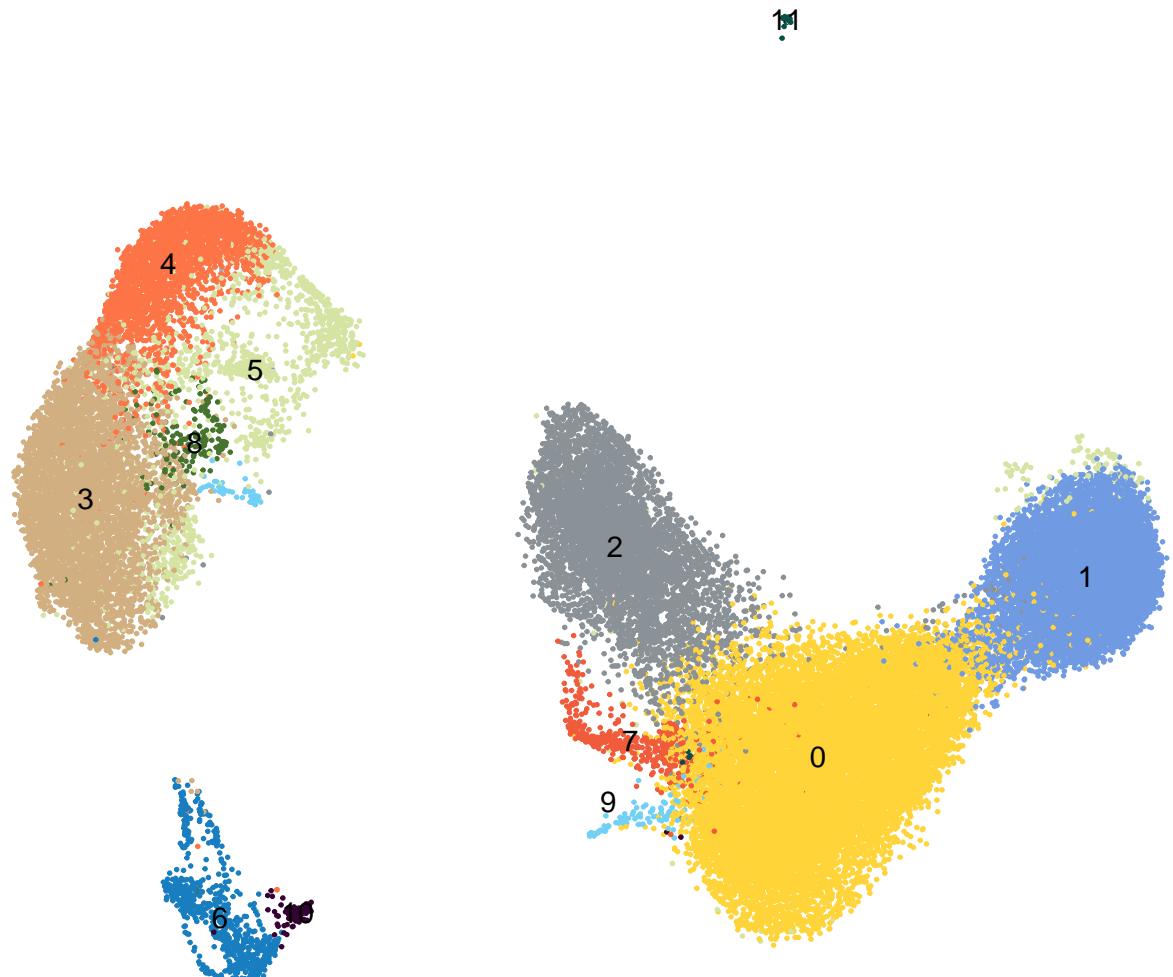
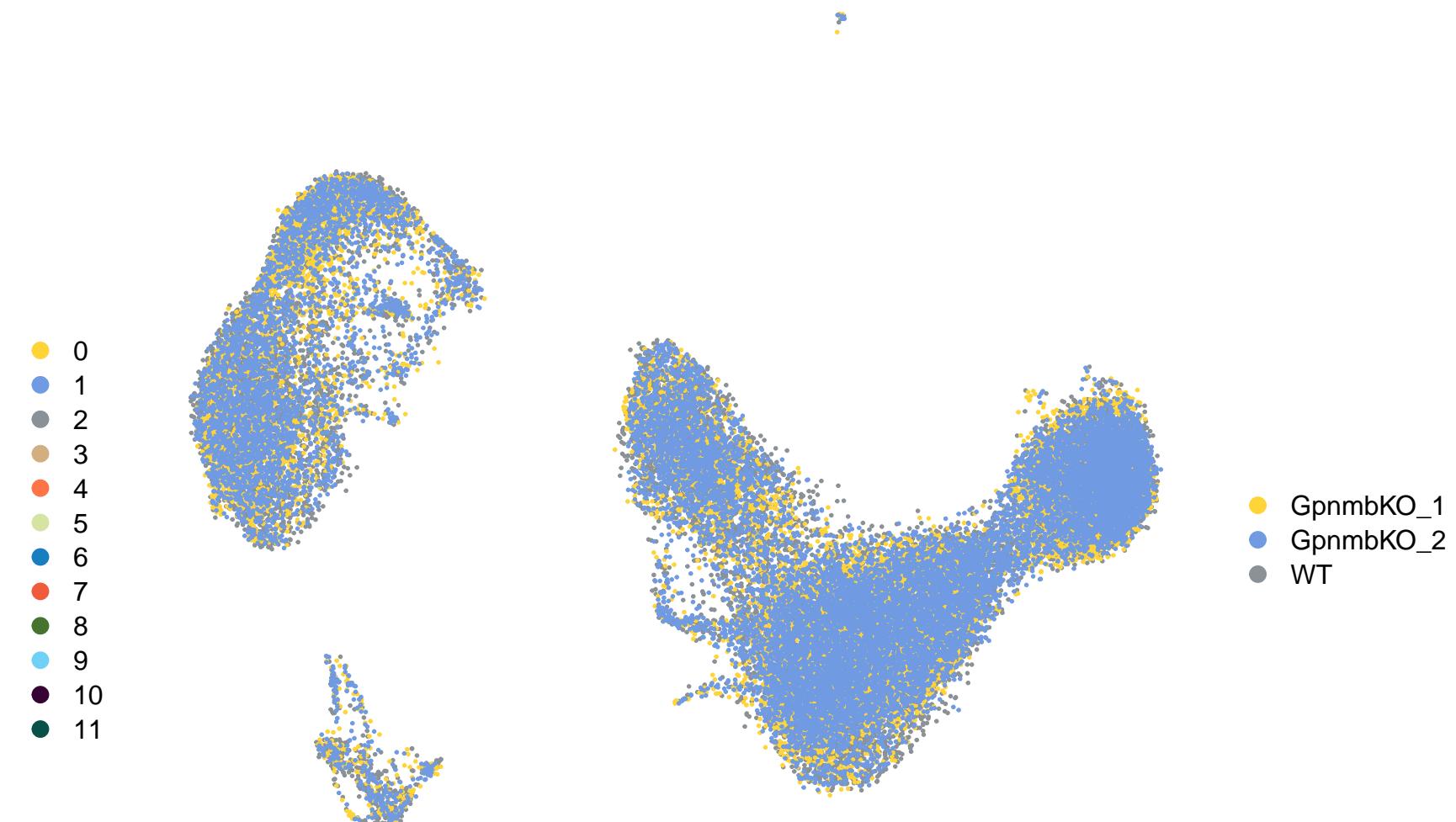


