

**Table 3:** Selected TF motifs extracted) by ISMARA and sorted by z-value in the outlet vs middle area analysis.

“TF motif” represents a set of transcription factors with similar target nucleotide sequence pattern identified by CAGE. “PCC” is the gene with strongest Pearson correlation coefficient for the TF motif identified. “Pattern” describes the nucleotide sequence pattern of the motif for the PCC selected genes.

<b>TF motif</b>	<b>Z-value of motif activity</b>	<b>PCC</b>	<b>Pattern</b>	<b>Potential liver functions<sup>2</sup></b>
PATZ1_KLF4 Up in the middle area	1,47	PATZ1	GGGGGAGG GGCCG	neoglucogenesis Hypoxia response TGBb related signaling
WT1_MTF1_ZBTB7B Up at the outlet	1,25	MTF1	GCGGGGGC GGGGG	Hypoxia, Wnt, and AP1 signaling
TAF1 Up in the middle area	1,09	TAF1	GCCGCCATC TT	Mitochondria respiration
ESRA_ESR2 Up in the middle area	1,04	ESRA	CAAAGGTCA G	Estrogen regulation
YY1_YY2 Up in the middle area	0,97	YY1	GCCATC	Glucose homeostasis Mitochondria respiration Lipid metabolism Liver disease
FOXM1_TBL1XR1 Up at the outlet	0,96	TBL1RX1	TTTCTTTTTC TGTTTTCT	Mitochondria translation Response to NO Liver metastasis Wnt signaling
SP4_PML Up at the outlet	0,95	SP4	GGGGCCAG GGGGGGGG CGGGGCCG	BMP, SMAD signaling E cadherin stabilisation Fatty acid oxidation
ZEB1 Up in the middle area	0,94	ZEB1	CTCACCTG	Tight junction Fatty acid/lipid metabolism
ID4_TCF4_SNAI2 Up in the middle area	0,68	ID4	TACACCTGT C	Tight junction AP1 complex Fatty acid oxidation
GATA3 Up in the middle area	0,67	GATA3	AGATGG	Mitochondria respiration Apolipoprotein receptor SMAD1 E cadherin/cell junction signaling

2 From Supp. File 6, data extracted with top target analysis in ISMARA