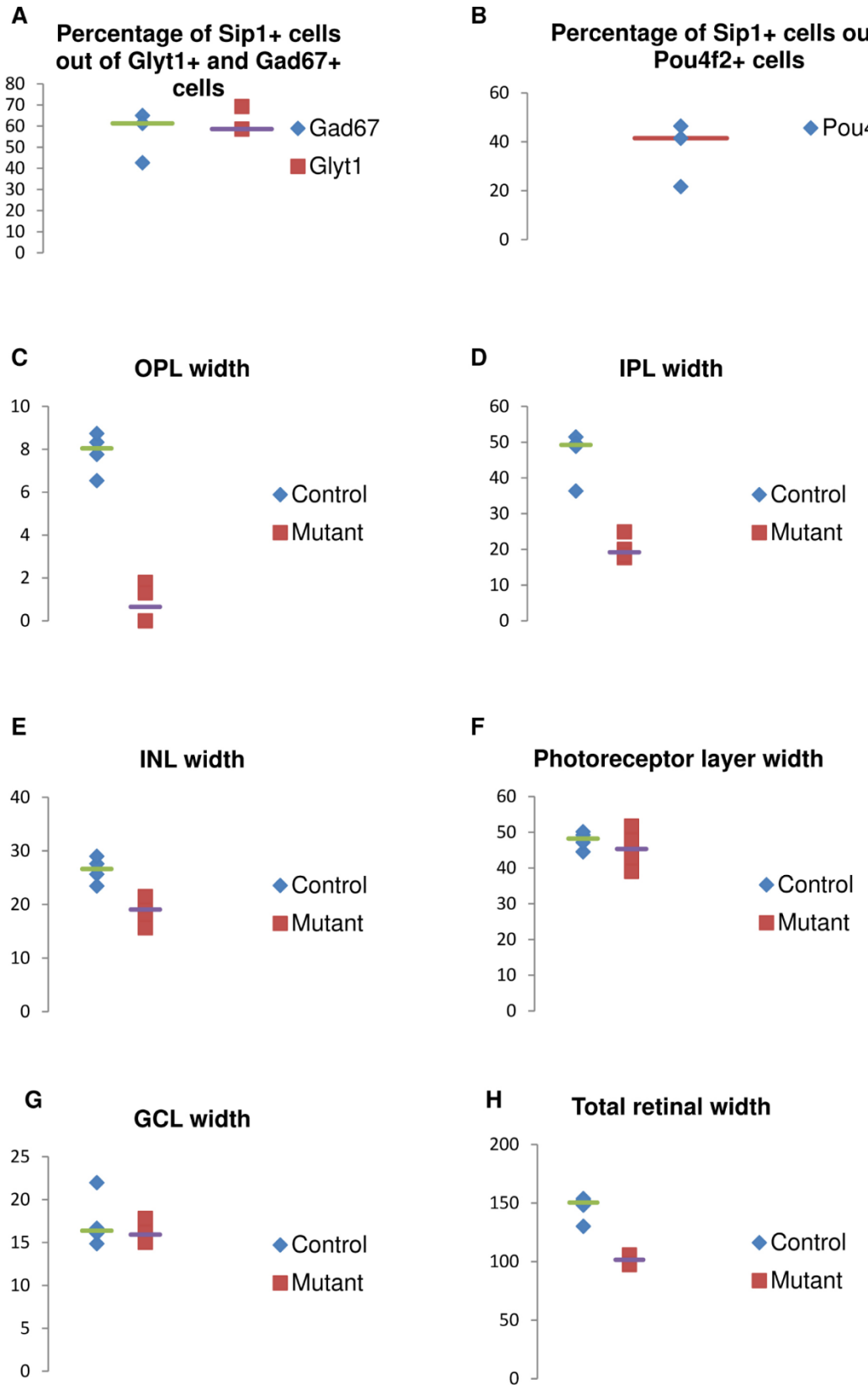


Figure S1: Measurements of the percentage of ACs and RGCs expressing Sip1 and the width of the different retinal layers in control and *Sip1$^{loxp/loxp}$;aCre* retinae.

