Supplemental Methods

runx1, *gata2a* and *gata2b* mutant generation and genotyping

TALENs targeting exon 4 of *runx1* were assembled using the Golden Gate TALEN system[34,35]. Synthesized TALEN RNA (75pg left arm and 75pg right arm) was injected in zebrafish embryos and founder fish and F1 heterozygous adults were screened as previously described by fluorescent PCR[36]. CRISPRs for *runx1* del(e3-8), *gata2a* and *gata2b* exon 3 were synthesized using the clone free method as previously described[37]. Zebrafish embryos were injected with 50pg of sgRNA(s) mixed with 300pg of Cas9 RNA. The *gata2b* exon 4 CRISPR was synthesized as a crRNA and the ALT-R-CRISPR-Cas9 System (IDT) was used to make the injection mix. Briefly, crRNA was incubated with tracrRNA to form a gRNA complex followed by a second incubation with Cas9 protein (PNA Bio) to form the ribonucleoprotein complex (RNP). The RNP complex was then injected into embryos (50pg gRNA and 1μg protein). Founder fish screening and identification of F1 heterozygous adults by fluorescent PCR was performed as previously described[38]. All subsequent genotyping was performed using fluorescent PCR as described previously[36,38]. To amplify both the WT and mutant alleles in the same reaction for genotyping of *runx1* del(e3-8) mutants, we used a mixture of 4 primers as follows: a forward primer in exon 3, a forward primer in exon 8, common reverse primer in exon 8 and FAM-labeled M13F primer. This leads to the amplification of 280bp fragment in the WT fish (exon 8 primers) and 347bp fragment in the mutant fish (exon 3 forward and exon 8 reverse primers). To amplify both the WT and mutant alleles in the same reaction for genotyping of *gata2a* i4del194 mutants, we used a mixture of 4 primers as follows: a forward primer 5' of the mutation, a forward primer within the deletion, common reverse primer 3' to the mutation and FAM-labeled M13F primer. This leads to the amplification of 235bp and 452bp fragments in the WT fish and 255bp fragment in the mutant fish.

Whole-mount *in situ* hybridization (WISH) and imaging

WISH were carried out essentially as described by Thisse[39]. The following DIG-labeled antisense mRNA probes were generated by using UTP-digoxigenin (Roche): *c-myb*, *mpx*, *ae1-globin* (*hbae1*), *rag1*. Imaging and embryo observation was done using a Leica MZ16F stereo microscope equipped with a Leica DC7000T camera using Leica LFS 4.6.0. Images were collected using an Upright Zeiss Axio Imager D2 microscope (Carl Zeiss Inc., Thornwood, NY, USA).

Histology and blood smears

Blood smears were performed from 22-day-old larvae, euthanized with tricaine (MS-222), tail clipped and stained (Protocol Hema 3 system; Thermo Fisher Scientific). Paraffin sectioning (sagittal) and HE were performed by Histoserv, Inc. (Germantown, MD). Images were acquired using an AxioCam HRm CCD camera with a 1388 pixel x 1040 pixel imaging field. Zeiss ZEN blue pro 2011 software package was used for collection of all images.

Kidney RNA extraction and RNA sequencing

Wild type and *runx1*$^{del25/del25}$ kidneys were dissected from ~2.5 months old fish (n= 3 for each genotype, pool of 3 kidneys/replicate) and immediately collected in Trizol (#15596018, Invitrogen). Samples were then put in a heatblock at 52°C for 10 min and then overnight in -80°C, RNA was extracted following the manufacturer protocol using Direct-zol™ RNA MiniPrep Kit (Zymo Research #R2051).

Time lapse and confocal imaging

Dechorionated embryos were anesthetized with tricaine, mounted in 0.8% low melting agarose and imaged using a Zeiss LSM 510 NLO Meta system(Thornwood, NY, USA) mounted on a Zeiss Axiovert 200M microscope with a Plan-Apochromat 20x/0.75 objective lens. Images were acquired every 10 minutes for a period of 15 hours. A range of 12-17 z-slices were used depending on the zebrafish orientation with a 1.94µm interval. Images were collected using the Zeiss ZEN 2009 V5.5 SP2 software package. Embryos were then recovered and genotyped according to the above protocol.

FACS-sorting and single cell capture and sequencing with 10X Genomics Chromium

Single cell suspensions were generated using a previously published protocol[44] and sorted on a FACS AriaIII (Becton Dickinson, Franklin Lakes, NJ) using FACS DIVA software. Sorted cells were first gated on Forward Scatter Area versus Side Scatter Area dot plot. Two additional dot plots were used to remove cell clumps by using a singlet gate on Forward Scatter Area versus Forward Scatter Width followed by a second singlet gate on Side Scatter Area versus Side Scatter Width. Cells falling within these three gate regions were then evaluated for GFP^{+} cells on a dot plot of GFP (488nm laser excitation, emission 530/30nm bandpass) versus PE (488nm laser excitation, emission 576/26nm bandpass). GFP^{low} cells were collected in a small volume of DMEM-10%FBS (25-30 ul) in a PCR-tube and the final volume was then adjusted according to the 10X Chromium protocol.

Single cell data processing, clustering and trajectory analysis

For all our analysis raw data matrices of two or more Seurat objects were merged to generate a new Seurat object with the resulting combined raw.data matrix. The original identifiers for each dataset were set and only recovered at the end of the analysis. Cells with <200 and >4000 detected genes or with >5 percentage of UMIs mapped to mitochondrial genes were excluded from further analysis. The Seurat objects were processed according to the Seurat-guided clustering tutorial at https://satijalab.org/seurat/vignettes.html. Differential expression analysis between the wild type and mutant HSC/HSPC was done using Seurat default function "FindMarkers". To perform single-cell trajectory reconstruction, we used STREAM software (Version 1.0)[17] to analyze single-cell gene expression matrix exported from Seurat. In the dimension reduction step, we applied "se" method on "top_pcs" as features, and n_neighbors=50. In the elastic principal graph calculation step, parameters include epg_alpha=0.01, epg_mu=0.05, epg_lambda=0.01 were used. For other STREAM analysis procedurals, default parameters were used. Additional subway plot that reflect sample information and Seurat clustering information were generated with matplotlib (DOI: 10.1109/MCSE.2007.55). All R analyses were performed using R version 3.6.0. scRNA-seq are available at GEO under accession number #GSE158101.

Mouse RNA-seq

For RNA-sequencing of mouse c-Kit$^+$ bone marrow cells, 8-12-week-old *Runx1$^{f/f}$, Mx1-Cre* mice and their littermate controls (*Runx1$^{f/f}$* or *Mx1-Cre*) were injected intraperitoneally with 250 μg of poly(I:C) (pIpC; InvivoGen) every other day for 3 doses to induce *Runx1* knockout. Two weeks after the last pIpC treatment, bone marrow cells were isolated and c-Kit$^+$ cells sorted out by BD FACSAria IIIu cell sorter (BD Biosciences). Total RNA was extracted with AllPrep DNA/RNA/Protein Mini Kit (QIAGEN). Poly-A selected stranded mRNA libraries were constructed using the Illumina TruSeq Stranded mRNA Sample Prep Kits and sequenced with a HiSeq2500 sequencer at the NIH Intramural Sequencing Center. HTseq-count (0.9.1)[29] were used to calculate the read count of each gene, based on the gene model from ensembl database (GRCm38.95). We used DESeq2 (1.22.2)[21] to perform differential gene expression analysis between two groups. Genes with fold change > 2 and padj<0.05 were treated as DE genes. Data were analyzed through the use of IPA (QIAGEN Inc., https://www.qiagenbioinformatics.com/products/ingenuity- pathway-analysis).

Mouse quantitative PCR

Quantitative PCR (qPCR) was performed using Power SYBR Green PCR Master Mix (Applied Biosystems) according to manufacturer's instruction. *Runx1* un-excised primers were used to detect un-excised Runx1 flox allele, and genomic control primers were used as internal controls for genomic DNA. The following primers were used: *Runx1* un-excised F 5'-ACTAGTGGATCCCTCGAGATAA-3', *Runx1* un-excised R 5'-GGACTTGTTCTCCTGGTACAC-3', Genomic control F 5'-CAGCCGTGGAGATTTAGGAG-3', Genomic control R 5'-AGTGGGAGAACTGAGCGATG-3', *Mx1-Cre* Genotype F 5'-CGATGCAACGAGTGATGAGG-3', *Mx1-Cre* Genotype R 5'-GCATTGCTGTCACTTGGTCGT-3', *Runx1* flox Genotype F 5'-CCCACTGTGTGCATTCCAGATTGG-3', *Runx1* flox Genotype R 5'-GACGGTGATGGTCAGAGTGAAGC-3'.

Statistical analysis

Results are expressed as mean ± standard error of the mean. The statistical analysis was conducted using two-tailed Student's t-test or a one-way ANOVA analysis using using GraphPad Prism v6.

