**Supplementary file**

# Assessment of a complete and classified platelet proteome from genome-wide transcripts of human platelets and megakaryocytes covering platelet functions

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## Supplementary Methods

**Novel combined proteome analysis for validation.** Well-purified platelet samples were obtained from 30 healthy subjects, and digested with trypsin using filter aided sample preparation, as described in the methods section. After digestion, 2 µg of peptide mixture from each sample were pooled. The pooled sample was desalted using a SpecVarian $C_{18}$ cartridge, according to manufacturer instructions (Agilent, Santa Clara, California). 50 µg of the pooled sample was fractionated by high pH-

reversed phase chromatography ($C_{18}$ column; BioBasic-18, 0.5 mm ID x 15 cm, 5 µm particle size, 300 Å pore size, (Thermo Scientific) using a linear gradient ranging from 5-38% of solvent B (mobile phase A: 10 mM ammonium formate, pH 8.0, B: 10 mM ammonium formate 84% acetonitrile, pH 8.0) for 90 minutes. Thirty fractions were collected every minute in a concatenated mode and dried under vacuum. Each fraction was analyzed on a Q Exactive HF mass spectrometer on line coupled to a U3000 RSLCnano (both from Thermo Scientific). Separate peptides fractions were loaded onto a trap column (Acclaim PepMap100 $C_{18}$ trap column; 100 µm x 2 cm) with 0.1% trifluoroacetic acid at a flow rate of 20 µL/min, followed by separation of peptides on the main column (PepMap100 C18; 75 µm × 50 cm), using a non-linear gradient ranging from 7-24-38% of solvent B (84% acetonitrile, 0.1% formic acid) for 150 minutes. On the Q Exactive HF, a 90 min acquisition time was used, where survey scans were acquired at resolution of 30,000 using an automatic gain control (AGC) target value of 3 $x10^6$. MS/MS spectra of the top 15 most intense ions were acquired with a resolution of 15,000 an isolation width of 1.2 *m/z*, a normalized collision energy of 27%, an AGC target value of 5 $x10^4$ ions, a maximum injection time of 200 ms. Raw data were searched in Proteome Discoverer (Thermo Scientific) using Uniprot-KD (Human Uniprot 23/07/2018), with trypsin as an enzyme, carbamido-methylation as fixed modification, and oxidation of methionine as variable modification. For MS spectra, the mass tolerance was set to 10 ppm, and for MS/MS spectra, the mass tolerance was set to 0.02 Da. Obtained in the validation cohort were 5,505 unique proteins, which were separated into previously identified and newly identified, and were compared per corresponding gene with transcriptome data (Suppl. Datafile 2).

**Technical limitations for obtaining the full platelet proteome.** Integral membrane proteins ($C_{10}$ and vesicular protein classes) with low relative abundance and high hydrophobicity are usually under-represented[1,2]. Use of specific enrichment steps can help here[3]. Second, while trypsin is the common choice as a digesting enzyme (cleaving at lysine and arginine residues), it is less efficient for domains rich in negatively charged amino acids[4]. This can be overcome by the use of other proteases or by changing digestion conditions. Third, loss of peptides is unavoidable in digested samples during sample preparation (FASP, precipitation, enrichment, desalting, elution)[5], and by the choice of protein denaturation agent Proc, 2010 #480}. Fourth, data-dependent acquisition (DDA) is the most common procedure to obtain mass

spectrometric data, however due to the TopN method used in DDA experiments, some precursors could be under- represented due to the defined threshold. Alternatively, in the data-independent acquisition (DIA) all precursors detected within a defined mass window are selected for MS/MS fragmentation and acquisition. This window is stepped across the entire mass range to collect MS/MS data from all detected precursors[6]. Furthermore, partial post-translational modifications (N-terminal acetylation, serine/threonine phosphorylation) can complicate the data analysis[7,8]. Concerning mass spectra analysis, current algorithms search for peptide-spectrum matches with 1% false discovery rate, estimated by a target-decoy search strategy[9-11], but this threshold may be less reliable for large data sets[12,13]. From our own data, we calculated that (with the exception of classes $C_{02}$, $C_{17}$, $C_{21}$).

