Supplementary Methods

Dietary Se deficient mice

C57BL/6 mice were purchased from Taconic at age of three weeks, and fed on custom Se diets (from Harlan Teklad) that only differed in the amount of Se (Se-D diet: Se < 0.01ppm; Se-A diet: Se 0.08-0.1 ppm). Mice were provided with double distilled water and kept on the abovementioned diets for three months prior to use in experiments.

BM cell culture, stress BFU-E colony assays, and CFU-GM colony assays

BM cells were isolated and cultured in the two-phase culture system as described[1]. In brief, BM cells were cultured in stress erythroid expansion media (SEEM), comprised of Iscove's Modified Dulbecco's Media (IMDM) with 1% (*m/v*) BSA, 0.0007% (*v/v*) β-mercaptoethanol, 10% (*v/v*) FBS, 4mM L-glutamine, Insulin (10μg/mL), Transferrin (200μg/mL), Scf (50ng/mL), Bmp4 (15ng/mL), Gdf15 (30ng/mL), and Shh (25ng/mL), for 5 to 7 days to enrich for SEPs. Human BM cells from three subjects were purchased from Reachbio Research Labs. Human BM culture was the same condition with corresponding human factors[1]. To induce deletion of the second *Trsp* allele in *Trsp* $^{fl/\Delta}$;CreERT BM cells, cells were cultured for 48Hrs in 10μM 4-hydroxytamoxifen (4-OHT, Sigma). Following expansion, the whole cell culture was shifted to stress erythroid differentiation media (SEDM), which is SEEM supplemented with Epo (3U/mL), and the cultures grown in hypoxia conditions (1% O_2, 5% CO_2, 37^{o}C) for 3 days. Following differentiation, cells (1x10^5 cells/mL) were replated in methylcellulose (StemCell Technology M3334) containing Epo and grown at 20% O_2 to assay for mature stress BFU-Es. In addition, colony assays were done in methylcellulose media containing Epo supplemented with Bmp4 (15ng/mL) and Scf (50ng/mL), and cells were cultured in hypoxia conditions (1% O_2) to assay for total stress BFU-E potential as previously described[1-3]. For CFU-GM colony quantitation, *Trsp* $^{fl/\Delta}$;CreERT BM cells or control cells were plated in IMDM with with 1% (*m/v*) BSA, 0.0007% (*v/v*) β-mercaptoethanol, 10% (*v/v*) FBS, 4mM L-glutamine, Scf (50ng/mL), IL-3 (20ng/mL) and 10μM 4-OHT for 24Hrs to induce *Trsp* deletion. Then cells (2x10^4 cells/mL) were replated in methylcellulose (StemCell Technology M2434) supplemented with GM-CSF(10ng/mL), Scf (50ng/mL) and IL-3 (20ng/mL), and cultured at 20% O_2, 5% CO_2, and 37^{o}C for 7 days. Total colonies in the culture were counted.

Estimation of SEPs in spleen and peripheral blood by stress BFU-E colony assays

For quantitation of splenic SEPs post PHZ treatment, splenocytes were isolated and plated at 1x10^6 cells/mL in methylcellulose containing Epo for stress BFU-Es in normoxia. To assess migration of BM erythroid-lineage potential progenitors, peripheral blood mononuclear cells (PBMC) were collected from peripheral blood by Histopaque (Sigma 1083-1) gradient centrifugation. Isolated PBMCs were cultured in SEDM for 3 days in hypoxia, and replated in M3334 methylcellulose (Stem Cell Technologies) at concentration of 1x10^5 cells/mL for stress BFU-Es, with addition of Bmp4 (15ng/mL) and Scf (50ng/mL), cultured in hypoxia, which assays both stress BFU-Es and cells committed to become stress BFU-Es.

Histology

Tissues were fixed in 4% paraformaldehyde and prepared for tissue sectioning and hematoxylin-eosin (H&E) staining (performed by the Animal Diagnostic Laboratory, Pennsylvania State University).

Quantitative polymerase chain reaction (qPCR) and gene expression analysis

RNA isolation from cells or tissues was performed using TRIzol reagent (Invitrogen) according to the manufacturer's instructions. cDNA was synthesized by using High Capacity cDNA Reverse Transcriptase kit (Applied Biosystems). qPCR reactions were performed with Taqman probes (Thermo Fisher), and PerfeCTa qPCR SuperMix Master mix (Quanta Biosciences) or SYBR™

green (Quanta Biosciences). Primer sequences and probes are provided in the supplementary Table S2 and S3.

Flow cytometry, Flow imaging, and Cell sorting

Spleen and BM cells were harvested from PHZ treated mice at the indicated time points. Cells were first stained with Brilliant Violet 510 live/dead dye (BD) to exclude dead and autofluorescent cells, and then processed with standard extracellular staining. For reticulocyte analysis, the whole blood was examined by thiazol orange co-staining with Ter119. For intracellular ROS staining, prior to regular cell staining, spleen cells were first stained with CellROX® reagent (Thermo Fisher C10422) in cell culture media for 30min at 37ºC in dark. Fortessa LSR (Becton Dickinson) and Accuri (Becton Dickinson) flow cytometers were used for analyses. Flow cytometry data were analyzed with FlowJo software. Imaging data were collected by FlowSight® (Amnis) and analyzed using IDEAS software. For sorting of ProEs and BasoEs by FACS, spleen cells were first enriched for $CD71^+$ cells with EasySep® magnet beads positive selection with anti-CD71 antibody, and then stained for live/dead cells and Ter119. Astrios (Becton Dickinson) cell sorter was used for cell sorting. Apoptosis was analyzed by Annexin V staining (BD). See supplementary Table S1 for detailed antibody information.

Western blotting

Whole cell lysates were prepared using standard RIPA or M-PER (Thermo-Pierce) cell lysis buffer containing protease inhibitor cocktail (Roche#04693116001). Primary antibodies used included anti-mouse-Bach1 (R&D AF5777), anti-mouse-GATA-1 (Santa Cruz sc-265), anti-mouse-Lamin B1 (Cell Signal 13435), anti-mouse-SelenoW (Rockland 600-401-A29), and anti-mouse-Yap (Santa Cruz sc-376830), followed by appropriate secondary antibody conjugated to horseradish peroxidase.

