Supplementary Table S1. siRNA sequences used in this study

siRNAs	**Sequences (5’-3’)**
si-NC (sense)	UUCUCCGAACGUGUCACGUTT
si-NC (antisense)	ACGUGACACGUUCGGAGAATT
si-Myc1 (sense)	CCGUACAGCCCUAUUUCAUTT
si-Myc1 (antisense)	AUGAAAUAGGGCUGUACGGTT
si-Myc2 (sense)	GACGAGACCUUCAUCAAGATT
si-Myc2 (antisense)	UCUUGAUGAAGGUCUCGUCTT

Supplementary Table S2. Primers used for ChIP-qPCR and qRT-PCR

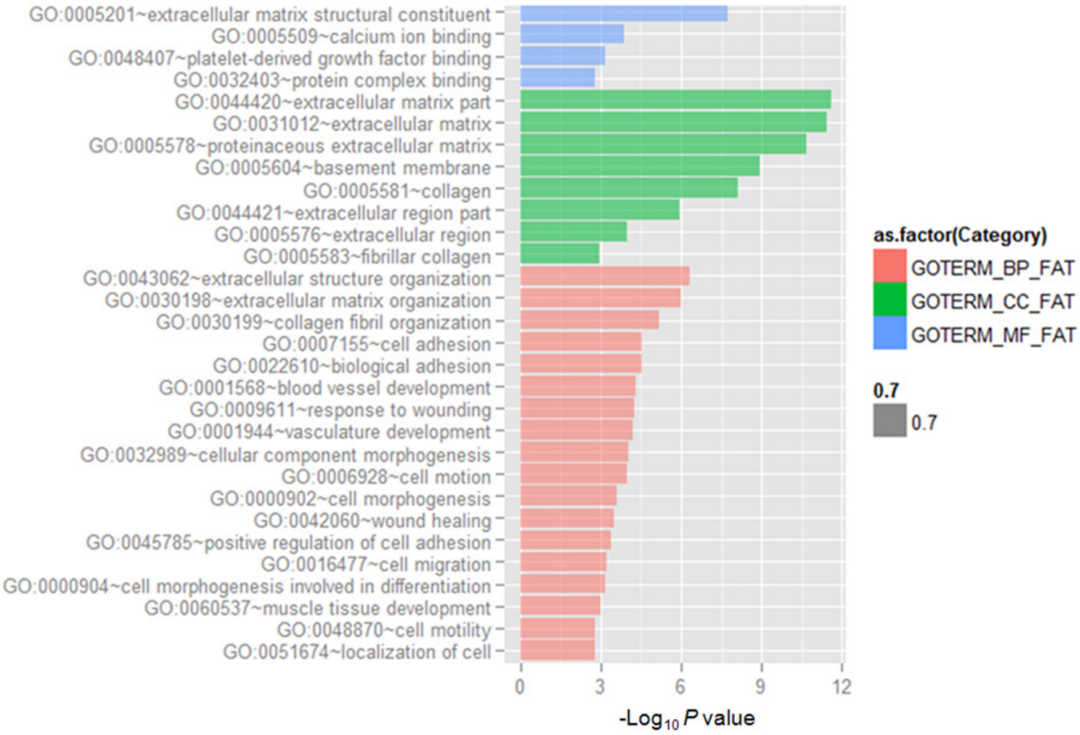
	Genes	**Forward primer (5'→3')**	**Reverse primer (5'→3')**
Primers for ChIP-qPCR	***mouse-ABI3BP***	GTTGCCTGAGTAGTTCTT	TATCATCACATTTCCCTC
	mouse-GIMAP6	CGCTGGCTCAACAAAGTA	TCGGGAACAGGAAACACT
	mouse-HOPX	ATTGTCTCATACGGGTCG	ACTCGGGTTAGATGTTGC
	mouse-PDZD2	TGACAGCCCTAGCATTAA	AAACTCCTACCCAACCAG
	mouse-PTPRD	CTTCAAGATAACCAGCACGAT	AATGTAGGGACCAGAGCAGTA
	mouse-RSPO2	TTCTGGAGAAAGGCTAAT	GAGGGATGGTCTAAACTG
	mouse-MTSS1	TTATCAAGCCCACCTCAGTCT	GGCATCAGGGTTCCTAATCAC
	mouse-NRXN3	CTCTACCTCCTTATTCTTGC	AATCCCTAAGTCACCTAAA
	mouse-EZH2	GCCAACTTGTGTGCTTTTGA	GGGAAACGTGACCCACTAAA
	mouse-SUZ12	AAATAGGTCGCTCCCTTTCG	CTGGGTTGTCGGACGTGAAG
	mouse-JARID2	CAGTGGAATGGTCGTGACTCG	CTTCCTCTCTCTCCTCCCG
	mir-26a	CTTACCATTCACAAAGCACCAA	TCCTCCTGAGCCTCACCTC
	mir-200b	GGCAGCATTGGATAGTGTC	CGTCATCATTACCAGGCAG
	mir-155	CTAATTGTGATAGGGGTTT	GTAGGAGTCAGTCAGAGGC
Primers for qRT-PCR	***mouse-ABI3BP***	CCGAGTTCTGTCTTCCTG	AGTAGCTGGGCAGAGTTG
	mouse-GIMAP6	ATCCTTGTCCAGAGTCCAGG	AAGTCGGGGAACAGAGACCT
	mouse-HOPX	AGGCAAGCCTTCTGACCG	CGGAGGACCAGGTGGAGA
	mouse-PDZD2	AGGTCAGAAGCGGACAGAG	CAACGATAGCGTGAGGTGA
	mouse-PTPRD	TCCAAGTTTGAGTGTTCCCA	GGCTAGCCATCCTCCAATAC
	mouse-RSPO2	GGGTTGTTTGTCTTGTTCG	AAAGCCTACTTTGCACTTCGT
	mouse-MTSS1	ATCAGGCAATCGATCAAAGC	TCAGAAAGTGGCTGACATGG
	mouse-NRXN3	TGAAGGCCACTCAGAAGAA	CCCTCCAGGTCGAGAATT
	mouse-EZH2	AAACCAAGAGTGGAAGCAGC	TCAGGGTCTTTAACGGGATG
	mouse-SUZ12	TCGAAATTCCAGAACAAGCA	TGTGGAAGAAACCGGTAAATG
	mouse-JARID2	GGTCCTGGGCAGTTTTGG	ATCTCAGGGCATCACCAT
	mouse-MYC	TCTCCTTCCTCGGACTCGC	GGTTTGCCTCTTCTCCACAG
	human-EZH2	TTCCCAATAACAGTAGCAG	TGTTTGACACCGAGAATT
	human-SUZ12	AAAGAGCAACATGGGAGA	GGCAATAGGAGCCGTAGA
	human-JARID2	GGTCCTGGGCAGTTTTGG	ATCTCAGGGCATCACCAT
	human-BRAF	GTTCAACGGGGACATGGA	AATTTGTCCAATAGGGCCTC
	mir-26a	TTCAAGTAATCCAGGATAGGCT	Universal qPCR Primer
	mir-200b	TAATACTGCCTGGTAATGATGA	Universal qPCR Primer
	mir-155	TTAATGCTAATCGTGATAGGGGT	Universal qPCR Primer
	18S	CGCCGCTAGAGGTGAAATTC	CTTTCGCTCTGGTCCGTCTT
	U6	CTCGCTTCGGCAGCACA	Universal qPCR Primer