Clusters

seurat_clusters



orig.ident

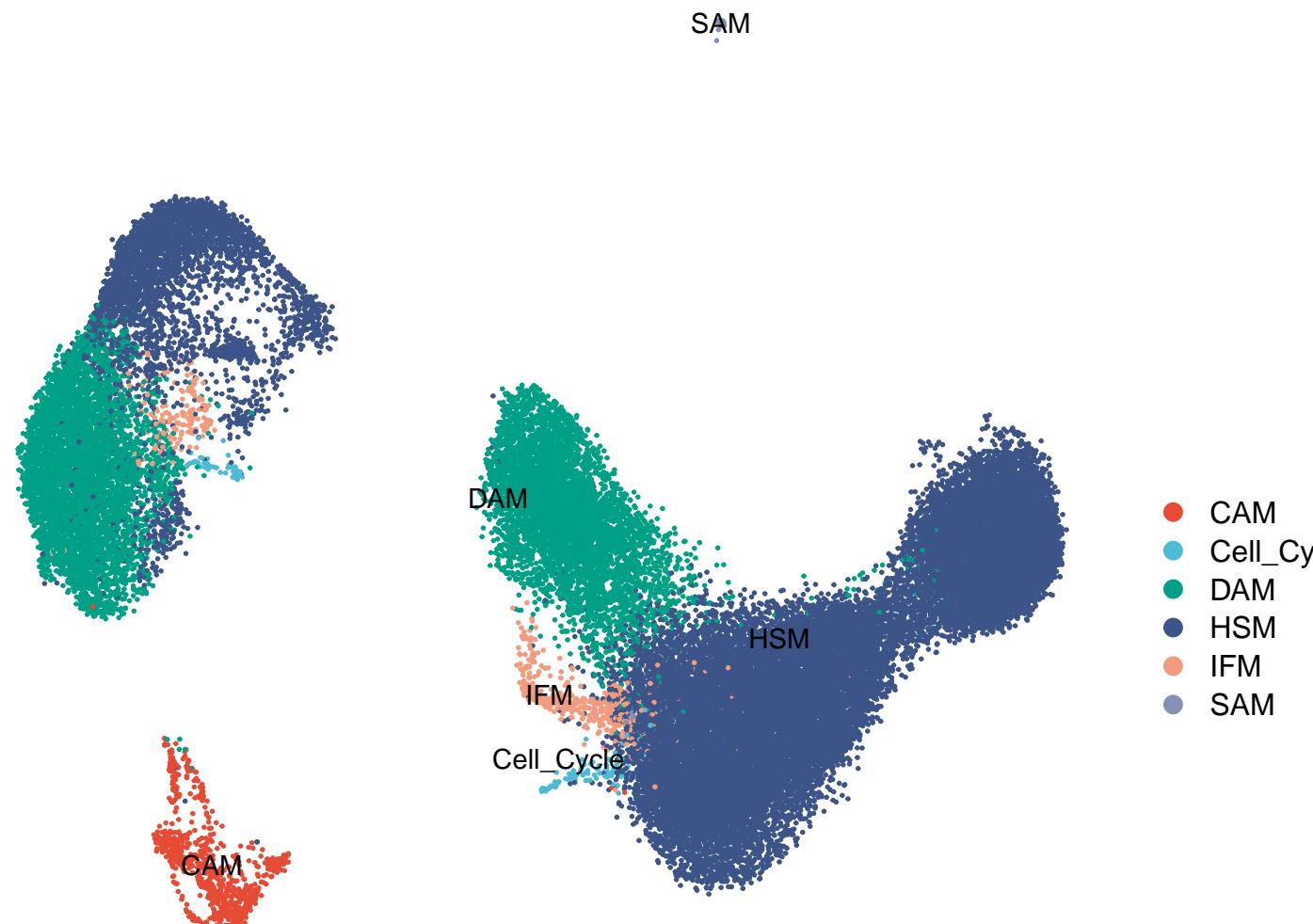


0
1
2
3
4
5
6
7
8
9
10
11

