

**Table S1.** Breast cancer datasets with *SETD7* expression (mRNA or protein), mutation or copy number information. HPA – Human Protein Atlas; MBC – Metastatic Breast Cancer; NA – not available; NGS – Next Generation Sequencing; RPPA – Reverse Phase Protein Arrays; WES – Whole Exome Sequencing.

Online Tool	Type of data (method)	Dataset (information about the sample, n = sample size)	PAM50 Subtypes (LumA / LumB / Her2 / Basal / Normal)	Stage (0 / 1 / 2 / 3 / 4)	Grade (1 / 2 / 3)	Lymph node status (positive / negative)	Therapy (none / chemotherapy / hormone therapy / both)
TNMplot	mRNA (RNA-seq)	TCGA, TARGET, GTEx (paired tumour and adjacent normal tissues, n = 112)	NA	NA	NA	NA	NA
KM plotter	mRNA (Gene chip)	E-MTAB-365 (n = 426)	174 / 149 / 53 / 49 / 1	NA	NA	285 / 134	NA
		GSE12276 (tumours with known site of relapse – focus on brain, n = 204)	34 / 72 / 38 / 59 / 1	NA	NA	NA	NA
		GSE16391 (Primary ER+/PR-/HER2- tumours of endocrine-treated patients, includes relapses, n = 48)	27 / 19 / 2 / 0 / 0	NA	2 / 30 / 16	30 / 18	0 / 0 / 30 / 18

		GSE16446 (Primary ER-negative tumours of anthracycline- treated patients (neoadjuvant), n = 107)	0 / 0 / 34 / 72 / 1	NA	2 / 19 / 81	59 / 48	0 / 107 / 0 / 0
		GSE17907 (Tumours with amplification of the <i>ERBB2</i> locus, n = 38)	5 / 5 / 24 / 2 / 2	NA	0 / 8 / 29	24 / 11	0 / 23 / 1 / 13
		GSE19615 (n = 115)	45 / 23 / 17 / 30 / 0	NA	23 / 28 / 64	53 / 62	7 / 38 / 21 / 42
		GSE20685 (n = 327)	117 / 91 / 69 / 42 / 8	NA	NA	NA	NA
		GSE20711 (n = 88)	16 / 32 / 17 / 23 / 0	NA	13 / 5 / 70	59 / 29	NA
		GSE21653 (n = 230)	73 / 59 / 21 / 69 / 8	NA	43 / 77 / 107	119 / 108	55 / 43 / 52 / 80
		GSE42568 (naïve tumours, n = 104)	27 / 28 / 12 / 30 / 7	NA	11 / 40 / 53	59 / 45	104 / 0 / 0 / 0
		GSE48390 (breast tumours from Taiwanese women, n = 80)	27 / 28 / 10 / 8 / 7	NA	NA	NA	NA
		GSE58812 (triple-negative (IHC), n = 107)	6 / 4 / 13 / 80 /	NA	NA	NA	NA
		GSE61304 (n = 58)	16 / 15 / 11 / 16 / 0	NA	5 / 16 / 37	37 / 20	NA

		GSE65194 (n = 130)	29 / 17 / 43 / 41 / 0	NA	NA	53 / 58	NA
		GSE9195 (ER+ primary breast tumors of patients treated by Tamoxifen in adjuvant setting, n = 77)	41 / 28 / 7 / 1 / 0	NA	14 / 20 / 24	36 / 41	0 / 0 / 77 / 0
	mRNA (RNA-seq)	GSE96058 (n = 2976)	1504 / 668 / 295 / 309 / 200	NA	449 / 1394 / 1074	1067 / 1820	313 / 340 / 1448 / 854
	Protein (LC-MS/MS)	Tang_2018 (n = 65)	NA	0 / 6 / 46 / 13 / 0	8 / 19 / 28	27 / 37	NA
	HPA	mRNA (RNA-seq)	TCGA (n = 1075)	NA	0 / 180 / 609 / 243 / 20	NA	NA
cBioPortal	Mutation (WES)	CPTAC, Cell 2020* (treatment-naïve primary tumors, n = 122)	57 / 17 / 14 / 29 / 5	0 / 4 / 70 / 33 / 0 (15 NA)	NA	NA	122 / 0 / 0 / 0
	Copy number (WES)						
	mRNA (RNA-seq)						
	Protein (LC-MS/MS)						
	Phosphoproteome						

	(LC-MS/MS)						
	Acetylproteome (LC-MS/MS)						
	Mutation (Gene chip)	METABRIC, Nature 2012 & Nat Commun 2016 (n = 2509)	700 / 475 / 224 / 209 / 148  (218 claudin-low / 529 NA / 6 NC)	24 / 630 / 979 / 144 / 11 (721 NA)	214 / 976 / 1198 (121 NA)	1047 / 1196 (266 NA)	543 / 221 / 1025 / 191 (529 NA)
	Copy number (Gene chip)						
	mRNA (Gene chip)						
	Promoter methylation (RRBS)						
	Mutation (WES)	SMC 2018* (tumors from a Korean BC cohort, n = 187)	47 / 65 / 18 / 36 / 2 (19 NA)	0 / 27 / 101 / 58 / 1	NA	NA	(info only on neoadjuvant chemotherapy: no = 178; yes = 9)
	mRNA (RNA-seq)						
	Mutation (WES)	TCGA PanCancer Atlas (n = 1084)	499 / 197 / 78 / 171 / 36  (103 NA)	0 / 277 / 628 / 137 / 39 (3 NA)	NA	687 / 33 (364 NA)	(neoadjuvant therapy: no = 1077; yes = 6; NA = 1)
	Copy number (WES)						
	mRNA (RNA-seq)						
	Protein (RPPA)						
	Mutation (WES)	MBC Project, Provisional, February 2020*	NA			23 / 92 (65 NA)	(any therapy for more than

	Copy number (WES)	(n = 180)		14 / 44 / 43 / 0 (79 NA)	11 / 27 / 21 / 51 (70 NA)		2 years after diagnosis: no = 131; yes = 46; NA = 3)
	mRNA (RNA-seq)						
	Mutations (NGS)	MSK, Cancer Discovery 2021* (n = 1116)	NA	NA	NA	NA	NA
	Copy number (NGS)						
	Mutations (NGS)	MSK, Cancer Cell 2018 (n = 1756)	NA	556 / 563 / 390 / 395 (14 NA)	98 / 456 / 1175 (189 NA)	765 / 745 (246 NA)	NA
	Copy number (NGS)						
	Mutations (NGS and Sequenom)	MSK, Nature Cancer 2020* (n = 51)	51 / 0 / 0 / 0 / 0	NA	NA	NA	0 / NA / 51 / NA
	Copy number (NGS)						
	Mutations (WES)	MSK, Cancer Res 2020* (n = 32)	NA	NA	NA	NA	NA
	Mutations (NGS)	MSKCC, NPJ Breast Cancer 2019* (n = 68)	68 / 0 / 0 / 0 / 0	NA	NA	NA	NA
	Copy number (NGS)						
	Mutations (targeted)	British Columbia, 2012* (n = 65)	0 / 0 / 0 / 38 / 0 (27 NA)	NA	4 / 3 / 56 (2 NA)	27 / 26 (12 NA)	NA

	deep amplicon sequencing)						
	Mutations (WES)	Broad, Nature 2012* (n = 130)	37 / 21 / 18 / 13 / 9 (5 NA)	11 / 73 / 19 / 0	4 / 29 / 26 (44 NA)	NA	NA
	Mutations (WES)	INSERM, PLoS Med 2016* (n = 216)	NA	NA	NA	NA	NA
	Copy number (WES)						
	Mutations (WES)	Sanger, Nature 2012* (n = 100)	NA	NA	8 / 41 / 51	NA	NA

\*No survival data

**Table S2.** Association of *SETD7* expression with therapy, grade and stage using datasets in cBioPortal. Chi-squared test p-value and Benjamini-Hochberg FDR correction q-value. NA – Not available; ND – not determined, either because all samples were treatment-naïve or less than 10% of the patients received therapy; DE – Differentially expressed