Splenic EBI enrichment

Procedure for the isolation and enrichment of splenic EBIs was as described[4] with modifications. Briefly, whole spleens were minced into small pieces, gently pressed with the syringe plunger, and then incubated in RPMI1640 media containing 0.075% (*m/v*) Collagenase IV (Gibco 17104019) and 0.004% (*m/v*) DNase I (Invitrogen DN25) for 30min at 37ºC with constant shaking. The suspension was passed through an 18-guage needle several times and cells were washed by centrifugation. The cell pellet was resuspended with 200-1000μL RPMI1640 containing 0.004% DNAse I and layered on top of 30% (*v/v*) FBS in IMDM. Aggregates were enriched by gravity sedimentation for 45min at room temperature. The supernatant was carefully removed and the pellet was resuspended in 50% (*v/v*) Percoll (in IMDM) and layered on top of 100% (*v/v*) Percoll (Sigma P1644) followed by centrifugation at 400*g* for 20min. Red colored aggregates at the 50% (*v/v*) Percoll and 100% (*v/v*) Percoll interface were collected, washed with PBS, and used for flow cytometry and imaging flow cytometry.

Monocyte transfer

Monocytes were sorted using EasySep magnetic beads (Stem Cell Technologies 19761A), to enrich $CD11b^+Ly6G^-$ cells. $1x10^6$ sorted wild type monocytes were injected into Se-D mice by retro-orbital injection at 6Hrs post PHZ treatment.

Microarray, RNA sequencing and ChIP sequencing

Splenic ProEs and BasoEs were sorted by FACS post 50% PHZ treatment from Se-D or Se-A mice. Total RNA was isolated using TRIzol reagent (Sigma), quantified, and RNA integrity tested using an Agilent Bioanalyzer. Microarray was performed by GeneChip® Mouse Transcriptome Assay 1.0 (Affymetrix). Gene normalization was conducted by using Expression Console Software (Affymetrix). The data have been deposited into NCBI's Gene Expression Omnibus

(GEO) and are accessible through GEO Series accession number GSE102056 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE102056). Gene expression profile was generated with normalized data by using Transcriptome Analysis Console Software (TAC) program. The cutoff was set at absolute value of fold change of Se-D compared to Se-A greater than 2, |fold change (Se-D vs. Se A)|>2. Gene ontology and signaling pathways were analyzed based on the gene profile by Ingenuity Pathway Analysis (IPA) Software program. RNA sequencing (RNA-Seq) and ChIP sequencing (ChIP-Seq) were performed as previously described[5,6].

SelenoW mutation using CRISPR/Cas9 and CRISPRi/Cas9 system

Mouse SelenoW knockout was generated using CRISPR/Cas9 system. Human *SelenoW* (*huSelenoW*) knockdown was generated using CRISPRi/Cas9 transcription inhibitory system. Both mouse and human SelenoW sgRNA sequences were designed using the MIT CRISPR/Cas9 design tool (http://crispr.mit.edu). Sequences with scores over 85 with minimum off-targets were selected. Mouse sgRNA lentivectors with puromycin and mCherry dual selection markers were purchased from VectorBuilder. The target sequence is 5'-CTTCAAAGAACCCGGTGACC-3'. BM cells isolated from B6J.129(Cg)-Gt(ROSA)26Sor$^{tm1.1(CAG-cas9-EGFP)Fezh}$/J mice (TgCas9-GFP mice, expressing Cas9 and GFP fusion protein) or Cas9 expressing murine erythroblast cell line G1E and G1E-ER4 cells (G1E cells where GATA-1 expression is induced by activation of estrogen receptor with treatment of 100 μM β-estradiol, E2) were transduced with the lentivirus expressing non-targeting control (NTC) or mouse *SelenoW* sgRNA. G1E and G1E-ER4 cells were cultured in IMDM media supplemented with 15% (v/v) FBS, Kit ligand (provided by Dr. Hardison's laboratory), Epo (2U/mL), and 0.00124% (v/v) monothioglycerol. Knockdown of *huSelenoW* utilized pLV-hU6-sgRNA hUbC-dCas9-KRAB-T2a-GFP that was a gift from Charles Gersbach (Addgene#71237) expressing deactivated dCas9-KRAB fusion protein[7]. We cloned huSelenoW sgRNA target sequence, 5'-AGCAGTAAGCGAGTTTATAC-3', into the vector plasmid. The knockdown efficiency was tested by qPCR using SYBR™ green (Quanta Biosciences). The primer sequences were listed in supplementary Table S2. Both mouse and human *SelenoW* sgRNA lentivirus was packaged using HEK293TN cells.

References

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3 Harandi, O. F., Hedge, S., Wu, D. C., McKeone, D. & Paulson, R. F. Murine erythroid short-term radioprotection requires a BMP4-dependent, self-renewing population of stress erythroid progenitors. *J Clin Invest* **120**, 4507-4519, doi:41291 10.1172/JCI41291 (2010).

4 Sadahira, Y., Mori, M. & Kimoto, T. Isolation and short-term culture of mouse splenic erythroblastic islands. *Cell Struct Funct* **15**, 59-65 (1990).

5 Jain, D. *et al.* Dynamics of GATA1 binding and expression response in a GATA1-induced erythroid differentiation system. *Genom Data* **4**, 1-7, doi:10.1016/j.gdata.2015.01.008 (2015).
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7 Thakore, P. I. *et al.* Highly specific epigenome editing by CRISPR-Cas9 repressors for silencing of distal regulatory elements. *Nat Methods* **12**, 1143-1149, doi:10.1038/nmeth.3630 (2015).

Supplemental tables

Supplementary Table S1. Flow cytometry antibodies

Antibodies	Source	Catalog
FITC-anti-mouse-CD71	BD	553266
PE-anti-mouse-CD71	Biolegend	113808
Brilliant Violet 421-anti-mouse-Ter119	Biolegend	116233
Alexa647-anti-mouse-Ter119	Biolegend	116218
APC/Cy7-anti-mouse-Ter119	Biolegend	116233
PE-anti-mouse-Ter119	BD	553673
PE-anti-mouse-CD133	eBiosciences	12-1331-82
Brilliant Violet 421-anti-mouse-cKit	BD	562609
PE- anti-mouse-CD49d	Biolegend	103705
PE-Cy7- anti-mouse-CD44	Biolegend	103030
PE/Cy7- anti-mouse-F4/80	Biolegend	123114
APC- anti-mouse-F4/80	Biolegend	142418
Percp/Cy5.5- anti-mouse-CD11b	BD	550993
APC-anti-mouse-CD11b	Biolegend	101212
PE-anti-mouse- CD11b	Biolegend	101207
FITC- anti-mouse-Vcam-1	BD	553332
Alexa 647- anti-mouse- Vcam-1	Biolegend	105712
PE- anti-mouse-CD169	Biolegend	142404
APC- anti-mouse-CD169	Biolegend	142418
FITC- anti-mouse-Ly6C	BD	553104
APC/Cy7- anti-mouse-Ly6C	BD	560596
Brilliant Violet 421- anti-mouse-CD115	Biolegend	135513
FITC-Annexin V	BD	556419

