

Supplementary Table 1. nLC-MS^E identification of differential expressed proteins in ERCR+ and ERCR- groups.

Accession	Description	Score	Seq. cov [%]	Peptide mass	Peptide Score	Sequence	RT	z
P61603	10 kDa heat shock protein mitochondrial	712.04	45.1	1076.59	6.16	VLLPEYGGTK	69.19	2
				1529.79	6.17	VVLDDKDYFLFR	96.68	3
				1013.56	6.12	GGEIQPVSVK	52.11	2
				1315.75	5.61	VLQATVVAVGSGSK	64.11	2
				1331.66	5.95	LDDKDYFLFR	96.68	2
				751.36	5.86	PEYGGTK	69.19	1
P19483	ATP synthase subunit alpha mitochondrial	311.80	34.9	1667.79	4.93	NVQAEEMVEFSSGLK	67.30	3
				1624.89	6.18	TGAIVDVPVGEELLGR	99.95	2
				1391.70	5.42	TGTAEVSSILEER	77.96	2
				1000.57	5.81	VLSIGDGIAR	71.63	2
				2338.16	5.05	EVAFAQFGSDLDAATQQLLSR	131.66	3
				1287.69	5.29	HALIYDDLK	76.44	2
				1026.59	5.83	AVDSLVPPIGR	75.24	2
				892.48	5.60	LELAQYR	61.94	2
				1171.63	4.27	VVDALGNAIDGK	72.72	2
				845.51	5.10	STVAQLVK	61.07	2
				2309.15	4.92	QGQYSPMAIEEQVAVIYAGVR	131.97	3
				2104.03	4.40	GMSLNLEPDNVGVVVFNDK	76.70	3
				789.42	4.46	VGSAAQTR	45.31	2
				1081.49	4.99	RFNDGTDEK	38.55	2
				1710.93	5.04	VVDALGNAIDGKPIGSK	74.43	3
				1730.96	4.73	QTGKTSIAIDTIINQK	134.02	2
				1728.86	4.53	GMSLNLEPDNVGVVVFNDK	76.69	2
				1033.56	3.87	VGVVVFNDK	76.71	2
				788.42	5.44	SIGDGIAR	71.64	1
				740.39	4.29	VVDALGNA	72.67	1
1126.54	4.58	EMVEFSSGLK	67.28	2				
982.56	4.47	VLSIGDGIAR	71.65	2				
2320.15	5.00	EVAFAQFGSDLDAATQQLLSR	131.69	3				
P05630	ATP synthase subunit delta mitochondrial	830.29	58.33	4122.23	6.22	QVDVPTQTGAFGILAAHVPTLQVLRPGLVVVHAEDGTTSK	118.06	5
				986.55	5.68	IEANEALVK	55.32	2
				1431.70	6.32	AQSELLGADEATR	68.16	2
				3600.79	5.62	YFVSSGSVTVNADSSVQLLAEAVTLDMLDLGAAK	133.78	4
				744.42	5.13	ANEALVK	55.35	1
969.52	4.83	IEANEALVK	55.29	2				
P62157	Calmodulin	2244.05	71.14	1754.87	7.27	VFDKDGNGYISAAELR	74.51	3
				1844.89	7.30	EAFSLFDKDGDTITTK	84.27	3
				1596.71	6.39	DTDSEEEIREAFR	73.91	3
				1855.84	6.46	MKDTDSEEEIREAFR	68.90	3
				1693.84	5.50	DGDGTITTKELGTVMR	126.03	2