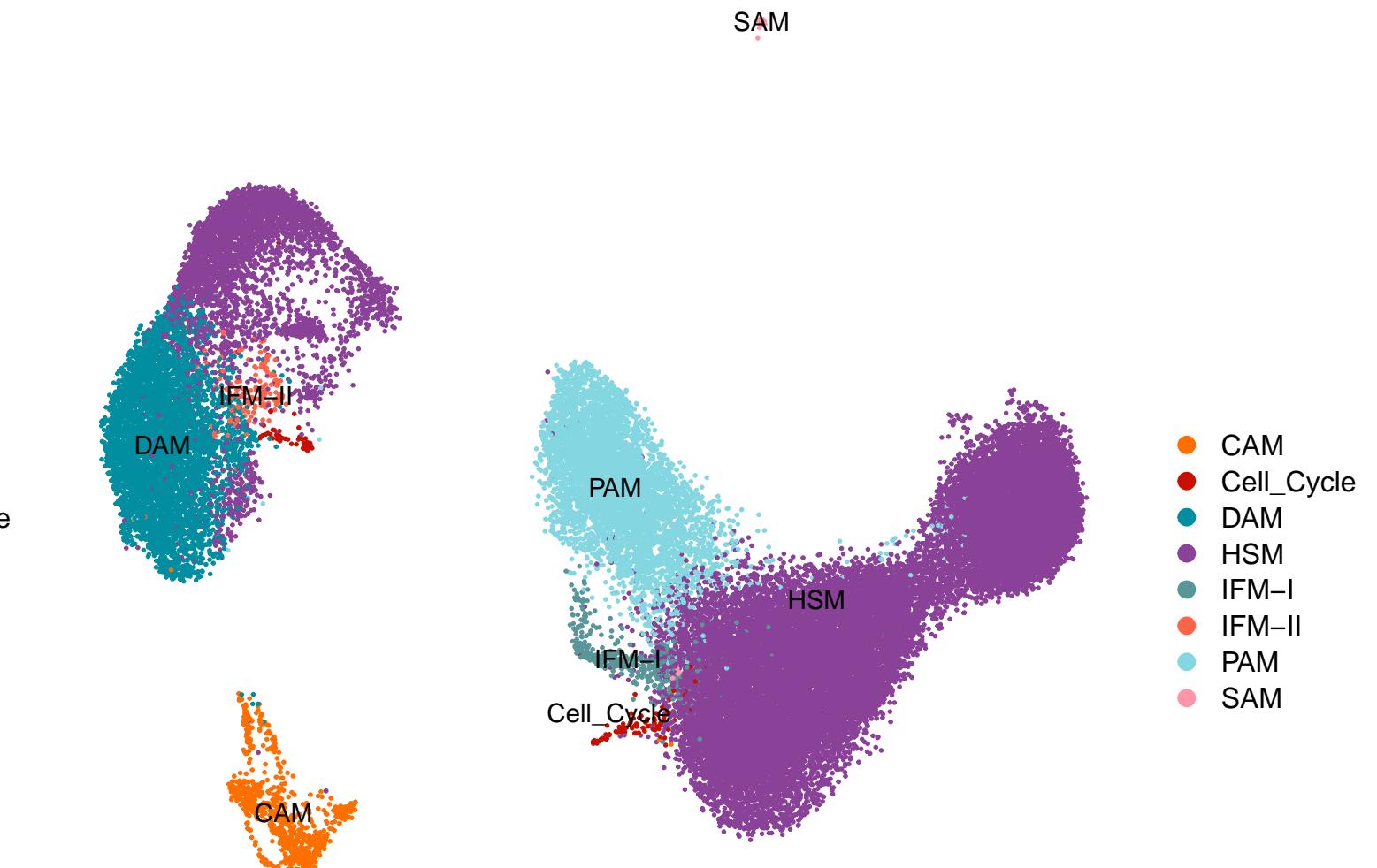
GpnmbKO_1
GpnmbKO_2
WT

Automated vs. Calibrated cell type annotation

cluster_auto