Supplemental Figure Legends and Movies Legends

Supplemental figure 1. Characterization of three new zebrafish *runx1* mutants.
A. Sanger sequencing confirmation of the generated mutations. Upper panels show the presence of a deletion of 8 bp and a deletion of 25 bp in the *runx1* targeted with TALENs (*runx1*^{del8} hg96 and *runx1*^{del25} hg97). In the lower panel, the deletion in *runx1*$^{del(e3-8)}$ hg98 was confirmed, which was localized between exon 3 and 8, as well as a 66 bp insertion in the middle. **B.** Alignment of the WT RUNX1 protein sequence with the predicted protein sequences resulting from the three mutations: *runx1*^{del8}, *runx1*^{del25}, and *runx1*$^{del(e3-8)}$. **C.** Expression of full length *runx1* mRNA can be detected in the AGM of *runx1*$^{del8/del8}$ and *runx1*$^{del25/del25}$ embryos at 36 hpf (black arrowheads) but not in the *runx1*$^{del(e3-8)/del(e3-8)}$ embryo by in situ hybridization. **D**. RT-PCR shows that the wild type *runx1* transcript is not detectable, but a mutant transcript is still present in the *runx1*$^{del(e3-8)}$ homozygous embryos (expected sizes of the PCR products: F2R1 (WT), 457 bp; F2R4 (del(e3-8)), 463bp). **E.** WISH showing the expression of definitive hematopoietic markers in the three *runx1* mutant lines and wildtype controls. The HSC marker *c-myb* is absent at 36 hpf in the AGM and at 3 dpf in the CHT. The myeloid progenitor marker *mpx* (3 dpf) and the erythroid marker *hbae1* (5 dpf) are also abrogated in the CHT of the *runx1* nulls. The lymphoid marker *rag1* is not detectable in the thymus (black arrowheads) of the *runx1*$^{-/-}$. **F.** Size measurement of adult (3 months old) female and male wild type and *runx1*$^{del8/del8}$.

Supplemental figure 2. Data from single cell RNA-sequencing with 2.5 dpf embryos.
A. Gating strategy for FACS isolation of *cd41*:GFP^{low} HSC/HSPC population from 2.5 dpf wild type and *runx1*$^{del8/del8}$ embryos. **B.** Counts of the *cd41*:GFP^{low} cells obtained from flow cytometric analysis of *Tg(cd41:GFP) runx1*$^{del8/del8}$ and wild type embryos at 2.5 dpf. For each experiment a pool of 25 - 130 embryos were analyzed for each genotype (n=4 wild type, n=6 *runx1*$^{del8/del8}$). **C.** Table listing single cell quality control metrics generated by 10X Cell Ranger. **D.** Feature plots showing the expression of selected markers (purple is high, grey is low) at 2.5 dpf. HSC: *tal1*, *fli1a*; erythroid EMPs: *alas2*, *hbbe1.1*; myeloid: *spi1b*; myeloid EMPs *mpeg1.1*, *mpx.*

Supplemental figure 3. Data from single cell RNA-sequencing of *cd41*:GFP^{low} at larval stages .
A. Gating strategy for FACS isolation of *cd41*:GFP^{low} HSC/HSPC population at larval stages. Data from 16 dpf wild type and *runx1*$^{del8/del8}$ embryos are presented and are representatives of

all time-points. **B.** Table showing cell quality control metrics generated by 10X Cell Ranger. **C, D.** Feature plots showing the expression of selected markers (purple is high, grey is low) representing different populations at 6 dpf (C) and 10 dpf (D). HSC: *lmo2, tal1, c-myb, fli1a;* HSC mutant specific *meis1b, gata2b* are expressed but not *meis1a* or *gata2a.* Multipotent progenitors: *ccr9a, cebpb, csf1rb;* erythroid markers: *alas2, hbbe1.1.* Myeloid markers: *spi1b*, *mpx*, *mpeg1.1, lyz*; B/T prog cells: *sox13.*

Supplemental figure 4. Single cell RNA-sequencing on 16 dpf larvae

A. UMAP showing *cd41*:GFP^{low} cells from bloodless and recovered *runx1*$^{del8/del8}$ at 16 dpf. Colored clusters represent hematopoietic cells, grey clusters are non-hematopoietic (based on expression profile). **B.** UMAP showing the projection of the two genotypes merged for analysis. **C.** Feature plots showing the expression of selected markers (purple is high, grey is low) . HSC: *lmo2*, *tal1*, *c-myb*, *fli1a*; erythroid cells: *gata1a*, *alas2*, *hbbe1.1, hbaa1*; myeloid: *spi1b*, *lyz* and *mpeg1.1.* **D.** Feature plots showing the expression of selected markers (purple is high, grey is low) at 16 dpf (projection on UMAP presented in Fig. 3G). HSC: *lmo2, tal1, c-myb, fli1a;* expression of HSC mutant specific markers *meis1b, gata2b.* Multipotent progenitors: *ccr9a, cebpb, csf1rb;* erythroid markers: *alas2, hbbe1.1.* Myeloid markers: *spi1b*, *mpx*, *mpeg1.1, lyz.*

Supplemental figure 5. Hematopoietic differentiation and pseudotime trajectories in *runx1*$^{del8/del8}$ and wildtype larvae at 6, 10, and 16 dpf

A. UMAP showing merged wild type *cd41*:GFP^{low} cells from 6, 10 and 16 dpf. **B.** Distribution of the three time points used to generate the merged UMAP in figure A. **C.** Flat tree plot representing pseudotime trajectory projection and branches identities (STREAM) of wild type *cd41*:GFP^{low} cells from panel A. **D.** UMAP obtained by merging datasets from multiple larval timepoints 6, 10 and 16 (bloodless and recovered) dpf of *runx1*$^{del8/del8}$ *cd41*:GFP^{low} cells. In both A and D colored clusters represent hematopoietic cells, grey clusters are non-hematopoietic (based on expression profile). **E.** Projection of the timepoints on the UMAP in figure D. **F.** Flat tree plot showing the results of the trajectory analysis (STREAM) relative to UMAPs from *runx1*$^{del8/del8}$ (presented in panel D) merged dataset. **G.** Stream plots showing the expression of representative markers in wild types. HSC/HSPCs: *c-myb.* Erythroid markers: *alas2, gata1a, hbbe1.1*, *hbaa1*. Myeloid markers: *spi1b*, *mpx*, *mpeg1.1, lyz;* multipotent progenitors: *cebpb.* **H.**

Stream plots showing the expression of representative markers in *runx1*$^{del8/del8}$. HSC/HSPCs: *c-myb*, *fli1a.* Erythroid markers: *gata1a, hbbe1.1*, *hbaa1*. Myeloid markers: *spi1b*, *mpx*, *mpeg1.1.*

Supplemental figure 6. GATA2 target genes are upregulated in c-Kit+ bone marrow cells from *Runx1* conditional knockout mice. A-C. qPCR analysis on *Runx1*$^{-/-}$ (n=10) and *Runx1*$^{+/+}$ littermates (n=7) dissected AGM at E10.5. Expression of exon 5 is lost in *Runx1*$^{-/-}$ upon excision of the floxed allele (D) but the expression of the mutant mRNA appeared unchanged (E). Expression of *Gata2* in the *Runx1*$^{-/-}$ AGM was comparable to *Runx1*$^{+/+}$ (F). **D.** RNA-seq reads coverage plot of *Runx1* isoform ENSMUST00000023673 exon regions (three biological replicates) confirmed the complete excision of Exon 4 in all the *Runx1* knockout mice used for RNA-seq. **E, F.** The Volcano plot on the left displays the differentially expressed genes (padj <0.05, FC>2) between *Runx1* knockout group and control group, related to Figure 4B,C. Red dots represent the genes known to be regulated by the transcription factor GATA2 (H), which are also listed in the table on the right (G).

