Supplemental table 1. Preeclampsia-like symptoms of systolic blood pressure (SBP), proteinuria, fetal and placental weight in each group.

	CTRL	**L**	**LA**	**A**
SBP	95.50±5.47	117.75±7.23*	99.25±5.15$^{\#}$	93.75±5.42
Albumin /creatinine	70.72±16.35	128.28±39.42*	99.06±23.95$^{\#}$	78.50±17.07
Fetal weight	1.37±0.19	1.18±0.17*	1.28±0.19$^{\#}$	1.38±0.16
Placental weight	0.11±0.02	0.09±0.02*	0.10±0.02$^{\#}$	0.09±0.02

All parameters were measured at E18.5. *, $P<0.05$, L vs. CTRL; #, $P<0.05$, LA vs. L. Data are expressed as the mean ± standard deviation. CTRL, the control group; L, LPS-treated group; LA, LPS+aspirin co-treatment group; A, aspirin-treated group; SBP, (systolic blood pressure).

Supplemental table 2. Quantitation of phosphorylation site changes involved in apoptotic pathway in PPI network.

Sequence	PSMs	Protein Group Accessions	Modifications	phosphoRS Site Probabilities	phosphoRS Binomial Peptide Score	IonScore A2	IonScore B2	IonScore C2	MH+ [Da]	CTRL/REF	L/REF	LA/REF	A/REF
ASPAPGGR	5	A0A087WR00	N-Term(iTRAQ4plex); S2(Phospho)	S(2): 100.0	152.1574615	16.95	18.59	20.67	936.4426	1.1707	0.8581	0.8957	0.9918
ETWDTAEEDSGTDSEYDESGK	32	A0A1L1SV73	N-Term(iTRAQ4plex); S10(Phospho); T12(Phospho); K21(iTRAQ4plex)	T(2): 0.0; T(5): 0.2; S(10): 99.8; T(12): 99.8; S(14): 0.2; Y(16): 0.0; S(19): 0.0	201.2710884	33.1	48.37	57.45	2799.0362	1.0745	1.1618	0.7397	1.2659
LVDSDGSLAEVPK	39	D3YTP0	N-Term(iTRAQ4plex); S7(Phospho); K13(iTRAQ4plex)	S(4): 0.0; S(7): 100.0	453.9650794	65.47	64.04	68.32	1697.8602	0.7701	1.0263	1.2550	0.8277
LVDSDGSLAEVPK	26	D3YTP0	N-Term(iTRAQ4plex); S4(Phospho); S7(Phospho); K13(iTRAQ4plex)	S(4): 100.0; S(7): 100.0	480.4813881	55.34	52.18	54.85	1777.8278	0.7885	1.1446	1.1231	0.8022
RLVDSDGSLAEVPK	45	D3YTP0	N-Term(iTRAQ4plex); S5(Phospho); S8(Phospho); K14(iTRAQ4plex)	S(5): 100.0; S(8): 100.0	576.2780547	49.38	60.3	49.25	1933.9283	0.8404	0.9926	1.1434	0.8732