The different repeats of the measurements of the percentage of Sip1+ cells out of Glyt1+ and Gad67+ cells (A) and Pou4f2+ cells (B) are presented in scatter plots (N=3). The different repeats of the measurement of the width of the OPL (C), IPL (D), INL (E), photoreceptors layer (F), GCL (G) and the total retina (H) in control and *Sip1$^{loxp/loxp}$;aCre* retinae are presented in scatter plots (N=4). The median in the scatter plots is represented by a line passing through the data points

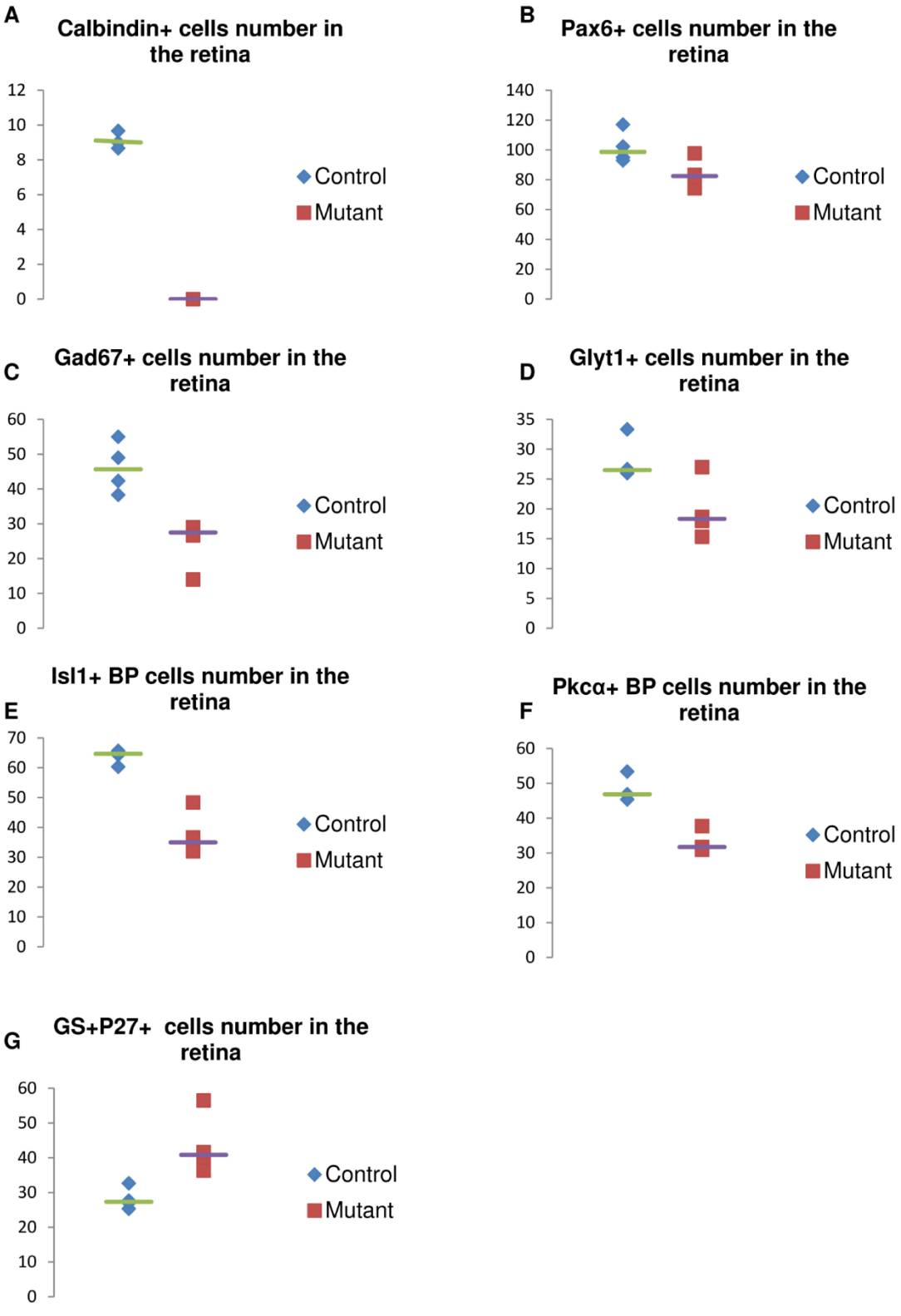


Figure S2: Measurements of the number of the different INL cells types in control and *Sip1*$^{loxp/loxp}$*;aCre* retinae.

The different repeats of the quantification of the number of Calbindin+ HCs (A), Pax6+ ACs (B), Gad67+ GABAergic ACs (C), Glyt1+ glycinergic ACs (D), Isl1+ BPs (E), Pkcα+ BPs (F) and GS+P27+ Muller glia (G) in control and *Sip1*$^{loxp/loxp}$*;aCre* retinae are presented in scatter plots (N=3 for Pkcα, N=4 for the rest). The median in the scatter plots is represented by a line passing through the data points.

