

Table S2: Gene Set Enrichment Analysis (GSEA) using MSigDB V7.5.1 of genes up- or down-regulated upon DSCAM-AS1 knockdown in HEC-1A cells by calculation of gene set overlaps. (<http://www.gsea-msigdb.org/gsea/index.jsp>) (FDR = false detection rate)

Genes down-regulated upon DSCAM-AS1 knockdown: overlapping gene sets				
Gene Set Name [# Genes (K)]	Description	# Genes in Overlap	P-value	FDR
KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3 [845]	Genes with promoters occupied by SMAD2 or SMAD3 [GeneID=4087, 4088] in HaCaT cells (keratinocyte) according to a ChIP-chip analysis.	20	4.38 e ⁻¹³	1.41 e ⁻⁸
ANDERSEN_CHOLANGIOCARCINOMA_CLASS2 [175]	Genes overexpressed in cholangiocarcinoma class 2 associated with poor prognosis.	11	3.87 e ⁻¹²	6.22 e ⁻⁸
ONDER_CDH1_TARGETS_2_DN [473]	Genes down-regulated in HMLE cells (immortalized nontransformed mammary epithelium) after E-cadherin (CDH1) [GeneID=999] knockdown by RNAi.	14	1.02 e ⁻¹⁰	1.09 e ⁻⁶
CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_SAL_DN [456]	Genes down-regulated in luminal-like breast cancer cell lines compared to the basal-like ones.	12	8.78 e ⁻⁹	4.07 e ⁻⁵
GOBP_LOCOMOTION [1921]	Self-propelled movement of a cell or organism from one location to another.	22	2.61 e ⁻⁸	9.81 e ⁻⁵
ENK_UV_RESPONSE_EPIDERMIS_DN [513]	Genes down-regulated in epidermis after to UVB irradiation.	12	3.2 e ⁻⁸	1.03 e ⁻⁴
FORTSCHEGGER_PHF8_TARGETS_DN [783]	Genes down-regulated in HeLa cells (cervical carcinoma) upon knockdown of PHF8 [GeneID=23133] by RNAi.	14	6.12 e ⁻⁸	1.79 e ⁻⁴
KIM_WT1_TARGETS_12HR_DN [217]	Genes down-regulated in UB27 cells (osteosarcoma) at 12 hr after inducing the expression of a mutated form of WT1 [GeneID=7490].	8	2.34 e ⁻⁷	4.43 e ⁻⁴
PASINI_SUZ12_TARGETS_DN [316]	Genes down-regulated in ES (embryonic stem cells) with deficient SUZ12 [GeneID=23512].	9	3.56 e ⁻⁷	6.37 e ⁻⁴
GOBP_CELL_MIGRATION [1556]	The controlled self-propelled movement of a cell from one site to a destination guided by molecular cues. Cell migration is a central process in the development and maintenance of multicellular organisms.	18	4.9 e ⁻⁷	7.89 e ⁻⁴

Genes up-regulated upon DSCAM-AS1 knockdown: overlapping gene sets				
Gene Set Name [# Genes (K)]	Description	# Genes in Overlap	P-value	FDR
DOUGLAS_BMI1_TARGETS_UP [563]	Genes up-regulated in A4573 cells (Ewing's sarcoma, ESFT) after knockdown of BMI1 [GeneID=648] by RNAi.	33	7.07 e ⁻²⁶	7.27 e ⁻²²
MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3_H3K27ME3 [1073]	Genes with high-CpG-density promoters (HCP) bearing histone H3 dimethylation at K4 (H3K4me2) and trimethylation at K27 (H3K27me3) in brain.	27	2.87 e ⁻¹²	1.47 e ⁻⁸
MIR217_5P [187]	Genes predicted to be targets of miRBase v22 microRNA hsa-miR-217-5p in miRDB v6.0 with MirTarget v4 prediction scores > 80 (high confidence targets).	13	8.99 e ⁻¹²	3.08 e ⁻⁸
MIR8485 [1034]	Genes predicted to be targets of miRBase v22 microRNA hsa-miR-8485 in miRDB v6.0 with MirTarget v4 prediction scores > 80 (high confidence targets).	24	2.61 e ⁻¹⁰	6.71 e ⁻⁷
WONG_ADULT_TISSUE_STEM_MODULE [721]	The 'adult tissue stem' module: genes coordinately up-regulated in a compendium of adult tissue stem cells.	20	4.34 e ⁻¹⁰	8.92 e ⁻⁷
ESC_V6.5_UP_LATE.V1_UP [182]	Genes up-regulated during late stages of differentiation of embryoid bodies from V6.5 embryonic stem cells.	11	1.64 e ⁻⁹	2.81 e ⁻⁶
MIR6807_3P [142]	Genes predicted to be targets of miRBase v22 microRNA hsa-miR-6807-3p in miRDB v6.0 with MirTarget v4 prediction scores > 80 (high confidence targets).	10	2.1 e ⁻⁹	2.81 e ⁻⁶
LEF1_UP.V1_DN [187]	Genes down-regulated in DLD1 cells (colon carcinoma) over-expressing LEF1 [Gene ID=51176].	11	2.19 e ⁻⁹	2.81 e ⁻⁶
MIR548AV_5P_MIR548K [307]	Genes predicted to be targets of miRBase v22 microRNA hsa-miR-548av-5p, hsa-miR-548k in miRDB v6.0 with MirTarget v4 prediction scores > 80 (high confidence targets).	13	4.05 e ⁻⁹	4.16 e ⁻⁶
MIR8054 [307]	Genes predicted to be targets of miRBase v22 microRNA hsa-miR-8054 in miRDB v6.0 with MirTarget v4 prediction scores > 80 (high confidence targets).	13	4.05 e ⁻⁹	4.16 e ⁻⁶