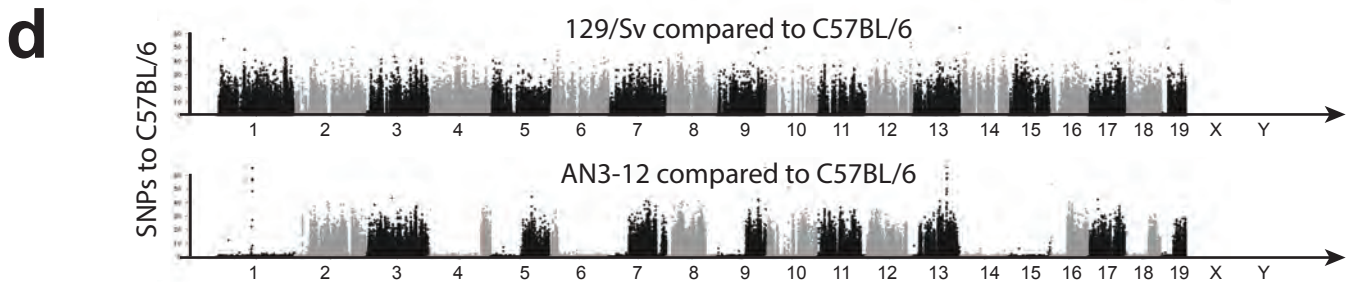
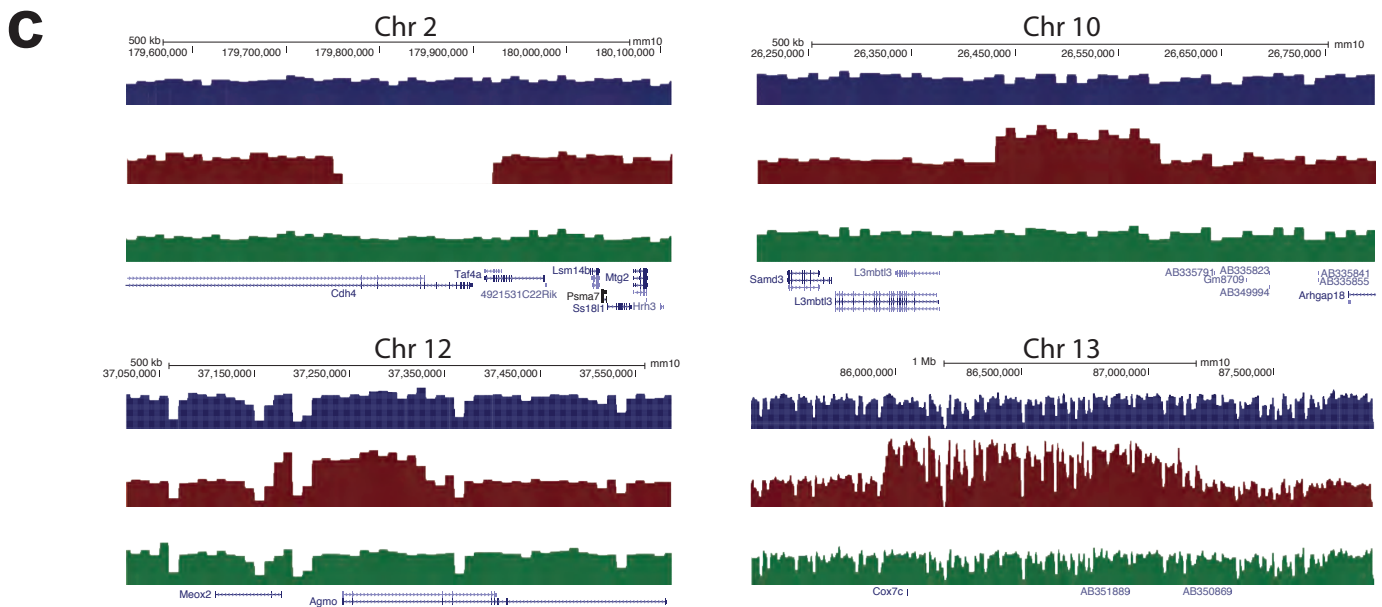
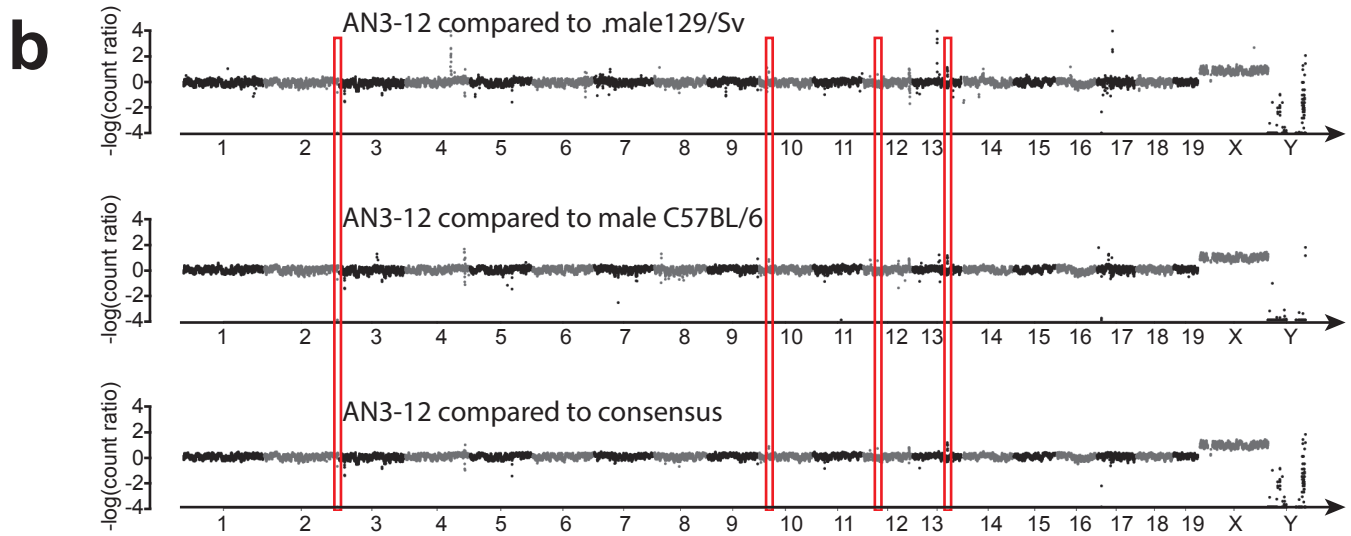
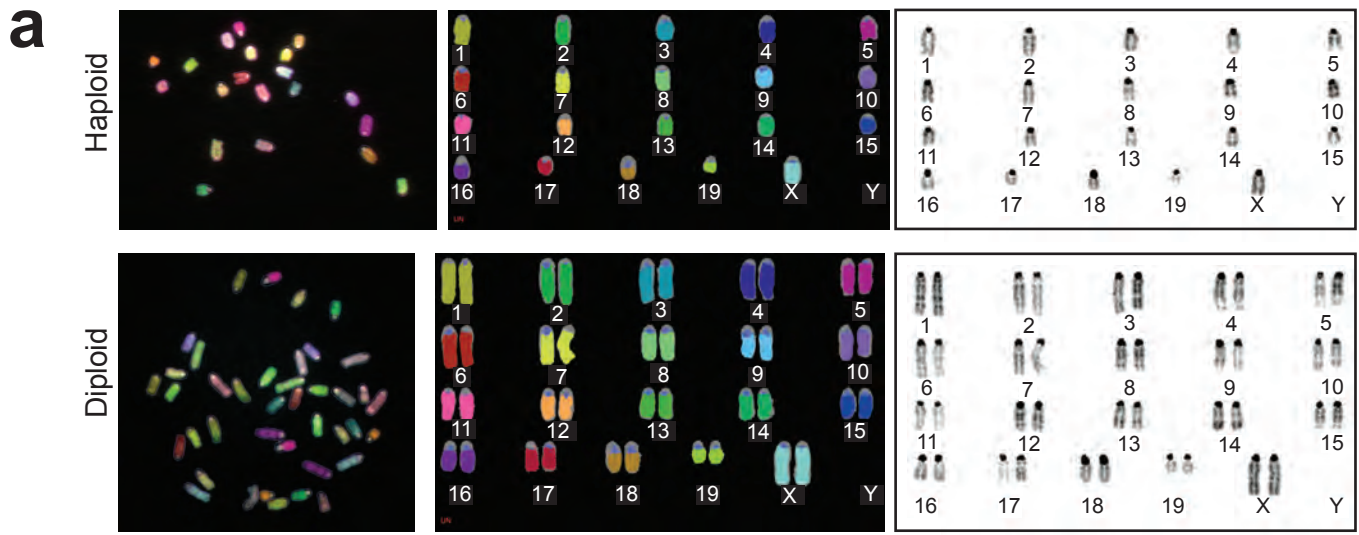
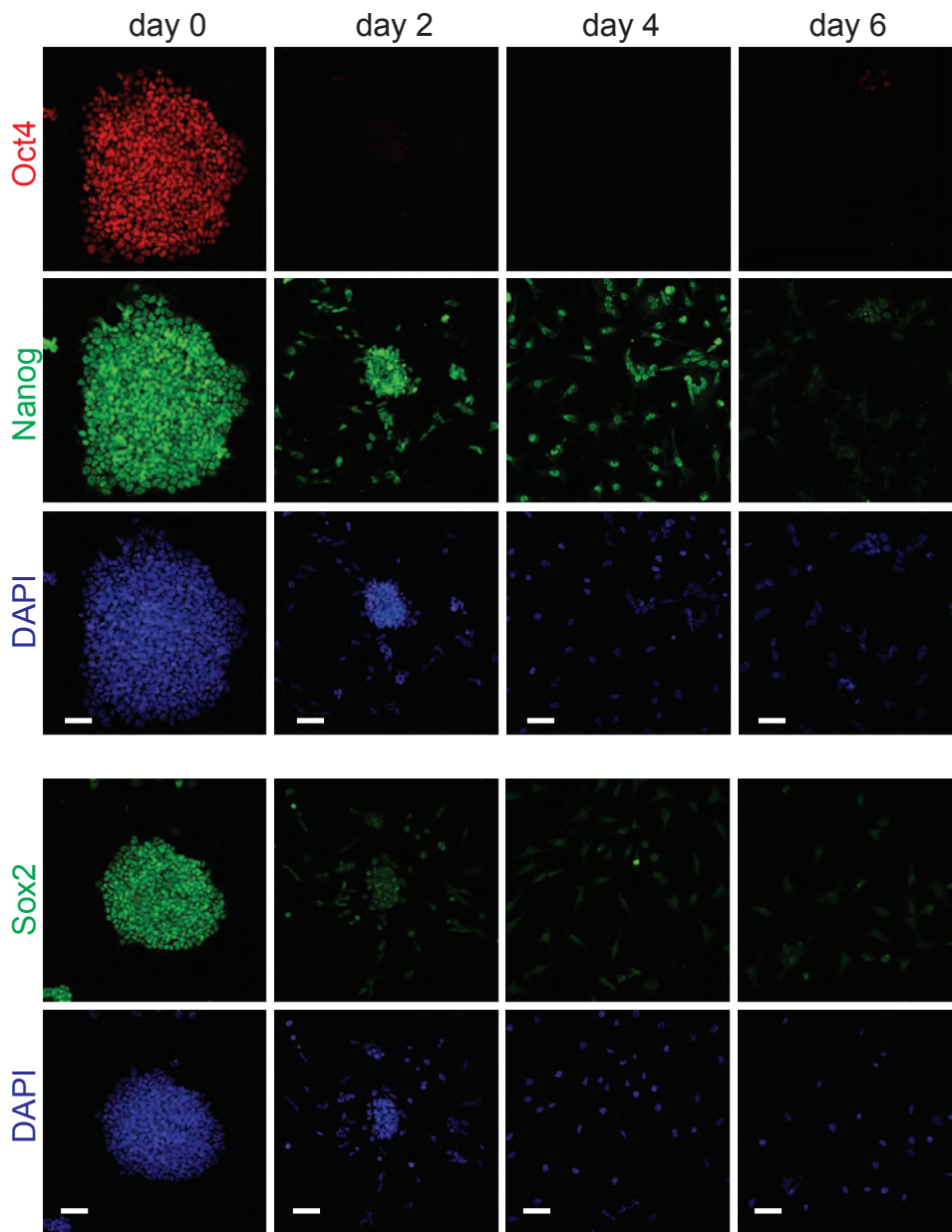
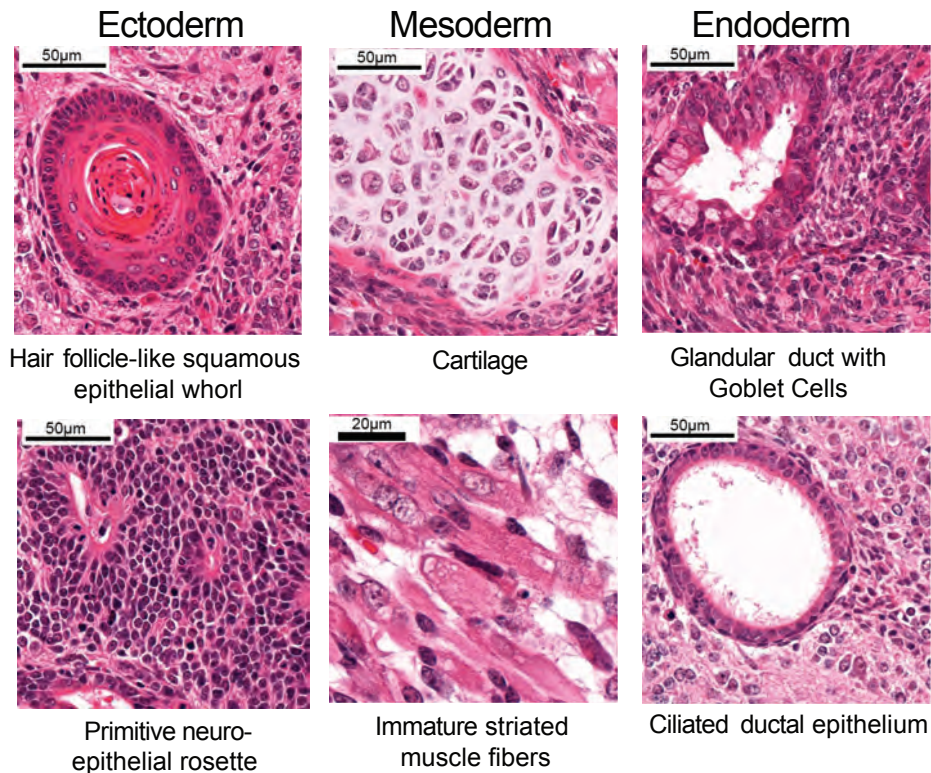


