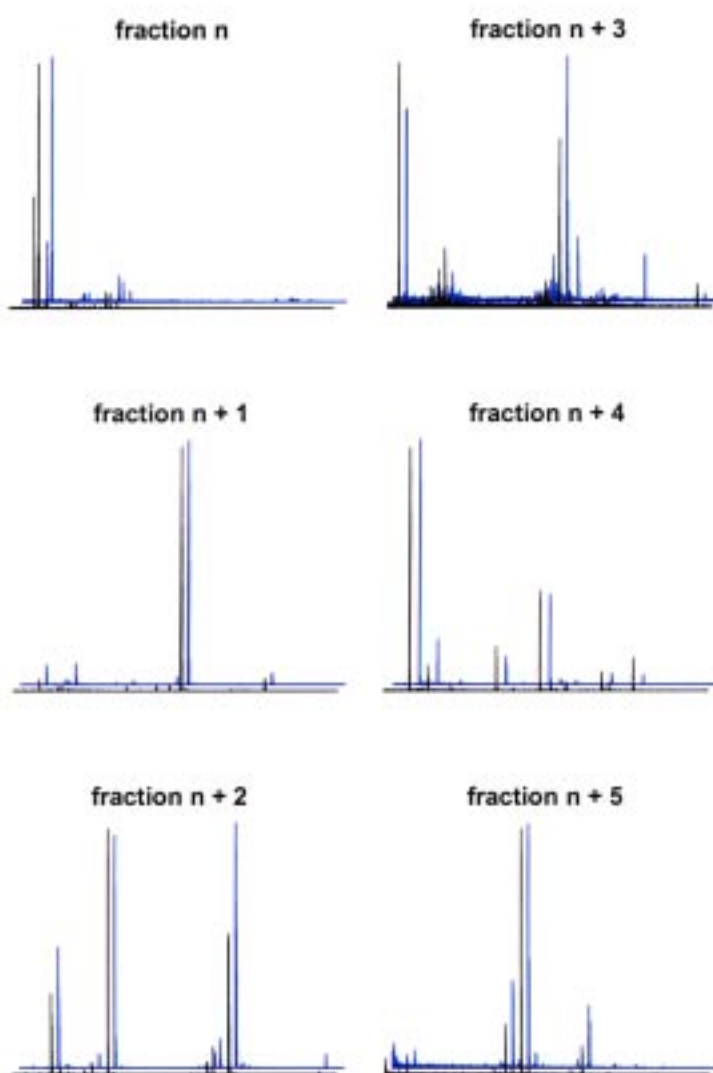
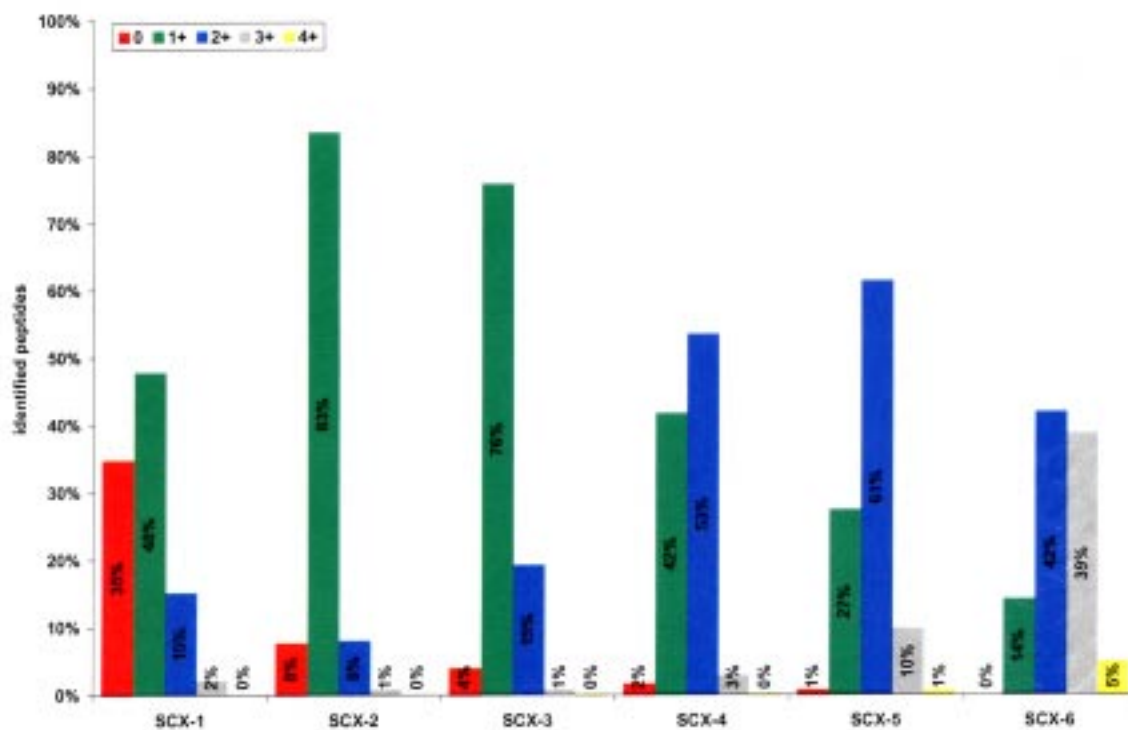


Supplementary figure 1: Reproducibility of the peptide sorting protocol. MALDI-MS spectra of six consecutive LC-MALDI fractions (labeled n to $n + 5$) following the four-stages LC enrichment of methionyl peptides from Jurkat proteome digests are shown. Clearly, the mass spectra obtained from the two preparations (traces shown in black and blue) are very similar and typically an overlap between 70 to 90% of peptide masses is observed between (see text). The m/z -interval (horizontal axis) was fixed between 1000 and 2000 Da. For each spectrum, ion intensities are normalized against the most intense ion.