Dataset	Analysis (nSETD7 DE / nTotal samples)	Therapy	Grade	Stage
CPTAC - RNA	Overall (61 / 122)	ND	NA	p = 0.24 q = 0.35
	Luminal A (29 / 57)	ND	NA	p = 0.38 q = 0.57
	Luminal B (9 / 17)	ND	NA	p = 0.45 q = 0.94
	Her2-enriched (7 / 14)	ND	NA	p = 0.37 q = 0.71
	Basal (15 / 29)	ND	NA	p = 0.95 q = 0.95
	Normal-like	-	-	-

	(2 / 5)			
CPTAC - protein	Overall (61 / 122)	ND	NA	p = 0.72 q = 0.80
	Luminal A (29 / 57)	ND	NA	p = 0.64 q = 0.85
	Luminal B (9 / 17)	ND	NA	p = 0.55 q = 0.81
	Her2-enriched (7 / 14)	ND	NA	p = 0.65 q = 0.86
	Basal (15 / 29)	ND	NA	p = 0.45 q = 0.70
	Normal-like (2 / 5)	-	-	-
METABRIC	Overall (952 / 2509)	Hormone therapy: p = 0.13 q = 0.45	p = 0.92 q = 0.95	p = 0.05 q = 0.31



		Chemotherapy: p = 0.35 q = 0.62		
	luminal A (339 / 700)	Hormone therapy: p = 0.88 q = 0.99	p = 0.30 q = 0.99	p = 0.72 q = 0.99
	luminal B (231 / 475)	Hormone therapy: p = 0.90 q = 0.98	p = 0.36 q = 0.98	p = 0.13 q = 0.98
	Her2-enriched (110 / 224)	Hormone therapy: p = 0.08 q = 0.89  Chemotherapy: p = 0.33	p = 0.14 q = 0.89	p = 0.09 q = 0.89

		q = 0.89		
	Basal (99 / 209)	Hormone therapy: p = 0.61 q = 0.95  Chemotherapy: p = 0.37 q = 0.95	p = 0.54 q = 0.95	p = 0.92 q = 0.97
	Normal-like (70 / 148)	Hormone therapy: p = 0.63 q = 1.00  Chemotherapy: p = 0.78 q = 1.00	p = 0.86 q = 1.00	p = 0.07 q = 0.79

	Caludin-low (99 / 218)	Hormone therapy: p = 0.92 q = 0.98  Chemotherapy: p = 0.95 q = 0.98	p = 0.17 q = 0.89	p = 0.18 q = 0.89
SMC	Overall (84 / 187)	ND	NA	p = 0.67 q = 0.71
	Luminal A (23 / 47)	ND	NA	p = 0.44 q = 0.97
	Luminal B (33 / 65)	ND	NA	p = 0.64 q = 0.76
	Her2-enriched (9 / 18)	ND	NA	p = 0.29 q = 0.60
	Basal (18 / 36)	ND	NA	p = 0.12 q = 0.43

	Normal-like (- / 2)	-	-	-
TCGA PanCancer Atlas	Overall (541 / 1084)	ND	NA	p = 0.10 q = 0.19
	Luminal A (249 / 499)	ND	NA	p = 0.42 q = 0.62
	Luminal B (99 / 197)	ND	NA	p = 0.46 q = 0.95
	Her2-enriched (39 / 78)	ND	NA	p = 0.24 q = 0.81
	Basal (85 / 171)	ND	NA	p = 0.56 q = 0.88
	Normal-like (18 / 36)	ND	NA	p = 0.47 q = 0.69
MBC Project	Overall (73 / 180)	Any: p = 0.62 q = 0.91	p = 0.69 q = 0.97	p = 0.47 q = 0.88
	ER+	Any:	p = 0.23	p = 0.38

	(33 / 113)	p = 0.36 q = 0.93	q = 0.93	q = 0.93
	ER- (7 / 23)	Any: p = 0.91 q = 0.94	p = 0.33 q = 0.94	p = 0.29 q = 0.94
	PR+ (25 / 85)	Any: p = 0.25 q = 0.91	p = 0.15 q = 0.91	p = 0.13 q = 0.91
	PR- (14 / 43)	Any: p = 0.88 q = 0.99	p = 0.39 q = 0.99	p = 0.35 q = 0.99
	HER2+ (11 / 37)	Any: p = 0.89 q = 0.99	p = 0.91 q = 0.99	p = 0.42 q = 0.83
	HER2- (28 / 85)	Any: p = 0.11 q = 0.98	p = 0.92 q = 0.98	p = 0.42 q = 0.98

**Table S3.** Association of *SETD7* differentially expression and known *SETD7* targets and their methylation sites and other sites known to compete with *SETD7* methylation. Significant associations are highlighted in bold (Benjamini-Hochberg q-val  $\leq 0.05$  and  $|\log FC| < 0.4$ ). NA – not available; NS – not significant.

Protein (gene)	Methylation site	Competing processes (sites)	TCGA PanCancer (RPPA)		CPTAC- protein (LC -MS/MS)		
			Overall (n = 541 / 1084)	Luminal A (n = 249 /499)	Overall (n = 60 / 122)		
					Acetylproteome	Phosphoproteome	Total Proteome
AKAP-6 ( <i>AKAP6</i> )	K604 [1]	-	NA	NA	NA	NS (AKAP6_S1007s)	NA
Androgen Receptor ( <i>AR</i> )	K630 [2] and K632 [3]	-	<b>High SETD7 (AR)</b>	NS (AR)	NA	<b>High SETD7 (AR_S310s, AR_S651s)</b> NS (AR_S516s, AR_S96s)	<b>High SETD7</b>
Catenin beta- 1 ( <i>CTNNB1</i> )	K180 [4]	-	NS* (CTNNB1)	NS* (CTNNB1)	NA	<b>Low SETD7 (CTNNB1_S191s)</b>	NS

						NS (CTNNB1_S179s, CTNNB1_S389s_S 425s_T428t, CTNNB1_T42t, CTNNB1_S552s, CTNNB1_S675s)	
Centromere protein C ( <i>CENPC</i> / <i>CENPC1</i> )	K414 [1]	-	NA	NA	NA	<b>Low SETD7</b> ( <i>CENPC_S177s</i> , <i>CENPC_S225s</i> , <i>CENPC_S538s</i> , <i>CENPC_S709s_S7</i> <i>10s</i> , <i>CENPC_S73s</i> , <i>CENPC_S773s</i> , <i>CENPC_T130t</i> , <i>CENPC_T734t</i> ) NS ( <i>CENPC_S528s</i> , <i>CENPC_S763s_S77</i>	<b>Low SETD7</b>

						3s, CENPC_S384s, CENPC_S709s_S71 0s_S713s, CENPC_S620s, CENPC_S333s, CENPC_S316s, CENPC_S276s, CENPC_S709s)	
Cullin 1 ( <i>CUL1</i> )	K73 [1]	-	NA	NA	NA	NA	Low SETD7
Dnmt1 ( <i>DNMT1</i> )	K142 [5]	-	NA	NA	NS (DNMT1_K189k, DNMT1_K973k)	Low SETD7 (DNMT1_S1105s, DNMT1_S127s, DNMT1_S154s, DNMT1_S398s, DNMT1_S714s, DNMT1_S732s, DNMT1_T253t)	Low SETD7



						NS (DNMT1_T328t, DNMT1_S6s, DNMT1_S143s, DNMT1_S141s_S1 43s, DNMT1_T166t, DNMT1_S1447s, DNMT1_S312s)	
ER $\alpha$ ( <i>ESR1</i> )	K302 [6]	-	<b>High SETD7 (ESR1)</b> NS (ESR1_PS118)	<b>High SETD7 (ESR1)</b> NS* (ESR1_PS118)	NS (ESR1_K171k)	<b>High SETD7 (ESR1_S296s)</b> NS (ESR1_S167s)	NS
E2F-1 ( <i>E2F1</i> )	K185 [7]	Phosphor ylation (S31 and S364)	NA	NA	NA	NS (E2F1_S375s, E2F1_S307s)	NA