**Extended Data Figure 1**



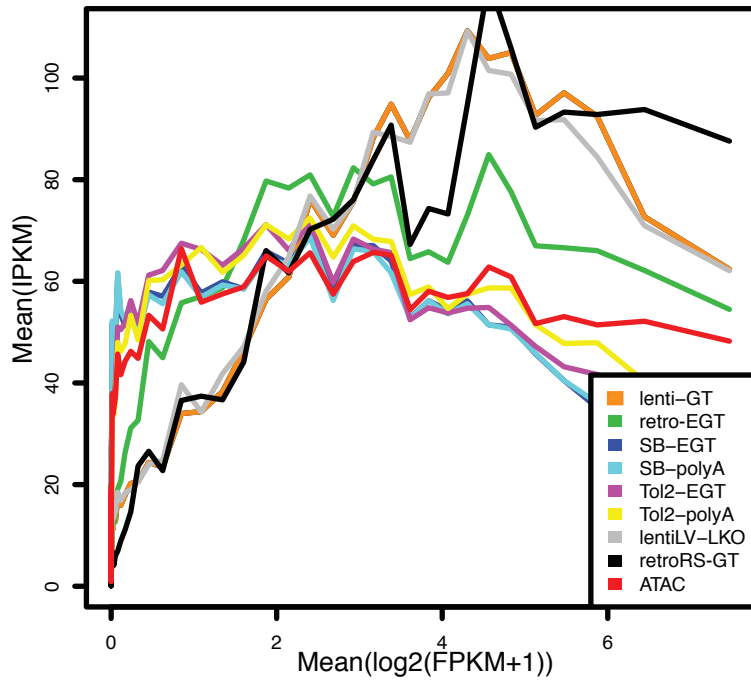
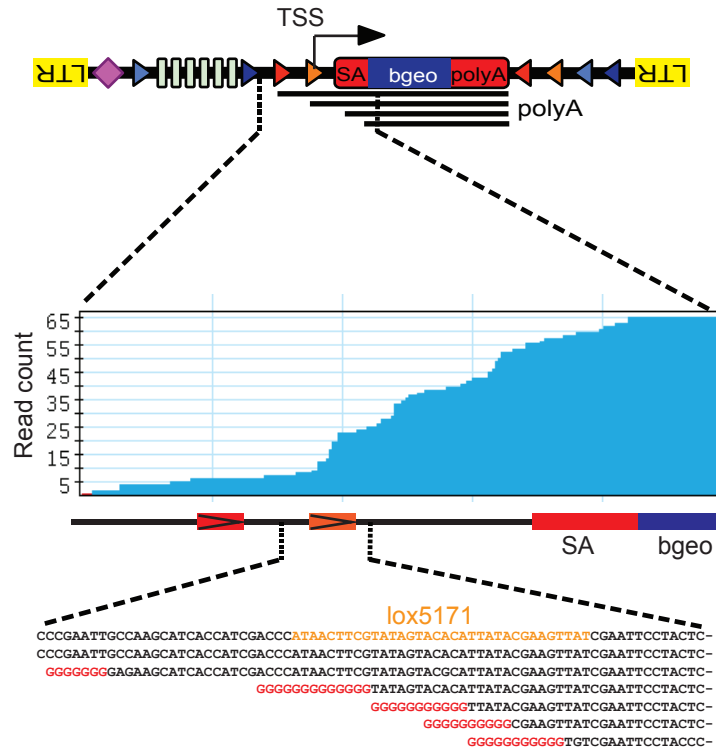
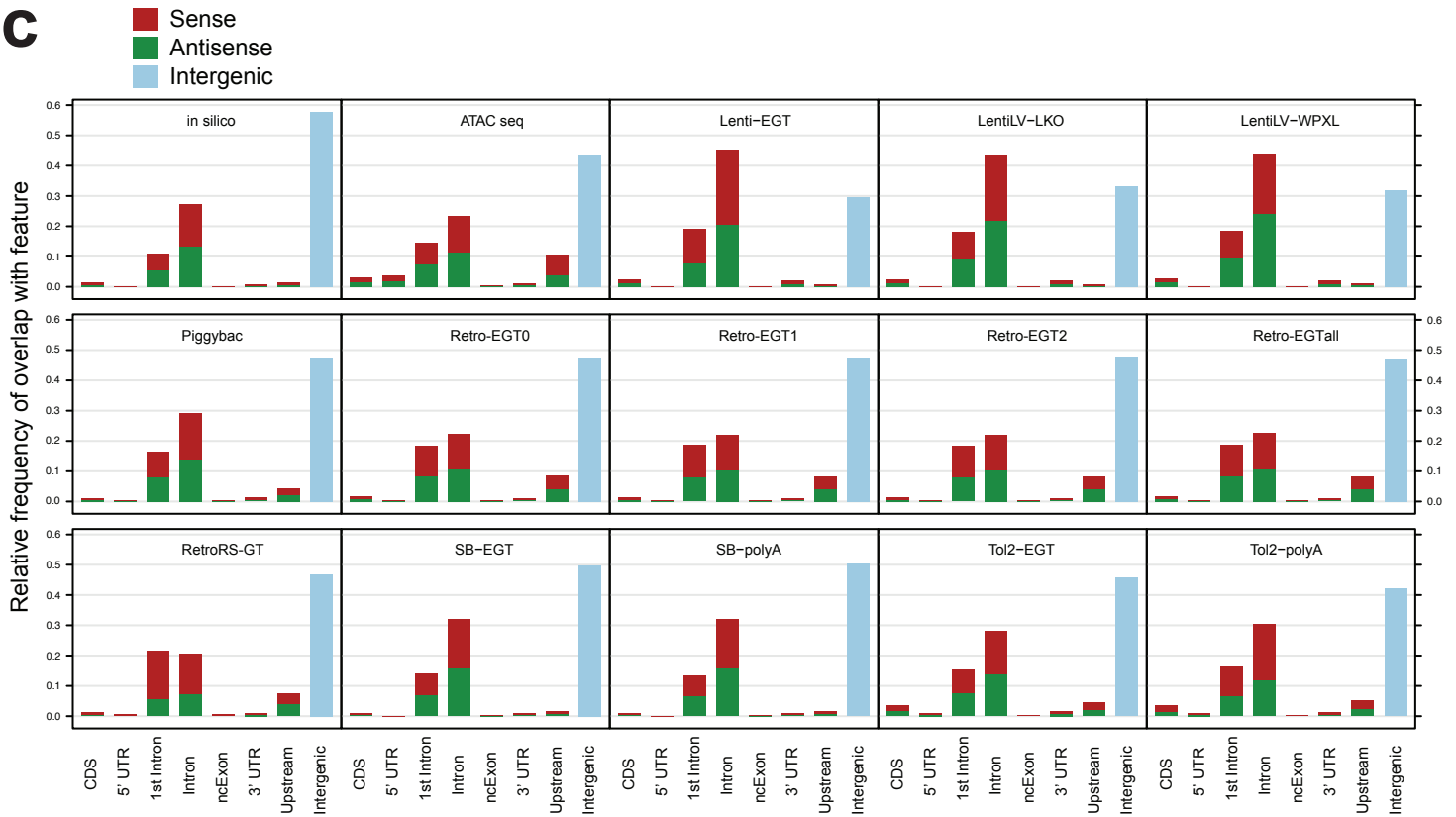
**Extended Data Figure 2**

