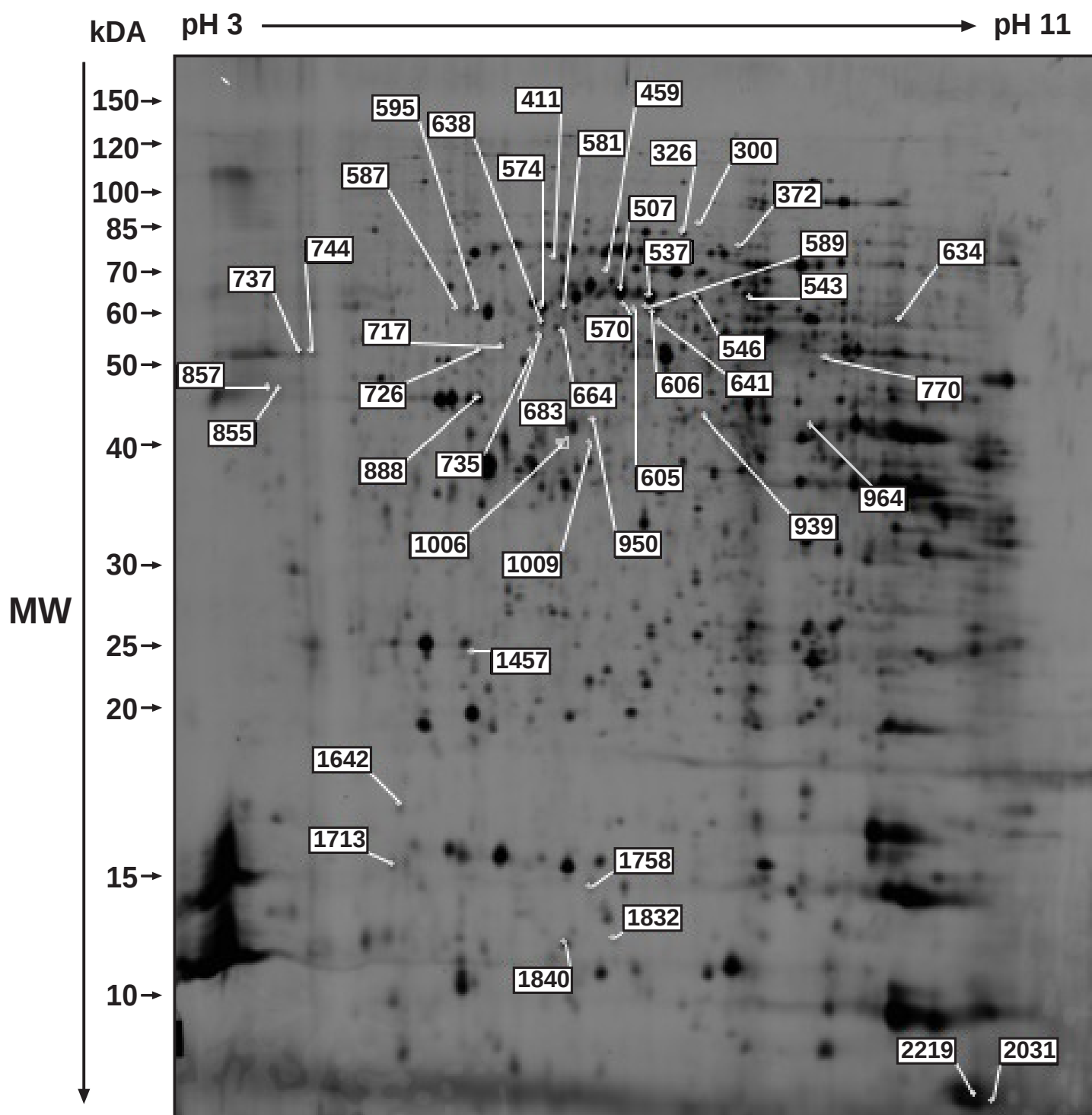




Supplemental Figure 1
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Supplemental Table 1. Proteins identified significantly altered by hypoxic-ischemic brain injury including contaminant proteins^a

