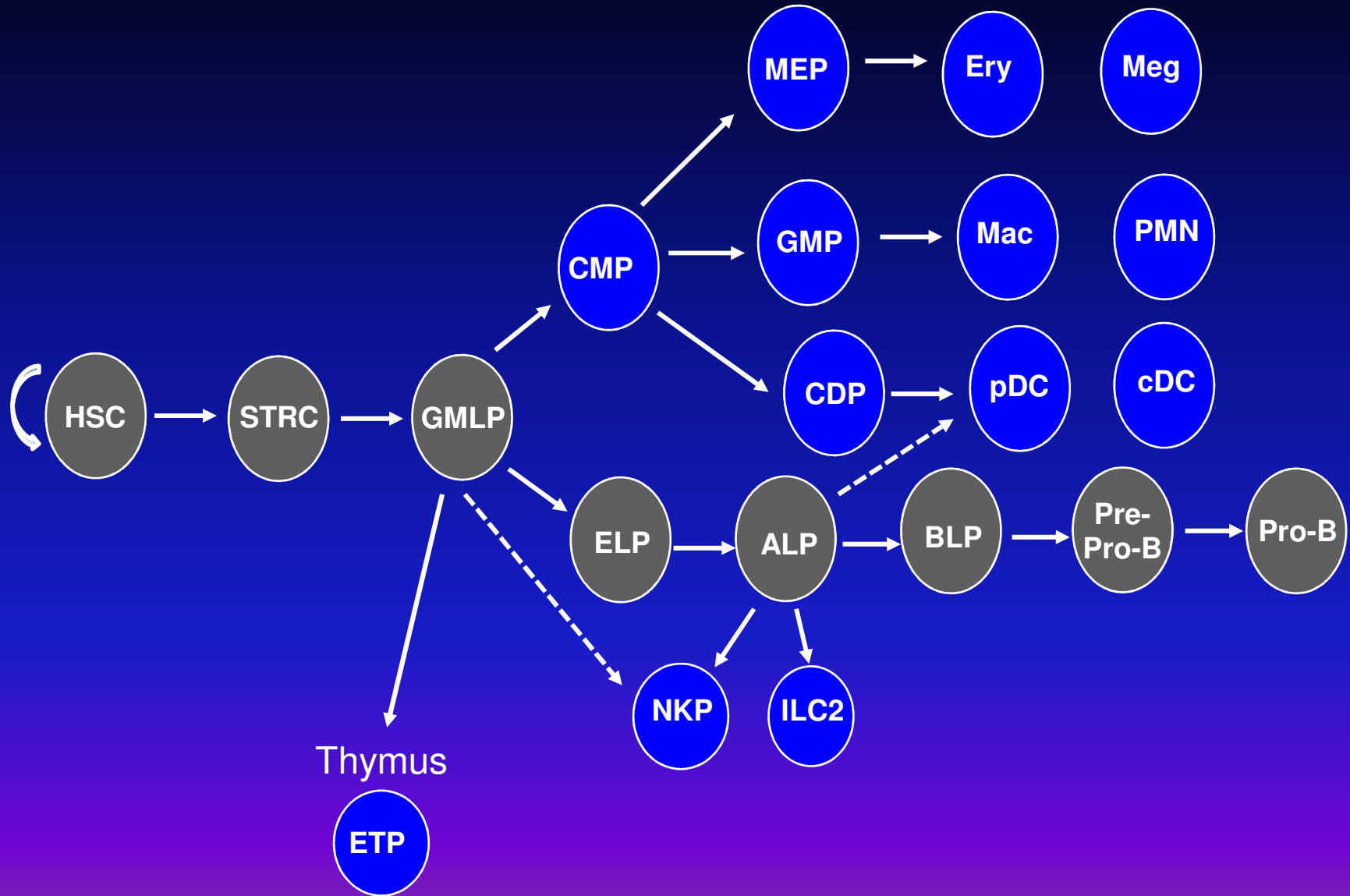


# Deciphering HoxA9 function in multipotential progenitor biology and B cell development

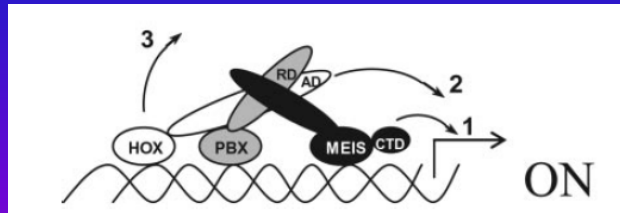
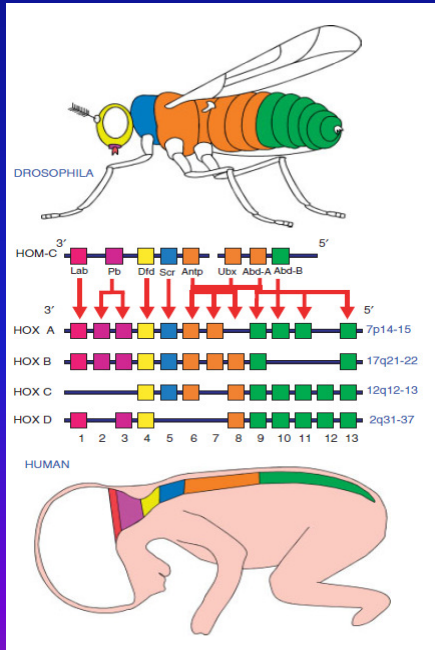
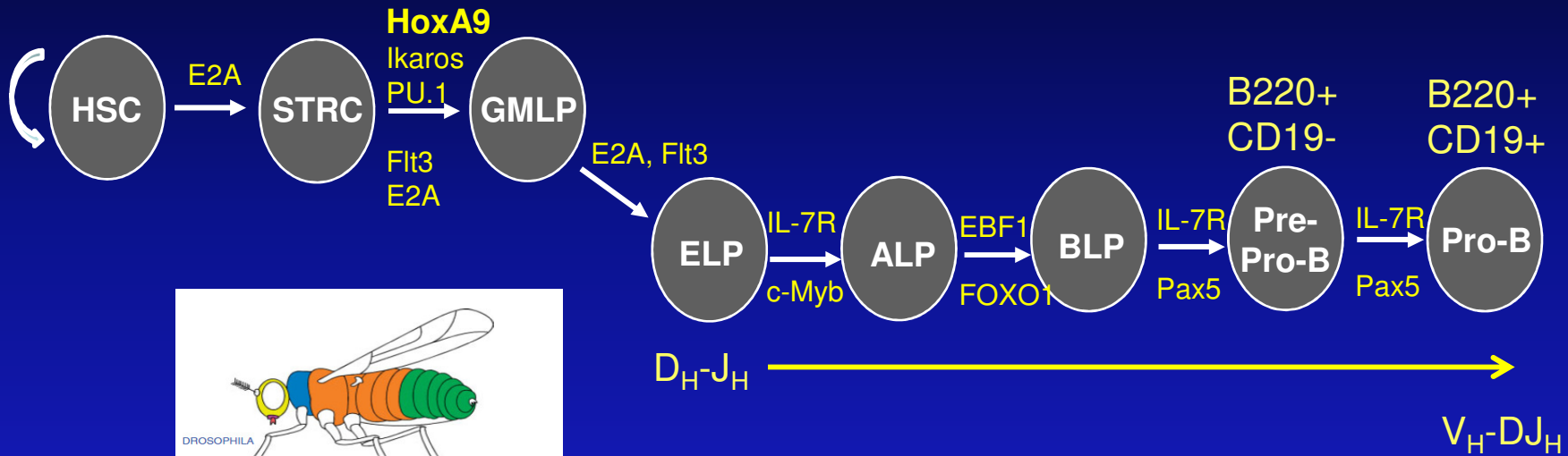
Kay L. Medina, PhD  
Associate Professor  
Dept. of Immunology  
Mayo Clinic College of Medicine