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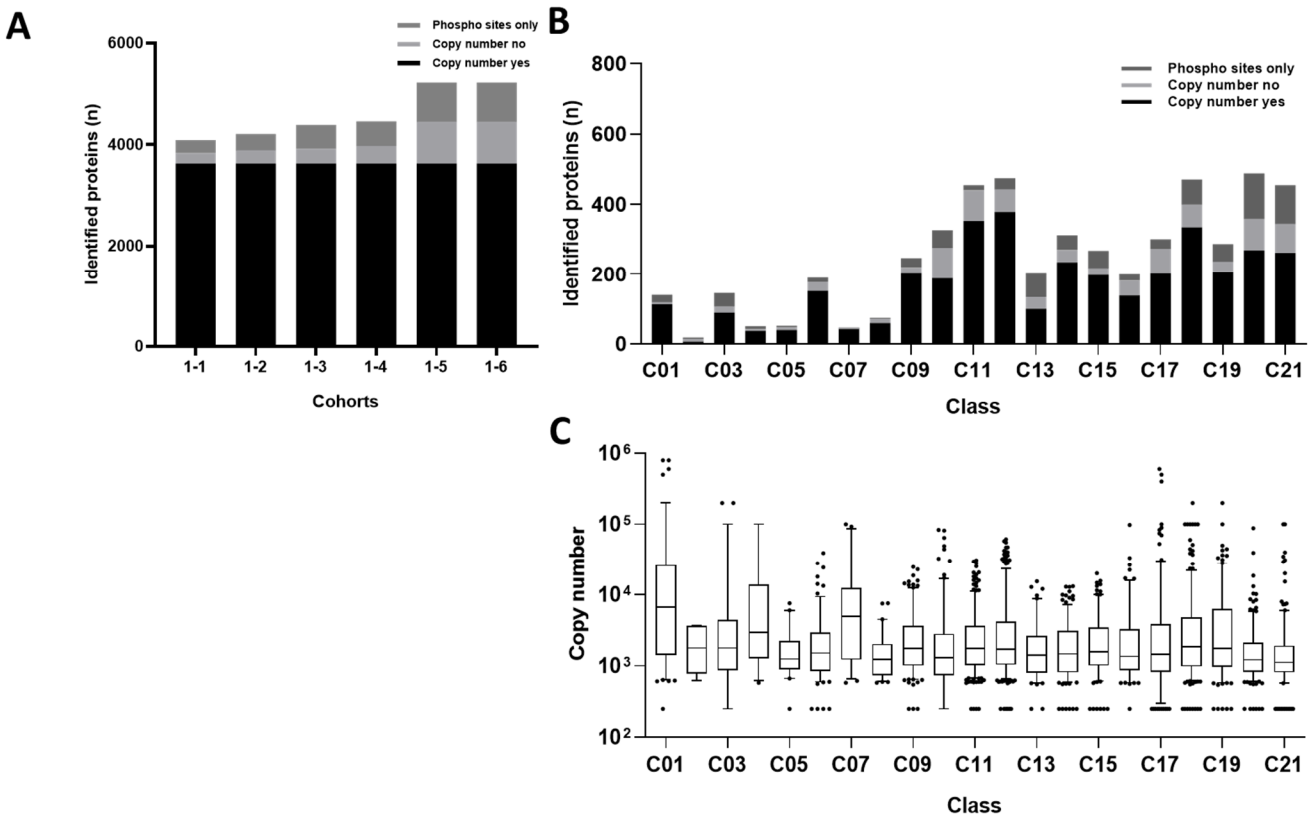
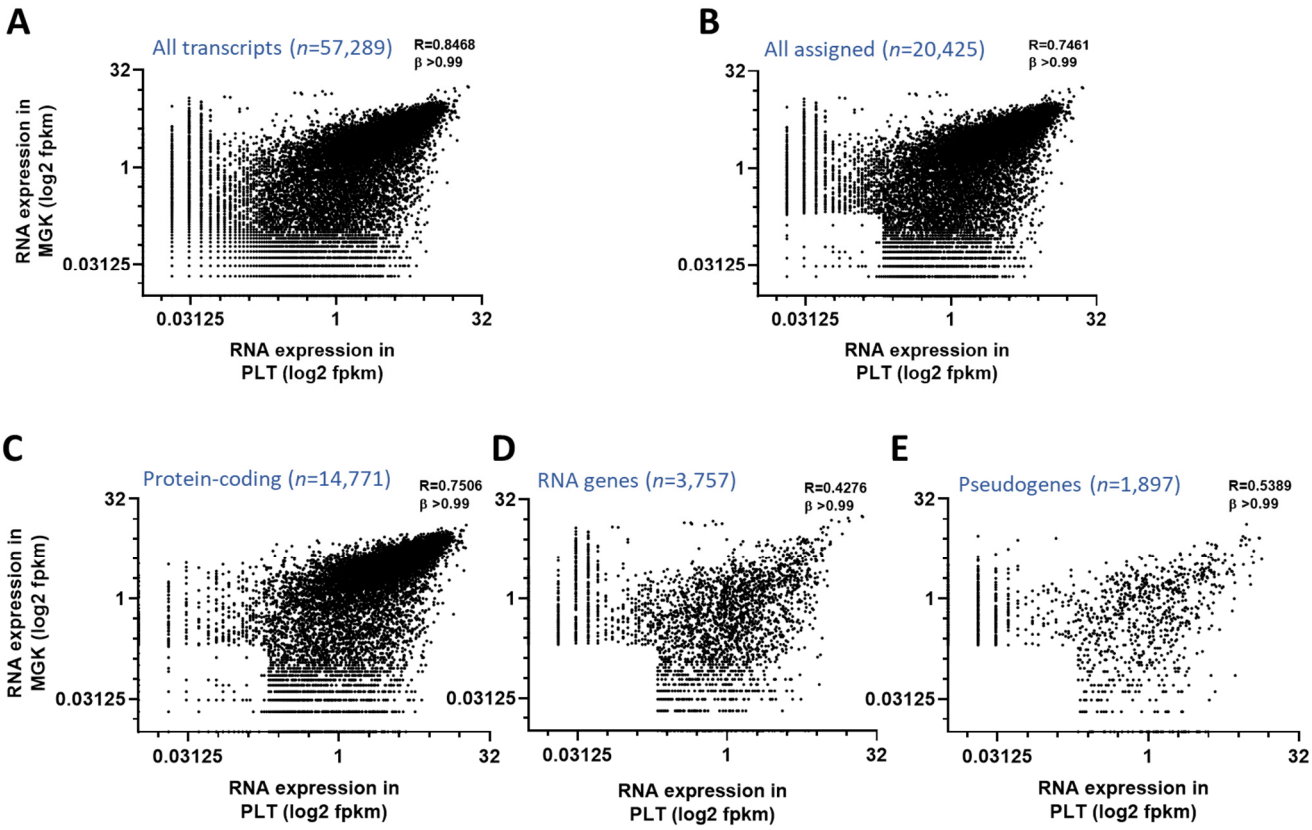