**a****b**

# Extended Data Figure 3



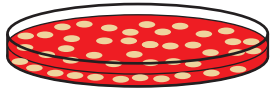


**a****b****c**

# Extended Data Figure 5

**a**

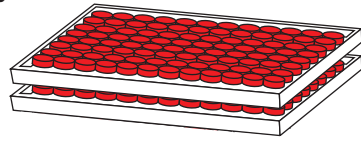
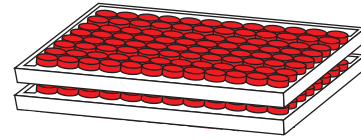
Insertional mutagenesis  
Neomycin selection



FACS sort for haploidy  
Grow out colonies



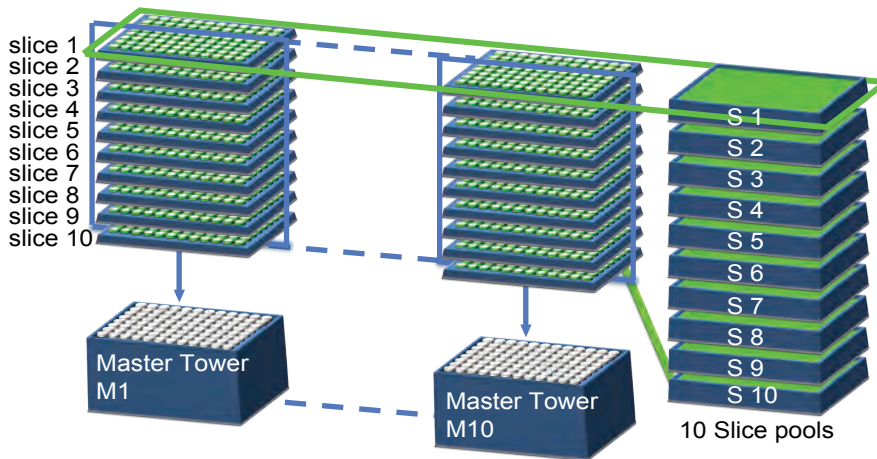
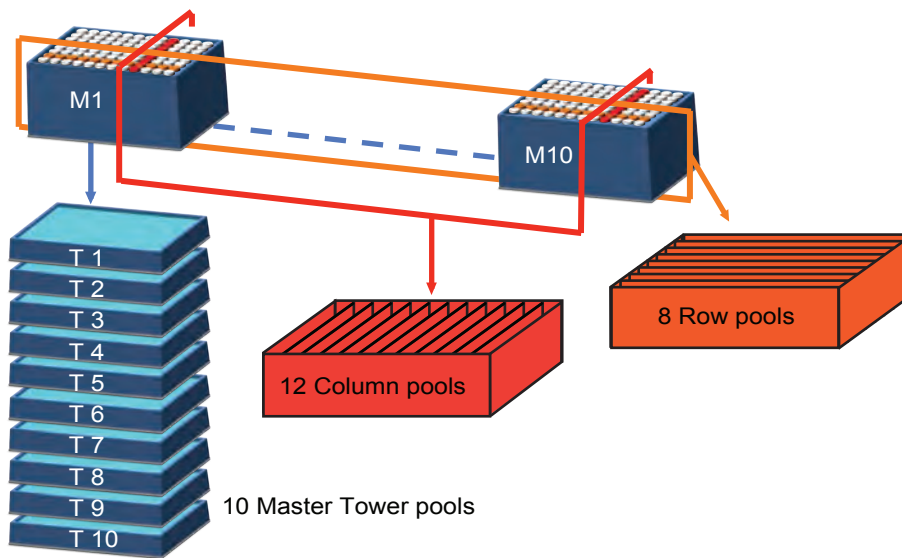
pick  
array



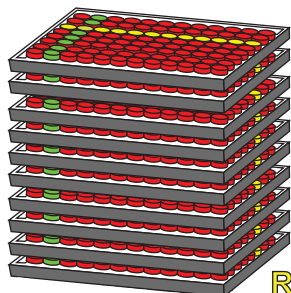
Cell banking

Sequencing

Cell lysis

**b****c****d**

4-Dimensional pooling



sum: 9 600 clones  
in 40 pools

PCR

read 1

iPCR1 genomic read

iPCR2 genomic read

bcPCR barcode

NGS on illumina platform

read 2

barcode

barcode

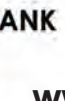
barcode

experimental index

4D coordinates

4D coordinates

4D coordinates



www.haplobank.at

# Extended Data Figure 6

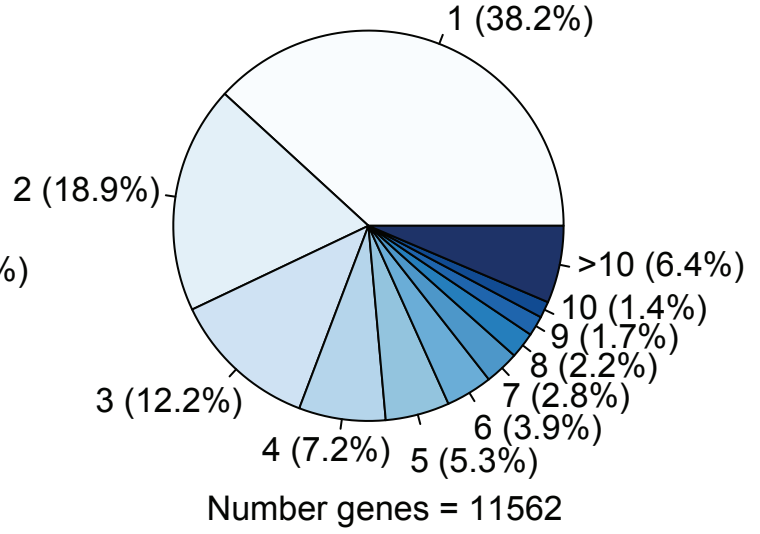
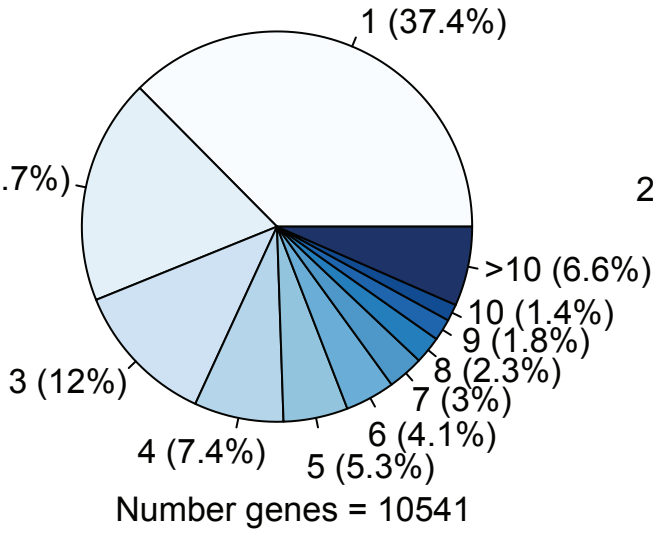
## Available Clones per Gene