		Acetylation (K117, K120 and K125) [8]					
Forkhead box protein O3 ( <i>FOXO3</i> )	K271 [9,10]	-	NS* ( <i>FOXO3</i> ) NS ( <i>FOXO3</i> _PS318_S321)		NS ( <i>FOXO3</i> _K259k, <i>FOXO3</i> _K242k)	NS ( <i>FOXO3</i> _S555s, <i>FOXO3</i> _S253s, <i>FOXO3</i> _S413s, <i>FOXO3</i> _T433t, <i>FOXO3</i> _S55s, <i>FOXO3</i> _S294s_S300s, <i>FOXO3</i> _S284s, <i>FOXO3</i> _S311s, <i>FOXO3</i> _S294s, <i>FOXO3</i> _T32t, <i>FOXO3</i> _T433t_S439s, <i>FOXO3</i> _S215s, <i>FOXO3</i> _S280s,	NS

						FOXO3_T427t, FOXO3_S300s)	
Transcription al activator GLI3 ( <i>GLI3</i> )	K436 and K595 [11]	-	NA	NA	NA	<b>High SETD7</b> ( <b>GLI3_S1006s,</b> <b>GLI3_S445s</b> ) NS (GLI3_S980s, GLI3_S849s, GLI3_S664s, GLI3_S313s, GLI3_S907s, GLI3_S865s, GLI3_S877s, GLI3_S1038s)	<b>High SETD7</b>
Hif1-alpha ( <i>HIF1A</i> )	K32 [12]	-	NA	NA	NS (HIF1A_K733k)	NS (HIF1A_S475s)	NA
HIV Tat- specific factor 1	K51 [13] and K71 [14]	-	NA	NA	NS (HTATSF1_K661k)	<b>Low SETD7</b> ( <b>HTATSF1_S702s,</b> <b>HTATSF1_S713s,</b>	<b>Low SETD7</b>

(HTATSF1)						HTATSF1_S521s, HTATSF1_S676s, HTATSF1_S494s, HTATSF1_S616s_ S624s, HTATSF1_S494s_ S498s, HTATSF1_S521s_ S529s, HTATSF1_S713s_ S714s, HTATSF1_S721s, HTATSF1_S529s, HTATSF1_S481s, HTATSF1_S616s, HTATSF1_S600s) NS (HTATSF1_S624s,	
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						HTATSF1_S597s_S 600s, HTATSF1_S407s, HTATSF1_T633t, HTATSF1_S498s, HTATSF1_S387s, HTATSF1_S445s_S 452s_S453s, HTATSF1_S85s_S4 98s, HTATSF1_S713s_S 714s_S721s, HTATSF1_S561s, HTATSF1_S479s, HTATSF1_S485s, HTATSF1_S453s, HTATSF1_S452s_S 453s,	
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						HTATSF1_S544s, HTATSF1_S241s, HTATSF1_S616s_S 624s_T633t, HTATSF1_S403s_S 407s, HTATSF1_S642s, HTATSF1_S579s, HTATSF1_S387s_S 389s, HTATSF1_S445s, HTATSF1_S702s_S 713s, HTATSF1_359s, HTATSF1_S597s_S 600s_S607s, HTATSF1_S403s)	
IRF-1 ( <i>IRF1</i> )	K126 [1]	-	NA	NA	NA	NA	NA

Histone acetyltransferase KAT2B ( <i>KAT2B</i> / <i>PCAF</i> )	K78, K89, K638, K671, K672 and K692 [15]	-	NA	NA	NA	NA	NA
KH domain-containing, RNA-binding, signal transduction-associated protein 1, Sam68 ( <i>KHDRBS1</i> )	K208 [16]	-	NA	NA	<b>Low SETD7 (KHDRBS1_K169k, KHDRBS1_K175k)</b> NS (KHDRBS1_K152k, KHDRBS1_K165k, KHDRBS1_K139k, KHDRBS1_K194k)	NS (KHDRBS1_S20s, KHDRBS1_S35s, KHDRBS1_S58s, KHDRBS1_S137s, KHDRBS1_T33t, KHDRBS1_T61t, KHDRBS1_S90s, KHDRBS1_T84t)	NS
Protein lin-28 homolog A ( <i>LIN28A</i> )	K135 [17]	-	NA	NA	NA	NA	NA

MeCp2 (MECP2)	K347 [1]	-	NA	NA	NS (MECP2_K222k, MECP2_K461k, MECP2_K333k, MECP2_K231k MECP2_K343k, MECP2_K316k, MECP2_K34k)	<b>High SETD7</b> <b>(MECP2_S286s,</b> <b>MECP2_T323t,</b> <b>MECP2_T323t_S32</b> <b>5s)</b> NS (MECP2_S325s, MECP2_T240s, MECP2_S92s, MECP2_S176s, MECP2_S25s, MECP2_S435s, MECP2_S82s, MECP2_S372s, MECP2_413s, MECP2_161s, MECP2_S368s_S37 2s)	NS
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Mediator of RNA polymerase II transcription subunit 1 ( <i>MED1</i> / <i>PPARBP</i> )	K1006 [1]	-	NA	NA	Low SETD7 ( <b>MED1_K699k</b> ) NS (MED1_K2k, MED1_K1210k, MED1_K1529k, MED1_K1309k, MED1_K1126k, MED1_K994k, MED1_K1354k, MED1_K991k)	Low SETD7 ( <b>MED1_S1207s,</b> <b>MED1_S1207s_T1</b> <b>215t</b> ) NS (MED1_S1481s_S1 482s, MED1_S1463s, MED1_T1215t, MED1_S1453s_S14 63s, MED1_S1479s, MED1_T1051t, MED1_S1463s_S14 65s, MED1_S588s, MED1_S1302s, MED1_S1192s, MED1_S1251, MED1_T628t,	
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						MED1_S1433s_T14 40t, MED1_S1479s_S14 81s_S1482S, MED1_S1156s, MED1_S953s, MED1_S1437s, MED1_T1017t_T10 32t, MED1_S1130s, MED1_S664s, MED1_T1051t_T10 57t, MED1_S1433s, MED1_S1401s, MED1_S1023s)	
Bile acid receptor ( <i>NR1H4</i> / <i>FXR</i> )	K206 [18]	-	NA	NA	NA	NA	NA

PARP-1 ( <i>PARP1</i> )	K508 [19]	-	NA	NA	<b>Low SETD7</b> <b>(PARP1_K621k,</b> <b>PARP1_K400k,</b> <b>PARP1_K662k,</b> <b>PARP1_K108k,</b> <b>PARP1_K633k,</b> <b>PARP1_K418k,</b> <b>PARP1_K105k,</b> <b>PARP1_K134k)</b> NS (PARP1_K700k, PARP1_K637k, PARP1_K796k, PARP1_K600k, PARP1_K433k, PARP1_K683k, PARP1_K654k, PARP1_K221k, PARP1_K84k,	<b>Low SETD7</b> <b>(PARP1_S179s,</b> <b>PARP1_S782s,</b> <b>PARP1_T368t)</b> NS (PARP1_S519s, PARP1_S257s)	<b>Low SETD7</b>
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					PARP1_K518k, PARP1_K119k, PARP1_K521k, PARP1_K505k, PARP1_K148k, PARP1_K192k, PARP1_K548k)		
PDX-1 ( <i>PDX1</i> )	K123 and K131 [20]	-	NA	NA	NA	NA	NA
PGC-1-alpha ( <i>PPARGC1A</i> )	K779 [21]	-	NA	NA	NA	NA	NA
Protein phosphatase 1 regulatory subunit 12A ( <i>PPP1R12A</i> )	K442 [22]	-	NA	NA	NA	<b>Low</b> SETD7 ( <i>PPP1R12A_S422s</i> ) <b>High</b> SETD7 ( <i>PPP1R12A_S427s</i> _S473s, <i>PPP1R12A_S479s</i> , <i>PPP1R12A_S507s</i> ,	<b>High</b> SETD7