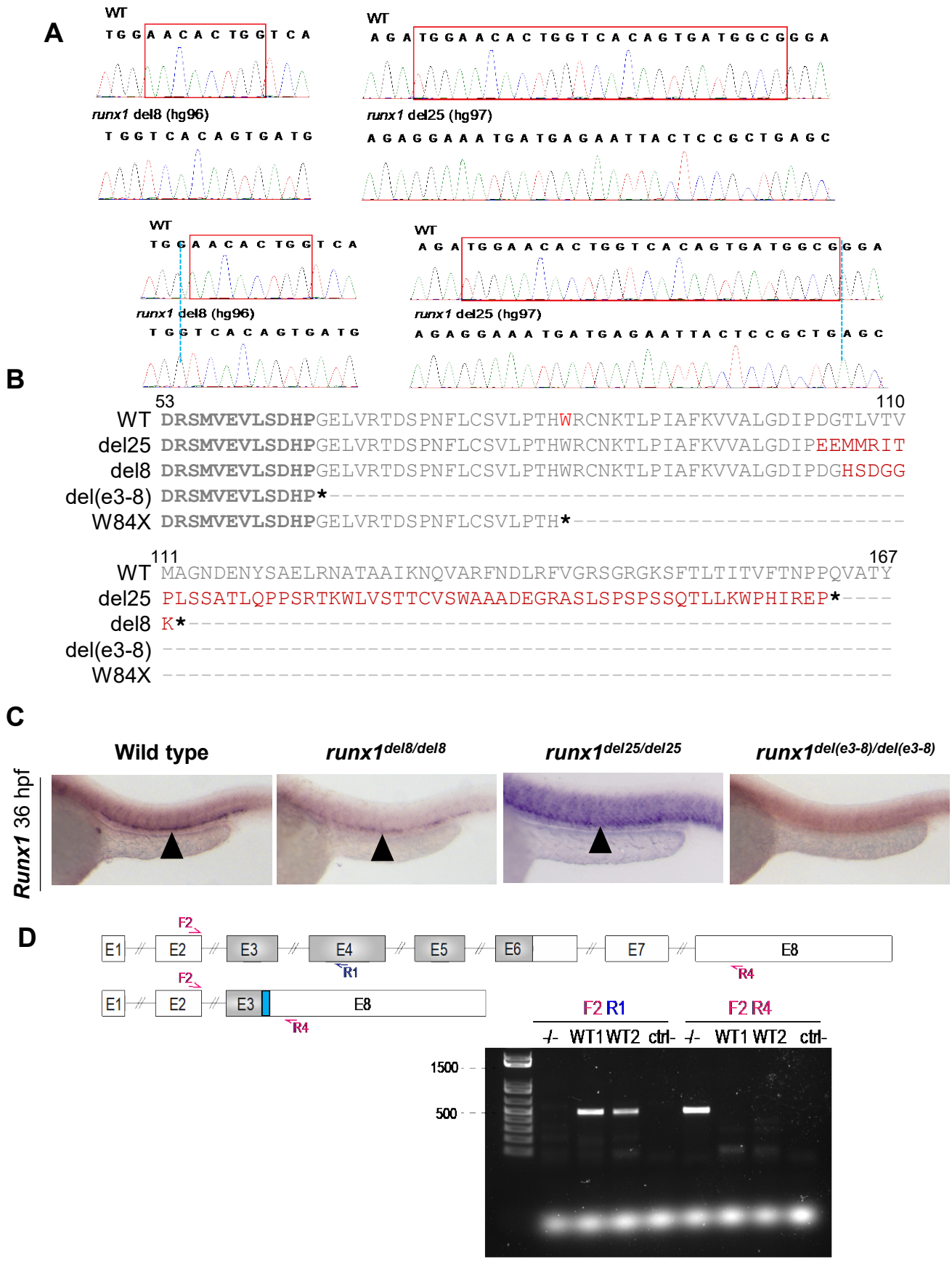
Supplemental figure 7. Characterization of new zebrafish *gata2b* and *gata2a* mutants. **A.** Sanger sequencing shows the presence of an insertion of 5 bp (*gata2b*^{ins5} hg94) in exon 3 and a deletion of 7 bp (*gata2b*^{del7} hg95) in exon 4 of the *gata2b* gene. **B.** Predicted protein sequences of the mutant lines *gata2b*^{ins5} and *gata2b*^{del7}. **C.** Survival of zebrafish *gata2b*^{ins5} and *gata2b*^{del7} lines. Progenies of both lines were obtained from heterozygous incrosses. Red dashed lines indicate the expected Mendelian ratio. Segments on the bars show % of fish recovered for each genotype. The numbers in each segment depict the numbers of fish for each genotype. Adult *gata2b*$^{-/-}$ fish can be recovered according to Mendelian ratio. **D.** Survival of adult *runx1*^{del8}*/gata2b*^{ins5} double mutants obtained from the incross of *runx1*$^{del8/del8}$*; gata2b*$^{+/ins5}$ parents. Red dashed lines indicate the expected ratio of *runx1*$^{-/-}$ recovery based on our previous experimental data (Fig. 1E). Each bar segment shows the percentage and number of fish recovered for each genotype. **E.** *gata2b* knock down experiments in the *runx1*^{del8}; *Tg*(*cd41*:GFP) background. *cd41*:GFP^{+} cells were reduced in the *runx1*$^{+/del8}$ embryos and completely absent in the *runx1*$^{del8/del8}$ embryos after injection of *gata2b*-MO (9) (11.7 ng). Representative pictures of the phenotype at 5 dpf are shown in the left. Asterisks mark the *cd41*:GFP^{+} cells in the CHT, white arrowhead marks *cd41*:GFP^{+} cells in the pronephric duct. Right panel shows a quantification of the phenotype observed and the number of embryos analyzed. **F.** Survival of uninjected and *gata2b*-MO injected *runx1*$^{del8/del8}$ mutants (1 month old) obtained from incrossing

runx1$^{+/del8}$ parents. 17% of the uninjected *runx1*$^{del8/del8}$ fish were recovered while no *runx1*$^{del8/del8}$ fish injected with *gata2b*-MO were recovered. **G.** Sanger sequencing confirming the deletion of 194 bp in the intron4 enhancer of *gata2a.* **H.** Presence or absence of blood circulation at 8 and 15 dpf in larvae obtained from *runx1*$^{+/-}$;*gata2b*$^{-/-}$;*gata2a*$^{+/-}$ incross. Segments on the bar show % of fish recovered for each genotype. Bloodless larvae are observed only in presence of *runx1*$^{-/-}$.

Supplemental Movie 1. *cd41:*GFP^{+};*kdrl:mCherry*$^{+}$ cells emerge and are released from the AGM through the axial vein in wild type embryo *Tg(cd41:GFP); Tg(kdrl:mCherry)*.
Time lapse imaging of the AGM region of a wild type embryo at 2.5 dpf. mCherry marks endothelial cells, GFP is expressed in thrombocytes, HSCs and non-hematopoietic cells. HSCs derived from hemogenic endothelium are mCherry^{+}GFP^{+} (yellow).
Images were acquired every 10 minutes for a period of 15 hours. A range of 12-17 z-slices were used depending on the zebrafish orientation with a 1.94µm interval.

Supplemental Movie 2. *cd41:*GFP^{+};*kdrl:mCherry*$^{+}$ are present in the *runx1*$^{-/-}$ AGM and are released through the axial vein in a *Tg(cd41:GFP); Tg(kdrl:mCherry) embryo*.
Time lapse imaging of the AGM region of a *runx1*$^{-/-}$ embryo at 2.5 dpf. mCherry marks endothelial cells, GFP is expressed in thrombocytes, HSCs and non-hematopoietic cells. HSCs derived from hemogenic endothelium are mCherry^{+}GFP^{+} (yellow).
Images were acquired every 10 minutes for a period of 15 hours. A range of 12-17 z-slices were used depending on the zebrafish orientation with a 1.94µm interval.

