Supplemental_Table_S6 :Transcription factor motifs enriched in differentially hydroxymethylated regions in pancreatic cancer

No.	NAME	NES	P Value	Binding Motif
1	STAT3	1.71	<0.01	NNNTTCCN
2	ELK1	1.65	<0.01	NAAACMGGAAGTNCVH
3	CREB	1.61	<0.01	NNGNTGACGTNN
4	ETF	1.54	<0.01	GVGGMGG
5	ATF3	1.45	<0.01	TGAYRTCA
6	E4F1	1.44	0	GTGACGY
7	NF1	1.43	0	NNTTGGCNNNNNNCCNNN
8	ELK1	1.33	0	SCGGAAGY
9	ISRE	1.55	0.01	CAGTTTCWCTTTYCC
10	CMYB	1.40	0.01	NCNRNNGRCNGTTGGKGG