318 chip on the PGM. For Cases 2-4, samples were mulitplexed and sequenced on Ion PI chips on the Proton Sequencer.[1]The comprehensive cancer panel (CCP) targets 1,688,650 bases in 409 genes.

Table S2: Somatic non-synonymous mutations identified in mutlifocal urothelial carcinoma subjected to targeted next generation sequencing

Sample	Case	Type	Location	Gene	Ref. allele	Var. allele	AA Change	FAO	FDP	Variant allele frequency (FAO/FDP)	Validated	Function	RefSeq	Nucleotide Change	ESP	1000G	dbSNP135	FSAF	FSAR	Homopolymer run (HRUN)
BL194	1	pTa	chr1:98348909	DPYD	G	A	R21X	63	166	0.38	Yes	stopgain SNV	NM_000110	C61T			rs72549310	32	31	1
BL195	1	pTa	chr2:148654005	ACVR2A	G	C	W64S	119	396	0.30	Yes	nonsyn SNV	NM_001616	G191C				72	47	2
BL194	1	pTa	chr3:142268985	ATR	G	C	R989G	101	311	0.32	Yes	nonsyn SNV	NM_001184	C2965G				59	42	1
BL190	1	> pTa	chr3:178952085	PIK3CA	A	T	H1047L	129	437	0.30	Yes	nonsyn SNV	NM_006218	A3140T			rs121913279	67	62	1
BL191	1	pTa	chr3:178952085	PIK3CA	A	T	H1047L	166	404	0.41	Yes	nonsyn SNV	NM_006218	A3140T			rs121913279	80	86	1
BL192	1	pTa	chr3:178952085	PIK3CA	A	T	H1047L	83	304	0.27	Yes	nonsyn SNV	NM_006218	A3140T			rs121913279	37	46	1
BL194	1	pTa	chr3:178952085	PIK3CA	A	T	H1047L	65	138	0.47	Yes	nonsyn SNV	NM_006218	A3140T			rs121913279	39	26	1
BL195	1	pTa	chr3:178952085	PIK3CA	A	T	H1047L	128	416	0.31	Yes	nonsyn SNV	NM_006218	A3140T			rs121913279	57	71	1
BL196	1	pTa	chr3:178952085	PIK3CA	A	T	H1047L	144	358	0.40	Yes	nonsyn SNV	NM_006218	A3140T			rs121913279	71	73	1
BL190	1	> pTa	chr5:180047236	FLT4	G	A	Q827X	27	121	0.22	Yes	stopgain SNV	NM_002020	C2479T				14	13	1
BL191	1	pTa	chr5:180047236	FLT4	G	A	Q827X	55	217	0.25	Yes	stopgain SNV	NM_002020	C2479T				30	25	1
BL192	1	pTa	chr5:180047236	FLT4	G	A	Q827X	25	106	0.24	Yes	stopgain SNV	NM_002020	C2479T				18	7	1
BL194	1	pTa	chr5:180047236	FLT4	G	A	Q827X	20	54	0.37	Yes	stopgain SNV	NM_002020	C2479T				11	9	1
BL195	1	pTa	chr5:180047236	FLT4	G	A	Q827X	40	191	0.21	Yes	stopgain SNV	NM_002020	C2479T				24	16	1
BL196	1	pTa	chr5:180047236	FLT4	G	A	Q827X	23	54	0.43	Yes	stopgain SNV	NM_002020	C2479T				14	9	1
BL192	1	pTa	chr6:152708232	SYNE1	A	G	F2828S	25	65	0.38	Yes	nonsyn SNV	NM_033071	T8483C	7.7E-05			23	2	3
BL190	1	> pTa	chr11:533874	HRAS	T	A	Q61L	47	102	0.46	Yes	nonsyn SNV	NM_001130442	A182T			rs121913233	22	25	1
BL191	1	pTa	chr11:533874	HRAS	T	A	Q61L	171	242	0.71	Yes	nonsyn SNV	NM_001130442	A182T			rs121913233	80	91	1
BL192	1	pTa	chr11:533874	HRAS	T	A	Q61L	69	166	0.42	Yes	nonsyn SNV	NM_001130442	A182T			rs121913233	39	30	1
BL194	1	pTa	chr11:533874	HRAS	T	A	Q61L	55	75	0.73	Yes	nonsyn SNV	NM_001130442	A182T			rs121913233	22	33	1
BL195	1	pTa	chr11:533874	HRAS	T	A	Q61L	29	51	0.57	Yes	nonsyn SNV	NM_001130442	A182T			rs121913233	15	14	1
BL196	1	pTa	chr11:533874	HRAS	T	A	Q61L	38	52	0.73	Yes	nonsyn SNV	NM_001130442	A182T			rs121913233	24	14	1
BL190	1	> pTa	chr12:49426888	MLL2	-	GCTGTTCA	Q3867fs	52	254	0.20	Yes	fs	NM_003482	11600_11601insTGAACAGC				4	48	1
BL191	1	pTa	chr12:49426888	MLL2	-	GCTGTTCA	Q3867fs	140	433	0.32	Yes	fs	NM_003482	11600_11601insTGAACAGC				52	88	1
BL194	1	pTa	chr12:49426888	MLL2	-	GCTGTTCA	Q3867fs	22	97	0.23	Yes	fs	NM_003482	11600_11601insTGAACAGC				1	21	1
BL195	1	pTa	chr12:49426888	MLL2	-	GCTGTTCA	Q3867fs	63	248	0.25	Yes	fs	NM_003482	11600_11601insTGAACAGC				19	44	1
BL196	1	pTa	chr12:49426888	MLL2	-	GCTGTTCA	Q3867fs	50	153	0.33	Yes	fs	NM_003482	11600_11601insTGAACAGC				26	24	1
BL190	1	> pTa	chr15:88678541	NTRK3	G	A	T332M	55	224	0.25	Yes	nonsyn SNV	NM_001007156	C995T	0.00015	0.0005	rs145157285	28	27	1