Supplemental figure 1



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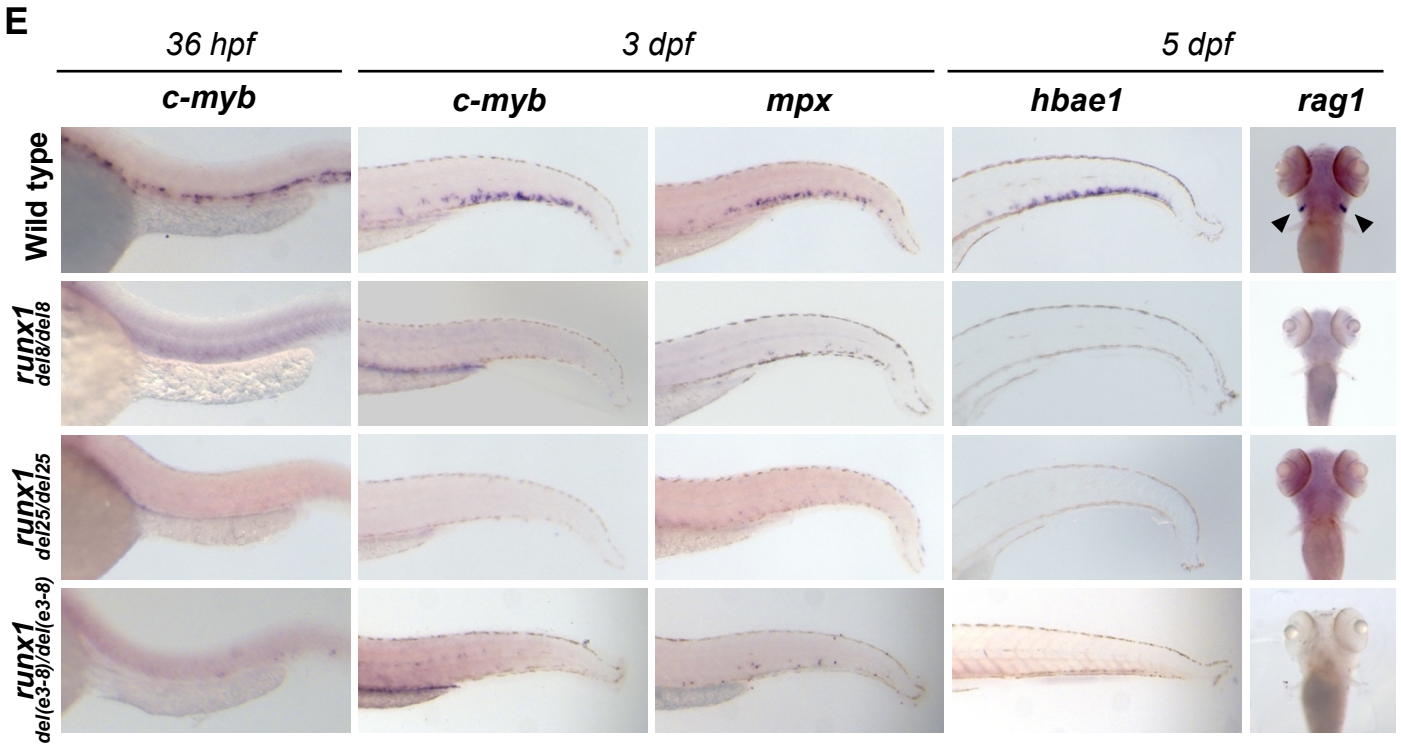
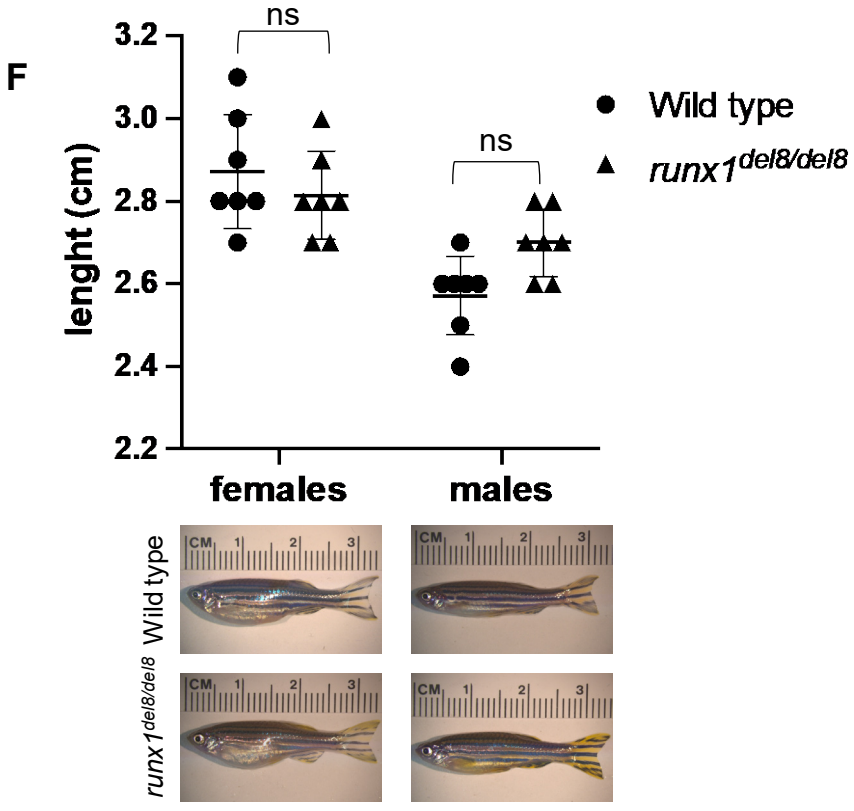
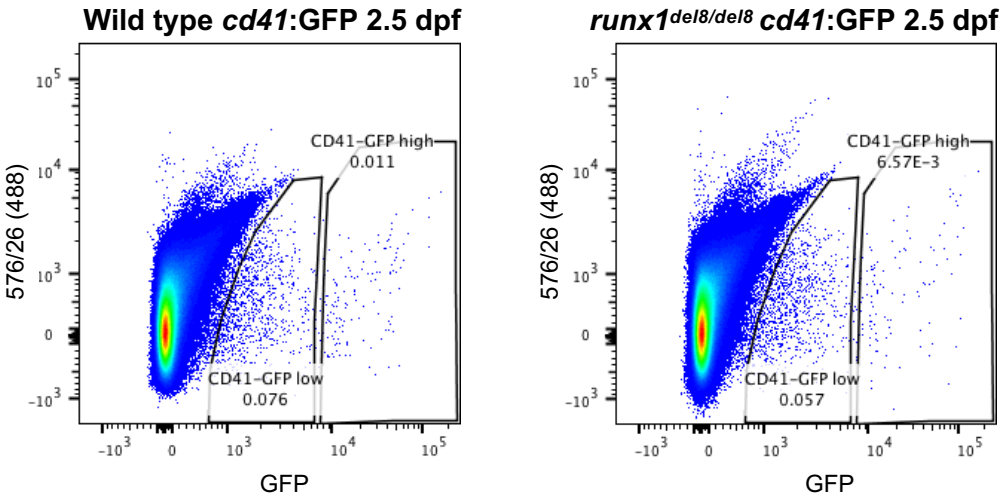




(Age of the fish 3 mths)

Supplemental figure 2

A



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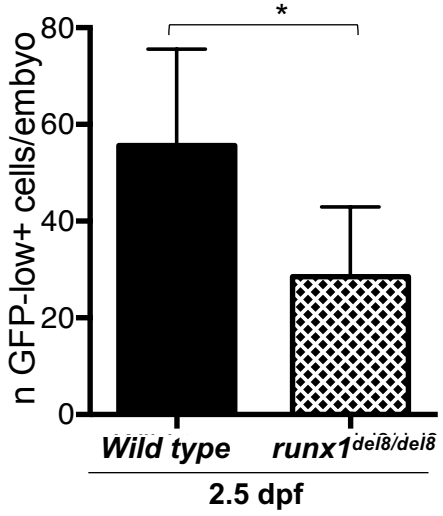
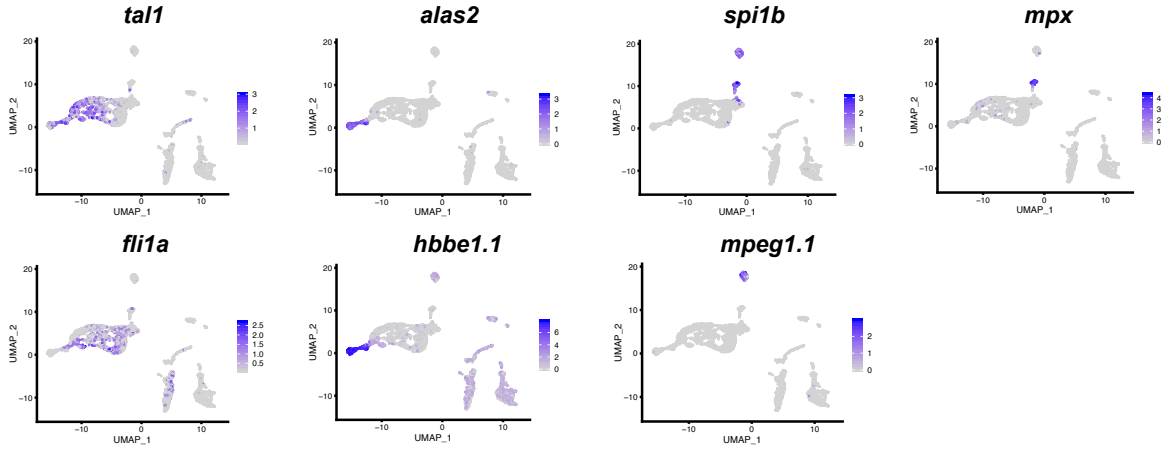


