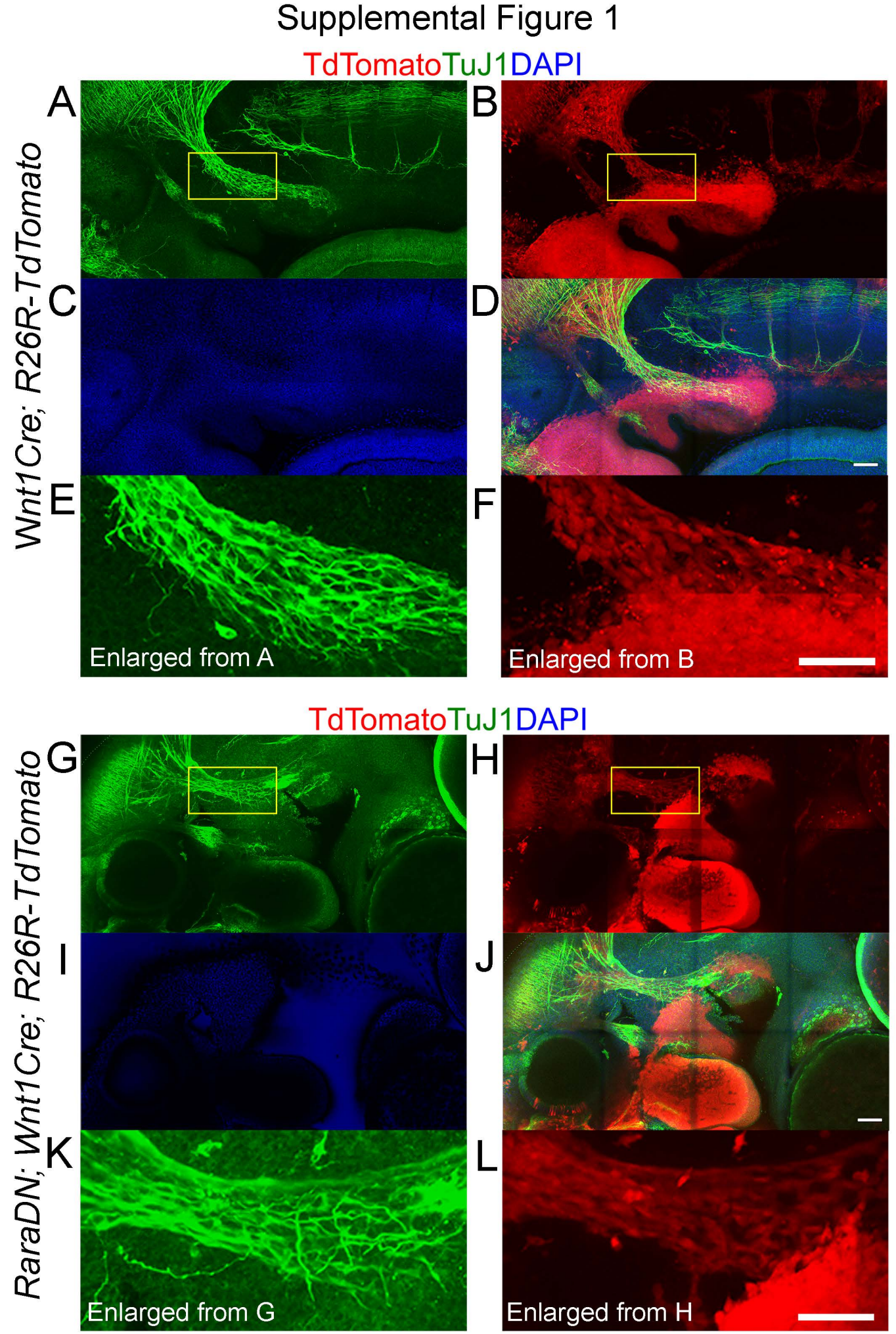