				4069.84	5.36	SLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMAR	101.04	5
				2631.29	5.43	EAFSLFDKDGDTITTKELGTVMR	115.55	3
				4265.06	5.12	MADQLTEEQIAEFKEAFSLFDKDGDTITTKELGTVMR	93.57	4
				4101.83	5.72	SLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMAR	109.33	5
				996.44	5.65	VFDKDGNGY	74.50	2
				1380.63	5.92	DSEEEIREAFR	73.91	2
				759.43	7.13	ISAAELR	74.49	1
				1049.53	5.11	EEIREAFR	68.89	2
				1644.81	7.02	FSLFDKDGDTITTK	84.31	2
				1150.55	7.14	DKDGDGTITTK	84.28	2
				833.37	5.78	VFDKDGNG	74.49	1
				1467.67	5.87	VFDKDGNGYISAAE	74.47	2
				1578.70	5.53	DTDSEEEIREAFR	73.93	3
				1837.83	5.04	MKDTDSEEEIREAFR	68.89	4
Q32LG3	Malate dehydrogenase mitochondrial	610.62	35.8	2393.24	6.36	LTYDIAHTPGVAADLSHIETR	102.46	4
				1233.72	6.03	IFGVTTLDIVR	103.00	2
				1793.08	6.08	VAVLGASGGIGQPLSLLLK	120.19	2
				1370.77	6.19	TIPLISQCTPK	87.91	2
				1489.73	5.06	GYLGPQLPDCLK	85.86	2
				1338.71	5.98	GCDVVVIPAGVPR	80.97	2
				962.53	5.40	ANAFVAELK	71.93	2
				1153.55	5.32	EGVVECSFVK	66.20	2
				2462.20	5.15	FVFSLVDAMNGKEGVVECSFVK	62.20	4
				2179.11	6.24	LYDIAHTPGVAADLSHIETR	102.45	3
				1156.56	4.95	GPEQLPDCLK	85.85	2
				783.53	5.37	PLSLLLK	120.17	2
				632.30	4.38	PDCLK	85.85	1
				1043.55	5.11	PLISQCTPK	87.91	2
Q9BG11	Peroxiredoxin 5 mitochondrial	693.72	58.9	3204.65	6.27	LLADPSGTFGKETDLLLDDSLFLFGNHR	149.48	4
				2118.08	5.70	ETDLLLDDSLFLFGNHR	137.39	3
				1607.82	5.93	GVLFGLPGAFTPGCSK	108.33	2
				1525.80	6.20	THLPGFVEQADALK	80.13	3
				1405.72	5.20	ATIVEGASTTAAGTR	97.23	2
				2406.21	5.12	GIQVVACLTVNDVFVTEEWAR	125.29	3
				3633.83	4.77	FSMVIEDGIVKSLNVEPDGTGLTCSLAPNLSQL	106.88	5
				752.40	5.59	THLPGFV	80.11	1
				881.45	5.49	THLPGFVE	80.14	2
				774.39	4.89	EQADALK	80.11	1
				645.35	5.05	QADALK	80.11	1
				873.46	4.90	VEQADALK	80.12	2
				1009.51	5.57	THLPGFVEQ	80.12	2
				2100.07	5.24	ETDLLLDDSLFLFGNHR	137.39	3
Q32KL7	Sperm equatorial segment protein 1	781.53	22.68	2981.36	6.84	EPFIEKDEPEPEPEPEPEPEVHR	68.77	4
				984.55	5.70	QLLNNNIR	55.93	2

				1186.59	5.74	SPNNANFIGPR	57.15	2
				2974.40	5.90	YTHDVGPGDNDVLINPVSEETTTFPTR	90.03	3
				2237.98	5.89	DEPEPEPEPEPEPEVHR	56.91	3
				1204.66	5.30	ILHILDTHDK	137.37	2
				1401.72	5.48	SKSPNNANFIGPR	50.49	2
				810.44	5.26	QLLNNNI	55.95	2
				1993.91	5.88	PEPEPEPEPEPEVHR	56.92	3
				863.43	5.65	PEPVEHR	68.76	2
P02784	Seminal plasma protein PDC 109	9678.98	43.28	1187.59	8.46	CVFPIYGGK	101.15	2
				2739.20	8.60	HFDCTVHGSLFPWCSLDADYVGR	104.69	3
				2333.01	7.08	IGSMWMSWCSLSPNYDKDR	103.93	3
				1315.68	6.82	CVFPIYGGKK	89.13	3
				2061.88	6.12	IGSMWMSWCSLSPNYDK	31.25	2
				2867.30	7.76	KHFDCTVHGSLFPWCSLDADYVGR	98.23	4
				1664.81	5.98	DYAKCVFPIYGGK	107.70	2
				2365.01	8.00	IGSMWMSWCSLSPNYDKDR	87.56	3
				2349.01	7.72	IGSMWMSWCSLSPNYDKDR	97.09	3
				1301.57	7.81	HFDCTVHGSLF	104.68	2
				1584.70	8.11	HFDCTVHGSLFPW	104.69	2
				2130.91	7.94	HFDCTVHGSLFPWCSLDA	104.69	3
				2059.87	7.79	HFDCTVHGSLFPWCSLD	104.69	3
				2508.07	7.93	HFDCTVHGSLFPWCSLDADYV	104.70	3
				995.47	7.72	SLDADYVGR	104.68	2
				1831.76	7.66	HFDCTVHGSLFPWCS	104.70	3
				2259.01	7.33	KHFDCTVHGSLFPWCSLDA	98.28	3
				795.36	7.13	DADYVGR	98.27	1
				609.29	7.26	DYVGR	104.69	1
				2374.03	7.44	KHFDCTVHGSLFPWCSLDAD	98.27	3
				1959.86	7.21	KHFDCTVHGSLFPWCS	98.25	3
				2636.16	7.13	KHFDCTVHGSLFPWCSLDADYV	98.26	3
				1282.59	6.97	KHFDCTVHGSL	98.22	2
				1915.78	6.13	IGSMWMSWCSLSPNYD	31.24	3
				680.33	7.48	ADYVGR	98.29	1
				1155.51	7.46	CSLDADYVGR	98.27	2
				552.31	6.47	YGGKK	89.10	1
				651.29	6.65	CVFPF	89.09	1
				1056.58	6.08	FPFIYGGKK	89.13	2
				909.51	6.29	PFIYGGKK	89.13	2
				908.44	7.39	LDADYVGR	98.25	2
				1398.60	8.01	HFDCTVHGSLFP	104.71	3
				2693.19	7.16	KHFDCTVHGSLFPWCSLDADYVGR	98.23	3