Peer victimization in adolescence alters gene expression and cytokine profiles (Heumann et al. 2024)

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- ▶ *Can we see molecular effects of PV? Differentially expressed (DE) genes? Altered cytokine levels?*

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- 32.5 mL peripheral blood: mRNA, genotyping DNA, plasma cytokine data

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A
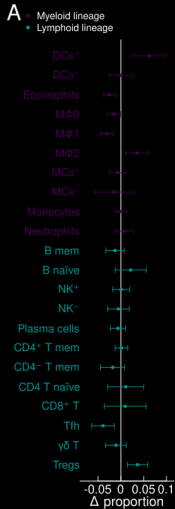
Fig. 1: A Leukocytes
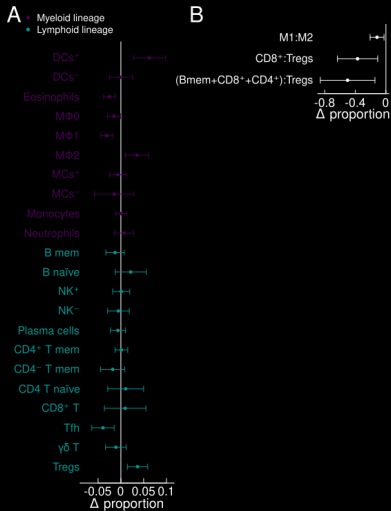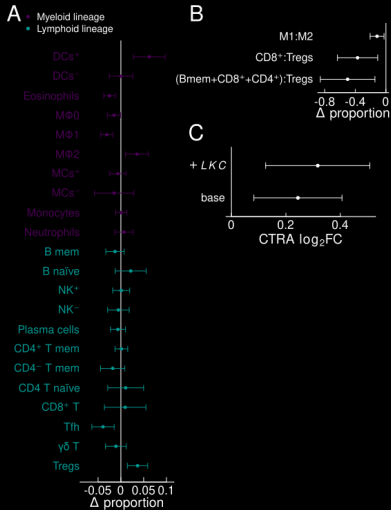
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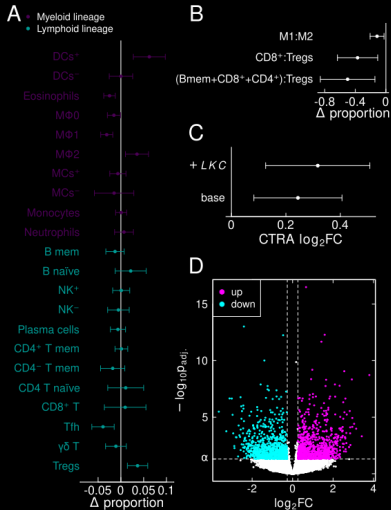**Fig. 1: A-B** Leukocytes

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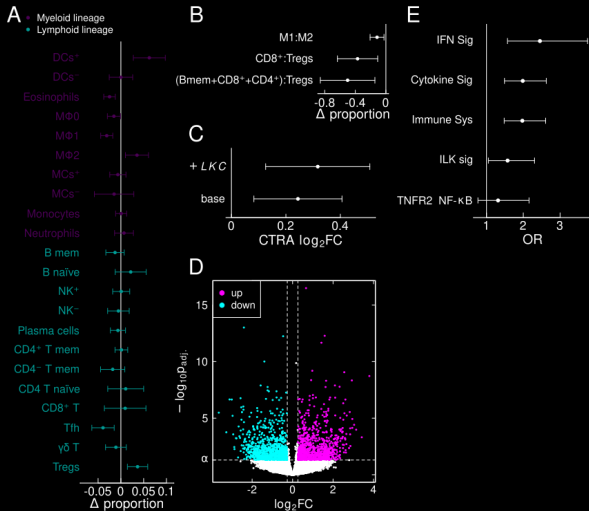**Fig. 1: A-B** Leukocytes, **C** CTRA, **D** DE genes