**Suppl. Figure 1.** *Buildup of identified human platelet proteome.* **A**, Progressive buildup of platelet proteome, obtained in six cohort studies (numbered 1 to 6) with healthy subjects. Black = 3,629 proteins with copy numbers; light gray = additional protein without copy numbers; dark gray = additional proteins by $TiO_2$ enrichment of phosphoproteome. **B**, Assignment of 5,211 identified proteins (all 6 cohorts) to 21 function classes (see Fig. 1). **C**, Ranges of copy numbers per function class.




**Suppl. Figure 2.** *Correlation of platelet (PLT) and megakaryocyte (MGK) transcriptomes.* **A**, Correlation of all transcript levels in PLT *vs.* MGK genome-wide. **B**, Correlation of relevant transcripts (log2fpkm ≥0.20) in PLT and MGK. **C-E**, Correlation of relevant transcripts separated out between protein-coding genes (**C**), RNA genes (**D**) and pseudogenes (**E**).

**A**

| PLT and/or MGK | Transcripts with proteins: total >0.20 | yes >0.20 | no >0.20 | yes <0.20 |
|---|---|---|---|---|
| C01 Cytoskeleton actin-myosin | 237 | 132 | 105 | 9 |
| C02 Cytoskeleton intermediate | 27 | 8 | 19 | 11 |
| C03 Cytoskeleton microtubule | 420 | 140 | 280 | 6 |
| C04 Cytoskeleton receptor-linked | 69 | 51 | 18 | 0 |
| C05 Endosome proteins | 101 | 52 | 49 | 0 |
| C06 ER & Golgi proteins | 568 | 190 | 378 | 1 |
| C07 Glucose metabolism | 58 | 46 | 12 | 1 |
| C08 Lysosome & peroxisome proteins | 168 | 74 | 94 | 1 |
| C09 Membrane & protein trafficking | 349 | 243 | 106 | 4 |
| C10 Membrane receptors & channels | 1430 | 318 | 1112 | 9 |
| C11 Mitochondrial proteins | 814 | 454 | 360 | 1 |
| C12 Other metabolism | 877 | 469 | 408 | 6 |
| C13 Other nuclear proteins | 1469 | 200 | 1269 | 3 |
| C14 Proteasomal proteins | 677 | 311 | 366 | 1 |
| C15 Protein kinases & phosphatases | 481 | 266 | 215 | 2 |
| C16 Protein processing | 308 | 199 | 109 | 1 |
| C17 Secretory proteins | 811 | 228 | 583 | 73 |
| C18 Signaling & adapter proteins | 1024 | 463 | 561 | 8 |
| C19 Small GTPases & regulators | 483 | 284 | 199 | 3 |
| C20 Transcription & translation | 2280 | 485 | 1795 | 3 |
| C21 Uncharacterized & other proteins | 2120 | 437 | 1683 | 18 |
| Protein coding | 14771 | 5050 | 9721 | 161 |
| RNA genes | 3757 | 0 | 3757 | 0 |
| Pseudogenes | 1897 | 0 | 1897 | 0 |
| **Total transcripts** | **20425** | 5050 | 15375 | 161 |

