Hematopoiesis after anti-CD117 monoclonal antibody treatment in the settings of wild-type and Fanconi anemia mice

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Received: Accepted: Early view: October 5, 2023. March 26, 2024. April 4, 2024.

https://doi.org/10.3324/haematol.2023.284275

©2024 Ferrata Storti Foundation Published under a CC BY-NC license 🖭 🔅 Supplementary Table 1: Untreated group compared with treated group genes upregulated or downregulated for each cluster. (See Excel file)



Supplementary Figure 1: FACS plot representative of the gating strategy used following micronuclei assay staining.



Supplementary Figure 2: FACS plot representative of the gating strategy following staining.



Supplementary Figure 3: Bubble plot showing all the cell types that were considered as the most probable by ScType for cluster annotation.



-10 -5 0 5 10 -10 -5 ò 5 10 -10 -5 ò 5 10 -10 -5 5 10 -10 UMAP_1 10 -10 -5 10 -10 -5 ò 5

Supplementary Figure 4: Integrated analysis for each group and identification of sub-clusters of distinct cell types. (A) UMAP of concatenate sample. The UMAP embedding and Leiden clustering were performed on the integrated gene expression, Cells are labeled based on their cluster identity. (B) Dot plot showing the average expression of selected marker genes for each cluster. The size of dots represents the fraction of cells expressing a given gene (>0 expression value) and the color intensity reflects the average expression level within each cluster. (C) Heatmap of cluster signature genes highlighted on left. Expression of the 10 top differentially expressed genes across the cells. (D) UMAP split by samples representing the distribution of cells by cluster.



Supplementary Figure 5: Heatmap of the top 100 differential pathways by Reactome gene set analysis.



Supplementary Figure 6: Single-Cell RNA Sequencing reveals antagonistic anti-CD117 mAb effects on MAPK pathway. (A-D) Pathway enrichment is expressed as the –log[p.value] adjusted for multiple comparisons and WikiPathways_2019_Mouse data base was used²⁶. (A) Up and down regulated pathways in 1-week WT ACK2 groups compare with untreated groups. (D) Up and down regulated pathways in 1-week FANCD2-/- ACK2 groups compare with untreated groups. (C) Up and down regulated pathways in 24-weeks WT ACK2 groups compare with untreated groups. (D) Up and down regulated pathways in 24-weeks FANCD2-/- ACK2 groups compare with untreated groups. (D) Up and down regulated pathways in 24-weeks FANCD2-/- ACK2 groups compare with untreated groups. (E) Dot plot showing the average expression of selected marker genes for each group. The size of dots represents the fraction of cells expressing a given gene (>0 expression value) and the color intensity reflects the average expression level within each cluster. (F) Downregulation of MAPK pathways after c-Kit mAb inhibition.



Supplementary Figure 7: Differential gene expressions for each subgroup in untreated versus ACK2 treated for cluster 0 – Monocytes. (A) Venn diagram. (B) Genes in common that were upor down-regulated across groups. (C) Volcano plot for each comparison. p-value < 0.05 and an average log2 fold change (avg log2FC) < \pm 0.5.



Supplementary Figure 8: Differential gene expressions for each subgroup in untreated versus ACK2 treated for cluster 1 – Neutrophils. (A) Venn diagram. (B) Genes in common that were upor down-regulated across groups. (C) Volcano plot for each comparison. p-value < 0.05 and an average log2 fold change (avg_log2FC) < ± 0.5 .



Supplementary Figure 9: Differential gene expressions for each subgroup in untreated versus ACK2 treated for cluster 2 – B cell progenitor (A) Venn diagram. (B) Genes in common that were up- or down-regulated across groups. (C) Volcano plot for each comparison. p-value < 0.05 and an average log2 fold change (avg_log2FC) < ± 0.5 .



