Supplementary Table 1

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| Cell of Interest | Marker | Amount | Time point | Protocol | Quantification Method | Reference |
| **Photo-receptors** | CRX | 15% | D90 | AGG | CRXp-GFP H9 line; FACS; n=3; >1000 cells/n; L=1 | 1 |
| 12-18% | D126 | AGG | CRX::Venus hESC line; IHC; n=4; >1000cells/n; L=1 | 2 |
| 69% | D135 | CLUMP | IHC of dissociated cells from CRX+/tdTomato+ OV; CRX+ cells; n=3; L=1 | 3 |
| 4% | D30 | CYST | IHC; CRX+ cells/DAPI+ cells; N=3/L; n=16-27/L; L=2 (calculated mean) (Fig.4C) | this study |
| 19% | D60 | CYST | IHC; CRX+ cells/DAPI+ cells; N=3/L; n=16-27/L; L=2 (calculated mean) (Fig.4C) | this study |
| 28% | D90 | CYST | IHC; CRX+ cells/DAPI+ cells; N=3/L; n=16-27/L; L=2 (calculated mean) (Fig.4C) | this study |
| 33% | D120 | CYST | IHC; CRX+ cells/DAPI+ cells; N=1-5/L; n=7-23/L; L=5 (calculated mean) (Fig.4C) | this study |
| 41% | D200 | CYST | IHC; CRX+ cells/DAPI+ cells; N=2-3/L; n=9-28/L; L=7 (calculated mean) (Fig.4E) | this study |
| **Cones** | ARR3 | 12% | D90 | AGG | IHC; ARR3+ cells/DAPI+ cells; N=3; L=1 | 1 |
| ~20% of ONL |  ≥D120 (W17) | CLUMP | IHC; ARR3+ cells/ONL; n≥6/L; L=3 | 4 |
| 18% | D140 (W20) | CLUMP | IHC; ARR3+ cells/image; N=3, n=30 images; L=1 | 5 |
| 25% | D200 | CYST | IHC; ARR3+ cells/DAPI+ cells; N=2/L; n=10/L; L=2 (calculated mean for 5A line) | 8 (Fig.1c) |
| 23% | D200 | CYST | IHC; ARR3+ cells/DAPI+ cells; N=13, ≥5n/N, L=4 (calculated mean for 5A, CRTD1, CRTD2, IMR90) | 8 (Fig.S11) |
| 38% | D200 | CYST | Flow cytometry; ARR3+ cells, L=2; N=1-2/L; 2-3 samples/N (calculated mean) | 8 (Fig.2e) |
| 18% | D200 | CYST | IHC; ARR3+ cells/DAPI+ cells; N=2-7/L; n=22-50/L; L=7 (calculated mean) (Fig.5C) | this study |
| 15% | D200 | AGG | IHC; ARR3+ cells/DAPI+ cells; N=2, n=7, L=1 (5A) (Fig.3C) | this study |
| OPN1SW | 9% | D135 | CLUMP | IHC of dissociated cells from CRX+/tdTomato+ OV; OPN1SW+ cells; n=3; L=1 | 3 |
| THRB | 17% | D135 | CLUMP | IHC of dissociated cells from CRX+/tdTomato+ OV; THRß + cells; n=3; L=1 | 3 |
| OPN1LW/MW | 176 cells | D215 | CYST | whole mount IHC; 6 stacks of optical sections; n=4 (calculated mean); L=1 | 6 |
| Top 20 markers/cluster | 34% | D240 | CYST | single cell RNA-seq; L=1 | 6 |
| Top 20 markers/cluster | 28% | D200 | CYST | single cell RNA-seq; L=1 | 8 (Fig.1g) |
| manual annotation(Suppl. Table 4) | 26% | D200 | CYST | single cell RNA-seq; Manual annotation; L=1; (integrated data HRO1 + HRO2) | this study |
| CaSTLE annotation (Suppl. Table 4) | 40% | D200 | CYST | single cell RNA-seq; CaSTLe annotation; L=1; (integrated data HRO1 + HRO2) | this study |
| **Rods** | NRL | 23% | D90 | AGG | IHC; NRL+ cells/DAPI+ cells; N=3; L=1 | 1 |
| ~80% of ONL | ≥D120 (W17) | CLUMP | IHC; NRL+ cells/ONL; n≥6/L; L=3 | 4 |
| 33% | D135 | CLUMP | IHC of dissociated cells from CRX+/tdTomato+ OV; NRL+ cells; n=3; L=1 | 3 |