Fig. 1: A-B Leukocytes, **C** CTRA, **D-E** DE genes/Reactome
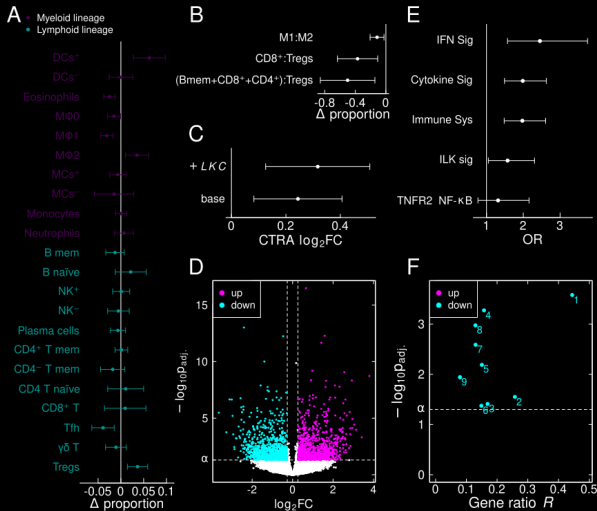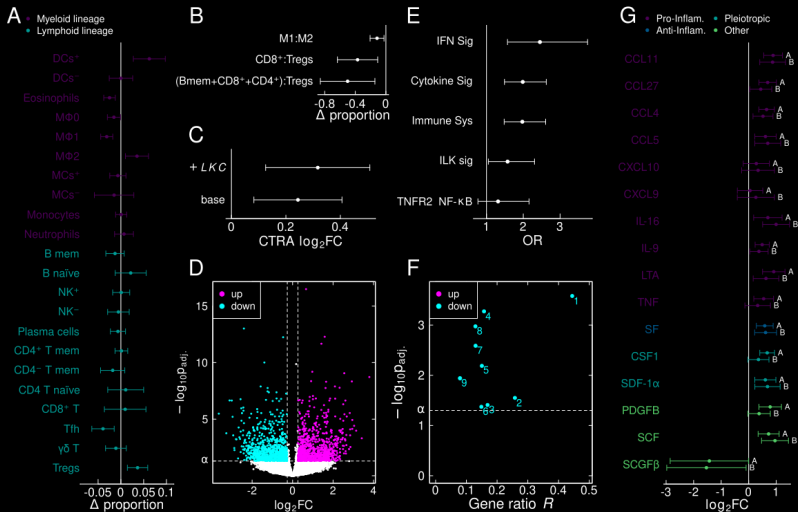
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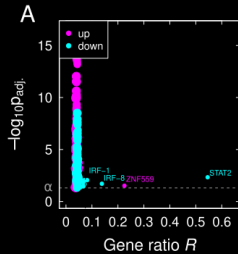
IV.2 Results
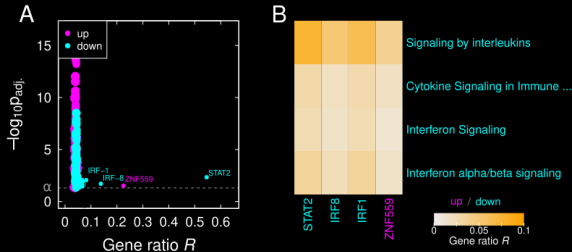
IV.2 Results

Fig. 2: **A** TFs
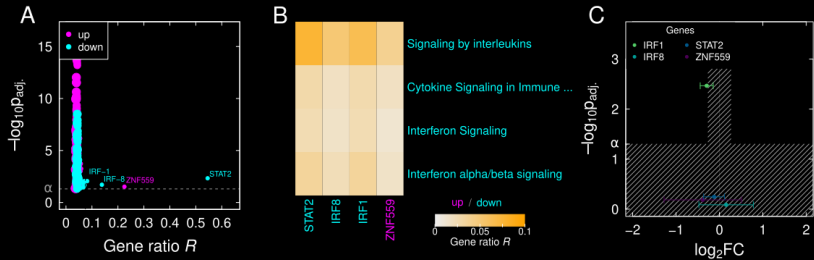
Fig. 2: **A** TFs, **B** TF target genes