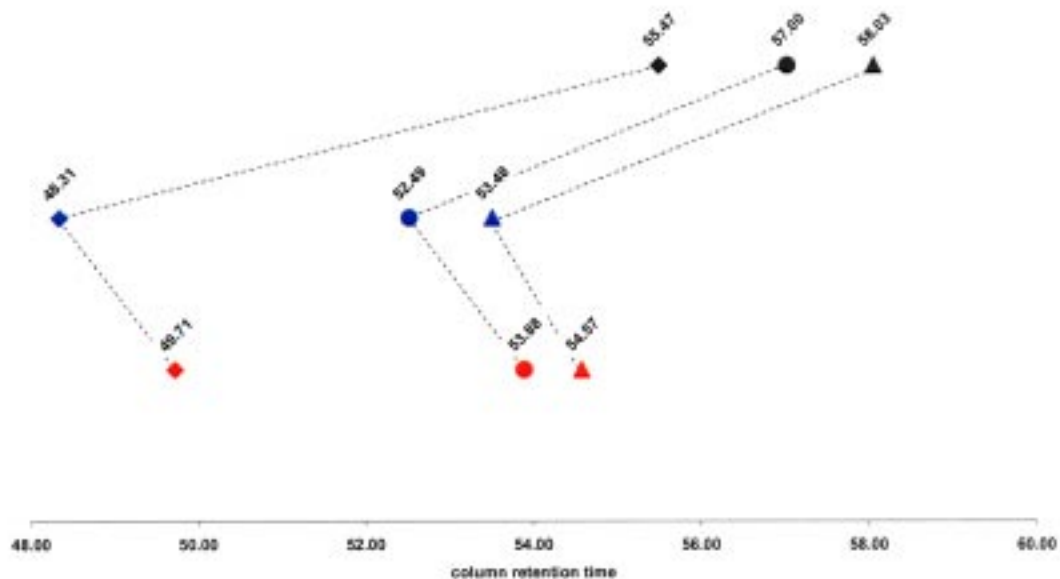


Supplementary figure 2: Charge distribution of MAPC peptides identified in the six different SCX fractions. Most peptides that are neutral at pH 3 are not retained by the column and thus present in the first fraction. As column retention increases, the overall peptide charge shifts to higher values indicating ample fractionation of tryptic peptides by SCX.

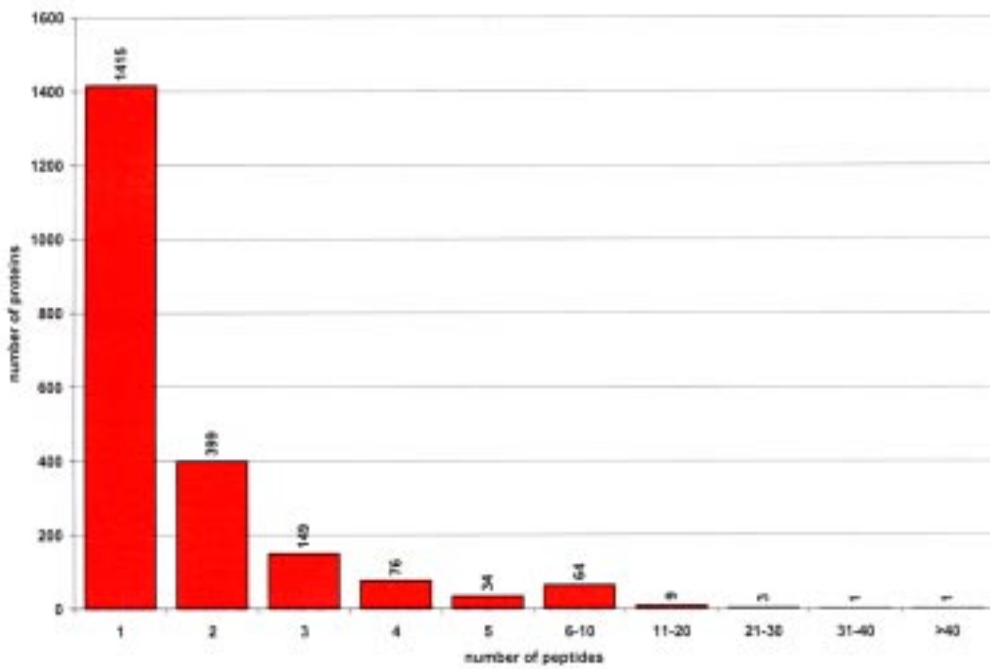
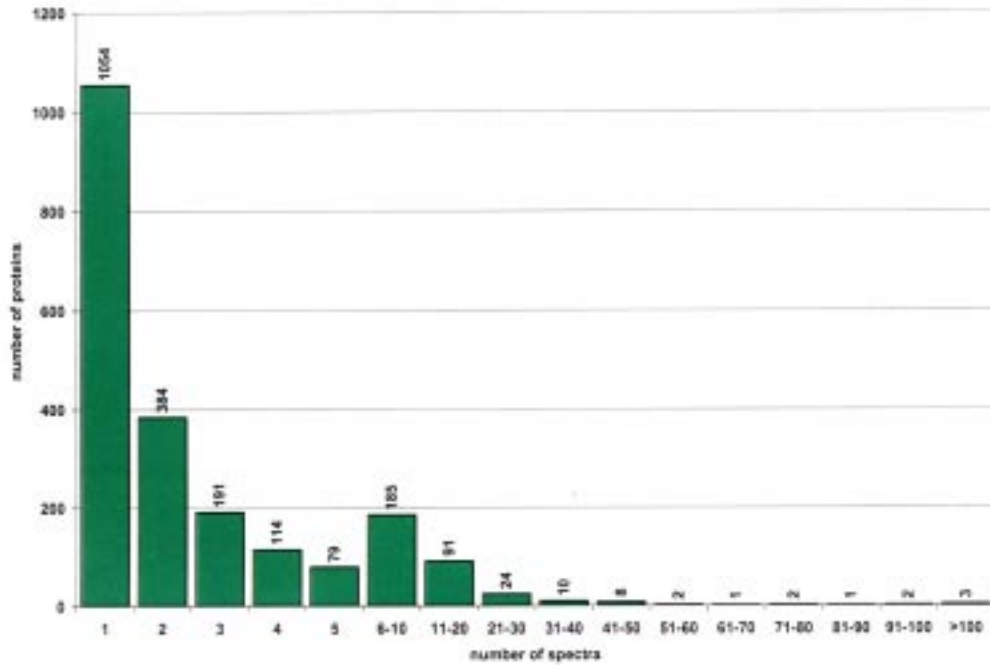


Supplementary figure 3: Shuffling of methionyl peptides by two oxidation stages.

