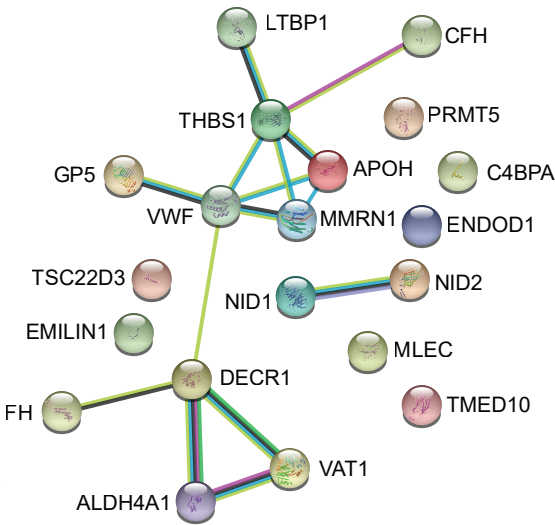


Total
DE proteins



Biological Process

| #pathway ID | pathway description | Gene Nr. | FDR |
|-------------|--|----------|----------|
| GO.0072376 | protein activation cascade | 5 | 5.70E-05 |
| GO.0007597 | blood coagulation, intrinsic pathway | 3 | 0.00229 |
| GO.0030198 | extracellular matrix organization | 6 | 0.00229 |
| GO.0072378 | blood coagulation, fibrin clot formation | 3 | 0.005 |
| GO.0031589 | cell-substrate adhesion | 4 | 0.0275 |
| GO.1903034 | regulation of response to wounding | 5 | 0.0357 |

Molecular Function

| #pathway ID | pathway description | Gene Nr. | FDR |
|-------------|----------------------|----------|----------|
| GO.0001948 | glycoprotein binding | 5 | 1.57E-05 |
| GO.0005518 | collagen binding | 4 | 0.000165 |
| GO.0043394 | proteoglycan binding | 3 | 0.000609 |

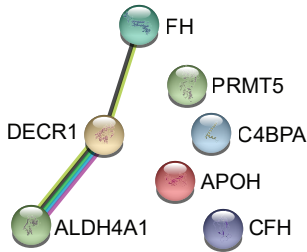
Cellular Component

| #pathway ID | pathway description | Gene Nr. | FDR |
|-------------|------------------------------------|----------|----------|
| GO.0005576 | extracellular region | 15 | 0.000177 |
| GO.0044421 | extracellular region part | 14 | 0.000177 |
| GO.0031012 | extracellular matrix | 6 | 0.000206 |
| GO.0031988 | membrane-bounded vesicle | 13 | 0.000206 |
| GO.0070062 | extracellular exosome | 12 | 0.000206 |
| GO.0005578 | proteinaceous extracellular matrix | 5 | 0.00199 |
| GO.0031093 | platelet alpha granule lumen | 3 | 0.002 |
| GO.0031091 | platelet alpha granule | 3 | 0.0036 |
| GO.0030141 | secretory granule | 4 | 0.0162 |
| GO.0044420 | extracellular matrix component | 3 | 0.0182 |

KEGG

| #pathway ID | pathway description | Gene Nr. | FDR |
|-------------|-------------------------------------|----------|--------|
| 4512 | ECM-receptor interaction | 3 | 0.0108 |
| 4610 | Complement and coagulation cascades | 3 | 0.0108 |

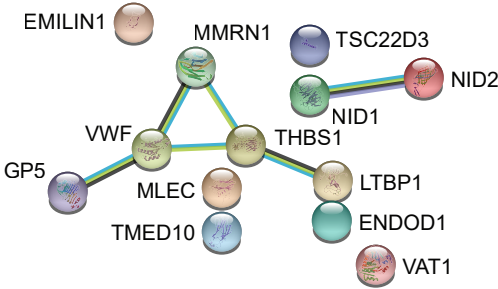
Upregulated
DE proteins



Biological Process

| #pathway ID | pathway description | Gene Nr. | FDR |
|-------------|----------------------------|----------|--------|
| GO.0072376 | protein activation cascade | 3 | 0.0146 |