C

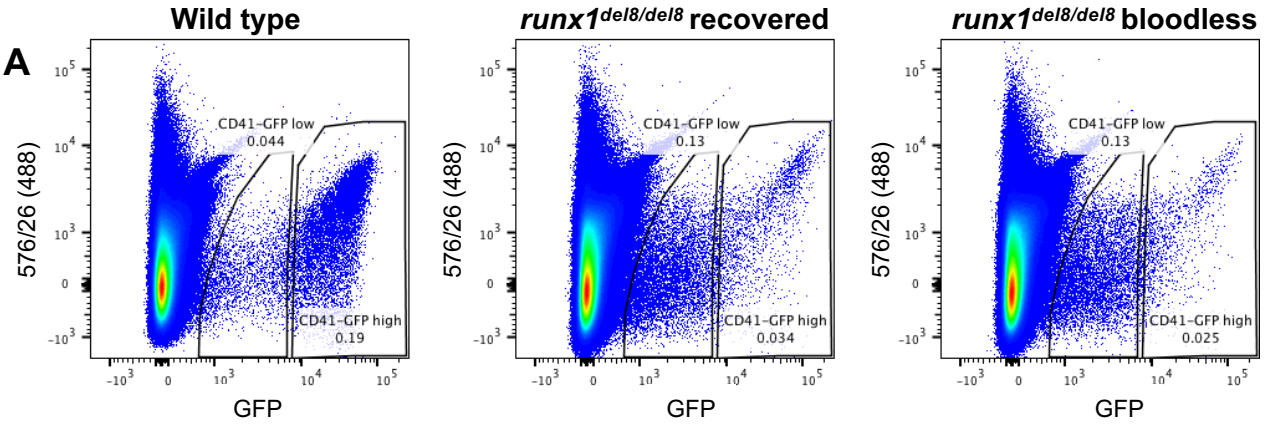
cd41:GFP^{low}	Wild type	*runx1*$^{del8/del8}$
Total # of cells	2200	1173
Mean reads/cell	112,873	251,483
Median Genes/Cell	1856	1258
Median UMI/Cell	12,290	7,757

D



Supplemental figure 3

A

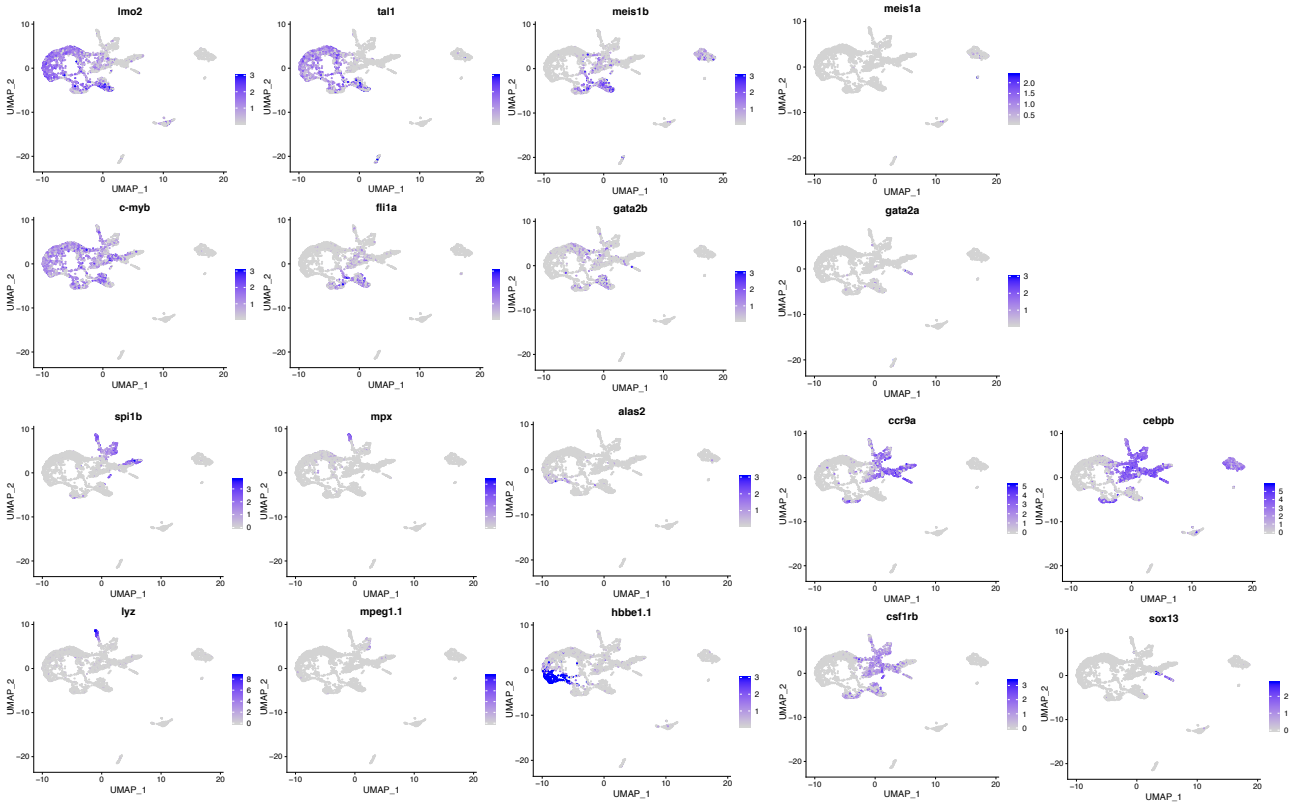


B

cd41:GFP^{low}	cd41-GFP^{low} **6 dpf**		cd41-GFP^{low} **10 dpf**		cd41-GFP^{low} **16 dpf**		
	Wild type	***runx1^{del8}***	***Wild type***	***runx1^{del8}***	***Wild type***	***Runx1^{del8}*** ***Bloodless***	***Runx1^{del8}*** ***Recovered***
Total # of cells	2754	799	2711	3505	6218	3674	7883
Mean reads/cell	59341	226492	36914	33640	41619	64970	28464
Median Genes/Cell	1493	983	1731	1506	1769	1830	1713
Median UMI/Cell	13288	4054	10432	7145	12284	9372	10497

