Supplementary table 1. Summary of ZNF545 methylation in cell lines and primary carcinomas

Samples	Promoter methylation (%)
Carcinoma cell lines	
Nasopharyngeal	6/6 (100%)
Esophageal	12/18 (67%)
Lung	3/5 (60%)
Gastric	8/8 (100%)
Colorectal	10/10 (100%)
Hepatocellular	5/13 (38%)
Breast	5/9 (56%)
Renal	5/7 (71%)
Cervical	3/4 (75%)
Prostate	0/3
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Primary tumors	22/20 (050/)
Nasopharyngeal Ca	33/39 (85%)
Esophageal Ca	21/31 (68%)
Gastric Ca	11/13 (85%)
Colorectal Ca	10/11 (91%)
Breast Ca	5/22 (23%)
Lung Ca	2/13 (15%)
Immortalized normal epithelial cell lines	
NP69, NE1, NE3, Het-1A, NE083, HEK293,	1/10 (10%)
CCD841-CoN, HMEC, HMEpC, RHEK1	(1.073)
Normal tissues	
Normal nasopharyngeal tissues	0/6
Normal esophageal epithelial tissues	0/7
Surgical-margin esophageal tissue from	3/31 (10%)
esophageal cancer patients	