Three synthetic, single methionyl peptides were used for this study: GIHETTFNSIMK (P1, diamonds), MDGIVPDIAVGKTR (P2, circles) and PMFIVNTNVPR (P3, triangles). The elution times of their three oxidized states (unmodified (black), sulfoxide (blue) and sulphone (red)) are given. Clearly, the hydrophilic shift introduced by H_2O_2 treatment and the hydrophobic shift introduced by performic acid oxidation are not uniform (e.g. following H_2O_2 oxidation P1 shifts more than 7 min while P3 shifts only 4.5 min, whereas this is 1.4 min for P1 and about 1 min for P3 after performic acid oxidation). The net result of such different back-and-forth shuffles is an improved separation of methionyl peptides, thus allowing a more efficient selection of peptide ions for further fragmentation analysis.



Supplementary figure 4: Distribution of proteins identified by a single spectrum (upper panel) and by a single peptide (lower panel). The number of proteins identified by a give number of spectra or peptides (x-axis) is given above the colored bars.



Supplementary Table 1: List of enzymes involved in ubiquitination and de-ubiquitination identified in the MAPC proteome. Proteins are ranked according to their function in the ubiquitination process and the number of spectra and peptides linked to each protein is indicated. Clearly, enzymes involved in all steps of ubiquitination are present – either in an active form or dormant – in the MAPC proteome and a potential equilibrium between ubiquitination and de-ubiquitination appears to exist in these cells.

| Acc. Numb. | Protein Description | Number of spectra | Number of peptides | Comment |
|-------------|--|-------------------|--------------------|----------------------------|
| P22314 | Ubiquitin-activating enzyme E1 | 7 | 4 | E1 (Ub-activating) |
| O95352 | Autophagy protein 7-like | 1 | 1 | E1 (Ub-activating) |
| P41228 | Ubiquitin-activating enzyme E1 homolog | 1 | 1 | E1 (Ub-activating) |
| Q8TBC4 | Ubiquitin-activating enzyme E1C | 1 | 1 | E1 (Ub-activating) |
| O14933 | Ubiquitin-conjugating enzyme E2 L6 | 2 | 1 | E2 (conjugating) |
| Q13404 | Ubiquitin-conjugating enzyme E2 variant 1 | 1 | 1 | E2 (conjugating) |
| Q15819 | Ubiquitin-conjugating enzyme E2 variant 2 | 1 | 1 | E2 (conjugating) |
| P61086 | Ubiquitin-conjugating enzyme E2-25 kDa | 1 | 1 | E2 (conjugating) |
| Q7Z6Z7 | E3 Ubiquitin-protein ligase URE-B1 | ? | 4 | E3 (ligase) |
| Q96J02 | Itchy homolog E3 Ubiquitin-protein ligase | 4 | 2 | E3 (ligase) |
| Q15386 | Ubiquitin-protein ligase E3C | 2 | 2 | E3 (ligase) |
| O95071 | Ubiquitin-protein ligase EDD | 2 | 1 | E3 (ligase) |
| Q8UWE0 | Ubiquitin-ligase protein LRSAM1 | 1 | 1 | E3 (ligase) |
| Q05086 | Ubiquitin-protein ligase E3A | 1 | 1 | E3 (ligase) |
| Q8NG27 | Ubiquitin-protein ligase Praja1 | 1 | 1 | E3 (ligase) |
| Q14139 | Ubiquitin-conjugation factor E4 A | 4 | 4 | E4 (Ub-conjugation factor) |
| P45974 | Ubiquitin-carboxyl-terminal hydrolase 5 | 7 | 2 | de-ubiquitination |
| P09936 | Ubiquitin-carboxyl-terminal hydrolase isozyme L1 | 7 | 1 | de-ubiquitination |
| Q93008 | Probable Ubiquitin-carboxyl-terminal hydrolase FAF-X | 5 | 4 | de-ubiquitination |
| P51784 | Ubiquitin-carboxyl-terminal hydrolase 11 | 4 | 2 | de-ubiquitination |
| P54578 | Ubiquitin-carboxyl-terminal hydrolase 14 | 2 | 2 | de-ubiquitination |
| Q9UPU5 | Ubiquitin-carboxyl-terminal hydrolase 24 | 2 | 2 | de-ubiquitination |
| Q93009 | Ubiquitin-carboxyl-terminal hydrolase 7 | 2 | 2 | de-ubiquitination |
| Q14694 | Ubiquitin-carboxyl-terminal hydrolase 10 | 1 | 1 | de-ubiquitination |
| Q92995 | Ubiquitin-carboxyl-terminal hydrolase 13 | 1 | 1 | de-ubiquitination |
| Q94966 | Ubiquitin-carboxyl-terminal hydrolase 19 | 1 | 1 | de-ubiquitination |
| Q9UHP3 | Ubiquitin-carboxyl-terminal hydrolase 25 | 1 | 1 | de-ubiquitination |
| P15374 | Ubiquitin-carboxyl-terminal hydrolase isozyme L3 | 1 | 1 | de-ubiquitination |
| Q9Y5K5 | Ubiquitin-carboxyl-terminal hydrolase isozyme L5 | 1 | 1 | de-ubiquitination |
| IP100297593 | Ubiquitin-specific proteinase 34 | 1 | 1 | de-ubiquitination |

Supplementary Table 2: List of identified ubiquitinated peptides. These peptides were identified by re-searching the data, now allowing for diglycine motif on internal lysine residues (such modified lysines are indicated in the peptide sequence with an asterisk).

| Protein Description & Accession Number | Identified Peptide | Protein Function |
|---|---|---|
| 26S protease regulatory subunit 4 (P62191) | ⁸¹ NQEQMKPLEEK*QEEER ⁹⁸ | involved in ATP-dependent degradation of ubiquitinated proteins |
| CD166 antigen precursor (Q13740) | ²⁶¹ NATVVMK*DNIR ²⁷² | cell adhesion, signal transduction |
| DNA replication licensing factor MCM7 (P33993) | ⁷⁶⁸ MNK*SEDESAGELTREELR ⁸²⁵ | involved in DNA replication |
| Krev interaction trapped protein 1 (O00522) | ³³⁵ ILLEK*GK ³⁴⁵ | small GTPase regulator activity |
| Multiple EGF-like-domain protein 8 precursor (Q99944) | ²⁶³ EAEK*DER ²⁶⁹ | secreted? calcium ion binding |

