Supplementary Table 1. Genes included on the MSK-IMPACT panel.

ABL1	ACVR1	AGO2	AKT1	AKT2	AKT3	ALK	ALOX12B	ANKRD11
APC	AR	ARAF	ARID1A	ARID1B	ARID2	ARID5B	ASXL1	ASXL2
ATM	ATR	ATRX	AURKA	AURKB	AXIN1	AXIN2	AXL	B2M
BABAM1	BAP1	BARD1	BBC3	BCL10	BCL2	BCL2L1	BCL2L11	BCL6
BCOR	BIRC3	BLM	BMPR1A	BRAF	BRCA1	BRCA2	BRD4	BRIP1
BTK	CALR	CARD11	CARM1	CASP8	CBFB	CBL	CCND1	CCND2
CCND3	CCNE1	CD274	CD276	CD79A	CD79B	CDC42	CDC73	CDH1
CDK12	CDK4	CDK6	CDK8	CDKN1A	CDKN1B	CDKN2A	CDKN2B	CDKN2C
CEBPA	CENPA	CHEK1	CHEK2	CIC	CREBBP	CRKL	CRLF2	CSDE1
CSF1R	CSF3R	CTCF	CTLA4	CTNNB1	CUL3	CXCR4	CYLD	CYSLTR2
DAXX	DCUN1D1	DDR2	DICER1	DIS3	DNAJB1	DNMT1	DNMT3A	DNMT3B
DOT1L	DROSHA	DUSP4	E2F3	EED	EGFL7	EGFR	EIF1AX	EIF4A2
EIF4E	ELF3	EP300	EPAS1	EPCAM	EPHA3	EPHA5	EPHA7	EPHB1
ERBB2	ERBB3	ERBB4	ERCC2	ERCC3	ERCC4	ERCC5	ERF	ERG
ERRFI1	ESR1	ETV1	ETV6	EZH1	EZH2	FAM123B	FAM175A	FAM46C
FAM58A	FANCA	FANCC	FAT1	FBXW7	FGF19	FGF3	FGF4	FGFR1
FGFR2	FGFR3	FGFR4	FH	FLCN	FLT1	FLT3	FLT4	FOXA1
FOXL2	FOXO1	FOXP1	FUBP1	FYN	GATA1	GATA2	GATA3	GLI1
GNA11	GNAQ	GNAS	GPS2	GREM1	GRIN2A	GSK3B	H3F3A	H3F3B
H3F3C	HGF	HIST1H1C	HIST1H2BD	HIST1H3A	HIST1H3B	HIST1H3C	HIST1H3D	HIST1H3E
HIST1H3F	HIST1H3G	HIST1H3H	HIST1H3I	HIST1H3J	HIST2H3C	HIST2H3D	HIST3H3	HLA-A
HLA-B	HNF1A	HOXB13	HRAS	ICOSLG	ID3	IDH1	IDH2	IFNGR1
IGF1	IGF1R	IGF2	IKBKE	IKZF1	IL10	IL7R	INHA	INHBA
INPP4A	INPP4B	INPPL1	INSR	IRF4	IRS1	IRS2	JAK1	JAK2
JAK3	JUN	KDM5A	KDM5C	KDM6A	KDR	KEAP1	KIT	KLF4
KMT2B	KMT5A	KNSTRN	KRAS	LATS1	LATS2	LMO1	LYN	MALT1
MAP2K1	MAP2K2	MAP2K4	MAP3K1	MAP3K13	MAP3K14	MAPK1	MAPK3	MAPKAP1
MAX	MCL1	MDC1	MDM2	MDM4	MED12	MEF2B	MEN1	MET
MGA	MITF	MLH1	MLL	MLL2	MLL3	MPL	MRE11A	MSH2
MSH3	MSH6	MSI1	MSI2	MST1	MST1R	MTOR	MUTYH	MYC
MYCL1	MYCN	MYD88	MYOD1	NBN	NCOA3	NCOR1	NEGR1	NF1