**a**

**RefSeq Genes**

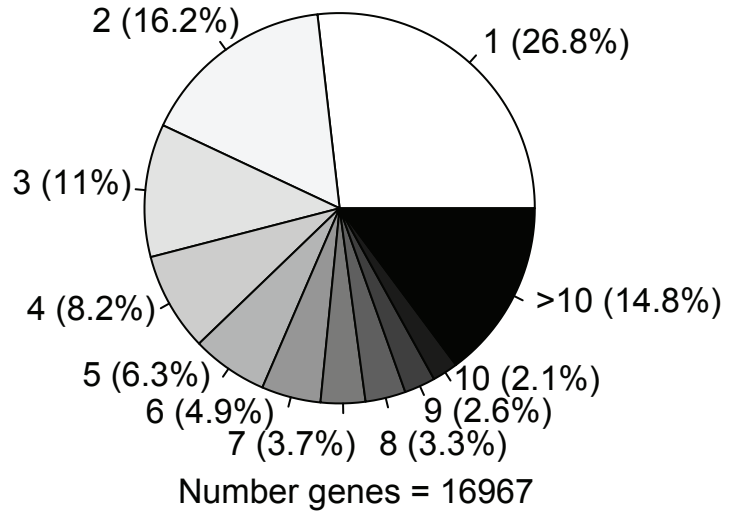
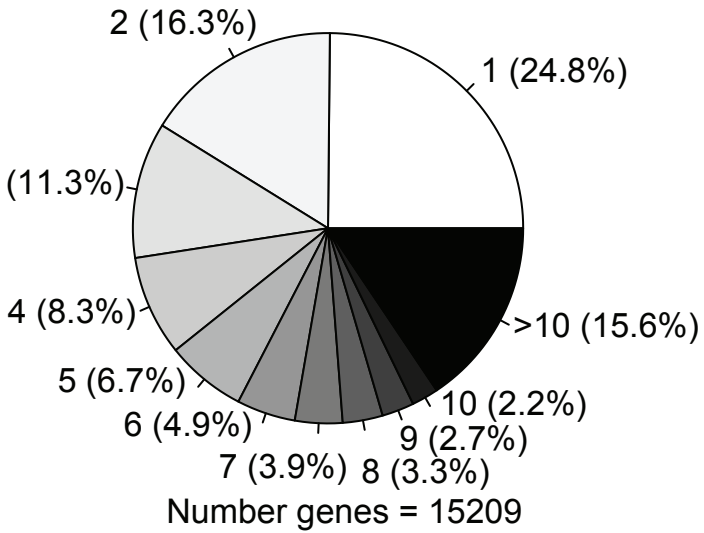
**Ensembl Genes**

**Single integrations**

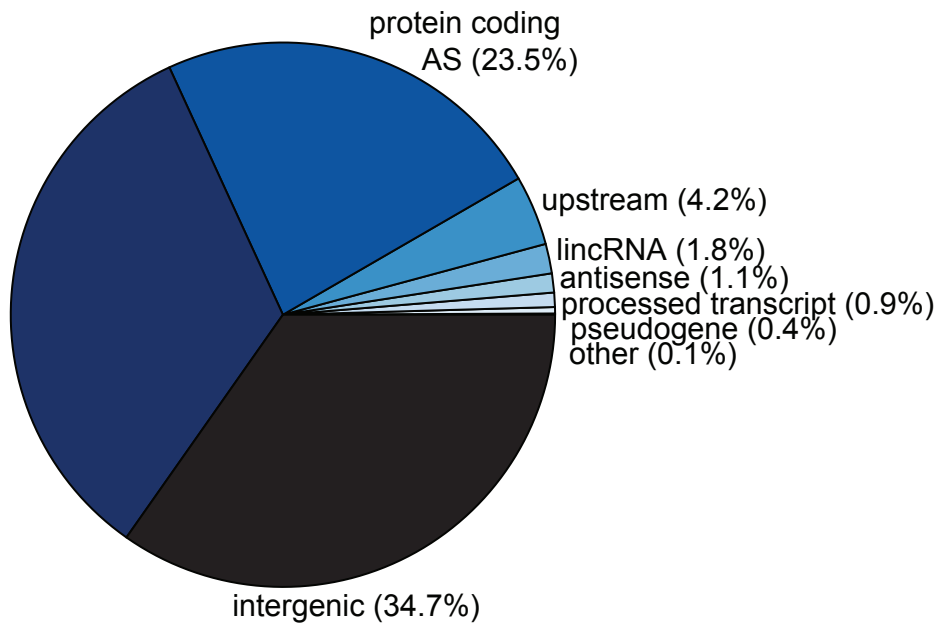


**b**

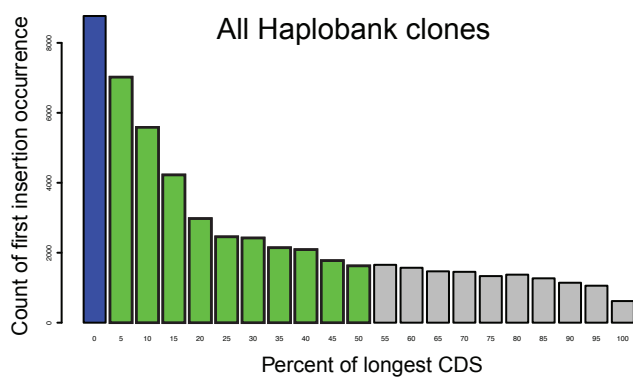
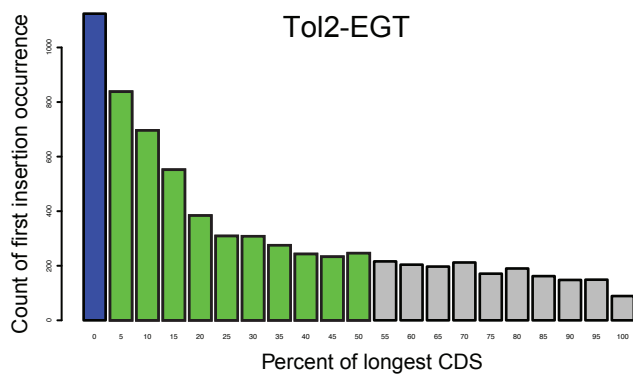
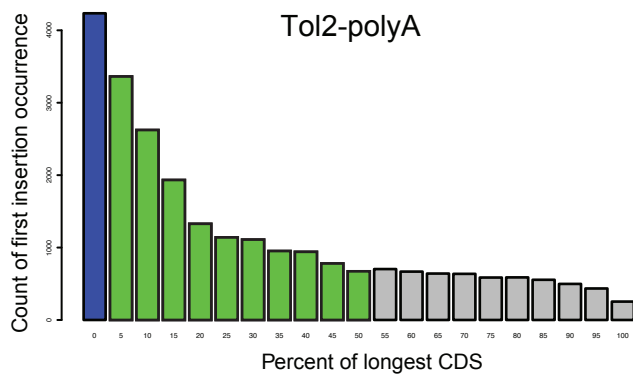
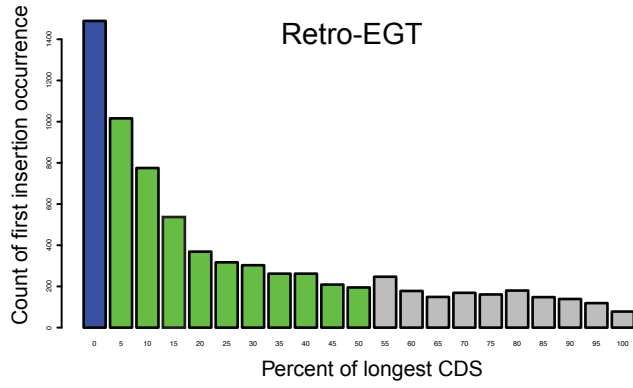
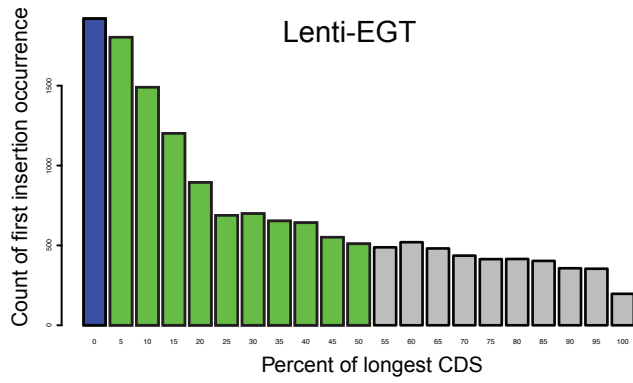
**All integrations**