Supplementary Table 3: List of 163 identified MAPC proteins known or predicted to cross the plasma membrane. The TMHMM Server version 2.0 at <http://www.cbs.dtu.dk/services/TMHMM-2.0/> was first used to indicate MAPC proteins that had at least one predicted helix crossing a biological membrane. Their corresponding information stored in the SwissProt database at <http://us.expasy.org/sprot/> was then browsed and only those proteins known or predicted to penetrate the plasma membrane are listed here. The number of predicted helices (column "PredHel") and the number of MALDI-MS/MS spectra coupled to the proteins (column "Spectra") are given. **Furthermore when these proteins were identified in other, non-proteomic studies this is indicated by references to these studies (see main text).**

| Protein description and database accession number | Predhel | Spectra | Identified in other studies? |
|--|---------|---------|------------------------------|
| ST4 oncofetal antigen precursor (Q13641) | 1 | 1 | |
| 8D6 antigen variant (Fragment) (Q53HF7) | 2 | 1 | |
| ADAM 9 precursor (Q13443) | 1 | 2 | |
| Adipocyte plasma membrane-associated protein (QBHDC9) | 1 | 5 | |
| Aminopeptidase N (P15144) | 1 | 10 | 21, 44, 46 |
| Amyloid beta A4 protein precursor (P05067) | 1 | 3 | |
| Amyloid-like protein 2 precursor (Q06481) | 2 | 2 | |
| Ancient ubiquitous protein 1 precursor (QBY679) | 2 | 2 | |
| Angiopoietin 1 receptor precursor (Q02763) | 1 | 1 | |
| Anthrax toxin receptor 1 precursor (Q9H6X2) | 1 | 1 | |
| Aquaporin-4 (P55067) | 6 | 1 | |
| ARL6IP2 (Q8NH8) | 2 | 1 | |
| ARMCX2 protein (Q7L311) | 1 | 1 | |
| ATP-sensitive inward rectifier potassium channel 14 (Q9JNX9) | 3 | 2 | |
| Autophagy protein 9-like 1 (Q7Z3C6) | 5 | 1 | |
| Beta platelet-derived growth factor receptor precursor (P09619) | 1 | 1 | |
| Calcium-activated potassium channel alpha subunit 1 (Q12781) | 6 | 1 | |
| Carbonic anhydrase XII precursor (Q43570) | 1 | 1 | |
| Carboxypeptidase D precursor (Q75976) | 1 | 1 | |
| CD166 antigen precursor (Q13740) | 1 | 5 | 44 |
| CD44 antigen precursor (P16070) | 1 | 13 | 21, 44, 45 |
| CD82 antigen (P27701) | 4 | 4 | |
| CD97 antigen precursor (P48960) | 7 | 3 | |
| Cell surface glycoprotein MUC18 precursor (P43121) | 1 | 4 | |
| Chemokine-like factor super family member 6 (Q9NX76) | 3 | 1 | |
| Cholinesterase precursor (P06276) | 2 | 1 | |
| Chromosome 10 open reading frame 74 (Q6NUK4) | 3 | 1 | |
| CLCN3 protein (Fragment) (Q7Z4M4) | 1 | 2 | |
| Contactin associated protein 1 precursor (P78357) | 1 | 2 | |
| Coxsackievirus and adenovirus receptor precursor (P78310) | 1 | 1 | |
| DFIT212 (Q6UX59) | 1 | 1 | |
| Dipeptidyl peptidase 4 (P27487) | 1 | 1 | |
| Discoilin, CLB and LCCL domain containing protein 1 precursor (Q8N8Z6) | 1 | 1 | |
| DnaJ homolog subfamily B member 12 (Q9NXW2) | 1 | 1 | |

| | | | |
|---|----|----|--------|
| Ectonucleotide pyrophosphatase/phosphodiesterase 1 (P22413) | 1 | 1 | |
| ELOVL5 protein (Fragment) (Q7L2S5) | 2 | 1 | |
| Endothelial protein C receptor precursor (Q9UNN8) | 1 | 1 | |
| Endothelin-converting enzyme 1 (P42892) | 1 | 3 | |
| Ephrin type-A receptor 2 precursor (P29317) | 1 | 1 | |
| Ephrin type-B receptor 2 precursor (P29323) | 1 | 1 | |
| Ephrin type-B receptor 4 precursor (P54760) | 1 | 1 | |
| FLJ14466 protein (Q96D31) | 3 | 1 | |
| GL004 (Q9NRG8) | 1 | 3 | |
| Granulocyte colony stimulating factor receptor precursor (Q99062) | 1 | 1 | |
| High-affinity cationic amino acid transporter-1 (P30825) | 14 | 2 | |
| High-affinity copper uptake protein 1 (O15431) | 2 | 2 | |
| HSPC009 (Q9Y2R0) | 1 | 1 | |
| HSPC039 protein (Q9Y5U9) | 1 | 1 | |
| HSPC179 (Q9NZZ1) | 1 | 2 | |
| HSPC202 (Q9P0S3) | 2 | 4 | |
| Hypothetical protein (Q8NFQ8) | 1 | 1 | |
| Hypothetical protein (Fragment) (Q53G17) | 11 | 1 | |
| Hypothetical protein DKFZp434C2415 (Q9GZZ9) | 1 | 1 | |
| Hypothetical protein DKFZp564A026 (Fragment) (Q9Y438) | 1 | 1 | |
| Hypothetical protein DKFZp666D0510 (Fragment) (Q658X6) | 1 | 1 | |
| Hypothetical protein DKFZp781O20198 (Q68CQ7) | 1 | 2 | |
| Hypothetical protein FLJ12436 (Q9HA01) | 2 | 1 | |
| Hypothetical protein FLJ14363 (Q96KC3) | 1 | 3 | |
| Hypothetical protein FLJ14400 (Q96KA5) | 6 | 2 | |
| Hypothetical protein FLJ22969 (Q9H5V8) | 1 | 3 | |
| Hypothetical protein FLJ30001 (Q96NW2) | 2 | 1 | |
| Hypothetical protein FLJ30107 (Q96NT5) | 11 | 1 | |
| Hypothetical protein FLJ40269 (Q8N7W5) | 2 | 5 | |
| Hypothetical protein FLJ40946 (Q8N7K6) | 1 | 1 | |
| Hypothetical protein FLJ90251 (Q8NCH3) | 2 | 1 | |
| Hypothetical protein FLJ90433 (Q8NC77) | 1 | 1 | |
| Hypothetical protein FLJ90509 (Q8NC37) | 7 | 1 | |
| Hypothetical protein FLJ90709 (Q8NBW4) | 11 | 1 | |
| Hypothetical protein FLJ90767 (Q8N211) | 11 | 1 | |
| Hypothetical protein LOC196463 (Q8NHP8) | 1 | 2 | |
| Hypothetical protein MGC15523 (Q96C66) | 9 | 1 | |
| Hypothetical protein MGC17943 (Q8WUH6) | 2 | 6 | |
| Hypothetical protein PSEC0198 (Q8N2F6) | 1 | 1 | |
| Hypothetical protein PSEC0249 (Q8NB18) | 1 | 1 | |
| Hypothetical protein PSEC0252 (Q8NB15) | 11 | 1 | |
| Integrin alpha-1 (P56199) | 1 | 1 | 44 |
| Integrin alpha-2 precursor (P17301) | 1 | 1 | 44, 45 |
| Integrin alpha-3 precursor (P26006) | 2 | 12 | 44 |
| Integrin alpha-5 precursor (P08648) | 1 | 3 | 44, 46 |
| Integrin alpha-V precursor (P06756) | 1 | 11 | 44 |
| Integrin beta-1 precursor (P05556) | 1 | 8 | 44, 46 |
| Interferon-induced transmembrane protein 3 (Q01628) | 2 | 1 | |
| Interleukin-6 receptor beta chain precursor (P40189) | 1 | 1 | |
| KIAA0747 protein (Fragment) (O94848) | 1 | 4 | |
| KIAA1201 protein (Fragment) (Q9ULL9) | 1 | 1 | |
| KIAA1250 protein (Fragment) (Q9ULH0) | 4 | 1 | |
| Leucine-rich repeats and calponin homology domain containing protein 4 (O75427) | 1 | 1 | |
| Leucyl-cystinyl aminopeptidase (Q9UIQ6) | 1 | 2 | |
| LOC51337 protein (Q8WUY1) | 1 | 1 | |