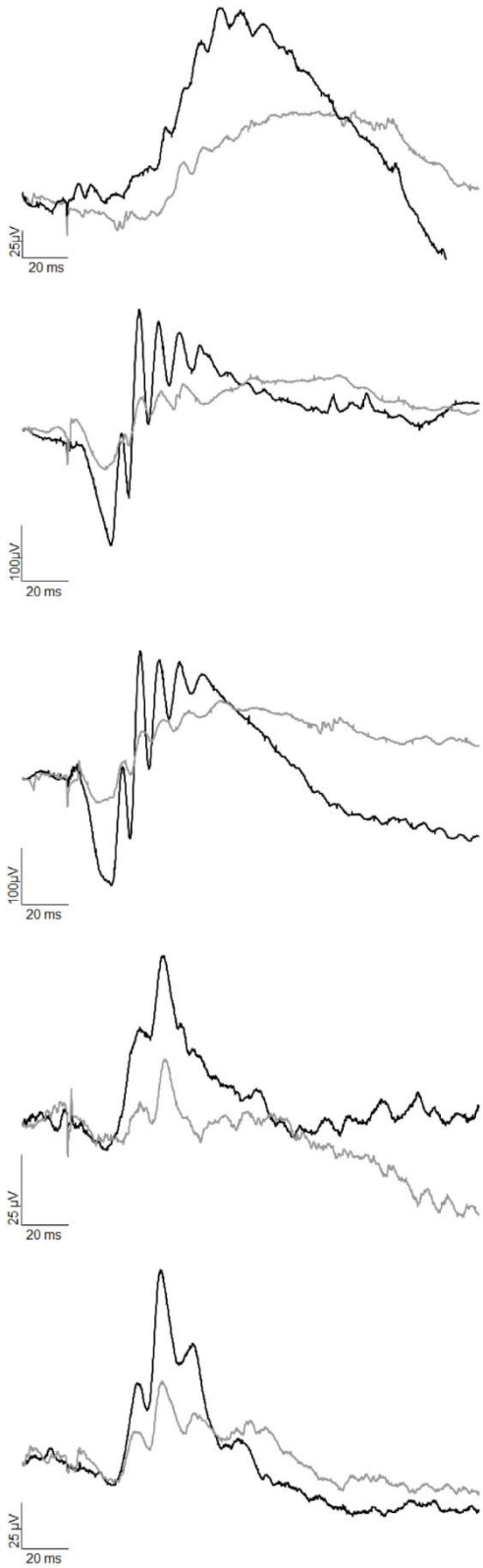
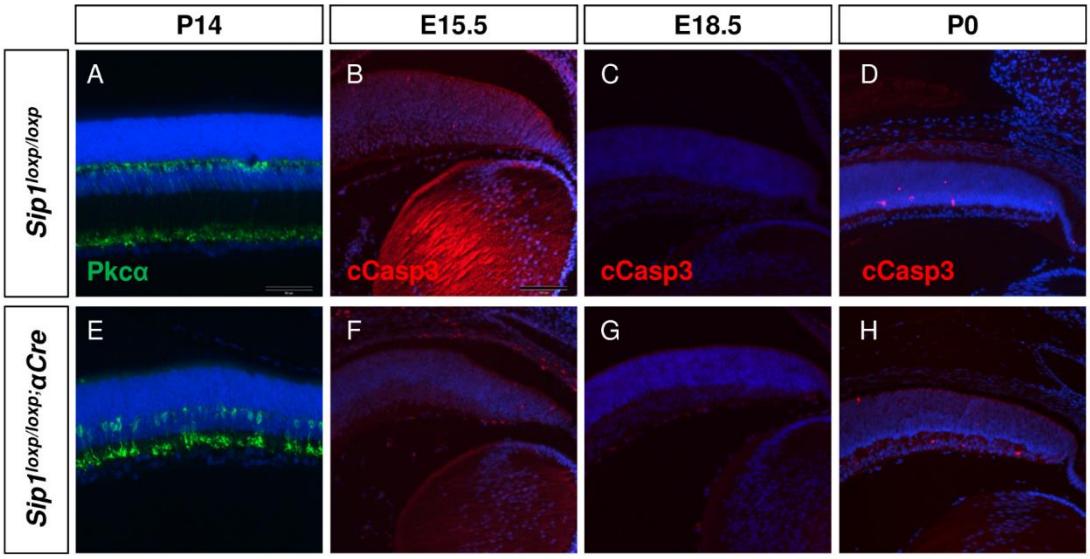
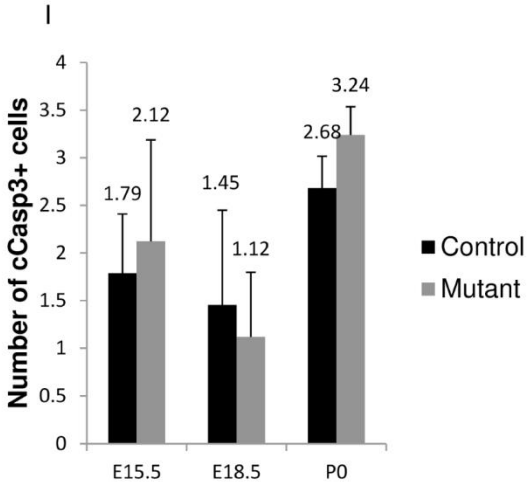


Figure S3: ERG traces.