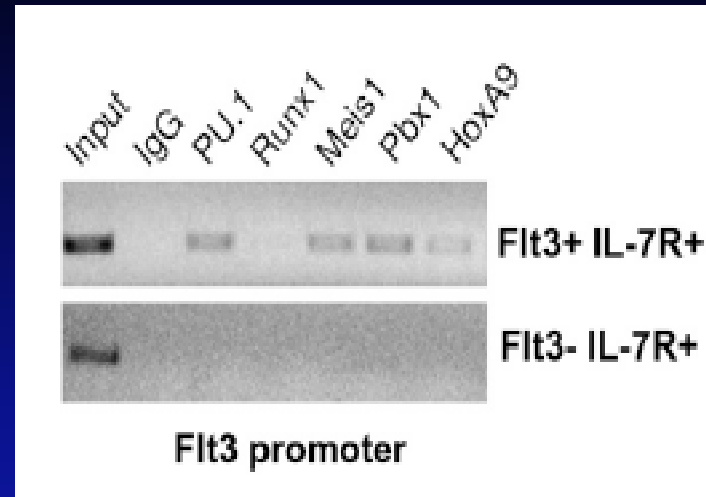
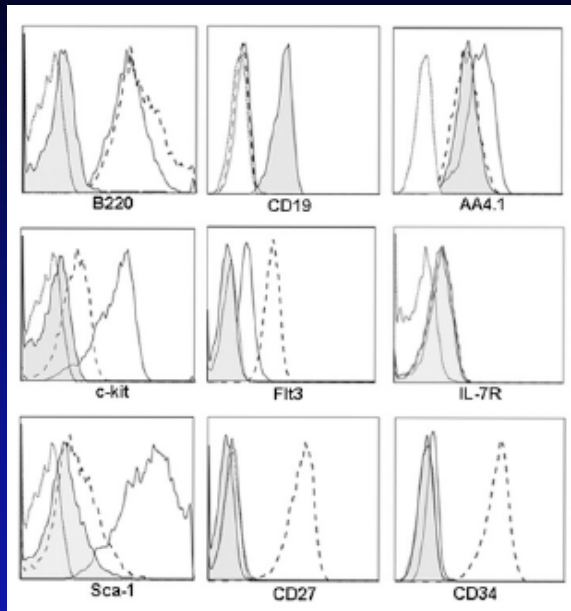
## Overview of adult hematopoiesis in the mouse



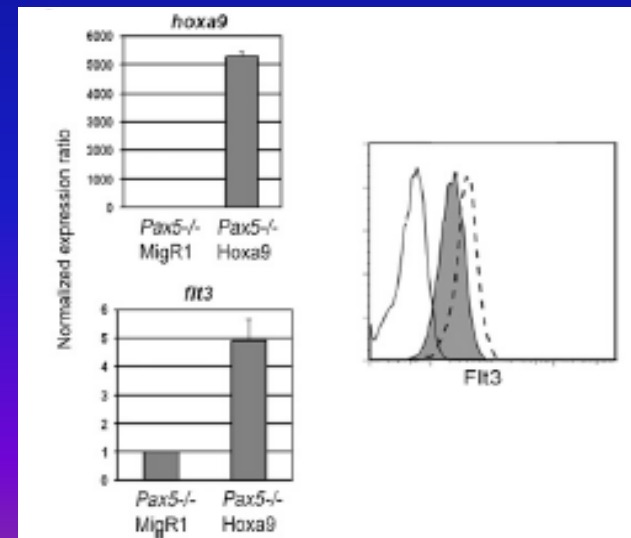
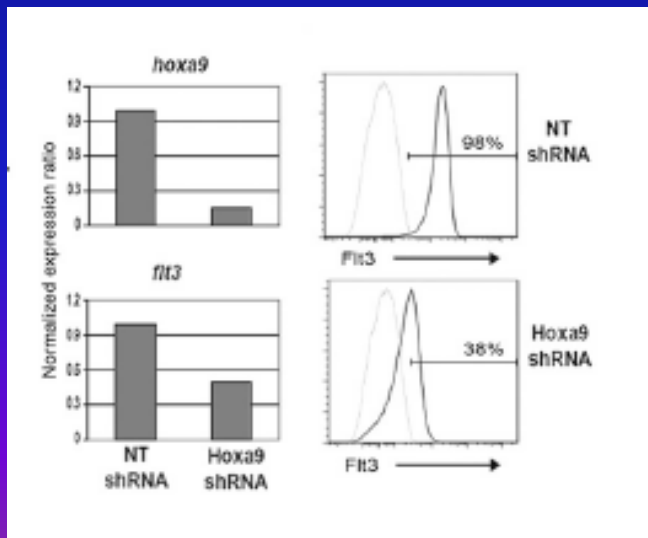
# Sequentially-acting regulatory circuits orchestrate B cell fate specification and commitment



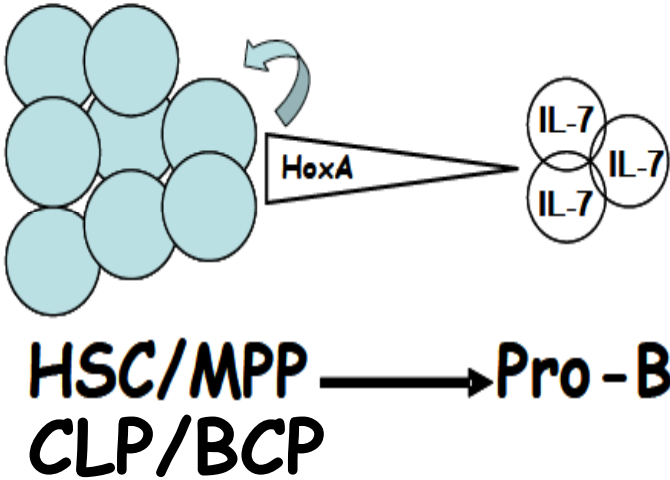
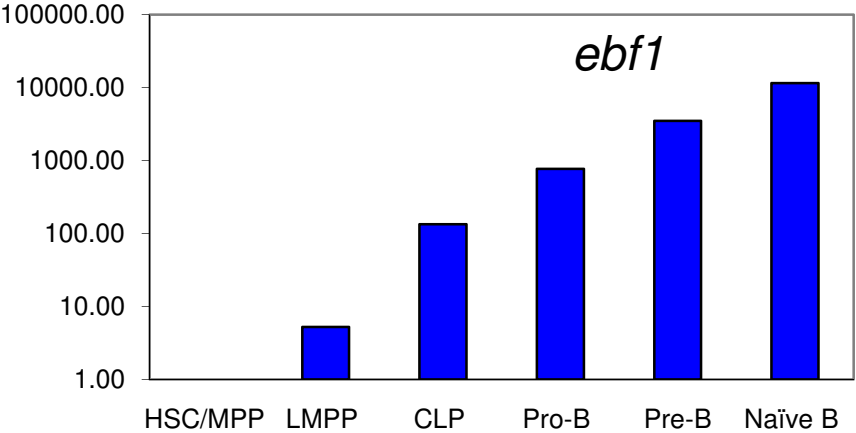
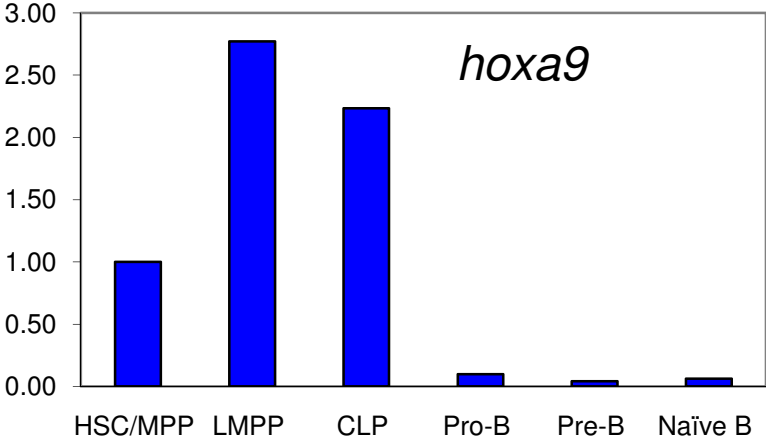
# Hoxa9 regulates Flt3 in lymphohematopoietic progenitors



