

**Supplementary Table S1. 52 Melanomas from Various Institutions Genotyped by FoundationOne™**

	Sample Information						Commonly Mutated Genes				
	Name	Gender	Age	Stage	Site (if not skin)	Median Sequencing Depth <sup>a</sup>	BRAF	NRAS	KIT	GNAQ	GNA11
Driver-Positive Melanomas	FM-Mel1	M	46	IV		589	V600E	Q61L			
	FM-Mel2	M	85	IV		1012	V600E				
	FM-Mel3	F	51	III		1155	V600E				
	FM-Mel4	M	48	IV		1341	V600E				
	FM-Mel5	F	43	IV		1550	V600E				
	FM-Mel6	M	62	III		1833	V600E				
	FM-Mel7	F	74	III		1102	V600K				
	FM-Mel8	M	56	IV		1255	V600K				
	FM-Mel9	F	35	IV		1360		Q61K			
	FM-Mel10	M	83	IV		1684		Q61K			
	FM-Mel11	F	76	III		1054		Q61L			
	FM-Mel12	M	65	III		1623		Q61L			
	FM-Mel13	M	56	IV		1276		Q61R			
	FM-Mel14	M	71	IV		1012		Q61R			
	FM-Mel15	M	42	IV		924		Q61R			
	FM-Mel16	F	71	n/a		1445		Q61R			
	FM-Mel17	F	57	IV		673		Q61R			
	FM-Mel18	M	65	IV	Uveal/Ocular	956				Q209P	
	FM-Mel19	M	40	IV	Uveal/Ocular	1703				Q209P	
	FM-Mel20	M	71	IV		743					Q209L
	FM-Mel21	F	44	IV	Uveal/CNS	808					Q209L
	FM-Mel22	F	32	IV		1416	D594N				
	FM-Mel23	M	78	IV		1809	G469S				
	FM-Mel24	M	63	IV		1104	G469V				
	FM-Mel25	F	55	IV		1023	K601E/amp				
	FM-Mel26	M	n/a	III		872	L597Q				
	FM-Mel27	M	71	IV		1602	L597R				
	FM-Mel28	M	83	IV		1779	T599_V600insT				
Pan-Negative Melanomas	FM-Mel29	F	59	IV		775	TRIM24-BRAF				
	FM-Mel30 <sup>b</sup>	F	27	III		1207	PAPSS1-BRAF				
	FM-Mel31	n/a	n/a	n/a		1417					
	FM-Mel32	F	54	IV		1568					
	FM-Mel33	M	n/a	IV		1116					

<b>Pan-Negative Melanomas</b>	FM-Mel34	M	73	IV		1232					
	FM-Mel35	F	50	IV		961					
	FM-Mel36	M	62	IV		1240					
	FM-Mel37	M	54	IV		1032					
	FM-Mel38	F	44	IV		1477					
	FM-Mel39 <sup>b</sup>	F	22	n/a		1364					
	FM-Mel40	F	68	IV		793					
	FM-Mel41	F	41	IV		1547					
	FM-Mel42	M	46	III		220					
	FM-Mel43	F	54	IV		966					
	FM-Mel44	F	70	III		254					
	FM-Mel45	F	55	IV		1196					
	FM-Mel46	M	52	IV		1342					
	FM-Mel47	M	44	IV		1665					
	FM-Mel48	M	61	IV	Anal	1128					
	FM-Mel49	F	50	IV		1463					
	FM-Mel50	M	38	IV		1396					
	FM-Mel51	F	67	IV		807					
FM-Mel52 <sup>b</sup>	M	58	IV	Uveal/Ocular	1226						

<sup>a</sup>Median Sequencing Depth refers to the median number of unique reads covering each base in the targeted genomic regions.

<sup>b</sup>Cases from Vanderbilt-Ingram Cancer Center

n/a – not available

**Supplementary Table S2. Cloning Primers**

<b>Primer Name:</b>	<b># Bases:</b>	<b>Sequences (5'--&gt;3')</b>
EcoRI-PAPSS1_Fwd	45	GCCGCCGAATTCGCGCCACCATGGAGATCCCCGGGAGCCTGTGC
EcoRI_PAPSS1_Rev	37	CGGCGGGAATTCCTAAGCTTTCTCCAAGGATTTGTAG
EcoRI-PAPSS1_FLAG_Rev	72	CGGCGGGAATTCCTACTTGTTCATCGTCGTCCTTGTAGTCAGCTTTCTCCAAGGATTTGTAGTATTCTGTCAG
PAPSS1-BRAF_Fwd	45	CTTCTACAGGAACGGGACTTGATTAGAGACCAAGGATTTTCGTGGT
PAPSS1-BRAF_Rev	45	GTCTCTAATCAAGTCCCGTTCCTGTAGAAGTTCCACAATTGCTG
EcoRI-BRAF_Rev	40	CGGCGGGAATTCCTCACTTGTTCATCGTCGTCCTTGTAGTCG
NheI-TRIM24_Fwd	45	GCCGCCGCTAGCGCCGCCACCATGGAGGTGGCGGTGGAGAAGGCG
TRIM24-BRAF_Fwd	45	TCCATCTCTCATCAGGACTTGATTAGAGACCAAGGATTTTCGTGGT
TRIM24-BRAF_Rev	45	GTCTCTAATCAAGTCTGATGAGAGATGGAAGGTTGCTGGATGGG
NotI-BRAF_Rev	42	CGGCGGGCGGCCGCTCACTTGTTCATCGTCGTCCTTGTAGTCG

Text Color Code:

Black = Restriction enzyme "landing pad"

Purple = Restriction enzyme sequence

Red = *PAPSS1* sequence

Blue = *BRAF* sequence

Green = Kozak or FLAG sequence

Orange = *TRIM24* sequence