Representative tracings of a control (black) and a mutant (gray) animal to the 5 stimulus conditions presented in Fig. 2K, L.





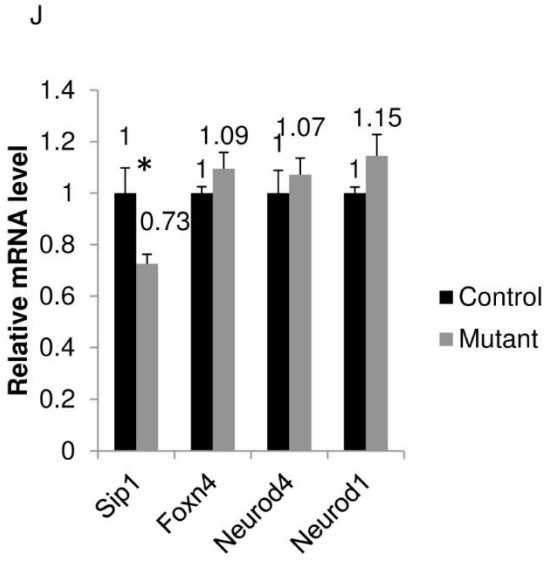


Figure S4: Pkcα and cleaved Caspase3 positive cells and the mRNA levels of *Sip1*, *Foxn4, Neurod4 and Neurod1* in control and *Sip1*$^{loxp/loxp}$*;aCre* eyes

IIF was used for the detection of Pkcα+ cells in P14 control (A) and *Sip1*$^{loxp/loxp}$*;aCre* (E) retinae. IIF was also used for the detection of cCasp3+ cells in E15.5 (B,F), E18.5(C,G) and P0 (D,H) control and *Sip1*$^{loxp/loxp}$*;aCre* retinae. The number of cCasp3+ cells in a normalized field of 180 μM was quantified in each of the stages (I). qPCR analysis was used in order to quantify the relative mRNA levels of *Sip1*, *Foxn4*, *NeuroD4* and *NeuroD1* in whole eyes of E15.5 control (N=3) and *Sip1*$^{loxp/loxp}$*;aCre* (N=5) embryos (J). Significant differences ($P<0.05$) are marked with an asterisk. Scalebars: 50 μm for A and E and 100 μm for B-D and F-H.

