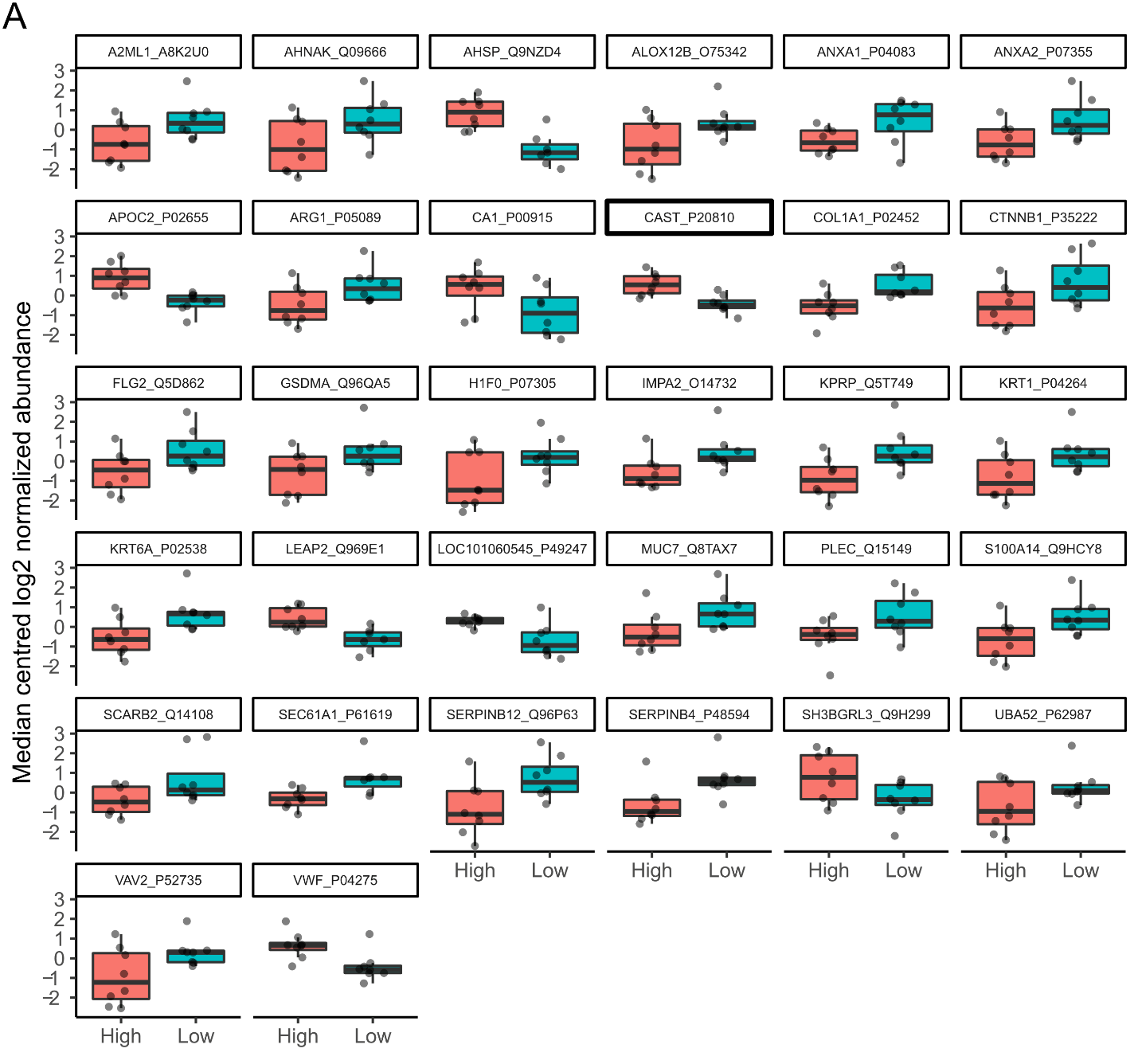
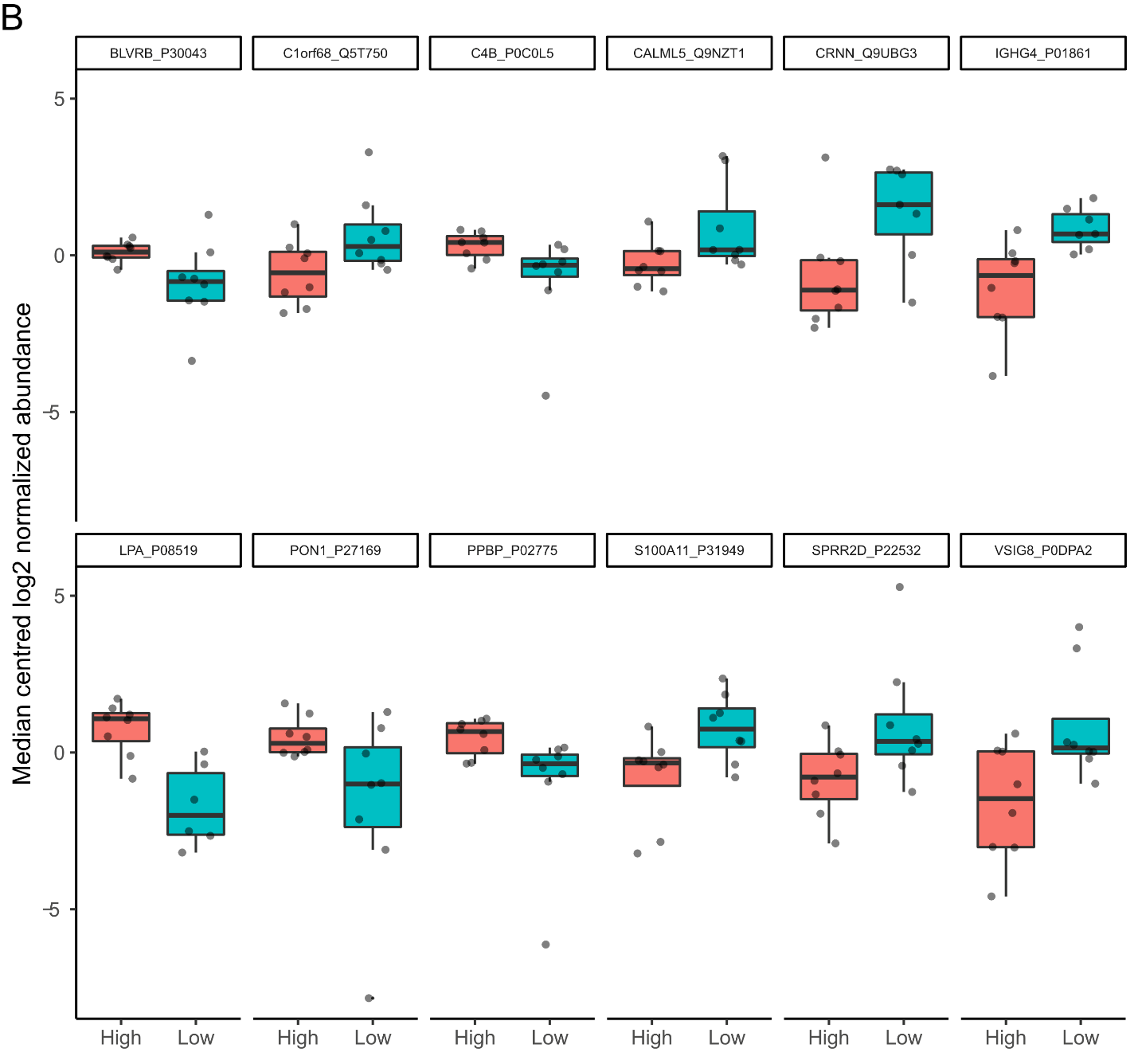
**The proteome signature of cord blood plasma with high hematopoietic stem and progenitor cell count**

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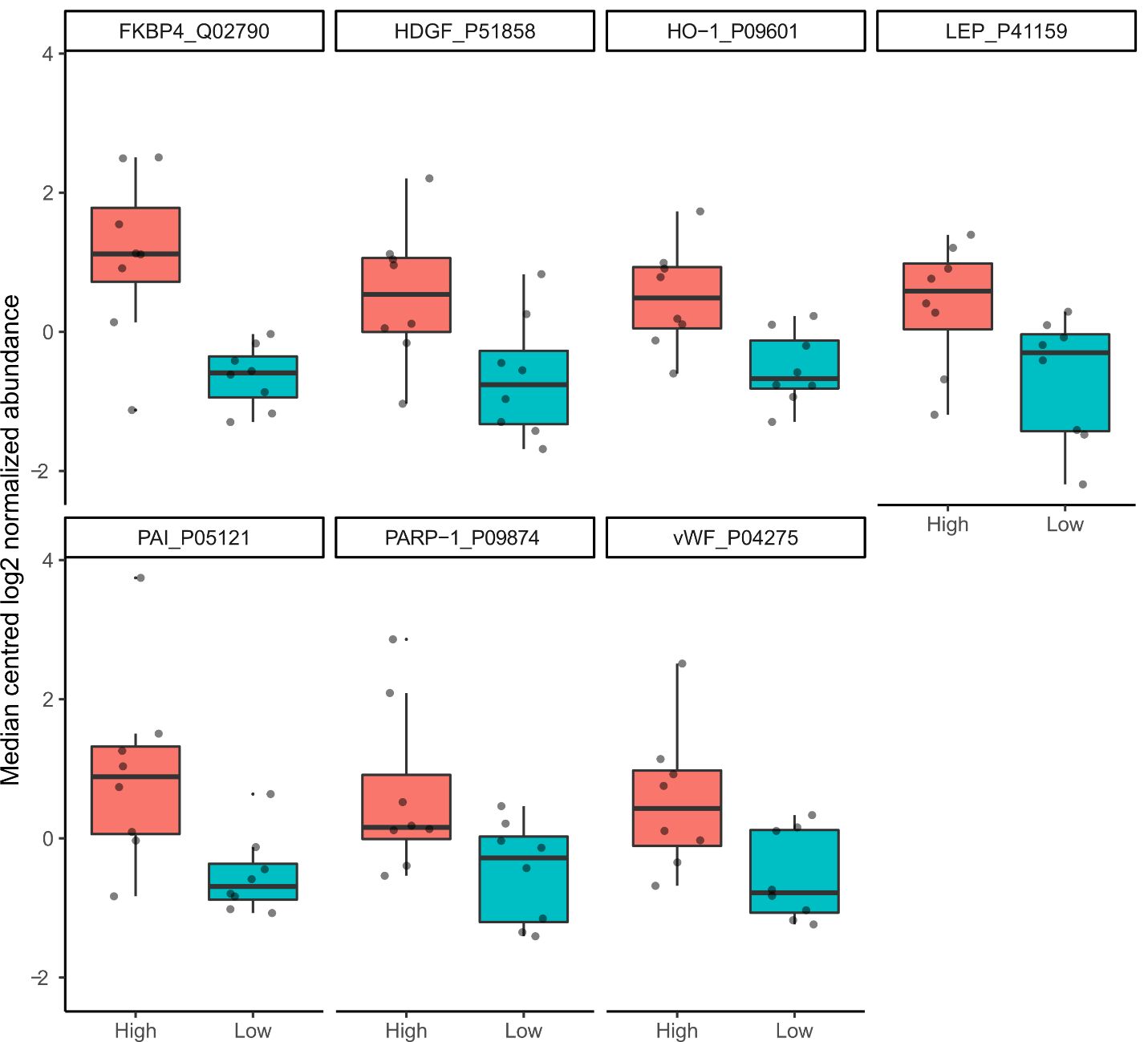
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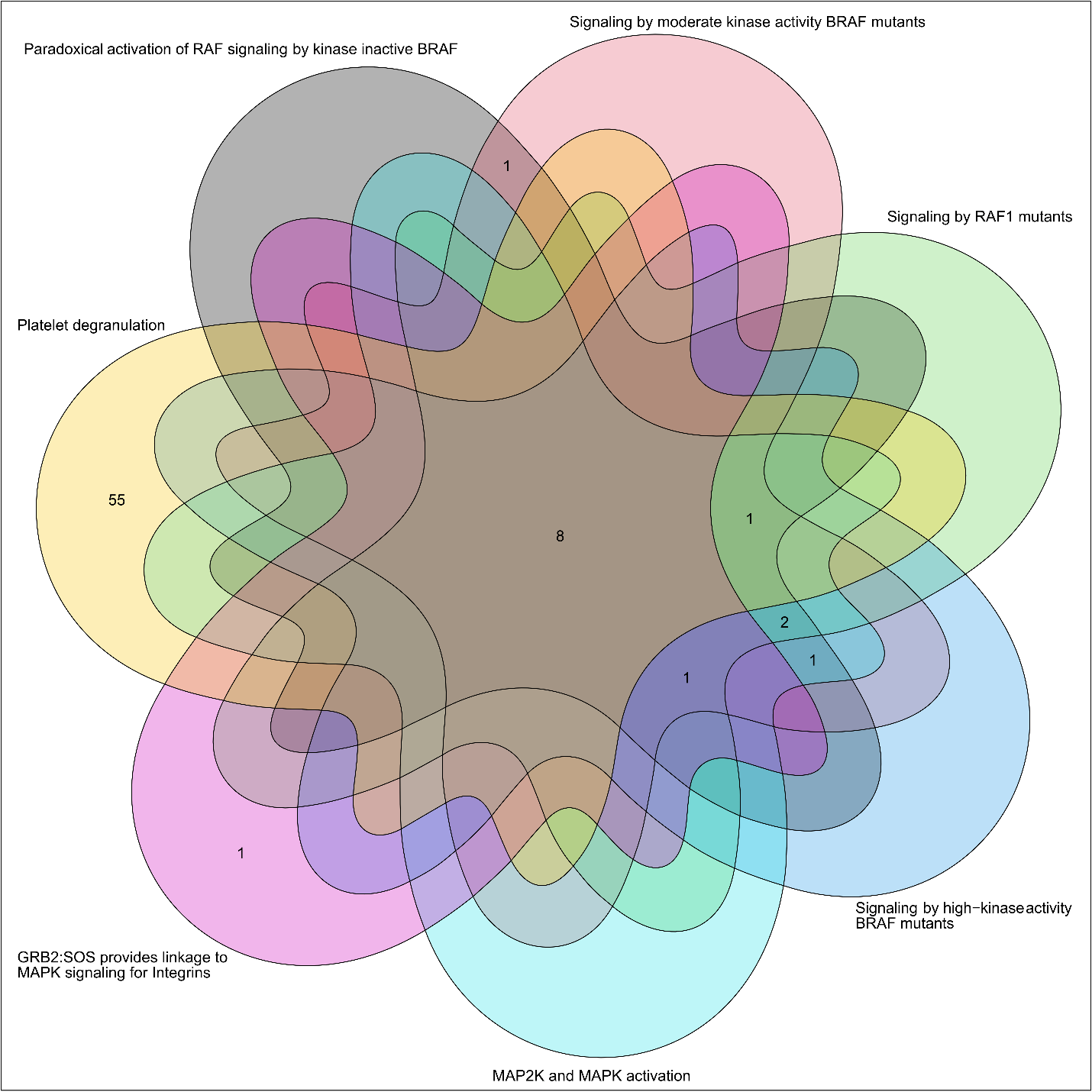
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**Figure S1.