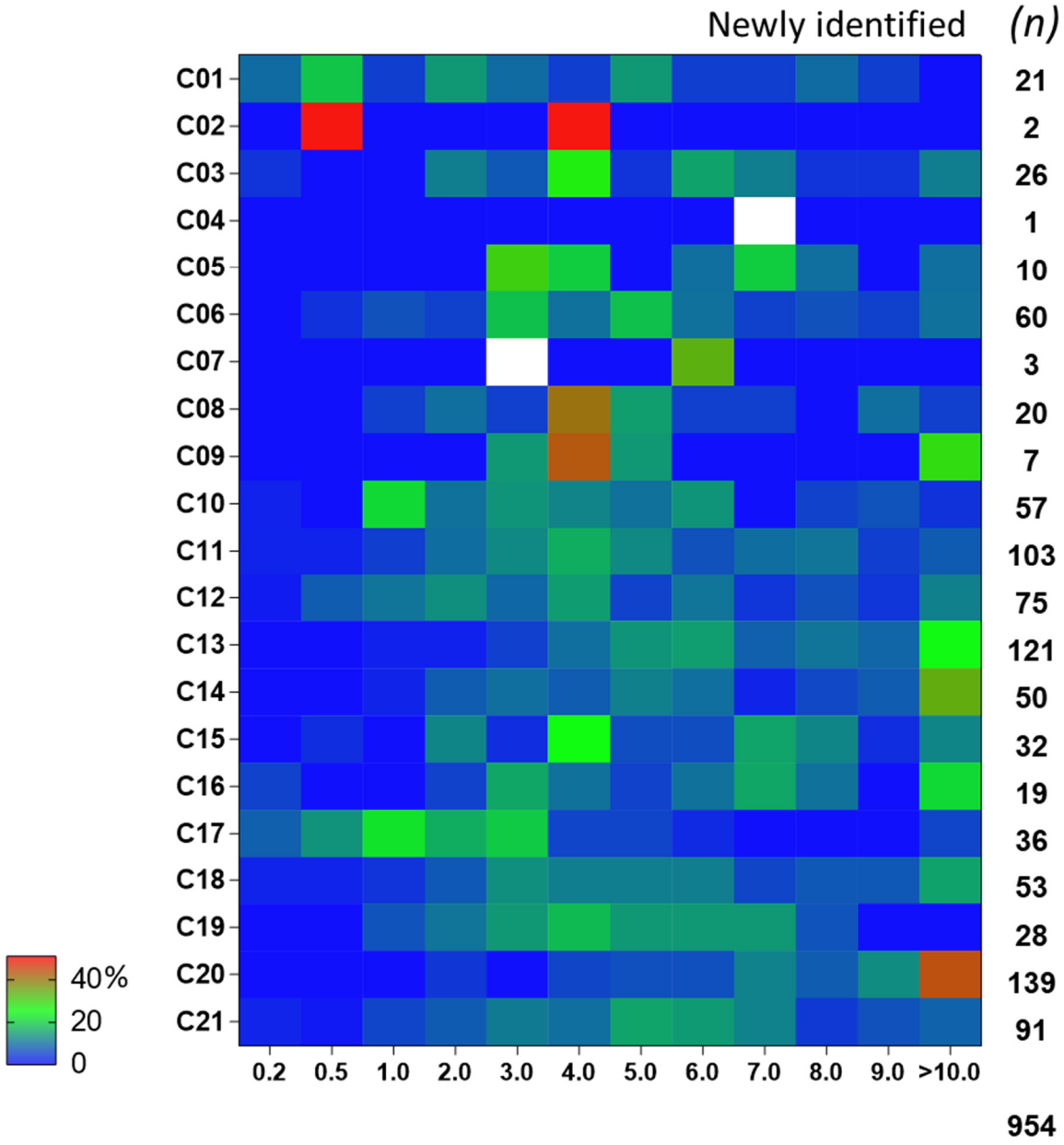
**B**

| PLT | Transcripts with proteins: total >0.20 | yes >0.20 | no >0.20 | yes <0.20 |
|---|---|---|---|---|
| C01 | 230 | 132 | 98 | 9 |
| C02 | 26 | 8 | 18 | 11 |
| C03 | 416 | 139 | 277 | 7 |
| C04 | 69 | 51 | 18 | 0 |
| C05 | 98 | 52 | 46 | 0 |
| C06 | 549 | 190 | 359 | 1 |
| C07 | 58 | 46 | 12 | 1 |
| C08 | 164 | 74 | 90 | 1 |
| C09 | 344 | 242 | 102 | 5 |
| C10 | 1344 | 315 | 1029 | 12 |
| C11 | 805 | 454 | 351 | 1 |
| C12 | 855 | 467 | 388 | 8 |
| C13 | 1442 | 200 | 1242 | 3 |
| C14 | 665 | 310 | 355 | 2 |
| C15 | 477 | 266 | 211 | 2 |
| C16 | 301 | 197 | 104 | 3 |
| C17 | 756 | 223 | 533 | 78 |
| C18 | 1008 | 462 | 546 | 9 |
| C19 | 478 | 284 | 194 | 3 |
| C20 | 2230 | 484 | 1746 | 4 |
| C21 | 1982 | 434 | 1548 | 21 |
| | 14297 | 5030 | 9267 | 181 |
| | 2480 | 0 | 2480 | 0 |
| | 852 | 0 | 852 | 0 |
| | **17629** | 5030 | 12599 | 181 |

**C**

| MGK | Transcripts with proteins: total >0.20 | yes >0.20 | no >0.20 | yes <0.20 |
|---|---|---|---|---|
| C01 | 186 | 125 | 61 | 16 |
| C02 | 20 | 6 | 14 | 13 |
| C03 | 355 | 133 | 222 | 13 |
| C04 | 64 | 48 | 16 | 3 |
| C05 | 88 | 52 | 36 | 0 |
| C06 | 478 | 190 | 288 | 1 |
| C07 | 52 | 45 | 7 | 2 |
| C08 | 152 | 74 | 78 | 1 |
| C09 | 313 | 240 | 73 | 7 |
| C10 | 914 | 300 | 614 | 27 |
| C11 | 783 | 454 | 329 | 1 |
| C12 | 781 | 463 | 318 | 12 |
| C13 | 1378 | 196 | 1182 | 7 |
| C14 | 638 | 311 | 327 | 1 |
| C15 | 432 | 264 | 168 | 4 |
| C16 | 289 | 198 | 91 | 2 |
| C17 | 429 | 155 | 274 | 146 |
| C18 | 829 | 446 | 383 | 25 |
| C19 | 432 | 281 | 151 | 6 |
| C20 | 2111 | 482 | 1629 | 6 |
| C21 | 1772 | 419 | 1353 | 36 |
| | 12496 | 4882 | 7614 | 329 |
| | 2783 | 0 | 2783 | 0 |
| | 1564 | 0 | 1564 | 0 |
| | **16843** | 4882 | 11961 | 329 |

