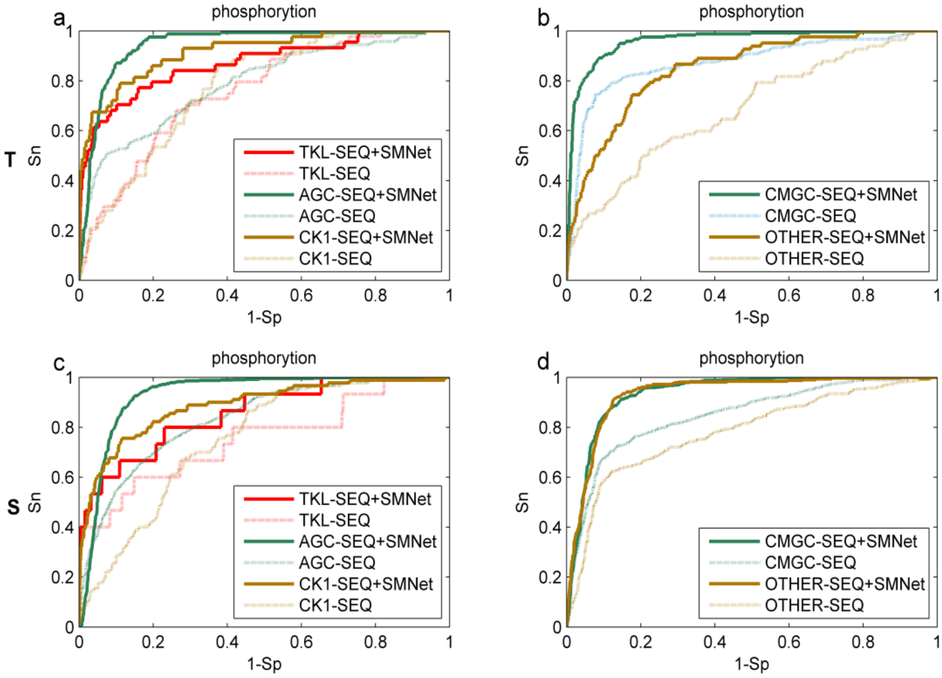

Figure S1. ROC curves of five phosphorylation kinase groups on S and T sites. Subplots *a* and *b* are the kinase groups performed on T sites, *c* and *d* are the kinase groups performed on S sites. The solid lines represent the SVM model constructed with SMNet profiles as well as local sequences, and the *dotted lines* represent the performance of the proposed method with only local sequences. SEQ and SMNet represent sequence and site-modification network.