						<p>PPP1R12A_S618s, PPP1R12A_S554s, PPP1R12A_S668s, PPP1R12A_S695s, PPP1R12A_S862s, PPP1R12A_S862s_ S871s, PPP1R12A_S910s, PPP1R12A_T443t) NS (PPP1R12A_S445s, PPP1R12A_S292s, PPP1R12A_S995s, PPP1R12A_S903s, PPP1R12A_T853, PPP1R12A_S477s, PPP1R12A_S409s, PPP1R12A_S507s_</p>	
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						T508t, PPP1R12A_T524st, PPP1R12A_T853t_ S682s_S871s, PPP1R12A_S509s, PPP1R12A_S608s, PPP1R12A_S299s, PPP1R12A_S527s, PPP1R12A_T406t_ S409s, PPP1R12A_S356s_ S357s_S365s, PPP1R12A_T305t)	
pRb ( <i>RB1</i> )	K810 [23] ad K873 [24]	Phosphor ylation (S807 and S811) [23]	NS* (RB1_PS807_ S811)	NS (RB1_PS807_ S811)	NA	<b>High SETD7</b> <b>(RB1_T601t)</b> NS (RB1_T841t, RB1_Y805yS807s, RB1_S780s_S788s,	

						RB1_T356t, RB1_S37s, RB1_S807s, RB1_S249s, RB1_T373t, RB1_T601t_S612s, RB1_S780s, RB1_S795s, RB1_T821t_T826t, RB1_T826t, RB1_T821t, RB1_S249s_T252t)	
Transcription factor p65, NFkB-p65 ( <i>RELA</i> )	K37 [25], K315 and K316 [26]	-	NA	NA	NS ( <i>RELA</i> _K122k, <i>RELA</i> _K195k, <i>RELA</i> _K310k)	<b>High SETD7</b> <b>(<i>RELA</i>_S205s)</b> NS ( <i>RELA</i> _S238s, <i>RELA</i> _S338s, <i>RELA</i> _S45s)	NS

Serine/threonine-protein kinase RIO1 ( <i>RIOK1</i> )	K411 [27]	Phosphorylation (T410) [27]	NA	NA	NA	<b>Low SETD7 (RIOK1_S21s_S22s, RIOK1_S22s)</b> NS (RIOK1_S21s_S22s_S24s)	<b>Low SETD7</b>
Nuclear receptor ROR-alpha ( <i>RORA</i> )	K87 [28]	-	NA	NA	NA	NS (RORA_S49s)	NA
60S ribosomal protein L29 ( <i>RPL29</i> )	K5 [29]	-	NA	NA	NA	NS (RPL29_S142s, RPL29_S158s)	NS
hSIRT1 ( <i>SIRT1</i> )	K233, K235, K236 and K238 [30]	-	NA	NA	NA	NS (SIRT1_T719t, SIRT1_S47s, SIRT1_S27s, SIRT1_S14s, SIRT1_747s,	NS



						SIRT1_S615s, SIRT1_S14s_S16s)	
Mothers against decapentaple gic homolog 7 ( <i>SMAD7</i> )	K70 [31]	-	NA	NA	NA	NA	NA
Transcription factor SOX-2 ( <i>SOX2</i> )	K119 [32]	-	NA	NA	NA	NA	NA
Msx2- interacting protein ( <i>SPEN</i> / <i>MINT</i> )	K2076 [1]	-	NA	NA	NS ( <i>SPEN_K21k</i> )	<b>High</b> <b>SETD7</b> ( <i>SPEN_S1425s</i> ) <b>Low</b> <b>SETD7</b> ( <i>SPEN_S1636s</i> , <i>SPEN_S2114s_S21</i> <i>26s</i> , <i>SPEN_S2120s</i> , <i>SPEN_S2126s</i> , <i>SPEN_S736s_S740</i>	NS

						s, SPEN_S749s, SPEN_T1633t_S16 36s, SPEN_T2393t, SPEN_T2421t) NS (SPEN_S2412s, SPEN_T1910t, SPEN_1619t_S1622 s, SPEN_S1252s, SPEN_S1222s, SPEN_T3467t, SPEN_T3139t, SPEN_S1380s_S138 2s, SPEN_S1918s, SPEN_T1619t, SPEN_T1947t, SPEN_S2366s, SPEN_T1140t, SPEN_S725s_S727s	
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						, SPEN_S727s, SPEN_S1857, SPEN_S1287s, SPEN_S1283s_S128 7s, SPEN_S623s, SPEN_S3433s, SPEN_S1278s, SPEN_S2101s, SPEN_S2466s, SPEN_S190s_2, SPEN_S2159s, SPEN_S1268s, SPEN_S190s_1, SPEN_S736s, SPEN_S1261s, SPEN_T3236t, SPEN_S2493s, SPEN_T2918t,	
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						SPEN_S1268s_S1278s, SPEN_S1062s, SPEN_S1380s, SPEN_T1826t, SPEN_S1006s)	
Signal transducer and activator of transcription 3 ( <i>STAT3</i> )	K140 [33]	-	NS (STAT3_PY705)	NS (STAT3_PY705)	<b>Low SETD7 (STAT3_K631k)</b> NS (STAT3_K370k, STAT3_K383k)	NA	NS
Histone-lysine N-methyltransferase SUV39H1 ( <i>SUV39H1</i> )	K105 and K123 [34]	-	NA	NA	NA	<b>Low SETD7 (SUV39H1_S402s)</b>	NS

Transcription initiation factor TFIID subunit 7 ( <i>TAF7</i> )	K5 [35]	-	NA	NA	NS (TAF7_K291k)	<b>Low SETD7 (TAF7_T274t)</b> NS (TAF7_S201s, TAF7_S171s, TAF7_S213s, TAF7_S264s, TAF7_S159s)	NS
Transcription initiation factor TFIID subunit 10 ( <i>TAF10</i> )	K189 [36]	-	NA	NA	NA	NS (TAF10_S44s)	NS*
Cellular tumor antigen p53 ( <i>TP53</i> )	K372 [37]	-	NS* (TP53)	NS	NS (TP53_K381k_K382k )	NS (TP53_S315s, TP53_S367s, TP53_S15s, TP53_S392s)	NS
Dual specificity	K708 [1]	-	NA	NA	NA	NA	<b>Low SETD7</b>

protein kinase TTK ( <i>TTK</i> / <i>MPS1</i> )							
Transcription al coactivator YAP1 ( <i>YAP1</i> )	K494 [38]	-	NS* (YAP1, YAP1_PS127)	NS (YAP1) NS* (YAP1_PS127 )	NS (YAP1_K97k, YAP1_K346k)	<b>High SETD7</b> <b>(YAP1_S109s_T11</b> <b>0t, YAP1_S128s,</b> <b>YAP1_S164s,</b> <b>YAP1_S386s,</b> <b>YAP1_T365t)</b> NS (YAP1_S109s, YAP1_S131_T143t, YAP1_S289s, YAP1_T432t, YAP1_S274s, YAP1_S61s, YAP1_S276s, YAP1_S217s,	<b>High</b> <b>SETD7</b>

						YAP1_S229s, YAP1_S344s)	
Transcription al repressor protein YY1 (YY1)	K173 and K411 [39]	-	NA	NA	<b>Low</b> <b>SETD7</b> <b>(YY1_K339k)</b> NS (YY1_K351k)	<b>Low</b> <b>SETD7</b> <b>(YY1_S118s)</b> NS (YY1_S187s)	NS
Transcription factor YY2 (YY2)	247 [40]	-	NA	NA	NA	NA	NA
Palmitoyltran sferase ZDHHC8 (ZDHHC8)	K300 [1]	-	NA	NA	NA	NS (ZDHHC8_S606s, ZDHHC8_S526s, ZDHHC8_S453s, ZDHHC8_S675s)	NA

\* not significant because  $|\log_{FC}| < 0.4$

**Table S4.** SETD7 association with survival outcomes. Significant values are highlighted in bold and strong tendencies (p-val ≤ 0.1) are shown in italic. Log rank test. BC – Breast Cancer, **CI – Confidence Interval**, DE – Differential Expression, DFS – Disease Free Survival, DSFS – Disease-Specific Free Survival, HPA – Huma Protein Atlas, **HR – Hazard Ratio**, OS – Overall survival, PFS – Progression Free Survival, PPS – Palliative Performance Score, RFS – Recurrence Free Survival, DMFS – Distant Metastasis Free Survival.

