1M_Org – Cluster Validation (Original Annotations)
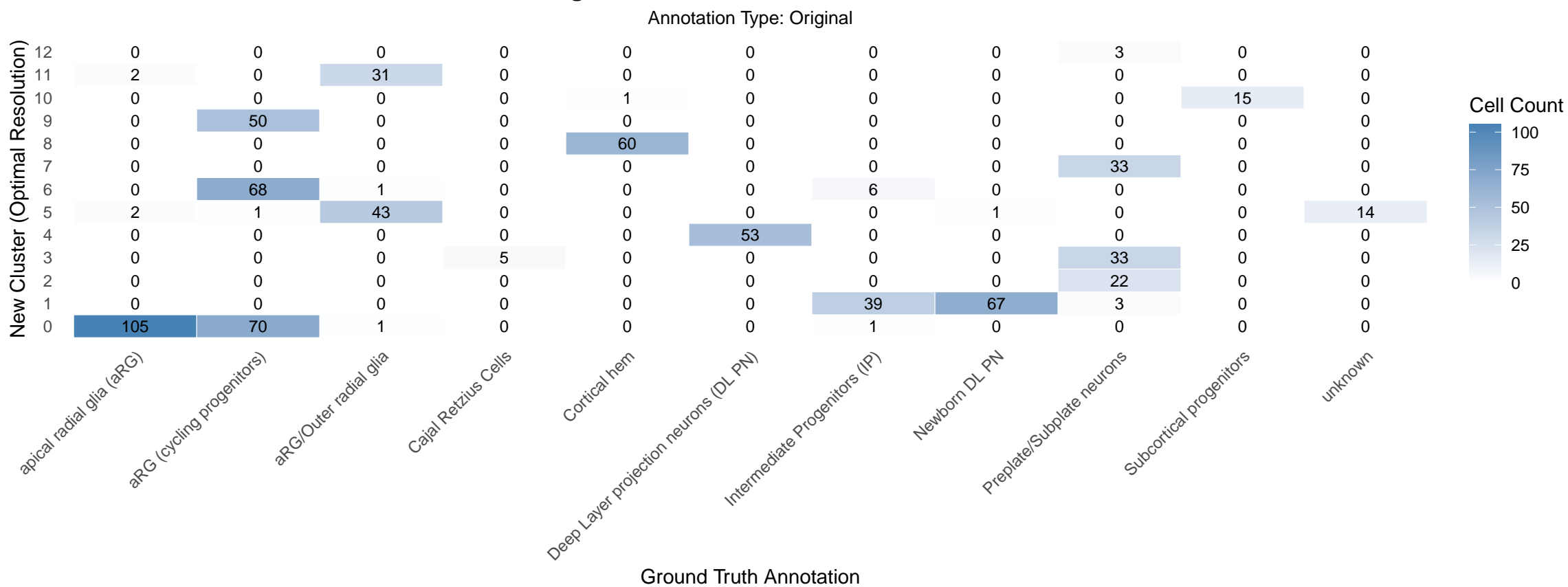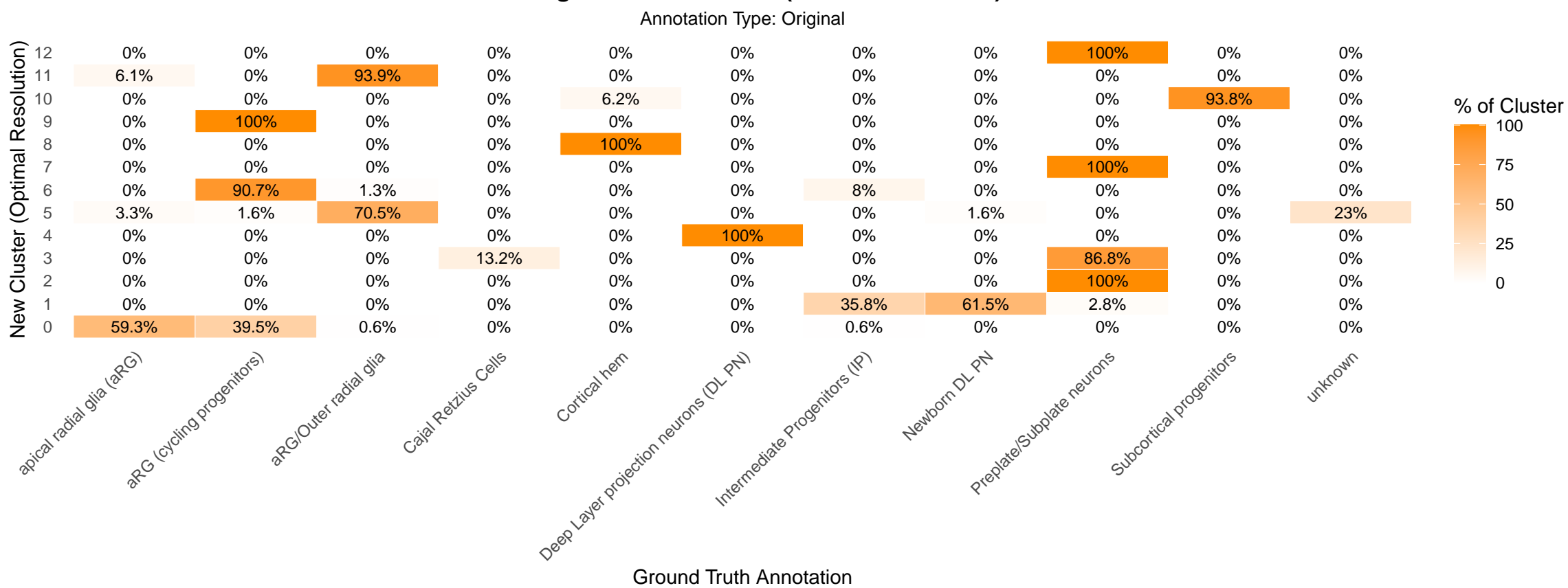
New Object: 2116 cells | Ground Truth: 2364 cells | Overlapping: 730 cells (34.5% / 30.9%)

