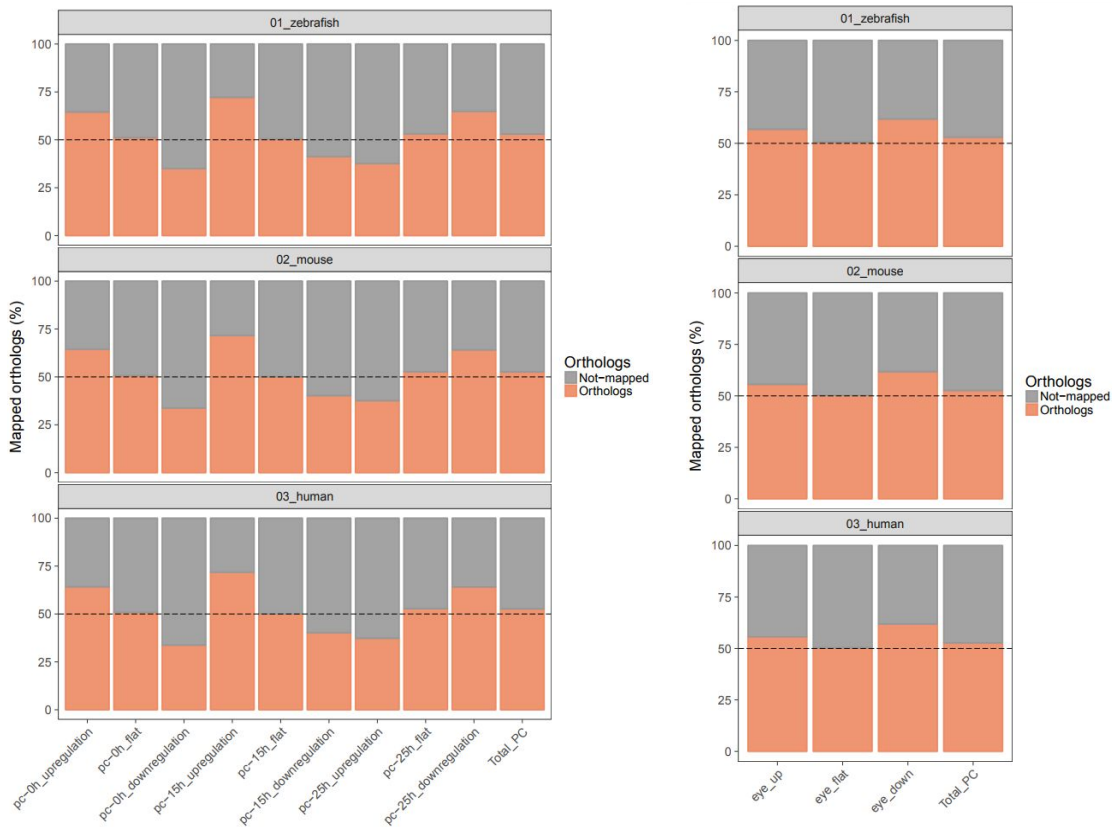


Orthologs

Number of orthologs in the different gene sets

Our regeneration Data:

High conservation of upregulated genes compared to the other gene sets in the early time points



Comparison: Eye development

Both up and down-regulated genes are more conserved than flat genes

Chi square test

Our regeneration data

p-value						
	Human		Mouse		Zebrafish	
	up	down	up	down	up	down
0h	0	0,00001807	0	0,00002067	0	0,00016437
15h	0	0,00610516	0	0,00263558	0	0,01103296
25h	0	1,70E-07	0	1,40E-07	0	6,00E-08

Chi-Value						
	Human		Mouse		Zebrafish	
	up	down	up	down	up	down
0h	122	18	130	18	123	14,2
15h	271	8	243	9	272	6,46
25h	57	27	54	28	56,46	29

Comparison: Eye development

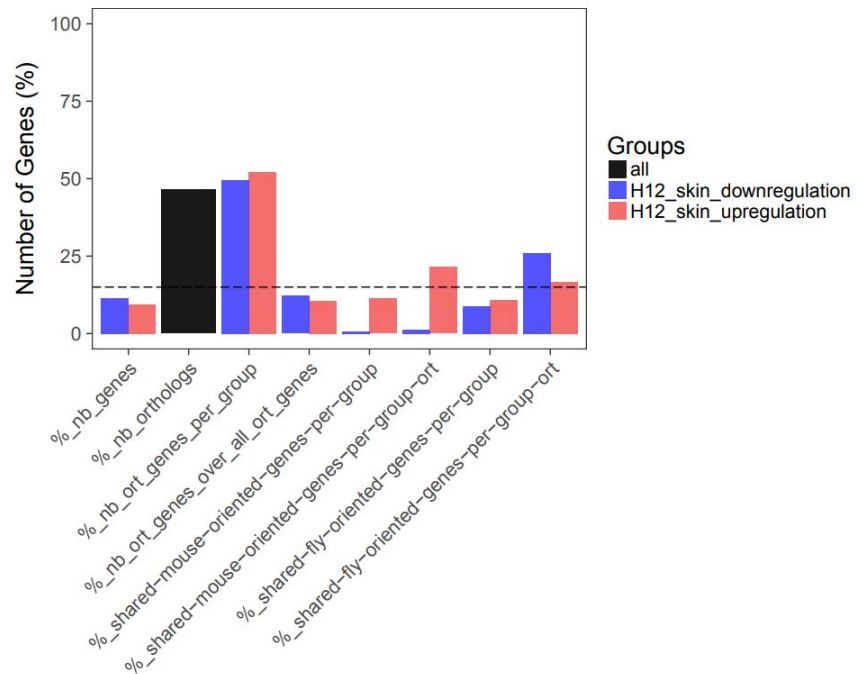
eye differentiation						
	Human		Mouse		Zebrafish	
	up	down	up	down	up	down
chi-test	17	83	17	83	23,76	79
p-value	0,00003467	0	0,00003561	0	0,00000109	0