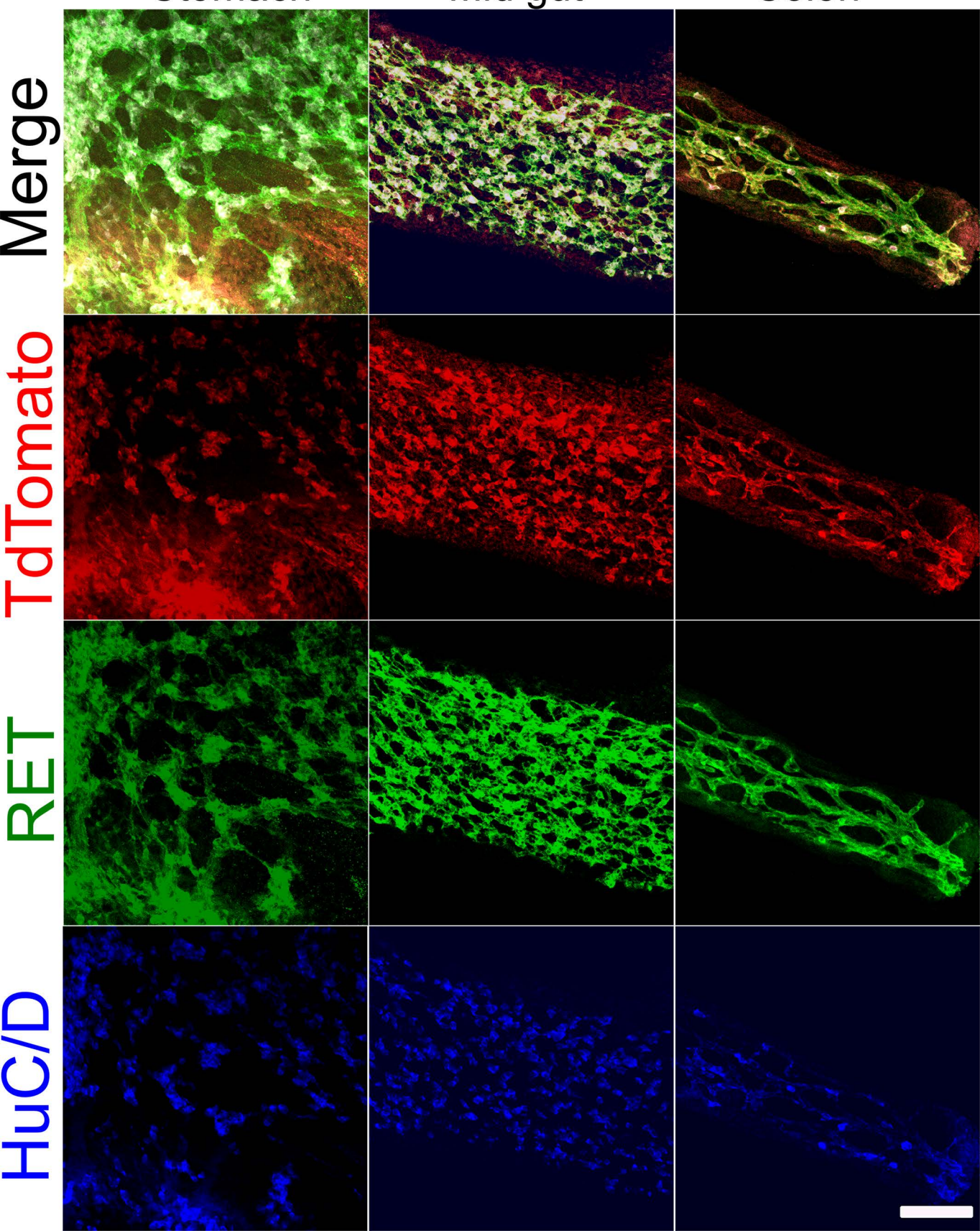
Supplemental Figure 1