1M_Org: Cluster vs Ground Truth Annotation

Annotation Type: Original

New Cluster (Optimal Resolution)	apical radial glia (aRG)	aRG (cycling progenitors)	aRG/Outer radial glia	Cajal Retzius Cells	Cortical hem	Deep Layer projection neurons (DL PN)	Intermediate Progenitors (IP)	Newborn DL PN	Preplate/Subplate neurons	Subcortical progenitors	unknown
12	0	0	0	0	0	0	0	0	3	0	0
11	2	0	31	0	0	0	0	0	0	0	0
10	0	0	0	0	1	0	0	0	0	15	0
9	0	50	0	0	0	0	0	0	0	0	0
8	0	0	0	0	60	0	0	0	0	0	0
7	0	0	0	0	0	0	0	0	33	0	0
6	0	68	1	0	0	0	6	0	0	0	0
5	2	1	43	0	0	0	0	1	0	0	14
4	0	0	0	0	0	53	0	0	0	0	0
3	0	0	0	5	0	0	0	0	33	0	0
2	0	0	0	0	0	0	0	0	22	0	0
1	0	0	0	0	0	0	39	67	3	0	0
0	105	70	1	0	0	0	1	0	0	0	0

Ground Truth Annotation

1M_Org: Row–Normalized (% of Each Cluster)