IACEEEFSDSDEEGEGGRK	25	D3YYI8	N-Term(iTRAQ4plex); C3(Carbamidomethyl); S8(Phospho); S10(Phospho); K19(iTRAQ4plex)	S(8): 100.0; S(10): 100.0	518.039343	43.28	28.75	20.76	2592.0088	0.8324	1.0387	1.0335	0.8937
GQPSPLAQVQQ	13	D3Z1Z4	N-Term(iTRAQ4plex); S4(Phospho)	S(4): 100.0	258.6666284	45.19	53.25	43.23	1376.6719	1.2620	0.8129	0.8824	0.9274
IGEGTYGVVYK	22	D3Z2T9	N-Term(iTRAQ4plex); T5(Phospho); Y6(Phospho); K11(iTRAQ4plex)	T(5): 100.0; Y(6): 100.0; Y(10): 0.0	325.9440051	55.33	48.97	51.73	1633.7547	0.7896	1.1240	1.0768	0.8263

Sequence	PSMs	Protein Group Accessions	Modifications	phosphoRS Site Probabilities	phosphoRS Binomial Peptide Score	IonScore A2	IonScore B2	IonScore C2	MH+ [Da]	CTRL/REF	L/REF	LA/REF	A/REF
IGEGTYGVVYK	5	D3Z2T9	N-Term(iTRAQ4plex); T5(Phospho); K11(iTRAQ4plex)	T(5): 50.0; Y(6): 50.0; Y(10): 0.0	167.0642347	8.38	32.28	27.61	1553.7876	1.0210	0.8716	0.9927	0.9301
VSPVPSPSQPAR	7	E9PUI4	N-Term(iTRAQ4plex); S2(Phospho); S6(Phospho)	S(2): 100.0; S(6): 98.5; S(8): 1.5	276.4829658	19.3	22.8	29.72	1525.6983	1.4680	0.8734	0.7661	0.8881
DTAATFQSVDGSPQAEQSPLESTSK	28	H3BKM2	N-Term(iTRAQ4plex); S12(Phospho); K25(iTRAQ4plex)	T(2): 0.0; T(5): 0.0; S(8): 1.4; S(12): 98.5; S(18): 0.0; S(22): 0.0; T(23): 0.0; S(24): 0.0	418.7364117	98.88	84.19	94.38	2949.3640	0.9340	0.9025	1.0996	1.0617
LCSSSSSDTSPR	21	H3BKM2	N-Term(iTRAQ4plex); C2(Carbamidomethyl); S7(Phospho)	S(3): 0.0; S(4): 0.0; S(5): 33.3; S(6): 33.3; S(7): 33.3; T(9): 0.0; S(10): 0.0	210.7347483	34.68	24.64	30.49	1507.6213	0.9521	0.8122	1.1492	0.8807
DYEEVGVDSVEGEGEEEGEEY	14	P05213	N-Term(iTRAQ4plex); S9(Phospho)	Y(2): 0.0; S(9): 100.0; Y(21): 0.0	205.6229578	74.55	56.51	57.84	2572.9668	1.3049	1.2021	0.8279	0.9830