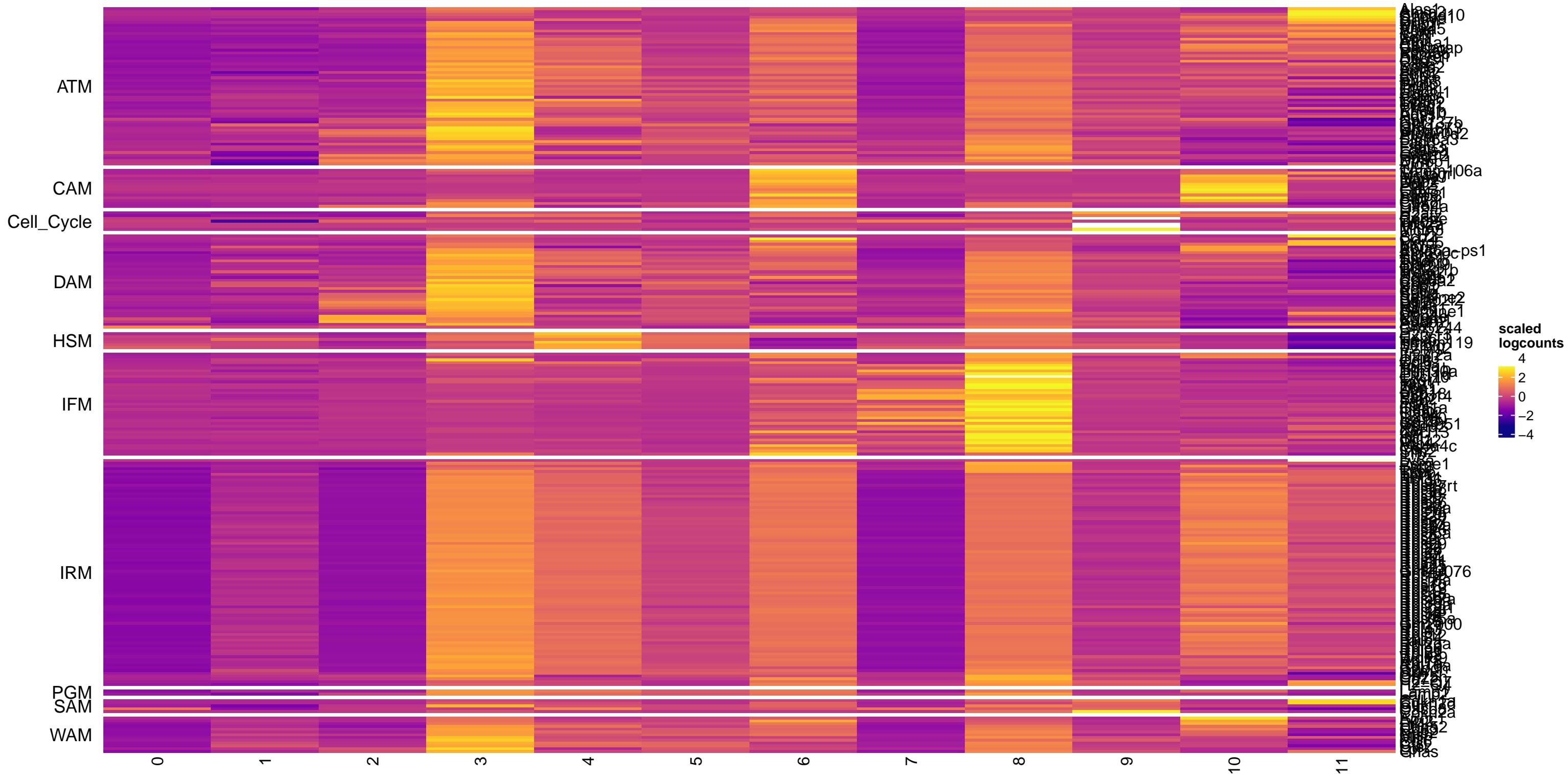


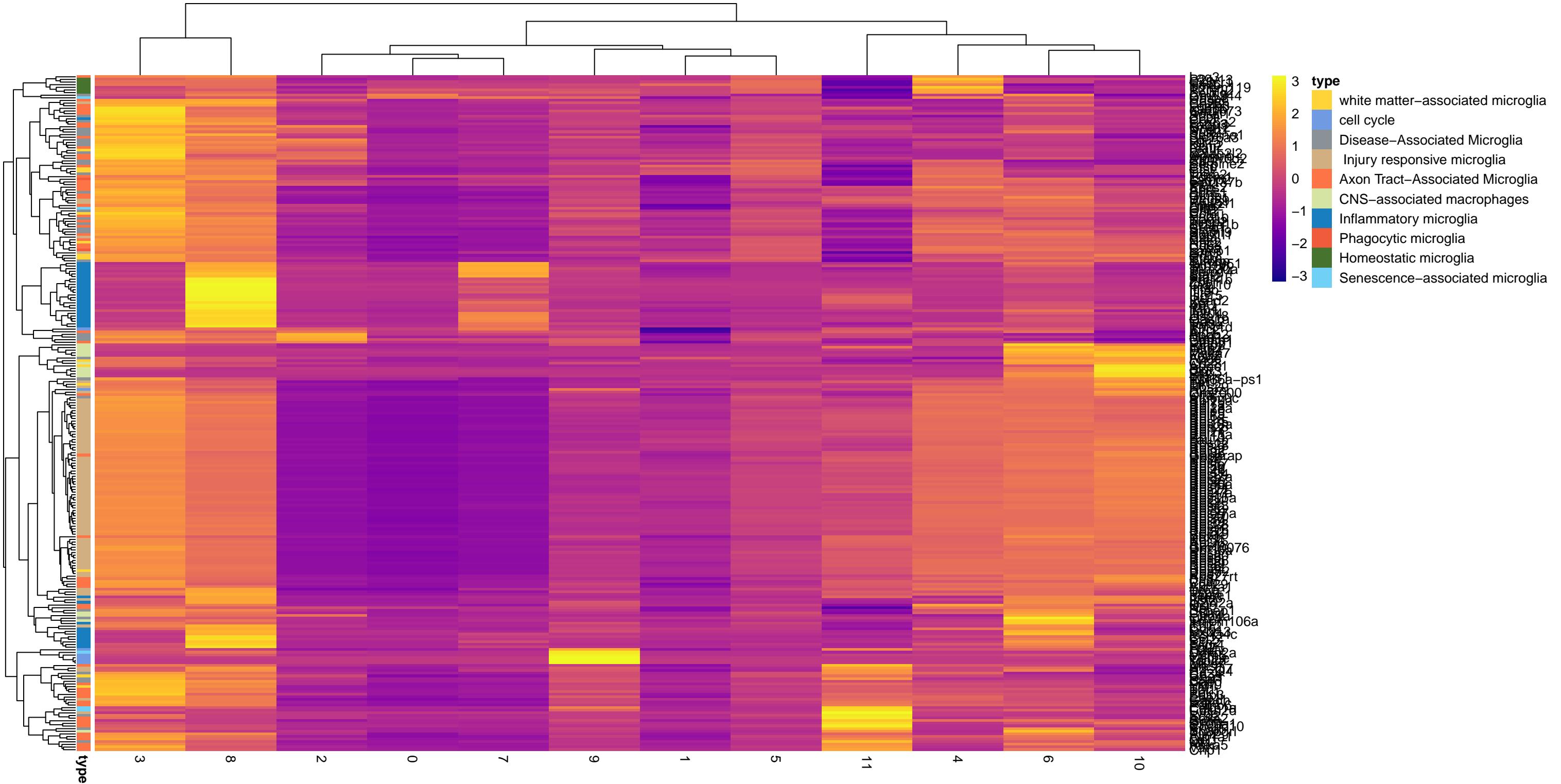
cluster_calibrated

