

**Table W1.** Clinicopathologic Characteristics and *EHMT2* Expression.

Tissue	Sample Name	EHMT2	Stage	Grade
Tumor	BT2	38.154	T4	3
	BT5	7.597	Ta	
	BT6	2.488	Ta	2
	BT8	0.809	Ta	2
	BT9	0.021	Ta	2
	BT10	9.196	T2	3
	BT15	3.718	T2	3
	BT16	2.943	Ta	2
	BT18	8.825	Ta	3
	BT20	0.305	T1	2
	BT21	4.680	Ta	3
	BT22	18.100	T2	2
	BT23	7.790	T1	2
	BT27	2.243	T3	3
	BT28	22.929	Ta	1
	BT31	7.520	Ta	2
	BT32	1.898	T2	3
	BT33	2.310	T1	2
	BT34	2.800	Ta	2
	BT36	0.963	T2	3
	BT38	7.842	Ta	2
	BT39	0.302	T1	3
	BT40	1.259	T2	3
	BT41	0.633	T1	2
	BT42	0.644	T2	3
	BT43	2.295	Ta	1
	BT44	0.481	T1	2
	BT46	4.627	Ta	2
	BT48	8.698	T2	3
	BT49	5.598	Ta	1
	BT50	10.781	T1	3
	BT51	31.680	Ta	2
	BT52	2.046	T3	3
	BT53	9.685	Ta	2
	BT54	0.722	T1	3
	BT56	16.182	T2	3
	BT57	1.752	T1	2
	BT58	9.347	Ta	2
	BT59	0.662	T2	3
	BT60	3.617	Mets	3
	BT64	1.602	Ta	2
	BT66	2.831	Ta	1
	BT67	0.402	T1	2
	BT68	4.220	Ta	2
	BT69	10.400	Ta	2
	BT70	3.590	T1	2
	BT71	2.750	T1	3
	BT72	27.900	Ta	1
	BT74	12.300	Ta	1
	BT76	2.730	T1	1
	BT77	4.420	Ta	2
	BT78	1.629	T1	3
	BT79	0.921	Ta	2
	BT80	2.485	Ta	2
	BT81	2.243	Ta	2
	BT82	1.629	T1	3
	BT83	0.921	Ta	2
	BT84	27.809	Ta	2
	BT85	1.874	T1	2
	BT87	2.045	T2	2
	BT88	12.620	T1	3
	BT90	4.001	Ta	2
	BT92	3.184	T1	2
	BT93	1.557	T2	3
	BT94	3.563	Ta	1
	BT95	1.111	T3a	3
	BT96	2.485	Ta	1
	BT97	0.192	Ta	2
	BT98	2.121	Ta	2
	BT99	2.078	T1	2
	BT100	53.775	T1	3
	BT101	5.750	T2	3
	BT103	3.240	T1	2

