Table S1: Bliss Index for Effect of MEK-I/SHP099 Combination on Cancer Cell Proliferation

Cell Lines	Ea	Eb	Bliss Index	Observed	Synergistic
Pancreas					
HPAFII	27.72%	72.09%	79.83%	90.82%	Yes
PANC2.03	43.25%	88.88%	93.69%	93.04%	
MIAPACA2	11.89%	38.60%	45.90%	87.95%	Yes
PANC10.05	62.97%	75.92%	91.08%	91.50%	
HUPT3	-6.35%	56.66%	53.90%	91.41%	Yes
PANC 08.13	78.60%	83.92%	96.56%	91.79%	
HPAC	-22.93%	63.95%	55.68%	91.84%	Yes
PANC 03.27	44.98%	59.74%	77.85%	90.92%	Yes
HUPT4	38.55%	83.33%	89.76%	96.52%	Yes
HS766T	2.92%	87.12%	87.50%	90.76%	Yes
CFPAC-1	-11.08%	47.94%	42.18%	89.70%	Yes
PANC 02.13	-12.78%	33.81%	25.35%	88.79%	Yes
PANC 04.03	80.48%	83.57%	96.79%	84.11%	
DAN-G	29.92%	62.68%	73.84%	80.69%	Yes
CAPANII	20.60%	28.10%	42.91%	80.15%	Yes
ASPC1	22.58%	62.71%	71.13%	77.40%	Yes
SW1990	17.37%	35.54%	46.74%	67.58%	Yes
PATU8902	5.73%	27.25%	31.42%	62.88%	Yes
SU8686	41.27%	48.90%	69.99%	58.33%	
PSN1	-1.26%	49.39%	48.76%	55.98%	Yes
Breast					
CAL85-1	56.76%	37.25%	**72.86747%**	87.79%	Yes
HCC1954	28.80%	45.72%	**61.35185%**	84.87%	Yes
MDA-MB-468	46.60%	26.91%	**60.97000%**	82.25%	Yes
MDA-MB-231	8.84%	61.15%	**64.58711%**	79.94%	Yes
HS578T	18.95%	20.25%	**35.36184%**	73.86%	Yes
HCC1143	1.51%	17.04%	**18.28644%**	71.62%	Yes
CAL120	7.53%	24.22%	**29.92618%**	58.22%	Yes
CAL 51	19.78%	7.69%	**25.94499%**	36.83%	Yes
MACLS2	2.12%	13.15%	**14.98970%**	36.48%	Yes
HCC38	0.62%	3.65%	**4.25298%**	7.02%	
Ovarian					
OV90	8.44%	96.88%	**97.14333%**	99.30%	Yes
ES2	48.98%	88.08%	**93.91842%**	96.65%	Yes
PEO1	68.43%	64.12%	**88.67268%**	93.33%	Yes
CAOV3	63.11%	56.49%	**83.94916%**	89.89%	Yes
OVCAR8	36.02%	28.04%	**53.95999%**	88.79%	Yes

TOV1369TR	60.03%	50.03%	**80.02699%**	87.17%	Yes
KURAMOCHI	47.41%	21.77%	**58.85884%**	85.32%	Yes
OVSAHO	59.16%	61.98%	**84.47263%**	84.73%	
TYKNU	2.05%	76.30%	**76.78585%**	81.34%	Yes
COV362	66.30%	61.68%	**87.08616%**	80.77%	
OV17R	60.50%	25.49%	**70.56855%**	72.88%	Yes
OVCAR3	29.74%	51.66%	**66.03632%**	66.95%	
COV504	41.01%	42.99%	**66.36980%**	60.44%	
OAW28	35.41%	42.31%	**62.73803%**	58.74%	
TOV3133G	28.97%	37.81%	**55.82644%**	41.72%	
COV318	20.37%	2.90%	**22.67927%**	28.96%	Yes