Baseline: flat genes

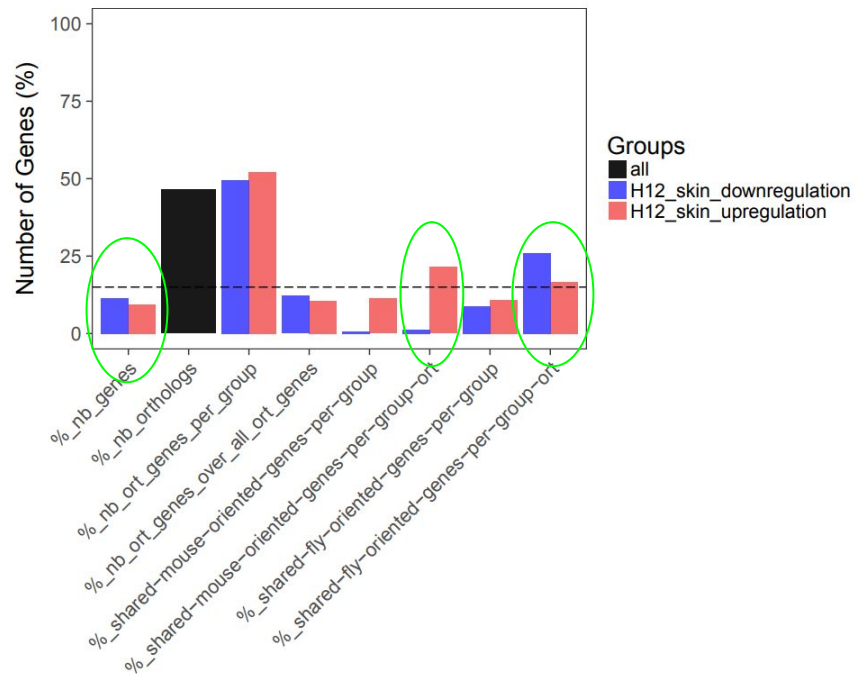
Goal comparison to eye: we would like to find a negative control, however the eye development is conserved [1]. We were not able to find a negative control.

[1] [http://dx.doi.org/10.1016/S0960-9822\(00\)00821-6](http://dx.doi.org/10.1016/S0960-9822(00)00821-6)