TIGGGDDSFNTFFSETGAGK	13	P05213;P68373	N-Term(iTRAQ4plex); S8(Phospho); K20(iTRAQ4plex)	T(1): 0.0; S(8): 100.0; T(11): 0.0; S(14): 0.0; T(16): 0.0	246.0016619	34.55	32.31	40.68	2376.0670	0.9471	0.8506	1.0791	0.9842
LLEDGEDFSLNDALDSSNSMQTVQK	10	P05784	N-Term(iTRAQ4plex); S17(Phospho); K25(iTRAQ4plex)	S(9): 0.0; S(16): 49.5; S(17): 49.5; S(19): 1.0; T(22): 0.0	224.7907442	6.6	7.51	56.92	3124.4264	1.2336	1.6828	1.6504	1.2451
EVEEDSEDEEMSEDEDDSSGEEEVVIPQK	70	P09405	N-Term(iTRAQ4plex); S6(Phospho); S18(Phospho); S19(Phospho); K29(iTRAQ4plex)	S(6): 100.0; S(12): 5.8; S(18): 97.1; S(19): 97.1	330.7818374	83.16	66.29	76.3	3841.4088	1.4374	1.5595	0.9266	1.0538

Sequence	PSMs	Protein Group Accessions	Modifications	phosphoRS Site Probabilities	phosphoRS Binomial Peptide Score	IonScore A2	IonScore B2	IonScore C2	MH+ [Da]	CTRL/REF	L/REF	LA/REF	A/REF
EVEEDSEDEEMSEDEDDSSGEEEVVIPQK	41	P09405	N-Term(iTRAQ4plex); S6(Phospho); M11(Oxidation); S12(Phospho); S18(Phospho); K29(iTRAQ4plex)	S(6): 100.0; S(12): 98.9; S(18): 50.6; S(19): 50.6	310.8705636	69.8	73.72	49.16	3857.4199	1.7213	1.7831	1.1794	0.7435
EVEEDSEDEEMSEDEDDSSGEEEVVIPQK	17	P09405	N-Term(iTRAQ4plex); S18(Phospho); K29(iTRAQ4plex)	S(6): 0.0; S(12): 0.9; S(18): 49.5; S(19): 49.5	213.4372153	38.01	45.54	47.89	3681.4944	1.3992	1.4882	1.0823	0.9227
IEDVGSDEEDDSGK	263	P11499	N-Term(iTRAQ4plex); S6(Phospho); K14(iTRAQ4plex)	S(6): 100.0; S(12): 0.0	427.5441553	110.99	109.9	110.28	1862.7797	0.9851	1.1221	0.9195	0.8551
IEDVGSDEEDDSGKDK	422	P11499	N-Term(iTRAQ4plex); S6(Phospho); K14(iTRAQ4plex); K16(iTRAQ4plex)	S(6): 100.0; S(12): 0.0	538.3861467	86.85	89.21	88.2	2250.0037	0.7157	1.1257	1.0287	0.8924
IEDVGSDEEDDSGKDKK	292	P11499	N-Term(iTRAQ4plex); S6(Phospho); K14(iTRAQ4plex); K16(iTRAQ4plex); K17(iTRAQ4plex)	S(6): 100.0; S(12): 0.0	369.6984741	46.57	38.06	37.77	2522.1934	0.6316	1.1128	1.1473	0.9198