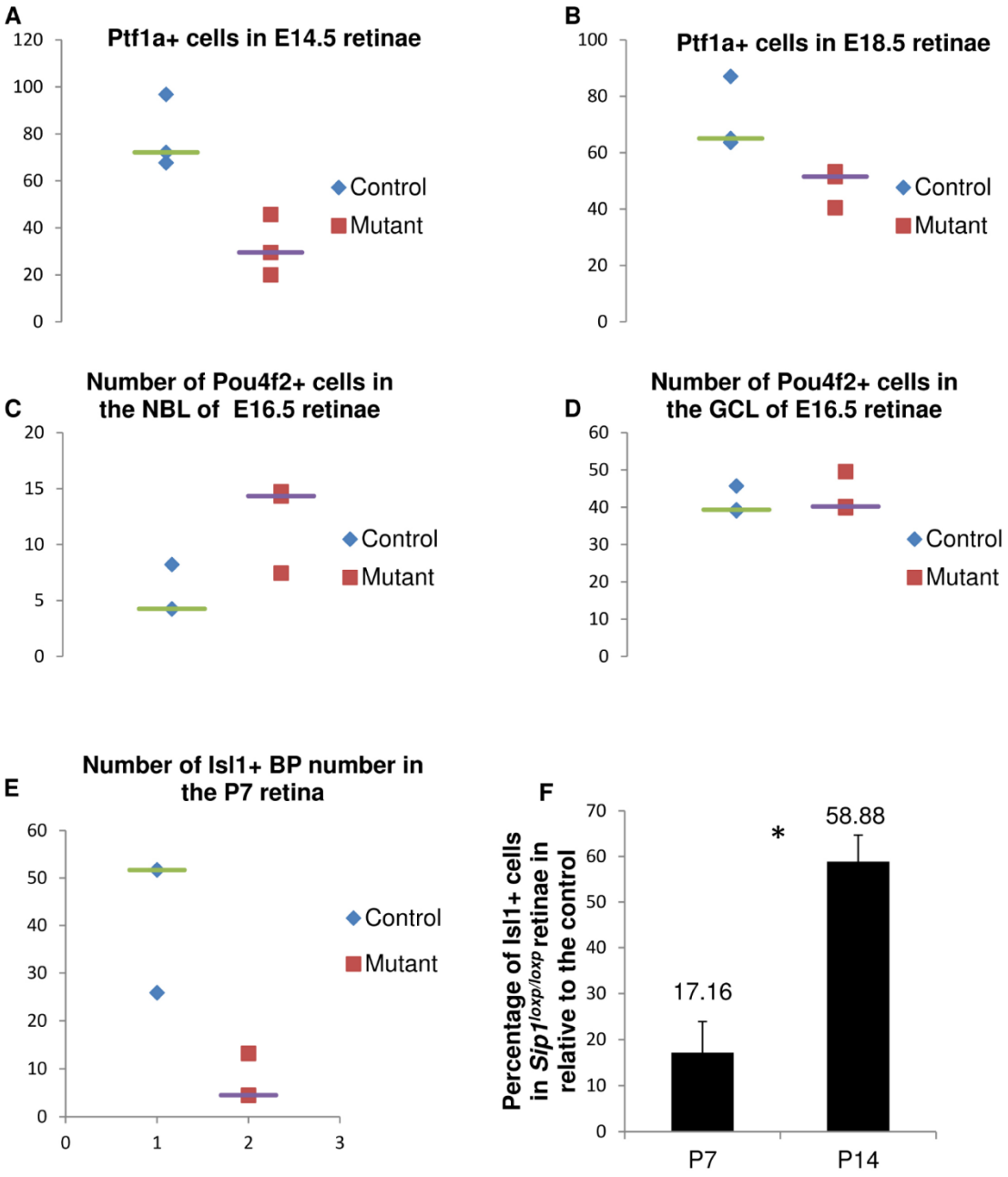


Figure S5: The number of Ptf1a+ and Pou4f2+ and Isl1+ cells in control and *Sip1*$^{loxp/loxp}$*;aCre* retinae.

The different repeats of the quantification of the number of Ptf1a+ cells at E14.5 (A) and E18.5 (B), Pou4f2+ in the NBL (C) and GCL (D) at E16.5 and Isl1+ cells at P7 (E) are presented in scatter plots (N=3 for all counts). The median in the scatter plots is represented by a line passing through the data points. The mean percentage of Isl1+ cells in *Sip1*$^{loxp/loxp}$*;aCre* retinae at P7 and P14 in comparison to their respective control is also presented (N=3 for P7 and N=4 for P14) (F). Significant differences ($P<0.05$) are marked with an asterisk.