Online tool	Type of data	Dataset (additional information)	PAM50 Subtypes (lumA / lumB / Her2-enriched / basal / normal-like)	nSETD7 DE / nTotal samples	Survival	p-value	<b>HR (CI) / Prognosis associated with high SETD7</b>
<b>KM plotter</b>	Gene chip	All (E-MTAB-365 and 13 GEO studies)	631 / 566 / 358 / 442 / 35	1015 / 2032	RFS	0.96	1.01 (0.81 – 1.25)
		All (7 GEO studies)	259 / 183 / 218 / 283 / 15	482 / 958	DMFS	0.25	0.79 (0.54 – 1.18)
		All (7 GEO studies)	222 / 200 / 198 / 296 / 27	473 / 943	OS	0.066	0.69 (0.46 – 1.03) <i>Good</i>
		All (3 GEO studies)	36 / 53 / 47 / 38 / 6	90 / 108	PPS	<b>0.007</b>	<b>0.49 (0.29 – 0.83)</b> <b>Good</b>
		E-MTAB-365	174 / 149 / 53 / 49 / 1	212 / 426	RFS	0.57	0.86 (0.52 – 1.43)



		GSE12276 (tumours with known site of relapse – focus on brain)	34 / 72 / 38 / 59 / 1	104 / 204	RFS	0.13	0.74 (0.5 – 1.09)
		GSE16391 (Primary ER+/PR-/HER2- tumours of endocrine-treated patients, includes relapses)	27 / 19 / 2 / 0 / 0	24 / 48	RFS	0.1	5.04 (0.59 – 43.35) <i>Bad</i>
		GSE16446 (Primary ER-negative tumours of anthracycline-treated patients (neoadjuvant))	0 / 0 / 34 / 72 / 1	54 / 107	RFS / DMFS	0.017	8.46 (1.05 – 68.32) <b>Bad</b>
					OS	0.25	3.46 (0.37 – 32.02)
		GSEE17907 (tumours with amplification of the <i>ERBB2</i> locus)	5 / 5 / 24 / 2 / 2	20 / 54	RFS / DMFS	0.79	0.83 (0.21 – 3.34)
		GSE19615	45 / 23 / 17 / 30 / 0	58 / 115	RFS / DMFS	0.98	1.02 (0.29 – 3.52)

		GSE20685	117 / 91 / 69 / 42 / 8	164 / 327	RFS / DMFS	0.12	0.58 (0.29 – 1.16)
					OS	<b>0.039</b>	<b>0.47 (0.23 – 0.98)</b> <b>Good</b>
			25 / 26 / 20 / 7 / 3	40 / 81	PPS	<b>0.034</b>	<b>0.47 (0.23 – 0.96)</b> <b>Good</b>
		GSE20711	16 / 32 / 17 / 23 / 0	44 / 90	RFS	0.33	1.56 (0.64 – 3.84)
					OS	0.98	1.02 (0.33 – 3.15)
			4 / 18 / 11 / 9 / 0	20 / 42	PPS	0.26	0.48 (0.13 – 1.76)
		GSE21653	73 / 59 / 21 / 69 / 8	116 / 266	RFS	0.58	0.83 (0.43 – 1.61)
		GSE42568	27 / 28 / 12 / 30 / 7	52 / 104	RFS	<b>0.02</b>	<b>0.41 (0.19 – 0.89)</b> <b>Good</b>
					OS	<b>0.001</b>	<b>0.22 (0.08 – 0.62)</b> <b>Good</b>
			6 / 8 / 6 / 10 / 3	16 / 33	PPS	<b>0.031</b>	<b>0.2 (0.04 – 1)</b> <b>Good</b>
		GSE48390 (breast tumours from Taiwanese women)	27 / 28 / 10 / 8 / 7	40 / 109	RFS	0.97	1.04 (0.15 – 7.39)
					OS	0.99	1.03 (0.06 – 16.41)
		GSE58812 (triple-negative (IHC))	6 / 4 / 13 / 80 / 4	54 / 107	OS	0.55	1.38 (0.48 – 3.97) <i>Bad</i>
					DMFS	0.96	1.03 (0.36 – 2.93)
		GSE61304	16 / 15 / 11 / 16 / 0	28 / 58	RFS	<b>0.009</b>	<b>0.11 (0.01 – 0.83)</b>

							<b>Good</b>
					DMFS	<b>0.042</b>	<b>0.15 (0.02 – 1.23)</b> <b>Good</b>
					RFS	0.15	625e7 (0 – Inf)
		GSE65194	29 / 17 / 43 / 41 / 0	63 / 130	DMFS	0.84	1.15 (0.29 – 4.63)
					OS	0.81	1.21 (0.24 – 6.05)
					RFS	0.36	0.46 (0.08 – 2.51)
		GSE9195 (ER+ primary breast tumors of patients treated by Tamoxifen in adjuvant setting)	41 / 28 / 7 / 1 / 0	38 / 77	DMFS	0.89	0.87 (0.12 – 6.19)
	RNA-seq	GSE96058	1504 / 668 / 295 / 309 / 200	1486 / 2976	OS	<b>0.016</b>	<b>0.68 (0.49 – 0.93)</b> <b>Good</b>
	Protein	Tang_2018	NA	65 *	OS	<b>0.014</b>	<b>2.6 (1.18 – 5.75)</b> <b>Bad</b>
<b>HPA</b>	RNA-seq	TCGA	NA	1075 *	OS	<b>0.001</b>	<b>Bad</b>
<b>cBioPortal</b>	Gene chip	METABRIC	700 / 475 / 224 / 209 / 148 (218 claudin-low / 529 NA / 6 NC)	952 / 2976 (- 605 NA)	OS	0.362	
					RFS	0.073	<i>Bad</i>
	RNA-seq	TCGA PanCancer Atlas	499 / 197 / 78 / 171 / 36 (103 NA)	541 / 1084 (- 2 NA)	OS	<b>0.012</b>	<b>Bad</b>
					PFS	0.227	-
					DSFS	0.273	-
					DFS	0.909	-

\*Differentially expressed method is automatic (by median), for all other analysis samples were divided by high (upper quartile) *vs* low (lower quartile) SETD7 expression.

**Table S5.** Prognosis associated with high *SETD7* in BC subtypes. Significant values are highlighted in bold and strong tendencies (p-val  $\leq 0.1$ ) are shown in parenthesis. Log rank test. DFS – Disease free survival; DMFS – Distant metastasis free survival; DSFS – Disease-specific free survival; NA – not available, either because the number of samples were too low for each subgroup or because KM plotter didn't perform the analysis; OS – overall survival; PFS – Progression free survival; PPS – Palliative performance score; RFS – Recurrence/Relapse free survival.