Annotation Type: Original

New Cluster (Optimal Resolution)	apical radial glia (aRG)	aRG (cycling progenitors)	aRG/Outer radial glia	Cajal Retzius Cells	Cortical hem	Deep Layer projection neurons (DL PN)	Intermediate Progenitors (IP)	Newborn DL PN	Preplate/Subplate neurons	Subcortical progenitors	unknown
12	0%	0%	0%	0%	0%	0%	0%	0%	100%	0%	0%
11	6.1%	0%	93.9%	0%	0%	0%	0%	0%	0%	0%	0%
10	0%	0%	0%	0%	6.2%	0%	0%	0%	0%	93.8%	0%
9	0%	100%	0%	0%	0%	0%	0%	0%	0%	0%	0%
8	0%	0%	0%	0%	100%	0%	0%	0%	0%	0%	0%
7	0%	0%	0%	0%	0%	0%	0%	0%	100%	0%	0%
6	0%	90.7%	1.3%	0%	0%	0%	8%	0%	0%	0%	0%
5	3.3%	1.6%	70.5%	0%	0%	0%	0%	1.6%	0%	0%	23%
4	0%	0%	0%	0%	0%	100%	0%	0%	0%	0%	0%
3	0%	0%	0%	13.2%	0%	0%	0%	0%	86.8%	0%	0%
2	0%	0%	0%	0%	0%	0%	0%	0%	100%	0%	0%
1	0%	0%	0%	0%	0%	0%	35.8%	61.5%	2.8%	0%	0%
0	59.3%	39.5%	0.6%	0%	0%	0%	0.6%	0%	0%	0%	0%

Ground Truth Annotation

1M_Org – Cluster Validation (Simplified Annotations)
New Object: 2116 cells | Ground Truth: 2364 cells | Overlapping: 730 cells (34.5% / 30.9%)
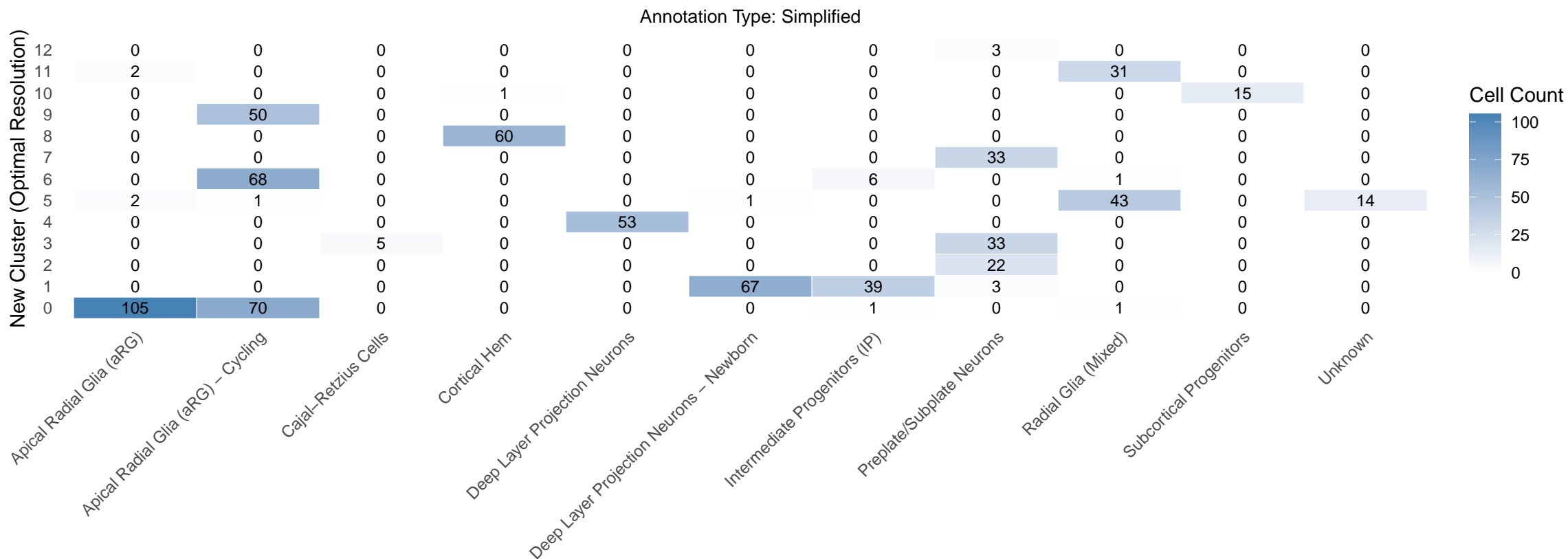**1M_Org: Cluster vs Ground Truth Annotation**
Annotation Type: Simplified

1M_Org: Row–Normalized (% of Each Cluster)
Annotation Type: Simplified