TSVQTEDDQLIAGQSAR	50	P26231	N-Term(iTRAQ4plex); S2(Phospho); T5(Phospho)	T(1): 1.3; S(2): 98.7; T(5): 100.0; S(15): 0.0	413.2292838	104.07	88.22	91.67	2122.9198	1.1540	1.1286	0.9129	0.9770
SRTSVQTEDDQLIAGQSAR	43	P26231	N-Term(iTRAQ4plex); S1(Phospho)	S(1): 33.3; T(3): 33.3; S(4): 33.3; T(7): 0.0; S(17): 0.0	299.4105712	61.52	60.1	47.17	2286.0879	1.0349	0.9155	1.1683	1.0186

Sequence	PSMs	Protein Group Accessions	Modifications	phosphoRS Site Probabilities	phosphoRS Binomial Peptide Score	IonScore A2	IonScore B2	IonScore C2	MH+ [Da]	CTRL/REF	L/REF	LA/REF	A/REF
KVMDSDEDDADY	19	P56812	K1(iTRAQ4plex); N-Term(iTRAQ4plex); M3(Oxidation); S5(Phospho)	S(5): 100.0; Y(12): 0.0	364.9596871	36.37	39.31	31.43	1786.7001	0.7853	1.0685	0.9834	0.9931
ASTSKSESSQK	31	P62754	N-Term(iTRAQ4plex); K5(iTRAQ4plex); S6(Phospho); S9(Phospho); K11(iTRAQ4plex)	S(2): 0.0; T(3): 0.0; S(4): 2.1; S(6): 97.8; S(8): 0.0; S(9): 100.0	247.2383084	28.77	21.77	30.65	1731.7928	0.6436	1.0753	1.0329	1.0091
LSSLRASTSK	26	P62754	N-Term(iTRAQ4plex); S3(Phospho); S7(Phospho); K10(iTRAQ4plex)	S(2): 0.0; S(3): 100.0; S(7): 100.0; T(8): 0.0; S(9): 0.0	303.139586	22	21.27	20.45	1497.7342	0.8368	1.0504	0.9799	0.9151
SASSDTSEELNSQDSPK	35	P70441	N-Term(iTRAQ4plex); S4(Phospho); T6(Phospho); K17(iTRAQ4plex)	S(1): 0.0; S(3): 97.8; S(4): 2.2; T(6): 50.0; S(7): 50.0; S(12): 0.0; S(15): 0.0	275.7832941	64.62	28.36	60.22	2229.9073	0.8378	1.1440	0.9919	0.9370
SASSDTSEELNSQDSPKR	19	P70441	N-Term(iTRAQ4plex); S1(Phospho); S15(Phospho); K17(iTRAQ4plex)	S(1): 0.0; S(3): 100.0; S(4): 0.0; T(6): 0.0; S(7): 0.0; S(12): 0.0; S(15): 100.0	414.1226565	56.09	51.32	52.08	2386.0069	0.7145	1.0256	1.0129	1.0646
ETQDSGSGNDDGGFSEEWEAQR	27	Q3TDW2	N-Term(iTRAQ4plex); S7(Phospho)	T(2): 0.0; S(5): 1.7; S(7): 98.3; S(15): 0.0	431.8363658	76.52	61.1	39.96	2625.0170	1.4796	1.1841	1.1932	1.0109