Gwin and Medina, JI, 2010

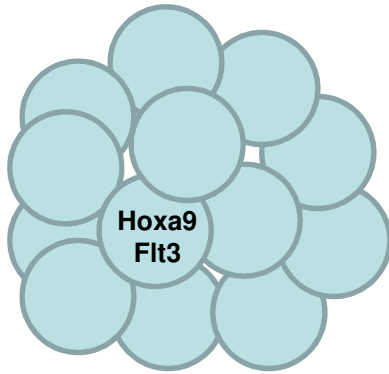


# Inverse expression of HoxA9 and EBF1 in lymphoid/B cell precursors

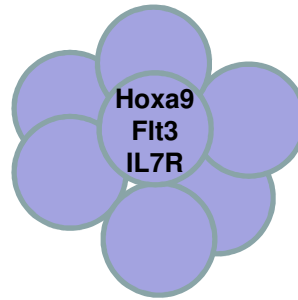


HSC/MPP program

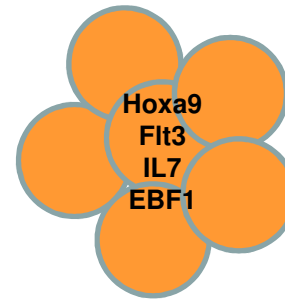
Alternate lineage programs



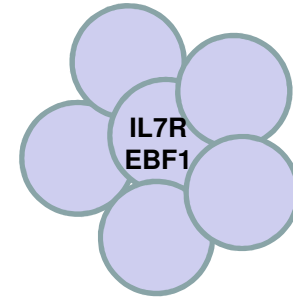
Myeloid-Lymphoid progenitor



All-Lymphoid progenitor



B-Lymphoid progenitor

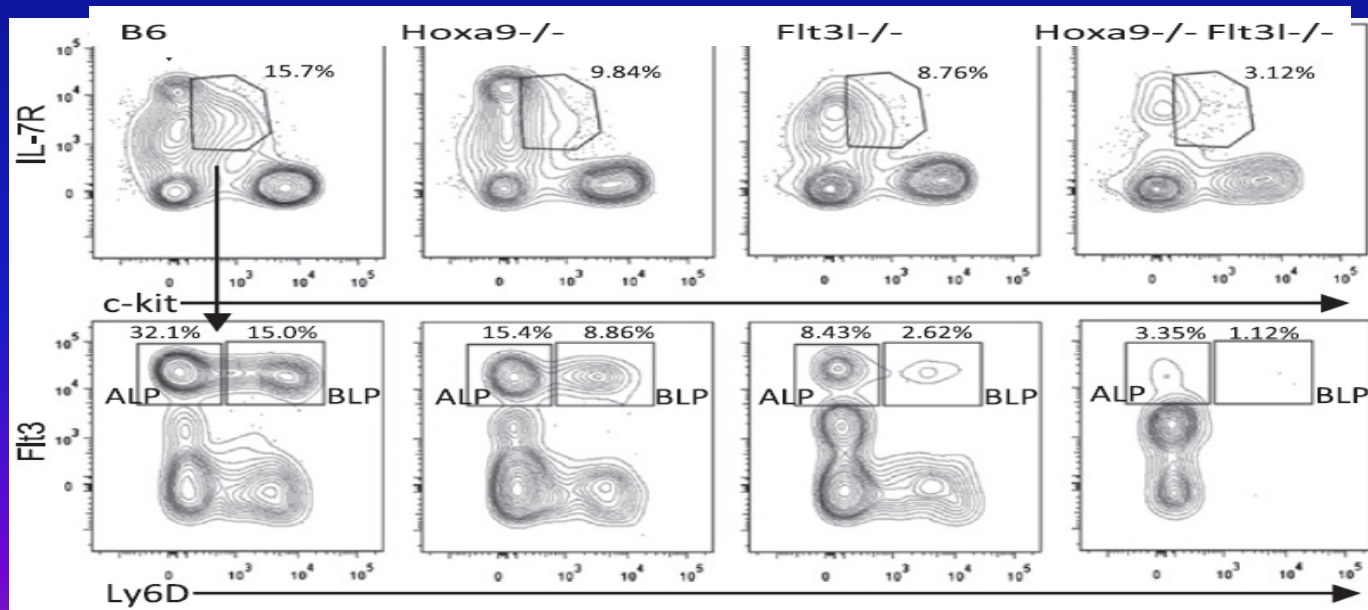
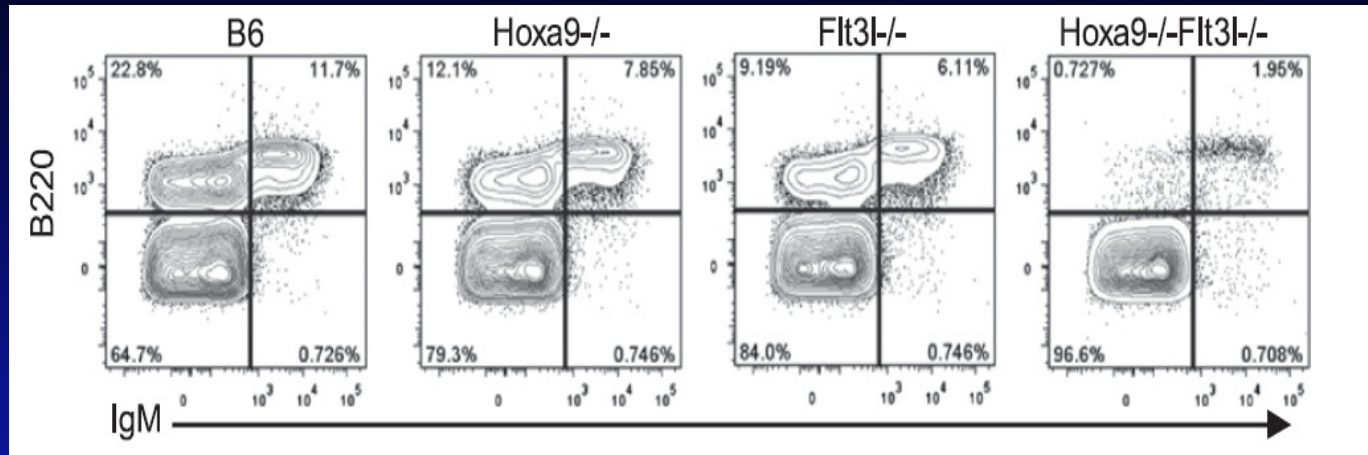