**Suppl. Figure 3.** *Comparison of relevant transcripts with or without identified platelet proteins.* **A, C**. Listing per function class of numbers of relevant transcripts (log2fpkm ≥0.20) that were yes/no identified in the platelet proteome. Transcriptomes were combined from platelets (PLT) and megakaryocytes (MGK), or used from PLT or MGK only. Indicated in gray are proteins without relevant mRNA expression (log2fpkm <0.20). Transcripts were summed as protein coding, RNA genes and pseudogenes. Data are shown for: **A**, Combined PLT/MGK transcriptome; **B**, PLT transcriptome; **C**, MGK transcriptome.




**Suppl. Figure 4.** *Distribution profile of transcripts of newly identified proteins per protein function class.* Heatmap of percentual distribution of transcript levels per function class (rainbow colors; blue = low, red = high) for 954 newly identified proteins in validation cohort. Numbers per class are indicated in right column.

**Suppl. Table 1.** *Clustering of proteins per class in quantitative proteome-transcriptome space. P*-values are given, representing significance of over-representation of protein in defined areas I-V of proteome-transcriptome matrix, based on transcript levels in platelets (PLT) or megakaryocytes (MGK). For visualization of areas I-V, see Fig. 4C-D. Modelling was as described in the methods section. Statistical significance increasing with red coloring.