Mouse skin regeneration data



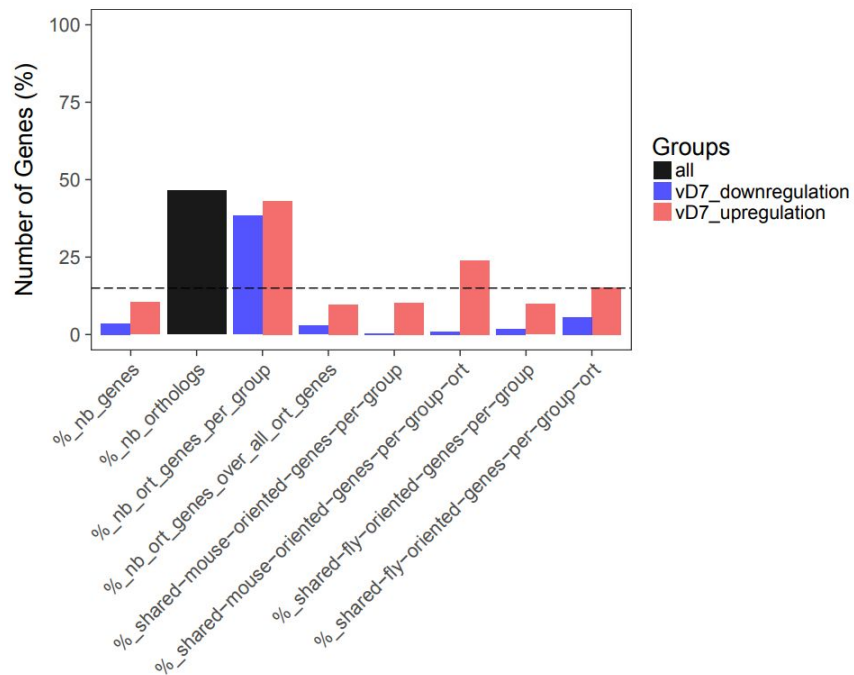
Mouse skin regeneration data



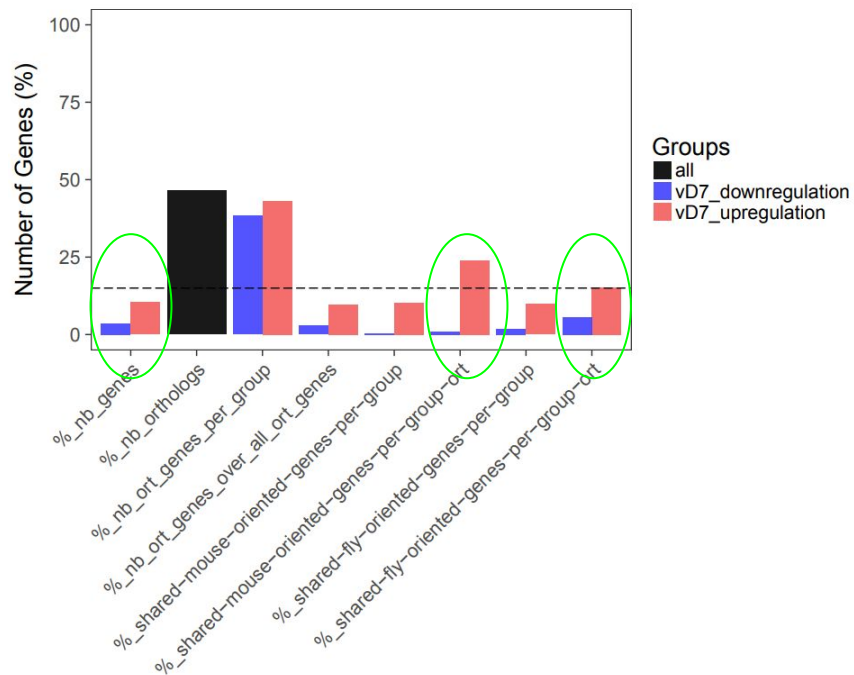
Mouse skin

Category	Term	Count	PValue
GOTERM_CC_DIRECT	GO:005737~cytoplasm	51	1,12E+11
GOTERM_BP_DIRECT	GO:006955~immune response	8	4,06E+10
GOTERM_MF_DIRECT	GO:005515~protein binding	27	1,85E+11
GOTERM_MF_DIRECT	GO:0016019~peptidoglycan receptor activity	3	0.001046778627076806
GOTERM_BP_DIRECT	GO:0001751~compound eye photoreceptor cell differentiation	5	0.0013541522087532239
GOTERM_CC_DIRECT	GO:0016020~membrane	17	0.00154262933721966101
GOTERM_BP_DIRECT	GO:0007476~imaginal disc-derived wing morphogenesis	12	0.00154206663154347
GOTERM_MF_DIRECT	GO:0050839~cell adhesion molecule binding	5	0.00200454137001363
GOTERM_MF_DIRECT	GO:0008745~N-acetylmuramoyl-L-alanine amidase activity	4	0.002056336522177214
GOTERM_BP_DIRECT	GO:0009253~peptidoglycan catabolic process	4	0.002073126267653188
GOTERM_BP_DIRECT	GO:0045087~innate immune response	8	0.0023306330901306928
KEGG_PATHWAY	dme04144:Endocytosis	10	0.0026170070839328105
GOTERM_BP_DIRECT	GO:0008063~Toll signaling pathway	5	0.0031473414813169135
GOTERM_MF_DIRECT	GO:0042834~peptidoglycan binding	4	0.004361492653905138
GOTERM_CC_DIRECT	GO:0031594~neuromuscular junction	6	0.004444336794147326
GOTERM_BP_DIRECT	GO:0007298~border follicle cell migration	8	0.008257629762045353
GOTERM_CC_DIRECT	GO:0005925~focal adhesion	4	0.00846532154636451
GOTERM_BP_DIRECT	GO:0007616~long-term memory	6	0.00856107336624281
GOTERM_CC_DIRECT	GO:0005912~adherens junction	5	0.011720489804138198
GOTERM_BP_DIRECT	GO:0009950~dorsal/ventral axis specification	4	0.012629891923736493
GOTERM_BP_DIRECT	GO:0055085~transmembrane transport	12	0.013408701411461315
GOTERM_BP_DIRECT	GO:0008299~isoprenoid biosynthetic process	3	0.015188480189017278
GOTERM_BP_DIRECT	GO:0006950~response to stress	3	0.015188480189017278
GOTERM_BP_DIRECT	GO:0006964~positive regulation of biosynthetic process of antibacterial peptides activ	3	0.018017762245826307
GOTERM_CC_DIRECT	GO:0000151~ubiquitin ligase complex	4	0.01870968431927909
GOTERM_BP_DIRECT	GO:0035220~wing disc development	6	0.01917905130958334
GOTERM_BP_DIRECT	GO:0030431~sleep	7	0.020436893387287748
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	23	0.02185287794818437
GOTERM_BP_DIRECT	GO:0007465~R7 cell fate commitment	3	0.024278997219393254
GOTERM_BP_DIRECT	GO:0007155~cell adhesion	6	0.02472742152681488
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2 cascade	4	0.024860952835202482
GOTERM_CC_DIRECT	GO:0005887~integral component of plasma membrane	16	0.02780013640225199
GOTERM_BP_DIRECT	GO:0007423~sensory organ development	5	0.029918315731241547
GOTERM_BP_DIRECT	GO:0007464~R3/R4 cell fate commitment	3	0.031291927223918325
GOTERM_BP_DIRECT	GO:0010025~wax biosynthetic process	3	0.031291927223918325
GOTERM_BP_DIRECT	GO:0035195~gene silencing by miRNA	3	0.031291927223918325
GOTERM_BP_DIRECT	GO:0035336~long-chain fatty-acyl-CoA metabolic process	3	0.031291927223918325
GOTERM_CC_DIRECT	GO:0043195~terminal bouton	4	0.03363727855494449
GOTERM_BP_DIRECT	GO:0002781~antifungal peptide production	2	0.034797175408941665
GOTERM_BP_DIRECT	GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense-mediated dec	3	0.03506161002368078
GOTERM_BP_DIRECT	GO:0046579~positive regulation of Ras protein signal transduction	4	0.03705084443634689
GOTERM_MF_DIRECT	GO:0052692~raffinose alpha-galactosidase activity	2	0.037345951142604576
GOTERM_MF_DIRECT	GO:0004557~alpha-galactosidase activity	2	0.037345951142604576
GOTERM_BP_DIRECT	GO:0005975~carbohydrate metabolic process	6	0.03868274370620692

