

Supplementary Figure S2

I. MaxQuant settings for TTC30A/B protein identification

PARAMETER	VALUE	Max. peptide mass [Da]	4600
VERSION	1.6.0.16	Min. peptide length for unspecific search	8
USER NAME	MPCADMIN	Max. peptide length for unspecific search	25
MACHINE NAME	ADMIN-PC	Razor protein FDR	True
DATE OF WRITING	02/16/2019 20:05:05	Disable MD5	False
FIXED MODIFICATIONS	CARBAMIDOMETHYL (C)	Max mods in site table	3
INCLUDE CONTAMINANTS	TRUE	Match unidentified features	True
PSM FDR	0.01	MS/MS tol. (FTMS)	20 ppm
PROTEIN FDR	0.01	Top MS/MS peaks per Da interval. (FTMS)	12
SITE FDR	0.01	Da interval. (FTMS)	100
USE NORMALIZED RATIOS FOR OCCUPANCY	TRUE	MS/MS deisotoping (FTMS)	True
MIN. PEPTIDE LENGTH	7	MS/MS deisotoping tolerance (FTMS)	7
MIN. SCORE FOR UNMODIFIED PEPTIDES	0	MS/MS deisotoping tolerance unit (FTMS) ppm	
MIN. SCORE FOR MODIFIED PEPTIDES	40	MS/MS higher charges (FTMS)	True
MIN. DELTA SCORE FOR UNMODIFIED PEPTIDES	0	MS/MS water loss (FTMS)	True
MIN. DELTA SCORE FOR MODIFIED PEPTIDES	6	MS/MS ammonia loss (FTMS)	True
MIN. UNIQUE PEPTIDES	0	MS/MS dependent losses (FTMS)	True
MIN. RAZOR PEPTIDES	1	MS/MS recalibration (FTMS)	False
MIN. PEPTIDES	1	MS/MS tol. (ITMS)	0.5 Da
USE ONLY UNMODIFIED PEPTIDES AND FALSE		Top MS/MS peaks per Da interval. (ITMS)	8
PEPTIDES USED FOR PROTEIN QUANTIFICATION	RAZOR	Da interval. (ITMS)	100
DISCARD UNMODIFIED COUNTERPART PEPTIDES	TRUE	MS/MS deisotoping (ITMS)	False
LABEL MIN. RATIO COUNT	2	MS/MS deisotoping tolerance (ITMS)	0.15
USE DELTA SCORE	FALSE	MS/MS deisotoping tolerance unit (ITMS) Da	
IBAQ	FALSE	MS/MS higher charges (ITMS)	True
IBAQ LOG FIT	FALSE	MS/MS water loss (ITMS)	True
MATCH BETWEEN RUNS	TRUE	MS/MS ammonia loss (ITMS)	True
MATCHING TIME WINDOW [MIN]	0.7	MS/MS dependent losses (ITMS)	True
ALIGNMENT TIME WINDOW [MIN]	20	MS/MS recalibration (ITMS)	False
FIND DEPENDENT PEPTIDES	FALSE	MS/MS tol. (TOF)	40 ppm
FASTA FILE	C:\DATABASES\SP-HUMAN-2014-11.FASTA	Top MS/MS peaks per Da interval. (TOF)	10
DECOY MODE	REVERT	Da interval. (TOF)	100
INCLUDE CONTAMINANTS	TRUE	MS/MS deisotoping (TOF)	True
ADVANCED RATIOS	TRUE	MS/MS deisotoping tolerance (TOF)	0.01
FIXED ANDROMEDA INDEX FOLDER		MS/MS deisotoping tolerance unit (TOF) Da	
TEMPORARY FOLDER		MS/MS higher charges (TOF)	True

