

Figure S1. Retinal cell types labeled in Cre driver lines visualized by Cre-dependent transgenic reporters and comparison with rAAV, Related to Figure 1 and Table 1. (a) Table lists the Cre driver lines crossed to a Cre-dependent reporter line for visualizing transgene expression and the locations and classes of labeled cells. (b) Retinal images of reporter expression are shown for three Cre driver lines after crossing with the Ai14 reporter line (red) or following intravitreal injection of Cre-dependent rAAV reporter (green). Sections were also stained with anti-VAChT (white). In each case, the rAAV labels a subset of the cell types labeled by the Ai transgenic reporter. Scale bar 25µm.

Figure S2. Cre is expressed in a variety of RGC types in the Htr2a-Cre_KM207 line, Related to Figure 2. Sections from an Htr2a-Cre KM207 retina injected with Cre-dependent rAAV were stained with anti-GFP (green in merge), anti-VAChT, anti-RBPMS (both blue in merge), and other antibodies that mark specific RGC subtypes. (a) anti-osteopontin (OPN) labels alpha RGCs. (b) anti-parvalbumin (Pvalb) labels 8 RGC types including ooDSGCs and alpha RGCs. (c) anti-CART labels ooDSGCs. (d) anti-Foxp2 labels four F-RGC types. (e) anti-melanopsin (Opn4), labels ipRGC types M1 and M2. Scale bar 25µm.

Figure S3. Cre lines that mark alpha RGCs, Related to Figures 1 and 2. (a-d) Vertical retina sections were stained with anti-GFP (green in merge), anti-VAChT and anti-RBPMS (both blue in merge), and (a-d) anti-OPN to label alpha RGCs (red in merge). Etv1-CreERT2 (a), Gal-Cre_KI87 (b), Kcng4-Cre (c), and Crh-IRES-Cre (BL) (d) selectively label osteopontin-positive alpha RGCs.

Figure S4. Alternative distance measures used to cluster individual experiments, Related to Figure 4. The resulting dendrograms are shown following unsupervised hierarchical clustering of the experiments using Pearson (a) and Spearman rank (b) correlation values as the distance measure. Cluster membership for each experiment was relatively stable across all distance measures used, although some experiments moved around (e.g. Gpr26-Cre lines are in the larger Cluster 1-2 in (a) and (b) as opposed to Cluster 3 in Figure 4. The colors indicate cluster assignment shown in Figure 4. Blue=Cluster 1, Green=Cluster 2, Orange=Cluster 3, Red=Cluster 4.

T**able S2.** List of all retinorecipient regions identified after tracing the central projections of Thy1-Cre expressing retinal ganglion cells (n=3), Related to Figure 3. *excluded from quantitative analysis, very sparse

Table S3. Verified projections from four Cre lines enriched for alpha RGCs, Related to Figure 4. -; no projection, * terminals observed in n=1, ** n=2, *** n=3. Note that Crh-IRES-Cre (BL) had only n=2. The others had n=3.

Movie S1. Whole brain images of Thy1-Cre retinal ganglion cell axons, related to Figure 3. The movie shows the stack of 140 coronal plane images acquired every 100 μ m using serial two-photon tomography. GFP-labeled axons from Thy1-Cre+ retinal ganglion cells can be seen entering the brain at the optic chiasm and radiating to many targets brain-wide, described in Figure 3.

Data S1. Log-transformed normalized projection values for each experiment and target, related to Figure 4.

Projection strengths were measured as the sum of all algorithmically-detected fluorescent pixels within a given target region (projection volume), and normalized by the injection volume in the optic chiasm. These values were log-transformed and underlie the color map shown in Figure 4.

Supplemental Experimental Procedures

Transgenic mice

Mouse lines were maintained as heterozygotes by crossing with C57Bl6/J mice. Mice were group-housed in a 12 hour light/dark cycle. Food and water were provided *ad libitum*. Some Cre driver mice were crossed with the Credependent tdTomato expressing reporter Ai14 (Madisen et al., 2010) or YFP expressing reporter Thy1-stop-YFP (Buffelli et al., 2003) for **Figure S1**.