BL191	1	pTa	chr15:88678541	NTRK3	G	A	T332M	104	290	0.36	Yes	nonsyn SNV	NM_001007156	C995T	0.00015	0.0005	rs145157285	54	50	1
BL192	1	pTa	chr15:88678541	NTRK3	G	A	T332M	42	157	0.27	Yes	nonsyn SNV	NM_001007156	C995T	0.00015	0.0005	rs145157285	23	19	1
BL194	1	pTa	chr15:88678541	NTRK3	G	A	T332M	29	80	0.36	Yes	nonsyn SNV	NM_001007156	C995T	0.00015	0.0005	rs145157285	9	20	1
BL195	1	pTa	chr15:88678541	NTRK3	G	A	T332M	66	217	0.30	Yes	nonsyn SNV	NM_001007156	C995T	0.00015	0.0005	rs145157285	36	30	1
BL196	1	pTa	chr15:88678541	NTRK3	G	A	T332M	72	171	0.42	Yes	nonsyn SNV	NM_001007156	C995T	0.00015	0.0005	rs145157285	41	31	1
BL190	1	> pTa	chr19:42798995	CIC	C	G	F1493L	21	124	0.17	Yes	nonsyn SNV	NM_015125	C4479G				9	12	2
BL190	1	> pTa	chr22:36690245	MYH9	C	T	E1244K	35	209	0.17	No	nonsyn SNV	NM_002473	G3730A				16	19	2
BL190	1	> pTa	chr22:36691693	MYH9	C	T	E1115K	17	123	0.14	No	nonsyn SNV	NM_002473	G3343A				9	8	1
BL300	2	pTa	chr1:27058033	ARID1A	C	T	Q581X	135	442	0.31	N/A	stopgainSNV	NM_006015	C1741T	NA	NA	NA	95	40	1
BL300	2	pTa	chr1:27099397	ARID1A	C	T	Q1212X	1170	2000	0.59	N/A	stopgainSNV	NM_006015	C3634T	NA	NA	NA	622	548	1
BL301	2	> pTa	chr1:27099397	ARID1A	C	T	Q1212X	305	606	0.50	N/A	stopgainSNV	NM_006015	C3634T	NA	NA	NA	164	141	1
BL300	2	pTa	chr11:108224499	ATM	C	T	A2893V	856	1851	0.46	N/A	onsynonymousSN	NM_000051	C8678T	NA	NA	NA	506	350	1
BL300	2	pTa	chr17:37868208	ERBB2	C	T	S310F	255	1999	0.13	N/A	onsynonymousSN	NM_004448	C929T	NA	NA	NA	110	145	2
BL301	2	> pTa	chr17:37868208	ERBB2	C	T	S310F	313	848	0.37	N/A	onsynonymousSN	NM_004448	C929T	NA	NA	NA	165	148	2
BL300	2	pTa	chr17:7572986	TP53	G	A	Q375X	623	671	0.93	N/A	stopgainSNV	NM_000546	C1123T	NA	NA	NA	613	10	1
BL301	2	> pTa	chr17:7572986	TP53	G	A	Q375X	83	109	0.76	N/A	stopgainSNV	NM_000546	C1123T	NA	NA	NA	80	3	1
BL300	2	pTa	chr17:78326838	RNF213	G	A	A3468T	412	1994	0.21	N/A	onsynonymousSN	NM_001256071	G10402A	7.7E-05	NA	rs143778568	177	235	1
BL300	2	pTa	chr18:48584787	SMAD4	C	T	Q289X	402	937	0.43	N/A	stopgainSNV	NM_005359	C865T	NA	NA	NA	189	213	1
BL301	2	> pTa	chr18:48584787	SMAD4	C	T	Q289X	106	210	0.50	N/A	stopgainSNV	NM_005359	C865T	NA	NA	NA	40	66	1
BL300	2	pTa	chr3:178952074	PIK3CA	G	A	M1043I	529	1102	0.48	N/A	onsynonymousSN	NM_006218	G3129A	NA	NA	NA	422	107	1
BL301	2	> pTa	chr3:178952074	PIK3CA	G	A	M1043I	43	144	0.30	N/A	onsynonymousSN	NM_006218	G3129A	NA	NA	NA	17	26	1
BL301	2	> pTa	chr6:152651006	SYNE1	C	G	L4867F	21	138	0.15	N/A	onsynonymousSN	NM_033071	G14601C	NA	NA	NA	14	7	1
BL302	3	pTa	chr1:27101105	ARID1A	C	T	R1463C	170	397	0.43	N/A	onsynonymousSN	NM_006015	C4387T	NA	NA	NA	71	99	2
BL303	3	> pTa	chr1:27101105	ARID1A	C	T	R1463C	148	428	0.35	N/A	onsynonymousSN	NM_006015	C4387T	NA	NA	NA	44	104	2
BL302	3	pTa	chr1:27106592	ARID1A	C	T	S2068L	162	371	0.44	N/A	onsynonymousSN	NM_006015	C6203T	NA	NA	NA	92	70	1
BL303	3	> pTa	chr1:27106592	ARID1A	C	T	S2068L	141	435	0.32	N/A	onsynonymousSN	NM_006015	C6203T	NA	NA	NA	62	79	1
BL302	3	pTa	chr10:89711908	PTEN	TAT	-	176_176del	123	266	0.46	N/A	onframeshiftdeletic	NM_000314	526_528del	NA	NA	NA	78	45	1
BL303	3	> pTa	chr10:89711908	PTEN	TAT	-	176_176del	167	430	0.39	N/A	onframeshiftdeletic	NM_000314	526_528del	NA	NA	NA	116	51	1
BL302	3	pTa	chr11:71727272	NUMA1	G	A	A426V	207	373	0.56	N/A	onsynonymousSN	NM_006185	C1277T	NA	NA	NA	118	89	1
BL303	3	> pTa	chr11:71727272	NUMA1	G	A	A426V	252	506	0.50	N/A	onsynonymousSN	NM_006185	C1277T	NA	NA	NA	121	131	1
BL302	3	pTa	chr13:110435726	IRS2	C	T	R892H	2*	2*	*1.00	N/A	onsynonymousSN	NM_003749	G2675A	NA	NA	NA	1	1	1