| | | | |
|--|----|----|--------|
| Low-density lipoprotein receptor-related protein 1 precursor (Q07954) | 1 | 13 | |
| Low-density lipoprotein receptor-related protein 10 precursor (Q7Z4F1) | 1 | 2 | |
| Lutheran blood group glycoprotein precursor (P50895) | 1 | 1 | |
| MARCH9 protein (Q96GG2) | 2 | 1 | |
| Mast/stem cell growth factor receptor precursor (P10721) | 2 | 1 | |
| Matrix metalloproteinase-14 precursor (P50281) | 1 | 2 | |
| Melanoma-associated chondroitin sulfate proteoglycan (Q92675) | 1 | 7 | |
| Membrane associated progesterone receptor component 2 (O15173) | 1 | 1 | |
| MLN64 N-terminal domain homolog (O95772) | 4 | 1 | |
| Multidrug resistance-associated protein 1 (P33527) | 16 | 1 | |
| Multidrug resistance-associated protein 4 (O15439) | 11 | 1 | |
| Myeloid-associated differentiation marker (Q96S97) | 8 | 1 | |
| Myoferlin (Q9NZM1) | 1 | 25 | |
| Neprilysin (P08473) | 1 | 2 | 44, 46 |
| Neural-cadherin precursor (P19022) | 1 | 5 | |
| Neurofascin precursor (O94856) | 1 | 1 | |
| Neuropilin-2 precursor (O60462) | 1 | 1 | |
| ORM1-like 3 (Q6UY83) | 2 | 3 | |
| OTTHUMP00000016463 (Fragment) (Q5JTD2) | 4 | 2 | |
| P63 protein (Q07065) | 1 | 7 | |
| Plasma membrane calcium-transporting ATPase 1 (P20020) | 7 | 2 | |
| Plasma membrane calcium-transporting ATPase 4 (P23634) | 8 | 3 | |
| Platelet-endothelial tetraspan antigen 3 (P48509) | 4 | 1 | |
| Poliovirus receptor precursor (P15151) | 1 | 3 | |
| Poliovirus receptor related protein 2 precursor (Q92692) | 1 | 1 | |
| Polycystin-2 (Q13563) | 7 | 1 | |
| Polyposis locus protein 1 (Q00765) | 2 | 4 | |
| Potassium channel subfamily K member 5 (O95279) | 6 | 1 | |
| Probable cation-transporting ATPase 13A1 (Q9HD20) | 7 | 1 | |
| Probable G-protein coupled receptor 144 (Q7Z7M1) | 5 | 1 | |
| Probable G-protein coupled receptor 37 precursor (O15354) | 7 | 1 | |
| Pro-neuregulin-1 precursor (Q02297) | 1 | 1 | |
| Protein BAT5 (O95870) | 2 | 2 | |
| Protein C10orf70 (Q9NZ45) | 1 | 1 | |
| Protein C1orf8 precursor (Q9BXS4) | 1 | 1 | |
| Protein HSPC163 (Q9P003) | 3 | 1 | |
| Protein KIAA0152 precursor (Q14165) | 1 | 1 | |
| Protein OS-9 precursor (Q13438) | 1 | 1 | |
| Protocadherin gamma B5 precursor (Q9Y5G0) | 1 | 1 | |
| Receptor-type tyrosine-protein phosphatase kappa precursor (Q15262) | 2 | 1 | |
| Receptor-type tyrosine-protein phosphatase-like N precursor (Q16849) | 1 | 1 | |
| Rhomboid family 1 (Q96CC6) | 6 | 1 | |
| Ryanodine receptor 3 (Q15413) | 6 | 1 | |
| SDFR1 protein (Q6NVX7) | 1 | 1 | |
| Secretory carrier-associated membrane protein 1 (O15126) | 4 | 1 | |
| Seprase (Q12884) | 1 | 5 | |
| Signal peptide peptidase-like 2B (Q8TCT7) | 8 | 1 | |
| Signal-regulatory protein beta-2 precursor (Q9P1W8) | 1 | 1 | |
| SLC15A4 protein (Q8TAH0) | 10 | 1 | |
| Sodium bicarbonate cotransporter NBC1 (Q9NRZ1) | 7 | 1 | |
| Sodium/calcium exchanger 2 precursor (Q9UPR5) | 9 | 1 | |
| Solute carrier family 12, member 5 (Q9H2X9) | 12 | 2 | |
| SPFH domain protein 1 precursor (O75477) | 1 | 5 | |
| Stomatin-like protein 1 (Q9UBI4) | 1 | 1 | |
| Stromal interaction molecule 1 precursor (Q13586) | 1 | 1 | |