Table S2: Primer Sequences for qRT-PCR

Primer Name	Species	Sequence
AXL Forward	Human	GACTATCTGCGCCAGGGAAA
AXL Reverse	Human	TAAAACTTGGCCGGTCCTGG
EGF Forward	Human	CAGCTGTGTCATTGGATGTGC
EGF Reverse	Human	ACGGTCACCAAAAAGGGACA
EGFR Forward	Human	GCGTCCGCAAGTGTAAGAAG
EGFR Reverse	Human	TCCAGAGGAGGAGTATGTGTGA
ETV1 Forward	Human	CTTAGCCGTTCACTCCGCTAT
ETV1 Reverse	Human	TCTGTCTTCAGCAGTGGACG
ETV4 Forward	Human	GCCCATTTCATTGCCTGGAC
ETV4 Reverse	Human	TACACGTAACGCTCACCAGC
ETV5 Forward	Human	TAGAACCGGAAGAGGTTGCTC
ETV5 Reverse	Human	TTATCCGGGAAAGCCATGGAG
FGF2 Forward	Human	AGCAGAAGAGAGAGGAGTTGTG
FGF2 Reverse	Human	TCGTTTCAGTGCCACATACCA
FGFR1 Forward	Human	CAGAGACCCACCTTCAAGCA
FGFR1 Reverse	Human	AGCGGCTCATGAGAGAAGAC
FGFR2 Forward	Human	GTGATGTCTGGTCCTTCGGG
FGFR2 Reverse	Human	GAACGTTGGTCTCTGGGAGG
FGFR3 Forward	Human	AGGAGCTCTTCAAGCTGCTG
FGFR3 Reverse	Human	AGGTCCAGGTACTCGTCGG
FGFR4 Forward	Human	CTCCCAGAGGCCTACCTTCA
FGFR4 Reverse	Human	CACCAGAGGGGGAATAGGGT
FOSL1 Forward	Human	CAGCCCAGCAGAAGTTCCA
FOSL1 Reverse	Human	ACTGAGGGTAGGTCAGAGGC
GAPDH Forward	Human	GAGTCAACGGATTTGGTCGT
GAPDH Reverse	Human	TTGATTTTGGAGGGATCTCG
HER2 Forward	Human	CAGGAGTGCGTGGAGGAATG
HER2 Reverse	Human	GGCCACACACTGGTCAGC
HER3 Forward	Human	GTGGTGATGGGGAACCTTGA
HER3 Reverse	Human	CGGAGGTTGGGCAATGGTAG
IGF1R Forward	Human	CTTCGCTTCGTCATGGAGGG
IGF1R Reverse	Human	CAGCTTGTTCTCCTCGCTGT
MET Forward	Human	CTGAATCTGCAACTCCCCCT
MET Reverse	Human	CCTTTAACTGCTTCAGGGTCAA
PDGFA Forward	Human	CAACACGAGCAGTGTCAAGTG
PDGFA Reverse	Human	CCGGATTCAGGCTTGTGGT
PDGFB Forward	Human	ACAAGACGGCACTGAAGGAG
PDGFB Reverse	Human	CAGACGGACGAGGGAAACAA
PDGFC Forward	Human	CTGGTTAAACGCTGTGGTGG
PDGFC Reverse	Human	CTGACACCGGTCTTTGGTCT
PDGFD Forward	Human	TGTGGCTGTGGAACTGTCAA
PDGFD Reverse	Human	ATCGAGGTGGTCTTGAGCTG

PDGFRA Forward	Human	ACCACCCAGAGAAGCCAAAG
PDGFRA Reverse	Human	GTATCAGCCTGCTTCATGTCC
PDGFRB Forward	Human	AGCCCAATGAGGGTGACAAC
PDGFRB Reverse	Human	TGACTTCATTCAGGGTGGAGC
RET Forward	Human	GGATGGAGAGGCCAGACAAC
RET Reverse	Human	GAGTCAGATGGAGTGGACGC
VEGFA Forward	Human	GGAGGAGGGCAGAATCATCAC
VEGFA Reverse	Human	ATGTCCACCAGGGTCTCGAT
VEGFB Forward	Human	TGTATACTCGCGCTACCTGC
VEGFB Reverse	Human	ATCTGCATCCGGACTTGGTG
VEGFR1 Forward	Human	ATCAAGTGGTTCTGGCACCC
VEGFR1 Reverse	Human	TATTGCCATGCGCTGAGTGA
VEGFR2 Forward	Human	GACAACCAGACGGACAGTGG
VEGFR2 Reverse	Human	CTGGGCACCATTCCACCAAA
Cftr Forward	Mouse	TTGCGCTGGTTCCAAATGAG
Cftr Reverse	Mouse	CTGCTCACAGATCGCATCAAG
Gata4 Forward	Mouse	CCAGCGGTAACTCCAGCAAT
Gata4 Reverse	Mouse	ATGCATAGCCTTGTGGGGAC
Gcg Forward	Mouse	ACTTCCCAGAAGAAGTCGCC
Gcg Reverse	Mouse	GTGACTGGCACGAGATGTTG
Hnf1b Forward	Mouse	CTCAACACCTCAACAAGGGC
Hnf1b Reverse	Mouse	TCTGTTGACTGAACTGTCGG
Hnf6 Forward	Mouse	CCTGGAGCAAACTCAAGTCG
Hnf6 Reverse	Mouse	TCTGTCCTTCCCGTGTTCTTG
Ins1 Forward	Mouse	GGACTATAAAGCTGGTGGGCA
Ins1 Reverse	Mouse	AGGTGGGGACCACAAAGATG
Ins2 Forward	Mouse	GTCAAGCAGCACCTTTGTGG
Ins2 Reverse	Mouse	GTCTGAAGGTCACCTGCTCC
Mafa Forward	Mouse	CAAGGAGGAGGTCATCCGAC
Mafa Reverse	Mouse	CTCTCCAGAATGTGCCGCTG
Mafb Forward	Mouse	AGAACGAGAAGACGCAGCTC
Mafb Reverse	Mouse	GCACTTGACCTTGTAGGCGT
Mist1 Forward	Mouse	GAGCAATGAGCGAGAGAGGC
Mist1 Reverse	Mouse	AGCGTGAGGGTCTCGATCTT
Muc1 Forward	Mouse	CCCTACCTACCACACTCACG
Muc1 Reverse	Mouse	GCCATTACCTGCCGAAACCT
Ngn3 Forward	Mouse	ACACTGACCCTATCCACTGCT
Ngn3 Reverse	Mouse	GTGGGGTGGAATTGGAACTGA
Nkx2.2 Forward	Mouse	CCTTTCTACGACAGCAGCGA
Nkx2.2 Reverse	Mouse	GTCATTGTCCGGTGACTCGT
Nkx6.1 Forward	Mouse	GCACGCTTGGCCTATTCTCT
Nkx6.1 Reverse	Mouse	TTCGGGTCCAGAGGTTTGTT
Pax4 Forward	Mouse	TCCAGTGACACCTCATCCCA
Pax4 Reverse	Mouse	GGGTTGATGGCACTTGTCCT
Spp1 Forward	Mouse	CTCCAATCGTCCCTACAGTCG
Spp1 Reverse	Mouse	CCTCATCTGTGGCATCAGGA