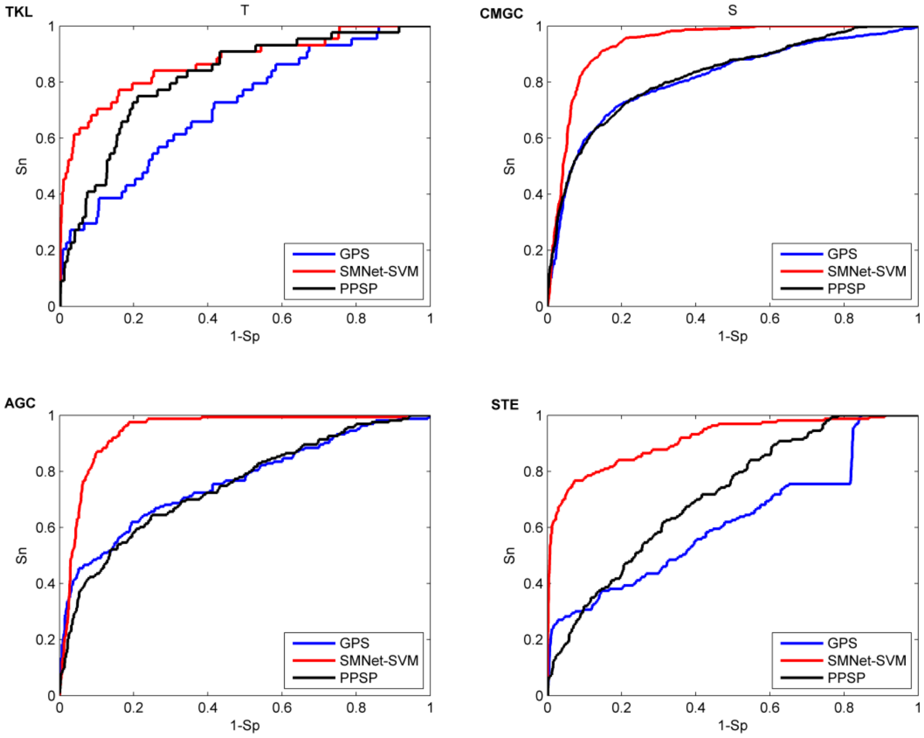

Figure S2. Performance of phosphorylation ROC curves in kinase group TKL, CMGC, AGC and STE with different methods. The red lines mean the performance of the SMNet method, and the blue and black lines show the GPS and PPSP, respectively. The kinase group TKL and AGC are response to T sites, and kinase group CMGC and STE are response to S sites.

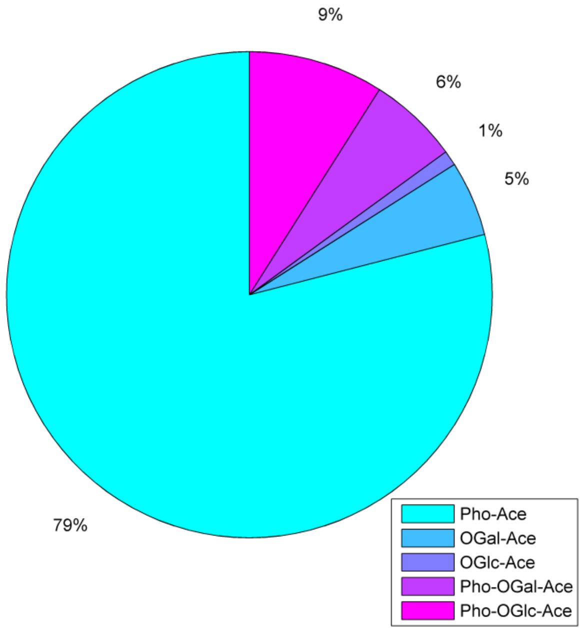

Figure S3. The distribution of different kinds of potential *in situ* PTMs for acetylation on S sites. Pho-Ace, OGal-Ace, OGlc-Ace, Pho-OGal-Ace and Pho-OGlc-Ace mean the sites that are both modified by two or three PTMs. Pho, OGal, OGlc, Ace are namely phosphorylation, O-GalNAc, O-GlcNAc and acetylation.

Table S1. The statistic of phosphorylation sites in kinase groups

Kinase group	**TKL**	**AGC**	**Atypical**	**CAMK**	**CK1**	**CMGC**	**STE**	**OTHER**
S sites	15	528	76	121	37	515	42	116
T sites	8	132	19	43	11	204	14	42
ALL	23	660	95	164	48	719	56	158

Table S2. Performance comparison of SMNet profiles and local sequences on S/T sites at high stringency level (*sp*=99.0%)

	PTM	Features	***Sn*(%)**	***MCC*(%)**	***Pre*(%)**	***Acc*(%)**
	Phosphorylation	SEQ	5.26	6.80	13.6	96.3
	(Atypical)	SEQ+SMNet	**31.6**	**37.8**	**48.7**	**97.0**
	Phosphorylation	SEQ	18.4	26.1	42.4	95.9
	(CAMK)	SEQ+SMNet	**32.9**	**41.6**	**56.8**	**96.4**
T	**Phosphorylation**	SEQ	14.6	18.4	26.9	96.9
	(STE)	SEQ+SMNet	**47.9**	**50.1**	**54.8**	**97.8**
	O-GalNAc	SEQ	4.84	10.1	89.7	38.5
		SEQ+SMNet	**37.2**	**40.4**	**98.5**	**59.3**
	Acetylation	SEQ	92.2	82.9	75.6	98.8
		SEQ+SMNet	92.2	82.9	75.6	98.8
	Phosphorylation	SEQ	12.3	21.7	48.2	92.8
	(Atypical)	SEQ+SMNet	**34.4**	**47.5**	**72.3**	**94.4**
	Phosphorylation	SEQ	2.81	4.76	20.6	91.0
	(CAMK)	SEQ+SMNet	**18.5**	**31.3**	**63.0**	**92.3**
S	**Phosphorylation**	SEQ	3.7	5.8	17.7	93.8
	(STE)	SEQ+SMNet	**52.8**	**61.4**	**75.4**	**96.5**
	O-GalNAc	SEQ	9.68	21.3	78.6	74.0
		SEQ+SMNet	9.32	20.7	78.0	73.9
	Acetylation	SEQ	87.9	89.5	94.3	97.3
		SEQ+SMNet	**90.0**	**90.8**	**94.4**	**97.6**