| | | | |
|---|---|---|----|
| Synaptic glycoprotein SC2 (Q9NZ01) | 4 | 1 | |
| T-cell surface glycoprotein E2 precursor (P14209) | 2 | 2 | |
| Transferrin receptor protein 1 (P02786) | 1 | 1 | 44 |
| Transient receptor potential cation channel subfamily V member 2 (Q9Y5S1) | 6 | 6 | |
| Transient receptor potential cation channel subfamily V member 5 (Q9NQA5) | 7 | 1 | |
| Transmembrane 9 superfamily protein member 3 precursor (Q9HD45) | 9 | 3 | |
| Transmembrane 9 superfamily protein member 4 (Q92544) | 9 | 2 | |
| Transmembrane anchor protein 1 (P84157) | 1 | 2 | |
| Transmembrane protein 16C (Q9BYT9) | 8 | 1 | |
| Transmembrane protein 24 (O14523) | 1 | 1 | |
| Tyrosine-protein kinase-like 7 precursor (Q13308) | 2 | 1 | |
| UPF0347 protein LOC55831 (Q9P0I2) | 2 | 3 | |
| Vacuolar proton translocating ATPase 116 kDa subunit a isoform 1 (Q93050) | 7 | 4 | |
| Vang-like protein 1 (Q8TAA9) | 4 | 1 | |
| Very low-density lipoprotein receptor precursor (P98155) | 1 | 1 | |
| V-set and immunoglobulin domain containing protein 2 precursor (Q96IQ7) | 1 | 1 | |
| X-linked interleukin-1 receptor accessory protein-like 2 precursor (Q9NP60) | 1 | 1 | |
| YIF1B protein (Q96C02) | 4 | 3 | |
| Zinc finger protein 179 (Q9ULX5) | 2 | 1 | |

Supplementary Table 4: Comparative analysis of the frequency of GO “cellular compartment”, “biological process” and

“molecular function” terms between the MAPC proteome and four proteomes of differentiated cells. The GO terms found in

the MAPC proteome are ranked according to the number of MAPC proteins coupled to a term (column “MAPC”). For each of the four

proteomes of differentiated cells, the number of identified proteins belonging to a GO term is indicated (columns entitled “Jurkat”,

“A549”, “SH-SY5Y” and “DLD1”) and the ratio of this GO term’s normalized frequency in the MAPC proteome versus that in the

differentiated proteome is given (normalized frequencies were calculated by dividing the number of proteins coupled to a GO term by

the total number of proteins coupled to GO cellular compartment terms). Ratio values higher than 2.24 hint to a significant increase of

the number of MAPC proteins linked to the corresponding GO term (see text) and are indicated in a green background. Whenever

such increased values were seen in two or more differentiated proteomes, the GO term is indicated in a green background as well.

Only GO-terms that hold 10 or more MAPC proteins were considered for this analysis. “#DIV/0!” points to the absence of a particular

set of GO term-associated proteins in the analyzed proteome.

| CELLULAR COMPARTMENT | | | | | | | | | | |
|-----------------------------|------------|------|--------|-------|------|-------|---------|-------|------|-------|
| GO name | GO ID | MAPC | Jurkat | ratio | A549 | ratio | SH-SY5Y | ratio | DLD1 | ratio |
| nucleus | GO:0005634 | 162 | 68 | 0.82 | 51 | 0.92 | 47 | 0.76 | 76 | 0.90 |
| cytoplasm | GO:0005737 | 145 | 76 | 0.79 | 56 | 0.89 | 49 | 0.85 | 65 | 1.00 |
| integral to plasma membrane | GO:0005887 | 55 | 4 | 5.04 | 12 | 1.42 | 8 | 1.61 | 19 | 1.30 |
| mitochondrion | GO:0005739 | 52 | 9 | 2.12 | 10 | 1.61 | 13 | 0.94 | 26 | 0.90 |
| cytosol | GO:0005829 | 39 | 18 | 0.78 | 12 | 1.01 | 10 | 0.91 | 24 | 0.73 |
| plasma membrane | GO:0005886 | 36 | 10 | 1.39 | 7 | 1.68 | 4 | 2.23 | 16 | 1.07 |
| integral to membrane | GO:0015021 | 36 | 1 | 13.21 | 4 | 3.78 | 2 | 6.22 | 8 | 2.02 |
| membrane fraction | GO:0005624 | 34 | 7 | 1.78 | 9 | 1.17 | 7 | 1.14 | 14 | 1.09 |
| endoplasmic reticulum | GO:0005783 | 29 | 3 | 3.55 | 8 | 1.12 | 7 | 0.97 | 13 | 1.09 |
| soluble fraction | GO:0005625 | 27 | 20 | 6.50 | 12 | 0.70 | 8 | 0.79 | 17 | 0.71 |
| cytoskeleton | GO:0005856 | 23 | 6 | 1.41 | 4 | 1.76 | 5 | 1.06 | 8 | 1.29 |