**c**



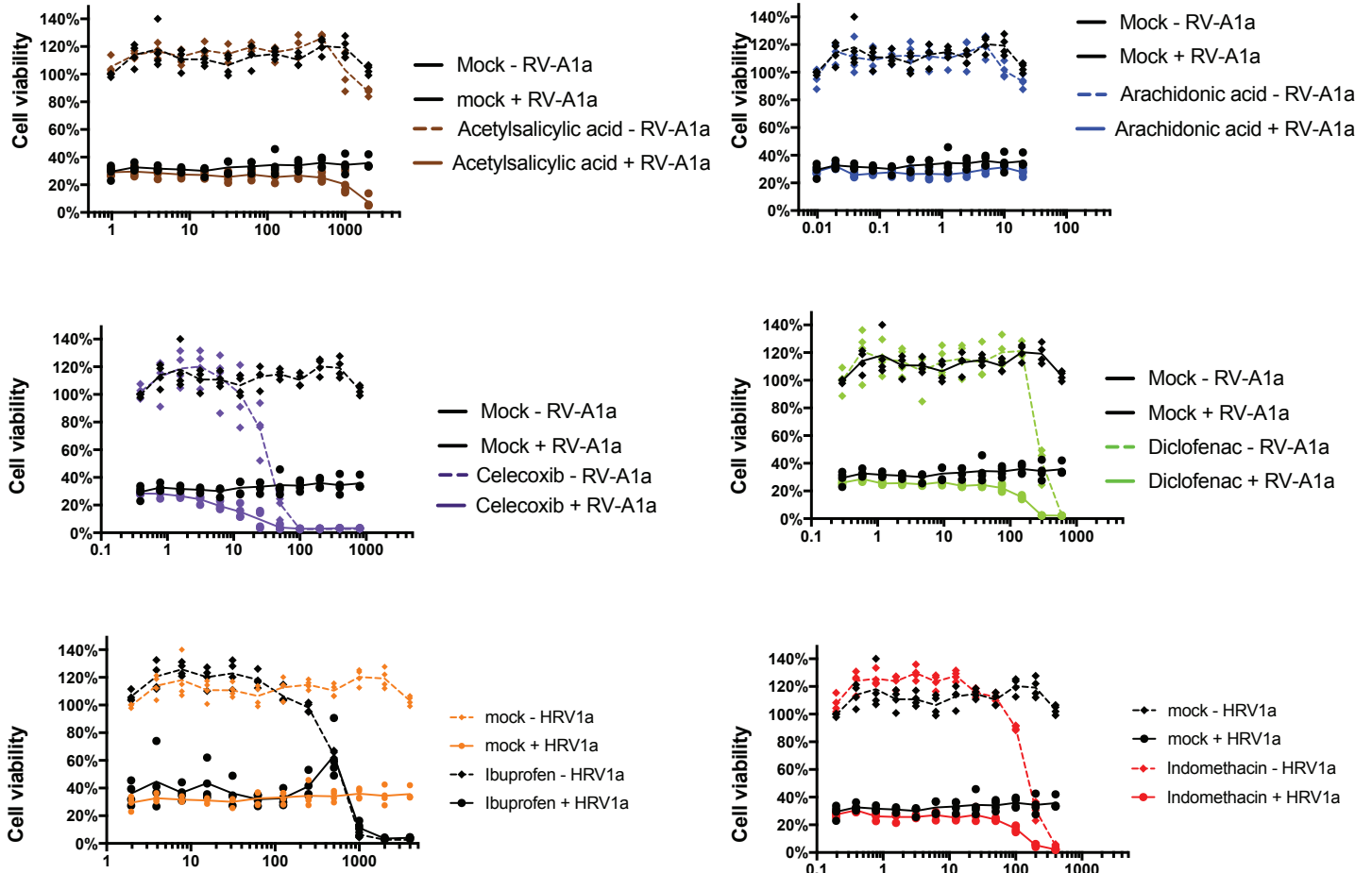
# Extended Data Figure 7



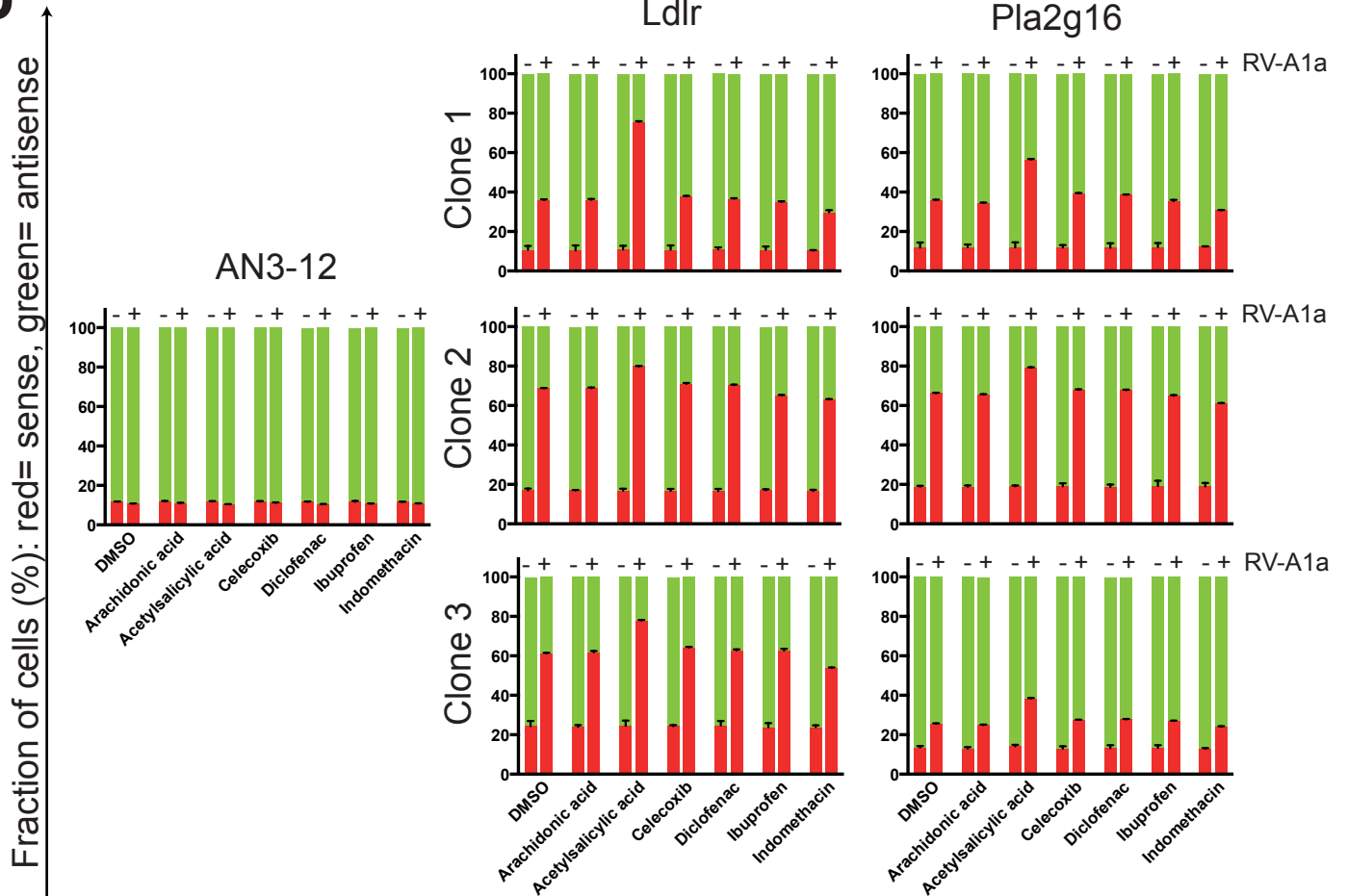
# Extended Data Figure 8



# a mES cells + RV-A1a

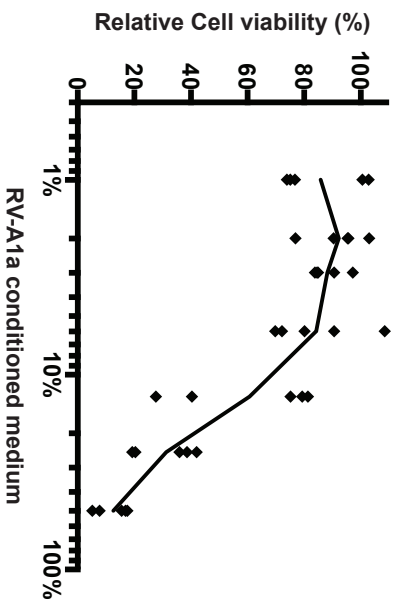


# b

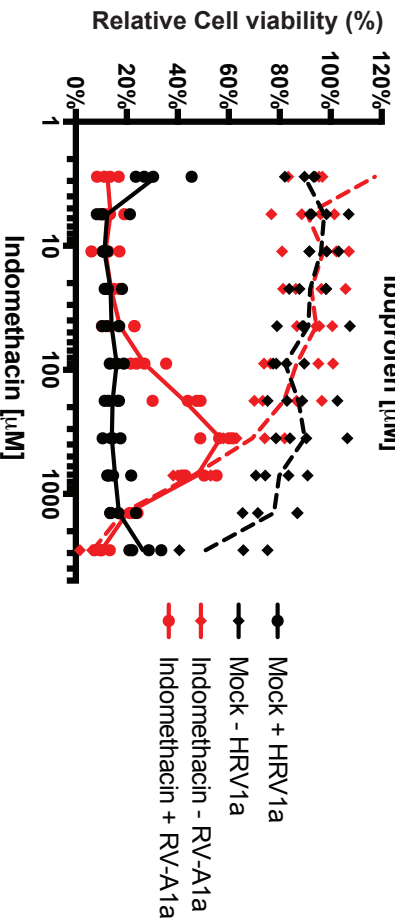
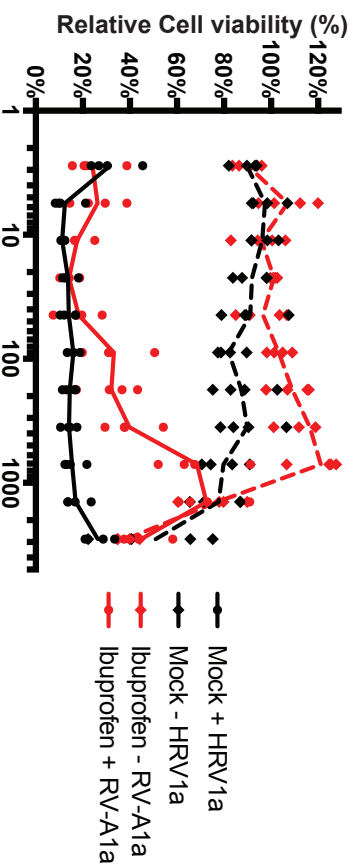