Table S3. Performance comparison of different methods for phosphorylation kinase group AGC, TKL, CMGC and STE (*sp*=95.0%)

	Groups	Methods	*Sn*(%)	*MCC*(%)	*Pre*(%)	*Acc*(%)
T	AGC	Proposed	**63.2**	**53.9**	**53.4**	**92.4**
		PPSP	34.4	30.9	38.4	90.0
		GPS	43.6	38.8	44.1	90.7
	TKL	Proposed	**61.4**	**34.4**	**22.0**	**94.2**
		PPSP	27.3	14.5	11.1	93.5
		GPS	27.3	14.5	11.1	93.5
S	CMGC	Proposed	**56.9**	**57.9**	**75.7**	**86.8**
		PPSP	43.3	46.5	70.4	83.9
		GPS	41.7	45.0	69.4	83.6
	STE	Proposed	**73.0**	**54.8**	**45.8**	**93.8**
		PPSP	19.0	13.7	18.0	90.9
		GPS	28.2	21.7	24.5	91.3

Table S4. Performance comparison of different methods for phosphorylation kinase group AGC, TKL, CMGC and STE (*sp*=99.0%)

	Groups	Methods	*Sn*(%)	*MCC*(%)	*Pre*(%)	*Acc*(%)
T	AGC	Proposed	13.5	24.4	55.0	91.9
		PPSP	9.20	17.6	45.5	91.5
		GPS	20.3	33.4	64.7	92.3
	TKL	Proposed	**40.9**	**43.5**	**48.7**	**97.7**
		PPSP	9.09	11.1	17.4	97.0
		GPS	20.5	24.3	32.1	97.3
S	CMGC	Proposed	**8.41**	**19.3**	**70.1**	**79.6**
		PPSP	16.8	31.8	82.4	81.4
		GPS	9.97	22.0	73.6	79.9
	STE	Proposed	**52.8**	**61.4**	**75.4**	**96.5**
		PPSP	7.36	12.6	30.0	94.0
		GPS	21.5	32.4	55.6	94.8

Table S5. Performance comparison of different methods for O-GlcNAc site prediction

	Method	*Sp*(%)	*MCC*(%)	*Pre*(%)	*Acc*(%)	*Sp*(%)	*MCC*(%)	*Pre*(%)	*Acc*(%)
T	O-GlcNAcPRED	99.0	5.23	21.7	90.9	95.0	7.88	17.4	88.0
	YinOYang		9.33	30.8	91.1		12.7	22.4	88.3
	PPSP		20.5	50.0	91.6		29.5	37.5	89.8
	SMNet-SVM		**52.9**	**78.3**	**94.0**		**68.5**	**60.7**	**94.1**
S	O-GlcNAcPRED	99.0	5.87	22.9	91.2	95.0	6.40	15.4	88.1
	YinOYang		19.5	48.1	91.8		19.3	28.2	89.1
	PPSP		29.7	60.9	92.4		28.7	36.3	89.9
	SMNet-SVM		**39.4**	**69.7**	**93.0**		**48.7**	**50.0**	**91.9**