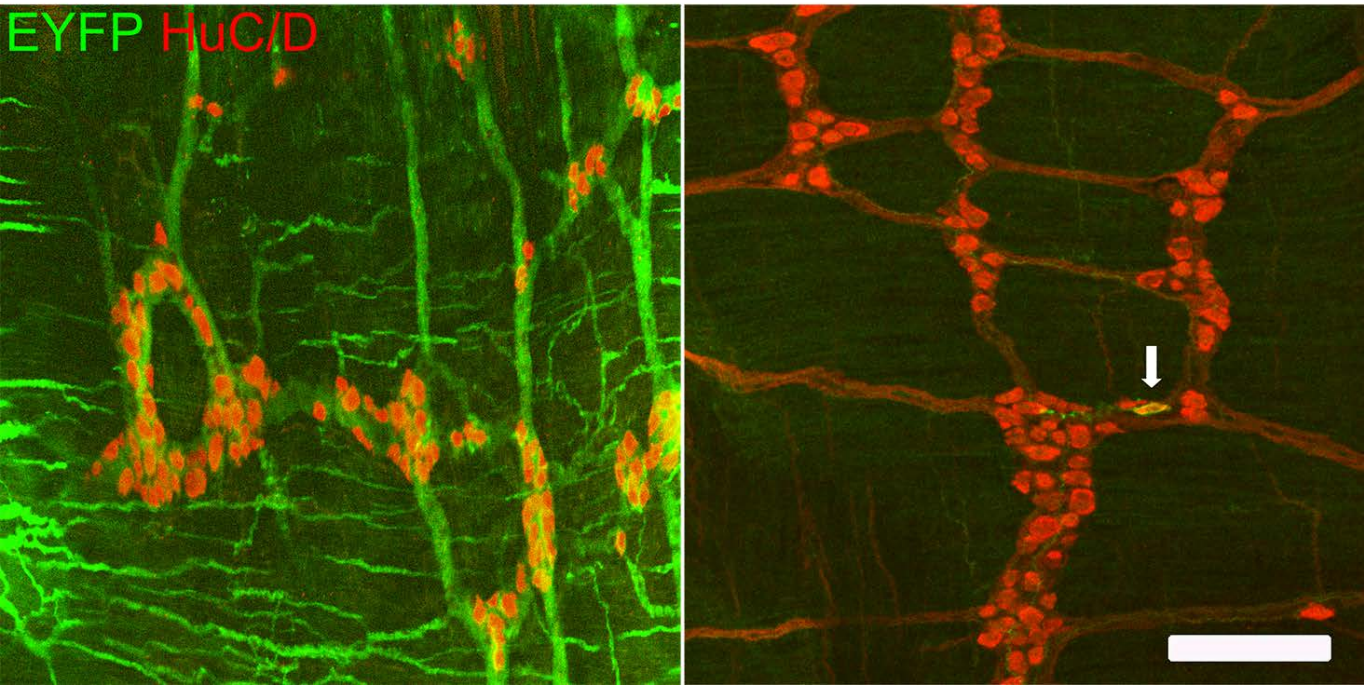
Supplemental Figure 2

E12.5 *SOX10Cre; R26R-TdTomato*

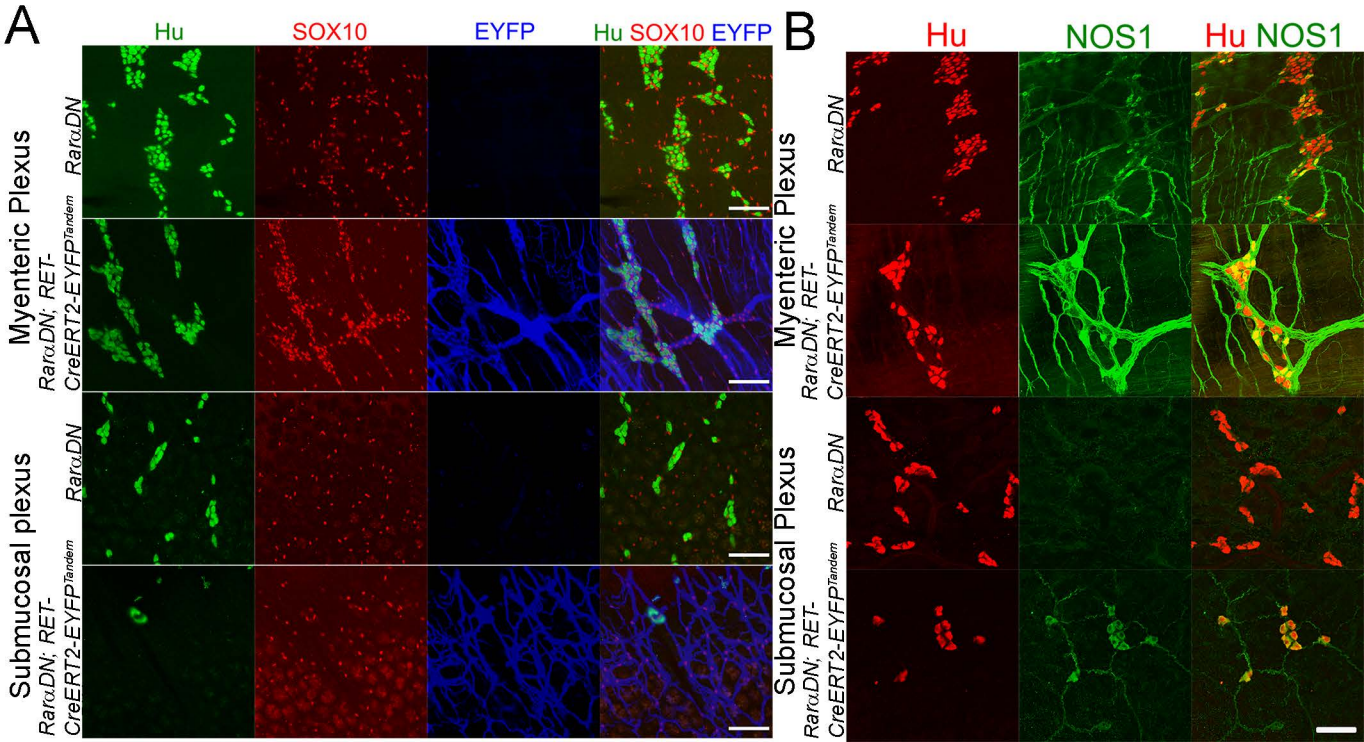


Supplemental Figure 3

RETCreERT2-EYFP^{Tandem}



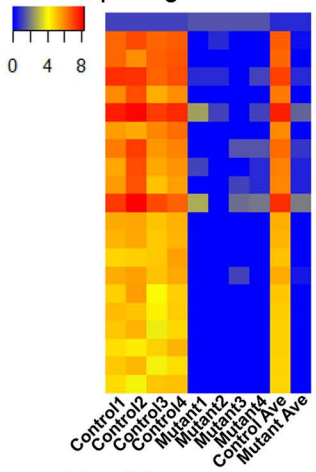
Supplemental Figure 4



Supplemental Figure 5

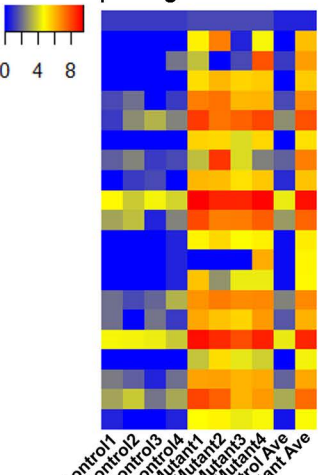
A E11.5 Stomach ENCDC

Top 20 genes less abundant in mutant



Gene	Fold change (log)	FDR
Miat	-9.2	3.7E-48
Fam163a	-9.2	4.9E-40
Chrna3	-9.2	2.9E-53
Th	-8.8	5.3E-23
Dbh	-8.6	1.5E-43
Nfasc	-8.4	2.5E-24
Stmn2	-8.0	1.1E-23
Rgs4	-7.9	2.oE-18
Stmn3	-7.8	3.3E-17
Gal	-7.8	7.4E-23
Chrna5	-7.5	5.4E-16
Btbd17	-7.4	7.0E-15