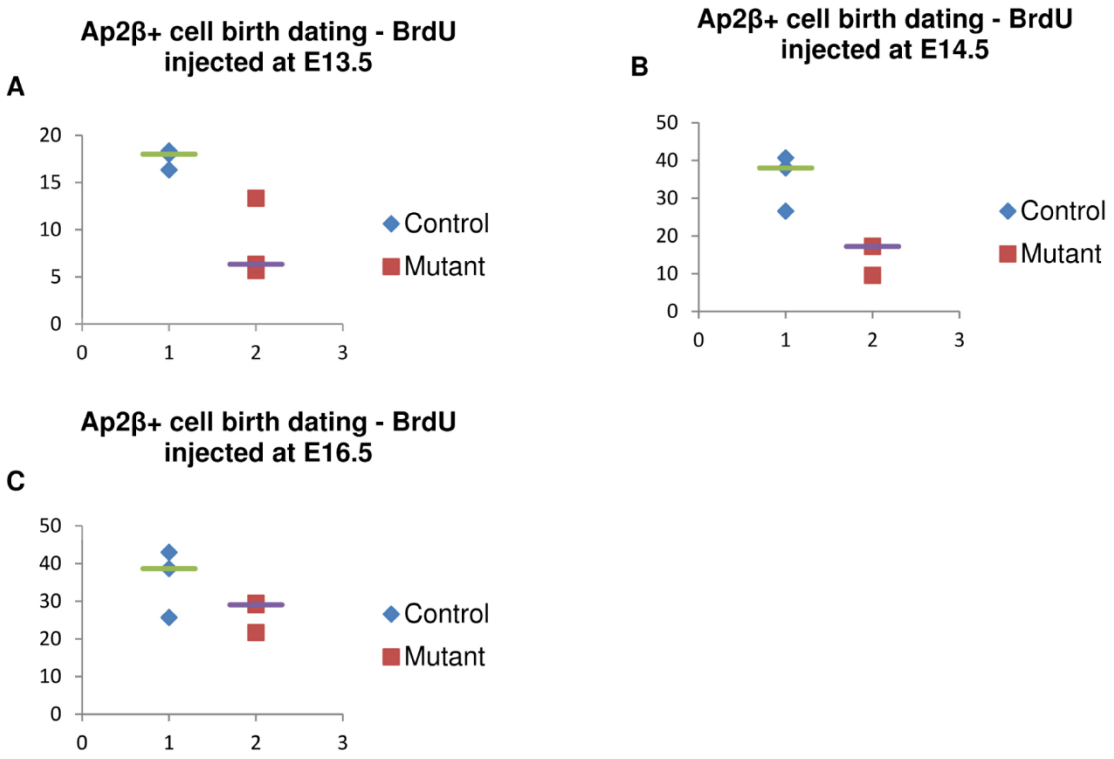
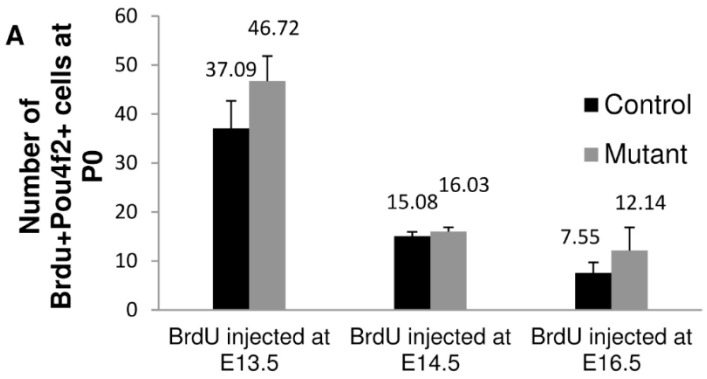
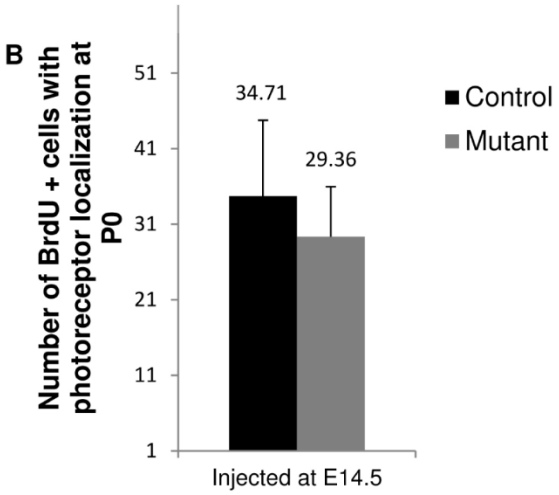
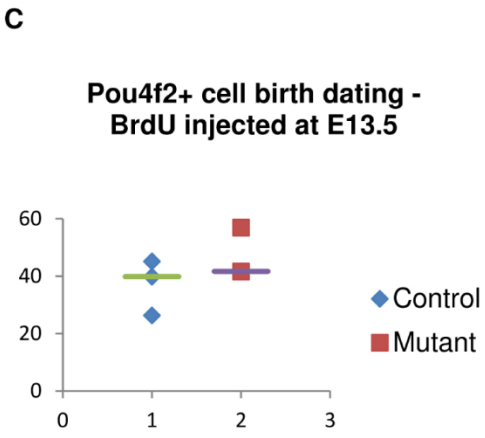


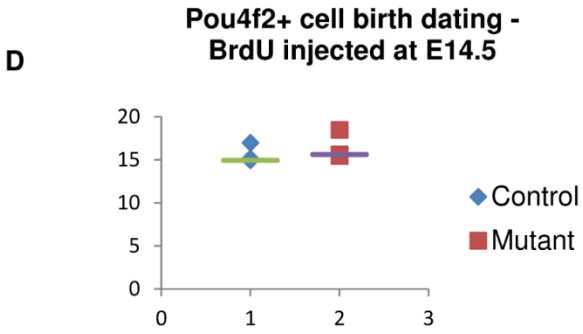
Figure S6: Birthdating of Isl1+ cells in control and *Sip1*$^{loxp/loxp}$*;aCre* retinae.

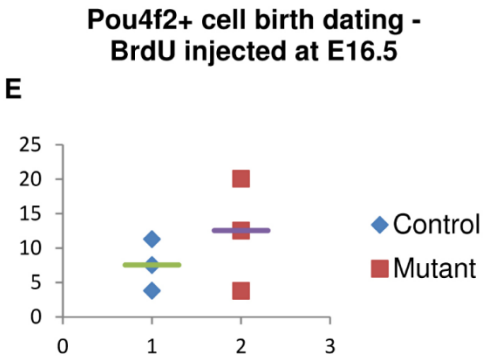
The different repeats of the quantification of the number of BrdU+Ap2β+ cells in P0 retinae that were injected with BrdU at E13.5 (A), E14.5 (B) and E16.5 (C) are presented in scatter plots (N=3 for E13.5 and E16.5, N=4 for E14.5). The median in the scatter plots is represented by a line passing through the data points