BL303	3	> pTa	chr13:110435726	IRS2	C	T	R892H	14	32	0.44	N/A	onsynonymousSN	NM_003749	G2675A	NA	NA	NA	10	4	1
BL302	3	pTa	chr14:81575017	TSHR	C	T	P252S	90	799	0.11	N/A	onsynonymousSN	NM_001018036	C754T	NA	NA	NA	59	31	2
BL302	3	pTa	chr16:68862116	CDH1	C	T	A735V	475	1022	0.46	N/A	onsynonymousSN	NM_004360	C2204T	NA	NA	NA	225	250	1
BL303	3	> pTa	chr16:68862116	CDH1	C	T	A735V	282	744	0.38	N/A	onsynonymousSN	NM_004360	C2204T	NA	NA	NA	126	156	1
BL302	3	pTa	chr17:37829458	PGAP3	G	A	R249W	79	615	0.13	N/A	onsynonymousSN	NM_033419	C745T	NA	NA	NA	20	59	1
BL302	3	pTa	chr20:36028689	SRC	T	C	M344T	43	265	0.16	N/A	onsynonymousSN	NM_005417	T1031C	NA	NA	NA	40	3	1
BL303	3	> pTa	chr20:36028689	SRC	T	C	M344T	57	125	0.46	N/A	onsynonymousSN	NM_005417	T1031C	NA	NA	NA	43	14	1
BL302	3	pTa	chr22:24176339	SMARCB1	G	A	R377H	55	105	0.52	N/A	onsynonymousSN	NM_003073	G1103A	NA	NA	NA	25	30	1
BL303	3	> pTa	chr22:24176339	SMARCB1	G	A	R377H	53	114	0.46	N/A	onsynonymousSN	NM_003073	G1103A	NA	NA	NA	25	28	1
BL302	3	pTa	chr22:41574128	EP300	C	T	A2138V	131	276	0.47	N/A	onsynonymousSN	NM_001429	C6413T	NA	NA	NA	45	86	1
BL303	3	> pTa	chr22:41574128	EP300	C	T	A2138V	217	520	0.42	N/A	onsynonymousSN	NM_001429	C6413T	NA	NA	NA	57	160	1
BL302	3	pTa	chr3:10140515	FANCD2	C	T	P1433S	260	487	0.53	N/A	onsynonymousSN	NM_033084	C4297T	NA	NA	NA	118	142	3
BL303	3	> pTa	chr3:10140515	FANCD2	C	T	P1433S	161	415	0.39	N/A	onsynonymousSN	NM_033084	C4297T	NA	NA	NA	62	99	3
BL302	3	pTa	chr3:128200112	GATA2	C	T	R398Q	194	405	0.48	N/A	onsynonymousSN	NM_032638	G1193A	NA	NA	NA	129	65	2
BL303	3	> pTa	chr3:128200112	GATA2	C	T	R398Q	205	447	0.46	N/A	onsynonymousSN	NM_032638	G1193A	NA	NA	NA	140	65	2
BL302	3	pTa	chr3:37089115	MLH1	G	T	E613X	301	724	0.42	N/A	stopgainSNV	NM_000249	G1837T	NA	NA	NA	164	137	1
BL303	3	> pTa	chr3:37089115	MLH1	G	T	E613X	300	823	0.36	N/A	stopgainSNV	NM_000249	G1837T	NA	NA	NA	143	157	1
BL302	3	pTa	chr3:65361515	MAGI1	T	C	N1063S	262	658	0.40	N/A	onsynonymousSN	NM_004742	A3188G	NA	NA	NA	134	128	3
BL303	3	> pTa	chr3:65361515	MAGI1	T	C	N1063S	436	1031	0.42	N/A	onsynonymousSN	NM_004742	A3188G	NA	NA	NA	212	224	3
BL302	3	pTa	chr4:1803564	FGFR3	C	T	R248C	248	397	0.62	N/A	onsynonymousSN	NM_000142	C742T	NA	NA	rs121913482	134	114	1
BL303	3	> pTa	chr4:1803564	FGFR3	C	T	R248C	93	173	0.54	N/A	onsynonymousSN	NM_000142	C742T	NA	NA	rs121913482	52	41	1
BL302	3	pTa	chr8:103311725	UBR5	C	T	A1053T	171	358	0.48	N/A	onsynonymousSN	NM_015902	G3157A	NA	NA	NA	85	86	1
BL303	3	> pTa	chr8:103311725	UBR5	C	T	A1053T	221	485	0.46	N/A	onsynonymousSN	NM_015902	G3157A	NA	NA	NA	136	85	1
BL302	3	pTa	chrX:63410021	AMER1	C	T	R1049Q	165	171	0.96	N/A	onsynonymousSN	NM_152424	G3146A	NA	NA	NA	62	103	1
BL303	3	> pTa	chrX:63410021	AMER1	C	T	R1049Q	218	247	0.88	N/A	onsynonymousSN	NM_152424	G3146A	NA	NA	NA	109	109	1
BL302	3	pTa	chrX:70598858	TAF1	C	T	A466V	246	271	0.91	N/A	onsynonymousSN	NM_004606	C1397T	NA	NA	NA	115	131	1
BL303	3	> pTa	chrX:70598858	TAF1	C	T	A466V	146	170	0.86	N/A	onsynonymousSN	NM_004606	C1397T	NA	NA	NA	54	92	1
BL302	3	pTa	chrX:76909629	ATRX	G	A	R1426X	39	39	1.00	N/A	stopgainSNV	NM_000489	C4276T	NA	NA	NA	26	13	1
BL303	3	> pTa	chrX:76909629	ATRX	G	A	R1426X	2*	5*	0.40*	N/A	stopgainSNV	NM_000489	C4276T	NA	NA	NA	1	1	1
BL306	4	> pTa	chr12:46245399	ARID2	C	T	Q1165X	35	150	0.23	N/A	stopgainSNV	NM_152641	C3493T	NA	NA	NA	5	30	2
BL305	4	pTa	chr12:49434196	KMT2D	GGCGA	-	2451_2453del	35	48	0.73	N/A	frameshiftdeletion	NM_003482	7353_7357del	NA	NA	NA	25	10	3
