

**Supplementary Table 4.** SATB1-regulated genes as identified by Han et al. [1] to be involved in metastasis suppression or promotion\*

Gene symbol	Probe_Id	Fold change	Raw $P$ †	FDR Adj. $P$ ‡
AREG	ILMN_1804421	ND	—	—
CDH11	ILMN_1672611	1.13	.06	.38
CDH2	ILMN_1779228	0.79	.00	.02
CDH5	ILMN_1719236	ND	—	—
CTGF	ILMN_1699829	1.06	.38	.79
CTGF	ILMN_2115125	1.04	.51	.86
EGFR	ILMN_1728858	ND	—	—
EGFR	ILMN_1798975	1.10	.14	.56
EGFR	ILMN_1696521	0.94	.31	.74
EGFR	ILMN_1755535	ND	—	—
ERBB2	ILMN_1717902	0.96	.48	.85
ERBB2	ILMN_1728761	ND	—	—
ERBB2	ILMN_2352131	0.90	.10	.49
ERBB3	ILMN_1751346	0.99	.83	.96
ERBB3	ILMN_2397602	1.05	.45	.83
ERBB3	ILMN_1737993	0.96	.50	.86
ERBB4	ILMN_1653728	1.08	.22	.67
FN1	ILMN_1778237	ND	—	—
FN1	ILMN_2366463	ND	—	—
FN1	ILMN_1675646	ND	—	—
ITGB4	ILMN_2334210	1.00	.95	.99
ITGB4	ILMN_2253707	ND	—	—
ITGB4	ILMN_1653965	ND	—	—
ITGB4	ILMN_2317543	1.04	.59	.89
MMP2	ILMN_1762106	1.5	.03	.29
MMP3	ILMN_1784459	0.96	.56	.88
MMP9	ILMN_1796316	1.03	.63	.91
NRG1	ILMN_1811954	ND	—	—
NRG1	ILMN_1737252	ND	—	—
NRG1	ILMN_2298888	ND	—	—
NRG1	ILMN_1731788	0.99	.84	.97
NRG1	ILMN_1657607	ND	—	—
S100A4	ILMN_1684306	0.99	.81	.96
S100A4	ILMN_1688780	1.02	.71	.94
SIP1	ILMN_2344007	1.20	.01	.10
SIP1	ILMN_2344002	1.21	.01	.08
SNAIL	ILMN_1758086	ND	—	—
TGFB1	ILMN_2129668	ND	—	—
VEGFB	ILMN_1772274	ND	—	—
VEGFB	ILMN_1801814	0.98	.69	.93
VEGFB	ILMN_1722855	0.97	.65	.92
VEGFB	ILMN_1726981	0.95	.39	.80

VIM	ILMN_1782538	1.03	.60	.90
VIM	ILMN_2058251	1.07	.27	.71

\*Fold change is the ratio of expression values from control vector MCF7 cells to pLXSN SATB1 MCF7 cells on a linear scale. Adjusted *P* values were adjusted for the false discovery rate by the R limma package [17]. Expression was determined by microarray analysis with the Illumina platform HumanWG-6. ND = not detected at detection a *P* value of less than .1; adj. = adjusted; ID = identification number.† Empirical Bayes analysis. All statistical tests are two-sided. ‡ FDR-adjusted empirical Bayes analysis.