Pro-B cell

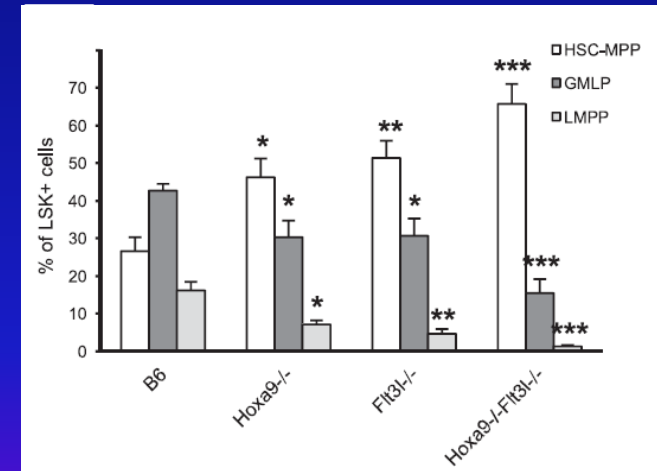
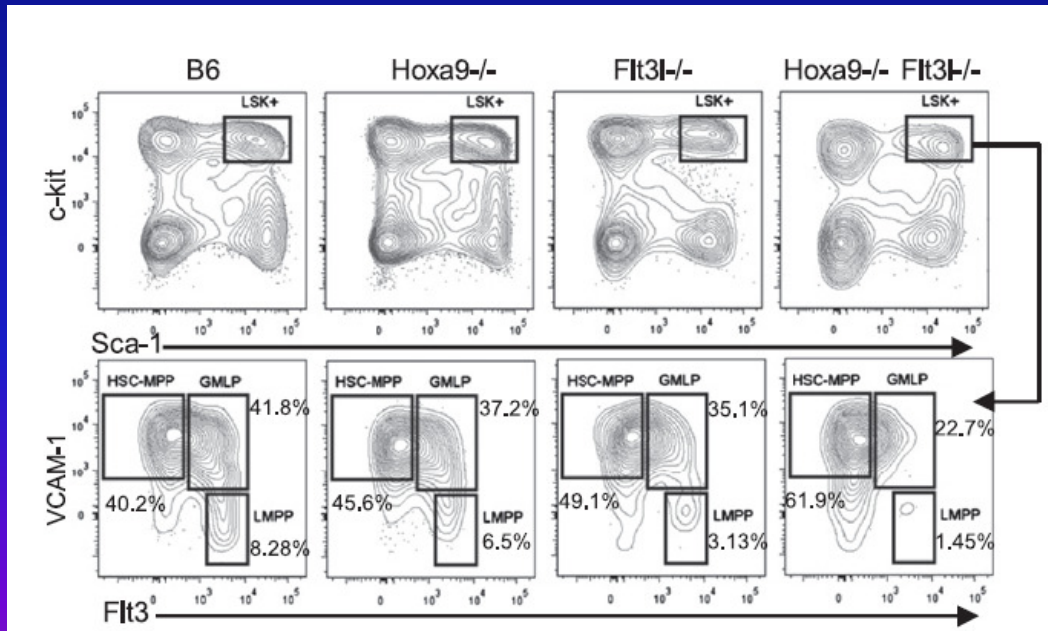
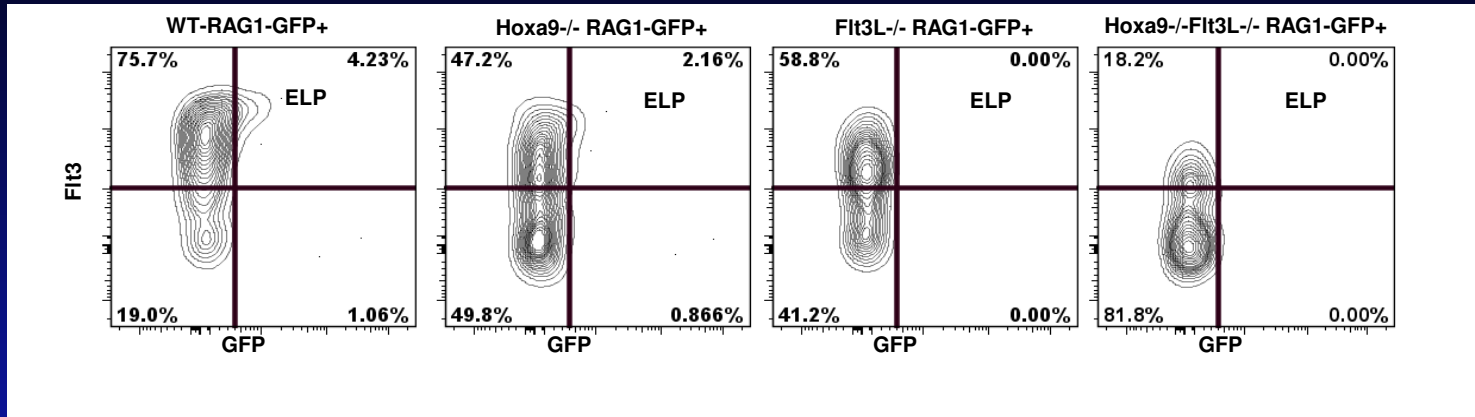
Transcription factors, signaling molecules, chemokines, microRNAs

B cell program

*hoxa9*<sup>-/-</sup> *flt3l*<sup>-/-</sup> mice exhibit a severe lympho-hematopoietic block



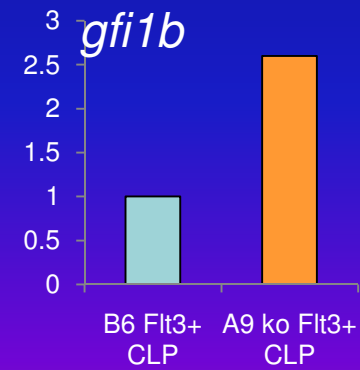
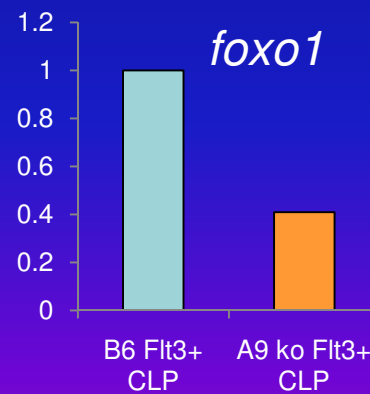
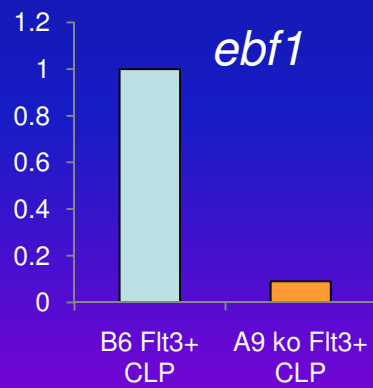
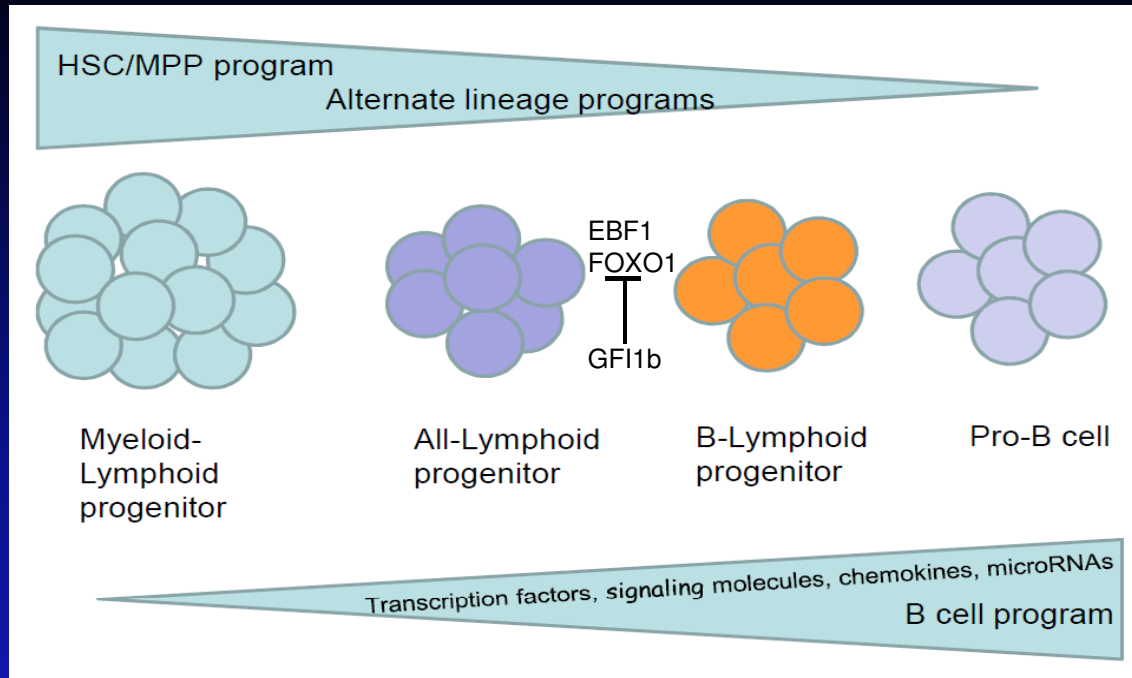
# HoxA9 and Flt3 signaling function together to establish the multipotential progenitor pool competent to undergo lymphoid priming