BL306	4	> pTa	chr12:49434196	KMT2D	GGCGA	-	2451_2453del	37	77	0.48	N/A	frameshiftdeletion	NM_003482	7353_7357del	NA	NA	NA	18	19	3
BL305	4	pTa	chr13:49027133	RB1	C	A	S567X	3*	3*	*1.00	N/A	stopgainSNV	NM_000321	C1700A	NA	NA	NA	1	2	1
BL306	4	> pTa	chr13:49027133	RB1	C	A	S567X	32	40	0.80	N/A	stopgainSNV	NM_000321	C1700A	NA	NA	NA	9	23	1
BL305	4	pTa	chr17:7577124	TP53	C	T	V272M	277	297	0.93	N/A	onsynonymousSN	NM_000546	G814A	NA	NA	NA	101	176	2
BL306	4	> pTa	chr17:7577124	TP53	C	T	V272M	262	284	0.92	N/A	onsynonymousSN	NM_000546	G814A	NA	NA	NA	126	136	2
BL305	4	pTa	chr17:78264475	RNF213	G	A	E407K	6	56	0.11	N/A	onsynonymousSN	NM_001256071	G1219A	NA	NA	NA	3	3	1
BL305	4	pTa	chr21:46330670	ITGB2	C	T	A10T	54	91	0.59	N/A	onsynonymousSN	NM_000211	G28A	NA	NA	NA	19	35	1
BL306	4	> pTa	chr21:46330670	ITGB2	C	T	A10T	140	228	0.61	N/A	onsynonymousSN	NM_000211	G28A	NA	NA	NA	27	113	1
BL305	4	pTa	chr3:142275301	ATR	G	A	R668W	116	161	0.72	N/A	onsynonymousSN	NM_001184	C2002T	NA	NA	NA	38	78	2
BL306	4	> pTa	chr3:142275301	ATR	G	A	R668W	118	270	0.44	N/A	onsynonymousSN	NM_001184	C2002T	NA	NA	NA	46	72	2
BL306	4	> pTa	chr9:133760006	ABL1	C	G	R777G	26	124	0.21	N/A	onsynonymousSN	NM_005157	C2329G	NA	NA	NA	8	18	3

All high confidence somatic non-synonymous variants (see Methods) identified in a case of multifocal urothelial carcinoma (Case 1) and paired invasive/non-invasive urothelial carcinomas (Cases 2-4) are indicated. For each variant the reference (Ref.) and variant (Var.) alleles, amino acid (AA) change, and read level information (FAO, FDP, FAO/FDP) are shown. FAO=flow corrected variant allele containing reads; FDP=flow corrected read depth. *indicates variants not called but with read level support. Variants validated by conventional Sanger sequencing are indicated. Allele frequencies in normal populations (ESP6500 and 1000 genomes project) and presence in dbSNP135 are given from Annovar. Variant allele support on both forward and reverse reads is given (FSAF=forward strand flow corrected variant allele calling reads; FSAR=reverse strand flow corrected variant allele calling reads). HRUN indicates the number of consecutive bases at the indicated variant allele position.

Table S3. Targeted multiplexed PCR based RNA sequencing statistics for urothelial carcinoma samples

Sample	Case	Type	RNA isolated	Sequencer	Mapped Reads[1]	On Target	Amplicons with at least 10 reads
BL193A*	1	Benign Urothelium	0.66ug	PGM	495,367	1	105
BL193B*	1	Benign Urothelium	1.04ug	PGM	449,622	1	106
BL190	1	> pTa	2.30ug	PGM	174,513	1	104
BL191	1	pTa	3.86ug	PGM	527,004	1	105
BL192	1	pTa	1.40ug	PGM	329,882	1	106
BL194	1	pTa	1.86ug	PGM	549,018	1	107
BL195	1	pTa	2.21ug	PGM	479,483	1	107
BL196	1	pTa	2.01ug	PGM	410,994	1	108
BL300	2	pTa	3.58ug	PGM	349,796	1	104
BL301	2	> pTa	0.40ug	PGM	272,113	1	106
BL303mn	3	Benign Urothelium	2.48ug	PGM	289,895	1	109
BL302^	3	pTa	6.80ug	PGM	500,996	1	108
BL302b^	3	pTa	N/A	PGM	392,154	1	105
BL303	3	> pTa	1.30ug	PGM	278,034	1	105
BL305^	4	pTa	0.68ug	PGM	470,339	1	99
BL305b^	4	pTa	N/A	PGM	512,697	1	100
BL306	4	> pTa	0.10ug	PGM	60,836	1	91

For each sample, the Case and whether the sample represented benign urothelium, pTa or > pTa urothelial carcinoma is indicated. Samples were multiplexed and sequenced on Ion Torrent 318 chips. * indicates biological replicates from different blocks. ^ indicates technical replicates, with "b" samples subjected to 3 extra cycles during multiplexed PCR. [1]The custom RNA Ampliseq panel consisted of 111 amplicons targeting 8 housekeeping genes and 103 target genes.