Supplementary Figure 10: Differential gene expressions for each subgroup in untreated versus ACK2 treated for cluster 3 – Monocyte/Neutrophil progenitor (A) Venn diagram. (B) Genes in common that were up- or down-regulated across groups. (C) Volcano plot for each comparison. p-value < 0.05 and an average log2 fold change (avg_log2FC) < ± 0.5 .



Supplementary Figure 11: Differential gene expressions for each subgroup in untreated versus ACK2 treated for cluster 4 – Myeloid progenitor 1 (A) Venn diagram. (B) Genes in common that were up- or down-regulated across groups. (C) Volcano plot for each comparison. p-value < 0.05 and an average log2 fold change (avg_log2FC) < ± 0.5 .



Supplementary Figure 12: Differential gene expressions for each subgroup in untreated versus ACK2 treated for cluster 5 – Myeloid progenitor 2 (A) Venn diagram. (B) Genes in common that were up- or down-regulated across groups. (C) Volcano plot for each comparison. p-value < 0.05 and an average log2 fold change (avg_log2FC) < ± 0.5 .



Hbb-bs Hba-a1

2mss1 6m42418

.cn2 Gm26917 Ngp fitm6

Supplementary Figure 13: Differential gene expressions for each subgroup in untreated versus ACK2 treated for cluster 6 – Myeloid progenitor 3 (A) Venn diagram. (B) Genes in common that were up- or down-regulated across groups. (C) Volcano plot for each comparison. p-value < 0.05 and an average log2 fold change (avg_log2FC) < ± 0.5 .



Supplementary Figure 14: Differential gene expressions for each subgroup in untreated versus ACK2 treated for cluster 7 – Macrophages (A) Venn diagram. (B) Genes in common that were upor down-regulated across groups. (C) Volcano plot for each comparison. p-value < 0.05 and an average log2 fold change (avg_log2FC) < \pm 0.5.



Supplementary Figure 15: Differential gene expressions for each subgroup in untreated versus ACK2 treated for cluster 8 – Immature B-cell (A) Venn diagram. (B) Genes in common that were up- or down-regulated across groups. (C) Volcano plot for each comparison. p-value < 0.05 and an average log2 fold change (avg_log2FC) < ± 0.5 .



Supplementary Figure 16: Differential gene expressions for each subgroup in untreated versus ACK2 treated for cluster 9 – CLP (A) Venn diagram. (B) Genes in common that were up- or down-regulated across groups. (C) Volcano plot for each comparison. p-value < 0.05 and an average log2 fold change (avg log2FC) < \pm 0.5.



Total

2

mss1 m42418

n2

Camp Igp 100a8 100a9 yz2

Supplementary Figure 17: Differential gene expressions for each subgroup in untreated versus ACK2 treated for cluster 10 – Dendritic cell (A) Venn diagram. (B) Genes in common that were up- or down-regulated across groups. (C) Volcano plot for each comparison. p-value < 0.05 and an average log2 fold change (avg_log2FC) < ± 0.5 .



Supplementary Figure 18: Differential gene expressions for each subgroup in untreated versus ACK2 treated for cluster 11 – Erythroblast (A) Venn diagram. (B) Genes in common that were up- or down-regulated across groups. (C) Volcano plot for each comparison. p-value < 0.05 and an average log2 fold change (avg_log2FC) < ± 0.5 .



Supplementary Figure 19: Differential gene expressions for each subgroup in untreated versus ACK2 treated for cluster 12 – B cells (A) Venn diagram. (B) Genes in common that were up- or down-regulated across groups. (C) Volcano plot for each comparison. p-value < 0.05 and an average log2 fold change (avg_log2FC) < ± 0.5 .



Supplementary Figure 20: Differential gene expressions for each subgroup in untreated versus ACK2 treated for cluster 13 – Plasma cells (A) Venn diagram. (B) Genes in common that were up- or down-regulated across groups. (C) Volcano plot for each comparison. p-value < 0.05 and an average log2 fold change (avg_log2FC) < ± 0.5 .