Supplementary Table S2. PCR primer sequences

Gene	Sequences 5'->3'	
Ptplad1 (Hacd3)	Fwd	CTGACGCCGCATGTCTACTG
	Rev	TTGAAATGCAGCACATTGTCTG
Cbr1	Fwd	TCAATGACGACACCCCCTTC
	Rev	CCTCTGTGATGGTCTCGCTTC
Casp3	Fwd	TGGTGATGAAGGGGTCATTTATG
	Rev	TTCGGCTTTCCAGTCAGACTC
Casp8	Fwd	TGCTTGGACTACATCCCACAC
	Rev	TGCAGTCTAGGAAGTTGACCA
Casp6	Fwd	GGAAGTGTTCGATCCAGCCG
	Rev	GGAGGGTCAGGTGCCAAAAG
Fech	Fwd	CAGACAGATGAGGCTATCAAAGG
	Rev	CACAGCTTGTTGGACTGGATG
mSelenoW	Fwd	GGTGCCTCCCCAGAATCTAC
	Rev	TGGGGGAATTCAGAGAGAGA
hSelenoW	Fwd	CCGTCCGAGTCGTTTATTGT
	Rev	CACGAGAACATCAGGGAAAGA
Txnrd1	Fwd	CCTATGTCGCCTTGGAATGTGC
	Rev	ATGGTCTCCTCGCTGTTTGTGG

Supplementary Table S3. qPCR Taqman probes

Gene	Identifier
Alas2	Mm00802083_m1
Bach1	Mm01344527_m1
Hmox1	Mm00516005_m1
Ihh	Mm00439613_m1
Dhh	Mm01310203_m1
Bmp4	Mm00432087_m1
Gdf15	Mm00442228_m1
Epo	Mm01202755_m1
Spic	Mm00488428_m1
Flvcr	Mm01320423_m1
Hrg1	Mm00728070_s1

Supplementary Figure Legends

Supplementary Figure S1. Kinetics of stress erythropoietic recovery post PHZ treatment.
(A - H) Characterization of 100% PHZ treated Se-D and Se-A mice.
(A) Representative pictures of hematocrits post PHZ treatment. Se-D mice exhibited severe hemolysis, shown by the dark red color of serum.
(B) *Gdf15* (C) *Bmp4* (D) *Dhh* and (E) *Ihh* mRNA levels in the whole spleen post treatment, n=3-7 per diet.
(F) Corticosteroid and (G) Epo serum level measurement by ELISA post treatment, n=3-6 per diet.
(H) Kidney *Epo* mRNA level post treatment, n=2-7 per diet.
(I - K) Characterization of the mobilization of BM stress erythroid precursors into periphery of 100% PHZ treated Se-D and Se-A mice, n=3-4 per diet.
(I) Phenotypic analysis and (J) proportions of SEPs in PBMCs isolated from peripheral blood of Se-D and Se-A mice on the indicated days.
(K) BFU-E colony assays. Stress BFU-E colony assays were performed to quantitate the number of potential SEPs mobilizing from BM into the peripheral blood. Stress BFU-E numbers are expressed as number generated per 1 x 10^5 PBMCs post 3-day SEDM culture.
Bars are representative of mean±SEM. *p<0.05, **p<0.001, *** p< 0.005, ****p<0.0001.

Supplementary Figure S2. Selenoproteins are required in early stress erythroid progenitors.
(A - C) Percent (A) live cells, (B) cells undergoing apoptosis or necrosis, and (C) ROS production in whole spleen post 50% PHZ treatment, n=4 per diet.
(D) Schematic for the stress erythropoiesis two-stage culture system. In the first stage, BM cells were cultured in SEEM in the presence of necessary factors including Gdf15, Bmp4, Scf and Shh, where SEPs were enriched. Then the culture was shifted to the second culture stage, where cells were cultured in SEDM and differentiated by Epo and hypoxia. For quantitation of SEPs, cells were replated for stress BFU-E colony assays.
(E and F) Colony assays of *Trsp*$^{fl/\Delta}$;CreERT or *Trsp*$^{fl/\Delta}$ control BM cells.
(E) CFU-GM colony assays. BM cells were cultured in complete IMDM media supplemented with IL-3, and Scf in the presence of 4OH-TM for 24Hrs to induce *Trsp* deletion. Cells were then shifted to methylcellulose culture containing IL-3, Scf and GM-CSF, for CFU-GM colony quantitation.
(F) Representative pictures of BFU-E and CFU-GM colony morphology of *Trsp*$^{fl/\Delta}$;CreERT or *Trsp*$^{fl/\Delta}$ BM cells. (G and H) Spleen sizes and total spleen cell counts of recipient mice transplanted with *Trsp*$^{\Delta/\Delta}$ or control BM cells post BMT on day 8 and day 10. (G) Spleen sizes(left) and representative pictures (right). (H) Cell counts. (I - K) Chimeric mice were generated by BMT using *Trsp*$^{fl/\Delta}$;CreERT or *Trsp*$^{fl/\Delta}$ mice as donors and *Trsp*$^{fl/fl}$ mice as recipients. After 8 weeks reconstitution, *Trsp* gene deletion was induced by i.p. tamoxifen. Mice were administrated with 100% PHZ a week later to induce stress erythropoiesis. (I) Schematic of the experiment workflow.
(J) Total cell numbers of spleen SEPs. SEPs were characterized by Kit$^+$Sca-1$^+$CD133$^+$CD34$^+$.
(K) Hematocrits post PHZ treatment, n=3-4 per group. Bars are representative of mean±SEM. *p<0.05, **p<0.001, *** p< 0.005, ****p<0.0001.

Supplementary Figure S3. Erythroblast terminal differentiation during Se deficiency.
(A) Characterization of Ter119^{hi}CD71^{lo}FSC^{lo} terminal cells with CD44 (shown in blue) in spleen of Se-D and Se-A mice post 50% PHZ treatment. On day 2, there were more reticulocytes and RBCs characterized by CD44^{lo}FSC^{lo} in the Se-A mice compared to Se-D mice. On day 3, there was accumulation of polychromatic and orthochromatic cells in Se-D mice.