Online Tool	Type of data	Datasets	Survival	Luminal A p-value (nSETD7 DE / nTotal samples)	Luminal B p-value (nSETD7 DE / nTotal samples)	Her2+ p-value (nSETD7 DE / nTotal samples)	Basal p-value (nSETD7 DE / nTotal samples)	Normal-like p-value (nSETD7 DE / nTotal samples)	Claudin-low p-value (nSETD7 DE / nTotal samples)
KM plotter	Gene chip	All studies	RFS	0.89 (317 / 631)	0.16 (284 / 566)	0.41 (180 / 358)	<b>0.009 (221 / 442)</b> <b>Bad</b>	0.64 (18 / 35)	-

			DMFS	0.027 (130 / 259) Good	0.93 (92 / 183)	0.64 (104 / 218)	0.27 (142 / 283)	0.73 (8 / 15)	-
			OS	0.41 (112 / 222)	0.47 (100 / 200)	0.091 (100 / 198)	0.33 (148 / 296)	0.99 (14 / 27)	-
			PPS	0.88 (18 / 36)	0.21 (26 / 53)	0.065 (24 / 47) (Good)	0.18 (20 / 38)	NA (NA / 6)	-
		E-MTAB-365	RFS	0.28 (88 / 174)	0.2 (74 / 149)	0.59 (26 / 53)	0.32 (25 / 49)	NA (- / 1)	-
		GSE12276	RFS	0.83 (16 / 34)	0.14 (36 / 72)	0.51 (20 / 38)	0.8 (30 / 59)	NA (- / 1)	-
		GSE16391	RFS	0.14 (14 / 27)	NA (NA / 19)	NA (- / 2)	-	-	-
		GSE16446	RFS / DMFS	-	-	NA (NA / 34)	0.029 (36 / 72) Bad	NA (- / 1)	-
			OS	-	-	NA (NA / 34)	0.061 (36 / 72) (Bad)	NA (- / 1)	-

		GSE17907	RFS / DMFS	NA (NA / 5)	NA (NA / 5)	0.77 (12 / 24)	NA (- / 2)	NA (- / 2)	-
		GSE19615	RFS / DMFS	0.53 (22/ 45)	NA (NA / 23)	NA (NA / 17)	0.14 (16 / 30)	-	-
		GSE20685	RFS / DMFS	0.21 (58 / 117)	0.72 (46 / 91)	0.86 (34 / 69)	0.15 (20 / 42)	NA (NA / 8)	-
			OS	0.19 (58 / 177)	0.62 (46 / 91)	0.29 (34 / 69)	0.1 (20 / 42)	NA (NA / 8)	-
			PPS	0.93 (12 / 25)	0.76 (12 / 26)	0.096 (10 / 20)	NA (NA / 7)	NA (NA / 3)	-
		GSE20711	RFS	NA (NA / 16)	0.57 (16 / 32)	NA (NA / 17)	<b>0.018 (12 / 23)</b> <b>Bad</b>	-	-
			OS	NA (NA / 16)	0.97 (16 / 32)	NA (NA / 17)	0.095 (12 / 23) (Bad)	-	-
			PPS	NA (NA / 4)	NA (NA / 18)	NA (NA / 11)	NA (NA / 9)	-	-
		GSE21653	RFS	0.66 (36 / 73)	0.075 (30 / 59)	0.7 (10 / 21)	0.46 (34 / 69)	NA (NA / 8)	-

					(Good)				
		GSE42568	RFS	0.47 (14 /27)	0.56 (14 / 28)	NA (NA / 12)	0.2 (16 / 30)	NA (NA / 7)	-
			OS	0.14 (14 /27)	0.1 (14 / 28)	NA (NA / 12)	0.063 (16 / 30) (Good)	NA (NA / 7)	-
			PPS	NA (NA / 6)	NA (NA / 8)	NA (NA / 6)	NA (NA / 10)	NA (NA / 3)	-
		GSE48390	RFS	NA (NA / 27)	NA (NA / 28)	NA (NA / 10)	NA (NA / 8)	NA (NA / 7)	-
			OS	NA (NA / 27)	NA (NA / 28)	NA (NA / 10)	NA (NA / 8)	NA (NA / 7)	-
		GSE61304	RFS	NA (NA / 16)	NA (NA / 15)	NA (NA / 11)	NA (NA / 16)	-	-
			DMFS	NA (NA / 16)	NA (NA / 15)	NA (NA / 11)	NA (NA / 16)	-	-
		GSE65194	RFS	NA (NA / 29)	NA (NA / 17)	NA (NA / 43)	NA (NA 41)	-	-

			DMFS	NA (NA / 29)	NA (NA / 17)	0.68 (22 / 43)	<b>0.024 (20 / 41)</b> <b>Bad</b>	-	-
			OS	NA (NA / 29)	NA (NA / 17)	0.9 (22 / 43)	<b>0.0052 (20 / 41)</b> <b>Bad</b>	-	-
		GSE9195	RFS	0.15 (20 / 41)	0.06 (14 / 28) (Bad)	NA (NA / 7)	NA (- / 1)	-	-
			DMFS	NA (NA / 41)	<b>0.045 (14 / 28)</b> <b>Bad</b>	NA (NA / 7)	NA (- / 1)	-	-
		GSE58812	OS	NA (NA / 6)	NA (NA / 4)	NA (NA / 13)	0.55 (40 / 80)	NA (NA / 4)	-
			DMFS	NA (NA / 6)	NA (NA / 4)	NA (NA / 13)	0.81 (40 / 80)	NA (NA / 4)	-
	RNA-seq	GSE96058	OS	0.31 (751 / 1504)	0.14 (334 / 668)	0.95 (149 / 295)	0.7 (154 / 309)	0.52 (100 / 200)	-
cBioPortal	Gene chip	METABRIC	OS	0.651 (339 / 700)	0.514 (232 / 475)	0.513 (110 / 224)	0.879 (99 / 209)	0.435 (70 / 148)	0.511 (99 / 218)



			RFS	0.721 (339 / 700)	0.111 (231 / 475)	0.967 (110 / 224)	0.830 (99 / 209)	0.392 (70 / 148)	0.133 (99 / 218)
	RNA-seq	TCGA PanCancer Atlas	OS	<b>0.044 (249 / 499) Bad</b>	0.712 (99 / 197)	0.0959 (39 / 78) (Bad)	0.456 (85 / 171)	0.381 (18 / 36)	-
			PFS	<b>0.0319 (249 / 499) Bad</b>	0.521 (99 / 197)	0.0511 (39 / 78) (Bad)	0.125 (85 / 171)	0.696 (18 / 36)	-
			DFS	0.701 (249 / 499)	0.577 (99 / 197)	0.154 (39 / 78)	0.0626 (85 / 171) (Bad)	0.371 (18 / 36)	-
			DSFS	0.0785 (249 / 499) (Bad)	0.370 (99 / 197)	0.169 (39 / 78)	0.610 (85 / 171)	0.967 (18 / 36) (Bad)	-

**Table S6.** Prognosis associated with high *SETD7* in BC considering therapy. Significant values are highlighted in bold (Log rank test p-val  $\leq 0.05$ ). CI – Confidence Interval, DFS – Disease Free Survival; DMFS – Distant metastasis free survival; DSFS – Disease-specific Free Survival; HR – Hazard Ratio, NA – Not Available, either because the number of samples were too low for each subgroup or because KM plotter didn't perform the analysis; OS – Overall Survival; PFS – Progression Free Survival; PPS – Palliative Performance Score; RFS – Recurrence/Relapse Free Survival.

Online Tool	Type of data	Datasets	Survival	No therapy p-value (nSETD7 DE / nTotal samples) HR (CI) / prognosis	Hormone plus Chemotherapy p-value (nSETD7 DE / n Total samples) HR (CI) / prognosis	Hormone therapy p-value (nSETD7 DE / n Total samples) HR (CI) / prognosis	Chemotherapy p-value (nSETD7 DE / n Total samples) HR (CI) / prognosis
KM plotter	Gene chip	All studies reporting treatment	RFS	0.18 (32 / 62) 0.39 (0.09 – 1.64)	0.052 (76 / 153) 0.33 (0.1 – 1.07)	0.99 (90 / 181) 0.99 (0.39 – 2.5)	0.0006 (106 / 211) 4.26 (1.73 – 10.5) Bad
			DMFS	0.81 (4 / 7) 1.41 (0.08 – 23.57)	0.28 (28 / 55) 3.24 (0.34 – 31.19)	0.3 (51 / 99) 0.32 (0.03 – 3.06)	0.0012 (84 / 168) 5.98 (1.75 – 20.47) Bad