Spot no.	Protein name	Accession number	expected pI	expected MW	observed pI	observed MW	Seq Cov (%)	Mascot score	Peptide Count	Fold change	Log2 Fold Change
300	Dihydropyrimidinase-related protein 2	IPI00870112	5.9	62.2	6.1	79	3.7	117.2	2	1.56	0.64
411	Heat shock 70 kDa protein 1A/1B	IPI00196751	5.5	70.1	5.5	70	3.9	112.9	3	-1.84	-0.88
459	Serum Albumin	IPI00191737	6.1	68.7	5.7	70	4.1	108.8	2	-1.64	-0.71
459	Dihydropyrimidinase-related protein 2	IPI00870112	5.9	62.2	5.7	70	19.9	614.7	11	-1.64	-0.71
507	T-complex protein 1 subunit alpha	IPI00200847	5.8	60.3	5.8	60	24.1	658.6	14	1.54	0.62
507	Isoform 1 of Dihydropyrimidinase-related protein 3	IPI00556970	6	61.9	5.8	60	19.6	568.5	10	1.54	0.62
507	Dihydropyrimidinase-related protein 2	IPI00870112	5.9	62.2	5.8	60	9.3	310.7	5	1.54	0.62
537	Glucose-6-phosphate 1-dehydrogenase	IPI00231637	5.9	59.3	5.9	60	4.9	95.8	3	1.52	0.60
537	Isoform 1 of Dihydropyrimidinase-related protein 3	IPI00556970	6	61.9	5.9	60	15.3	484.2	9	1.52	0.60
546	Keratin, type II cytoskeletal 1	IPI00421857	8.9	64.8	6.1	60	6.6	260.3	6	-1.62	-0.70
546	Krt10 uncharacterized protein	IPI00950839	4.9	49.7	6.1	60	8.4	280.6	6	-1.62	-0.70
546	Isoform 1 of Dihydropyrimidinase-related protein 3	IPI00556970	6	61.9	6.1	60	7.5	168.9	4	-1.62	-0.70
570	Isoform 1 of Dihydropyrimidinase-related protein 3	IPI00556970	6	61.9	5.8	59	5.3	143.6	3	-2.2	-1.18
570	Serum Albumin	IPI00191737	6.1	68.7	5.8	59	3.3	103.6	3	-2.2	-1.18
574	T-complex protein 1 subunit epsilon	IPI00470301	5.4	59.5	5.5	58	3.3	125.4	2	-6.82	-2.77
574	Serine/threonine-protein phosphatase (Calcineurin)	IPI00559849	5.9	57.5	5.5	58	4.3	94.1	2	-6.82	-2.77
574	Isoform 1 of Dihydropyrimidinase-related protein 3	IPI00556970	6	61.9	5.5	58	4.9	171.2	4	-6.82	-2.77
574	Dihydropyrimidinase-related protein 2	IPI00870112	5.9	62.2	5.5	58	15.9	404.3	8	-6.82	-2.77
589	Isoform 1 of Dihydropyrimidinase-related protein 3	IPI00556970	6	61.9	5.9	58	5.3	132.8	3	-3.34	-1.76
595	Tubulin alpha-1C chain	IPI00364046	4.8	49.9	5.4	57	9.6	234.3	5	-1.8	-0.85
595	Na ⁺ /H ⁺ exchange regulatory cofactor NHE-RF1	IPI00200898	5.6	38.8	5.4	57	6.5	99.6	2	-1.8	-0.85
605	Isoform 1 of Dihydropyrimidinase-related protein 3	IPI00556970	6	61.9	5.9	58	3.7	170.5	3	-3.3	-1.72
606	Coronin-1A	IPI00210071	6	51	6.0	58	18	277.4	7	-5.26	-2.4
606	Isoform 1 of Dihydropyrimidinase-related protein 3	IPI00556970	6	61.9	6.0	58	16.7	551	11	-5.26	-2.4
638	Tubulin alpha-1C chain	IPI00364046	4.8	49.9	5.5	53	9.1	217.2	5	-1.6	-0.68
638	Dihydropyrimidinase-related protein 2	IPI00870112	5.9	62.2	5.5	53	6.5	360.5	5	-1.6	-0.68

Spot no.	Protein name	Accession number	expected pI	expected MW	observed pI	observed MW	Seq Cov (%)	Mascot score	Peptide Count	Fold change	Log2 Fold Change
664	Isoform 1 of Dihydropyrimidinase-related protein 3	IPI00556970	6	61.9	5.6	51	6.5	207.9	4	-1.8	-0.86
664	Dihydropyrimidinase-related protein 2	IPI00870112	5.9	62.2	5.6	51	6.5	193.6	4	-1.8	-0.86
683	Dihydropyrimidinase-related protein 2	IPI00870112	5.9	62.2	5.5	51	3.7	175.9	3	-3.2	-1.69
683	Isoform 1 of Dihydropyrimidinase-related protein 3	IPI00556970	6	61.9	5.5	51	3.5	97.7	2	-3.2	-1.69
726	Rap1 GTPase-GDP dissociation stimulator 1	IPI00369496	5.5	52.2	5.4	49	6.3	153.5	3	-1.65	-0.72
726	Isoform 1 of Glial fibrillary acidic protein	IPI00190943	5.2	49.9	5.4	49	36.5	1103.2	23	-1.65	-0.72
726	Isoform 2 of Glial fibrillary acidic protein	IPI00210211	5.6	49.5	5.4	49	17.5	405.8	8	-1.65	-0.72
770	ATP synthase subunit alpha, mitochondrial	IPI00396910	9.7	59.7	6.7	49	7.2	263.5	4	1.59	0.67
888	Actin cytoplasmic 1	IPI00189819	5.2	41.7	5.3	43	14.1	247.6	6	1.54	0.62
1713	Eukaryotic translation initiation factor 5A-1	IPI00211216	4.9	16.8	5.1	16	10.4	118	3	1.75	0.81
1758	Superoxide dismutase (Cu-Zn)	IPI00231643	5.9	15.9	5.7	15	34.4	268.1	6	-1.87	-0.90
1758	Prefoldin 5	IPI00870220	5.9	17.3	5.7	15	5.2	94.1	2	-1.87	-0.90

^aProteins were extracted from left and right hemispheres of HI-treated rats at postnatal day 9, separated by 2D-DIGE and identified by LC-ESI-MS. To every significantly regulated spot (average ratio ± 1.5 ; p-value < 0.05), the table assigns IPI Accession number, expected (exp.) and observed (obs.) pI and MW, Mascot score, Peptide count, Fold change; Log2 Fold Change and Sequence coverage achieved by LC ESI-MS. Negative fold change means proteins were higher expressed in lesioned (left) hemispheres; positive fold change indicates that proteins were higher expressed in control (right) hemispheres. Peptide assignments with an ion score > 30 were accepted. Protein identifications with an ion score > 90 and a minimum of two peptides identified were approved.