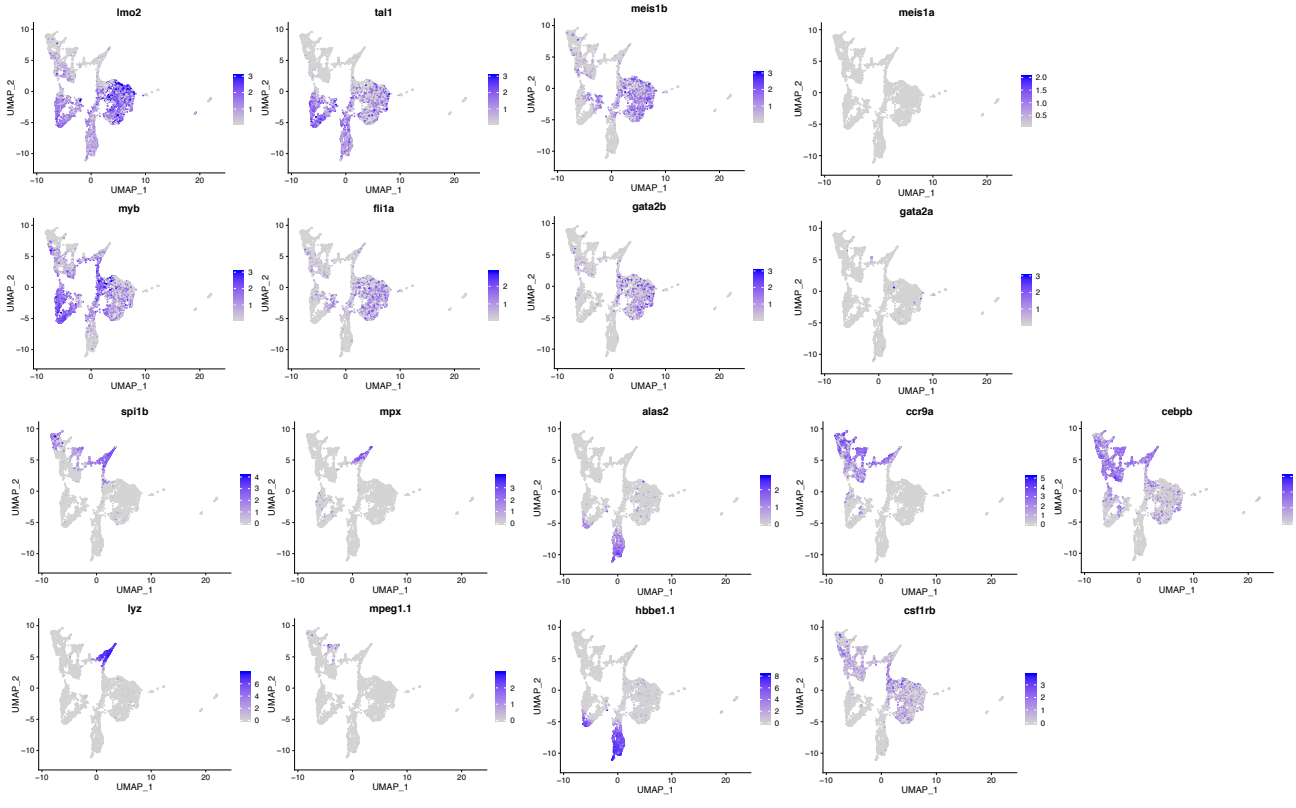
C

6 dpf

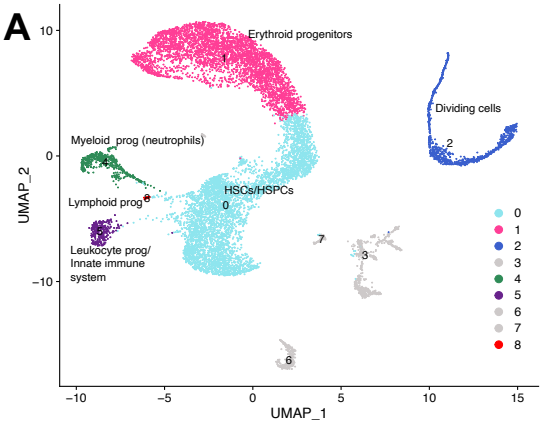


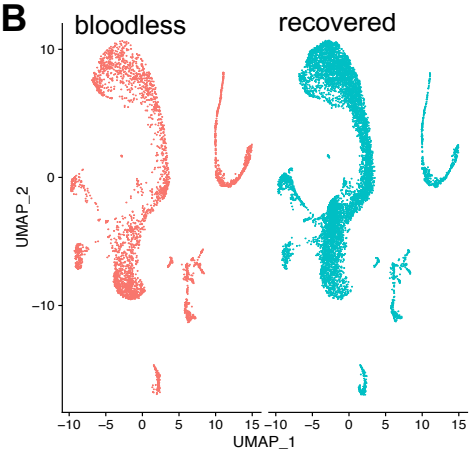
D

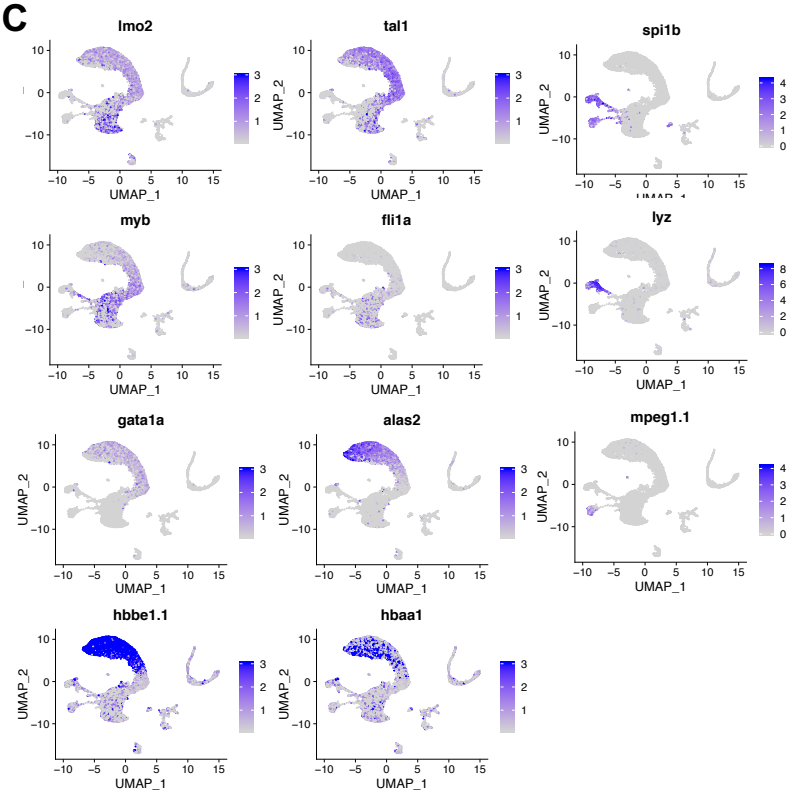
10 dpf

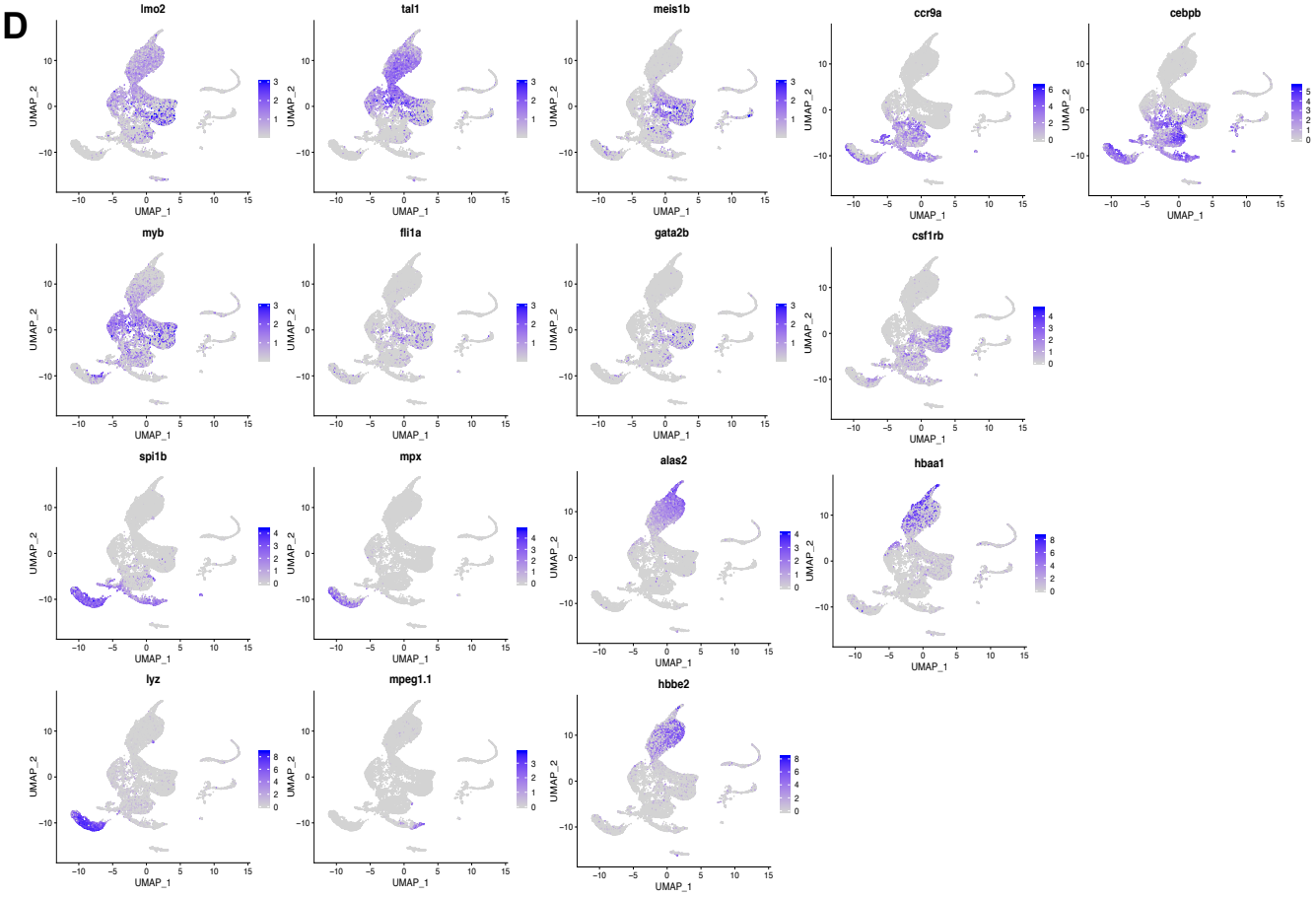


Supplemental figure 4

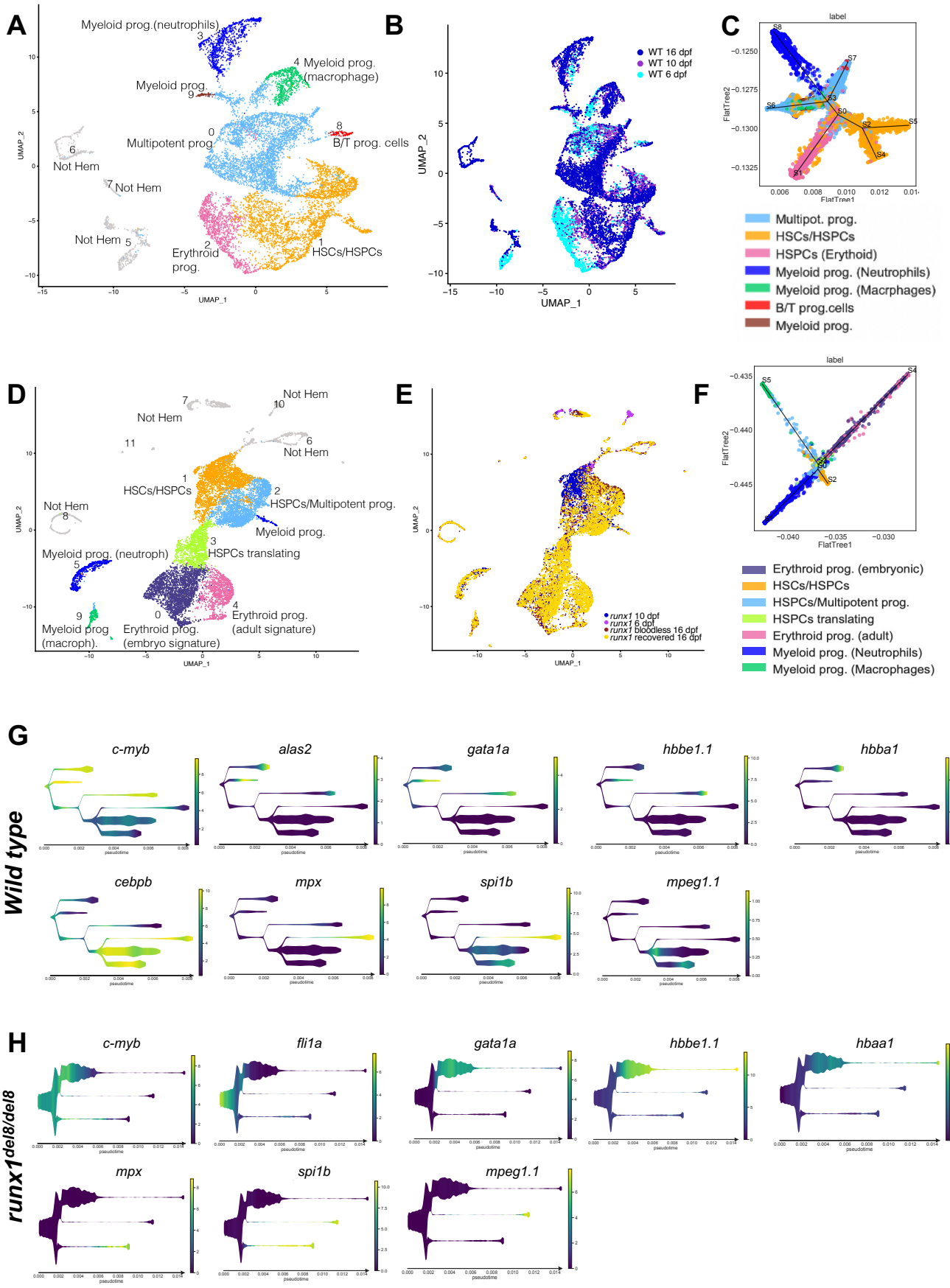




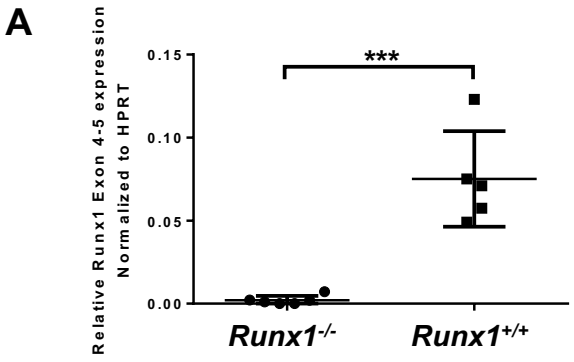