ETQDSGSGNDDGGFSEEWEAQR	12	Q3TDW2	N-Term(iTRAQ4plex); S5(Phospho); S7(Phospho)	T(2): 5.7; S(5): 97.1; S(7): 97.1; S(15): 0.0	160.4895975	28.47		38.52	2704.9793	1.0315	1.1739	0.7296	0.7574
LIVENLSSR	13	Q3TWW8	N-Term(iTRAQ4plex); S7(Phospho)	S(7): 50.0; S(8): 50.0	155.2703251	24.08	24.24	22.16	1254.6592	1.0110	0.8217	1.0679	0.9349

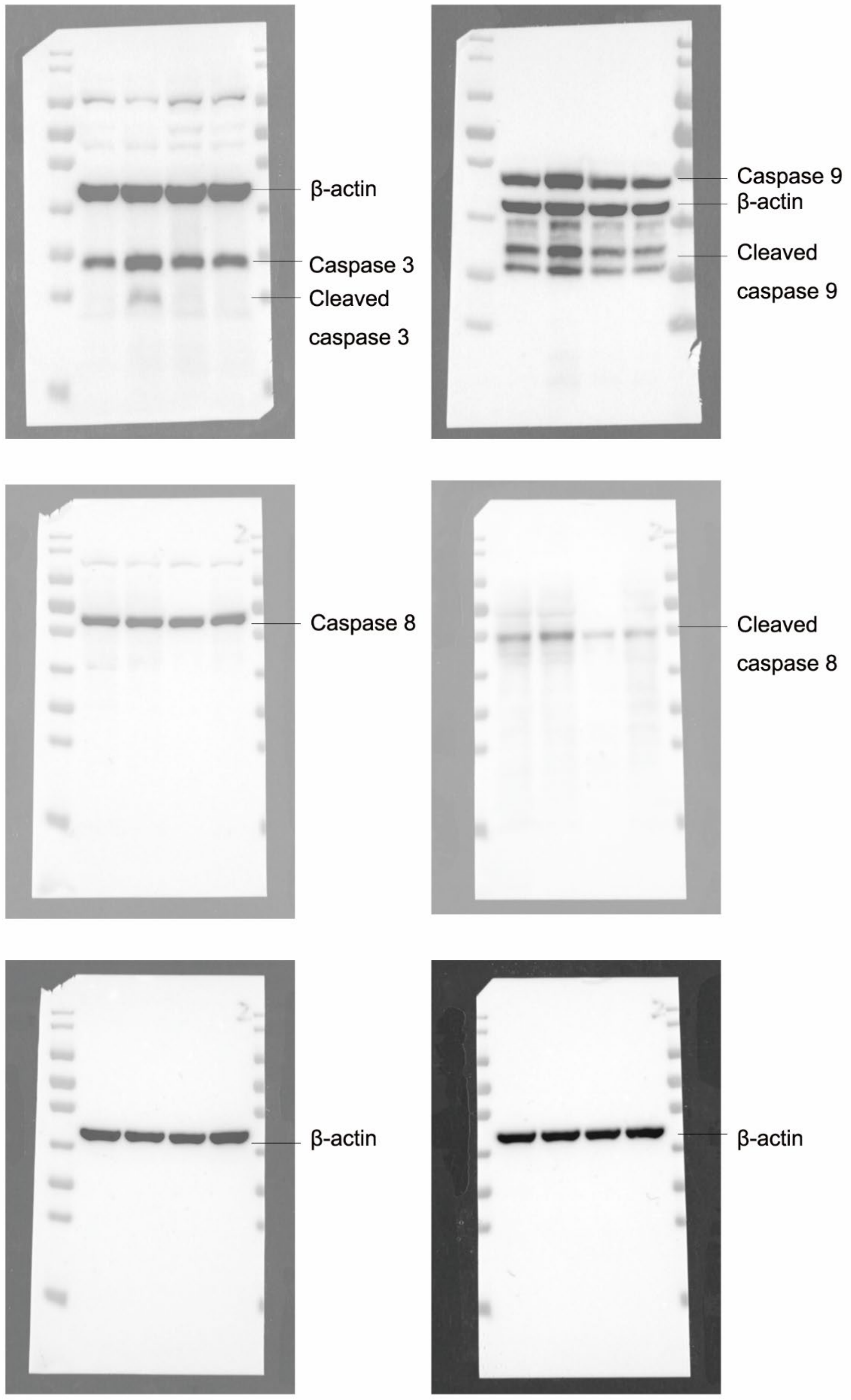
Sequence	PSMs	Protein Group Accessions	Modifications	phosphoRS Site Probabilities	phosphoRS Binomial Peptide Score	IonScore A2	IonScore B2	IonScore C2	MH+ [Da]	CTRL/REF	L/REF	LA/REF	A/REF
VQGEAVSNIQENTQTPTVQEESEEEEVDETGVEVK	454	Q3UK68	N-Term(iTRAQ4plex); S22(Phospho); K35(iTRAQ4plex)	S(7): 0.0; T(13): 0.0; T(15): 0.0; T(17): 1.3; S(22): 98.7; T(30): 0.0	492.5990996	107.86	120.36	115.3	4228.9442	1.0314	1.3253	1.2408	1.2216
IACDEEFSDSEDEGEGGRR	17	Q3URA2	N-Term(iTRAQ4plex); C3(Carbamidomethyl); S8(Phospho); S10(Phospho)	S(8): 100.0; S(10): 100.0	263.8597961	39.06	26.04	20.9	2461.8979	1.0120	0.8408	1.0238	0.9857
IACDEEFSDSEDEGEGGRR	2	Q3URA2	N-Term(iTRAQ4plex); C3(Carbamidomethyl); S8(Phospho)	S(8): 97.5; S(10): 2.5	101.2237634	1.41		7.44	2381.9377	0.8846	0.7839	1.1099	1.0457
EPSGQPEDSPEAETSTLDVFTEK	22	Q3V3Q7	N-Term(iTRAQ4plex); S9(Phospho); K23(iTRAQ4plex)	S(3): 0.0; S(9): 100.0; T(14): 0.0; S(15): 0.0; T(16): 0.0; T(21): 0.0	208.0398063	21.48	23.66	48.84	2861.2789	1.3763	1.1204	1.1592	1.3126
ANSLDNER	8	Q3V3Q7	N-Term(iTRAQ4plex); S3(Phospho)	S(3): 100.0	228.0292745	19.82	25.8	24.48	1142.4955	1.1019	0.8847	0.9295	1.0465
SRLTPTTPESSSTGTEDK	45	Q64337	N-Term(iTRAQ4plex); T4(Phospho); T6(Phospho); K18(iTRAQ4plex)	S(1): 50.0; T(4): 50.0; T(6): 100.0; T(7): 0.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; T(13): 0.0; T(15): 0.0	304.0963615	58.12	51.75	56.25	2342.0394	0.7658	1.1697	1.0686	0.8210