NF2	NFE2L2	NFKBIA	NKX2-1	NKX3-1	NOTCH1	NOTCH2	NOTCH3	NOTCH4
NPM1	NRAS	NSD1	NTHL1	NTRK1	NTRK2	NTRK3	NUF2	NUP93
PAK1	PAK7	PALB2	PARK2	PARP1	PAX5	PBRM1	PDCD1	PDCD1LG2
PDGFRA	PDGFRB	PDPK1	PGR	PHOX2B	PIK3C2G	PIK3C3	PIK3CA	PIK3CB
PIK3CD	PIK3CG	PIK3R1	PIK3R2	PIK3R3	PIM1	PLCG2	PLK2	PMAIP1
PMS1	PMS2	PNRC1	POLD1	POLE	PPARG	PPM1D	PPP2R1A	PPP4R2
PPP6C	PRDM1	PRDM14	PREX2	PRKAR1A	PRKCI	PRKD1	PTCH1	PTEN
PTP4A1	PTPN11	PTPRD	PTPRS	PTPRT	RAB35	RAC1	RAC2	RAD21
RAD50	RAD51	RAD51C	RAD51L1	RAD51L3	RAD52	RAD54L	RAF1	RARA
RASA1	RB1	RBM10	RECQL	RECQL4	REL	RET	RFWD2	RHEB
RHOA	RICTOR	RIT1	RNF43	ROS1	RPS6KA4	RPS6KB2	RPTOR	RRAGC
RRAS	RRAS2	RTEL1	RUNX1	RXRA	RYBP	SDHA	SDHAF2	SDHB
SDHC	SDHD	SESN1	SESN2	SESN3	SETD2	SF3B1	SH2B3	SH2D1A
SHOC2	SHQ1	SLX4	SMAD2	SMAD3	SMAD4	SMARCA4	SMARCB1	SMARCD1
SMO	SMYD3	SOCS1	SOS1	SOX17	SOX2	SOX9	SPEN	SPOP
SPRED1	SRC	SRSF2	STAG2	STAT3	STAT5A	STAT5B	STK11	STK19
STK40	SUFU	SUZ12	SYK	TAP1	TAP2	TBX3	TCEB1	TCF3
TCF7L2	TEK	TERT	TET1	TET2	TGFBR1	TGFBR2	TMEM127	TMPRSS2
TNFAIP3	TNFRSF14	TOP1	TP53	TP53BP1	TP63	TRAF2	TRAF7	TSC1
TSC2	TSHR	U2AF1	UPF1	VEGFA	VHL	VTCN1	WHSC1	WHSC1L1
WT1	WWTR1	XIAP	XPO1	XRCC2	YAP1	YES1	ZFHX3	ZRSR2

Supplementary Table 2. Clinicopathological characteristics of the 22 patients with paired molecular comparison of type 1 and type 2 areas.

Case #	Age	Sex	Surgery	Tumor Size (cm)	LVI	Necrosis (%)	Furhman grade (predominant)	Furhman grade (highest)	WHO/ISUP grade (predominant)	WHO/ISUP grade (highest)	Mitosis/10 HPF	Type 1 (%)	Type 2 (%)	pT	Recurrence/ Progression	F/u time (years)	Status
RCJ_1	72	M	Partial	2.9	N	7	2	2	3	3	0	15	85	1A	NONE	9.2	NED
RCJ_10	65	M	Total	14.8	N	75	2	2	1	2	0	80	20	3A	DISTANT METS	2.6	DOD
RCJ_11	63	M	Partial	3.4	N	30	2	3	2	3	0	90	10	1A	NONE	4.5	NED
RCJ_12	65	M	Partial	2.5	N	0	1	3	1	2	0	75	25	1A	NONE	2.6	NED
RCJ_13	69	M	Total	5.3	N	5	2	3	2	3	0	25	75	1B	NONE	9.9	DOC
RCJ_14	63	M	Partial	3	N	5	2	3	2	3	0	10	90	1A	NONE	9.7	NED
RCJ_15	71	M	Partial	3.2	N	5	2	2	2	3	0	80	20	1A	NONE	11.1	NED
RCJ_16	77	M	Total	7.8	N	85	1	2	2	3	0	70	30	2B	NONE	9.6	NED
RCJ_17	68	M	Partial	2.5	N	5	1	2	2	3	0	90	10	1A	NONE	9.0	NED
RCJ_18	75	F	Total	3.6	Y	20	2	2	1	2	19	75	25	3B	DISTANT METS	2.9	DOD
RCJ_19	69	M	Partial	4	N	7	2	3	3	3	1	5	95	1A	DISTANT METS	7.4	AWD
RCJ_2	60	M	Partial	3.7	N	0	2	2	2	3	0	75	25	1A	NONE	6.9	NED
RCJ_20	78	M	Total	6	N	40	2	3	3	3	0	5	95	1B	NONE	7.7	NED
RCJ_21	74	M	Total	6.4	N	20	2	3	2	3	1	95	5	3A	NONE	6.6	NED
RCJ_22	79	M	Total	7.5	Y	5	3	4	3	4	0	2	98	3A	DISTANT METS	3.6	DOD
RCJ_3	69	M	Partial	3.1	N	0	2	3	2	3	0	35	65	1A	NONE	6.9	NED
RCJ_4	83	M	Partial	8.5	N	40	2	3	2	3	0	85	15	3A	NONE	6.4	NED
RCJ_5	74	M	Partial	17	N	0	2	3	2	3	1	10	90	2B	NONE	6.3	NED
RCJ_6	53	M	Partial	4.8	N	0	2	2	2	2	2	60	40	1B	NONE	3.8	NED
RCJ_7	73	M	Total	4.7	N	40	2	3	2	3	0	65	35	1B	NONE	9.6	NED
RCJ_8	69	M	Partial	9.5	N	30	1	2	1	2	0	90	10	2A	NONE	7.6	NED
RCJ_9	64	M	Partial	1.8	N	0	1	2	1	2	0	75	25	1A	NONE	7.5	NED

Supplementary Figure 1. Distribution of fraction of copy number altered (FCNAg) compared between type 1 and type 2 areas.