# Extended Data Figure 9

**a** HEK293T cells + RV-A1a

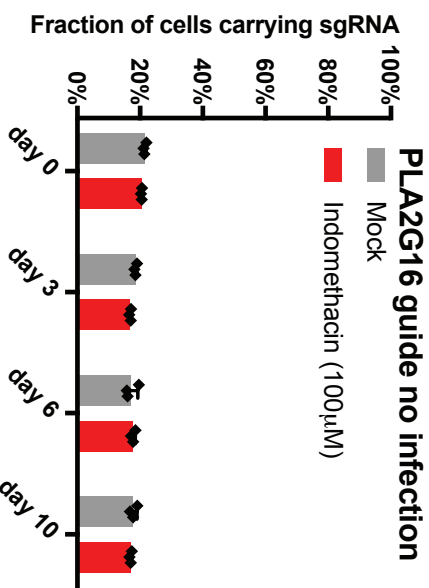


**b** HEK293T cells + RV-A1a

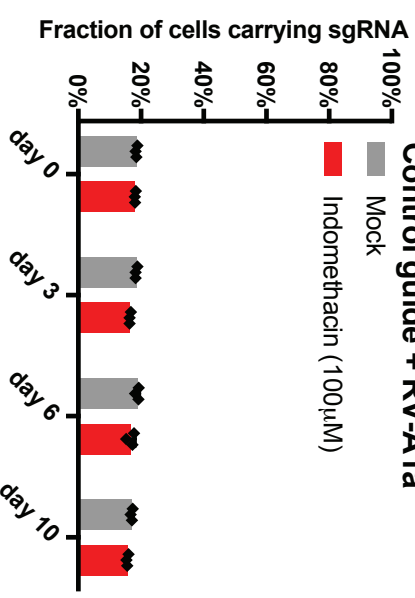
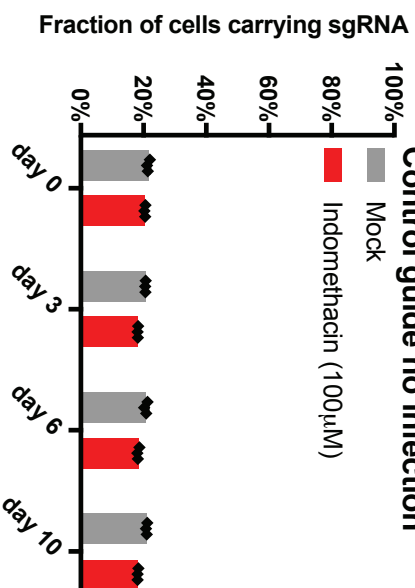
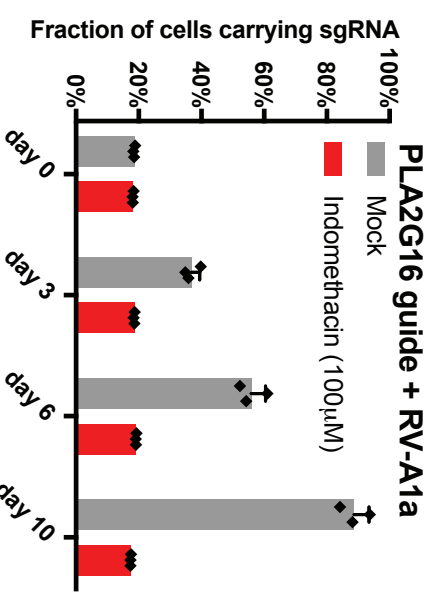


**c**

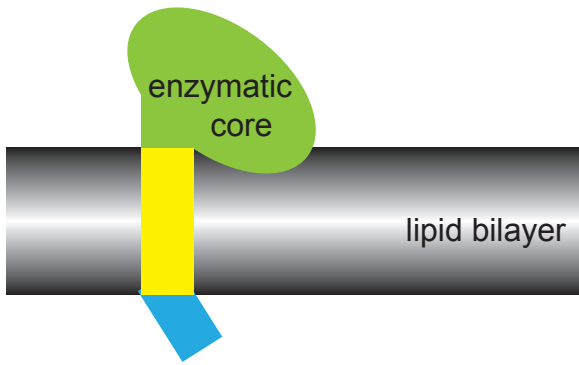
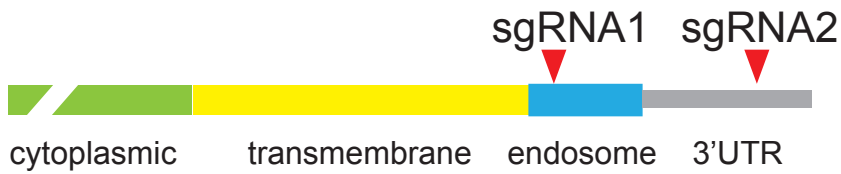
HEK293T cells no virus



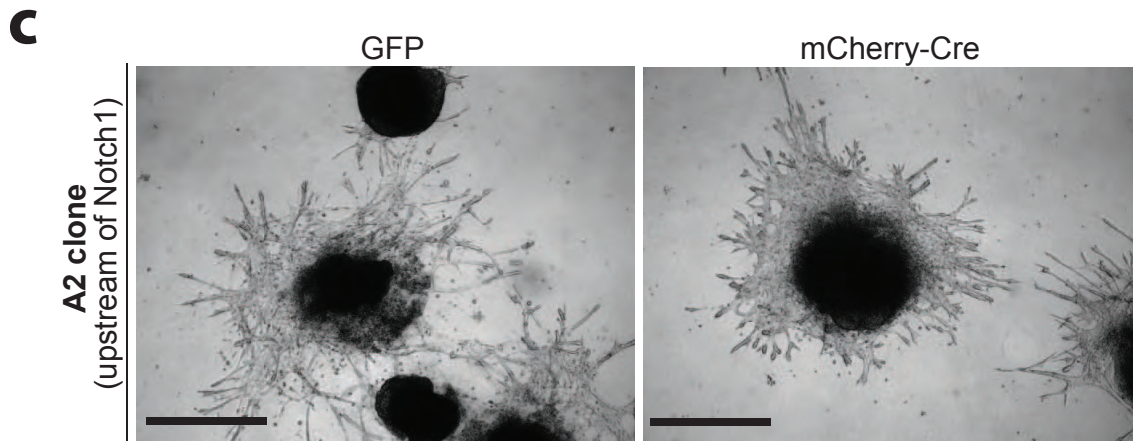
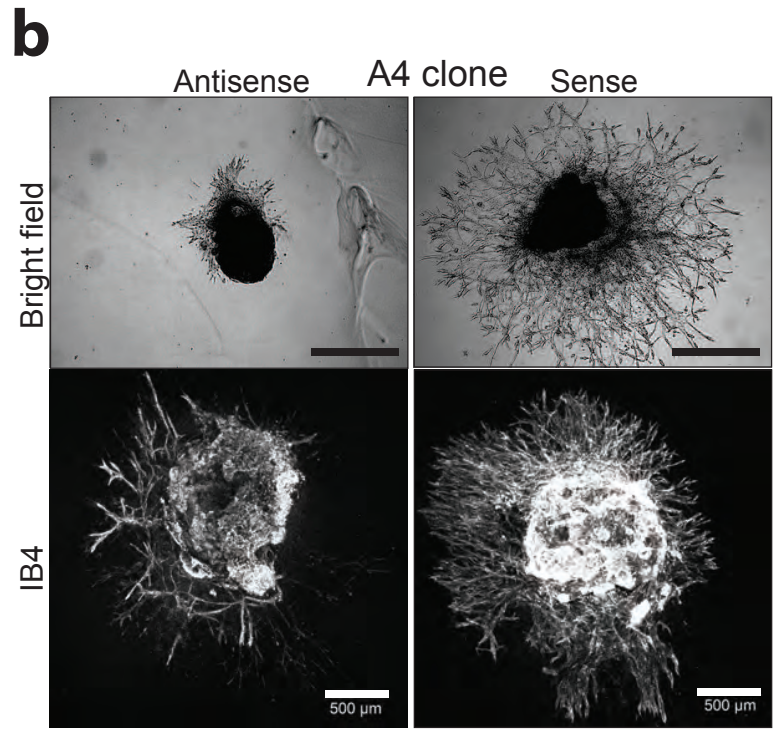
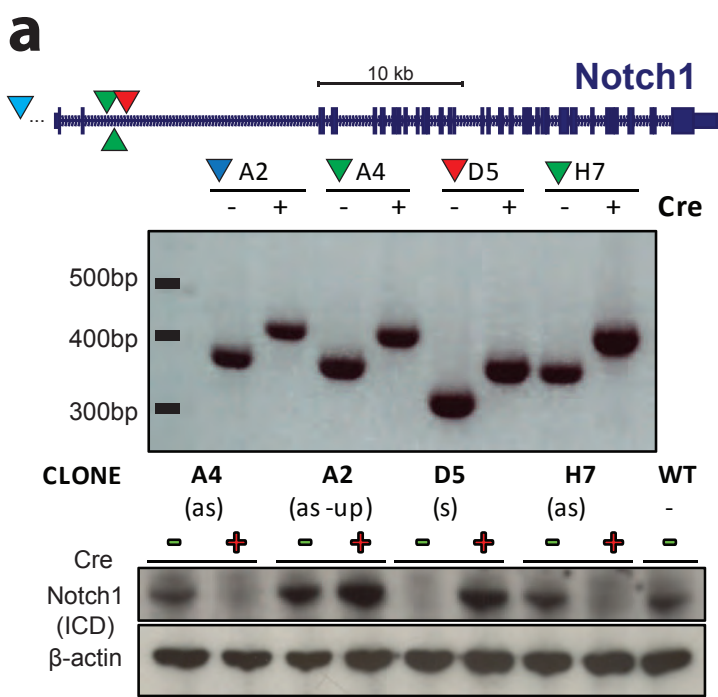
HEK293T cells + RV-A1a