Mouse heart regeneration data



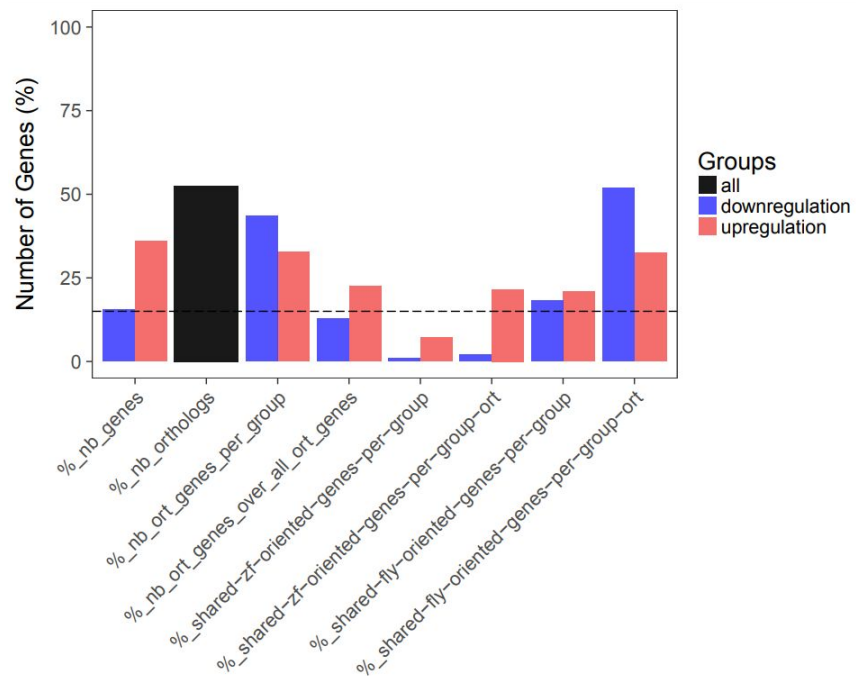
Mouse heart regeneration data



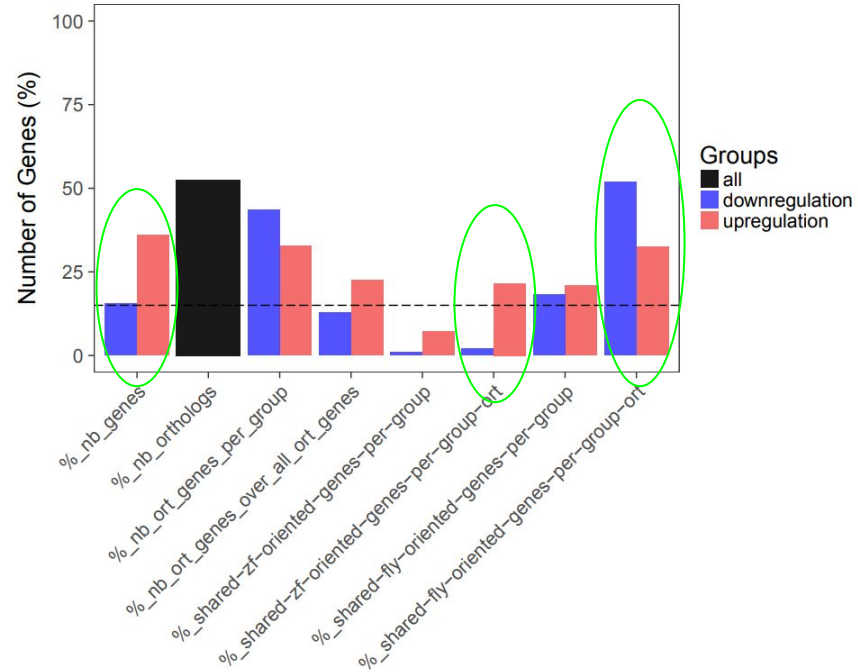
Mouse heart

Category	Term	PValue
GOTERM_BP_DIRECT	GO:0007422~peripheral nervous system development	5.86E+08
GOTERM_BP_DIRECT	GO:0007307~eggshell chorion gene amplification	7.90E+08
KEGG_PATHWAY	dme00830.Retinol metabolism	1.20E+12
GOTERM_BP_DIRECT	GO:0009253~peptidoglycan catabolic process	2.64E+11
GOTERM_MF_DIRECT	GO:0016019~peptidoglycan receptor activity	2.71E+12
GOTERM_MF_DIRECT	GO:0008745~N-acetylmuramoyl-L-alanine amidase activity	2.87E+11
KEGG_PATHWAY	dme00983.Drug metabolism - other enzymes	6.18E+11
GOTERM_MF_DIRECT	GO:0042834~peptidoglycan binding	6.26E+11
GOTERM_MF_DIRECT	GO:0016758~transferase activity, transferring hexosyl groups	6.69E+11
GOTERM_MF_DIRECT	GO:0005515~protein binding	0.0011433108656887288
GOTERM_BP_DIRECT	GO:0007155~cell adhesion	0.001296374949553805
GOTERM_BP_DIRECT	GO:0009813~flavonoid biosynthetic process	0.003079095812116281
GOTERM_BP_DIRECT	GO:0052696~flavonoid glucuronidation	0.003079095812116281
GOTERM_BP_DIRECT	GO:0007095~mitotic G2 DNA damage checkpoint	0.0034348830497672738
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	0.003924133701479878
GOTERM_BP_DIRECT	GO:0000082~G1/S transition of mitotic cell cycle	0.004607609546810708
GOTERM_MF_DIRECT	GO:0008194~UDP-glycosyltransferase activity	0.004838406242117356
GOTERM_BP_DIRECT	GO:0042127~regulation of cell proliferation	0.005620441227803466
GOTERM_BP_DIRECT	GO:0007419~ventral cord development	0.005956109539193618
GOTERM_MF_DIRECT	GO:0003677~DNA binding	0.006452392487151536
GOTERM_MF_DIRECT	GO:0008028~monocarboxylic acid transmembrane transporter activity	0.006617673779342341
GOTERM_MF_DIRECT	GO:0016538~cyclin-dependent protein serine/threonine kinase regulator activity	0.006617673779342341
GOTERM_MF_DIRECT	GO:0003678~DNA helicase activity	0.007672753657145244
GOTERM_BP_DIRECT	GO:0022008~neurogenesis	0.009301236943766104
GOTERM_BP_DIRECT	GO:0006260~DNA replication	0.00964248827042278
GOTERM_CC_DIRECT	GO:0005667~transcription factor complex	0.010422904774709814
GOTERM_BP_DIRECT	GO:0007476~imaginal disc-derived wing morphogenesis	0.011171192066803972
GOTERM_BP_DIRECT	GO:0006955~immune response	0.011273788270270256
GOTERM_BP_DIRECT	GO:0045087~innate immune response	0.012460793699813105
GOTERM_MF_DIRECT	GO:0001077~transcription activator activity, RNA polymerase II core promoter proximal r	0.013419058710738313
GOTERM_BP_DIRECT	GO:0000915~actomyosin contractile ring assembly	0.013939495616176752
GOTERM_MF_DIRECT	GO:0003700~transcription factor activity, sequence-specific DNA binding	0.016190497508208754
GOTERM_BP_DIRECT	GO:0010971~positive regulation of G2/M transition of mitotic cell cycle	0.017205148476260687
GOTERM_BP_DIRECT	GO:1900117~regulation of execution phase of apoptosis	0.017205148476260687
GOTERM_MF_DIRECT	GO:0016614~oxidoreductase activity, acting on CH-OH group of donors	0.017205148476260687
GOTERM_BP_DIRECT	GO:0000281~mitotic cytokinesis	0.018534707050843684
GOTERM_BP_DIRECT	GO:0048477~oogenesis	0.018551290314511068
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	0.01911653879914678
GOTERM_CC_DIRECT	GO:0005634~nucleus	0.01931550508090287
GOTERM_BP_DIRECT	GO:0002009~morphogenesis of an epithelium	0.01954001102585428
GOTERM_BP_DIRECT	GO:0007400~neuroblast fate determination	0.020979684425786856
GOTERM_CC_DIRECT	GO:0043231~intracellular membrane-bounded organelle	0.020979684425786856
GOTERM_BP_DIRECT	GO:0035561~regulation of chromatin binding	0.020979684425786856

