

Table S5. MicroRNAs differentially expressed between NCI-60 cell-lines with and without *BRAF* gene mutations^a

	<i>Fold-change</i>	<i>P</i>
<i>miR-509-3p</i>	5.31	<0.001
<i>miR-509-3-5p</i>	3.89	<0.001
<i>miR-513a-5p</i>	3.25	<0.001
<i>miR-506</i>	2.95	<0.001
<i>miR-584</i>	3.86	<0.001
<i>miR-146a</i>	6.68	<0.001
<i>miR-509-5p</i>	2.73	<0.001
<i>miR-510</i>	2.91	<0.001
<i>miR-502-5p</i>	1.73	<0.001
<i>miR-508-5p</i>	2.80	<0.001
<i>miR-513c</i>	2.09	<0.001
<i>miR-211</i>	1.99	0.0001
<i>miR-513b</i>	1.47	0.0002
<i>miR-92b</i>	-1.48	0.0003
<i>miR-30d</i>	1.03	0.0010
<i>miR-508-3p</i>	1.23	0.0022
<i>miR-425*</i>	-1.20	0.0056
<i>miR-501-5p</i>	1.00	0.0056
<i>miR-30b*</i>	1.12	0.0065
<i>miR-660</i>	1.58	0.0083
<i>miR-30b</i>	1.01	0.0084
<i>miR-335</i>	-0.99	0.0101
<i>miR-185</i>	1.08	0.0117
<i>miR-149</i>	-2.19	0.0171
<i>miR-339-5p</i>	-0.99	0.0171
<i>miR-204</i>	1.03	0.0216
<i>miR-502-3p</i>	1.38	0.0246
<i>miR-589*</i>	-1.14	0.0246
<i>miR-500*</i>	1.39	0.0294
<i>miR-501-3p</i>	1.37	0.0327
<i>miR-768-5p</i>	-0.72	0.0393
<i>miR-135a*</i>	0.71	0.0433
<i>miR-181c*</i>	-1.44	0.0433
<i>miR-331-3p</i>	-0.90	0.0433
<i>miR-1296</i>	-1.22	0.0434
<i>miR-532-3p</i>	1.20	0.0434
<i>miR-532-5p</i>	1.22	0.0434
<i>miR-663</i>	1.03	0.0434
<i>miR-768-3p</i>	-0.72	0.0434
<i>miR-29b-1*</i>	1.54	0.0453

^aDifferential expression was evaluated with empirical Bayes moderated t statistics provided with the limma Bioconductor package (version 3.10.0) in R. Log₂-transformed microarray signal values were used. The 40 microRNAs that are the most differentially expressed (P <0.05) in the group of 11 NCI-60 cell-lines with *BRAF* mutations compared to that of 48 without are tabulated along with fold-changes (difference of intra-group means) and P values adjusted by the Benjamini-Hochberg method for a maximum false discovery rate of 5%.