EVDPSTGELQSLQMPESEGPSSLDPSQEGPTGLK	21	Q64337	N-Term(iTRAQ4plex); M14(Oxidation); S22(Phospho); K34(iTRAQ4plex)	S(5): 0.0; T(6): 0.0; S(11): 0.0; S(17): 0.0; S(21): 0.0; S(22): 100.0; S(26): 0.0; T(31): 0.0	490.1682691	39.55	89.29	36.82	3910.8014	1.4089	1.4014	0.8676	1.2527
SGYHDDSDEDLLE	15	Q6PHU5	N-Term(iTRAQ4plex); S7(Phospho)	S(1): 0.0; Y(3): 0.0; S(7): 100.0	383.1595357	57.86	38.75	38.81	1718.6570	1.1938	0.8803	0.8757	1.0395

Sequence	PSMs	Protein Group Accessions	Modifications	phosphoRS Site Probabilities	phosphoRS Binomial Peptide Score	IonScore A2	IonScore B2	IonScore C2	MH+ [Da]	CTRL/REF	L/REF	LA/REF	A/REF
SLSPLSGTTDTK	26	Q80TU6	N-Term(iTRAQ4plex); S3(Phospho); K12(iTRAQ4plex)	S(1): 0.0; S(3): 100.0; S(6): 0.0; T(8): 0.0; T(9): 0.0; T(11): 0.0	251.8395801	68.75	68.65	47.72	1574.7920	0.9051	0.8528	1.0505	1.1001
TAQVPSPPR	43	Q80TU6	N-Term(iTRAQ4plex); S6(Phospho)	T(1): 0.0; S(6): 100.0	230.4992269	30.38	29.01	36.72	1176.5876	1.0309	0.8550	1.0519	0.8758
KQTPPASPSPQPIEDRPPSSPIYEDAAPFK	49	Q8BNA5	K1(iTRAQ4plex); N-Term(iTRAQ4plex); T3(Phospho); S7(Phospho); S19(Phospho); K30(iTRAQ4plex)	T(3): 100.0; S(7): 100.0; S(9): 99.9; S(19): 0.1; S(20): 0.0; Y(23): 0.0	291.1617471	16.63	21.83	15.79	3919.8475	0.9017	1.0753	0.8585	0.9801
GRESDEDTEDASETDLAK	10	Q8BR65	N-Term(iTRAQ4plex); S4(Phospho); T8(Phospho); S12(Phospho); K18(iTRAQ4plex)	S(4): 100.0; T(8): 100.0; S(12): 97.6; T(14): 2.4	322.8026394	31.03	23.89	44.91	2495.9348	1.3589	1.0912	1.0765	1.1072
GDMSAVNDESF	7	Q8CCI5	N-Term(iTRAQ4plex); S10(Phospho)	S(4): 0.0; S(10): 100.0	174.9876212	42.24		38.37	1395.5271	1.1324	0.8787	0.9015	0.9504
YLSFTPPEKDGFPSGTPALNTK	7	Q8CIN4	N-Term(iTRAQ4plex); S3(Phospho); K9(iTRAQ4plex); T16(Phospho); K22(iTRAQ4plex)	Y(1): 49.4; S(3): 49.4; T(5): 1.2; S(14): 50.0; T(16): 50.0; T(21): 0.0	148.4256343	16.46		8.66	2959.4257	0.9737	1.4336	1.6505	#DIV/0!