(B - E) Quantification of (A) splenic ProEs, (B) splenic BasoEs, (C) BM ProEs, and (D) BM BasoEs post 100% PHZ treatment, n=4-7 per diet. Top, percentage; bottom, total cell counts.
(F and G) Percent ROS^+ (E) BasoEs and (G) ProEs in the spleen post 50% PHZ treatment, n=4 per diet. (H) Percent apoptotic and necrotic spleen ProEs of the Se-D and Se-A mice post 50% PHZ treatment, n=4 per diet. (I) Schematic of Caspase-3 (Casp3) mediated ProE to BasoE transition. Cleavage of GATA-1 or insufficient cleavage of Lamin B mediated by Casp3 blocks ProE to BasoE maturation. (J) Western blotting (left) and densitometry (right) of Lamin B protein expression in sorted splenic ProEs from mice on day 3 post 50% PHZ treatment, n=2-3 per diet.
Bars are representative of mean±SEM. *p<0.05, **p<0.001, *** p< 0.005, ****p<0.0001.

Supplementary Figure S4. Transcriptomic analysis of BasoE during stress erythropoiesis.
(A - D) Affymetrix transcriptomic analysis of sorted spleen BasoEs from Se-D or Se-A mice on day 3 post 50% PHZ treatment, n=3 per diet. The analysis methods were the same as for the ProEs described in the main figure, Fig. 4. (A) Heat map of hierarchical clustering analysis with cutoff at |fold change|> 2. (B) Scatter plot of differential expression analysis with cutoff at |fold change|> 2. (C) Pathway enrichment analysis. Pathways of interest with *p<0.05* are shown.
(D) *SelenoW* average expression level in Se-D and Se-A BasoEs by transcriptomic analysis.

Supplementary Figure S5. SelenoW plays a role in erythroblast terminal differentiation.
(A) SelenoW protein expression in *Trsp*$^{fl/\Delta}$;CreERT or *Trsp*$^{fl/\Delta}$ BM cells with or without *in vitro* 4-OHT treatment for 48Hrs, Δ: *Trsp*$^{fl/\Delta}$;CreERT, Ctrl: *Trsp*$^{fl/\Delta}$.
(B) SelenoW expression in transduced TgCas9-GFP BM cells with sgRNA or control lentivectors post 7 day SEEM culture. (C) ENCODE ChIP-seq analysis of GATA-1 and CTCF binding of *SelenoW* in G1E-ER4 cells post E2 treatment, three replicates. (D - G) Analysis of SelenoW knockout or control G1E and G1E-ER4 cells post E2 treatment. (D) SelenoW and glutathione peroxidase 1 (Gpx1) expression at 48Hrs, n=3 per group. SelenoW was absent but Gpx1 was not affected. (E) Representative pictures of hemoglobin staining by neutral benzidine in G1E-ER4 cells post E2 treatment. (F) Representative spectrums of cellular heme level for G1E-ER4. Three independent measurements. (G) Cell cycle analysis. Percent G_0/G_1 phase and S-phase cells in the culture, n=3 per cell type. (H) *HuSelenoW* knockdown (KD) was confirmed by qRT-PCR represented by relative expression to *Gapdh*. Frozen human bone marrow cells from three subjects were thawed 24Hrs prior transduction with huSelenoW dCas9-KRAB/sgRNA lentivector or dCas9-KRAB empty lentivector control. The cells were transduced by spinoculation, and left in culture with virus overnight. On the second day, cells were transferred to SEEM and cultured for 7 days following by 3-day SEDM culture. Transduced (GFP^+) cells were purified by sorting.

Supplementary Figure S6. Macrophages are impaired in Se-D mice during stress erythropoiesis.
(A) Analysis of α_4 integrin expression on erythroblast precursors (left) post 100% PHZ treatment, n=3 per diet. $\alpha_4^+CD71^+$cells are $Ter119^+$ with relatively big cell sizes (middle). Right, quantitation of $\alpha_4^+CD71^+$cells in the spleen.
(B and C) Representative graphs of flow cytometry analysis of $F4/80^+$ cells in the spleen of Se-D and Se-A mice post (B) 100% and (C) 50% PHZ treatment.
(D) Representative graphs of flow cytometry analysis of macrophage CD11b expression in the spleen of Se-D and Se-A mice post 50% PHZ treatment.
(E) Flow cytometry analysis gating strategy of spleen RPMs and monocytes. RPMs were marked as $CD11b^{lo}$ $F4/80^+$ $Vcam\text{-}1^+$. Monocytes were identified as $CD11b^+CD115^+$.
Bars are representative of mean±SEM. *p<0.05, **p<0.001, *** p< 0.005, ****p<0.0001.

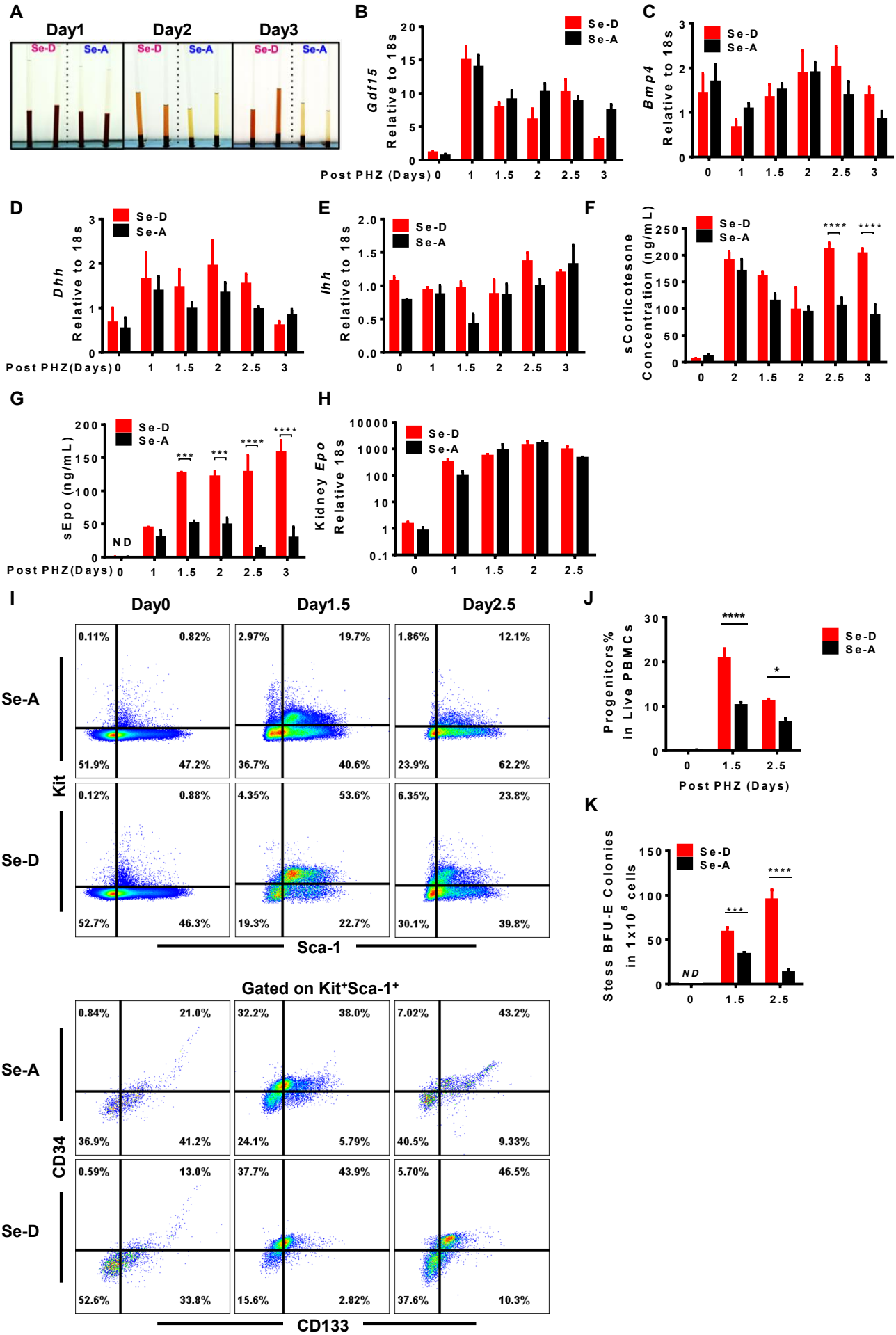
Supplementary Figure S7. Incompetency of erythroid forming microenvironment during Se deficiency.