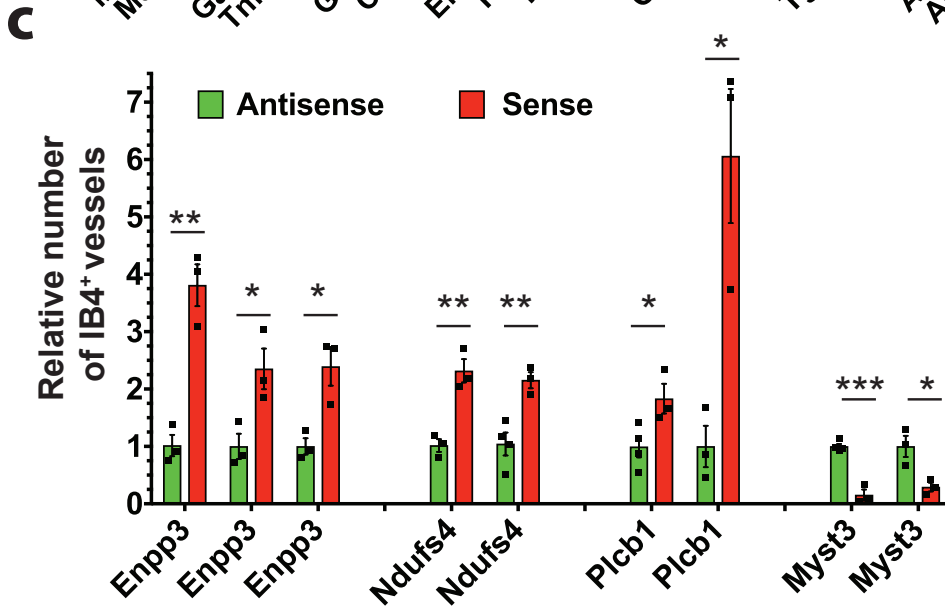
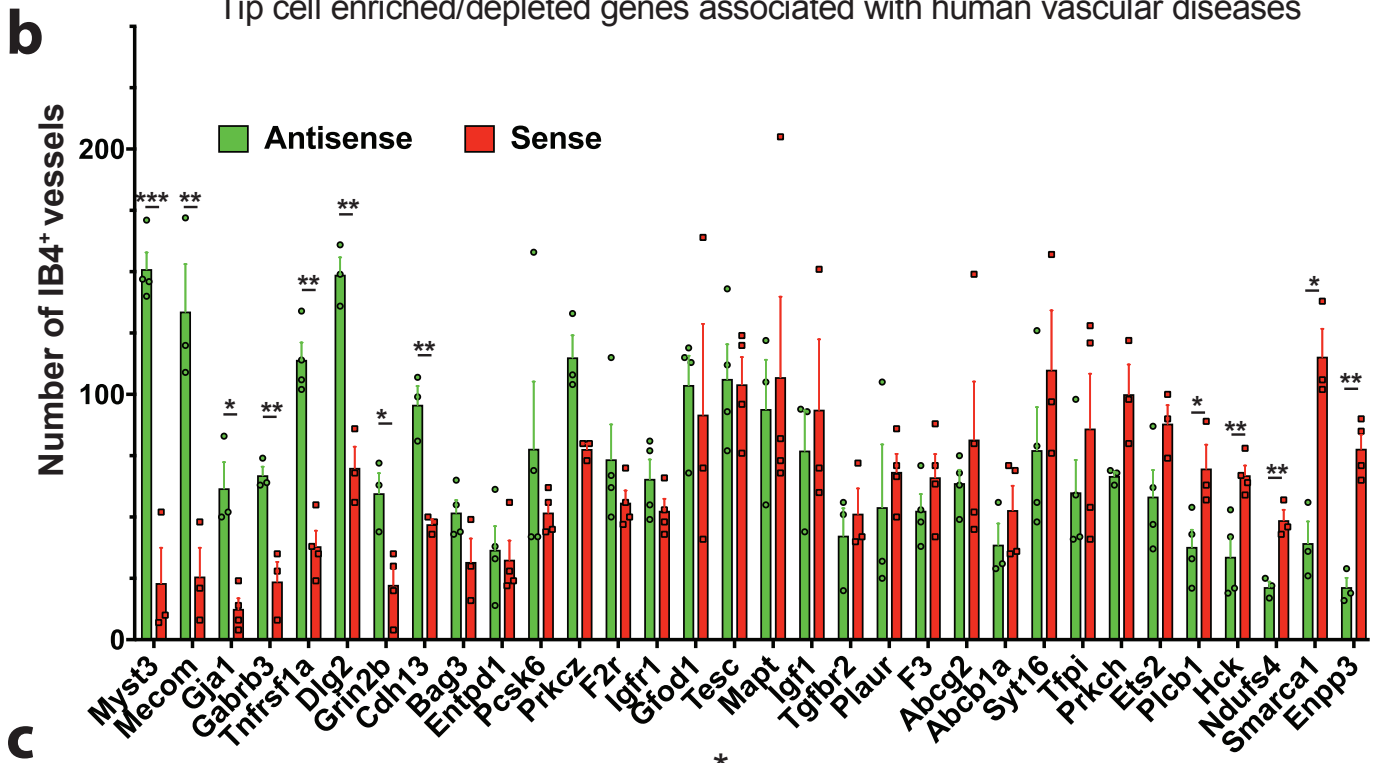
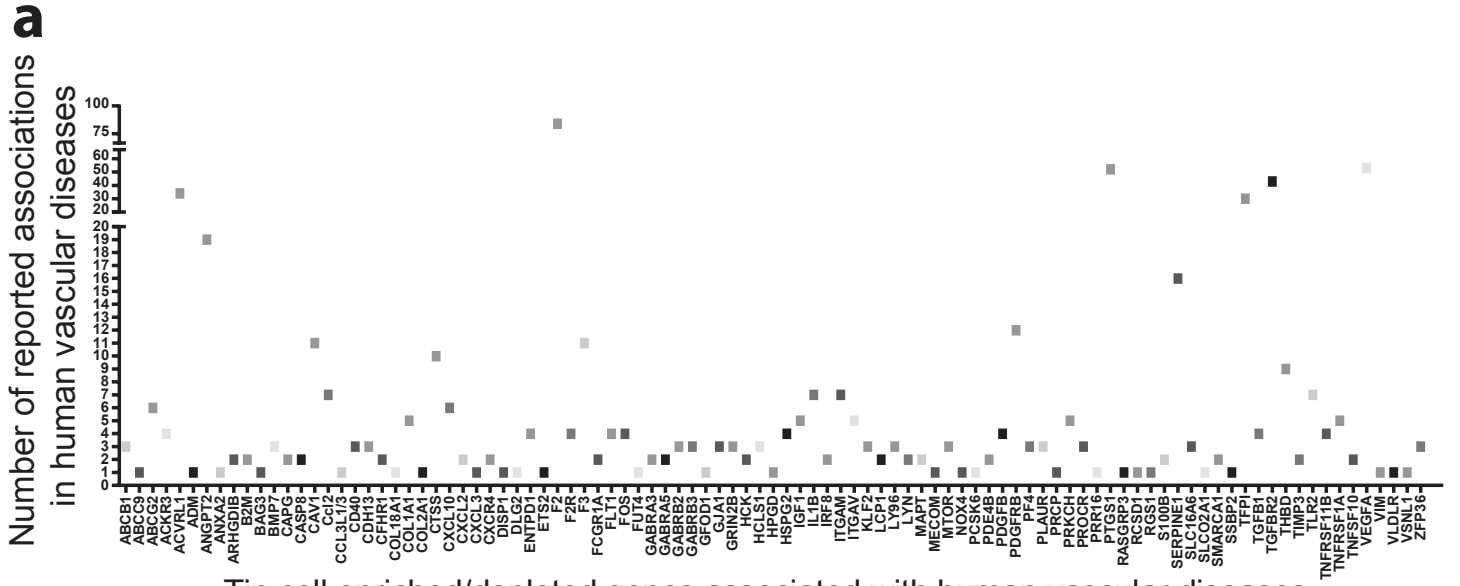
**Extended Data Figure 10**

**a****b****c**

wt	cytoplasmic	transmembrane	vesicular	
	V R D A V K A V G I A G V G L A A L G L V G V M L S R N N K K Q K Q Stop			
sgRNA1	V R D A V K A V G I A G V G L A A L G L V G V M L S R N N K K Q K Q Stop			Control
sgRNA1	V R D A V K A V G I A G V G L A A L G L V G V M L S R N N K K Q K Q Stop			+ RV-A1a
sgRNA2	V R D A V K A V G I A G V G L A A L G L V G V M L S R N N K K Q K Q Stop			Control
sgRNA2	V R D A V K A V G I A G V G L A A L G L V G V M L S R N N K K Q K Q Stop			+ RV-A1a