Table S4. Targeted RNAseq from FFPE multifocal and paired invasive/non-invasive urothelial carcinoma

Amplicon	Gene	BL302	BL302b	BL303	BL190	BL301	BL305	BL305b	BL306	BL300	BL191	BL192	BL194	BL195	BL196	BL193A	BL193B	BL303mn
AMPL7201391	*CTPS1*	0.217	-0.021	-0.568	-0.425	2.664	0.000	-0.535	-1.134	0.909	1.596	-0.075	-0.101	0.086	0.208	0.689	-0.427	0.675
AMPL10340053	*E2F3*	-0.639	-0.776	-0.123	-1.174	2.775	1.067	0.918	1.574	2.678	-0.599	-0.257	0.000	0.028	0.078	0.178	-0.493	-0.102
AMPL8788545	*CDH3*	0.264	0.286	0.000	4.279	0.881	0.932	1.001	0.510	-1.574	-0.859	-1.755	-0.609	-1.400	-0.223	-0.246	-0.227	0.713
AMPL34951177	*DSC2*	0.269	0.178	0.000	2.405	2.001	0.603	1.061	1.291	0.057	-4.139	-3.309	-1.732	-3.159	-2.544	-0.053	-0.580	-0.159
AMPL28541017	*EGFR*	0.169	0.414	1.303	0.000	0.343	-0.581	0.104	-0.010	-0.430	-2.075	-2.078	-0.995	-0.564	-0.695	0.487	0.508	0.907
AMPL3900751	*OSR2*	0.795	0.957	0.895	0.819	1.343	-1.159	-0.547	-0.634	0.015	-1.342	-1.524	-1.073	-2.482	-0.548	0.000	0.168	1.254
AMPL31461347	*USP18*	0.051	0.367	0.529	1.220	0.000	1.284	1.080	1.027	-0.165	-0.471	0.063	-1.009	-1.129	-0.500	-0.754	-0.581	-0.679
AMPL29181444	*AURKB*	1.881	1.852	1.303	3.017	1.553	0.060	-1.684	-0.101	1.882	0.119	-0.394	-0.287	-1.309	0.000	-5.797	-4.124	-0.331
AMPL513992	*BIRC5*	0.825	0.697	0.905	1.477	1.068	-0.947	0.358	-0.137	1.056	-0.264	-0.615	-0.755	-1.340	0.084	-7.035	-5.362	0.000
AMPL14157888	*CCNB1*	0.944	1.109	1.058	0.495	0.495	0.114	0.153	-0.372	1.393	-1.629	-1.065	-0.771	-1.285	0.000	-3.540	-3.870	-0.612
AMPL29290680	*BUB1*	0.904	1.073	0.733	-0.287	0.985	0.851	0.623	0.313	1.726	-0.344	0.000	-1.010	-0.905	-0.155	-4.790	-3.361	-0.224
AMPL9881690	*NEK2*	2.068	2.221	1.489	-0.368	1.447	1.250	0.861	0.415	2.477	-1.692	0.000	-1.278	-1.858	-0.739	-6.026	-6.131	-1.053
AMPL12243426	*KIF2C*	1.715	1.878	1.054	0.769	1.174	0.641	1.350	-0.296	2.000	-0.088	-0.926	-0.905	-1.067	0.000	-4.715	-5.305	-0.432
AMPL3666801	*TOP2A*	2.190	2.168	1.823	-0.088	1.549	0.375	0.389	-0.430	2.759	-0.078	0.158	-0.389	-0.675	0.000	-4.708	-4.767	-0.198
AMPL7721438	*CDK1*	0.718	0.652	0.343	-0.696	0.347	0.651	0.784	0.000	1.548	-0.371	0.179	-0.449	-0.804	-0.276	-5.375	-5.627	-0.936
AMPL12585044	*UBE2C*	0.166	0.000	0.154	0.547	0.886	1.035	1.219	0.217	1.923	-2.182	-1.191	-1.513	-1.641	-0.142	-7.638	-6.613	-1.946
AMPL5612106	*RRM2*	1.417	1.269	0.843	0.123	1.847	-1.248	-0.814	-1.701	2.879	-0.742	-0.001	-0.231	0.000	0.349	-5.509	-5.836	0.282
AMPL28634242	*CCNB2*	2.232	2.105	1.486	1.628	1.553	0.207	-0.286	-1.897	2.205	0.000	-0.389	-0.065	-0.160	0.798	-4.424	-3.768	-0.037
AMPL12119161	*TPX2*	1.595	1.837	1.124	1.249	1.394	0.985	1.032	-1.949	2.045	-0.320	0.000	-0.547	-0.525	-0.481	-3.535	-3.695	-0.754
AMPL8761772	*DSG1*	4.243	5.932	0.311	2.192	3.810	5.759	-0.801	6.274	-0.694	-1.091	-0.063	-0.782	-0.607	3.162	-1.007	-0.919	0.000
AMPL27941400	*KRT6A*	4.867	4.765	4.857	6.775	0.295	-6.077	-7.699	-4.530	-7.592	0.000	-1.030	-0.647	-1.165	2.201	0.376	-2.495	0.242
AMPL29984209	*KRT6B*	5.067	5.071	3.906	8.579	1.455	0.000	-3.207	-1.038	-4.100	-1.327	-1.884	-0.866	-0.691	2.130	0.979	-0.418	0.501
AMPL27010534	*KRT16*	4.069	3.871	2.909	6.060	2.817	-0.775	-0.983	0.000	-0.133	-0.328	-1.491	2.597	1.374	1.106	-1.071	-2.316	-1.459
AMPL1709242	*KRT14*	5.610	5.144	3.651	4.119	1.181	-1.155	-0.715	-1.724	2.058	-0.629	-1.752	0.254	-1.681	1.476	-3.169	-4.315	0.000
AMPL6916342	*S100A7*	8.280	8.252	6.345	3.192	5.557	-1.764	-1.801	1.367	-0.109	-0.091	-1.063	0.540	-0.022	5.457	-2.007	-1.919	0.000