(A - C) Representative graphs of flow cytometry analysis of splenic erythroblastic islands post 50% PHZ treatment. (A) RPMs in EBIs. (B) Analysis of Vcam-1 and (C) CD169 expression on EBI macrophages. (D) Schematic of heme delivery and synthesis pathways during erythroblast maturation in EBIs. Macrophages take up red cells by erythrophagocytosis and degraded in phagolysosome. Heme is then released to macrophage cytoplasm via heme transporter Hrg1. Free heme can be degraded into iron by Hmox1 or export out of macrophages through heme exporter Flvcr. In erythroblasts, heme is imported via Hrg1, and then further incorporated into hemoglobin. (E - H) Disrupted heme transportation and heme homeostasis in EBIs from 50% PHZ treated Se-D mice. (E) *Flvcr*, (F) *Hrg1* and (G) *Hmox-1* expression in EBIs, n=4 per diet. (H) *Hrg1* average expression level in ProEs from spleens of 50% PHZ treated Se-D and Se-A mice on day 3 by transcriptomic analysis. Bars are representative of mean±SEM. *p<0.05, **p<0.001, *** p< 0.005, ****p<0.0001.

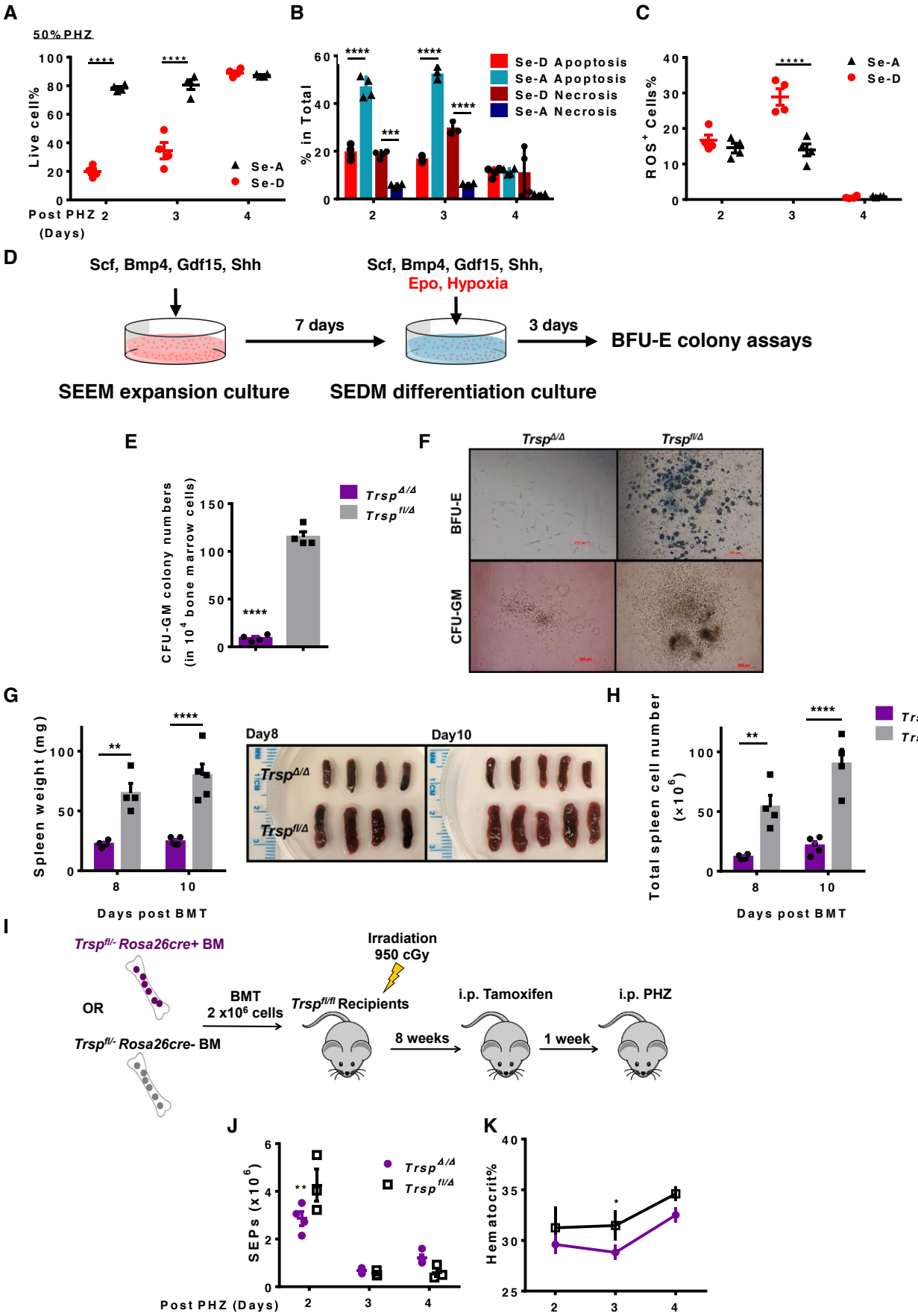
Supplementary Figure S8. SelenoW regulates erythroid differentiation potentially through Yap cellular translocation.