			OS	-	-	-	0.25 (54 / 107) 3.46 (0.37 – 32.02)
		GSE16391	RFS	-	NA (NA / 18) -	0.14 (16 / 30) 4.5 (0.5 – 40.38)	-
		GSE16446	RFS / DMFS	-	-	-	<b>0.017 (54 / 107)</b> <b>8.46 (1.05 -68.32)</b> <b>Bad</b>
			OS				0.25 (54 / 107) 3.46 (0.37 – 32.02)
		GSE17907	RFS / DMFS	-	NA (NA / 13)	NA (NA / 1)	0.6 (12 / 23) 0.65 (0.13 – 3.25)
		GSE19615	RFS / DMFS	NA (NA / 7)	0.15 (20 / 42) 171e7 (0 – Inf)	NA (NA / 21)	0.15 (20 / 38) 4.41 (0.49 – 39.51)
		GSE21653	RFS	0.16 (28 / 55) 0.31 (0.06 – 1.73)	0.13 (40 / 80) 0.41 (0.12 -1.35)	0.89 (26 / 52) 1.12 (0.22 – 5.61)	0.13 (22 / 43) 2.8 (0.69 – 11.29)
		GSE9195	RFS	-	-	0.36 (38 / 77) 0.46 (0.08 – 2.51)	-
			DMFS	-	-	0.89 (38 / 77)	-

						0.87 (0.12 – 6.19)	
		GSE42568	RFS	-	-	-	<b>0.02 (52 / 104)</b> 0.41 (0.19 – 0.89) Bad
			OS	-	-	-	<b>0.0016 (52 / 104)</b> 0.22 (0.08 – 0.62) Bad
			PPS	-	-	-	0.28 (8 / 17)
	RNA-seq	GSE96058	OS	<b>0.016 (156 / 313)</b> 0.36 (0.15 – 0.86) Good	0.088 (429 / 854) 0.44 (0.17 – 1.16)	0.68 (724 / 1448) 0.92 (0.6 – 1.39)	0.8 (170 / 340) 0.91 (0.41 – 1.98)
cBioPortal	Gene Chip	METABRIC	RFS	0.381 (258 / 543)	0.283 (91 / 191)	<b>0.0325 (495/1025)</b> Bad	0.965 (107 / 221)
			OS	0.458 (259 / 543)	0.625 (91 / 191)	0.325 (495 / 1025)	0.933 (107 / 221)
	RNA-seq	TCGA PanCancer Atlas	OS	<b>0.0295 (537 / 1077)</b> Bad	Any: 6	-	-
			PFS	0.279 (536 / 1077)	Any: NA (NA / 6)	-	-

			DSFS	0.345 (533 / 1077)	Any: NA (NA / 6)	-	-
			DFS	0.891 (454 / 1077)	Any: NA (NA / 6)	-	-

**Table S7.** Prognosis associated with high *SETD7* in BC considering stage. Significant values are highlighted in bold (Log rank test p-val  $\leq 0.05$ ) and strong tendencies (Log rank test p-val  $\leq 0.1$ ) are shown in italic. DFS – Disease Free Survival; DSFS – Disease-specific Free Survival; NA – Not Available, because the number of samples were too low for each subgroup; OS – Overall Survival; PFS – Progression Free Survival; RFS – Recurrence/Relapse Free Survival.

Online tool	Type of data	Dataset	Survival	Stage 0 p-value (nSETD7 DE / nTotal samples)	Stage I p-value (nSETD7 DE / nTotal samples)	Stage II p-value (nSETD7 DE / nTotal samples)	Stage III p-value (nSETD7 DE / nTotal samples)	Stage IV p-value (nSETD7 DE / nTotal samples)
HPA	RNA-seq	TCGA	OS	-	<i>0.095 (180 / 180)</i> <i>Bad</i>	<b>0.00027 (609 / 609)</b> <b>Bad</b>	0.84 (243 / 243)	0.90 (20 / 20)
cBioPortal	Gene chip	METABRIC	OS	NA (NA / 24)	0.634 (237 / 630)	0.668 (400 / 979)	<i>0.0957 (57 / 144)</i> <i>Good</i>	NA (NA / 11)

			RFS	NA (NA / 24)	0.249 (236 / 630)	<b>0.0396 (400 / 979)</b> <b>Bad</b>	0.217 (57 / 144)	NA (NA / 11)
	RNA-seq	TCGA PanCancer Atlas	OS	-	0.332 (138 / 277)	<b>0.0283 (313 / 628)</b> <b>Bad</b>	0.520 (69 / 137)	0.633 (19 / 39)
			DFS	-	0.567 (123 / 277)	<b>0.0569 (312 / 628)</b> <b>Bad</b>	0.624 (57 / 137)	0.241 (9 / 39)
			PFS	-	0.612 (137 / 277)	0.120 (313 / 628)	0.991 (69 / 137)	0.728 (19 / 39)
			DSFS	-	0.877 (137 / 277)	0.325 (270 / 628)	0.685 (67 / 137)	0.879 (19 / 39)
KM plotter	Protein	Tang_2018	OS	-	NA (6 / 6)	<b>0.036 (46 / 46)</b> <b>Bad</b>	NA (13 / 13)	-

**Table S8.** Prognosis associated with high *SETD7* in BC considering grade. Significant values are highlighted in bold (Log rank test p-val  $\leq 0.05$ ) and strong tendencies (Log rank test p-val  $\leq 0.1$ ) are shown in italic. **CI** – Confidence Interval, DMFS – Distant Metastasis Free Survival; **HR** – Hazard Ratio, NA – Not Available, either because the number of samples were too low for each subgroup or simply because KM plotter didn't perform the analysis; OS – Overall Survival; PPS – Palliative Performance Score; RFS – Recurrence/Relapse Free Survival.

Online Tool	Type of data	Datasets	Survival	Grade I p-value (nSETD7 DE / nTotal samples) <i>HR (CI) / prognosis</i>	Grade II p-value (nSETD7 DE / nTotal samples) <i>HR (CI) / prognosis</i>	Grade III p-value (nSETD7 DE / nTotal samples) <i>HR (CI) / prognosis</i>
KM plotter	Gene chip	All studies reporting Grade status	RFS	<b>0.03 (56 / 113)</b> <b>0 (0 – Inf) Good</b>	0.8 (121 / 243) <i>1.09 (0.56 – 2.14)</i>	0.74 (242 / 481) <i>0.93 (0.62 – 1.41)</i>
			DMFS	NA (NA / 44) -	0.5 (46 / 91) <i>1.54 (0.43 – 5.44)</i>	0.093 (116 / 234) <i>1.98 (0.88 – 4.44)</i>
			OS	0.48 (12 / 26) <i>2.35 (0.2 – 27.18)</i>	0.82 (32 / 64) <i>0.82 (0.14 – 4.9)</i>	<i>0.061 (102 / 204)</i> <i>0.52 (0.26 – 1.04) Good</i>
			PPS	0.69 (4 / 6) <i>1.62 (0.14 – 18.31)</i>	0.69 (6 / 13) <i>0.62 (0.05 – 7)</i>	<b>0.0022 (36 / 72)</b> <b>0.24 (0.09 – 0.64) Good</b>
		GSE16391	RFS	NA (NA / 2)	0.14 (16 / 30)	NA (NA / 16)

				-	-	-
		GSE16446	RFS / DMFS	NA (NA / 2) -	NA (NA / 19) -	<b>0.013 (40 / 81)</b> <b>173e7 (0 - Inf) Bad</b>
			OS	NA (NA / 2) -	NA (NA / 19) -	0.13 (40 / 81) 139e7 (0 – Inf)
		GSEE17907	RFS / DMFS	-	NA (NA / 8) -	0.49 (14 / 29) -
		GSE19615	RFS / DMFS	NA (NA / 23) -	0.06 (14 / 28) 195e7 (0 – Inf) Bad	0.63 (32 / 64) 1.54 (0.26 – 9.22)
			RFS	NA (NA / 13) -	NA (NA / 5) -	0.37 (36 / 70) 1.55 (0.59 – 4.11)
			OS	NA (NA / 13) -	NA (NA / 5) -	0.63 (36 / 70) 1.34 (0.41 – 4.4)
			PPS	NA (NA / 3) -	NA (NA / 2) -	0.21 (18 / 37) 0.4 (0.09 – 1.75)
		GSE21653	RFS	0.082 (22 / 43) 0 (0 – Inf) Good	0.79 (38 / 77) 1.16 (0.39 – 3.47)	0.92 (54 / 107) 0.95 (0.4 – 2.3)