**Table W1.** (continued).

Tissue	Sample Name	EHMT2	Stage	Grade	
	BT105	0.514	T2	2	
	BT106	1.300	Ta	3	
	BT107	1.570	Mets	3	
	BT108	0.027	T1	2	
	BT109	27.900	Ta	2	
	BT110	0.703	T1	2	
	BT112	92.800	Ta	3	
	BT113	0.984	T1	3	
	BT114	1.910	T2	3	
	BT115	1.800	T1	3	
	BT116	2.160	T2a	3	
	BT119	0.788	Ta	2	
	BT120	2.670	Ta	2	
	BT122	1.980	T1	3	
	BT125	1.970	T1	2	
	BT127	9.672	T1	2	
	BT128	6.160	Ta	1	
	BT129	0.576	Ta	2	
	BT130	7.240	Ta	2	
	BT131	1.574	T2	3	
	BT132	0.908	T2	3	
	BT133	1.367	T1	2	
	BT135	1.419	T2	3	
	BT137	0.221	Ta	2	
	BT138	2.925	Ta	1	
	BT139	1.194	T2	3	
	BT140	5.000	Ta	2	
	BT141	1.310	Mets	3	
	BT143	1.550	T1	3	
	BT145	1.320	T2	2	
	BT150	0.854	Ta	2	
	BT151	0.964	Ta	3	
	BT152	10.261	Ta	2	
	BT154	3.450	T1	3	
	BT158	10.420	Ta	2	
	BT160	0.780	T1	2	
	BT161	3.190	Ta	2	
	BT164	1.477	Ta	1	
	BT169	5.186	T2	3	
	BT178	2.940	Ta	2	
	BT180	0.955	T1	2	
	BT181	0.749	T2	3	
	BT187	2.364	Ta	2	
	BT188	18.595	T2	3	
	BT189	4.517	T1	2	
	Normal	BN11A	1.142	Normal	Normal
		BN11B	1.494	Normal	Normal
		BN12A	1.858	Normal	Normal
		BN13A	0.601	Normal	Normal
		BN13B	0.962	Normal	Normal
		BN14A	1.216	Normal	Normal
		BN14B	0.677	Normal	Normal
		BN15A	0.693	Normal	Normal
		BN17B	0.533	Normal	Normal
		BN18	3.260	Normal	Normal
		BN18B	9.540	Normal	Normal
		BN19A	0.765	Normal	Normal
		BN1A	0.863	Normal	Normal
		BN20B	0.900	Normal	Normal
		BN21A	0.955	Normal	Normal
		BN22A	1.157	Normal	Normal
		BN22B	0.876	Normal	Normal
		BN24B	0.881	Normal	Normal
		BN25A	0.765	Normal	Normal
		BN26A	1.350	Normal	Normal
	BN2A	1.840	Normal	Normal	
	BN2B	1.091	Normal	Normal	
	BN4A	1.151	Normal	Normal	
	BN4B	0.835	Normal	Normal	
	BN5B	0.610	Normal	Normal	
	BN6A	1.094	Normal	Normal	
	BN8A	0.891	Normal	Normal	
	BN9A	0.889	Normal	Normal	

**Table W2.** siRNA Sequence.

siRNA Name	Sequence
siEGFP	Sense: 5' GCAGCACGACUUCUUAAGTT 3' Antisense: 5' CUUGAAGAAGUCGUGCUGCTT 3'
siFFLuc	Sense: 5' GUGCGCUGCUGGUGCCAATT 3' Antisense: 5' GUUGGCACCAGCAGCGCACTT 3'
siNegative control (cocktail)	Target #1 Sense: 5' AUCCGCGCGAUAGUACGUA 3' Antisense: 5' UACGUACUAUCGCGCGGAU 3'
	Target #2 Sense: 5' UUACGCGUAGCGUAAUACG 3' Antisense: 5' CGUAUUACGCUACGCGUAA 3'
	Target #3 Sense: 5' UAUUCGCGCGAUAGCGGU 3' Antisense: 5' ACCGCUAUACGCGGAAUA 3'
siEHMT2 #1	Sense: 5' GAGUUUGGCUAUGAGGCUATT 3' Antisense: 5' UAGCCUCAUAGCCAAACUCTT 3'
siEHMT2 #2	Sense: 5' GCAAUUAUUUCACCGUCGATT 3' Antisense: 5' UGGCAGGUGAAAUAUUUGCTT 3'
siIAH1	Sense: 5' CGAUUGACUUGGGAAGCGATT 3' Antisense: 5' UCGCUUCCCAAGUCAUUCGTT 3'

