

Table S9 Expression patterns of common predicted regulators for altered microRNAs during different cancers (cancer data of 11 microarray studies: breast, colorectal, endometrial, gastric, liver, lung, ovarian, pancreatic, prostate and testicular cancers as well as glioblastoma). In total, 22 common regulators were predicted for different clusters of miRNAs which eight of them are located at PCSRs including YY1, SPIB, SOX10, NFIC, NR4A2, FOXD1, NFATC2 and HOXA5.

Gene symbol	Region	<sup>a</sup> PCSR	Breast	Endometrial	Ovarian	Prostate	Testicular	Colorectal	Liver	Gastric	Pancreatic	Lung	Glioblastoma
GATA3	chr10p14	-											
GATA2	chr3q21.3	-											
YY1	chr14q34.2	✓											
ETS1	chr11q23.3	-											
MZF1	chr19q13.43	-											
FOXL1	chr16q24.1	-											
ELK1	chrXp11.23	-											
FOXO3	Chr6q21	-											
HOXA5	chr7p15.2	✓											
SP1	chr12q13.13	-											
API(JUN)	chr1p32.1	-											
SPIB	chr19q13.33	✓											
ZNF354C	5q35.3	-											
SOX10	chr22q13.1	✓											
USF1	chr1q23.3	-											
NFIC	chr19p13.3	✓											
NR4A2	chr2q24.1	✓											
SPI1	chr11p11.2	-											
FEV	chr2q35	-											
FOXD1	chr5q13.2	✓											
NFATC2	chr20q13.2	✓											
TFAP2A	chr6p24.3	-											

<sup>a</sup> Predicted cancer-susceptibility region