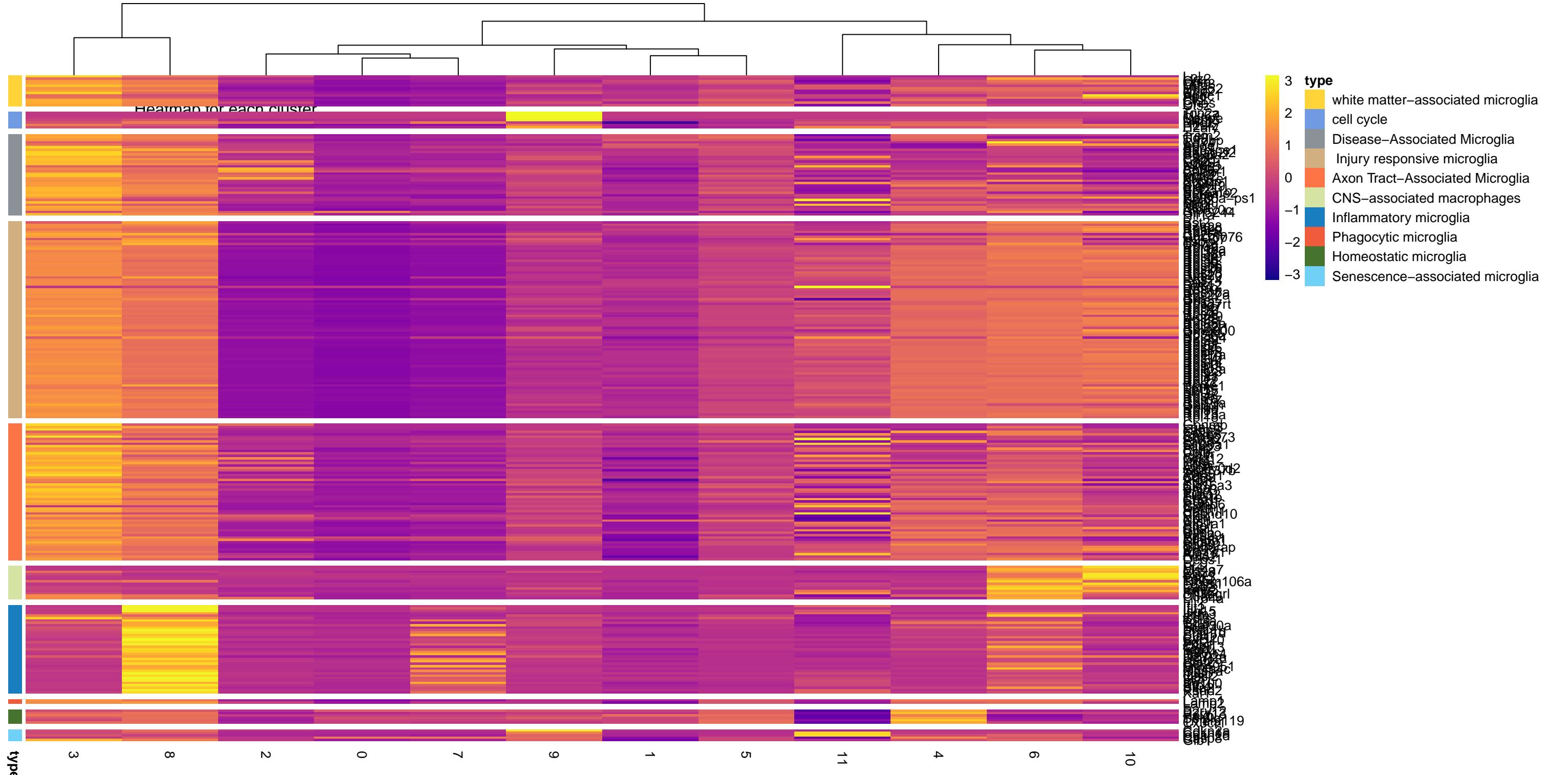


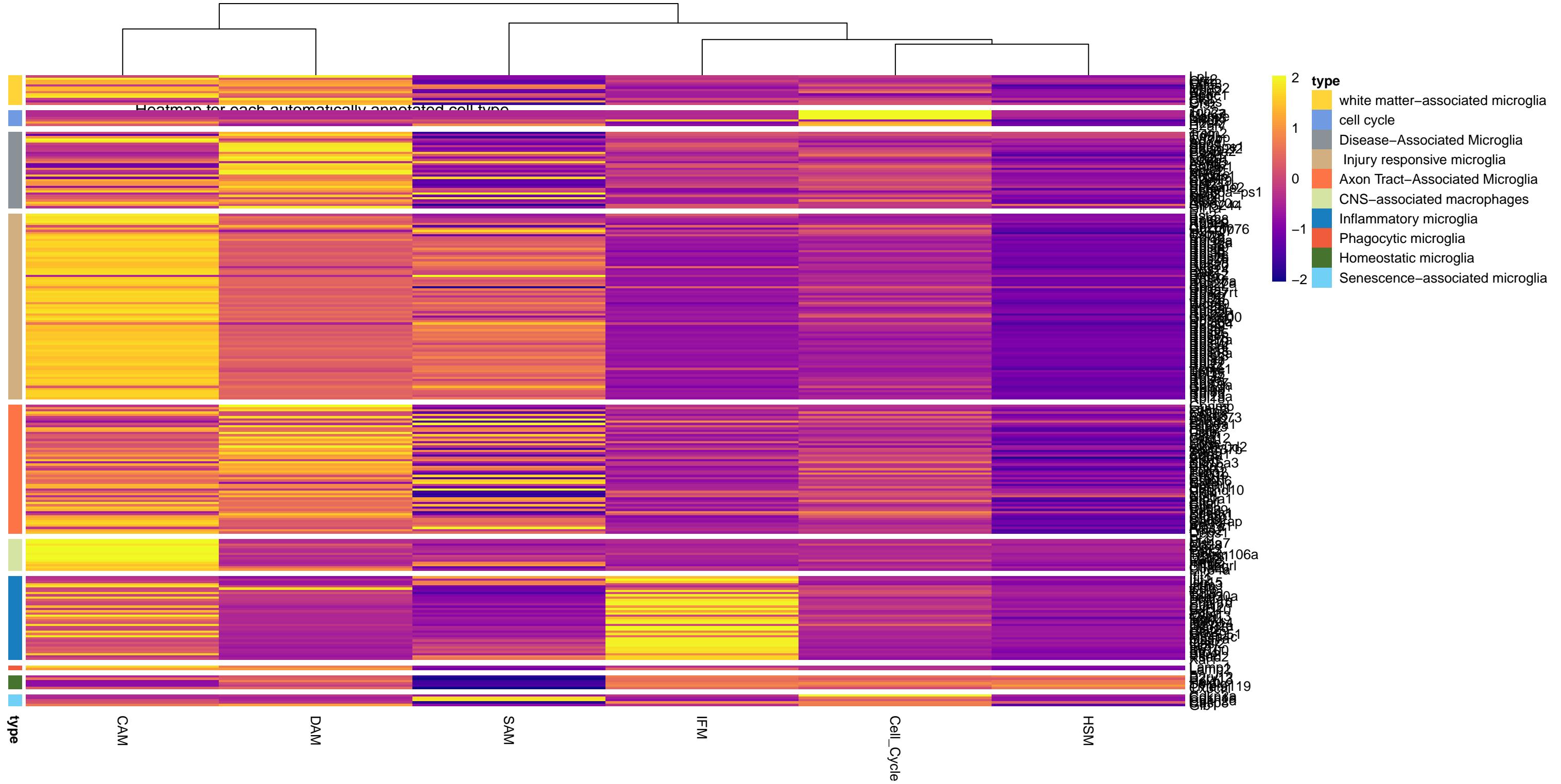
- CAM
- Cell_Cycle
- DAM
- HSM
- IFM
- SAM

