

Table S1. Ascl1, Ngn2 and retroviral lineages

Lineage	G*	H*	C*	dA*	A*	R*	B*	M*	Clumps [†]
E12.5/E13.5 Ascl1	7 (0.22%)	302 (9.70%)	483 (15.51%)	149 (4.78%)	447 (14.35%)	1416 (45.46%)	154 (4.94%)	157 (5.04%)	1591
E12.5/E13.5 Ngn2	22 (1.75%)	245 (19.54%)	527 (42.03%)	122 (9.73%)	265 (21.13%)	66 (5.26%)	3 (0.24%)	4 (0.32%)	1075
E12.5+E13.5 retroviral (all clones) [‡]	43 (0.43%)	8 (0.08%)	152 (1.52%)	NA	337 (3.36%)	8390 (83.67%)	987 (9.84%)	85 (0.85%)	312
E12.5+E13.5 Retroviral (clones <16 cells) [§]	23 (5.7%)	6 (1.5%)	75 (18.7%)	NA	26 (6.5%)	234 (58.2%)	33 (8.2%)	5 (1.2%)	130
E17.5 Ascl1	0 (0.00%)	3 (0.06%)	52 (1.09%)	18 (0.38%)	489 (10.30%)	3799 (80.00%)	230 (4.84%)	158 (3.33%)	2528
E17.5 Ngn2	1 (0.09%)	0 (0.00%)	20 (1.84%)	52 (4.78%)	276 (25.37%)	738 (67.83%)	1 (0.09%)	0 (0.00%)	827
Adult WT retina [¶]	0.6%	0.5%	2.2%	0.9%	7%	78.5%	7.4%	2.9%	NA

*Number of cells observed (% of the total).

[†]Number of clumps or clones counted.[‡]From Turner et al. (Turner et al., 1990). The two datasets are pooled.[§]Cell fate distribution of clones containing 1-15 cells from the pooled datasets.[¶]From Jeon et al. (Jeon et al., 1998).

G, retinal ganglion cell; H, horizontal; C, cone; dA, displaced amacrine; A, amacrine; R, rod; B, bipolar; M, Müller glia; WT, wild type.

NA, not available. All of the ganglion cell layer-labeled cells are in the retinal ganglion cell (RGC) category.