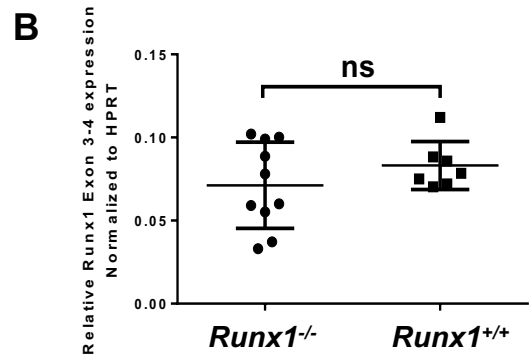


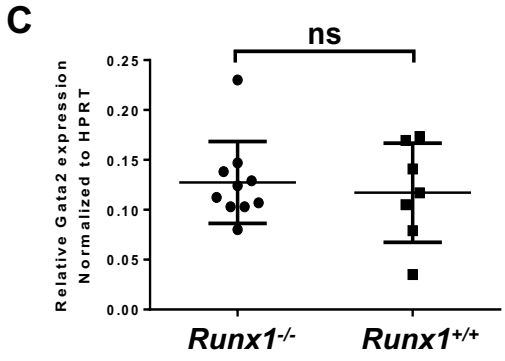
Supplemental figure 5

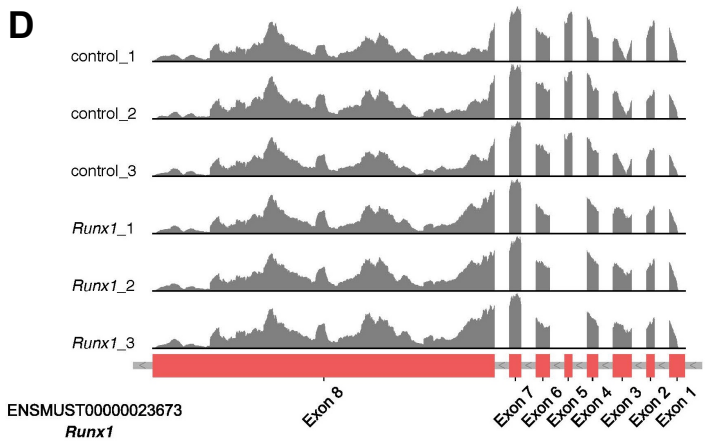


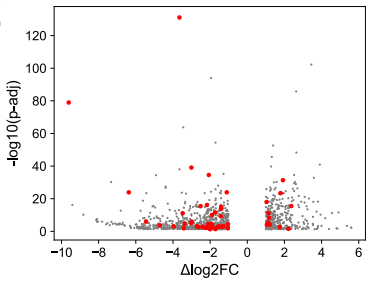
Supplemental figure 6











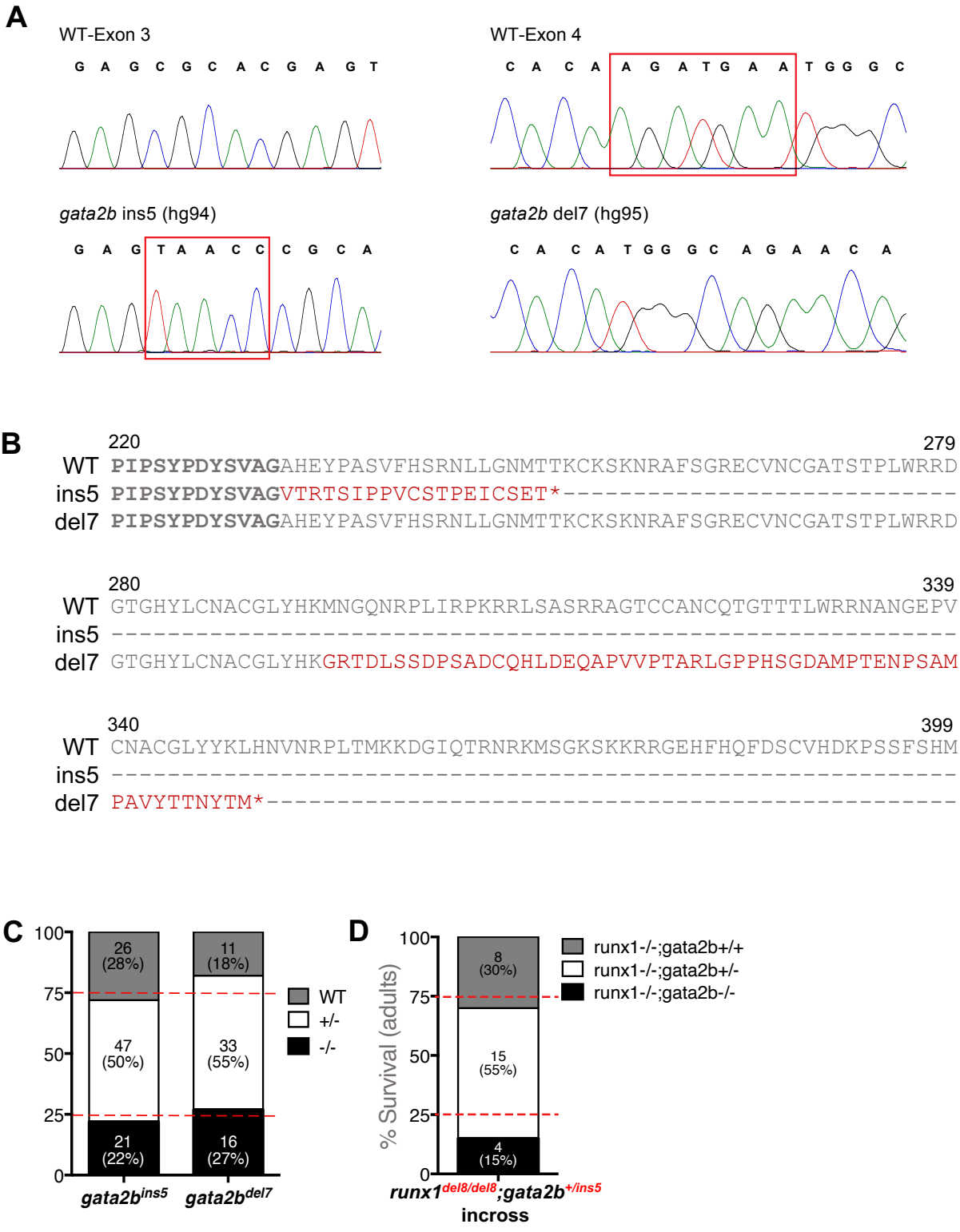
DE genes c-Kit+ *Runx1* KO vs control	
Total	1384
UP	414
DOWN	940

