

**Supplementary Table 2.** Comparison of somatic mutation frequencies between two clusters

	Cluster 1	Cluster 2	Fisher's p-value
<i>BRAF</i>			0.860
MUT	13	238	
WT	10	240	
<i>NRAS</i>			0.182
MUT	1	36	
WT	22	442	
<i>TERT</i>			8.05E-56*
MUT	1	1	
WT	22	477	
<i>EIF1AX</i>			3.20E-09*
MUT	1	5	
WT	22	473	
<i>ATM</i>			5.07E-18*
MUT	1	3	
WT	22	475	
<i>HRAS</i>			0.00E+00
MUT	0	15	
WT	23	463	
<i>KRAS</i>			0.00E+00
MUT	0	4	
WT	23	474	
<i>RET</i>			0.00E+00
MUT	0	0	
WT	23	478	
<i>ALK</i>			0.00E+00
MUT	0	1	
WT	23	477	
<i>NF1</i>			0.00E+00
MUT	0	3	
WT	23	475	
<i>TSHR</i>			0.00E+00
MUT	0	3	
WT	23	475	
<i>STK11</i>			0.00E+00
MUT	0	0	
WT	23	478	
<i>PIK3CA</i>			0.00E+00
MUT	0	2	
WT	23	476	
<i>PTEN</i>			0.00E+00
MUT	0	2	
WT	23	476	
<i>MET</i>			0.00E+00
MUT	0	1	
WT	23	477	
<i>TFF3</i>			0.00E+00
MUT	0	0	
WT	23	478	
<i>SERPINA1</i>			0.00E+00
MUT	0	0	
WT	23	478	
<i>TIMP1</i>			0.00E+00
MUT	0	0	
WT	23	478	
<i>FN1</i>			0.00E+00
MUT	0	1	
WT	23	477	
<i>TPO</i>			0.00E+00
MUT	0	0	
WT	23	478	
<i>TP53</i>			0.00E+00
MUT	0	1	
WT	23	477	
<i>RB1</i>			0.00E+00
MUT	0	2	
WT	23	476	
<i>NF2</i>			0.00E+00
MUT	0	0	
WT	23	478	
<i>MEN1</i>			0.00E+00
MUT	0	1	
WT	23	477	
<i>TG</i>			0.00E+00
MUT	0	11	
WT	23	467	
<i>DNAH9</i>			0.00E+00
MUT	0	8	
WT	23	470	
<i>PROS1</i>			0.00E+00
MUT	0	2	
WT	23	476	
<i>CRABP1</i>			0.00E+00
MUT	0	0	
WT	23	478	
<i>CDKN2A</i>			0.00E+00
MUT	0	0	
WT	23	478	
<i>CDKN2B</i>			0.00E+00
MUT	0	0	
WT	23	478	
<i>JAK2</i>			0.00E+00
MUT	0	0	
WT	23	478	
<i>KIT</i>			0.00E+00
MUT	0	0	
WT	23	478	
<i>KDR</i>			0.00E+00
MUT	0	2	
WT	23	476	
<i>NFE2L2</i>			0.00E+00
MUT	0	0	
WT	23	478	

p-values were obtained using Fisher's exact test. \*p < 0.05. MUT, mutation type; WT, wild type