| Protein function class | High transl. high transcr. | | High transl. low transcr. | | Low trans. low transcr. | | Mid transl. mid transcr. | | Unrelevant transl. | | Protein count | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Area I | | Area II | | Area III | | Area IV | | Area V | | Area I-V | | |
| *P-value (Matlab)* | PLT | MGK | PLT | MGK | PLT | MGK | PLT | MGK | PLT | MGK | PLT | MGK | Total |
| 01 Cytoskeleton actin-myosin | 1.31E-09 | 1.10E-10 | 9.92E-01 | 9.99E-01 | 6.32E-01 | 8.82E-02 | 9.92E-01 | 9.74E-01 | 1.71E-03 | 4.22E-04 | 66 | 66 | 114 |
| 02 Cytoskeleton intermediate | 1.00E+00 | 1.00E+00 | 8.15E-01 | 1.00E+00 | 1.00E+00 | 9.98E-02 | 1.00E+00 | 9.13E-01 | 3.93E-03 | 2.76E-04 | 4 | 6 | 7 |
| 03 Cytoskeleton microtubule | 5.27E-04 | 3.00E-03 | 5.93E-01 | 4.17E-01 | 6.76E-01 | 7.49E-01 | 5.69E-01 | 5.24E-01 | 9.06E-02 | 1.27E-01 | 60 | 56 | 91 |
| 04 Cytoskeleton receptor-linked | 2.90E-03 | 2.90E-03 | 7.36E-01 | 9.97E-01 | 7.70E-01 | 4.36E-01 | 6.67E-01 | 8.33E-01 | 8.65E-01 | 8.86E-01 | 22 | 16 | 38 |
| 05 Endosome proteins | 1.00E+00 | 1.00E+00 | 1.30E-01 | 1.99E-01 | 7.88E-01 | 1.00E+00 | 7.30E-01 | 7.85E-01 | 8.78E-01 | 1.00E+00 | 23 | 18 | 40 |
| 06 ER & Golgi proteins | 1.00E+00 | 1.00E+00 | 1.17E-01 | 3.41E-02 | 3.51E-01 | 6.69E-01 | 6.00E-01 | 7.24E-01 | 1.00E+00 | 1.00E+00 | 85 | 74 | 152 |
| 07 Glucose metabolism | 4.57E-03 | 4.57E-03 | 9.69E-01 | 9.56E-01 | 7.73E-02 | 1.00E+00 | 2.93E-01 | 1.01E-01 | 6.53E-01 | 9.14E-01 | 28 | 25 | 43 |
| 08 Lysosome & peroxisome proteins | 1.00E+00 | 1.00E+00 | 1.98E-01 | 6.34E-01 | 3.97E-01 | 1.00E+00 | 9.65E-01 | 9.34E-01 | 9.58E-01 | 9.68E-01 | 30 | 22 | 60 |
| 09 Membrane & protein trafficking | 1.00E+00 | 1.00E+00 | 4.10E-01 | 8.06E-01 | 9.85E-01 | 8.13E-01 | 3.27E-03 | 9.77E-03 | 9.81E-01 | 9.99E-01 | 122 | 105 | 202 |
| 10 Membrane receptors & channels | 2.20E-01 | 2.20E-01 | 1.03E-01 | 3.73E-02 | 9.53E-01 | 3.55E-01 | 1.00E+00 | 9.93E-01 | 5.88E-01 | 5.65E-01 | 98 | 103 | 202 |
| 11 Mitochondrial proteins | 1.00E+00 | 1.00E+00 | 1.00E+00 | 1.00E+00 | 5.49E-04 | 4.31E-01 | 1.31E-04 | 1.24E-04 | 1.00E+00 | 1.00E+00 | 187 | 170 | 353 |
| 12 Other metabolism | 7.40E-01 | 8.71E-01 | 1.00E+00 | 9.64E-01 | 1.19E-01 | 6.80E-01 | 2.82E-02 | 4.05E-02 | 9.96E-01 | 1.00E+00 | 203 | 186 | 379 |
| 13 Other nuclear proteins | 1.00E+00 | 1.00E+00 | 6.03E-01 | 4.69E-01 | 7.43E-01 | 1.00E+00 | 6.16E-01 | 7.64E-01 | 9.69E-01 | 9.25E-01 | 51 | 45 | 101 |
| 14 Proteasomal proteins | 1.00E+00 | 1.00E+00 | 3.58E-01 | 1.84E-02 | 9.82E-01 | 6.90E-01 | 6.62E-03 | 1.32E-02 | 1.00E+00 | 1.00E+00 | 136 | 134 | 235 |
| 15 Protein kinases & phosphatases | 1.00E+00 | 1.00E+00 | 1.77E-02 | 4.60E-01 | 9.83E-01 | 5.73E-01 | 1.74E-02 | 3.55E-03 | 9.93E-01 | 9.96E-01 | 126 | 112 | 198 |
| 16 Protein processing | 8.98E-01 | 8.98E-01 | 8.16E-01 | 3.14E-02 | 7.78E-02 | 6.20E-01 | 3.47E-01 | 7.43E-01 | 5.71E-01 | 1.00E+00 | 81 | 70 | 139 |
| 17 Secretory proteins | 8.43E-01 | 8.43E-01 | 1.00E+00 | 1.00E+00 | 8.38E-03 | 2.78E-05 | 1.00E+00 | 1.00E+00 | 1.43E-52 | 2.78E-18 | 141 | 155 | 202 |
| 18 Signaling & adapter proteins | 8.09E-02 | 3.67E-02 | 3.70E-02 | 8.74E-01 | 9.90E-01 | 7.47E-01 | 2.53E-01 | 2.28E-02 | 1.00E+00 | 2.53E-81 | 196 | 177 | 334 |
| 19 Small GTPases & regulators | 2.34E-01 | 2.34E-01 | 2.82E-02 | 5.65E-01 | 1.00E+00 | 1.00E+00 | 3.97E-01 | 3.46E-01 | 9.95E-01 | 1.00E+00 | 121 | 102 | 207 |
| 20 Transcription & translation | 9.89E-01 | 9.89E-01 | 2.78E-08 | 3.35E-11 | 9.98E-01 | 1.00E+00 | 9.95E-01 | 9.96E-01 | 9.99E-01 | 9.98E-01 | 156 | 146 | 268 |
| 21 Uncharacterized & other proteins | 9.87E-01 | 9.87E-01 | 2.64E-02 | 4.61E-01 | 8.46E-03 | 5.52E-01 | 1.00E+00 | 1.00E+00 | 1.75E-01 | 9.98E-01 | 148 | 108 | 261 |
| All classes | | | | | | | | | | | 2084 | 1896 | 3626 |

**Suppl. Table 2.** *Restraining factors per function class and prediction model of full platelet proteome.* Analysis of non-identified proteins (*n*=9,721) from the relevant, combined PLT/MGK transcriptome per function class. Indicated in **blue** are fractions transcripts present in the identified proteome, and fractions with low mRNA (arbitrarily set at log2fpkm <1.00). Indicated in **green** (ID) are well-identified classes with fractions >0.55 identified. Indicated in **red** is indication of one or more restraining factors per class: *(i)* over-representation of low copy number (areas II-III in Fig. 4D), *(ii)* low mRNA level (area V, LM = low mRNA >45%); *(iii)* retainment in megakaryocyte (peri)nucleus upon platelet shedding (RET).