Intravitreal injections and perfusions

Animals were anesthetized with ketamine/xylazine (100mg/kg ketamine, 10mg/kg xylazine). One drop of 0.5% proparacaine hydrochloride ophthalmic solution was applied as a topical anesthetic to the eye. A small incision was made by inserting a sharp 30 gauge needle to the depth of the bevel just below the limbus of the eye. A blunt 33 gauge needle attached to a Hamilton syringe was inserted to withdraw 2 μL of vitreous fluid. A second Hamilton syringe was used to inject 2 μL of virus. Needles were inserted between the len and the retina in order to minimize damage to either. Petroleum ophthalmic ointment was applied to the eye following surgery, and an analgesic was administered (ketoprofen for mice injected at the Allen Institute). Three weeks post-injection for Cre mice or posttamoxifen induction for CreER mice, mice were deeply anesthetized with 5% isoflurane (at the Allen Institute) or 25 µL/10g Euthasol (Virbac; Fort Worth, TX; at Harvard) and intracardially perfused with 10 ml of saline (0.9% NaCl)

followed by 50 ml of freshly prepared 4% paraformaldehyde (PFA) at a flow rate of 9 ml/min. Brains were rapidly dissected and post-fixed in 4% PFA at room temperature for 3-6 hours and overnight at 4°C. rAAV injected eyes were dissected entirely from the eye cup and a cautery was used to mark the dorsal orientation on each eye, and were then post-fixed in 4% PFA for 30-60 min. Brains and eyes were rinsed briefly with PBS and stored in PBS with 0.1% sodium azide.

Immunohistochemistry

For whole mounts, retinas were first immunostained for GFP. Briefly, retinas were blocked in 0.3% Triton X-100 and 5% normal donkey serum in PBS on a shaker overnight at 4°C. The next day they were placed into primary antibody (chicken anti-GFP, Abcam, 1:1000 in 0.3% Triton X-100 and 5% normal donkey serum) and incubated for 1 week on a shaker at 4°C. Retinas were rinsed well in PBS, followed by incubation with secondary antibody (donkey anti-chicken Alexa Fluor 488, Jackson Immunoresearch, 1:500) on a shaker overnight at 4°C. Following immunohistochemistry, relaxing cuts were made and the retina was transferred to filter paper, mounted on glass slides using Fluoromount-G with DAPI (Southern Biotech), and coverslipped.

Retinas to be sectioned were immersed in 30% sucrose solution overnight at 4°C, embedded in TFM (General Data Healthcare, Inc), frozen to -80°C and sectioned at 20 μm in a cryostat (Leica 1850). For immunostaining, slides were rehydrated in PBS, then blocked in 0.3% Triton X-100 and 3% normal donkey serum in PBS for at least 30 minutes. Each slide was stained with anti-GFP antibody (chicken anti-GFP, Abcam, 1:1000) and one of the following additional primary antibodies: anti-Brn3a (mouse, Millipore, 1:500), anti-VAChT (guinea pig, Chemicon, 1:500-1000), anti-CART (rabbit, Phoenix Pharmaceuticals, 1:2000), anti-osteopontin (goat, R&D Systems, 1:1000), anti-RBPMS (guinea pig, PhosphoSolutions, 1:1250-2500), anti-melanopsin (rabbit, Thermo Scientific, 1:5000), anti-Foxp2 (rabbit, Abcam, 1:1500), anti-parvalbumin (rabbit, Swant, 1:5000-10,000) all diluted in 0.3% Triton X-100 and 3% normal donkey serum. Slides were incubated in primary antibodies overnight at 4°C, then washed in PBS and incubated in the following secondary antibodies for 90 minutes at room temperature: donkey anti-chicken Alexa Fluor 488 for GFP (donkey, Jackson Immunoresearch, 1:500), and anti-guinea pig, antirabbit or anti-mouse Alexa Fluor 555 (donkey, Jackson Immunoresearch, 1:500) for the other primary antibody detections. Slides were coverslipped using Fluoromount-G with DAPI (Southern Biotech).