KPASVSPTTPTSPTEGEAS	57	Q8R1Q8	N-Term(iTRAQ4plex); K1(iTRAQ4plex); S6(Phospho)	S(4): 0.1; S(6): 97.7; T(8): 0.1; T(9): 2.2; T(11): 0.1; S(12): 0.0; T(14): 0.0; S(19): 0.0	225.0073763	36.42	32.63	36.06	2212.0652	1.1783	0.9848	0.8049	1.0269
DFQEYVEPGEDFPASPQRR	9	Q8R1Q8	N-Term(iTRAQ4plex); S15(Phospho)	Y(5): 0.0; S(15): 100.0	287.6293461	30.37	29.85	28.69	2491.1015	0.9835	0.7895	1.0442	0.8194

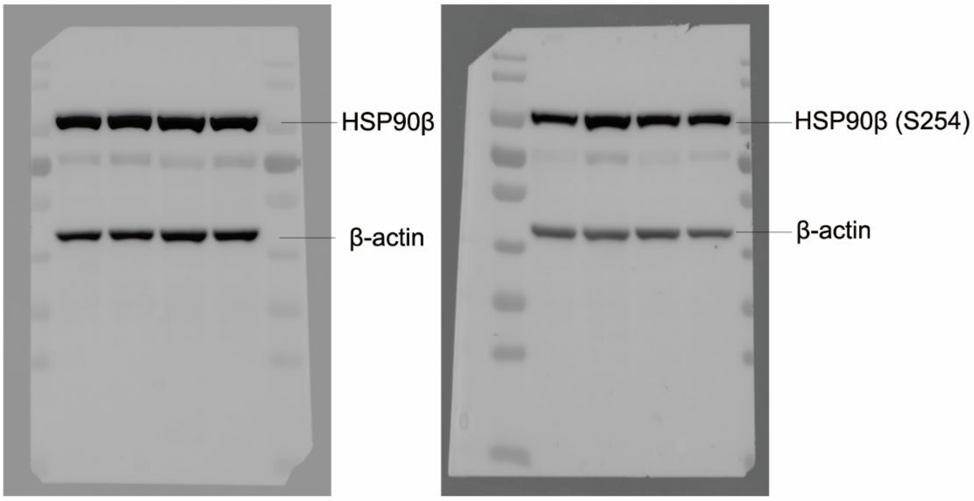
Sequence	PSMs	Protein Group Accessions	Modifications	phosphoRS Site Probabilities	phosphoRS Binomial Peptide Score	IonScore A2	IonScore B2	IonScore C2	MH+ [Da]	CTRL/REF	L/REF	LA/REF	A/REF
KPASVSPTTPTSPTEGEAS	7	Q8R1Q8	K1(iTRAQ4plex); N-Term(iTRAQ4plex); T8(Phospho); T9(Phospho); T11(Phospho)	S(4): 4.8; S(6): 95.4; T(8): 99.7; T(9): 1.6; T(11): 32.8; S(12): 32.8; T(14): 32.8; S(19): 0.0	63.0771435	9.64		14.74	2371.9995	0.9438	1.2964	0.8222	0.8169
SVASNQSEMEYSSLQDMPK	12	Q8VDP4	N-Term(iTRAQ4plex); S7(Phospho); K19(iTRAQ4plex)	S(1): 97.5; S(4): 1.3; S(7): 1.3; Y(11): 0.0; S(12): 0.0; S(13): 0.0	261.3475535	27.34		34.18	2499.1062	0.9134	1.1465	0.8535	0.9661
MEDSMDMDMSPLRPQNYLFGCELK	35	Q9DAY9	N-Term(Acetyl); M5(Oxidation); S10(Phospho); C21(Carbamidomethyl); K24(iTRAQ4plex)	S(4): 0.0; S(10): 100.0; Y(17): 0.0	324.7747034	38.03		56.7	3189.3281	1.6849	1.3889	1.6021	1.6362
MEDSMDMDMSPLRPQNYLFGCELK	40	Q9DAY9	N-Term(Acetyl); M1(Oxidation); S4(Phospho); M5(Oxidation); C21(Carbamidomethyl); K24(iTRAQ4plex)	S(4): 100.0; S(10): 0.0; Y(17): 0.0	117.5093217	15.36		6.72	3205.3220	2.0139	2.4357	1.6943	
HIVSNDSSDSDDEAQGPK	20	Q9DBX5	N-Term(iTRAQ4plex); S10(Phospho); K18(iTRAQ4plex)	S(4): 0.0; S(7): 0.0; S(8): 1.3; S(10): 98.7	304.6495926	68.62	21.55	45.14	2268.9904	0.8075	0.8162	1.2406	0.9684
CSVSLSNVEAR	3	Q9DBX5	N-Term(iTRAQ4plex); C1(Carbamidomethyl); S4(Phospho)	S(2): 0.1; S(4): 99.9; S(6): 0.1	114.9149999	12.65		9.64	1445.6574	1.0493	0.8431	1.0388	0.9323