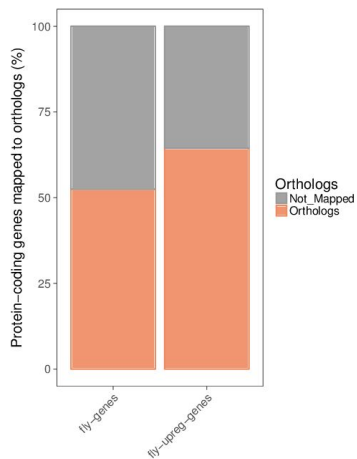
Zebrafish heart regeneration data



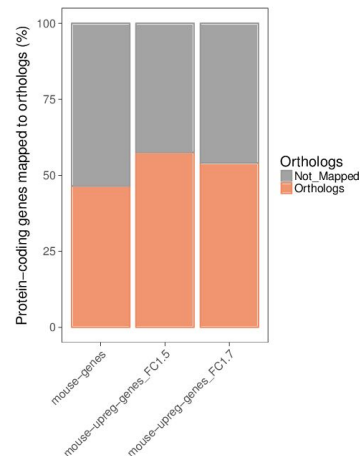
Zebrafish heart regeneration data



Fly gene stats

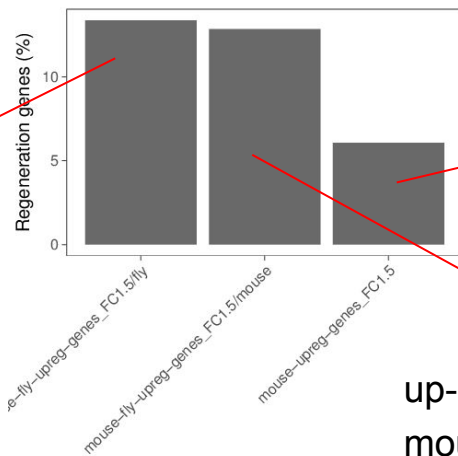


Mouse gene stats



Enrichment of regeneration genes shared by mouse and fly

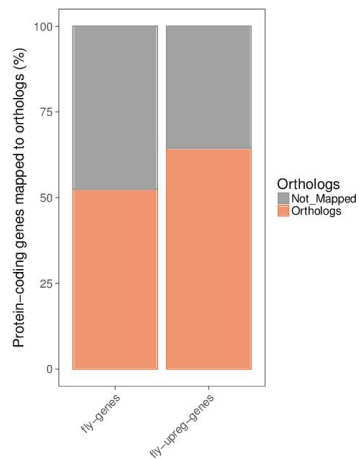
up-reg genes both fly and mouse/ fly up-reg genes



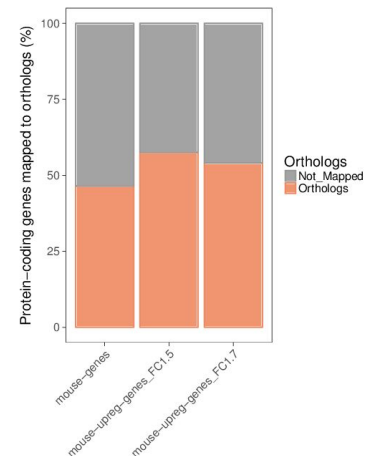
Mouse up-reg genes/all mouse protein-coding genes

up-reg genes both fly and mouse/ mouse up-reg genes

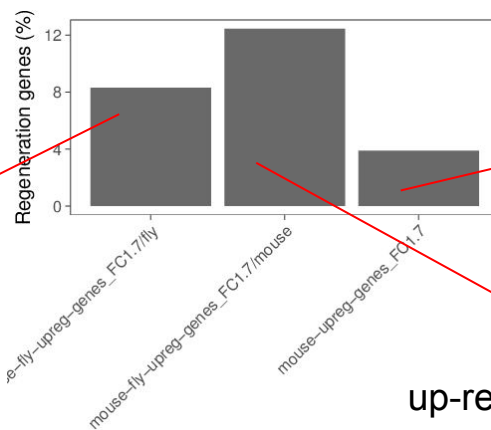
Fly gene stats



Mouse gene stats



Enrichment of regeneration genes shared by mouse and fly



up-reg genes both fly and mouse/ fly up-reg genes

Mouse up-reg genes/all mouse protein-coding genes

up-reg genes both fly and mouse/ mouse up-reg genes

New data for re-usage
analysis

New data for re-usage analysis



NATURE | LETTER

日本語要約

Stimulation of functional neuronal regeneration from Müller glia in adult mice

Nikolas L. Jorstad, Matthew S. Wilken, William N. Grimes, Stefanie G. Wohl, Leah S. VandenBosch, Takeshi Yoshimatsu, Rachel O. Wong, Fred Rieke & Thomas A. Reh

