Table S2. Identificaton of consensus sequence of TaREM using MEME and their function by prosite and Eukaryotic Linear Motif resource programs. The motif numbers are the same to those described in Figure5.

TaREM group/ genes names	Motif Number	Motif E-value	Motif size (aa)	Best possible match	Predicted Motif Function
All genes	†1	2.8^{e-34}	105	Remorin-C domain	-
Group1/ 1.1, 1.2, 1.3, 1.4, 1.5	*2	1.1^{e-07}	36-65	Remorin-N domain	-
Group1/ 1.1, 1.2, 1.3, 1.4	3	3^{e-05}	23	KITGGSIADERDAVALAKRV ETS	Casein kinase II (CK-2) phosphorylation site (PA)
Group 1/ 1.2, 1.3, 1.4, 1.5	4	4.545^{e-03}	14	DDSKALIAVVIVEV	(LIG_SUMO_SIM_par_1) Motif for the parallel beta augmentation mode of non-covalent binding to SUMO protein.
Group 1 / 1.2, 1.3, 1.4, 1.5	5	3^{e-05}- 4^{e-06}	13	KDVIAEEKAVIVP	GTF2I-like repeat profile
Group 1 / 1.1, 1.2, 1.5	6	0.16-0.084	10	MGAEVEEAAK	No hit
Group 1 / 1.5	7	5.324^{e-03}	29	KEKKSEGGSILDRDAVIAVL ARDLVEATK	CK2_PHOSPHO_SITE Casein kinase II phosphorylation site
Group 1 / 1.5	8	1.280^{e-02}	25	KVAPDEDESKALAVVTVEP KPNTKP	(MOD_SUMO_rev_2) Inverted version of Sumoylation motif recognized for modification by SUMO-1
Group 1/	9	3.252^{e-04}	12	MAEELEQAKKVE	(IG_BIR_II_1) IBMs are

1.3, 1.5, 6.6					function in the abrogation of caspase inhibition by Inhibitor of Apoptosis Proteins (IAPs) in apoptotic cells.
Group 1/ 1.2, 1.3, 1.4	10	1.280^{e-02}	16	KVDVADEEKAVIVAIP	(MOD_SUMO_rev_2) Inverted version of Sumoylation motif recognized for modification by SUMO-1
Group 4/ 4.1, 4.2, 4.3	11	6.4^{e-07}	27	TMPTMISREFNTSAMLVAIA GASASTM	ASN_GLYCOSYLATION N-glycosylation site
Group 4/ 4.1, 4.2	12	8.662^{e-03}	24	GDEDELEEETNPLAIVPDSH NYPI	(LIG_FHA_1) Phosphothreonine motif binding a subset of FHA domains, (LIG_PDZ_Class_2) The C-terminal class 2 PDZ-binding motif
Group 4/ 4.2	13	2.302^{e-04}	13	FVRDEIHAPLTSPP	BIG1 Big-1 (bacterial Ig-like domain 1) domain profile
Group 5/ (5.1, 5.3)	14	3^{e-7}	25	VMDDERQVTVLTRWSKKR HVTARLG	PKC_PHOSPHO_SITE Protein kinase C phosphorylation site
Group 6/ 6.1, 6.2, 6.3, 6.4, 6.5, 6.6	15	3^{e-2}	23	VSMRDMVGTEMTPIAGSQK EPS	Collagen IV carboxyl-terminal non-collagenous (NC1) domain profile
Group 6/ 6.1, 6.2, 6.3, 6.4,	16	4^{e-12}	25	FSRKPAPSKWDDAEQKWILS ASPTG	LDL-receptor class B (LDLRB) repeat profile (The

6.5, 6.6					low-density lipoprotein receptor)
Group 6/ 6.1, 6.2, 6.3, 6.6	17	3^{e-10}	24	TRREIMADLGTQRLGKMTN TIAAW	PKC_Protein kinase C phosphorylation site, CK2_PHOSPHO_SITE Casein kinase II phosphorylation site
Group 6/ 6.1, 6.2, 6.3, 6.6	18	5.200^{e-03}	12	MEDYERIHKPVQ	(LIG_LIR_Gen_1) Canonical LIR motif that binds to Atg8 protein family members to mediate processes involved in autophag
Group 0.1/ 0.1, 0.12	19	1.7^{e-12}	57	DAVNEWRLPKVSEEADEAV DQKDWQDDAMSSRVSSAR DWNFESDSAYEGSNHDGRA F	PKC_Protein kinase C phosphorylation site, CK2_PHOSPHO_SITE Casein kinase II phosphorylation site
Group 0.2/ 0.2, 0.23	20	1.7^{e-095}	54	GDLTPGQNVVGKVVDSVPN LKDDPSFTRKTPDKKRSRNF EQEEANQRAKPGVNPTTS	PKC_PHOSPHO_SITE Protein kinase C phosphorylation site

† Motif 1 represents of Remorin-C domain. * Motif 2 represents of Remorin-N domain. – unknown function.