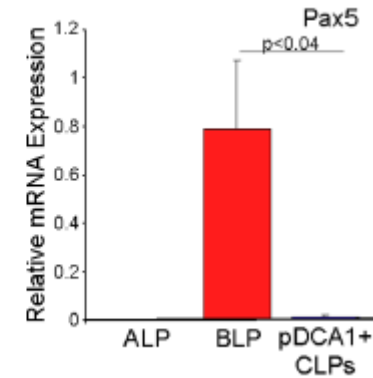
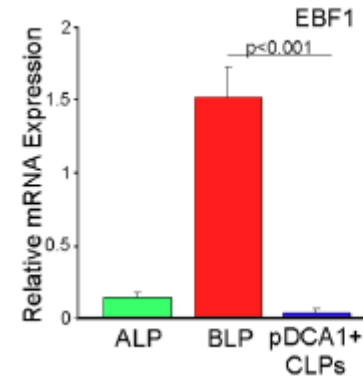
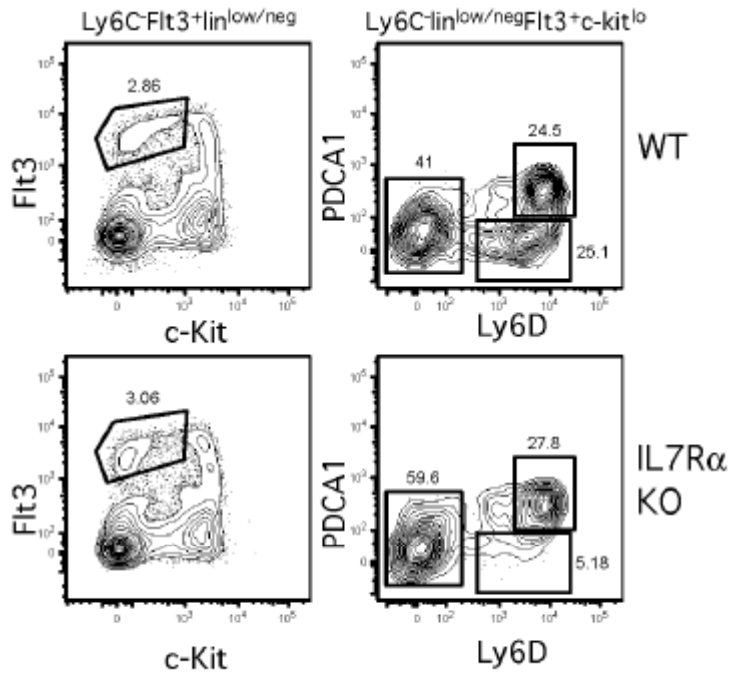
*hoxa9*<sup>-/-</sup> *flt3l*<sup>-/-</sup>



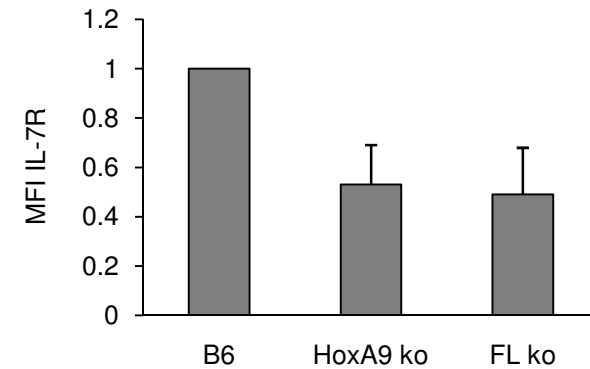
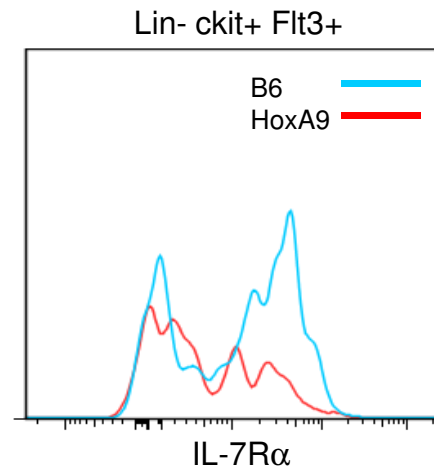
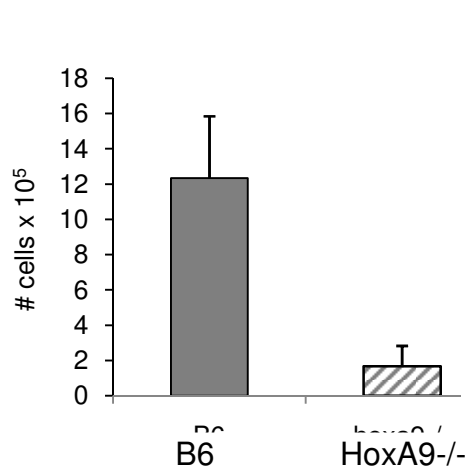
# The role of HoxA9 in B cell fate specification.



# HoxA9<sup>-/-</sup> hematopoietic progenitors have impaired IL-7 signaling

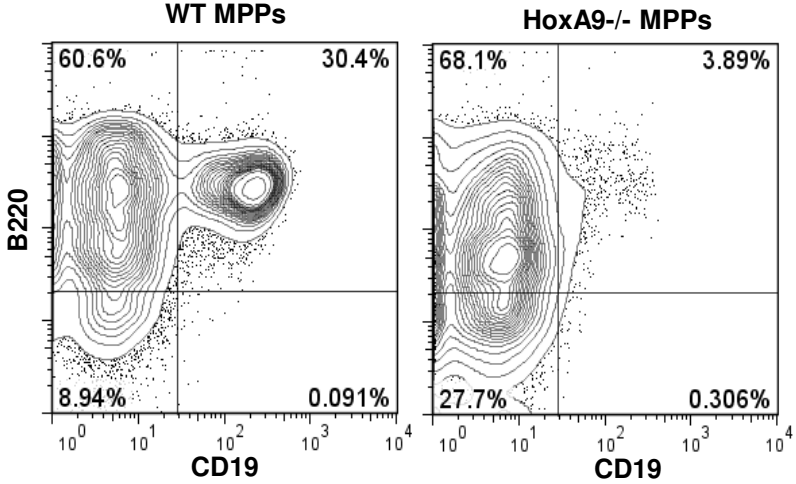
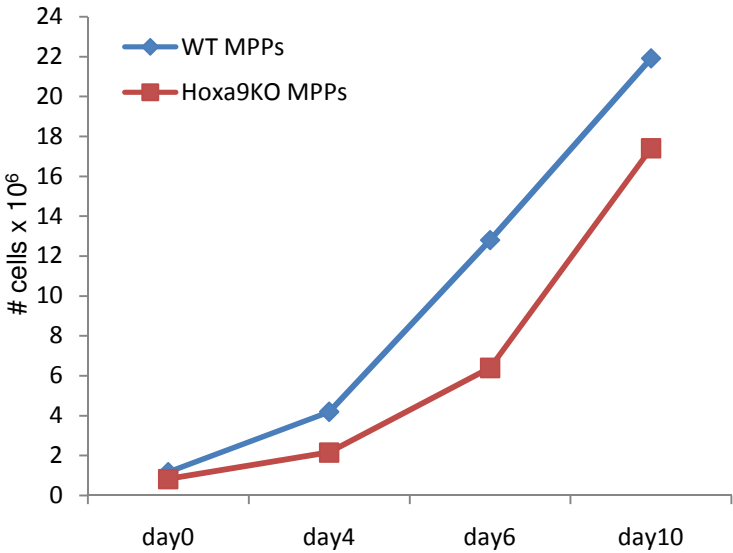
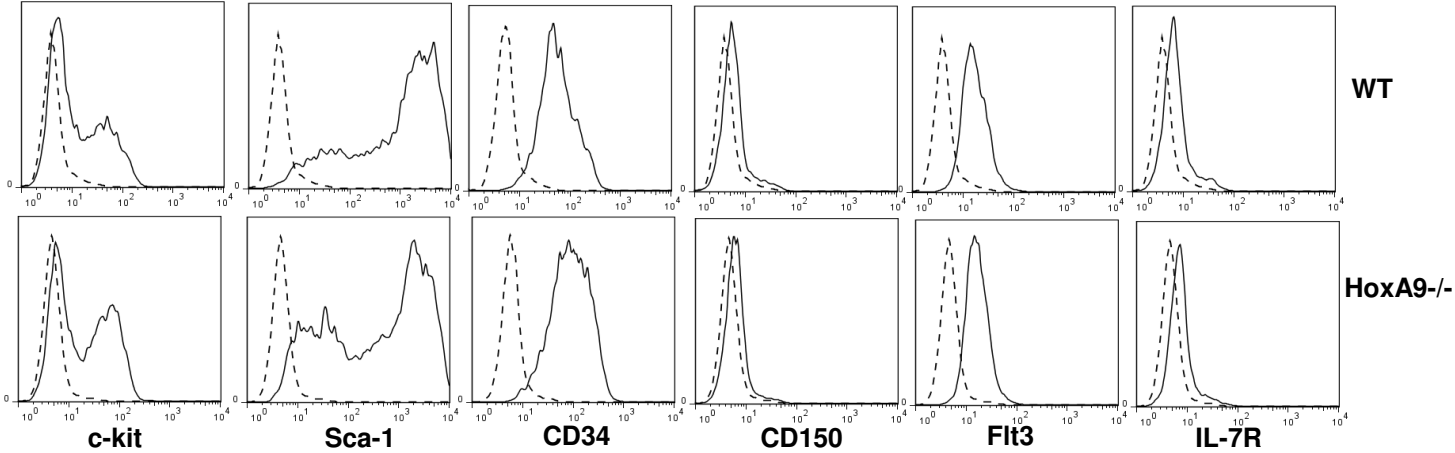