Adcyap1r	-7.1	2.2E-12
Mab21l2	-7.1	3.8E-16
Nap1l2	-7.0	4.2E-10
Nrsn1	-6.8	7.5E-11
Slc18a3	-6.8	2.1E-09
Myt1	-6.7	2.8E-10
St18	-6.7	2.9E-09
Frmpd1	-6.6	2.3E-09

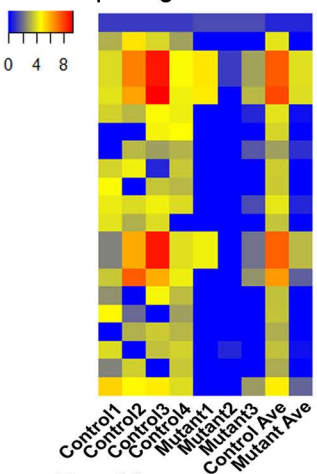
Top 20 genes more abundant in mutant



Gene	Fold change (log)	FDR
Bhlhe40	8.3	2.1E-07
Afp	8.3	0.00037
Csrp3	8.3	3.0E-23
Hspb2	7.9	1.7E-35
Gpnmb	7.9	6.9E-33
Slc45a2	7.8	4.2E-14
Hspa1a	7.6	2.1E-05
Trim63	7.5	3.4E-22
Pmel	7.3	1.8E-48
Anxa1	7.2	6.1E-25
Cxcl14	7.1	4.7E-14
Serpina6	7.0	0.0049
Trpm1	7.0	1.6E-07
Pax3	6.8	1.5E-39
Tyr	6.8	5.4E-21
Dct	6.8	3.3E-35
Wnt1	6.7	2.4E-45
Cxcl10	6.7	7.2E-08
Cryab	6.5	8.9E-20
C2	6.5	1.6E-10