Protein expression of Yap in cytosol and nucleus in SelenoW knockout BM cells in stress erythropoiesis two-stage culture (top). Densitometry ratio of cytoplasmic Yap over nuclear Yap in SelenoW knockout or control BM cells post SEEM (bottom left) and SEDM culture (bottom right), n=3-4 per group. Bars are representative of mean±SEM. *p<0.05, **p<0.001, *** p< 0.005, ****p<0.0001.

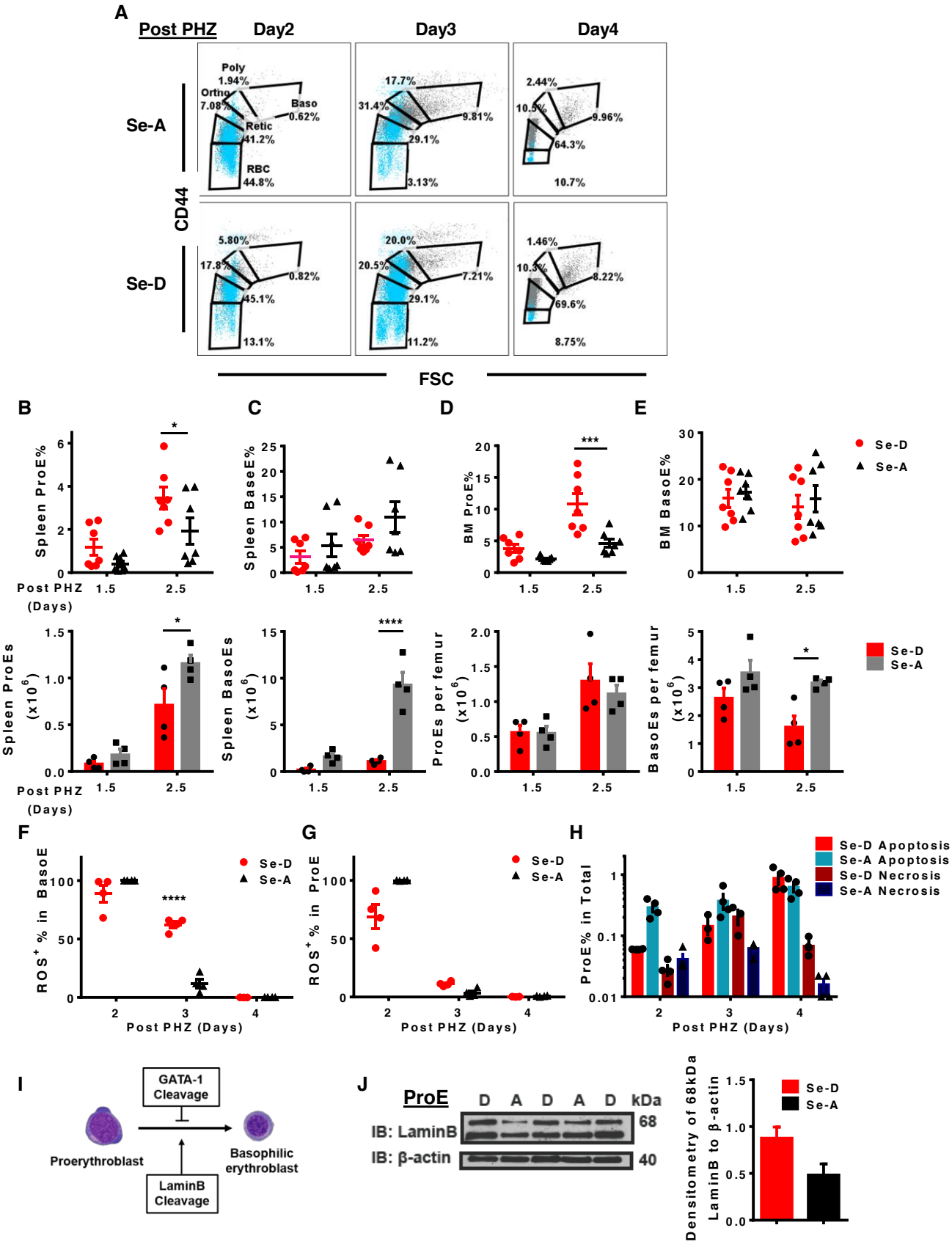
Supplementary Figure 1



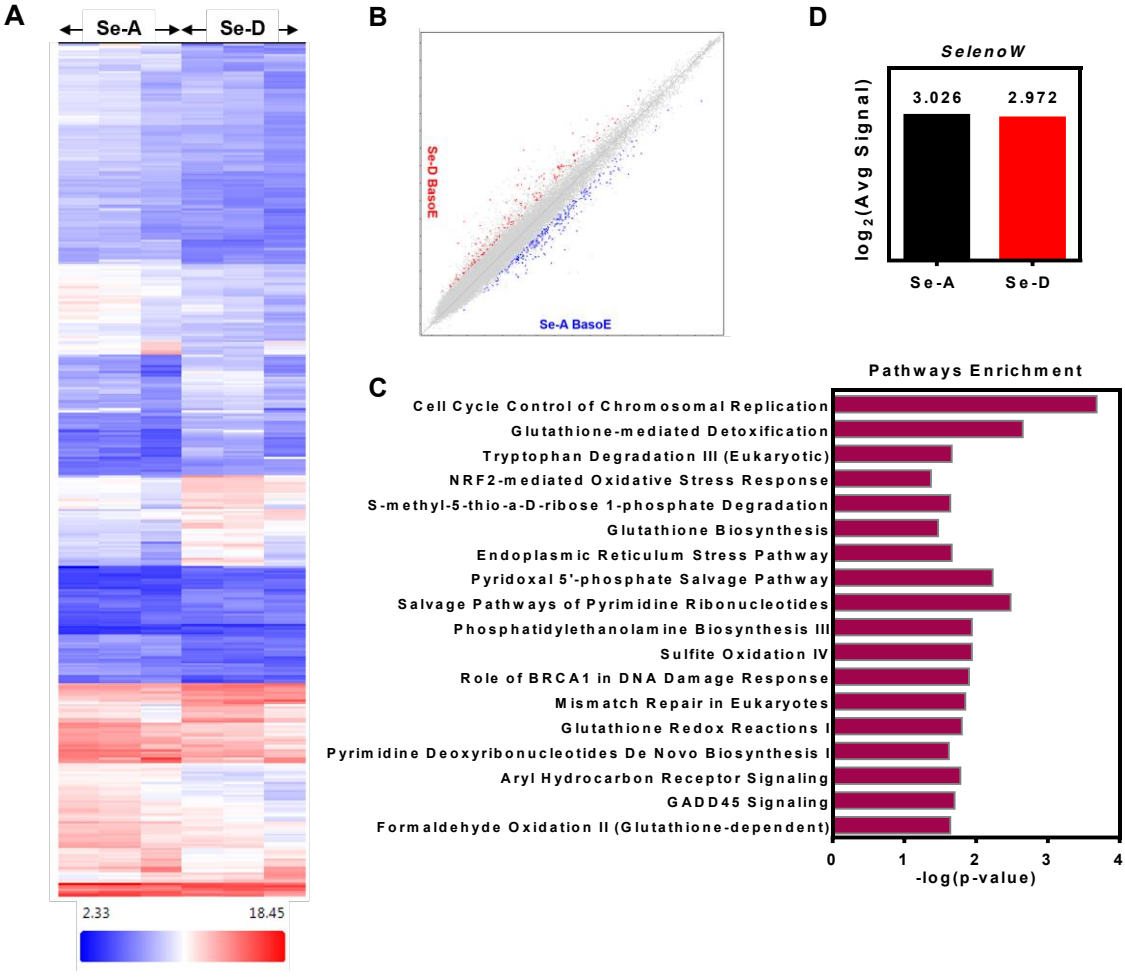
Supplementary Figure 2