		GSE42568	RFS	NA (NA/ 11) -	0.79 (20 / 40) <a href="#">0.83 (0.2 – 3.36)</a>	0.2 (26 / 53) <a href="#">0.51 (0.17 – 1.47)</a>
			OS	NA (NA/ 11) -	0.57 (20 / 40) <a href="#">0.6 (0.1 – 3.6)</a>	<b>0.02 (26 / 53)</b> <a href="#">0.22 (0.06 – 0.89) Good</a>
			PPS	NA (NA / 3) -	NA (NA / 8) -	<b>0.04 (12 / 22)</b> <a href="#">0.19 (0.03 – 1.09) Good</a>
		GSE61304	RFS	NA (NA / 5) -	NA (NA / 16) -	<b>0.042 (18 / 37)</b> <a href="#">0.09 (0.01 – 0.74) Good</a>
			DMFS	NA (NA / 5) -	NA (NA / 16) -	0.14 (19 / 36) 0.23 (0.03 – 1.94)
		GSE9195	RFS	NA (NA / 14) -	NA (NA / 20) -	0.84 (12 / 24) <a href="#">0.82 (0.11 – 5.83)</a>
			DMFS	NA (NA / 14) -	NA (NA / 20) -	0.6 (12 / 24) <a href="#">1.88 (0.17 – 20.82)</a>
	RNA-seq	GSE96058	OS	0.35 (224 / 449) <a href="#">0.52 (0.13 – 2.08)</a>	0.18 (698 / 1394) <a href="#">0.7 (0.41 – 1.18)</a>	0.9 (536 / 1074) <a href="#">0.97 (0.65 – 1.46)</a>
	Protein	Tang_2018	OS	NA (8 / 8) -	NA (19 / 19) -	<b>0.016 (28 / 28)</b> <a href="#">3.39 (1.14 – 10.14) Bad</a>

cBioPortal	Gene chip	METABRIC	OS	0.516 (83 / 214)	0.745 (370 / 976)	0.421 (463 / 1198)
			RFS	0.863 (83 / 214)	0.186 (370 / 976)	0.309 (462 / 1198)

**Table S9.** Prognosis associated with high *SETD7* in BC considering lymph node status. Significant values are highlighted in bold (Log rank test p-val  $\leq 0.05$ ) and strong tendencies (Log rank test p-val  $\leq 0.1$ ) are shown in italic. **CI – Confidence Interval**, DFS – Disease Free Survival; DFSF – Disease-specific Free Survival; **HR – Hazard Ratio**, NA – Not Available, either because the number of samples were too low for each subgroup or because the analysis wasn’t processed by KM plotter; OS – Overall Survival; PFS – Progression Free Survival; RFS – Recurrence/Relapse Free Survival.

Online Tool	Type of data	Dataset	Survival	Lymph node status	
				Positive p-value (nSETD7 DE / nTotal samples) <b>HR (CI) / Prognosis</b>	Negative p-value (nSETD7 DE / nTotal samples) <b>HR (CI) / Prognosis</b>

KM plotter	Gene chip data (EGA and GEO)	All studies reporting lymph node status	RFS	0.11 (408 / 814) <a href="#">0.76 (0.54 – 1.07)</a>	0.74 (288 / 574) <a href="#">0.91 (0.52 – 1.58)</a>
			DMFS	0.19 (130 / 261) 1.58 (0.79 – 3.18)	0.39 (120 / 240) <a href="#">0.62 (0.2 – 1.89)</a>
			OS	0.059 (116 / 230) <a href="#">0,53 (0.28 – 1.03)</a> <i>Good</i>	0.91 (90 / 180) <a href="#">0.93 (0.28 – 3.06)</a>
			PPS	<b>0.00013 (38 / 76)</b> <a href="#">0.15 (0.05 – 0.45)</a> <b>Good</b>	0.45 (12 / 23) <a href="#">0.5 (0.08 – 3.05)</a>
		E-MTAB-365	RFS	0.96 (142 / 285) 1.02 (0.54 – 1.9)	0.43 (68 / 134) 0.71 (0.31 – 1.65)
		GSE16391	RFS	0.14 (16 / 30) <a href="#">4.53 (0.5 – 40.94)</a>	NA (NA / 18) -
		GSE16446	RFS / DMFS	0.053 (30 / 59) <a href="#">6.39 (0.74 – 54.99)</a> <i>Bad</i>	0.5 (24 / 48) <a href="#">2.18 (0.21 – 22.2)</a>
			OS	0.48 (30 / 59) <a href="#">2.32 (0.21 – 25.8)</a>	0.31 (24 / 48) <a href="#">114e7 (0 – Inf)</a>
		GSEE17907	RFS / DMFS	0.51 (12 / 24)	NA (NA / 11)

				0.55 (0.09 – 3.33)	-
		GSE19615	RFS / DMFS	0.37 (26 / 53) 2.15 (0.39 – 11.74)	0.31 (32 / 62) 0.33 (0.03 – 3.15)
		GSE20711	RFS	0.99 (30 / 59) 1 (0.36 – 2.75)	0.11 (14 / 29) 4.99 (0.56 – 44.83)
			OS	0.45 (30 / 59) 0.61 (0.17 – 2.18)	0.14 (14 / 29) 175e7 (0 – Inf)
			PPS	0.055 (18 / 35) 0.26 (0.06 – 1.12) <i>Good</i>	NA (NA / 7) -
		GSE21653	RFS	0.77 (60 / 119) 0.88 (0.39 – 2.01)	0.71 (54 / 108) 0.79 (0.23 – 2.74)
		GSE42568	RFS	0.4 (30 / 59) 0.69 (0.29 – 1.64)	0.042 (22 / 45) 0.14 (0.01 – 1.26) <b>Good</b>
			OS	0.04 (30 / 59) 0.33 (0.11 – 1) <b>Good</b>	0.026 (22 / 45) 0 (0 – Inf) <b>Good</b>
			PPS	0.029 (14 / 28) 0.18 (0.03 – 0.98) <b>Good</b>	NA (NA / 5) -

		GSE61304	RFS	0.096 (18 / 37) 0.28 (0.06 – 1.39) <i>Good</i>	0.19 (11 / 20) 0 (0 – Inf)
			DMFS	0.3 (18 / 37) 0.42 (0.08 – 2.27)	0.19 (11 / 20) 0 (0 – Inf)
		GSE65194	RFS	NA (NA / 53)	NA (NA / 58)
			OS	0.31 (26 / 53) 3.08 (0.32 – 29.71)	NA (NA / 58) -
			DMFS	0.51 (26 / 53) 1.65 (0.37 – 7.42)	0.16 (28 / 58) 0 (0 – Inf)
		GSE9195	RFS	0.28 (18 / 36) 0.41 (0.07 – 2.23)	NA (NA / 41) -
			DMFS	0.81 (18 / 36) 0.79 (0.11 – 5.67)	NA (NA / 41) -
	RNA-seq	GSE96058	OS	0.47 (911 / 1067) 0.85 (0.55 – 1.32)	0.055 (534 / 1820) 0.63 (0.39 – 1.01)
	Protein	Tang_2018	OS	0.8 (27 / 27) 0.85 (0.24 – 3.01)	0.00019 (37 / 37) 7.28 (2.17 – 24.47) <b>Bad</b>

cBioPortal	Gene Chip	METABRIC	RFS	<b>0.038 (455 / 1047)</b> <b>Bad</b>	0.680 (496 / 1196)
			OS	0.423 (455 / 1047)	0.766 (497 / 1196)
	RNA-seq	TCGA PanCancer Atlas	OS	0.116 (343 / 687)	0.806 (17 / 33)
			DFS	0.337 (299 / 687)	0.407 (11 / 33)
			DSFS	0.447 (340 / 687)	0.806 (17 / 33)
			PFS	0.772 (342 / 687)	0.468 (17 / 33)

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