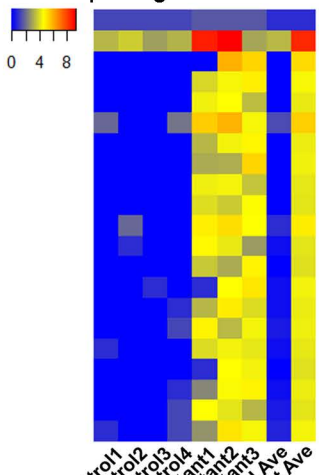
B E13.5 Colon ENCDC

Top 20 genes less abundant in mutant



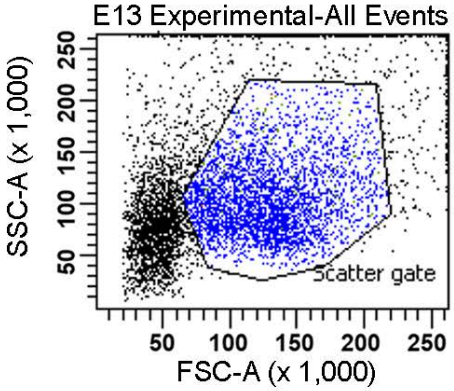
Gene	Fold change (log)	FDR
Hba.x	-7.4	2.8E-05
Hba.a1	-6.2	0.0006
Hba.a2	-6.0	0.021
Beta.s	-6.0	0.021
Npy	-5.7	0.0211
Lgals3	-5.6	0.00019
Scara5	-5.6	0.03
Chodl	-5.5	7E-05
Ptger3	-5.4	0.0074
Wnt11	-5.2	0.013
Hs3st2	-5.2	0.00011
Hbb.b2	-5.2	0.015
Hbb.b1	-5.1	0.02
Hbb.y	-5.1	0.02
Gabra5	-5.1	0.02
Klhl4	-4.9	0.02
Cd300a	-4.7	0.038
Gpr75	-4.7	0.00021
Ano4	-4.6	0.031
Scg2	-4.6	

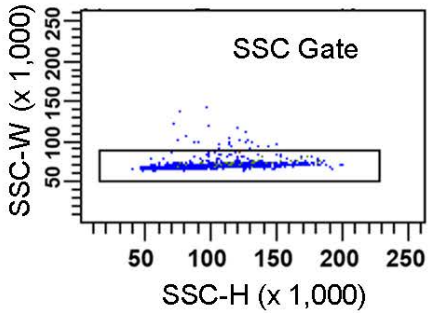
Top 20 genes more abundant in mutant

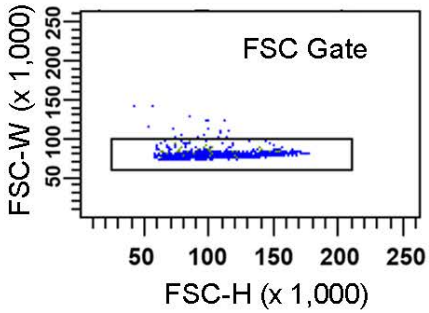


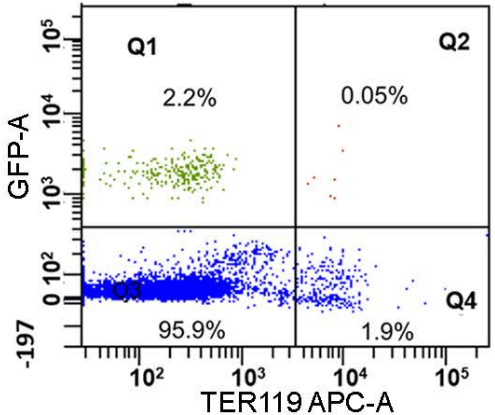
Gene	Fold change (log)	FDR
Slc7a11	6.2	2.1E-07
Slc40a1	6.0	0.00057
Galnt3	5.1	0.0002
Fzd4	4.9	0.0006
Sema3c	4.9	6.7E-05
X9130019O22Rik	4.9	0.00052
Bhlha15	4.9	0.0016
Bmp4	4.9	0.0007
Lifr	4.8	0.0007
X1700019G17Rik	4.7	0.00047
Adam22	4.6	0.0041
Igsf9b	4.6	0.0021
Enpp2	4.6	0.009
Mbnl3	4.6	0.0013
Prkcq	4.6	0.0016
Oprl1	4.6	0.00083
Trpc6	4.5	0.0071
Cdh24	4.5	0.0023
Parp9	4.5	0.003
Rapgef3	4.4	0.003