Downregulated
DE proteins



Biological Process

| #pathway ID | pathway description | Gene Nr. | FDR |
|-------------|-----------------------------------|----------|----------|
| GO.0030198 | extracellular matrix organization | 6 | 0.000224 |
| GO.0031589 | cell-substrate adhesion | 4 | 0.00844 |
| GO.0030168 | platelet activation | 4 | 0.0336 |
| GO.0002576 | platelet degranulation | 3 | 0.0403 |
| GO.0006887 | exocytosis | 4 | 0.0403 |
| GO.0071711 | basement membrane organization | 2 | 0.0403 |

Molecular Function

| #pathway ID | pathway description | Gene Nr. | FDR |
|-------------|---|----------|----------|
| GO.0005518 | collagen binding | 4 | 4.91E-05 |
| GO.0001948 | glycoprotein binding | 3 | 0.0168 |
| GO.0043236 | laminin binding | 2 | 0.0415 |
| GO.0043394 | proteoglycan binding | 2 | 0.0415 |
| GO.0050431 | transforming growth factor beta binding | 2 | 0.0415 |

Cellular Component

| #pathway ID | pathway description | Gene Nr. | FDR |
|-------------|------------------------------------|----------|----------|
| GO.0031012 | extracellular matrix | 6 | 6.52E-05 |
| GO.0005578 | proteinaceous extracellular matrix | 5 | 0.000903 |
| GO.0031093 | platelet alpha granule lumen | 3 | 0.00186 |
| GO.0031091 | platelet alpha granule | 3 | 0.00255 |
| GO.0005576 | extracellular region | 10 | 0.00379 |
| GO.0030141 | secretory granule | 4 | 0.00413 |
| GO.0031988 | membrane-bounded vesicle | 9 | 0.00413 |
| GO.0044420 | extracellular matrix component | 3 | 0.00521 |
| GO.0044421 | extracellular region part | 9 | 0.00521 |
| GO.0070062 | extracellular exosome | 8 | 0.00521 |
| GO.0044433 | cytoplasmic vesicle part | 4 | 0.0195 |

KEGG

| #pathway ID | pathway description | Gene Nr. | FDR |
|-------------|--------------------------|----------|---------|
| 4512 | ECM-receptor interaction | 3 | 0.00551 |