| | | | | | | | | | | |
|--|------------|------|---------|---------|------|---------|---------|---------|------|---------|
| intracellular | GO:0015622 | 22 | 11 | 0.73 | 3 | 2.27 | 4 | 1.29 | 15 | 0.66 |
| membrane | GO:0016020 | 22 | 5 | 1.81 | 8 | 0.85 | 3 | 1.72 | 10 | 0.99 |
| extracellular space | GO:0025115 | 18 | 2 | 3.39 | 2 | 2.79 | 2 | 2.11 | 3 | 2.89 |
| proteasome complex | GO:000502 | 17 | 13 | 0.48 | 7 | 0.75 | 3 | 1.33 | 10 | 0.76 |
| nucleolus | GO:0005730 | 16 | 4 | 1.47 | 4 | 1.24 | 4 | 0.94 | 3 | 2.59 |
| actin cytoskeleton | GO:0015629 | 15 | 5 | 1.10 | 7 | 0.66 | 3 | 1.17 | 11 | 0.61 |
| extracellular | GO:0005576 | 15 | 5 | 1.10 | 3 | 1.55 | 5 | 0.70 | 10 | 0.67 |
| Golgi apparatus | GO:0005794 | 13 | 5 | 0.95 | 4 | 1.01 | 2 | 1.52 | 6 | 0.97 |
| nucleoplasm | GO:0005654 | 13 | 4 | 1.19 | 4 | 1.01 | 3 | 1.02 | 4 | 1.46 |
| lysosome | GO:0005764 | 12 | 1 | 4.69 | 3 | 1.24 | 1 | 2.81 | 7 | 0.77 |
| nuclear pore | GO:0005643 | 11 | 6 | 0.67 | 7 | 0.49 | 3 | 0.86 | 9 | 0.55 |
| spliceosome complex | GO:0005681 | 10 | 8 | 0.46 | 2 | 1.55 | 2 | 1.17 | 5 | 0.96 |
| BIOLOGICAL PROCESS | | | | | | | | | | |
| GO name | GO ID | MAPC | Justif. | ratio | AS43 | ratio | SH-SY5Y | ratio | DL03 | ratio |
| signal transduction | GO:007165 | 93 | 29 | 1.18 | 22 | 1.31 | 17 | 1.28 | 34 | 1.23 |
| cell proliferation | GO:0008283 | 44 | 21 | 0.77 | 11 | 1.24 | 6 | 1.72 | 11 | 1.80 |
| protein amino acid phosphorylation | GO:0091468 | 36 | 11 | 1.29 | 2 | 5.57 | 5 | 1.69 | 11 | 1.47 |
| protein biosynthesis | GO:0006412 | 34 | 16 | 0.78 | 17 | 0.62 | 15 | 0.53 | 20 | 0.76 |
| protein folding | GO:0076457 | 29 | 17 | 0.63 | 8 | 1.12 | 10 | 0.68 | 17 | 0.77 |
| transport | GO:0006910 | 24 | 4 | 2.26 | 9 | 0.83 | 5 | 1.12 | 8 | 1.35 |
| proteolysis and peptidolysis | GO:0005268 | 22 | 7 | 1.15 | 0 | 8716091 | 2 | 2.58 | 6 | 1.65 |
| intracellular protein transport | GO:0016686 | 22 | 6 | 1.35 | 5 | 1.36 | 5 | 1.03 | 7 | 1.41 |
| cell adhesion | GO:0007155 | 22 | 0 | 8070001 | 5 | 1.36 | 3 | 1.72 | 10 | 0.99 |
| immune response | GO:0008225 | 21 | 6 | 1.26 | 2 | 3.25 | 2 | 2.46 | 5 | 1.89 |
| development | GO:0007275 | 21 | 3 | 2.57 | 5 | 1.39 | 3 | 1.64 | 2 | 4.71 |
| RNA splicing | GO:0008380 | 21 | 14 | 0.55 | 8 | 0.81 | 10 | 0.49 | 17 | 0.55 |
| neurogenesis | GO:0007399 | 20 | 7 | 1.05 | 4 | 1.55 | 6 | 0.78 | 8 | 1.12 |
| regulation of cell cycle | GO:0000874 | 19 | 20 | 0.35 | 13 | 0.45 | 0 | 8504001 | 0 | 8070001 |
| transcription from Pol II promoter | GO:0003068 | 18 | 8 | 0.83 | 4 | 1.39 | 4 | 1.05 | 6 | 1.35 |
| mRNA processing | GO:0006397 | 18 | 8 | 0.83 | 8 | 0.70 | 8 | 0.53 | 14 | 0.58 |
| protein complex assembly | GO:0004461 | 18 | 10 | 0.66 | 11 | 0.51 | 4 | 1.05 | 13 | 0.62 |
| RNA processing | GO:0006398 | 17 | 4 | 1.56 | 11 | 0.48 | 6 | 0.66 | 6 | 1.27 |
| regulation of translational initiation | GO:0006446 | 16 | 11 | 0.53 | 6 | 0.83 | 5 | 0.75 | 11 | 0.65 |