EVDQDDEENSEEDEMDSGTMVR	20	Q9JI11	N-Term(iTRAQ4plex); S10(Phospho); M20(Oxidation)	S(10): 100.0; S(17): 0.0; T(19): 0.0	448.4034381	97.48	96.36	77.83	2799.0223	1.0439	1.1152	0.8015	0.9595

Sequence	PSMs	Protein Group Accessions	Modifications	phosphoRS Site Probabilities	phosphoRS Binomial Peptide Score	IonScore A2	IonScore B2	IonScore C2	MH+ [Da]	CTRL/REF	L/REF	LA/REF	A/REF
GSGGSPGPEPPGRPDGSSLLYR	10	Q9R1Y5	N-Term(iTRAQ4plex); S5(Phospho)	S(2): 0.0; S(5): 100.0; S(17): 0.0; S(18): 0.0; Y(21): 0.0	198.0473986	8.61	5.81	15.98	2364.1133	1.2532	0.8231	0.9173	0.9554
GEPNVSYICSR	203	Q9WV60	N-Term(iTRAQ4plex); Y7(Phospho); C9(Carbamidomethyl)	S(6): 1.2; Y(7): 98.8; S(10): 0.0	319.6463526	45.42	44.98	52.5	1505.6586	1.1934	0.8469	0.9078	1.0005
GEPNVSYICSR	20	Q9WV60	N-Term(iTRAQ4plex); Y7(Phospho); C9(Carbamidomethyl); S10(Phospho)	S(6): 50.0; Y(7): 50.0; S(10): 100.0	241.9056184	29.85	17.9	33.88	1585.6268	1.1052	0.8234	0.9291	1.0788
TVSTQHSTESQDNDQPDYDSVASDEDTDVETR	26	Q9JLQ2	N-Term(iTRAQ4plex); S23(Phospho)	T(1): 0.0; S(3): 0.0; T(4): 0.0; S(7): 0.0; T(8): 0.0; S(10): 0.0; Y(18): 0.0; S(20): 0.0; S(23): 100.0; T(27): 0.0; T(31): 0.0	650.8430857	115.66	93.91	100.55	3795.5423	0.7724	1.1181	1.1751	0.9290
ATISDEEIER	15	Q8BJF9	N-Term(iTRAQ4plex); S4(Phospho)	T(2): 0.0; S(4): 100.0	307.0326547	51.12	48.2	55.01	1386.6280	1.1856	0.8251	0.9047	1.0532
QKSDAEEDGVTGSQDEEDSKPK	105	P35564	N-Term(iTRAQ4plex); K2(iTRAQ4plex); S3(Phospho); S13(Phospho); K20(iTRAQ4plex); K22(iTRAQ4plex)	S(3): 100.0; T(11): 49.5; S(13): 49.5; S(19): 0.9	379.579173	39.14	36.77	56.23	3115.3849	0.7717	1.2814	1.1659	0.7884
AGLEDSEEDVEEAEVEAEDKDH	33	A2AQ07	N-Term(iTRAQ4plex); S6(Phospho); K20(iTRAQ4plex)	S(6): 100.0	722.9092966	75.27	70.75	44.22	2813.1769	0.9231	1.2774	0.8048	0.9347

Original western blotting membranes of **Figure 5**



Original western blotting membranes of **Figure 7**



Original western blotting membranes of **Figure 8**