AMPL11163127	*SERPINB5*	1.598	1.606	1.644	0.000	-0.411	-0.721	-0.497	-0.827	-1.952	-0.008	0.029	1.071	0.181	0.018	0.858	-0.573	-0.114
AMPL8981496	*SNAI2*	0.843	0.773	1.488	2.327	-1.235	-0.389	-0.354	0.000	-0.798	0.817	0.591	0.946	-0.042	-0.149	-0.454	-1.056	0.174
AMPL11203502	*DSG3*	1.477	-0.523	-1.056	6.234	-2.365	-3.132	-3.169	0.000	-2.062	-1.458	1.154	0.020	-2.974	0.657	3.326	1.106	2.156
AMPL6582208	*KRT5*	0.000	0.059	3.538	7.036	-2.396	-2.841	-2.216	-2.163	-4.369	-0.939	-1.146	-0.469	1.323	0.477	2.748	2.834	3.530
AMPL2584612	*ALDH1A1*	-1.025	-0.757	2.223	0.389	2.476	-1.760	-5.604	0.735	-3.175	-1.370	1.492	0.000	-1.162	-2.515	2.587	2.339	3.559
AMPL9895722	*CLDN3*	-0.989	-0.851	0.312	0.063	2.317	-0.608	-0.760	-1.761	-0.122	0.190	-2.870	-0.519	0.756	0.000	1.930	1.452	1.558
AMPL35508166	*CDC42EP1*	-2.038	-2.261	-0.691	3.889	0.322	0.000	0.332	0.471	-0.422	-0.347	-0.543	1.400	0.888	0.879	-0.080	-0.333	0.920
AMPL11335505	*CTGF*	-2.056	-2.552	1.159	1.545	0.972	-1.408	-1.130	0.801	-2.021	-0.175	1.780	-2.028	-0.413	0.000	0.413	0.008	2.570
AMPL11574555	*COL6A1*	-1.732	-1.498	-0.502	1.670	0.365	0.267	0.319	0.747	-1.125	0.000	-0.076	-0.577	-0.477	-0.785	1.322	1.177	2.040
AMPL27933904	*COL6A3*	-2.477	-2.503	0.395	1.404	1.920	-2.569	-2.827	-2.073	0.194	-1.038	0.224	0.000	-0.360	-1.816	2.271	1.597	2.646
AMPL4472112	*CD44*	-4.116	-3.531	-1.798	2.451	0.827	-1.091	-1.135	-0.632	0.164	0.540	-0.011	0.635	0.000	-0.087	1.026	0.533	0.863
AMPL8310762	*EMP3*	-2.754	-2.342	0.000	2.663	2.246	-0.672	-1.261	-0.341	-1.214	-1.197	0.068	0.797	0.583	-0.109	1.434	1.067	1.136
AMPL30059936	*MT2A*	-4.288	-4.245	-1.678	3.932	2.792	-2.419	-1.490	0.423	-2.725	-1.995	-0.081	0.603	1.133	0.000	1.613	1.830	0.665
AMPL11346393	*PLAUR*	-2.776	-2.430	-1.441	2.591	1.981	-1.452	-1.621	-1.745	-1.999	-1.227	0.000	1.423	0.991	0.781	2.055	0.409	0.031
AMPL4491197	*TWIST1*	-2.739	-4.187	-2.814	3.436	2.381	-2.474	-2.511	-2.342	-1.011	-0.374	0.134	0.000	0.661	0.826	3.051	1.581	1.148
AMPL11822627	*LUM*	-3.248	-3.021	0.810	0.977	1.468	-1.154	-0.801	0.000	-0.534	-1.317	0.657	0.062	-0.512	-1.041	1.941	0.935	1.887
AMPL30534219	*CHST15*	-2.438	-2.258	-0.426	0.931	1.806	-0.037	0.000	0.276	-1.097	-1.330	-0.534	0.079	0.047	-1.144	1.647	0.921	1.621
AMPL7772539	*ZEB1*	-2.050	-1.634	0.000	1.557	1.541	0.042	-0.189	0.565	-0.954	-1.083	0.352	-0.676	-0.087	-0.126	0.860	0.423	1.431
AMPL25214228	*ZEB2*	-2.812	-2.334	0.370	0.057	1.904	-2.621	0.131	0.000	-1.453	-0.410	0.437	-0.302	-0.711	-0.739	1.185	0.572	1.238
AMPL30886125	*RHOJ*	-1.788	-1.797	0.021	0.451	0.625	0.032	0.243	-0.426	-1.461	-1.204	0.528	-0.008	-0.608	0.000	0.110	-0.070	1.121
AMPL27989111	*MMP9*	-1.019	-0.789	0.000	5.481	3.416	-3.491	-2.528	0.864	-0.683	-0.878	-0.089	2.140	3.099	-0.654	3.530	3.918	0.046
AMPL14012330	*TUBB6*	-0.370	0.057	-0.137	3.149	2.870	0.238	-0.189	-0.326	-0.183	-1.032	0.328	-0.342	0.000	-1.102	1.512	1.012	1.394
AMPL11256174	*PI3*	-2.457	-3.457	-1.406	5.234	1.495	0.000	0.886	0.236	-1.089	-6.393	-4.365	-2.277	0.676	1.259	2.965	2.338	-1.214
AMPL27488485	*BYSL*	-0.569	-0.662	-0.404	1.007	0.832	-0.719	0.000	0.570	0.162	0.416	0.495	-0.275	-0.448	0.490	0.402	-0.265	-1.300
AMPL29528964	*MMP11*	-2.731	-2.874	-0.805	2.448	4.266	0.161	0.914	0.971	1.997	2.371	0.000	-0.371	-0.928	0.280	-3.123	-3.035	-0.680
AMPL8073111	*COL4A2*	-1.000	-0.448	0.279	3.018	1.437	-0.402	-0.753	-1.003	0.574	1.146	0.929	-0.371	-0.038	-1.008	0.363	0.000	1.398
AMPL10760438	*SPARC*	-0.883	-0.630	0.750	2.619	1.258	-0.429	-0.002	-0.549	0.256	1.269	1.376	-0.214	-0.136	-0.468	0.000	0.033	1.714