| **Protein function class** (n) | **Fraction not identified** | | **Fraction low mRNA** | | **Mostly identified** | **Explanation for low identification** | | |
|---|---|---|---|---|---|---|---|---|
| UniProt-KB: in protein name (n≥10) | (fraction) | | (fraction) | | >55% | **Low copy number** (II, III) | **Low mRNA (>20%,** V) | **Retained in MGK** |
| **C01 Cytoskeleton actin-myosin** (237) | 0.44 | | 0.30 | | ID | | LM, V | |
| Actin (36) | | 0.14 | | 0.40 | | | | |
| Myosin (45) | | 0.44 | | 0.55 | | | | |
| **C02 Cytoskeleton intermediate** (27) | 0.70 | | 0.42 | | NID | | LM, V | |
| Keratin (12) | | 0.58 | | 0.57 | | | | |
| **C03 Cytoskeleton microtubule** (420) | 0.67 | | 0.19 | | NID | | | RET |
| Centromere (16) | | 0.88 | | 0.21 | | | | |
| Centrosomal (36) | | 0.75 | | 0.11 | | | | |
| Dynein (41) | | 0.61 | | 0.40 | | | | |
| Kinesin (38) | | 0.71 | | 0.37 | | | | |
| Mitotic spindle / HAUS (13) | | 0.69 | | 0.22 | | | | |
| Tubulin (74) | | 0.46 | | 0.29 | | | | |
| **C04 Cytoskeleton receptor-linked** (69) | 0.26 | | 0.17 | | ID | | | |
| LIM / Wiskott (10) | | 0.30 | | 0.33 | | | | |
| **C05 Endosome proteins** (101) | 0.49 | | 0.18 | | NID | ? | | |
| Multivesicular body (11) | | 0.18 | | 0.00 | | | | |
| WAS / WASH (11) | | 0.45 | | 0.00 | | | | |
| **C06 ER & Golgi proteins** (568) | 0.67 | | 0.24 | | NID | | LM | |
| AP-1/3 complex subunit (19) | | 0.21 | | 0.25 | | | | |
| ER membrane / lumen protein (34) | | 0.41 | | 0.36 | | | | |
| Golgi (59) | | 0.47 | | 0.57 | | | | |
| Trafficking protein particle (16) | | 0.25 | | 0.00 | | | | |
| Transferase (95) | | 0.96 | | 0.45 | | | | |
| **C07 Glucose metabolism** (58) | 0.21 | | 0.25 | | ID | | LM | |
| Glucose (18) | | 0.33 | | 0.17 | | | | |
| Fructose (11) | | 0.35 | | 0.25 | | | | |
| **C08 Lysosome & peroxisome proteins** (168) | 0.56 | | 0.13 | | NID | | LM | |
| Lysosome /lysosomal (21) | | 0.52 | | 0.09 | | | | |
| Peroxisome / peroxisomal (37) | | 0.54 | | 0.30 | | | | |
| V-type proton ATPase (17) | | 0.29 | | 0.40 | | | | |
| **C09 Membrane & protein trafficking** (349) | 0.30 | | 0.31 | | ID | | LM | |
| Exocyst complex (10) | | 0.10 | | 1.00 | | | | |
| Protein transport (11) | | 0.09 | | 0.00 | | | | |
| Sorting nexin (27) | | 0.37 | | 0.40 | | | | |
| Synapto (19) | | 0.74 | | 0.57 | | | | |
| Syntaxin (20) | | 0.20 | | 0.00 | | | | |
| Vacuolar protein sorting-associated (26) | | - | | - | | | | |

| Protein function class (n) | Fraction not identified | | Fraction low mRNA | | Mostly identified | Explanation for low identification | | |
|---|---|---|---|---|---|---|---|---|
| UniProt-KB: in protein name (n≥10) | (fraction) | | (fraction) | | >55% | Low copy number (II, III) | Low mRNA (>20%, V) | Retained in MGK |
| **C10 Membrane receptors & channels** (1430) | 0.78 | | 0.39 | | NID | | LM | |
| Calcium / Cal (42) | | 0.79 | | 0.55 | | | | |
| Chemokine/Interleukin receptor (18) | | 0.83 | | 0.60 | | | | |
| C-type lectin domain family (19) | | 0.95 | | 0.56 | | | | |
| Glycoprotein (32) | | 0.75 | | 0.38 | | | | |
| G-protein coupled (45) | | 0.98 | | 0.68 | | | | |
| Integrin (30) | | 0.57 | | 0.59 | | | | |
| Olfactory receptor (28) | | 1.00 | | 0.86 | | | | |
| Purinoceptor (14) | | 0.79 | | 0.36 | | | | |
| Solute carrier family / SLC (146) | | 0.64 | | 0.46 | | | | |
| Voltage-dependent/gated (38) | | 0.84 | | 0.63 | | | | |
| **C11 Mitochondrial proteins** (814) | 0.44 | | 0.10 | | ID | III | | |
| ATP synthase (23) | | 0.26 | | 0.17 | | | | |
| Cytochrome b/c (49) | | 0.37 | | 0.22 | | | | |
| Import (27) | | 0.22 | | 0.00 | | | | |
| NADH dehydrogenase (39) | | 0.18 | | 0.29 | | | | |
| Ribosomal protein (84) | | 0.44 | | 0.00 | | | | |
| tRNA (31) | | 0.39 | | 0.08 | | | | |
| **C12 Other metabolism** (877) | 0.47 | | 0.22 | | NID | | LM | |
| (Metabolite) kinase (69) | | 0.36 | | 0.40 | | | | |
| (Metabolite) phosphatase (53) | | 0.43 | | 0.35 | | | | |
| (Metabolite) reductase (49) | | 0.37 | | 0.44 | | | | |
| (Metabolite) synthase (57) | | 0.49 | | 0.29 | | | | |
| (Metabolite) transferase (162) | | 0.53 | | 0.43 | | | | |
| **C13 Other nuclear proteins** (1469) | 0.86 | | 0.07 | | NID | | | RET |
| Chromatin (17) | | 0.76 | | 0.08 | | | | |
| Histone (150) | | 0.89 | | 0.10 | | | | |
| Nuclear pore complex (34) | | 0.82 | | 0.32 | | | | |
| Polymerase (28) | | 0.86 | | 0.00 | | | | |
| Repair protein (29) | | 0.86 | | 0.12 | | | | |
| **C14 Proteasomal proteins** (677) | 0.54 | | 0.11 | | NID | II | | |
| COP9 signalosome (10) | | 0.10 | | 0.00 | | | | |
| E3 ubiquitin-protein ligase (180) | | 0.69 | | 0.17 | | | | |
| Kelch-like (20) | | 1.00 | | 0.30 | | | | |
| NEDD (15) | | 0.20 | | 0.33 | | | | |
| Proteasome/ proteasomal (45) | | 0.18 | | 0.13 | | | | |
| Ubiquitin-conjugating (32) | | 0.53 | | 0.12 | | | | |
| **C15 Protein kinases & phosphatases** (481) | 0.45 | | 0.20 | | NID | II | LM | |
| Mitogen-activated protein kinase (41) | | 0.44 | | 0.33 | | | | |
| Serine/threonine-protein kinase (144) | | 0.42 | | 0.34 | | | | |
| Serine/threonine-protein phosphatase (40) | | 0.38 | | 0.27 | | | | |
| Tyrosine (-protein) phosphatase (29) | | 0.45 | | 0.54 | | | | |
| Tyrosine-protein kinase (29) | | 0.34 | | 0.30 | | | | |