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- ▶ Downregulated key **TF**
  - ■ Underlying regulatory activity persisting independently of DE genes (possibly miRNA activity, protein-protein interactions, post-transcriptional modification)

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- Early vs. late victimization, or chronic vs. acute victimization $\rightsquigarrow$ larger sample sizes needed

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- ► potentially altering the immune profile in young adulthood
- ► results underscore the importance of health policies
- ► aimed at preventing peer victimization, building resilience, and mitigating its long-term effects

Thank you!

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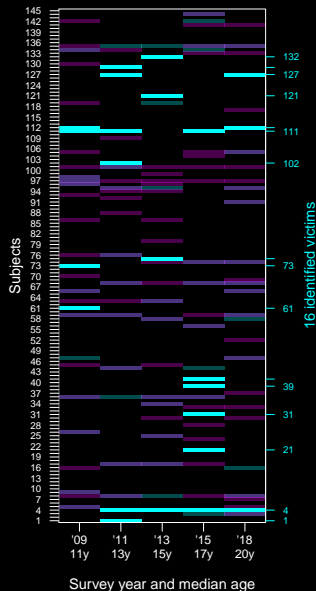www.jacobscenter.uzh.ch
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Appendix

Subordinate ■ Dominant □ Unaffected

Fig. S1: Peer victimization.

Prevalence of social peer adversity. The figure shows subordinate experiences and dominant behavior above 90% quantiles for each survey year. As the highest deciles, subjects above these thresholds are considered to be severely affected from the respective phenomenon. 16 individuals (7 male and 9 female) subjected to only subordinate experiences are identified as peer-victimized at the time of our study at around age 22.

Appendix

Fig. S2: Balancing after IPW. The lollipop plot shows absolute standardized differences between treated (PV) and control after IPW.
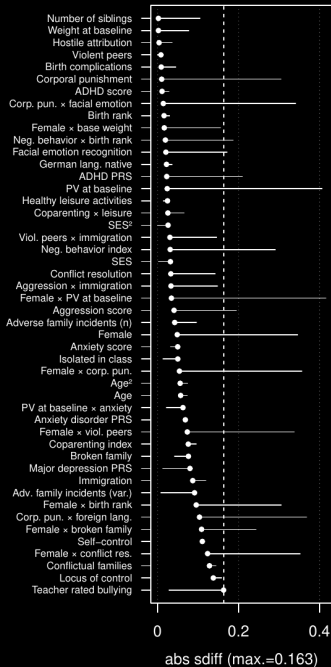
Appendix

Fig. S3: Hierarchy of queried Reactome pathways. The figure displays the hierarchical organization of pathways from the Reactome query with overrepresentation with downregulated genes (the query did not show any upregulation), as also visualized in the Reactome pathway browser. Node sizes represent relative term sizes, colors the gene ratio R. A=Immune system, a1=Cytokine Signaling in Immune system, a11=Signaling by Interleukins, a12=TNFR2 non-canonical NF-×B pathway, a13=Interferon signaling, a131=Interferon alpha/beta signaling, B=Metabolism, b1=The citric acid (TCA) cycle and respiratory electron transport, b3=Formation of ATP by chemiosmotic coupling, C=Metabolism of proteins, c1=Translation, c11=SRP-dependent cotranslational protein targeting to membrane, c12=Eukaryotic Translation Termination, D=Organelle biogenesis and maintenance, b1=Mitochondrial biogenesis, b2=Cristae formation. The Gene ratio indicates the proportion of DE genes within a specific pathway that are present in the query set.