COMBINED FOLDER LOCATION	MS/MS water loss (TOF)	True
SECOND PEPTIDES TRUE	MS/MS ammonia loss (TOF)	True
STABILIZE LARGE LFQ RATIOS TRUE	MS/MS dependent losses (TOF)	True
SEPARATE LFQ IN PARAMETER GROUPS FALSE	MS/MS recalibration (TOF)	False
REQUIRE MS/MS FOR LFQ	MS/MS tol. (Unknown)	0.5 Da
COMPARISONS FALSE	Top MS/MS peaks per Da interval. (Unknown)	8
CALCULATE PEAK PROPERTIES FALSE	Da interval. (Unknown)	100
MAIN SEARCH MAX. COMBINATIONS 200	MS/MS deisotoping (Unknown)	False
ADVANCED SITE INTENSITIES TRUE	MS/MS deisotoping tolerance (Unknown)	0.15
LFQ NORM FOR SITES AND PEPTIDES FALSE	MS/MS deisotoping tolerance unit (Unknown)	Da
WRITE MSSCANS TABLE TRUE	MS/MS higher charges (Unknown)	True
WRITE MSMSSCANS TABLE TRUE	MS/MS water loss (Unknown)	True
WRITE MS3SCANS TABLE FALSE	MS/MS ammonia loss (Unknown)	True
WRITE ALLPEPTIDES TABLE TRUE	MS/MS dependent losses (Unknown)	True
WRITE MZRANGE TABLE FALSE	MS/MS recalibration (Unknown)	False
WRITE PASEFMSMSSCANS TABLE FALSE	Site tables	Oxidation (M)Sites.txt
WRITE ACCUMULATEDPASEFMSMSSCANS TABLE FALSE		

An overview of the MaxQuant settings used for quantitative analysis of acquired mass spectrometry data sets.

II. Specific TTC30A/B peptide sequences and ratios

peptide sequence	specificity	TTC30A_x/y_TTC30B
AGLSGAQIPDGEFTALVYR	TTC30A	25.64221
ALIYEIIGWNK	TTC30A	26.56001
EEEQLSYDDPNR	TTC30A	23.57260
EEEQLSYDDPNRK	TTC30A	26.29461
GNYEFGISR	TTC30A	27.89663
IEKEEEQLSYDDPNR	TTC30A	22.45543
IEKEEEQLSYDDPNRK	TTC30A	23.60411
KIEKEEEQLSYDDPNR	TTC30A	25.73300
LDGLAGMLTEQLR	TTC30A	24.61827
NYEVAQETLTDMPPR	TTC30A	44.63029
NYEVAQETLTDMPPRAEEELDPVTLHNQALMNMDAR	TTC30A	24.72231
QHPELGVGMTTEGFDVR	TTC30A	27.93952
SLVEQLLSGEGGEESGGDNETDGQVNLGCLLYK	TTC30A	26.22704
YAEAVQLLGR	TTC30A	28.68934
ACLYAEATR	TTC30B	-25.61216
AGLSGAQIPDGEFTAVVYR	TTC30B	-22.61680
DSVIQECVQFLEHCELHGR	TTC30B	-26.44459
EEEQLSYDDPDKK	TTC30B	-22.61090
EGGEESGGENETDGQINLGCLLYK	TTC30B	-26.32410
GNYDFGISR	TTC30B	-25.62171
NIPAVIEQPLEEER	TTC30B	-27.35527
NTVTYESR	TTC30B	-24.41638
QHPELGVGMTTEGIDVR	TTC30B	-23.29323
SLVEQLPSR	TTC30B	-27.06034
YAEAVQLLGELQR	TTC30B	-27.13242

III. IFT-B interactors of TTC30A/B and ratios

TTC30A interactors	TTC30A_x/y_Control	TTC30B interactors	TTC30A_x/y_Control
TTC26	31,51712	TTC26	29,65243
IFT88	31,63776	IFT88	30,08411
TTC30A (Bait)	31,50176	TTC30A	29,40869
IFT20	29,13248	IFT20	27,07368
TTC30B	29,87241	TTC30B (Bait)	29,02791
TRAF3IP1	28,57022	TRAF3IP1	26,43966
IFT81	8,99273	IFT81	6,49532
CLUAP1	29,19903	CLUAP1	27,06651
IFT74	9,26959	IFT74	7,23361
IFT27	5,88090	IFT27	3,95420
IFT22	30,72643	IFT22	28,68761
IFT46	30,86946	IFT46	28,92667
IFT57	29,75482	IFT57	27,47053
IFT80	30,11855	IFT80	27,81675
IFT172	12,52627	IFT172	10,40726
IFT52	10,05262	IFT52	8,18796
HSPB11	5,39968	HSPB11	3,51236