| Protein function class (n) | Fraction not identified | Fraction low mRNA | Mostly identified | Explanation for low identification | | |
|---|---|---|---|---|---|---|
| UniProt-KB: in protein name (n≥10) | (fraction) | (fraction) | >55% | Low copy number (II, III) | Low mRNA (>20%, V) | Retained in MGK |
| **C16 Protein processing** (308) | 0.35 | 0.13 | ID | | | |
| Dol / dolichol (16) | 0.00 | - | | | | |
| Glucosyl / glycosyltransferase (17) | 0.18 | 0.00 | | | | |
| Methyltransferase (13) | 0.62 | 0.00 | | | | |
| Palmitoyl / sialyl (20) | 0.95 | 0.26 | | | | |
| Pept/ peptidyl (50) | 0.26 | 0.31 | | | | |
| **C17 Secretory proteins** (811) | 0.72 | 0.47 | NID | III | LM, V | |
| Collagen (33) | 0.73 | 0.71 | | | | |
| Growth factor (36) | 0.61 | 0.64 | | | | |
| Interleukin / chemokine (41) | 0.83 | 0.53 | | | | |
| Metalloproteinase (28) | 0.82 | 0.61 | | | | |
| Protease (21) | 0.81 | 0.59 | | | | |
| **C18 Signaling & adapter proteins** (1024) | 0.55 | 0.26 | NID | II | LM | |
| 14-3-3 / S100 protein (15) | 0.27 | 0.50 | | | | |
| Adapter / adaptor protein (35) | 0.63 | 0.41 | | | | |
| Bcl / Bax (18) | 0.50 | 0.44 | | | | |
| Calcium / calpain (38) | 0.61 | 0.52 | | | | |
| cAMP / A-kinase (34) | 0.76 | 0.46 | | | | |
| Caspase (19) | 0.42 | 0.13 | | | | |
| cGMP / G kinase (17) | 0.59 | 0.30 | | | | |
| Guanine nucleotide / G-protein (43) | 0.42 | 0.67 | | | | |
| Phosphatidyl /phosphoinositide (66) | 0.38 | 0.20 | | | | |
| **C19 Small GTPases & regulators** (483) | 0.41 | 0.20 | ID | II | LM | |
| Arf-GAP (18) | 0.61 | 0.27 | | | | |
| Rab (78) | 0.19 | 0.27 | | | | |
| Ral (12) | 0.33 | 0.50 | | | | |
| Rap (17) | 0.47 | 0.13 | | | | |
| Ras *(non RAb, Ral, Rap)* (20) | 0.70 | 0.50 | | | | |
| Rho (88) | 0.57 | 0.44 | | | | |
| **C20 Transcription & translation** (2280) | 0.79 | 0.09 | NID | II | | RET |
| Nuclear (127) | 0.67 | 0.04 | | | | |
| Ribosomal protein (96) | 0.65 | 0.03 | | | | |
| Transcription (303) | 0.87 | 0.82 | | | | |
| Translation (56) | 0.21 | 0.08 | | | | |
| tRNA (71) | 0.56 | 0.23 | | | | |
| Zinc finger (579) | 0.98 | 0.28 | | | | |
| **C21 Uncharacterized & other proteins** (2120) | 0.79 | 0.23 | NID | III | LM | |
| Coiled-coil (91) | 0.84 | 0.28 | | | | |
| FAM (255) | 0.77 | 0.40 | | | | |
| Leucine-rich repeat (36) | 0.83 | 0.60 | | | | |
| Putative (90) | 0.89 | 0.39 | | | | |
| Transmembrane (133) | 0.70 | 0.40 | | | | |
| Uncharacterized (249) | 0.92 | 0.48 | | | | |