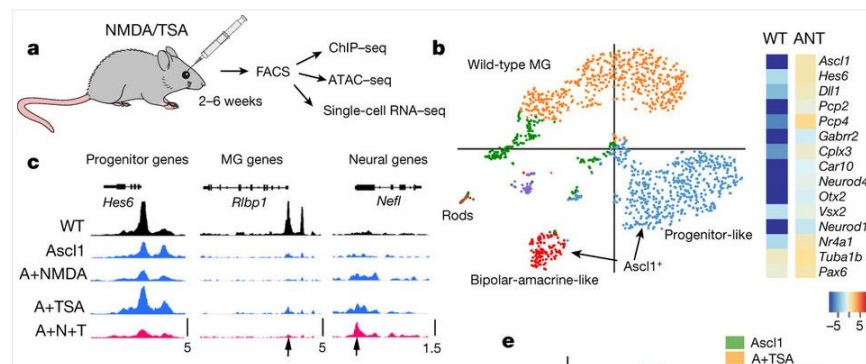
Affiliations | Contributions | Corresponding author

Nature 548, 103–107 (03 August 2017) | doi:10.1038/nature23283

Received 31 January 2017 | Accepted 13 June 2017 | Published online 26 July 2017



Many retinal diseases lead to the loss of retinal neurons and cause visual impairment. The adult mammalian retina has little capacity for regeneration. By contrast, teleost fish functionally regenerate their retina following injury, and Müller glia (MG) are the source of regenerated neurons^{1, 2, 3, 4, 5, 6}. The proneural transcription factor *Ascl1* is upregulated in MG after retinal damage^{4, 7} in zebrafish and is necessary for regeneration⁸. Although *Ascl1* is not expressed in mammalian MG after injury⁹, forced expression of *Ascl1* in mouse MG induces a neurogenic state *in vitro*¹⁰ and *in vivo* after NMDA (N-methyl-D-aspartate) damage in young mice¹¹. However, by postnatal day 16, mouse MG lose neurogenic capacity, despite *Ascl1* overexpression¹¹. Loss of neurogenic capacity in mature MG is accompanied by reduced chromatin accessibility, suggesting that epigenetic factors limit regeneration. Here we show that MG-specific overexpression of *Ascl1*, together with a histone deacetylase inhibitor, enables adult mice to generate neurons from MG after retinal injury. The MG-derived neurons express markers of inner retinal neurons, synapse with host retinal neurons, and respond to light. Using an assay for transposase-accessible chromatin with high-throughput sequencing (ATAC-seq), we show that the histone deacetylase inhibitor promotes accessibility at key gene loci in the MG, and allows more effective reprogramming. Our results thus provide a new approach for the treatment of blinding retinal diseases.



ENCODE data for re-usage analysis

Experiment Matrix

Click or enter search terms to filter the experiments included in the matrix.

Organism

<i>Homo sapiens</i>	373
<i>Mus musculus</i>	85

Biosample type

tissue	85
primary cell	22
immortalized cell line	17
in vitro differentiated cells	10
stem cell	9

Organ

brain	34
embryo	13
liver	8
eye	4
intestine	4

[+ See more...](#)

Project

Assay

DNase-seq	57
ATAC-seq	28

Assay category

DNA binding	796
Transcription	328
DNA accessibility	85
DNA methylation	72
DNA sequencing	72

Date released

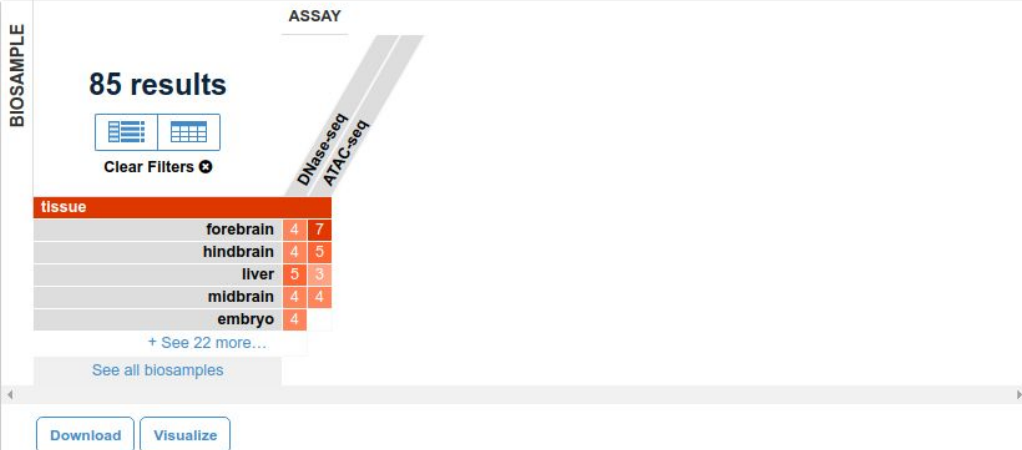
May, 2017	27
September, 2015	15
September, 2012	10
July, 2011	8
September, 2017	8

[+ See more...](#)

Available data

bam	85
bigWig	85
fastq	85
bed narrowPeak	57
bigBed narrowPeak	57

[+ See more...](#)



