

Table S1. Mean % Methylation and Standard Deviations (SD) at Individual CpGs for EVX1, CAV1, and FGF1

<i>Gene</i>	<i>CG position</i>	<i>*NTA (% Methylation)</i>	<i>SD</i>	<i>*TA (%Methylation)</i>	<i>SD</i>	<i>p-value (Wilcoxin Rank Sum)</i>	<i>p-value (t-test)</i>
EVX1	CG1	30.3	8.8	41.3	14.5	0.011	0.019
	CG2	28	8.2	37.9	12.5	0.016	0.016
	CG3	22.5	7	32.3	10.1	0.003	0.004
	CG4	49.7	14.1	59.6	13.1	0.058	0.029
	CG5	46.2	15	56.4	11.8	0.052	0.018
	CG6	37	13.6	48.1	12	0.022	0.01
CAV1	CG1	4.9	4.1	9	5.1	0.029	0.016
	CG2	13.8	7.2	22.5	8.8	0.011	0.003
	CG3	16.9	8.5	28.3	10	0.001	0.001
	CG4	13.2	7.3	24.3	11.2	0.002	0.003
	CG5	14.6	8.8	25.5	9.3	0.004	0.001
	CG6	14.4	5.3	24.1	11	0.003	0.006
	CG7	18.4	8.8	29.1	10.2	0.003	0.002
	CG8	8.2	4.9	14.4	5.9	0.004	0.002
	CG9	15.2	4.5	21.3	7.7	0.005	0.014
	CG10	17.4	5.3	25	8.9	0.004	0.009
FGF1	CG1	82	13.9	65.4	11.6	0.001	0.0001
	CG2	72.2	12.9	56.6	11.5	0.001	0.0001
	CG3	81.6	12.6	65.36	12.2	0.001	0.001
	CG4	81.6	12.1	65.4	13.5	0.002	0.001

*NTA = non-tumor associated; TA = tumor-associated