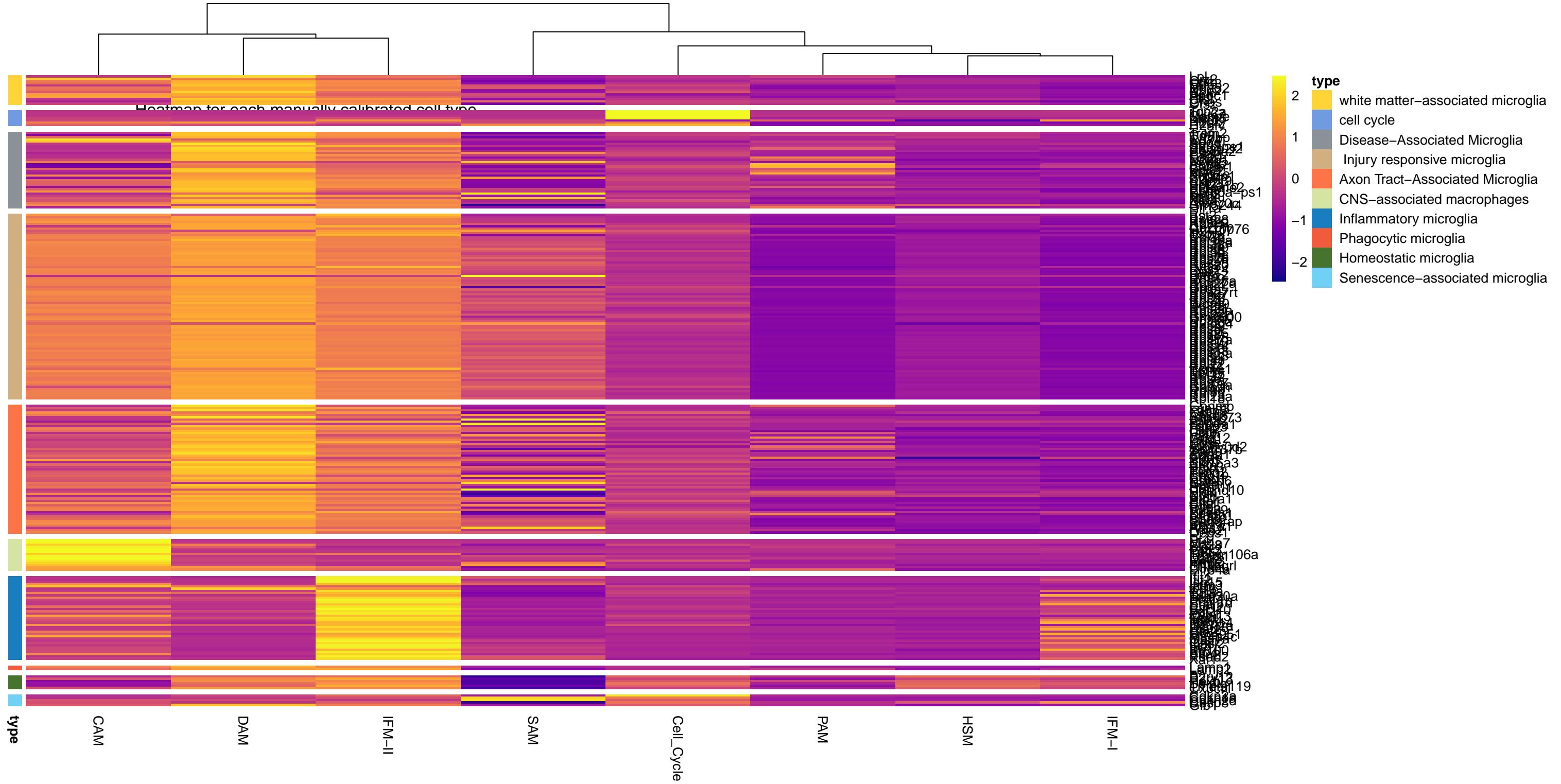
- CAM
- Cell_Cycle
- DAM
- HSM
- IFM-I
- IFM-II
- PAM
- SAM