**Table W3.** Gene Ontology Pathway Analysis Based on the Affymetrix's Microarray Data.

Entry ID	Name	Definition	P
GO0003677	DNA binding	Interacting selectively with DNA (deoxyribonucleic acid).	$4.7 \times 10^{-6}$
GO0045449	Regulation of transcription	Any process that modulates the frequency, rate, or extent of the synthesis of either RNA on a template of DNA or DNA on a template of RNA.	$4.0 \times 10^{-6}$
GO0051726	Regulation of cell cycle	Any process that modulates the rate or extent of progression through the cell cycle.	$3.0 \times 10^{-6}$
GO0006355	Regulation of transcription, DNA-dependent	Any process that modulates the frequency, rate, or extent of DNA-dependent transcription.	$3.2 \times 10^{-5}$
GO0004605	Phosphatidate cytidylyltransferase activity	Catalysis of the reaction: CTP + phosphatidate = diphosphate + CDP-diacylglycerol.	$9.7 \times 10^{-4}$
GO0031570	DNA integrity checkpoint	Any cell cycle checkpoint that delays or arrests cell cycle progression in response to changes in DNA structure.	$8.5 \times 10^{-4}$
GO0000075	Cell cycle checkpoint	A point in the eukaryotic cell cycle where progress through the cycle can be halted until conditions are suitable for the cell to proceed to the next stage.	$5.8 \times 10^{-4}$
GO0051338	Regulation of transferase activity	Any process that modulates the frequency, rate, or extent of transferase activity, the catalysis of the transfer of a group, e.g., a methyl group, glycosyl group, acyl group, phosphorus-containing, or other groups, from one compound (generally regarded as the donor) to another compound (generally regarded as the acceptor). Transferase is the systematic name for any enzyme of EC class 2.	$3.6 \times 10^{-4}$
GO0016481	Negative regulation of transcription	Any process that stops, prevents, or reduces the frequency, rate, or extent of transcription.	$2.2 \times 10^{-4}$
GO0000278	Mitotic cell cycle	Progression through the phases of the mitotic cell cycle, the most common eukaryotic cell cycle, which canonically comprises four successive phases called G <sub>1</sub> , S, G <sub>2</sub> , and M and includes replication of the genome and the subsequent segregation of chromosomes into daughter cells. In some variant cell cycles, nuclear replication or nuclear division may not be followed by cell division, or G <sub>1</sub> and G <sub>2</sub> phases may be absent.	$1.6 \times 10^{-4}$
GO0016564	Transcription repressor activity	Any transcription regulator activity that prevents or downregulates transcription.	$1.4 \times 10^{-4}$
GO0007346	Regulation of mitotic cell cycle	Any process that modulates the rate or extent of progress through the mitotic cell cycle.	$3.6 \times 10^{-3}$
GO0045892	Negative regulation of transcription, DNA-dependent	Any process that stops, prevents, or reduces the frequency, rate, or extent of DNA-dependent transcription.	$3.4 \times 10^{-3}$
GO0016568	Chromatin modification	The alteration of DNA or protein in chromatin, which may result in changing the chromatin structure.	$2.5 \times 10^{-3}$
GO0008629	Induction of apoptosis by intracellular signals	Any process induced by intracellular signals that directly activates any of the steps required for cell death by apoptosis.	$2.2 \times 10^{-3}$
GO0006281	DNA repair	The process of restoring DNA after damage. Genomes are subject to damage by chemical and physical agents in the environment and by free radicals or alkylating agents endogenously generated in metabolism. DNA is also damaged because of errors during its replication. A variety of different DNA repair pathways have been reported that include direct reversal, base excision repair, nucleotide excision repair, photoreactivation, bypass, double-strand break repair pathway, and mismatch repair pathway.	$1.52 \times 10^{-3}$
GO0007093	Mitotic cell cycle checkpoint	A signal transduction-based surveillance mechanism that ensures accurate chromosome replication and segregation by preventing progression through a mitotic cell cycle until conditions are suitable for the cell to proceed to the next stage.	$1.05 \times 10^{-3}$
GO0006350	Transcription	The synthesis of either RNA on a template of DNA or DNA on a template of RNA.	$1.02 \times 10^{-3}$
GO0006917	Induction of apoptosis	A process that directly activates any of the steps required for cell death by apoptosis.	$4.2 \times 10^{-2}$
GO0043065	Positive regulation of apoptosis	Any process that activates or increases the frequency, rate, or extent of cell death by apoptosis.	$4.2 \times 10^{-2}$
GO0008624	Induction of apoptosis by extracellular signals	Any process that activates or increases the frequency, rate, or extent of cell death by apoptosis.	$2.2 \times 10^{-2}$