** Box plots of proteins in the MS data with >two-fold abundance differences and p<0.05 between CD34+ high (red boxes) vs CD34+ low (blue boxes). **A** Proteins with narrow data distribution. **B** Proteins with wide data distribution. Raw and adjusted p-values as well as fold differences can be found in Table S2.

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**Figure S2.** Box plots of proteins in the PEA data with >two-fold abundance differences and p<0.05 between CD34+ high (red boxes) vs CD34+ low (blue boxes). Raw and adjusted p-values as well as fold differences can be found in Table S3.

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**Figure S3.** Venn diagram showing the number of shared proteins in Reactome pathways. Sub-pathways of the four branches “Oncogenic map signaling”, “Integrin signaling”, “Platelet degranulation”, and “MAP2K and MAPK activation” share 8 or more proteins. The only branch where these proteins are matching together with many other proteins is in “platelet degranulation”.

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Automatiskt genererad beskrivning**

**Figure S4.** Reactome hierarchical tree for the 18 significantly enriched sub-pathways for the MS data together with “parent” pathways. Sub-pathways within each of the 7 branches share many proteins. The leading number for each significant pathway indicates the rank when ordered by p-value. The trailing numbers within parenthesis indicate the number of proteins from the MS data sets matching with the pathway and the total number of proteins within the pathway.