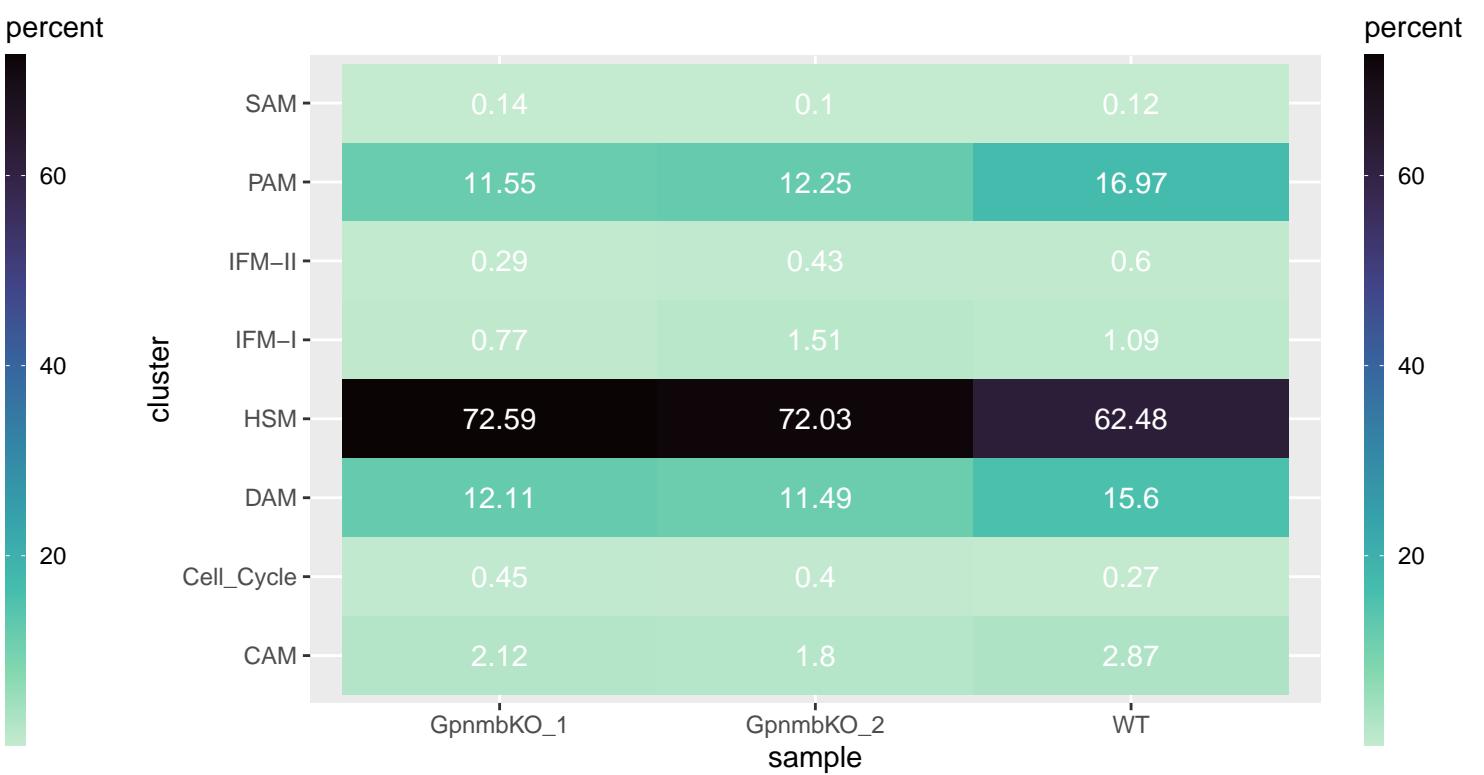
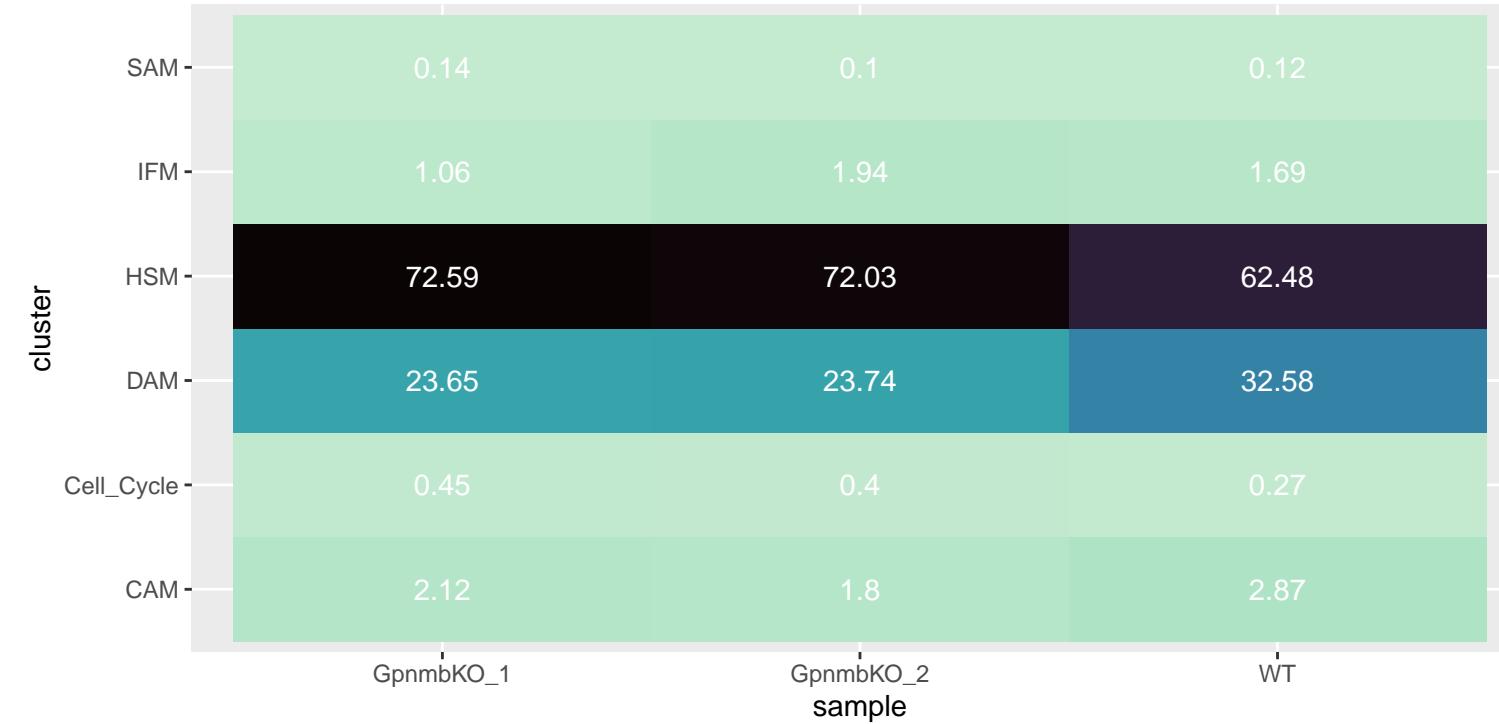