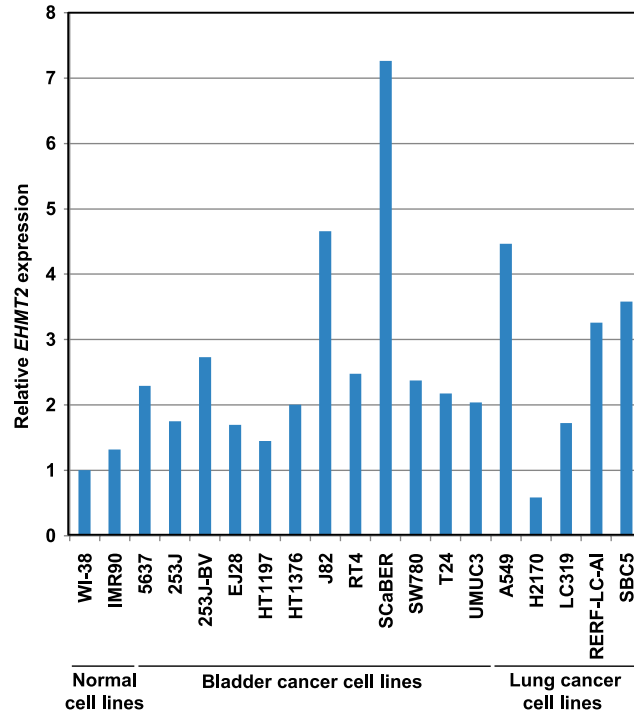
**Table W4.** Expression of *SLAH1* in Cancer Tissues Analyzed by cDNA Microarray\*.

Tissue Type	Case (n)	Ratio (Tumor/Normal)			
		Count < 1/2	Count < 1/3	Count < 1/5	Count < 1/10
Bladder cancer	33	19 (57.5%)	17 (51.5%)	15 (45.4%)	11 (33.3%)
Breast cancer	41	27 (65.8%)	23 (56.0%)	16 (39.0%)	9 (21.9%)
Cholangiocellular carcinoma	25	17 (68.0%)	14 (56.0%)	12 (48.0%)	11 (44.0%)