Supplementary Figure legends

Figure S1. Gene ontology (GO) terms of down-regulated genes.

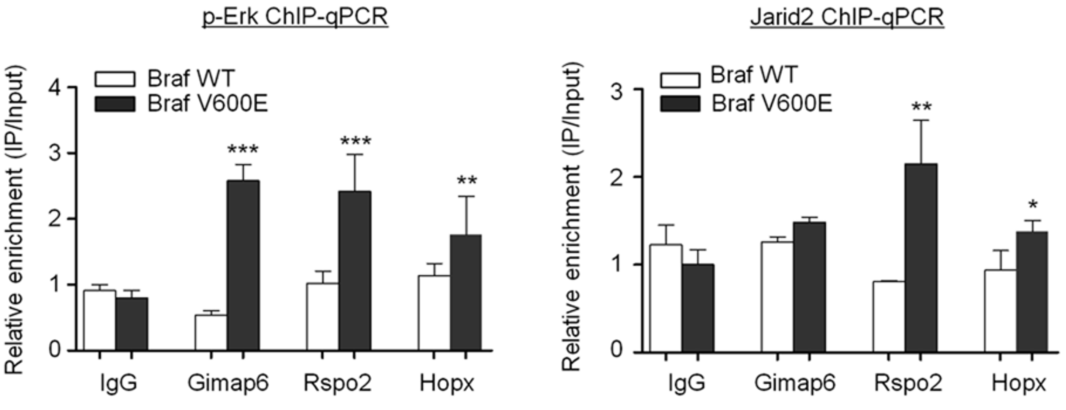
Figure S2. ChIP-qPCR analysis of the promoter regions of the indicated genes in Braf^{V600E} cells relative to that in Braf^{WT} cells. Data were presented as mean ± SD from three independent experiments. Statistically significant differences were indicated: *, $P<0.05$; **, $P<0.01$; ***, $P<0.001$.

Figure S1.



GO:0005201~extracellular matrix structural constituent
GO:0005509~calcium ion binding
GO:0048407~platelet-derived growth factor binding
GO:0032403~protein complex binding
GO:0044420~extracellular matrix part
GO:0031012~extracellular matrix
GO:0005578~proteinaceous extracellular matrix
GO:0005604~basement membrane
GO:0005581~collagen
GO:0044421~extracellular region part
GO:0005576~extracellular region
GO:0005583~fibrillar collagen
GO:0043062~extracellular structure organization
GO:0030198~extracellular matrix organization
GO:0030199~collagen fibril organization
GO:0007155~cell adhesion
GO:0022610~biological adhesion
GO:0001568~blood vessel development
GO:0009611~response to wounding
GO:0001944~vasculature development
GO:0032989~cellular component morphogenesis
GO:0006928~cell motion
GO:0000902~cell morphogenesis
GO:0042060~wound healing
GO:0045785~positive regulation of cell adhesion
GO:0016477~cell migration
GO:0000904~cell morphogenesis involved in differentiation
GO:0060537~muscle tissue development
GO:0048870~cell motility
GO:0051674~localization of cell
0
3
6
9
12
-Log$_{10}$ P value
as.factor(Category)
GOTERM_BP_FAT
GOTERM_CC_FAT
GOTERM_MF_FAT
0.7
0.7

Figure S2.


p-Erk ChIP-qPCR
Braf WT
Braf V600E
Relative enrichment (IP/Input)
0
1
2
3
4
***
***
**
IgG
Gimap6
Rspo2
Hopx
Jarid2 ChIP-qPCR
Braf WT
Braf V600E
Relative enrichment (IP/Input)
0
1
2
3
**
*
IgG
Gimap6
Rspo2
Hopx