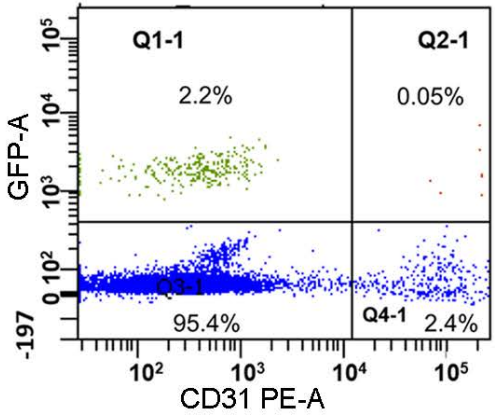
Supplemental Figure 6



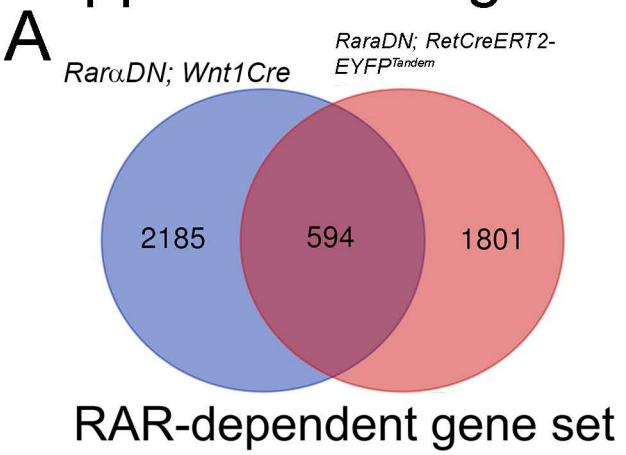


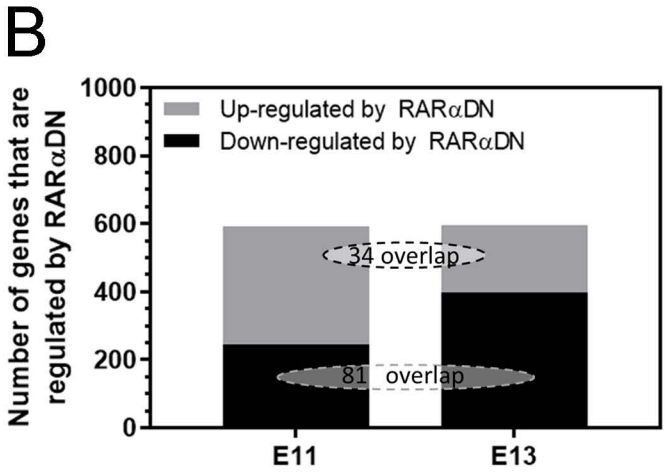






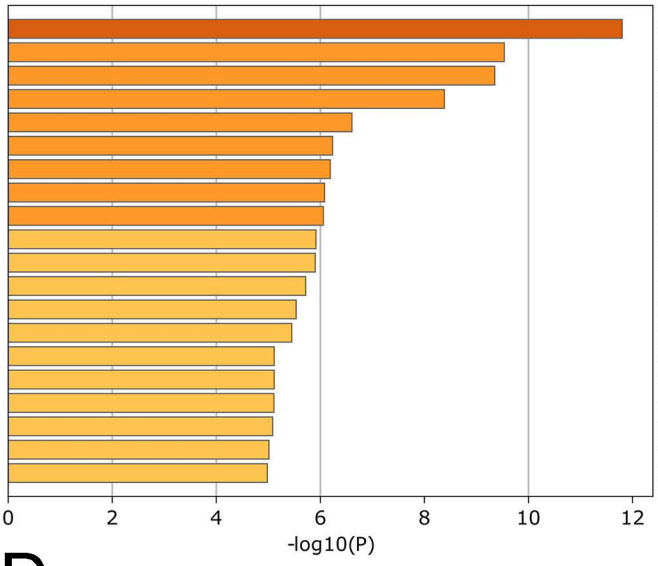
Supplemental Figure 7





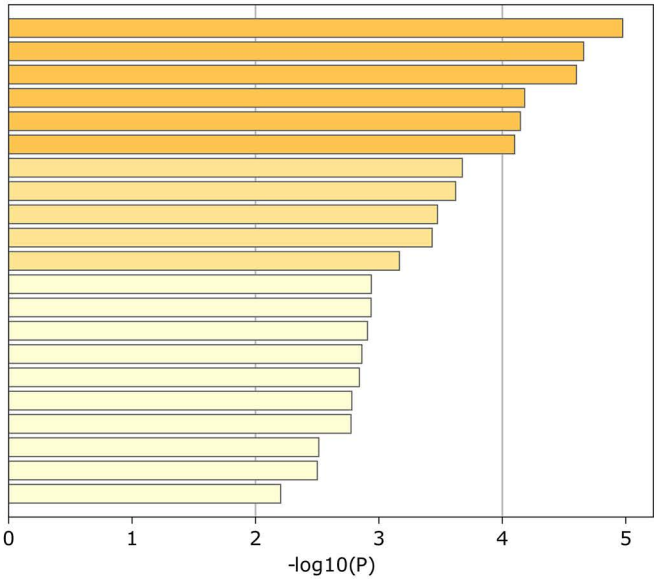
C

Gene enrichment pathway analysis



GO:0010631: epithelial cell migration
GO:0051129: negative regulation of cellular component organization
R-HSA-9675108: Nervous system development
GO:0097435: supramolecular fiber organization
GO:0007005: mitochondrion organization
GO:0051347: positive regulation of transferase activity
GO:0022411: cellular component disassembly
hsa05016: Huntington's disease
GO:0060485: mesenchyme development
GO:0046034: ATP metabolic process
GO:0031589: cell-substrate adhesion
GO:0052547: regulation of peptidase activity
GO:0045055: regulated exocytosis
GO:0097190: apoptotic signaling pathway
GO:0048732: gland development
GO:0048483: autonomic nervous system development
GO:0010721: negative regulation of cell development
GO:0008285: negative regulation of cell proliferation
GO:0007423: sensory organ development
GO:0030198: extracellular matrix organization