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 October 2013 | Volume 8 | Issue 10 | e78408

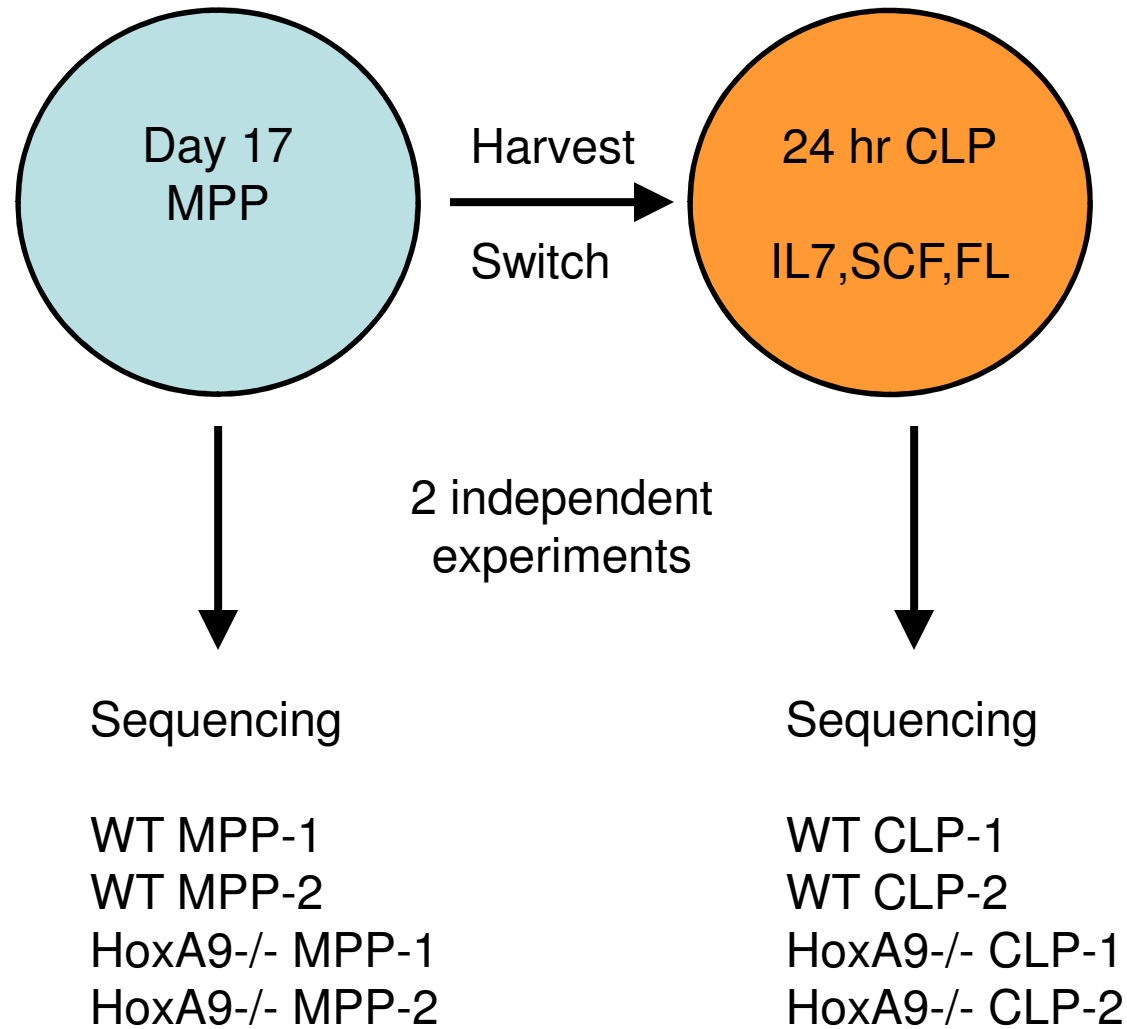


# Culture model to identify HoxA9 target genes critical for B cell development

Lin- c-kit cells cultured for 17 days in SCF+FL+Tpo+IL-6



# RNA-Seq Platform



# Summary of RNA-Seq Platform

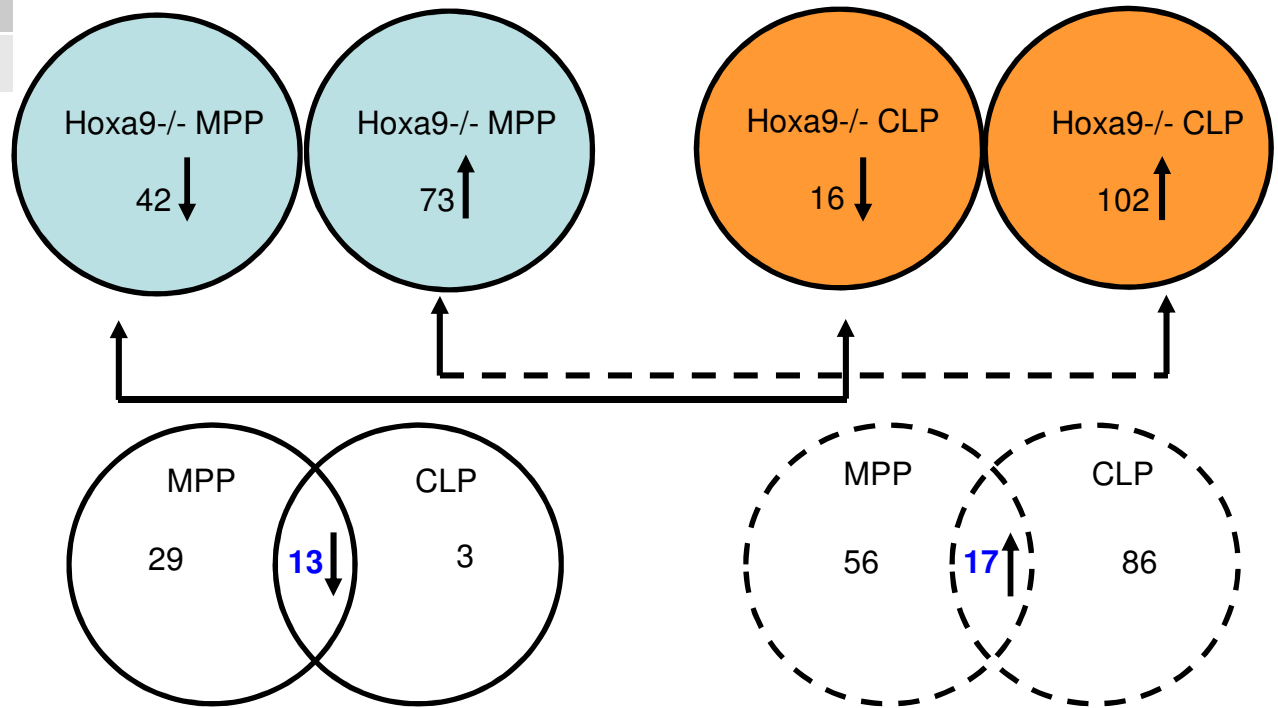
Sample	Total Reads
Hoxa9ko-CLP-1	89,662,470
Hoxa9ko-CLP-2	86,812,194
Hoxa9ko-MPP-1	79,030,174
Hoxa9ko-MPP-2	102,001,936
WT-CLP-1	108,111,316
WT-CLP-2	118,748,182
WT-MPP-1	98,958,636
WT-MPP-2	99,110,526