AMPL11579079	*PAFAH1B2*	0.080	-0.042	-0.181	1.686	1.193	-0.581	-1.031	-0.557	0.699	0.521	0.723	-0.287	0.000	0.629	-0.072	-0.126	0.457
AMPL27649163	*THY1*	-0.914	-0.923	0.000	2.919	1.761	-0.709	0.369	-0.832	0.308	0.556	1.022	-0.529	-0.380	0.107	-2.203	-1.639	1.143
AMPL8551205	*TP63*	0.290	-1.805	-0.544	2.620	0.809	1.358	-0.240	1.732	-0.017	0.353	0.765	-0.521	-0.468	-0.101	-0.482	0.000	0.116
AMPL11493373	*CDC45*	0.668	0.648	0.823	1.076	-0.113	-2.340	-5.377	-1.208	1.157	0.334	-0.317	0.000	-0.860	0.519	-5.583	-1.407	1.179
AMPL28173828	*ERBB2*	0.891	0.775	1.168	0.314	-0.054	-2.870	-3.270	-2.185	1.682	0.497	-1.184	-0.829	-0.741	0.000	-0.521	0.318	0.131
AMPL4088717	*DAXX*	0.490	0.416	0.357	0.082	-0.547	-0.919	-2.236	-2.990	0.000	0.395	-1.333	-0.017	-0.192	0.256	-0.270	0.072	0.761
AMPL9085863	*EVPL*	0.860	1.126	0.000	0.022	-1.396	-1.707	-2.334	-2.025	-0.783	2.174	-0.131	0.609	0.736	0.893	-0.675	0.617	-0.219
AMPL29080192	*DGCR2*	0.543	0.731	0.316	1.400	-0.794	-3.042	-2.332	-3.317	-0.607	1.551	-0.585	-0.086	0.000	0.713	-0.165	0.672	0.782
AMPL8197863	*JUP*	0.766	0.509	0.190	1.923	-0.603	-2.110	-2.229	-2.383	-0.820	1.117	0.000	0.500	0.243	0.379	-0.524	-0.155	-0.168
AMPL9223556	*KRT19*	0.000	-0.392	0.198	1.199	-0.476	-2.180	-2.052	-2.175	-0.987	0.965	-0.363	0.298	0.277	0.005	-0.338	0.050	0.166
AMPL12404256	*UPK1B*	0.574	0.737	0.260	-1.206	0.000	-11.788	-12.825	-6.849	-0.704	0.762	0.418	1.181	0.400	0.271	-1.669	-1.702	-1.549
AMPL10721356	*FGFR3*	2.734	2.747	2.057	-1.890	-6.643	-5.381	-5.033	-4.163	-0.754	1.276	-0.879	-0.773	0.336	0.525	0.000	1.984	0.744
AMPL29568183	*LAD1*	0.437	0.527	0.285	0.878	-4.104	-3.053	-3.210	-2.618	0.273	0.508	-0.895	-0.091	0.000	0.142	-0.330	-0.409	0.479
AMPL22071570	*RAB15*	0.593	0.262	0.000	-1.367	-1.329	-1.228	-1.304	-1.651	-0.518	0.769	-1.211	0.530	0.123	0.798	-0.498	0.560	0.551
AMPL32842362	*CYB5R2*	0.000	-0.253	-0.509	2.552	-0.550	-0.877	-1.336	-0.809	0.101	0.597	0.679	0.274	0.795	1.213	-0.783	-0.422	0.304
AMPL6425300	*KRT17*	0.024	0.000	0.563	3.067	-1.482	-2.100	-1.561	-1.572	-0.266	0.271	-0.011	0.863	1.115	0.077	0.806	-1.116	-1.177
AMPL11137028	*CLDN7*	-0.222	-0.059	-0.775	0.623	0.159	-0.743	-0.763	-0.904	0.131	0.719	-0.241	0.761	0.678	0.145	0.308	0.000	-0.028
AMPL5745909	*LAMB3*	-0.885	-1.101	-0.483	2.939	1.081	-2.189	-1.958	-1.426	-0.910	1.202	-0.601	0.581	0.520	0.411	0.694	0.000	0.251
AMPL12051348	*MYO10*	-0.949	-0.849	-0.522	1.066	0.936	-1.318	-0.987	-0.589	-1.148	0.404	-0.123	0.974	0.521	1.067	0.000	0.036	1.021
AMPL5549170	*CDK6*	0.287	0.000	0.627	1.817	1.268	-2.806	-1.843	-1.367	-1.554	-0.805	-1.485	0.387	-1.487	-1.171	0.504	0.023	1.080
AMPL6902314	*SPRR1B*	1.130	1.236	-0.143	3.260	2.100	-3.894	-3.271	-2.016	0.000	-3.474	-2.592	2.107	0.555	1.987	-1.265	-0.327	0.752
AMPL8121313	*S100A8*	0.276	-1.789	0.000	3.259	-0.460	-4.397	-4.434	-1.266	0.531	-4.724	-0.111	0.492	1.737	-1.346	2.060	1.425	0.689
AMPL8830067	*S100A9*	-0.066	-0.164	-0.006	0.825	3.929	-5.648	-5.053	-4.031	2.661	-1.562	0.000	-0.020	1.688	0.849	2.074	1.774	0.337
AMPL3374329	*SLFN11*	-3.533	-2.142	0.050	0.033	2.862	-7.383	-5.420	-3.251	2.136	-0.433	0.151	0.000	-0.611	-0.541	1.970	1.448	1.258
AMPL10442058	*MTX1*	1.222	0.031	1.285	0.569	0.660	-0.921	-0.874	-1.648	1.005	0.074	-0.555	-0.029	-0.238	-0.113	0.000	-0.159	0.692
AMPL28185772	*CDH1*	-0.215	0.070	-0.433	-1.013	-0.075	-0.779	-0.179	-0.992	0.414	0.372	0.547	0.878	0.698	0.679	-0.020	0.000	0.338
AMPL2320970	*IL1B*	-5.254	-3.895	-4.106	-2.448	-0.178	-4.819	-2.704	-2.272	0.000	1.385	1.494	2.333	2.933	3.041	2.242	0.522	1.426
