Supplemental Figure Legends

Table S1 Immunostaining defects in OFF Types 2 and 3 bipolar cells are summarized for the markers indicated in the table. Data for the Vsx1 and Irx5 single mutants are from this study (data not shown) and from previous studies (Chow et al, 2004; Cheng at al 2005). Identical immunostaining defects for the OFF Type 2 marker recoverin are observed in the single Vsx1 and Irx5 mutants, while non-overlapping defects are observed for the remaining markers. The Vsx1 Irx5 double mutants are characterized by the accumulation of immunostaining defects (this study) from the single Vsx1 and Irx5 mutants.

Figure S1 Regular arrangement of their constituents supports distinction of functional RGC types. In order to assess the regularity with which spatial receptive fields of the more frequently recorded fast ON and biphasic OFF RGCs types were distributed across the retinal surface we calculated a spacing ratio (s) of cell pairs according to $s = d / (r_1 + r_2)$, where d is the center-to-center distance for two cells and r_1 and r_2 signify the distance from the center to the 1-SD boundary of their receptive fields along the same trajectory (Devries and Baylor, 1997; Segev et al., 2006). The relative frequency with which different spacing ratios were observed was normalized by the retinal area covered by the respective bins as described previously by DeVries and Baylor (Devries and Baylor, 1997). Histograms of cells in a mosaics with little overlap or gaps in their receptive field coverage are expected to peak around one, whereas histograms obtained by pairing cells of different types are expected to show a monotonically

declining distribution (Wassle et al., 1981a; Wassle et al., 1981b; Devries and Baylor, 1997). *A* – *D* Histograms of the spacing ratio of cell pairs drawn from fast ON (*A* and *C*, solid line) or biphasic OFF cells (*B* and *D*, solid line) recorded from control (*A* and *B*) and dko (*C* and *D*) mice are compared to histograms of spacing ratios from the pairing of different cell types (dashed lines) in the same recordings. Indeed, histograms of the cell pairs drawn from within a functional RGC type peaked around one (solid lines) whereas those pairing cells of different type (dashed lines) declined monotonically. For the purpose of the present study this regular arrangement supports or grouping of RGCs into the different functional types based on their temporal receptive fields.

Figure S2 Perievent raster and histograms, and LN model representation of light responses of representative ON and OFF cells from control and dko mice. *A*, Peristimulus rasters and histograms of spike trains from fast ON (*upper row*) and biphasic OFF (*lower row*) RGCs recorded from control (*left column*) and dko (*right column*) mice during 22 cycles of a full-field stimulus square wave modulated at 0.125 Hz. Shaded areas indicate periods of darkness (~10^1 Rh*/M-cone/s) and unshaded areas indicate periods of illumination (~10^6 Rh*/M-cone/s). While the representative ON cell in dko mice reaches a peak firing rate similar to ON RGCs in control mice, a representative OFF RGC shows a much lower peak firing rate than its control counterpart. *B*, Space-time receptive fields of the cells shown in *A*. Waveforms depicting temporal structure of receptive field centers (*left panels*) were normalized to their amplitude and color-coded to indicate

control (black) and dko (red) genotype. Spatial extent and position of RGC receptive fields of the same cells, is depicted by plotting the 1-SD contours of 2D Gaussian fits to receptive field profiles. Positions are shown relative to the center of the recording array in each recording (*dots*). *C*, Comparison of static nonlinearities of the same representative RGCs as in *A* and *B*. Left panels show firing rate as a function of the generator signal for the ON (*upper left panel*) and OFF (*lower left panel*) RGCs recorded from control (black circles and line) or dko (red circles and line) mice. Bars on the right indicate the response threshold, gain and range for these cells. Threshold and gain were normalized by the median threshold and gain, respectively, of the population of all recorded and classified cells.