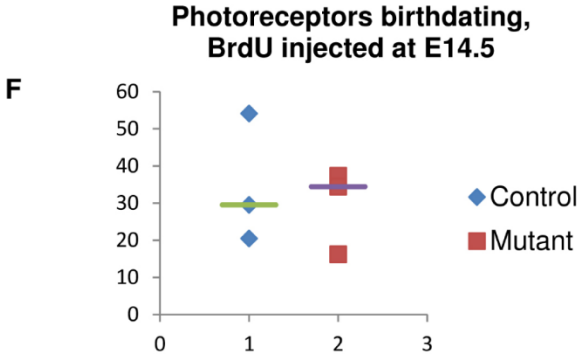


Figure S7: The birth dates of RGCs and cone photoreceptors are not delayed in the *Sip1*$^{loxp/loxp}$*;aCre* retina.

For RGCs birthdating BrdU was injected to control and *Sip1*-mutant embryos at E13.5, E14.5 or E16.5. The retinas were harvested at P0 and IIF was used in order to detect BrdU+;Pou4f2+ cells. The mean number of these cells was then quantified in control and mutant retinae injected at the three time points (N=3 for E13.5 and E16.5, N=4 for E14.5) (A). For photoreceptor birthdating BrdU was injected to control and *Sip1*-mutant embryos at E14.5. The retinae were harvested at P0 and IIF was used in order to detect BrdU+ cells which are found in the presumptive location of photoreceptors (N=3) (B). The number of BrdU+Pou4f2+ cells in control and *Sip1*-mutant embryos in the different repeats at E13.5 (C), E14.5(D) and E16.5 (E) (N=3 for E13.5 and E16.5, N=4 for E14.5) and the number of BrdU+ photoreceptors in the different repeats at E14.5 (N=3) (F) are also presented as scatter plots. The median in the scatter plots is represented by a line passing through the data points.