| | | | | | | | | | | |
|--|------------|------|--------|---------|-----|---------|---------|---------|------|-------|
| positive regulation of I-kappaB kinase/NF-kappaB cascade | GO:0043123 | 16 | 5 | 1.17 | 4 | 1.24 | 3 | 1.25 | 4 | 1.80 |
| carbohydrate metabolism | GO:0005875 | 15 | 2 | 2.75 | 4 | 1.16 | 2 | 1.76 | 3 | 2.24 |
| regulation of transcription | GO:0006355 | 15 | 9 | 0.61 | 4 | 1.16 | 4 | 0.88 | 10 | 0.67 |
| response to unfolded protein | GO:0006096 | 15 | 6 | 0.92 | 6 | 0.77 | 7 | 0.50 | 10 | 0.67 |
| regulation of transcription from Pol II promoter | GO:0006357 | 14 | 11 | 0.47 | 8 | 0.54 | 10 | 0.33 | 11 | 0.57 |
| protein modification | GO:0006484 | 14 | 1 | 5.14 | 6 | 0.72 | 3 | 1.09 | 4 | 1.57 |
| vesicle-mediated transport | GO:0016192 | 14 | 4 | 1.28 | 3 | 1.44 | 2 | 1.64 | 5 | 1.26 |
| energy pathways | GO:0008091 | 13 | 0 | EC00001 | 3 | 1.34 | 3 | 1.02 | 5 | 1.17 |
| lipid metabolism | GO:0006629 | 13 | 6 | 0.73 | 9 | 0.45 | 5 | 0.61 | 8 | 0.73 |
| cell motility | GO:0006938 | 13 | 5 | 0.95 | 6 | 0.67 | 2 | 1.52 | 9 | 0.65 |
| positive regulation of cell proliferation | GO:0008284 | 13 | 5 | 0.95 | 3 | 1.34 | 2 | 1.52 | 5 | 1.17 |
| DNA replication | GO:0006260 | 12 | 9 | 0.48 | 7 | 0.53 | 9 | 0.31 | 7 | 0.77 |
| G-protein coupled receptor protein signaling pathway | GO:0007186 | 12 | 1 | 4.49 | 2 | 1.66 | 2 | 1.41 | 2 | 2.89 |
| negative regulation of cell proliferation | GO:0008285 | 12 | 5 | 0.88 | 3 | 1.24 | 4 | 0.70 | 5 | 1.08 |
| DNA repair | GO:0006281 | 11 | 4 | 1.01 | 3 | 1.13 | 4 | 0.64 | 7 | 0.71 |
| induction of apoptosis | GO:0006917 | 11 | 7 | 0.56 | 3 | 1.13 | 2 | 1.29 | 9 | 0.55 |
| intracellular signaling cascade | GO:0007242 | 11 | 5 | 0.81 | 0 | EC00018 | 2 | 1.29 | 6 | 0.82 |
| cell-cell signaling | GO:0007257 | 11 | 1 | 4.34 | 0 | EC00018 | 0 | EC00018 | 5 | 0.99 |
| metabolism | GO:0008152 | 11 | 3 | 1.35 | 1 | 3.46 | 0 | EC00018 | 2 | 2.47 |
| actin cytoskeleton organization and biogenesis | GO:0030036 | 11 | 7 | 0.58 | 4 | 0.85 | 2 | 1.29 | 5 | 0.99 |
| apoptosis | GO:0006915 | 10 | 4 | 0.92 | 5 | 0.82 | 1 | 2.34 | 4 | 1.12 |
| membrane fusion | GO:0006544 | 10 | 1 | 3.67 | 1 | 3.10 | 0 | EC00018 | 1 | 4.48 |
| inflammatory response | GO:0006954 | 10 | 2 | 1.83 | 3 | 1.03 | 2 | 1.17 | 2 | 2.24 |
| central nervous system development | GO:0007417 | 10 | 4 | 0.92 | 2 | 1.55 | 3 | 0.78 | 4 | 1.12 |
| MOLECULAR FUNCTION | | | | | | | | | | |
| GO name | GO ID | MAPC | Juicer | ratio | AS4 | ratio | SH-SY5Y | ratio | DLD1 | ratio |
| protein binding | GO:0005515 | 105 | 39 | 0.99 | 30 | 1.68 | 25 | 0.98 | 49 | 0.96 |
| RNA binding | GO:0003723 | 61 | 23 | 0.97 | 32 | 0.69 | 21 | 0.68 | 29 | 0.94 |
| ATP binding | GO:0005524 | 60 | 29 | 1.10 | 15 | 1.24 | 11 | 1.28 | 25 | 1.08 |
| GTPase activity | GO:0003924 | 36 | 5 | 2.20 | 6 | 1.55 | 5 | 1.41 | 9 | 1.50 |
| electron transporter activity | GO:0006489 | 36 | 6 | 1.83 | 9 | 1.03 | 4 | 1.76 | 13 | 1.04 |
| DNA binding | GO:0003677 | 29 | 22 | 0.48 | 13 | 0.69 | 0 | EC00018 | 14 | 0.93 |
| signal transducer activity | GO:0004871 | 28 | 10 | 1.03 | 9 | 0.96 | 8 | 0.82 | 9 | 1.40 |

| | | | | | | | | | | |
|--|------------|----|----|--------|----|------|----|--------|----|------|
| structural constituent of ribosome | GO:0003735 | 27 | 12 | 0.83 | 15 | 0.56 | 14 | 0.45 | 18 | 0.67 |
| zinc ion binding | GO:0008270 | 27 | 10 | 0.39 | 6 | 1.39 | 3 | 2.11 | 14 | 0.87 |
| calcium ion binding | GO:0005509 | 26 | 4 | 2.38 | 7 | 1.15 | 8 | 0.76 | 12 | 0.97 |
| transporter activity | GO:0005215 | 23 | 5 | 1.69 | 9 | 0.79 | 9 | 0.69 | 9 | 1.15 |
| protein synthesis kinase activity | GO:0004674 | 22 | 6 | 1.35 | 3 | 2.27 | 2 | 2.59 | 9 | 1.10 |
| transcription factor activity | GO:0003709 | 21 | 16 | 0.48 | 10 | 0.65 | 6 | 0.82 | 11 | 0.86 |
| actin binding | GO:0003779 | 20 | 11 | 0.67 | 10 | 0.62 | 5 | 0.94 | 11 | 0.82 |
| receptor activity | GO:0004672 | 20 | 2 | 3.67 | 1 | 6.59 | 1 | 4.89 | 4 | 2.24 |
| nucleic acid binding | GO:0003676 | 19 | 4 | 1.74 | 6 | 0.98 | 0 | 6.0907 | 10 | 0.85 |
| structural molecule activity | GO:0005198 | 19 | 7 | 1.00 | 9 | 0.65 | 8 | 0.56 | 8 | 1.07 |
| structural constituent of cytoskeleton | GO:0005209 | 19 | 8 | 0.87 | 9 | 0.65 | 4 | 1.11 | 12 | 0.71 |
| transcription coactivator activity | GO:0003713 | 16 | 7 | 0.84 | 5 | 0.99 | 5 | 0.75 | 10 | 0.72 |
| GTP binding | GO:0005035 | 16 | 7 | 0.84 | 8 | 0.62 | 10 | 0.37 | 5 | 1.44 |
| pre-mRNA splicing factor activity | GO:0002048 | 16 | 8 | 0.73 | 10 | 0.50 | 8 | 0.47 | 13 | 0.55 |
| translation initiation factor activity | GO:0003743 | 15 | 13 | 0.42 | 4 | 1.16 | 5 | 0.70 | 10 | 0.67 |
| catalytic activity | GO:0003824 | 15 | 6 | 0.92 | 4 | 1.16 | 1 | 3.81 | 6 | 1.12 |
| receptor binding | GO:0003922 | 15 | 1 | 5.59 | 2 | 2.32 | 3 | 1.17 | 3 | 2.24 |
| protein kinase activity | GO:0004672 | 13 | 3 | 1.59 | 1 | 4.52 | 2 | 1.52 | 7 | 0.83 |
| structural constituent of nucleus | GO:0005937 | 11 | 0 | 6.0907 | 5 | 0.69 | 1 | 2.59 | 4 | 1.23 |
| microtubule motor activity | GO:0003777 | 10 | 3 | 1.22 | 6 | 0.52 | 3 | 0.78 | 6 | 0.56 |