Table S6. Functional enrichment analysis for different PTMs on S sites

	Category	Term	Count	*P-Value*
Phosphorylation kinase group CMGC	SP_PIR_KEYWORDS	phosphoprotein	74	2.13E-25
	SP_PIR_KEYWORDS	disease mutation	14	0.0112
	GOTERM_BP_FAT	GO:0007242~intracellular signaling cascade	24	8.93E-08
	GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	12	1.98E-05
	GOTERM_BP_FAT	GO:0051726~regulation of cell cycle	10	6.90E-05
	GOTERM_BP_FAT	GO:0010941~regulation of cell death	15	9.84E-05
	GOTERM_BP_FAT	GO:0022402~cell cycle process	12	2.07E-04
	GOTERM_BP_FAT	GO:0007049~cell cycle	14	2.31E-04
	GOTERM_BP_FAT	GO:0042127~regulation of cell proliferation	13	9.56E-04
	GOTERM_BP_FAT	GO:0007179~transforming growth factor beta receptor signaling pathway	4	4.14 E-03
	GOTERM_BP_FAT	GO:0010769~regulation of cell morphogenesis involved in differentiation	4	8.29 E-03
	KEGG_PATHWAY	hsa04110:Cell cycle	9	1.50E-05
	KEGG_PATHWAY	hsa04310:Wnt signaling pathway	7	2.44 E-03
	KEGG_PATHWAY	hsa05200:Pathways in cancer	10	2.66 E-03
	KEGG_PATHWAY	hsa04010:MAPK signaling pathway	7	0.0348
Phosphorylation kinase group CK1	SP_PIR_KEYWORDS	phosphoprotein	62	2.60E-18
	SP_PIR_KEYWORDS	disease mutation	13	0.0104
	SP_PIR_KEYWORDS	alzheimer disease	2	0.0422
	KEGG_PATHWAY	hsa05200:Pathways in cancer	8	5.15 E-03
	GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	8	0.0168
	GOTERM_CC_FAT	GO:0005667~transcription factor complex	5	0.0188
O-GlcNAc	SP_PIR_KEYWORDS	nucleus	46	1.32E-11
	SP_PIR_KEYWORDS	cytoplasm	32	2.36E-06
	SP_PIR_KEYWORDS	cell cycle	10	1.02E-04
	SP_PIR_KEYWORDS	Transcription	19	1.34 E-03
	UP_SEQ_FEATURE	glycosylation site: O-linked (GlcNAc)	6	5.92E-09
	GOTERM_CC_FAT	GO:0005856~cytoskeleton	24	4.57E-08
	GOTERM_MF_FAT	GO:0016563~transcription activator activity	13	8.81E-07
	GOTERM_BP_FAT	GO:0043254~regulation of protein complex assembly	7	8.72E-06
	GOTERM_BP_FAT	GO:0045449~regulation of transcription	25	3.89 E-03
	GOTERM_BP_FAT	GO:0006350~transcription	20	0.014
	KEGG_PATHWAY	hsa04930:Type II diabetes mellitus	3	0.0454
acetylation	SP_PIR_KEYWORDS	acetylation	53	4.10E-20
	SP_PIR_KEYWORDS	dna-binding	18	0.0142
	PIR_SUPERFAMILY	PIRSF002048:histone H2A	10	2.38E-16
	INTERPRO	IPR002119:Histone H2A	10	3.11E-16

	GOTERM_CC_FAT	GO:0032993~protein-DNA complex	10	1.26E-09
	GOTERM_CC_FAT	GO:0000785~chromatin	12	1.60E-08
	GOTERM_BP_FAT	GO:0006323~DNA packaging	10	4.71E-08
	GOTERM_BP_FAT	GO:0006325~chromatin organization	11	1.25E-04
	KEGG_PATHWAY	hsa00330:Arginine and proline metabolism	4	0.0174
	KEGG_PATHWAY	hsa05212:Pancreatic cancer	4	0.0385

Table S7. Information of top 10 potential *in situ* PTMs for acetylation on T sites

Ranking	UniProt ID	Protein name	Position	Known PTM	Potential *in situ* PTMs	Score
1	Q15125	EBP	2	O-GalNAc, O-GlcNAc	OGal-OGlc-Ace	0.964
2	P68431	HIST1H3A	4	Phosphorylation	Pho-Ace	0.752
3	P46734	MAP2K3	222	Phosphorylation	Pho-Ace	0.751
4	Q96KX2	CAPZA3	2	O-GlcNAc	OGlc-Ace	0.745
5	P45985	MAP2K4	261	Phosphorylation	Pho-Ace	0.727
6	Q15125	EBP	3	O-GalNAc, O-GlcNAc	OGal-OGlc-Ace	0.695
7	P21453	S1PR1	4	O-GalNAc,	OGal- Ace	0.646
8	P35579	MYH9	1800	Phosphorylation	Pho-Ace	0.554
9	P07900	HSP90AA1	7	Phosphorylation	Pho-Ace	0.534
10	P53779	MAPK10	221	Phosphorylation	Pho-Ace	0.505