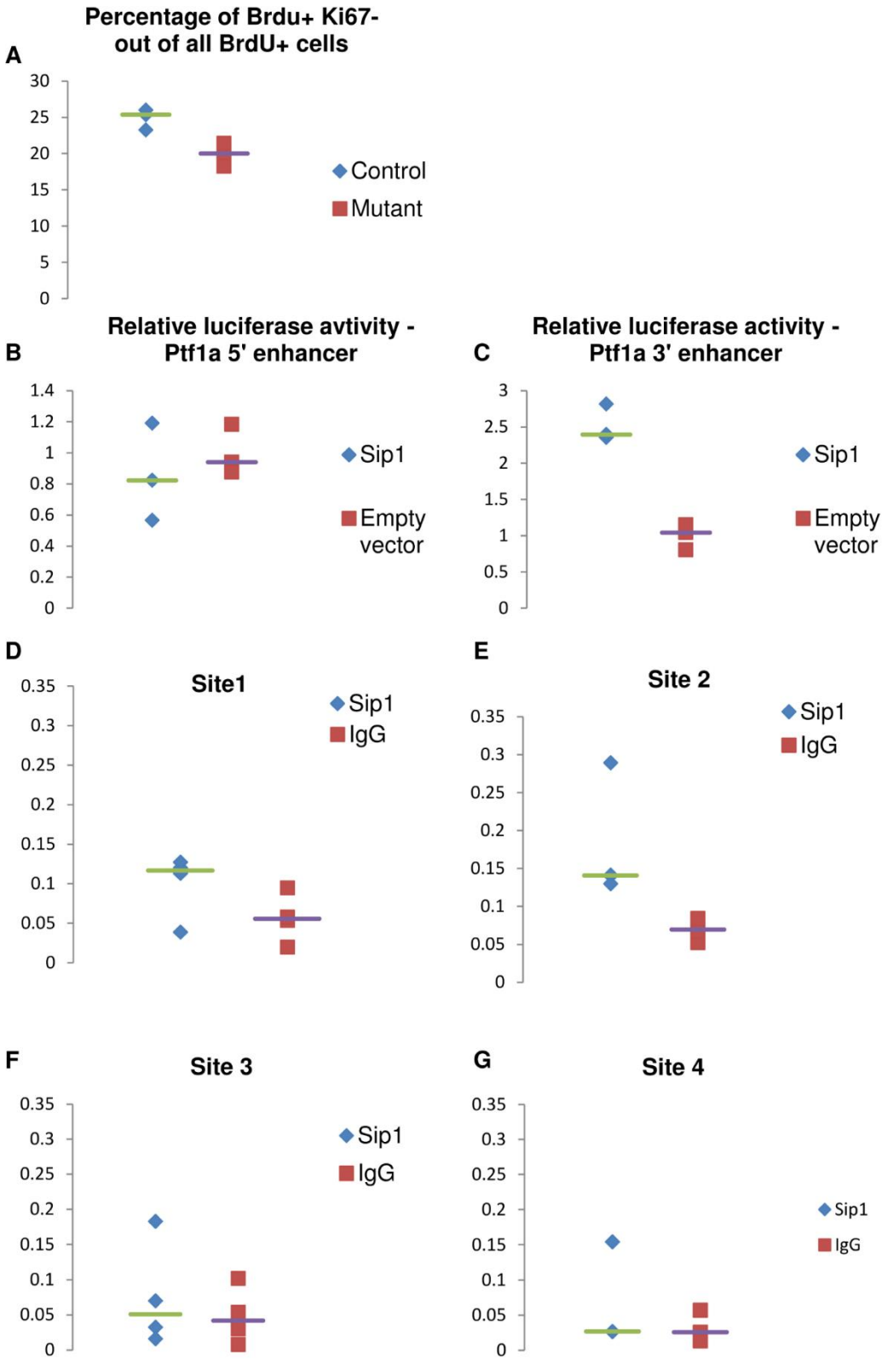


Figure S8: Measurements of Cell cycle exit, Luciferase and chromatin IP analysis

The different repeats of the quantification of the percentage of BrdU+ Ki67- cells out of the BrdU+ cell population in control and *Sip1*$^{loxp/loxp}$*;aCre* retinae (N=3) (A). The different repeats of the quantification of the relative luciferase activity in the presence of Sip1 expression vector achieved by the 5' Ptf1a enhancer (B) and the 3' enhancer (C) (N=3) are presented in scatter plots. The repeats of the measurements of the percentage of input which was immune-precipitated by Sip1 AB or IgG in the vicinity of Sip1 binding site 1 (D), 2 (E), 3 (F) or 4 (G) are also presented in scatter plots (N=4 for sites 1,2,3 and N=3 for site 4). The median in the scatter plots is represented by a line with the same color of the data points from which it is derived.

Table S1

Antigen	Source	Manufacturer	# Catalog	Dilution
Ap2α	Mouse	Santa Cruz	sc-12726	1:50
Ap2β	Rabbit	Cell signaling	2509	1:50
BrdU	Mouse	Chemicon	MAB3222	1:100
Calbindin	Mouse	Sigma	C9848	1:5000
Cleaved Caspase3	Rabbit	Cell signaling	9661	1:300
Crx	Mouse	Abnova	#H00001406-M02	1:400
Gad67	Mouse	Millipore	MAB5406	1:1000
Glutamin Synthetase	Mouse	BD	610517	1:100
Glyt1	Goat	Chemicon	AB1770	1:4000
Igg	Rabbit	Santa Cruz	sc-2027	
Isl1	Mouse	DSHB	40.2D6	1:100
Ki67	Rat	Dako	M7249	1:100
Nf165	Mouse	Hybridoma bank	AB 2314897	1:500
P27	Rabbit	Therno scientific	RB9019	1:50
Pax6	Rabbit	Convance	prb-278p	1:400
Pkcα	Rabbit	Santa Cruz	sc-208	1:1200
PNA		Vector		1:200
Pou4f2	Goat	Santa Cruz	sc-6026	1:100
Prox1	Rabbit	Acris	dp3501p	1:40
Ptf1a	Rabbit	Kind gift of Helena Edlund		1:500
Sip1	Rabbit	Santa Cruz	sc-48789	1:200

Table S2

Sip1 forward	GGCAAGGCCTTCAAGTACAA
Sip1 reverse	AAGCGTTTCTTGCAGTTTGG
Foxn4 forward	AGCCACACCCCAAACACTAC
Foxn4 reverse	AAGCTGCCTGTTTTGCTGTT
Neurod4 forward	GCTCCAGTCAGATCACAGGAG
Neurod4 reverse	CAGCTCCACCATGTCCTTG
Neurod1 forward	AATTCGCCCACGCAGAAGGC
Neurod1 reverse	TGAGACACTCATCTGTCCAGC
Actb forward	CACAGCTGAGAGGGAAATCGTGC
Actb reverse	GATCTTGATCTTCATGGTGCTAGG
Ptf1a site 1 forward	TTCCCACGACAGGATGTGAG
Ptf1a site 1 reverse	TTTCTGGCAGGCCTGTCTCT
Ptf1a site 2 forward	ATCAATCCCTGTCTTGGTTCTCT
Ptf1a site 2 reverse	TTAGGCAGCTGCAGTCCA
Ptf1a site 3 forward	AGTGTTGGTCCCTAAAGACATTG
Ptf1a site 3 reverse	ACGTTCCCTTCTTGATAAATGG
Ptf1a site 4 forward	GCTCCATTTCAACCATTGTG
Ptf1a site 4 reverse	GAAGAGCCCTTGAGCTTGG