ENCODE data for re-usage analysis

ATAC-seq of midbrain <i>Mus musculus</i> C57BL/6 midbrain embryo (16.5 days) Lab: Bing Ren, UCSD Project: ENCODE	Experiment ENCSR096JCC released
ATAC-seq of midbrain <i>Mus musculus</i> C57BL/6 midbrain embryo (15.5 days) Lab: Bing Ren, UCSD Project: ENCODE	Experiment ENCSR468GUI released
ATAC-seq of midbrain <i>Mus musculus</i> C57BL/6 midbrain embryo (13.5 days) Lab: Bing Ren, UCSD Project: ENCODE	Experiment ENCSR819QOJ released
ATAC-seq of midbrain <i>Mus musculus</i> C57BL/6 midbrain embryo (11.5 days) Lab: Bing Ren, UCSD Project: ENCODE	Experiment ENCSR382RUC released

ATAC-seq of liver <i>Mus musculus</i> C57BL/6 liver postnatal (0 days) Lab: Bing Ren, UCSD Project: ENCODE	Experiment ENCSR609OHJ released
ATAC-seq of liver <i>Mus musculus</i> C57BL/6 liver embryo (12.5 days) Lab: Bing Ren, UCSD Project: ENCODE	Experiment ENCSR302LIV released
ATAC-seq of liver <i>Mus musculus</i> C57BL/6 liver embryo (11.5 days) Lab: Bing Ren, UCSD Project: ENCODE	Experiment ENCSR785NEL released

Genes in/out side clusters

0h upregulated genes INSIDE clusters

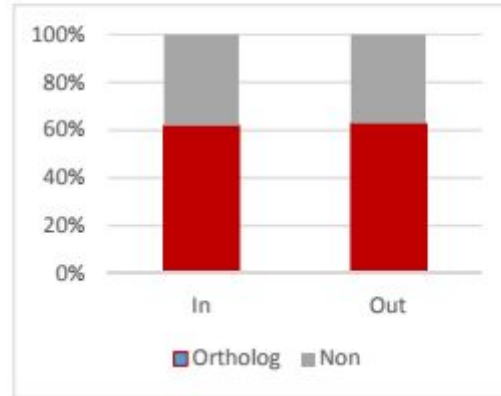
Category	Term	Count	PValue
GOTERM_BP_DIRECT	GO.0030707~ovarian follicle cell development	17	2.21E+08
GOTERM_BP_DIRECT	GO.0007399~nervous system development	18	7.96E+08
GOTERM_MF_DIRECT	GO.0003677~DNA binding	45	8.76E+08
GOTERM_BP_DIRECT	GO.0007095~mitotic G2 DNA damage checkpoint	13	1.15E+11
GOTERM_BP_DIRECT	GO.0048477~oogenesis	27	1.10E+12
GOTERM_BP_DIRECT	GO.0046425~regulation of JAK-STAT cascade	6	2.11E+12
GOTERM_CC_DIRECT	GO.0005634~nucleus	100	2.78E+12
GOTERM_BP_DIRECT	GO.0007219~Notch signaling pathway	11	2.97E+11
GOTERM_CC_DIRECT	GO.0005737~cytoplasm	87	3.54E+11
GOTERM_BP_DIRECT	GO.0035019~somatic stem cell population maintenance	6	5.13E+11
GOTERM_BP_DIRECT	GO.0051123~RNA polymerase II transcriptional preinitiation complex	6	8.44E+11
GOTERM_MF_DIRECT	GO.0004802~glutathione peroxidase activity	7	0.001027509437868212
GOTERM_CC_DIRECT	GO.0005700~polytene chromosome	17	0.001825478636670938
GOTERM_BP_DIRECT	GO.0007423~sensory organ development	9	0.0031706855101392814
GOTERM_BP_DIRECT	GO.0008283~cell proliferation	9	0.0031706855101392814
GOTERM_BP_DIRECT	GO.0000278~mitotic cell cycle	8	0.00399569142473899165
GOTERM_BP_DIRECT	GO.0007365~periodic partitioning	3	0.003999565424569938
GOTERM_MF_DIRECT	GO.0003682~chromatin binding	13	0.005391939827190603
GOTERM_BP_DIRECT	GO.0007067~mitotic nuclear division	13	0.005413548534288489
GOTERM_BP_DIRECT	GO.0019991~septate junction assembly	6	0.005980092676411749
GOTERM_BP_DIRECT	GO.0001708~cell fate specification	6	0.005980092676411749
GOTERM_MF_DIRECT	GO.0005515~protein binding	40	0.006229503724949665
GOTERM_BP_DIRECT	GO.0044804~nucleophagy	4	0.0066527383680596245
GOTERM_BP_DIRECT	GO.0042058~regulation of epidermal growth factor receptor signaling	4	0.0066527383680596245
GOTERM_MF_DIRECT	GO.0003700~transcription factor activity, sequence-specific DNA bin	21	0.0071006277023068845
GOTERM_BP_DIRECT	GO.0006749~glutathione metabolic process	7	0.007367015961335778
GOTERM_MF_DIRECT	GO.0016301~kinase activity	7	0.007637760324176527
GOTERM_BP_DIRECT	GO.0000706~meiotic DNA double-strand break processing	3	0.007803286413356147
GOTERM_BP_DIRECT	GO.0006367~transcription initiation from RNA polymerase II promote	8	0.009126199902704371
GOTERM_MF_DIRECT	GO.0000978~RNA polymerase II core promoter proximal region sequ	5	0.010364860296567718
GOTERM_BP_DIRECT	GO.0006357~regulation of transcription from RNA polymerase II prom	14	0.012033098157289333
GOTERM_BP_DIRECT	GO.0006351~transcription, DNA-templated	24	0.012497318333413156
GOTERM_BP_DIRECT	GO.0042059~negative regulation of epidermal growth factor receptor	6	0.01385007273141317
GOTERM_CC_DIRECT	GO.0019008~molybdopterin synthase complex	3	0.014096912478004651
GOTERM_MF_DIRECT	GO.0001046~core promoter sequence-specific DNA binding	3	0.014698540863274719
GOTERM_MF_DIRECT	GO.0001077~transcriptional activator activity, RNA polymerase II con	7	0.016886167182106705
GOTERM_BP_DIRECT	GO.0006777~Mo-molybdopterin cofactor biosynthetic process	3	0.01856901106354489
GOTERM_BP_DIRECT	GO.0046579~positive regulation of Ras protein signal transduction	6	0.01870569072873797
GOTERM_BP_DIRECT	GO.0006468~protein phosphorylation	18	0.02010765351329353
GOTERM_MF_DIRECT	GO.0046872~metal ion binding	38	0.020489186510212913
KEGG_PATHWAY	dme00980:Metabolism of xenobiotics by cytochrome P450	8	0.02063220607153842

