

Supplementary data, Table 5 – False Discovery Rate (FDR) for proteins found with two peptides using the MASCOT™ search engine in the SwissProt™ mus musculus database with an error tolerance of 1 ppm

proteins used for the MASCOT™ search at 1 ppm, with two or more MS/MS identified peptides.		Total number of peptide masses.	Number of combinations of two peptides.	False protein found within 1 ppm, with 2 peptides,	FDR for 2 peptides in a single Mascot™ search at 1 ppm.
Cbr2	Hba-a1	4	6	-	-
Cbr2	Rps27a	4	6	-	-
Cbr2	Hist1h4a	4	6	-	-
Hist1h4a	Rps27a	4	6	-	-
Hba-a1	Rps27a	4	6	-	-
Hba-a1	Hist1h4a	4	6	-	-
Rps27a	Alb	5	10	-	-
Hba-a1	Alb	5	10	-	-
Cbr2	Alb	5	10	-	-
Hist1h4a	Alb	5	10	-	-
Actb	Cbr2	5	10	-	-
Hist1h4a	Actb	5	10	-	-
Actb	Hba-a1	5	10	-	-
Actb	Rps27a	5	10	-	-
Actb	Alb	6	15	-	-
Actc1	Rps27a	6	15	-	-
Actc1	Hist1h4a	6	15	HOOK3_MOUSE	0.07
Actc1	Cbr2	6	15	-	-
Actc1	Hba-a1	6	15	-	-
Actb	Actc1	7	21	-	-
Alb	Actc1	7	21	-	-
Aldh1a1	Cbr2	7	21	-	-
Aldh1a1	Hba-a1	7	21	-	-
Aldh1a1	Hist1h4a	7	21	-	-
Aldh1a1	Rps27a	7	21	-	-
Hbb-b1 and Hbb-b2	Cbr2	7	21	-	-
Hbb-b1 and Hbb-b2	Hba-a1	7	21	-	-
Hbb-b1 and Hbb-b2	Hist1h4a	7	21	-	-
Hbb-b1 and Hbb-b2	Rps27a	7	21	-	-
Aldh2	Cbr2	8	28	CAN1_MOUSE	0.04
Aldh2	Hba-a1	8	28	-	-
Aldh2	Hist1h4a	8	28	-	-
Aldh2	Rps27a	8	28	-	-
Actc1	Aldh1a1	9	36	-	-
Actc1	Hbb-b1 and Hbb-b2	9	36	-	-
Actb	Aldh2	9	36	-	-
Alb	Aldh2	9	36	-	-

FDR = False Discovery Rate. The maximum false discovery rate was assessed using masses found in MALDI FTICR MS and sequenced by Orbi-trap analysis in lung samples. A Mascot search (1 ppm) was performed on all combinations of peptides attributed to two different proteins identified in Table 1, to determine the probability of finding an additional (false) identification (see supplementary data). In a total of 116 combinations, two additional identifications were found, which indicates an average FDR of 0.02. The highest FDR we observed was 0.07 in a single set of comparisons, and we took this conservative estimated threshold as FDR with two attributed peptides. For proteins with more than two peptides attributed to a single protein at (1 ppm), we postulate a lower FDR. In the case of a single peptide mass, we calculate the FDR from the inverse of the total number of proteins found in a 1 ppm Mascot search. Several proteins were identified with more than two peptides in a 2 ppm search, however, only one peptide deviates less than 1 ppm from the calculated value. In this case we attribute a high FDR, until supporting evidence is provided.