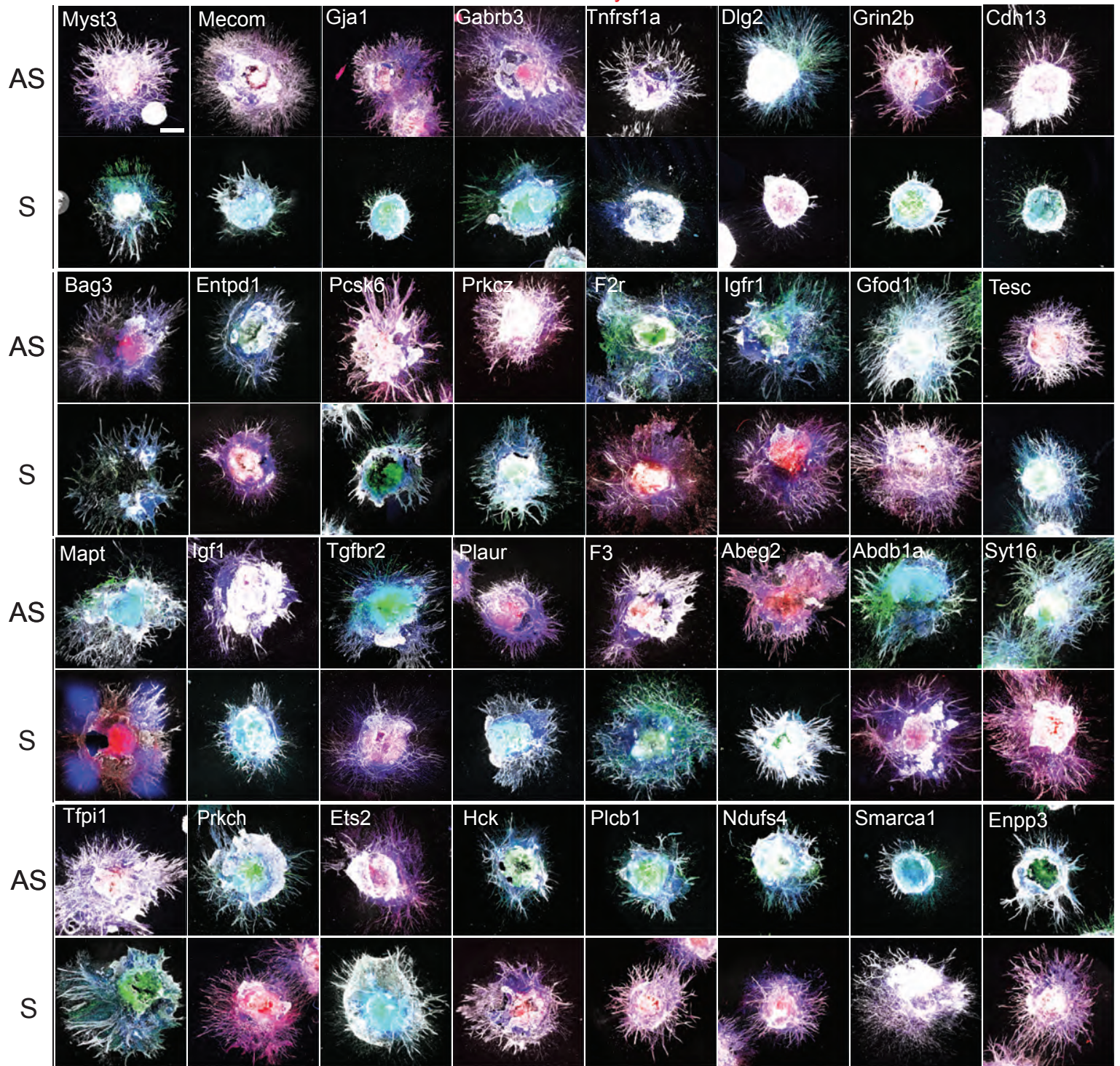
# Extended Data Figure 12



**Extended Data Figure 13**



IB4 GFP mCherry-Cre DAPI



**Extended Data Figure 14**

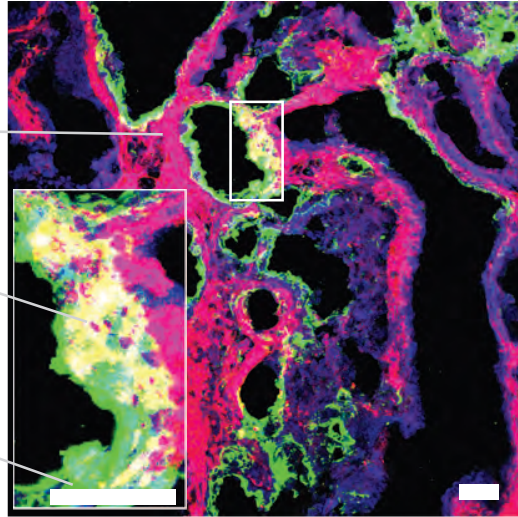


**a**

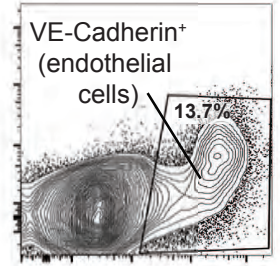
DAPI

mCherry<sup>+</sup>ES cell derived  
tissueIB4<sup>+</sup> mCherry<sup>+</sup>

Mosaic blood vessel

IB4<sup>+</sup>Endogenous  
endothelial cell**b**Myst3  
chimaeric EBs

Sense (GFP):Antisense (mCherry-Cre) 1:1



VE-Cadherin

mCherry (antisense)

Non-endothelial cells

7.82%

8.77%

8.77%

8.77%

8.77%

8.77%

8.77%

8.77%

8.77%

8.77%

8.77%

8.77%

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8.77%

8.77%

8.77%

8.77%

8.77%

8.77%

8.77%

8.77%

8.77%

8.77%

Endothelial cells

7.25%

2.17%

2.17%

2.17%

2.17%

2.17%

2.17%

2.17%

2.17%

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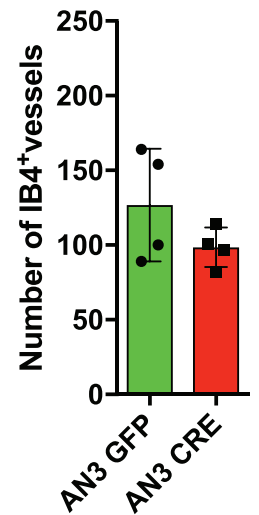
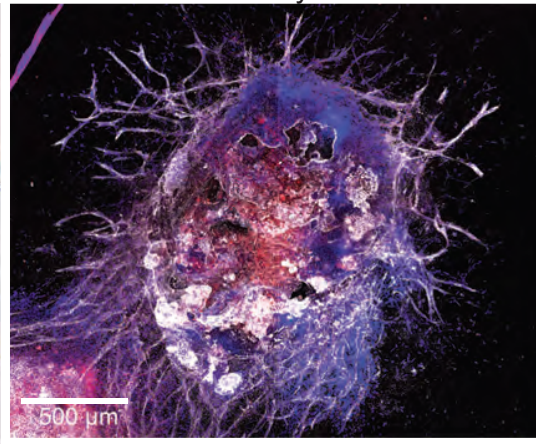
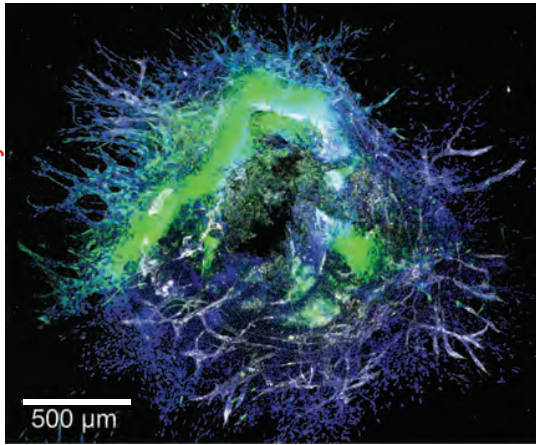
GFP (sense)

**c**

GFP

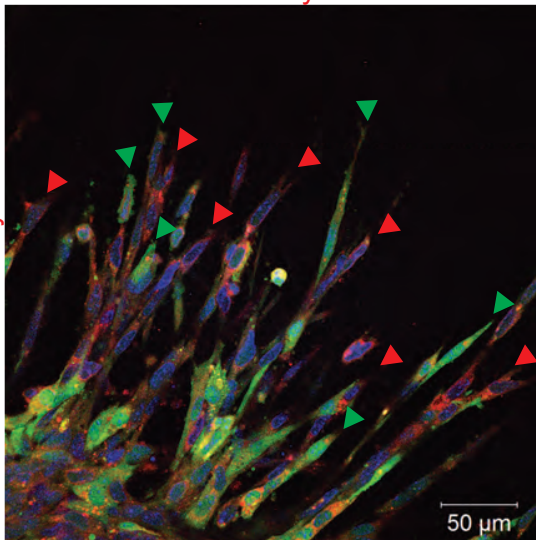
mCherry-Cre

IB4 GFP mCherry DAPI

**d**

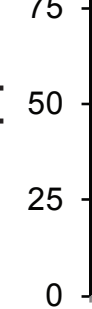
eV-GFP:mCherry-Cre 1:1

GFP mCherry DAPI

%Contribution to  
the tip position100  
75  
50  
25  
0

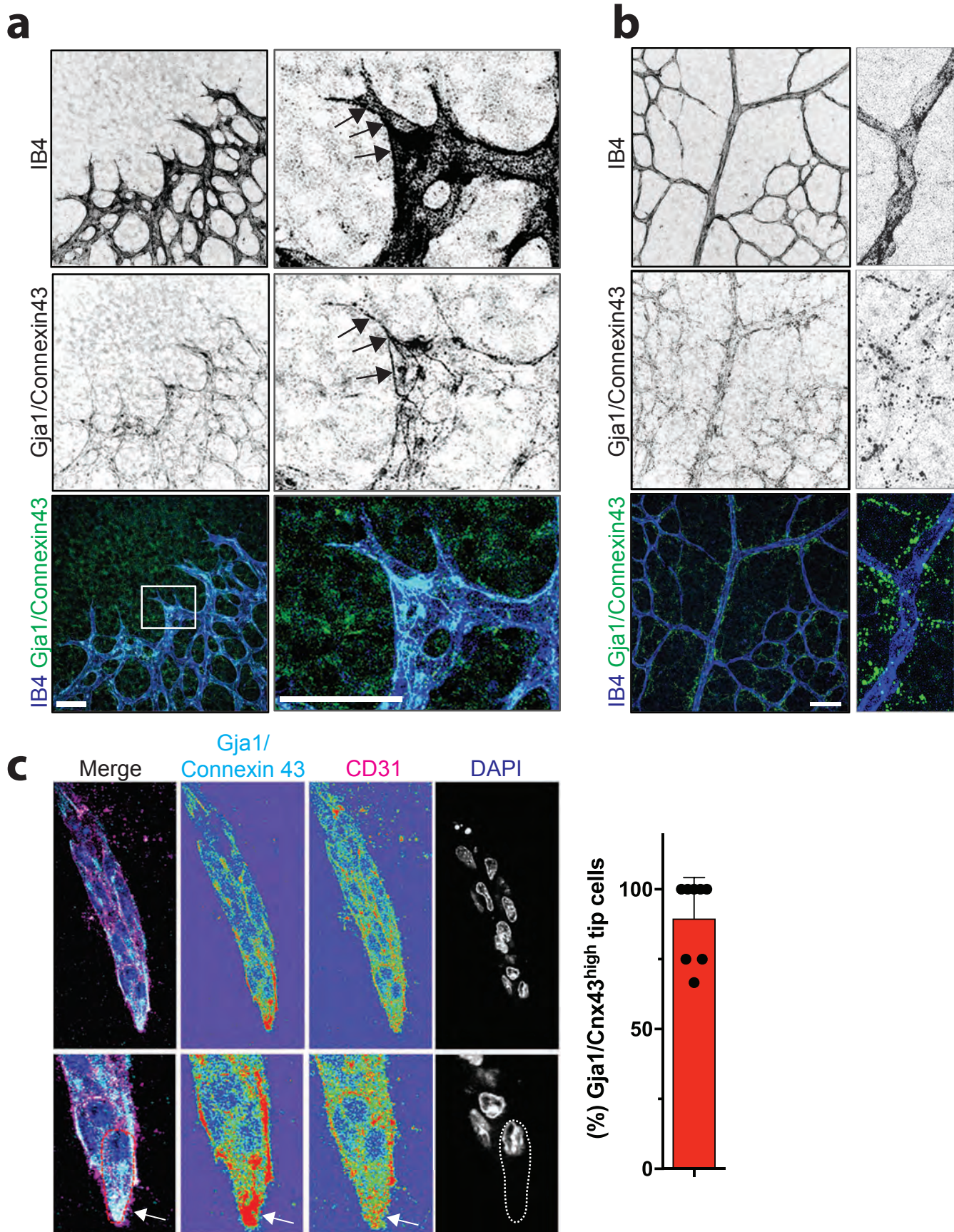
mCherry-Cre

GFP



# Extended Data Figure 15





**Extended Data Figure 16**