Fig. S1

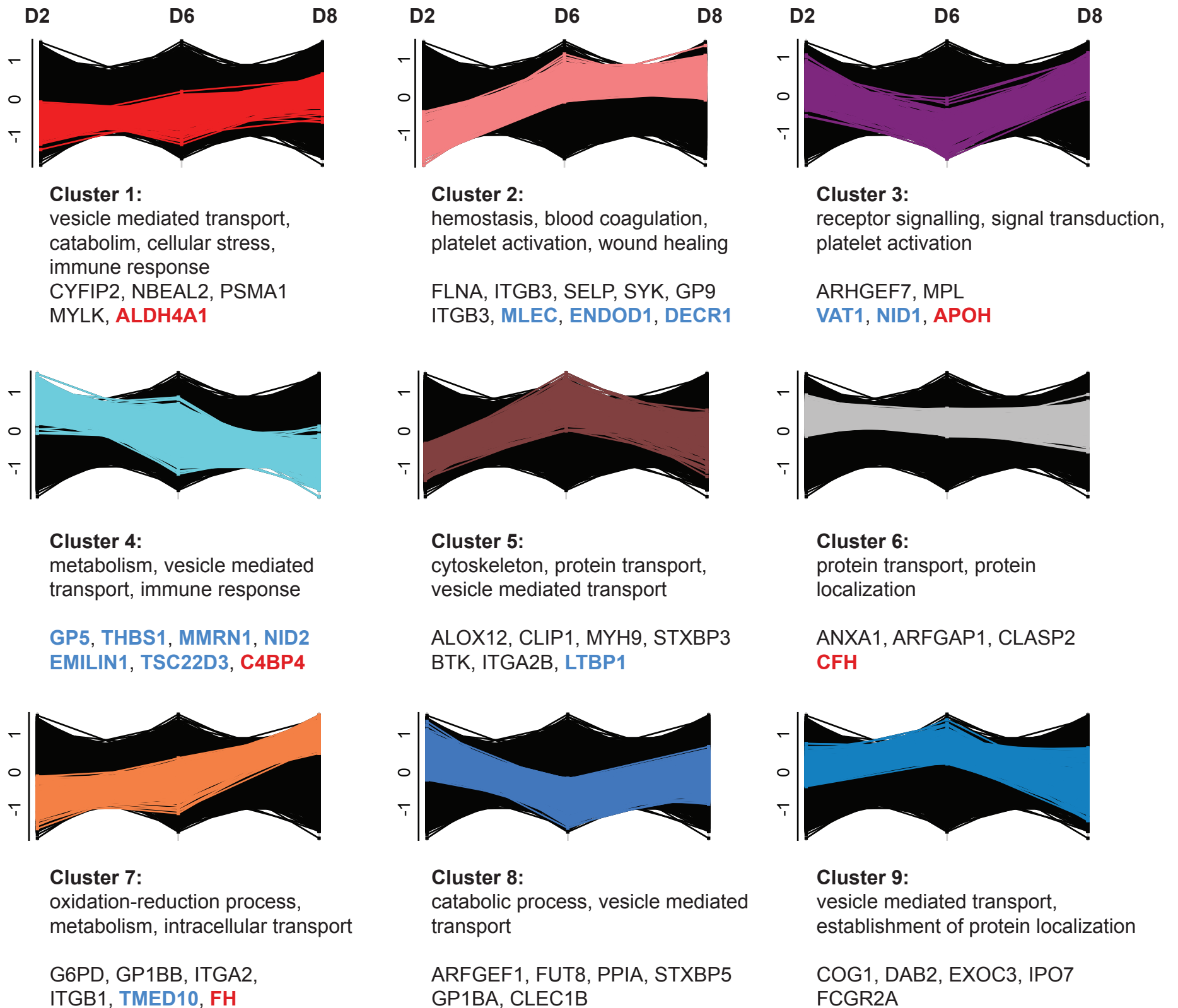


Fig. S2

SUPPORTING FILES LEGENDS

Figure S1: STRING analysis of differentially expressed (DE) proteins after Multiple Sample Test Analysis of Mirasol PRT vs Control PCs. Protein-protein functional interactions and GO-Term enrichment are depicted for the total of DE proteins, and separately for down- and upregulated DE proteins (Table S4).

Figure S2. Dynamics of platelet protein changes through storage. Dynamics of protein changes were analyzed by K-means using Perseus software. Time-course kinetics of significant proteins in 9 different clusters is shown. On the X-axis, time points indicate Day 2, Day 6 and Day 8 of platelet storage while on the Y-axis, the respective expression values of proteins in the cluster are depicted. The black lines represent the average expression of all proteins while coloured lines are the expression (LFQ intensity value) of the clustered proteins. Below, relevant enriched Biological Process GO-Terms are shown. Proteins DE in Mirasol vs Control PCs are also indicated (blue, downregulated and red, upregulated). Other proteins of interest within the cluster are indicated.

Table S1: Proteomic Analysis of Control vs Mirasol PC Lysates through Storage. Indicated are the Average Log2 LFQ of Control and Mirasol PCs samples at Days 2, 6 and 8 of Storage, Log2 LFQ fold ratios Mirasol vs Control at different Days, FDR (t test), Multiple Sample test ANOVA significant entries and corresponding FDR, and the individual Log2 LFQ values of individual Control and Mirasol Samples. LFQ = Label Free Quantification; FDR = false discovery rate; C = Control; M = Mirasol, D = Day.

Table S2: Gene Ontology (GO) Term (GO-Term) enrichment analysis of significantly differentially expressed (DE) proteins identified after Multiple Sample test comparing Control and Mirasol PRT PCs through storage. From the 20 significant DE proteins,

STRING-based GO-Term enrichment analysis was performed on the total, down-and upregulated datasets. All identified Terms are depicted, including Biological Process, Biological Function, Cellular component and KEGG pathway.

Table S3: Proteomic Analysis of Fresh Platelets and Control PC Lysates through Storage. Indicated are the Average Log2 LFQ of Fresh Platelets and Control PCs samples at Days 1, 2, 6 and 8 of Storage, Log2 LFQ fold ratios Control at different Days vs Fresh or Day 1 Platelets, FDR (T test), Multiple Sample test ANOVA FDR, and the individual Log2 LFQ values of Fresh Platelets and Control PC Samples. LFQ = Label Free Quantification; FDR = false discovery rate; C = Control; D = Day; D0 = Fresh Platelets.

Table S4: K-means cluster analysis of Control PCs through storage. First datasheet contains a table indicating the proteins enlisted on each identified cluster (See Fig. S2). Second datasheet contains significant Biological Processes (maximum 15) after STRING-based GO-Term enrichment performed separately with the protein list from each cluster.