Non-small cell lung cancer	26	16 (61.5%)	14 (53.8%)	11 (42.3%)	9 (34.6%)
Prostate cancer	50	22 (44.0%)	18 (36.0%)	15 (30.0%)	4 (8.0%)
Small cell lung cancer	15	11 (73.3%)	7 (46.6%)	1 (6.6%)	0 (0.0%)

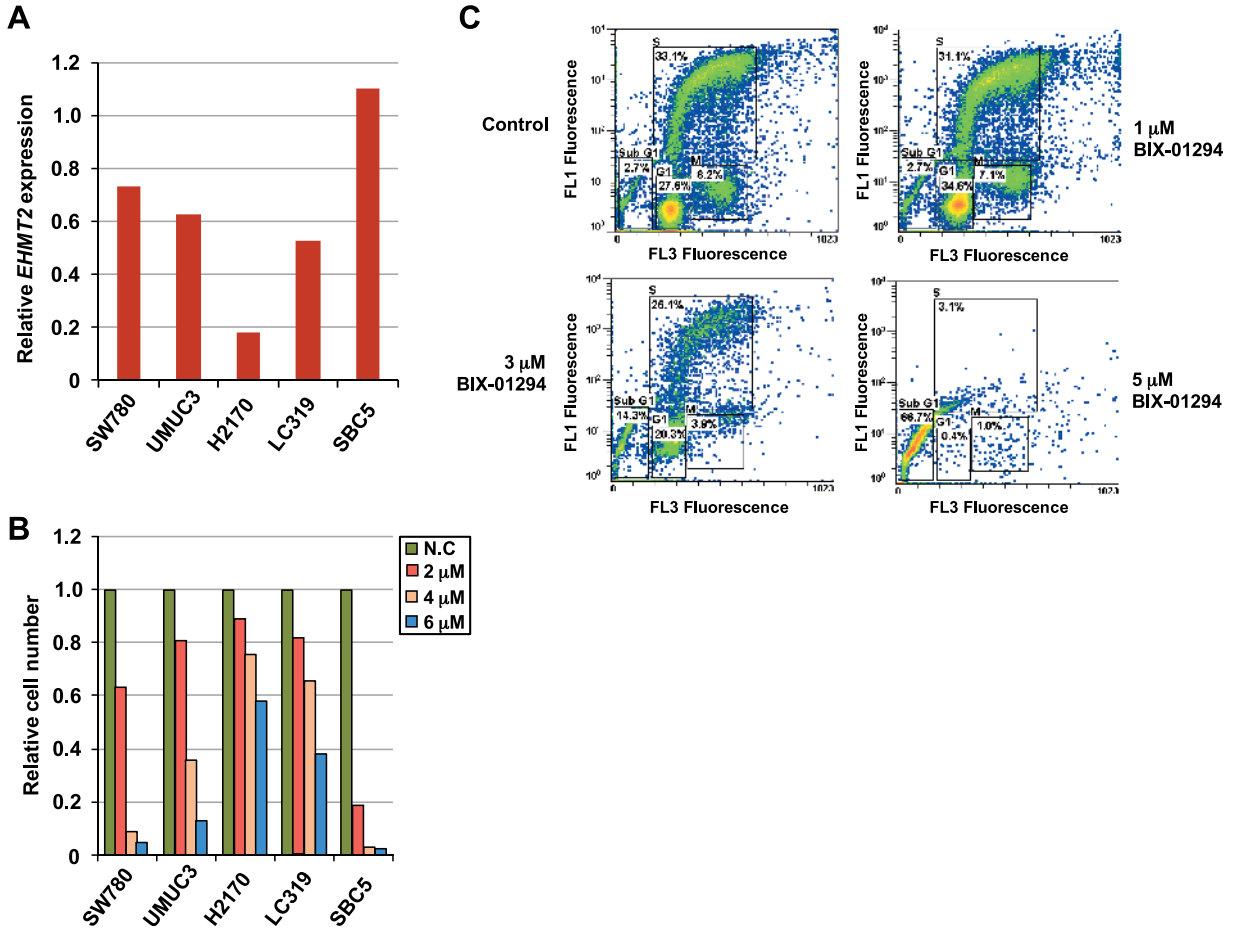
\*We compared the signal intensity of *SLAH1* between tumor tissues and corresponding nonneoplastic tissues derived from the same patient.