AMPL12645874	*UPK3A*	-4.168	-4.616	-2.626	-4.269	-2.551	-8.225	-2.870	-5.093	0.000	2.715	2.586	3.256	2.908	3.481	0.509	2.391	0.078
AMPL10761850	*SNCG*	-1.871	-1.966	-2.900	0.000	-2.569	-3.102	-3.078	-3.271	-1.078	2.927	2.055	1.538	1.600	1.894	0.161	1.966	1.752
AMPL12409979	*UPK2*	-0.661	-0.742	-1.739	-2.969	0.000	-9.733	-4.912	-3.601	0.015	2.985	3.444	3.664	3.550	3.728	-0.700	2.693	1.124
AMPL26958107	*HMGCS2*	-7.722	-8.070	-8.018	0.572	-9.912	-0.556	-0.270	0.000	-0.503	3.886	3.437	2.886	2.537	3.056	-1.939	1.723	2.274
AMPL8722244	*ALDH4A1*	0.048	0.140	0.422	-0.661	-2.450	-1.239	-0.446	0.000	-1.981	0.787	-0.537	-0.170	-0.264	0.211	0.538	1.184	1.900
AMPL13422619	*ANXA10*	-2.073	-1.975	-3.214	-2.924	-11.713	0.725	1.176	0.235	-2.429	-0.947	0.000	1.069	0.628	0.485	0.093	-0.110	0.178
AMPL29995295	*FOXA1*	-0.066	-0.048	0.026	-1.405	-4.645	0.200	0.401	0.780	-0.820	-0.083	-0.115	0.402	-0.150	0.533	0.297	0.304	0.000
AMPL29346377	*MECOM*	-0.296	-0.213	-0.368	-1.276	-2.987	0.250	0.320	1.036	-0.617	-0.672	0.259	-0.060	0.000	0.461	0.207	0.337	0.396
AMPL9338361	*SPINK1*	-0.023	-0.418	-0.608	-8.590	-9.364	0.740	0.572	1.237	-2.279	-0.495	-0.025	0.081	0.000	0.192	0.017	1.292	1.545
AMPL5861722	*GATA3*	0.492	0.556	0.000	-2.511	-0.969	-0.389	0.062	0.093	-0.356	0.527	-0.300	-0.030	-0.622	0.073	-1.344	0.668	0.338
AMPL27566624	*IDH1*	0.654	0.504	0.405	-2.564	-0.972	-0.788	-0.668	-0.922	-0.765	0.460	0.605	-0.055	0.000	0.241	-1.073	0.018	0.012
AMPL13952580	*PGAP1*	1.101	1.240	0.760	-2.927	-1.739	0.257	0.334	0.616	-2.244	0.415	0.000	-0.180	-0.104	0.309	-0.263	-0.037	-0.047
AMPL33781908	*PPARG*	0.589	0.715	0.094	-4.963	-0.898	0.069	0.618	0.622	-0.584	-0.779	-0.924	0.283	0.368	-0.186	-0.317	-0.247	0.000
AMPL26129724	*GPD1L*	1.263	1.269	1.646	-2.392	-1.112	-0.092	0.000	-0.216	-1.728	2.364	1.229	1.607	1.008	1.536	-0.284	-0.031	-0.443
AMPL30688193	*KRT20*	3.615	3.419	2.109	-1.417	-8.414	-2.806	-2.531	-1.801	-9.111	3.925	3.098	4.603	4.443	3.400	-2.358	0.000	-3.169
AMPL5886580	*TRAK1*	0.662	0.973	-0.132	0.000	-1.134	-0.371	-0.514	-0.553	-0.823	0.955	-0.263	0.258	0.311	0.916	-0.829	0.389	0.285
AMPL30493854	*FXR1*	0.622	0.259	0.612	-2.151	0.400	1.847	1.843	1.808	-0.213	-1.244	0.176	-0.321	-0.334	-0.136	-0.043	-0.397	0.000
AMPL11919253	*GCLC*	1.413	1.136	1.201	-2.530	-2.067	2.022	1.951	2.421	-2.010	-1.160	-0.675	-0.743	-0.370	-0.018	0.000	0.899	0.801
AMPL7551808	*EIF3E*	0.000	-0.098	0.083	-0.835	-0.946	1.091	1.419	1.173	-1.916	-0.633	1.011	0.305	0.099	0.725	-2.022	-1.227	-0.798
AMPL12397056	*RPL10A*	0.147	-0.346	0.914	-0.347	-0.688	-0.040	0.000	0.452	-1.487	-0.642	0.357	0.390	0.387	0.706	-0.775	-0.435	0.083
AMPL5024000	*BTF3*	0.400	-0.287	0.688	-2.099	0.000	0.220	-0.235	0.404	-0.226	-0.875	0.471	-0.013	0.082	0.481	-0.768	-0.647	0.115
AMPL1548435	*RPL23*	-0.008	-1.135	0.725	-0.805	0.310	0.603	0.000	1.124	0.105	-1.482	1.005	-0.037	0.109	1.115	-0.912	-0.733	-0.058
AMPL7944855	*SNRPE*	0.201	0.185	0.524	-1.023	0.376	0.354	0.621	0.279	0.534	-1.618	-0.148	-0.743	-0.573	0.000	-0.729	-1.088	-0.686
AMPL34905979	*SPINT2*	0.000	0.070	-0.832	-0.270	-0.439	1.775	2.144	0.811	-0.624	0.259	-0.113	0.381	0.406	0.162	-0.026	-0.163	-0.510

Normalized, median centered $\log_2$ gene expression for each target gene is shown from Fig 6. Housekeeping genes (and amplicon IDs) used for normalization were *CTCF* /AMPL12421284, *TARDBP* /AMPL12780081, *THRAP3* /AMPL27747452, *SAFB* /AMPL7581688, *HNRNPK* /AMPL14711065, *ZNF143* /AMPL6994781, *GTF2F1* /AMPL7860244 and *HNRNPA1* /AMPL14111542.