Imaging

Brains from mice injected with tracer into one eye were prepared and imaged by serial two-photon tomography as previously described (Oh et al., 2014) using TissueCyte 1000 systems (TissueVision, Cambridge,MA) coupled with Mai Tai HP DeepSee lasers (Spectra Physics, Santa Clara, CA). Single optical plane images 75 μ m below the tissue surface were acquired using 925 nm wavelength light through a Zeiss 320 water immersion objective (NA=1.0), with 250 mW light power at objective. In order to scan a full tissue section, individual tile images were acquired, and the entire stage was moved between each tile. Then, a vibratome cuts a $100 \mu m$ section and the imaging is repeated. Images are collected from 140 coronal sections covering the rostral-to-caudal extent of the brain, which takes \sim 18.5 h at an x,y resolution of \sim 0.35 µm per pixel.

Images were processed using the informatics data pipeline (IDP) set up and previously described in detail for the Allen Mouse Brain Connectivity Atlas (Oh et al., 2014;Kuan et al., 2015). Briefly, the two key algorithms are signal detection and image registration. The signal detection algorithm was applied to each image to segment positive fluorescent signals from background. The output is a full resolution mask that classifies each pixel as either signal or background. An isotropic 3-D summary of each brain is constructed by dividing each image into 10 m X 10 m grid voxels. Total signal is computed for each voxel by summing the number of signal-positive pixels in that voxel. The highly aligned nature from section to section allows for simply stacking the section images together to form a coherent reconstructed 3-D volume. Each image stack is then registered in a multi-step process using both global affine and local deformable registration to the 3-D Allen Common Coordinate Framework (CCF) as previously described (Oh et al., 2014;Kuan et al., 2015). Segmentation and registration results are combined to quantify signal for each voxel in the reference space and for each structure in the CCF ontology by combining voxels from the same structure.

Here, we used normalized projection volume as a measure of projection strength. Normalized projection volume is the sum of segmented pixels within a given brain structure divided by the sum of segmented pixels within the injection site. Because the injection site in these experiments was outside the imaged brain, we chose to normalize each target's value by the sum of segmented pixels within the optic chiasm. This signal should be more accurate as a value for injection size than what we could measure in the corresponding retinal whole mount as it includes all the RGC axons entering the brain from a particular experiment, and does not include other retinal cell types that might express Cre-dependent rAAV-EGFP. Connection weights were measured with pixel counts rather

than fluorescence intensity, because counts were previously determined to be more reliable (Oh et al., 2014). We chose to represent the weights in each target region by using volume (sum of detected pixels) and not density (sum of detected pixels / target structure volume). The scaling of results by injection size shows the proportion of axons going to each structure. In contrast, many anatomists are accustomed to categorizing projections by number rather than proportion of axons. As an illustration, imagine lines A and B that both project to area X. If line A has 5 axons at the chiasm and 5 in area X, Figure 10 shows a high value for the line A/area X box. If line B has 1000 axons at the chiasm and 50 in area X, the line B/area X box will have a low value. In contrast, conventional histology would categorize A as having a weak and B a strong projection to area X, because ratings are usually made on the basis of something closer to absolute density.

Unsupervised hierarchical clustering was done on the log-transformed normalized projection volumes using GENE-E or Morpheus software for algorithms and dendrogram visualization

(http://www.broadinstitute.org/cancer/software/GENE-E/index.html). True negative values ("0s") were converted to the half minimum of the positive array elements before calculating the logarithm.

To subdivide LGd for analyses shown in **Figure 6**, sections from Kcng4-Cre (alpha RGCs), Cart-Tg1-Cre (ooDSGCs) and CTB-injected mice (in the opposite eye) were matched for rostral-caudal location and aligned to the average template brain used as the basis for drawing structures in the Allen Mouse CCF. The strongest projections (avoiding passing fibers, and above a set threshold) were pseudocolored by line. Borders were drawn as shown in **Figure 6** using the pseudocolored projection signal, as well as anatomical data derived from the average template brain.

References

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