Condition composition in automated vs. calibrated cell type annotation



most likely cell type in each cluster

	0	1	2	3	4	5	6	7	8	9	10	11
1	HSM	HSM	DAM	DAM	HSM	HSM	CAM	IFM	IFM	Cell_Cycle	CAM	SAM
2	SAM	WAM	CAM	WAM	PGM	PGM	PGM	HSM	PGM	SAM	IRM	IRM
3	Cell_Cycle	DAM	Cell_Cycle	ATM	IRM	WAM	IRM	Cell_Cycle	DAM	HSM	WAM	ATM
4	IFM	CAM	ATM	PGM	ATM	DAM	IFM	SAM	IRM	ATM	PGM	Cell_Cycle

most expressed genes in each cluster

	0	1	2	3	4	5	6	7	8	9	10	11
1	Hexb	Ctsd	Ctsd	Ctsd	Ctsd	Ctsd	Apoe	Ctsd	Ctsd	Ctsd	Apoe	Apoe
2	Ctsd	Apoe	Apoe	Apoe	Hexb	Hexb	Lyz2	Hexb	Apoe	Hexb	Rps29	Ctsd
3	Apoe	Hexb	Hexb	Hexb	Cx3cr1	Apoe	Ctsd	Apoe	Hexb	Apoe	Ftl1	Tpt1
4	Cx3cr1	Tyrobp	Cadm1	Tyrobp	Rps29	Tyrobp	Rps29	Cx3cr1	Tyrobp	Tyrobp	Ctsd	Hexb
5	P2ry12	Trem2	Apbb2	Ctsb	Tyrobp	Cx3cr1	Ctsb	P2ry12	Ctsb	Cx3cr1	Lyz2	Rps29
6	Tyrobp	Ctsb	Ctsb	Trem2	P2ry12	Ctsb	Tpt1	Tyrobp	Rps29	Trem2	Tpt1	Rps21
7	Selplg	Cx3cr1	Tyrobp	Rps29	Fau	Trem2	Ftl1	Ctsb	B2m	Ctsz	Tyrobp	Fau
8	Ctsb	Rps29	Cd9	Fau	Trem2	Ctsz	Tyrobp	Trem2	Trem2	Ctsb	Hexb	Rps24
9	Trem2	Ctsz	Trem2	Ctsz	Tpt1	Rps29	Fau	Trim30a	Fau	Rps29	Fau	Rpl27a
10	Cadm1	B2m	Cx3cr1	B2m	B2m	Cd9	B2m	Selplg	Ctsz	P2ry12	Rps24	B2m
11	Ctsz	Cd9	Ctsz	Tpt1	Selplg	B2m	Hexb	Ctsz	Cx3cr1	Selplg	Ctsb	Gnas
12	Cd9	Tpt1	Myo1e	Cd9	Ctsb	Fau	Cd74	B2m	Cd9	Cd9	Rps12	Rps8
13	B2m	Fau	B2m	Rps21	Apoe	Tpt1	Rps24	Cd9	Tpt1	B2m	Rpl37a	Rpl37a
14	Rps29	Rps12	Rps29	Rps24	Ctsz	P2ry12	Rps21	Cadm1	Rps12	Cadm1	Rps21	Rpl13
15	Fau	Rps24	P2ry12	Rps12	Rps21	Ftl1	Rpl37a	Rps29	Rps24	Tpt1	Pf4	Ftl1
16	Tpt1	P2ry12	Gnas	Ftl1	Rps24	Ctsl	Rps12	Tpt1	Rpl13	Fau	Rpl27a	Rpl21
17	Grn	Rps21	Fau	Ctsl	Cd9	Selplg	Rpl35a	Grn	Rps21	Rps24	Rpl35a	Rpl18a
18	Rps21	Ctsl	Ctsl	Rpl21	Rps12	Rps21	Rpl13	Fau	Rpl37	Rps12	Rps8	Rps12
19	Rps24	Selplg	Tpt1	Cx3cr1	Rpl13	Rps12	Cx3cr1	Rps21	Rpl37a	Grn	B2m	Rpl41
20	Rps12	Rpl21	Rps21	Rpl13	Ftl1	Rpl13	Rpl39	Ly6e	Ftl1	Gnas	Rps28	Rpl35a

most expressed genes in each calibrated cell type

	CAM	Cell_Cycle	DAM	HSM	IFM-I	IFM-II	PAM	SAM
1	Apoe	Ctsd	Ctsd	Ctsd	Ctsd	Ctsd	Ctsd	Apoe
2	Lyz2	Hexb	Apoe	Hexb	Hexb	Apoe	Apoe	Ctsd
3	Ctsd	Apoe	Hexb	Apoe	Apoe	Hexb	Hexb	Tpt1
4	Rps29	Tyrobp	Tyrobp	Cx3cr1	Cx3cr1	Tyrobp	Cadm1	Hexb
5	Tpt1	Cx3cr1	Ctsb	Tyrobp	P2ry12	Ctsb	Apbb2	Rps29
6	Ftl1	Trem2	Trem2	Ctsb	Tyrobp	Rps29	Ctsb	Rps21
7	Ctsb	Ctsz	Rps29	P2ry12	Ctsb	B2m	Tyrobp	Fau
8	Tyrobp	Ctsb	Fau	Trem2	Trem2	Trem2	Cd9	Rps24
9	Fau	Rps29	Ctsz	Rps29	Trim30a	Fau	Trem2	Rpl27a
10	Hexb	P2ry12	B2m	Ctsz	Selplg	Ctsz	Cx3cr1	B2m
11	B2m	Selplg	Tpt1	B2m	Ctsz	Cx3cr1	Ctsz	Gnas
12	Rps24	Cd9	Cd9	Selplg	B2m	Cd9	Myo1e	Rps8
13	Rps21	B2m	Rps21	Cd9	Cd9	Tpt1	B2m	Rpl37a
14	Rps12	Cadm1	Rps24	Fau	Cadm1	Rps12	Rps29	Rpl13
15	Rpl37a	Tpt1	Rps12	Tpt1	Rps29	Rps24	P2ry12	Ftl1
16	Rpl35a	Fau	Ftl1	Rps12	Tpt1	Rpl13	Gnas	Rpl21
17	Rpl13	Rps24	Ctsl	Rps24	Grn	Rps21	Fau	Rpl18a
18	Rps8	Rps12	Rpl21	Rps21	Fau	Rpl37	Ctsl	Rps12
19	Rpl39	Grn	Cx3cr1	Cadm1	Rps21	Rpl37a	Tpt1	Rpl41
20	Rpl27a	Gnas	Rpl13	Ctsl	Ly6e	Ftl1	Rps21	Rpl35a