**Table W5.** Primer Sequences for Quantitative RT-PCR and ChIP Analyses.

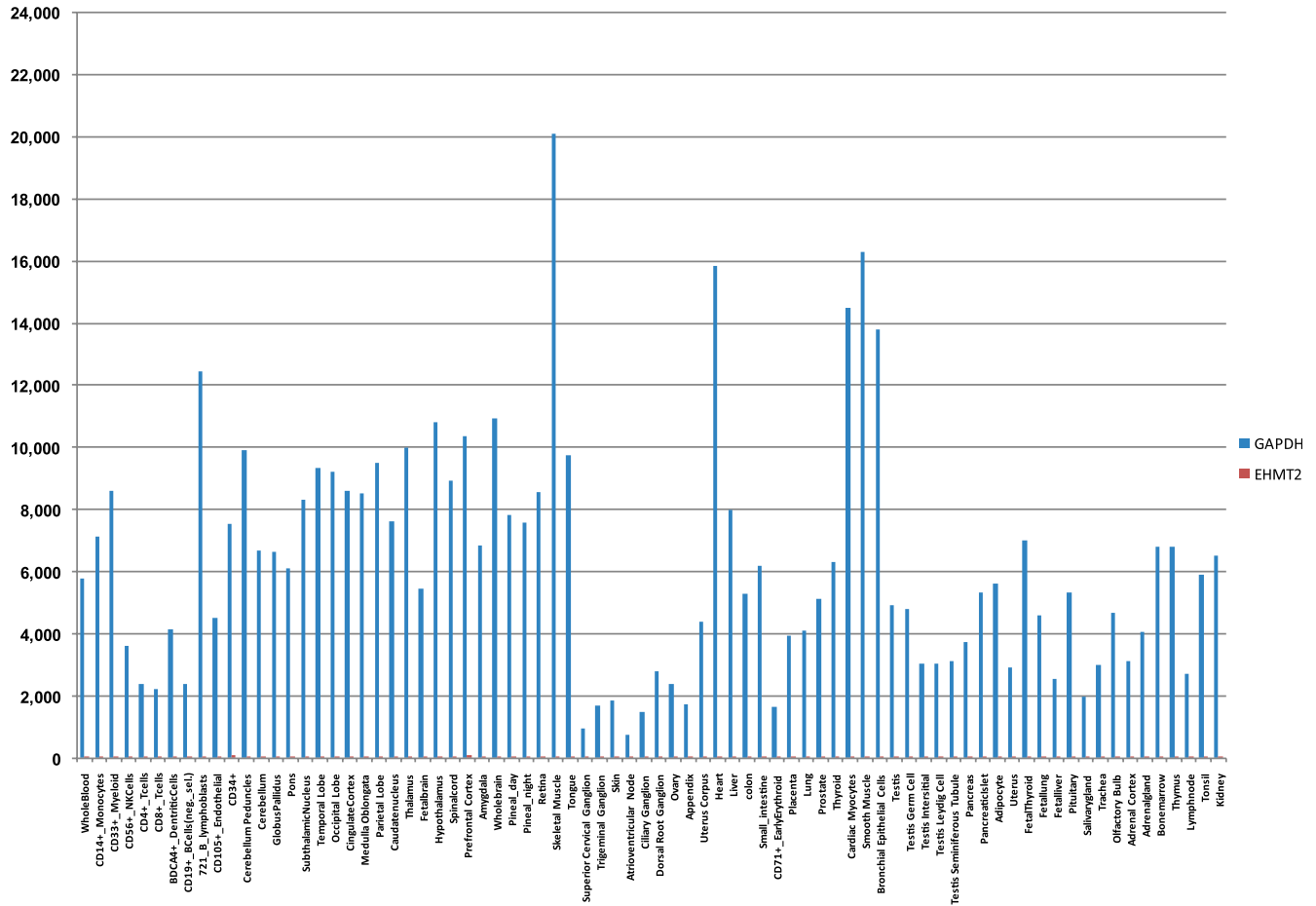
Gene Name	Primer Sequence
<i>GAPDH</i> (housekeeping gene)- f	5' GCAAATTCATGGCACCGTC 3'
<i>GAPDH</i> (housekeeping gene)- r	5' TCGCCCCACTTGATTTTGG 3'
<i>SDH</i> (housekeeping gene)- f	5' TGGGAACAAGAGGGCATCTG 3'
<i>SDH</i> (housekeeping gene)- r	5' CCACCACTGCATCAAATTCATG 3'
<i>EHMT2</i> - f1	5' GGAGGAAGCTGAACTCAGGAGG 3'
<i>EHMT2</i> - r1	5' GACTGAAGTCATCACCCACCAC 3'
<i>SLAH1</i> - f1	5' GTTACCGCCCATTCCTCAAT 3'
<i>SLAH1</i> - r1	5' GACAACATGTGAGCTTTGGG 3'
<i>SLAH1</i> -ChIP- f1	5' AGCAACGGTAGCCGAGTAG 3'
<i>SLAH1</i> -ChIP- r1	5' TGGCCGCCGCCGCCGTTTCGC 3'



**Figure W1.** Expression of *EHMT2* in 2 normal cell lines, 12 bladder cancer cell lines, and 5 lung cancer cell lines. Expression levels of *EHMT2* were analyzed by quantitative real-time PCR. Data were normalized by *GAPDH* and *SDH* expressions.



**Figure W2.** BIX-01294 reduces growth rate in five cancer cell lines. (A) Expression levels of *EHM2* in five cancer cells analyzed by quantitative real-time PCR. (B) Effect of BIX-01294 on the viability of cancer cell lines. Cancer cell lines were treated for 2 days with the inhibitor BIX-01294 (2, 4, and 6  $\mu$ M). This result was normalized by negative control (NC); pure water. Statistical analysis was done based on three independent experiments. *P* values were calculated using Student's *t* test. (C) Cell cycle distribution was analyzed by flow cytometry after coupled staining with fluorescein isothiocyanate (FITC)-conjugated anti-BrdU and 7-amino-actinomycin D (7-AAD) as described in Materials and Methods.



**Figure W3.** Expression levels of *EHTM2* in 78 normal tissues. Data were derived from BioGPS (<http://biogps.gnf.org/#goto=welcome>). *GAPDH* expression is shown as a control of the signal intensity.