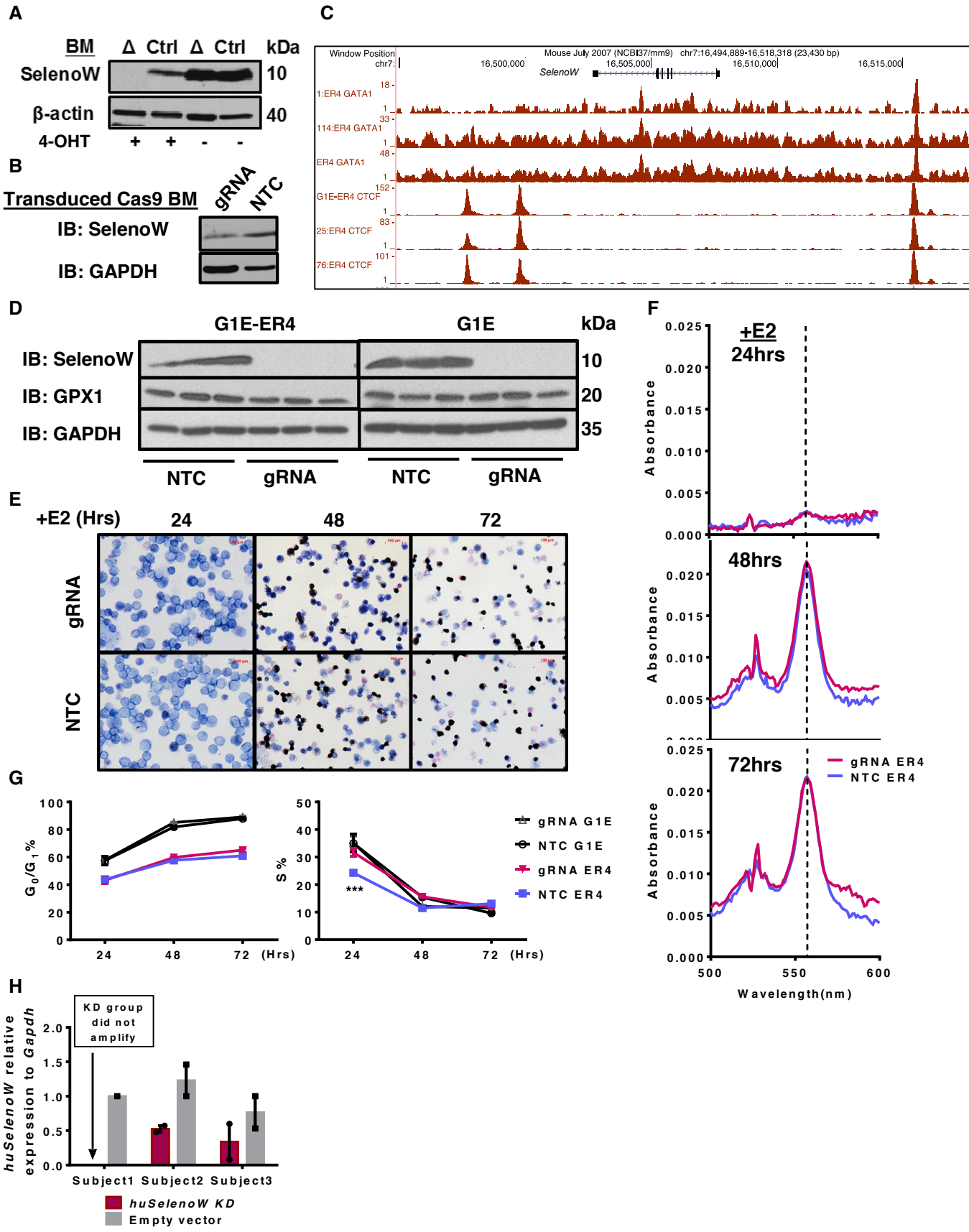
Supplementary Figure 3



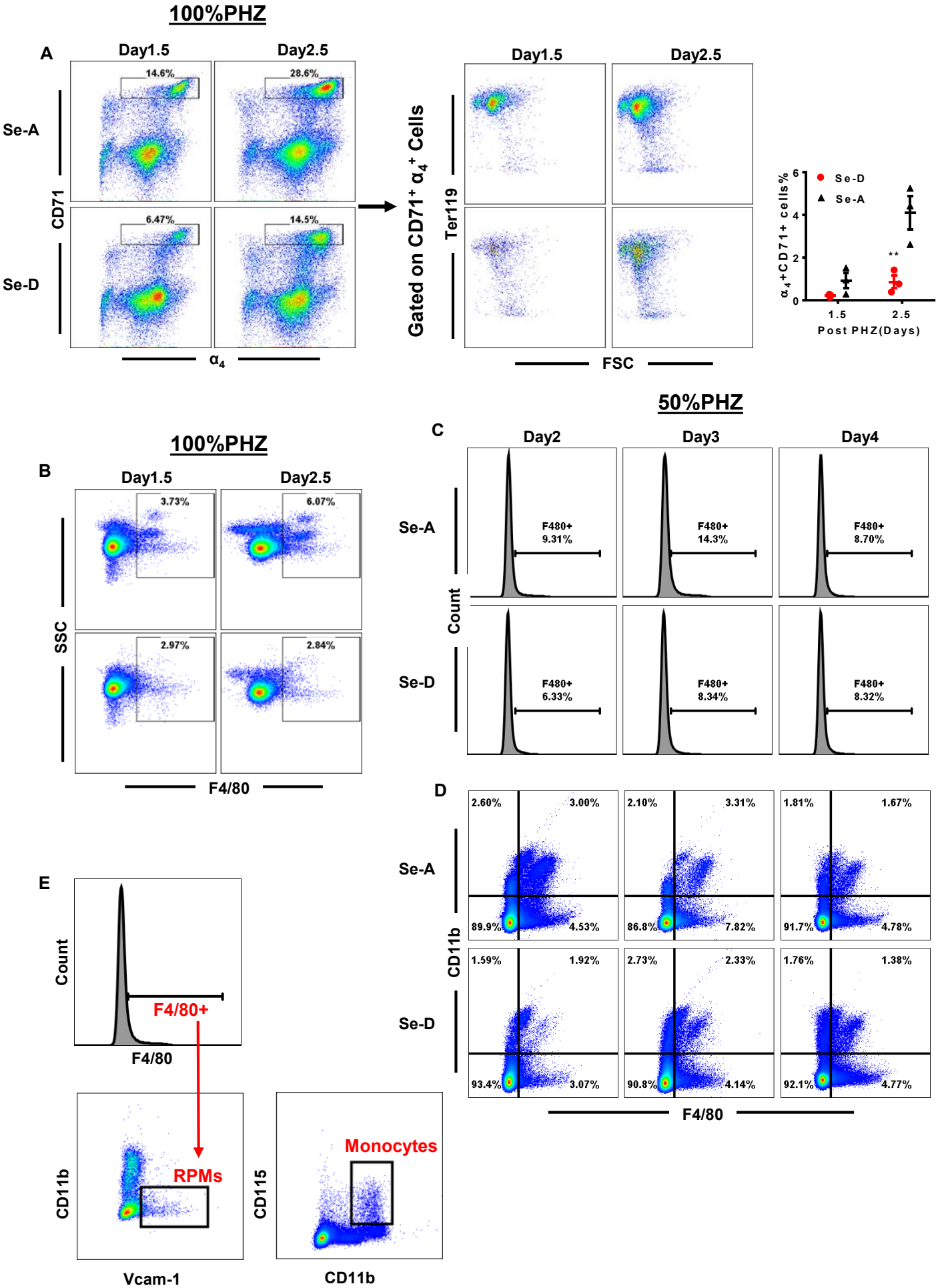
Supplementary Figure 4



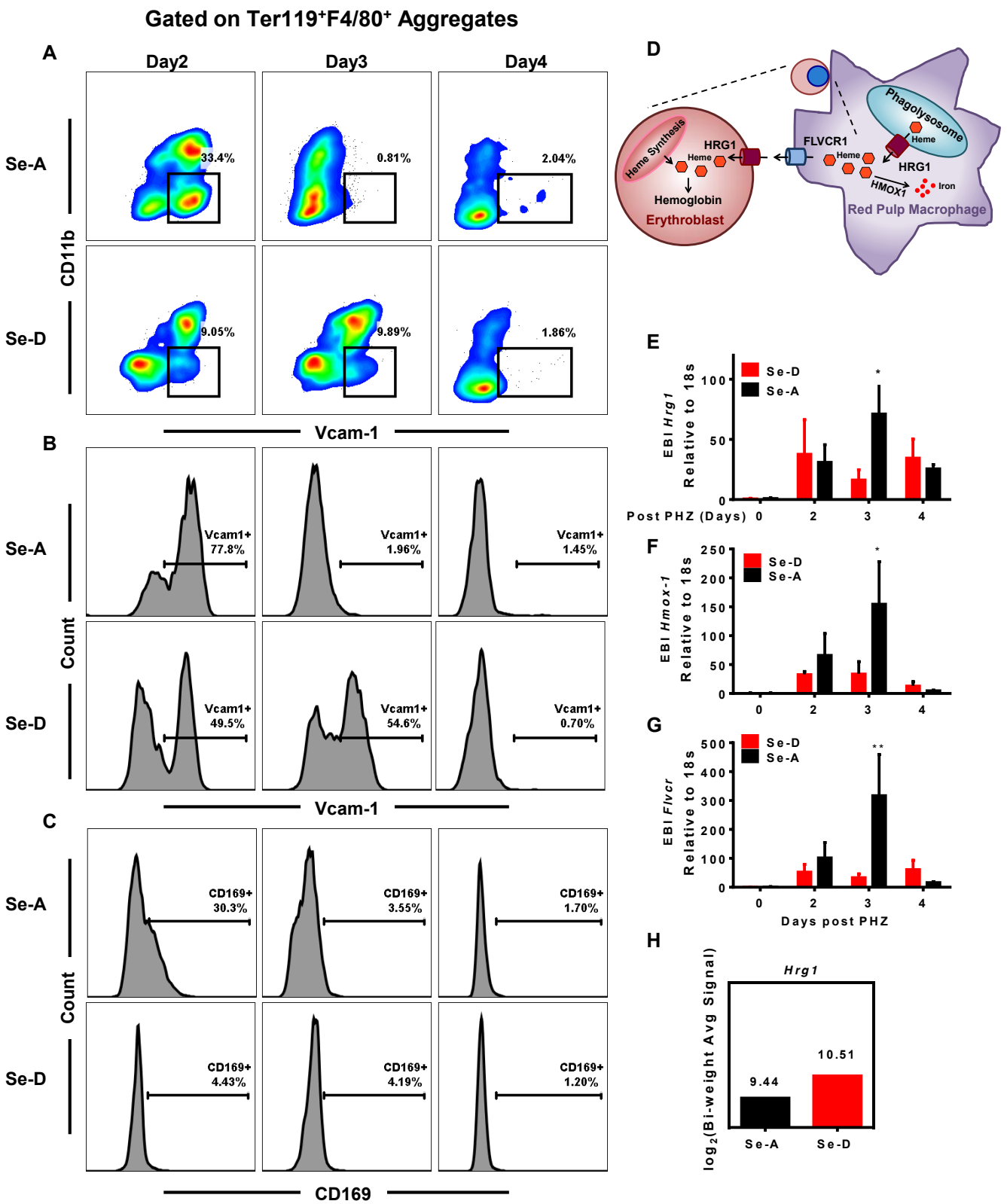
Supplementary Figure 5



Supplementary Figure 6



Supplementary Figure 7



Supplementary Figure 8