0h upregulated genes OUTSIDE clusters

Category	Term	Count	PValue
GOTERM_MF_DIRECT	GO:0005515--protein binding	119	4.57E+06
GOTERM_BP_DIRECT	GO:0016567--protein ubiquitination	39	3.90E+07
GOTERM_MF_DIRECT	GO:0004842--ubiquitin-protein transferase activity	44	3.47E+08
GOTERM_CC_DIRECT	GO:0005737--cytoplasm	221	7.69E+09
GOTERM_BP_DIRECT	GO:0000122--negative regulation of transcription from RNA polymerase II prom	33	3.57E+10
GOTERM_BP_DIRECT	GO:0007411--axon guidance	38	4.73E+10
GOTERM_BP_DIRECT	GO:0007476--imaginal disc-derived wing morphogenesis	42	7.39E+10
GOTERM_CC_DIRECT	GO:0005634--nucleus	248	7.58E+10
GOTERM_MF_DIRECT	GO:0008270--zinc ion binding	100	1.76E+12
GOTERM_MF_DIRECT	GO:0031624--ubiquitin conjugating enzyme binding	9	1.88E+12
GOTERM_CC_DIRECT	GO:0000151--ubiquitin ligase complex	12	3.63E+11
GOTERM_BP_DIRECT	GO:0001738--morphogenesis of a polarized epithelium	8	5.73E+11
GOTERM_BP_DIRECT	GO:0045892--negative regulation of transcription, DNA-templated	25	9.65E+11
GOTERM_MF_DIRECT	GO:0061630--ubiquitin protein ligase activity	19	0.0010640905301097917
GOTERM_BP_DIRECT	GO:0000209--protein polyubiquitination	16	0.0011713739408607104
GOTERM_BP_DIRECT	GO:0006897--endocytosis	16	0.0013948742174575187
GOTERM_BP_DIRECT	GO:0007391--dorsal closure	22	0.0015173617062416143
GOTERM_BP_DIRECT	GO:0045167--asymmetric protein localization involved in cell fate determination	7	0.0016472726924615064
GOTERM_BP_DIRECT	GO:0042787--protein ubiquitination involved in ubiquitin-dependent protein cata	19	0.0017920364097096964
GOTERM_BP_DIRECT	GO:0035050--embryonic heart tube development	8	0.00191832729806341
GOTERM_CC_DIRECT	GO:0032154--cleavage furrow	11	0.0020086419542603446
GOTERM_BP_DIRECT	GO:0043066--negative regulation of apoptotic process	16	0.002289973959461549
GOTERM_BP_DIRECT	GO:0006909--phagocytosis	36	0.0022937817376283863
GOTERM_MF_DIRECT	GO:0005524--ATP binding	107	0.0023724860212738642
GOTERM_BP_DIRECT	GO:0045746--negative regulation of Notch signaling pathway	13	0.0026400387579364245
GOTERM_BP_DIRECT	GO:0006727--onmochrome biosynthetic process	8	0.0026937316170383007
GOTERM_BP_DIRECT	GO:0030837--negative regulation of actin filament polymerization	5	0.002959338070500696
GOTERM_BP_DIRECT	GO:1902669--positive regulation of axon guidance	5	0.002959338070500696
GOTERM_BP_DIRECT	GO:0022008--neurogenesis	79	0.003409904063745352
KEGG_PATHWAY	dme00563_Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	8	0.0035106288492668617
GOTERM_BP_DIRECT	GO:0051301--cell division	16	0.003616217855481752
GOTERM_BP_DIRECT	GO:0007307--eggshell chorion gene amplification	8	0.003688562838048888
GOTERM_CC_DIRECT	GO:0005794--Golgi apparatus	29	0.004431059100334946
GOTERM_BP_DIRECT	GO:0007422--peripheral nervous system development	18	0.0044418440614410306
GOTERM_BP_DIRECT	GO:0008360--regulation of cell shape	21	0.004448220157697897
GOTERM_BP_DIRECT	GO:0000082--G1/S transition of mitotic cell cycle	6	0.004756767312969577
GOTERM_BP_DIRECT	GO:0006886--intracellular protein transport	21	0.004967734767808359
GOTERM_MF_DIRECT	GO:0008134--transcription factor binding	19	0.00517994844073751
GOTERM_BP_DIRECT	GO:0007029--endoplasmic reticulum organization	7	0.005190886947870575
GOTERM_BP_DIRECT	GO:0045773--positive regulation of axon extension	5	0.005441147136539997
GOTERM_CC_DIRECT	GO:0045179--apical cortex	11	0.006199954132911566
GOTERM_BP_DIRECT	GO:0007155--cell adhesion	19	0.006381975039181318

Orthologous genes in 0h upregulated clusters

0h Up				
	Ortholog	Non	Total	%
In	338	208	546	61,9047619
Out	968	573	1541	62,816353



chi test	0.143
p-value	0.70531663