Read length:50bp

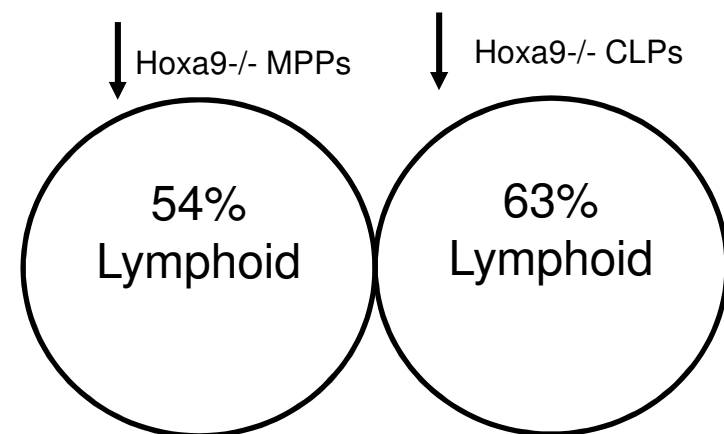
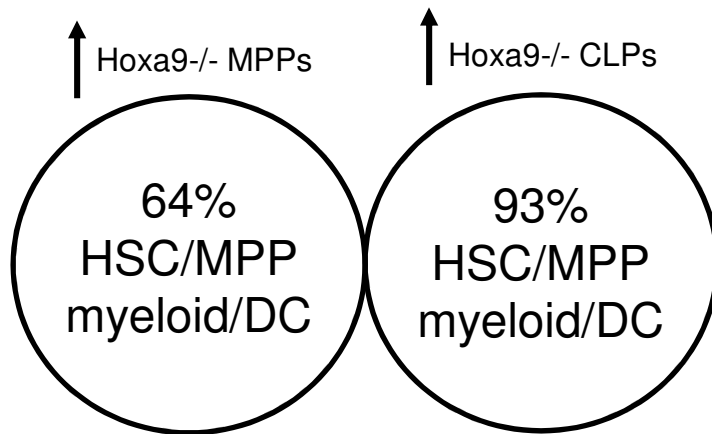
40-50X depth of coverage/gene

Differential expression cutoff: absolute fold change 1.4

False discovery rate of  $\geq 0.1$ ;  $p > 0.05$



# Hoxa9-deficiency impairs lymphoid priming and downregulation of HSC/MPP and/or alternative lineage gene programs



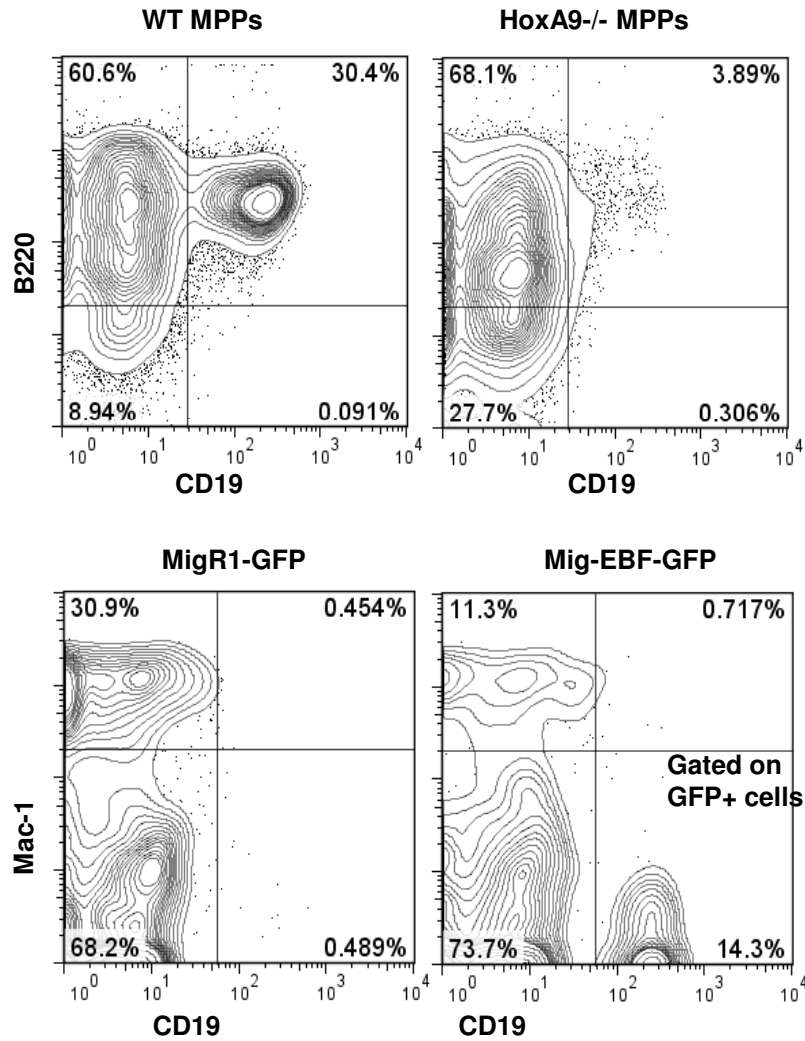
## Shared upregulated

Lcn2 – lipocalin 2 – **neutrophil**  
Mgam – maltase-glucoamylase - **neutrophil**  
Clec4b – ATP binding cassette - **DC**  
Adam23 – disintegrin and metalloproteinase - **DC**  
Pglyrp1 – peptidoglycan recognition protein - **neutrophil**  
Elane – elastase – **macrophage/HSC/MPP**  
Abca13 – ATP binding cassette - **neutrophil**  
Ehd3 – EH domain containing 3 – **T cells**  
Dio2 – deiodinase – **HSC/MPP**  
Mpo – myeloperoxidase - **monocytes**  
Vcam1 – vascular cell adhesion molecule 1 – **HSC/MPP**  
Dach1 – dachshund - **neutrophil**  
**Ppic** – peptidylprolyl isomerase C – **HSC/MPP**  
**Rab38** – member of RAS family - **macrophage**  
Mgl2 – **macrophage** galactose N-acetyl-galactosamine specific  
Ikzf2 – ikaros zinc finger 2; Helios – **HSC/T cells/T regs**  
**Gata2** – **HSC/MPP**

## Shared downregulated

**Rag1** – recombinase activating gene – **lymphocytes**  
**Gfra1** – sperm stem cell self renewal - **BCPs**  
Rag2 - recombinase activating gene - **lymphocytes**  
Ppfa4 – protein tyrosine phosphatase – spl DC / Macs  
Slc15a2 – H+/peptide transporter - **BCPs**  
P2rx3 – purinergic receptor P2X - **BCPs**  
Cdh17 – cadherin 17 - **BCPs**  
**Cecr2** – cat eye syndrome - **BCPs**  
Gimap4 – GTPase - **BCPs**  
**Lin28b** - regulator adult to fetal HSC; let7 biogenesis - **BCPs**  
**Cd27** – member of TNF receptor family – **MPPs/BCPs**  
**Igfbp3** – insulin growth factor 2 binding protein - **BCPs**