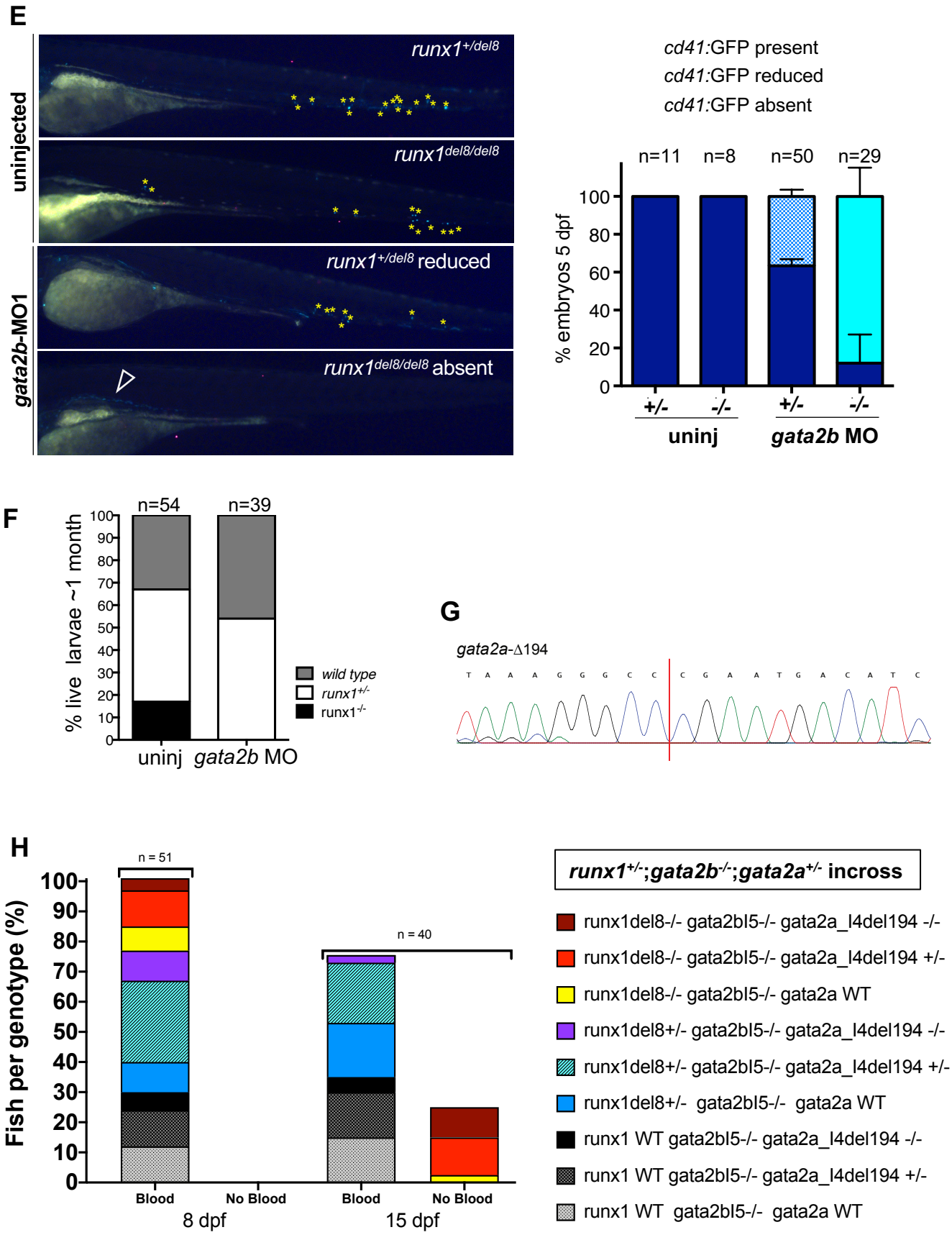
F

Gata2 targets	log2FC	padj
Mcpt8	-3.650321322	8.02E-132
Prss34	-9.611277313	1.0477E-79
Gpr141	-3.008077068	7.9349E-40
Fcnb	-2.069785301	2.6944E-35
Gp5	1.919783526	4.4589E-32
Fcer1a	-6.378849917	1.2049E-24
Trem3	-1.105839463	1.2049E-24
Selp	1.794588999	3.844E-24
Runx1	1.04126559	9.5457E-19
Ear2	-2.168092334	6.7056E-17
Treml1	2.369657329	3.193E-16
Hba-a2	-2.513858293	3.7829E-16
Ms4a2	-1.403797682	1.1998E-15
E2f2	-1.418846388	2.2369E-14
Wfdc21	-1.720175789	2.6872E-12
Mfsd2b	1.13729184	6.3402E-12
I830127L07Rik	-3.478864935	7.8395E-12
4930438A08Rik	-1.907219749	8.3059E-11
S100a8	-1.428756293	5.2125E-10
Il1rl1	1.170550668	4.6017E-09
Il6	-5.449056709	9.7035E-07
Gm5900	-2.99549301	1.1597E-06
Gfi1b	1.124317426	4.7116E-06
Alas2	-3.021702358	7.7742E-06
Olfm4	-3.37069312	2.4029E-05
Serpinb10	-1.939506569	2.7924E-05

Gata2 targets	log2FC	padj
Abca13	-1.0365411	4.6065E-05
Alox5	-2.0995171	4.7741E-05
Itgam	-1.905784	6.9314E-05
F2rl2	1.2110646	7.4512E-05
Aqp9	1.05463015	7.5652E-05
Fcrla	-4.7062151	0.00018768
Grap2	-1.2854677	0.00068623
Stfa1	-3.9614682	0.00081374
Cma1	-2.7080113	0.00086956
S100a9	-1.5008933	0.00119023
Cd96	-1.550776	0.00119049
Ngp	-2.409216	0.00138443
Epx	-1.3739083	0.00163303
Cd177	-2.6266039	0.002584
Tubb1	1.7535548	0.00287178
Cd300ld	-1.8882208	0.00337986
Mcemp1	-1.6334332	0.00348528
Camp	-2.1846944	0.00382526
Lcn2	-2.1893857	0.0052711
Ltf	-2.2461519	0.00719916
Trim10	-1.0451479	0.01234823
Gzmb	-3.4210466	0.01361247
Mpig6b	2.22068988	0.0295484
Slc4a1	-2.0049962	0.03829659
Sytl3	-1.9911064	0.04000622
Mctp2	-1.7169036	0.04123368

Supplemental figure 7




E
uninjected
gata2b-MO1
runx1+/del8
runx1del8/del8
runx1+/del8 reduced
runx1del8/del8 absent
cd41:GFP present
cd41:GFP reduced
cd41:GFP absent
n=11
n=8
n=50
n=29
% embryos 5 dpf
100
80
60
40
20
0
+/-
-/-
+/-
-/-
uninj
gata2b MO
F
n=54
n=39
% live larvae ~1 month
100
90
80
70
60
50
40
30
20
10
0
wild type
runx1+/-
runx1-/-
uninj
gata2b MO
G
gata2a-Δ194
T A A A G G G C C C G A A T G A C A T C
H
Fish per genotype (%)
n = 51
n = 40
100
90
80
70
60
50
40
30
20
10
0
Blood
No Blood
Blood
No Blood
8 dpf
15 dpf
runx1+/-;gata2b-/-;gata2a+/- incross
runx1del8-/- gata2bI5-/- gata2a_I4del194 -/-
runx1del8-/- gata2bI5-/- gata2a_I4del194 +/-
runx1del8-/- gata2bI5-/- gata2a WT
runx1del8+/- gata2bI5-/- gata2a_I4del194 -/-
runx1del8+/- gata2bI5-/- gata2a_I4del194 +/-
runx1del8+/- gata2bI5-/- gata2a WT
runx1 WT gata2bI5-/- gata2a_I4del194 -/-
runx1 WT gata2bI5-/- gata2a_I4del194 +/-
runx1 WT gata2bI5-/- gata2a WT