| 25% | D200 | CYST | IHC; NRL+ cells/DAPI+ cells; N=2/L; n=10/L; L=2 (calculated mean) | 8 (Fig.1c) |
| 21% | D200 | CYST | IHC; NRL+ cells/DAPI+ cells; N=2-4; n=13-50/L; L=7 (calculated mean) (Fig.5C) | this study |
| 22% | D200 | AGG | IHC; NRL+ cells/DAPI+ cells; N=2, n=7, L=1 (5A) (Fig.3C) | this study |
| RHO | 118 cells | D215 | CYST | whole mount IHC; 6 stacks of optical sections; n=4 (calculated mean); L=1 | 6 |
| RCVRN+ARR3− | 26% | D200 | CYST | Flow cytometry; RCVRN+ARR3− cells, L=2; N=1-2/L; 2-3 samples/N (calculated mean) | 8 (Fig.2e) |
| Top 20 markers/cluster | 25% | D240 | CYST | single cell RNA-seq; L=1 | 6 |
| manual annotation | 24% | D200 | CYST | single cell RNA-seq; Manual annotation; L=1; (integrated data HRO1 + HRO2) | this study |
| CaSTLE annotation  | 13% | D200 | CYST | single cell RNA-seq; CaSTLe annotation; L=1; (integrated data HRO1 + HRO2) | this study |
| Top 20 markers/cluster | 25% | D200 | CYST | single cell RNA-seq; L=1 | 8 (Fig.1g) |
| **Cone:Rod ratio** | ARR3:NRL | 1:2 | D90 | AGG |  | 1 |
| ARR3:NRL | 1:4 | ≥D120 | CLUMP |  | 4 |
| RXRγ:NRL | 1:4 | D126 | AGG | IHC; n=4; >200cells/n  | 2 |
| (OPN1SW+THRß):NRL | 1:1 | D135 | CLUMP |  | 3 |
| OPN1LW/MW: RHO | 1:1 | D215 | CYST | IHC and single cell RNA-seq | 6 |
| ARR3:NRL | 1:1 | D200 | CYST | IHC; N=2/L; n=10/L; L=2 (calculated mean) & single cell RNA-seq; L=1  | 8 (Fig.1c) |
| ARR3:NRL | 1:1 | D200 | CYST | IHC; ARR3+/DAPI+ cells; N=13, ≥5n/N, n>65, L=4 (mean for 5A, CRTD1, CRTD2, IMR90) | 8 (Fig.S11) |
| Top 20 markers/cluster | 1:1 | D200 | CYST | single cell RNA-seq; L=1 | 8 (Fig.2e) |
| ARR3:NRL | 1.1:1 | D200 | CYST | IHC; ARR3+ and NRL+ /DAPI+ cells; calculated mean of all hiPSC lines, N≥24, n≥184 L=7 (Fig.5E) | this study |
| ARR3:NRL | 0.7:1 | D200 | AGG | IHC; ARR3+ and NRL+ /DAPI+ cells; N=2, n=7, L=1 (5A) (Fig.3C) | this study |
| **Müller Glia** | SOX9 | 24% | D150 | CYST | IHC; SOX9+ cells/DAPI+ cells; N=1-2/L; n=5-10/L; L=2 (calculated mean) | 8 |
| SOX9 | 25% | D200 | CYST | IHC; SOX9+ cells/DAPI+ cells; N=2/L; n=10/L; L=2 (calculated mean) | 8 |
| SOX9 | 26% | D250 | CYST | IHC; SOX9+ cells/DAPI+ cells; N=2/L; n=10/L; L=2 (calculated mean) | 8 |
| SOX9 | 23% | D200 | CYST | Flow cytometry; SOX9+ cells, L=2; N=1-2/L; 2-3 samples/N (calculated mean) | 8 |
| SOX9 | 28% | D200 | CYST | IHC; SOX9+ cells/DAPI+ cells; N=2-4/L; n=16-50/L; L=7 (calculated mean) (Fig.5C) | this study |
| SOX9 | 28% | D200 | AGG | IHC; ARR3+ and NRL+ /DAPI+ cells; N=2, n=7, L=1 (5A) (Fig.3C) | this study |
| Top 20 markers/cluster | 25% | D200 | CYST | single cell RNA-seq; L=1 | 8 |
| Top 10 markers/cluster | 53% | D200 | CLUMP | single cell RNA-seq; L=1 | 7 |
| Top 20 markers/cluster | 25% | D240 | CYST | single cell RNA-seq; L=1 | 6 |
| SLC1A3, RLBP1, SFRP2 | 24% | D200 | CYST | single cell RNA-seq; Manual annotation; L=1; (integrated data HRO1 + HRO2) | this study |

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