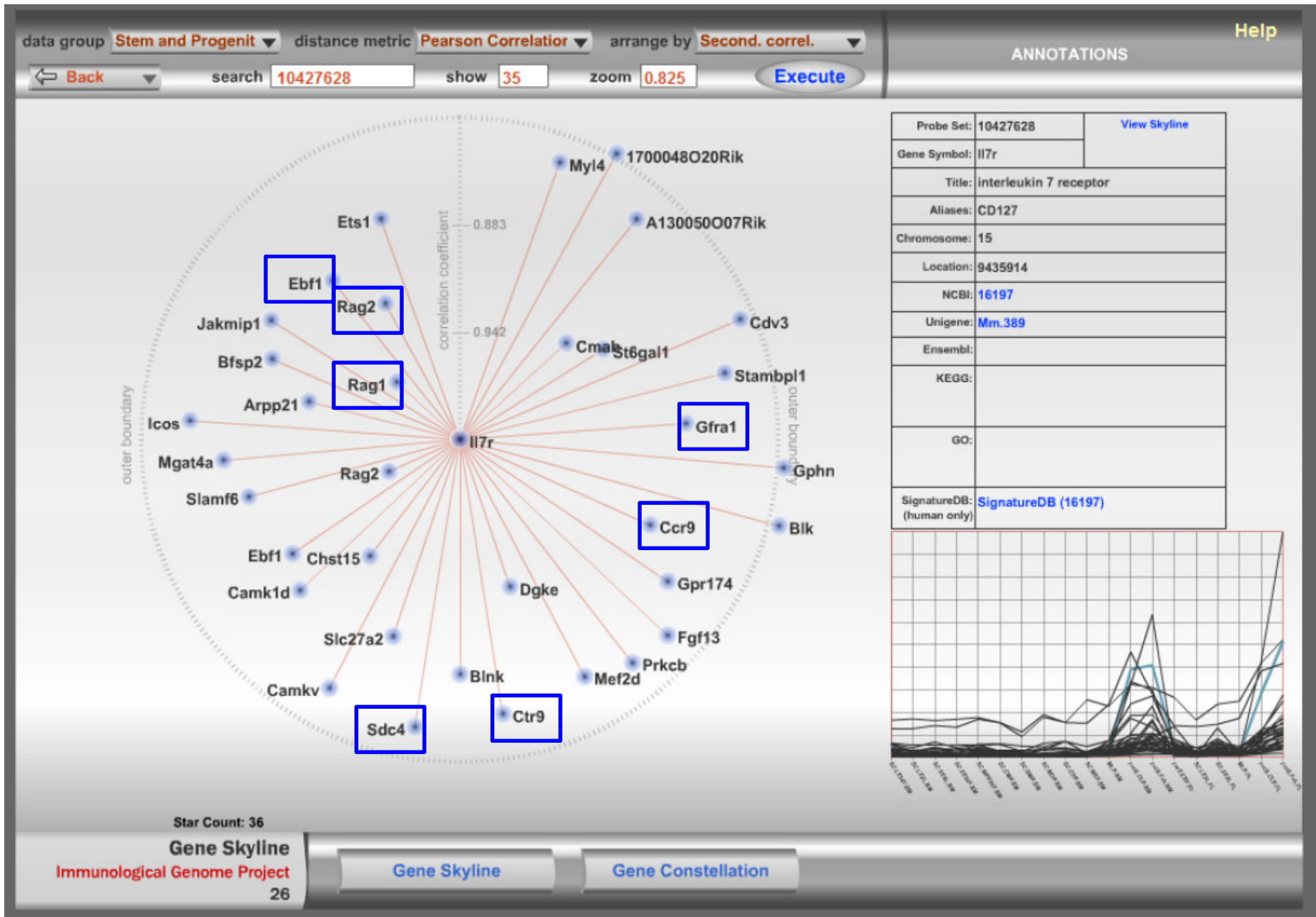
# Ectopic expression of EBF1 is sufficient to restore the generation of BCPs from *HoxA9*<sup>-/-</sup> MPPs



17 day MPP switched to SCF+FL+IL7 and cultured for an additional 6-8 days

*Hoxa9*<sup>-/-</sup> d17 MPP in SCF+FL+IL7 6-8 days after retroviral transduction

# Linking RNA-Seq and Microarray data to the IL-7R signaling pathway



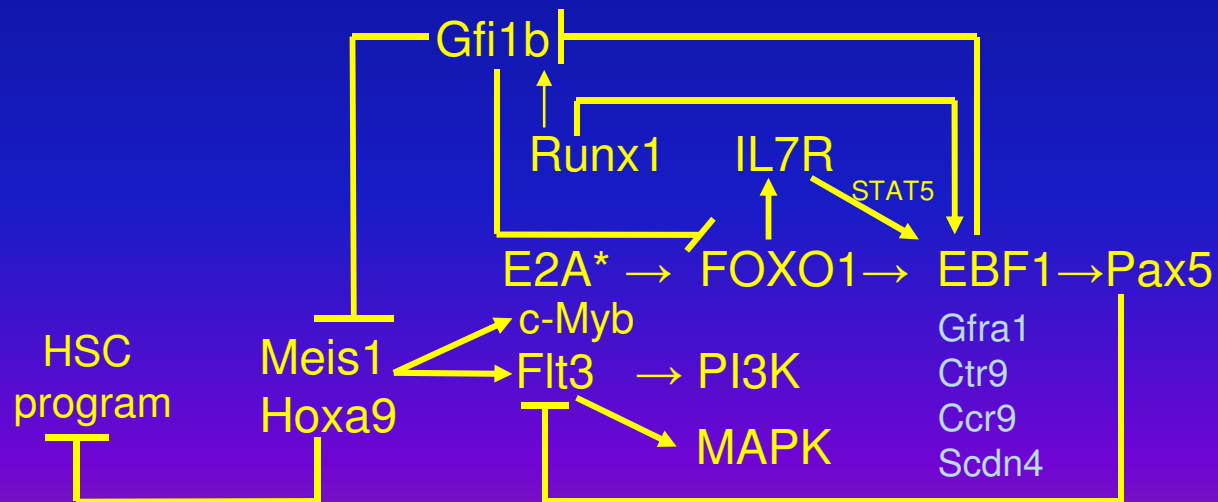


## Conclusions:

We developed a short-term in vitro culture model to expand MPPs from WT and HoxA9<sup>-/-</sup> mice that will be informative in the identification, characterization, and validation of HoxA9 regulated genetic circuits in early hematopoiesis.

RNA-Seq confirmed decreased lymphoid priming in MPPs and under B cell differentiation conditions due to HoxA9 deficiency independent of Flt3 signaling.

HoxA9 deficiency impairs IL-7R expression and signaling – enforced expression of EBF1 can bypass the IL-7 signaling defect.



## Underway:

1. Identify novel HoxA9 target genes : compare results to microarray platform of genes upregulated in EBF1<sup>-/-</sup> multipotent cells that express endogenous Hoxa9
  - underexpressed in Hoxa9<sup>-/-</sup> MPPs in RNA-Seq platform (transcriptional activation)
  - overexpressed in EBF1<sup>-/-</sup> MPPs in Affymetrix Array  
[Chd17](#), [CD27](#), [CCR9](#), [Ppfia4](#), [Sorcs2](#), [RAG2](#), [GPR25](#), [Jup](#), [Igf2bp3](#)
  - overexpressed in Hoxa9<sup>-/-</sup> MPPs in RNA-Seq platform (transcriptional repressor)
  - underexpressed in EBF1<sup>-/-</sup> MPPs in Affymetrix Array  
[Mgst1](#), [Tgm2](#), [Enpp4](#), [Plekha8](#), [Muc13](#), [Cpne2](#), [Tmem176a](#), [Mreg](#), [Adcy6](#), [STAT4](#), [Sulf2](#), [SpiB](#)
2. Identify novel EBF1 target genes : compare results to microarray platform of genes underexpressed in EBF1<sup>-/-</sup> multipotent cells to genes underexpressed in HoxA9-deficient MPPs or CLPs  
[P2rx3](#), [RAG1](#), [Rgs8](#), [Cecr2](#), [Egfl7](#), [Uaca](#), [Lax1](#), [Dntt](#), [Slc15a2](#), [Gimap4](#)
3. Perform gain-of-function and loss-of-function experiments in WT or HoxA9<sup>-/-</sup> MPPs to evaluate gene function in B cell development followed by molecular validation.
4. Determine if HoxA9 target genes are relevant to leukemogenesis.

# Acknowledgements

## Medina Lab

Kim Gwin

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Joe Dolence, PhD

Mike Bell

Elena Frank

Mariya Shapiro

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Gene Expression Core

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MAYO  
CLINIC