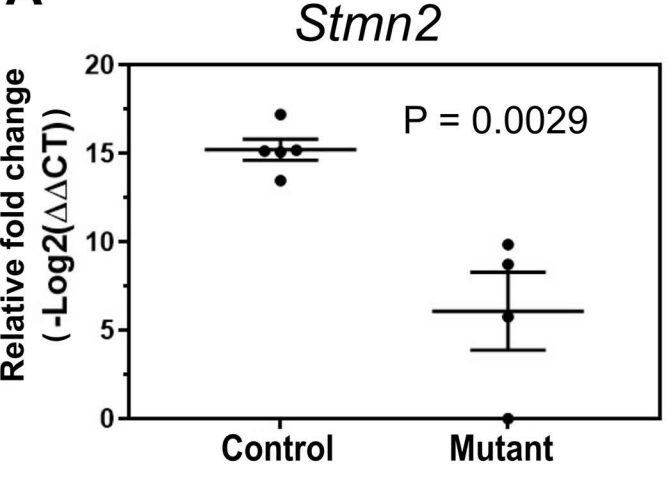
D

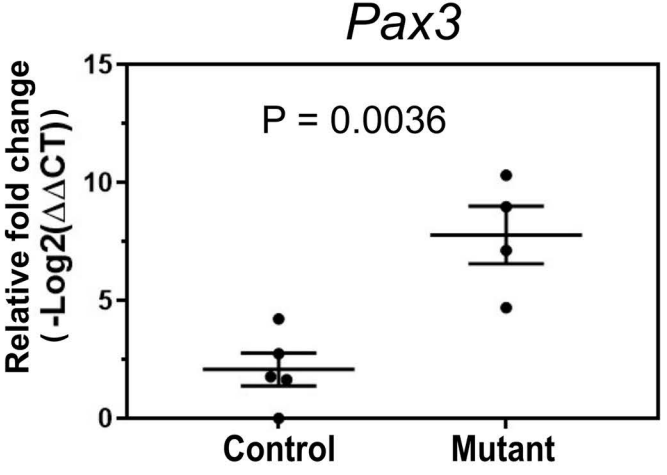


GO:0015850: organic hydroxy compound transport
GO:0001667: ameboidal-type cell migration
GO:0045859: regulation of protein kinase activity
GO:0009612: response to mechanical stimulus
GO:0050808: synapse organization
GO:1903053: regulation of extracellular matrix organization
GO:0042391: regulation of membrane potential
GO:0043269: regulation of ion transport
GO:1903531: negative regulation of secretion by cell
GO:0050804: modulation of chemical synaptic transmission
GO:1901216: positive regulation of neuron death
GO:0022411: cellular component disassembly
GO:0051493: regulation of cytoskeleton organization
R-MMU-1433557: Signaling by SCF-KIT
GO:0031646: positive regulation of neurological system process
GO:2001024: negative regulation of response to drug
GO:0048873: homeostasis of number of cells within a tissue
GO:0022612: gland morphogenesis
GO:0051954: positive regulation of amine transport
R-MMU-8957275: Post-translational protein phosphorylation
GO:0000381: regulation of alternative mRNA splicing, via spliceosome

Supplemental Figure 8

A





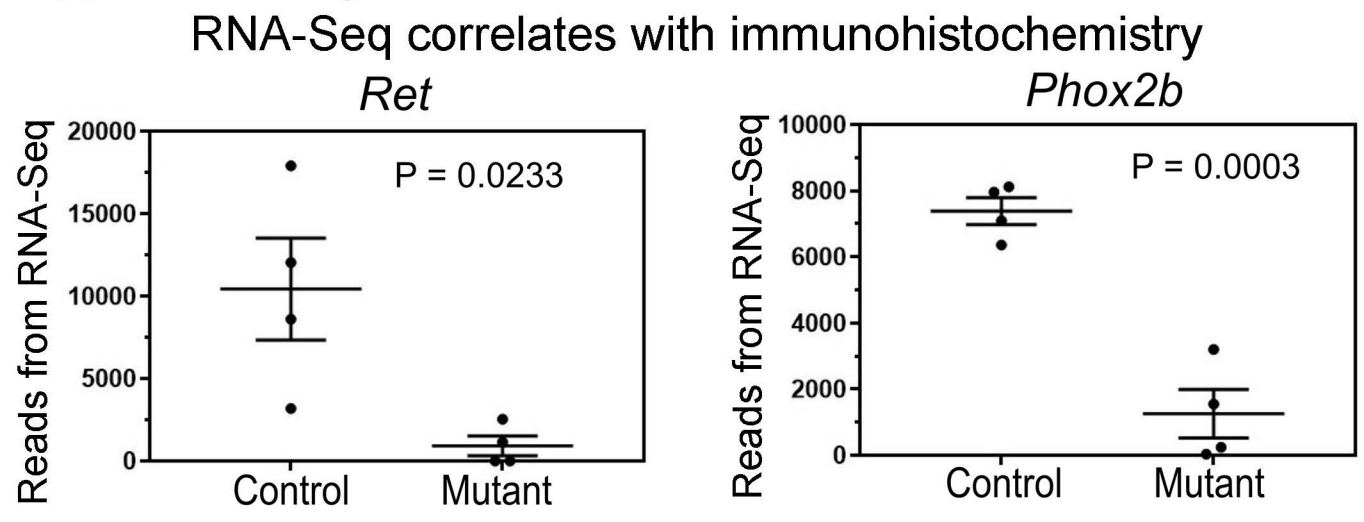
Control: *Wnt1Cre+; R26R-TdTomato+*

Mutant: *RarαDN$^{LoxP/+}$; Wnt1Cre+; R26R-TdTomato+*

B

	Stmn2	*Pax3*
Log2 fold change using qRT-PCR	- 9.1	5.7
Log2 fold change using RNA-Seq	- 8.0	6.8

Supplemental Figure 9



Control: *Wnt1Cre+; R26R-TdTomato+*

Mutant: *RarαDN$^{LoxP/+}$; Wnt1Cre+; R26R-TdTomato+*