

A

All Wnt-regulated Genes

<u>Motif Name</u>	<u>Consensus</u>	<u>P-value</u>
E2F4(E2F)/K562-E2F4-ChIP-Seq(GSE31477)/Homer	GGCGGGAAAH	1.00E-07
E2F(E2F)/Hela-CellCycle-Expression/Homer	TTSGCGGAAAA	1.00E-06
Sp1(Zf)/Promoter/Homer	GGCCCCGCCCC	1.00E-03
KLF5(Zf)/LoVo-KLF5-ChIP-Seq(GSE49402)/Homer	DGGGYGKGGC	1.00E-03
KLF3(Zf)/MEF-Klf3-ChIP-Seq(GSE44748)/Homer	NRGCCCRCCCHBNN	1.00E-03

B

Overlap Angiogenic Switch and Wnt-regulated Genes

<u>Motif Name</u>	<u>Consensus</u>	<u>P-value</u>
JunB(bZIP)/DendriticCells-Junb-ChIP-Seq(GSE36099)/Homer	RATGASTCAT	1.00E-02
HNF6(Homeobox)/Liver-Hnf6-ChIP-Seq(ERP000394)/Homer	NTATYGATCH	1.00E-02
Atf3(bZIP)/GBM-ATF3-ChIP-Seq(GSE33912)/Homer	DATGASTCATHN	1.00E-02
Cux2(Homeobox)/Liver-Cux2-ChIP-Seq(GSE35985)/Homer	HNRAATCAAT	1.00E-02
Mef2b(MADS)/HEK293-Mef2b.V5-ChIP-Seq(GSE67450)/Homer	GCTATTTTGGM	1.00E-02

Supplemental Table 1. (A) Motif analysis of all Wnt-regulated genes, as identified by RNA-sequencing of CHLA25 cells in the presence or absence of Wnt3a conditioned media. (B) Motif analysis of angiogenic switch genes that were identified among Wnt-regulated genes. Motif analysis was performed using HOMER, and transcription binding sites were searched within promoter regions +/- 2 kb from the transcription start site of each gene. Top 5 motifs for each gene set are shown, along with their consensus sequence and p-value.