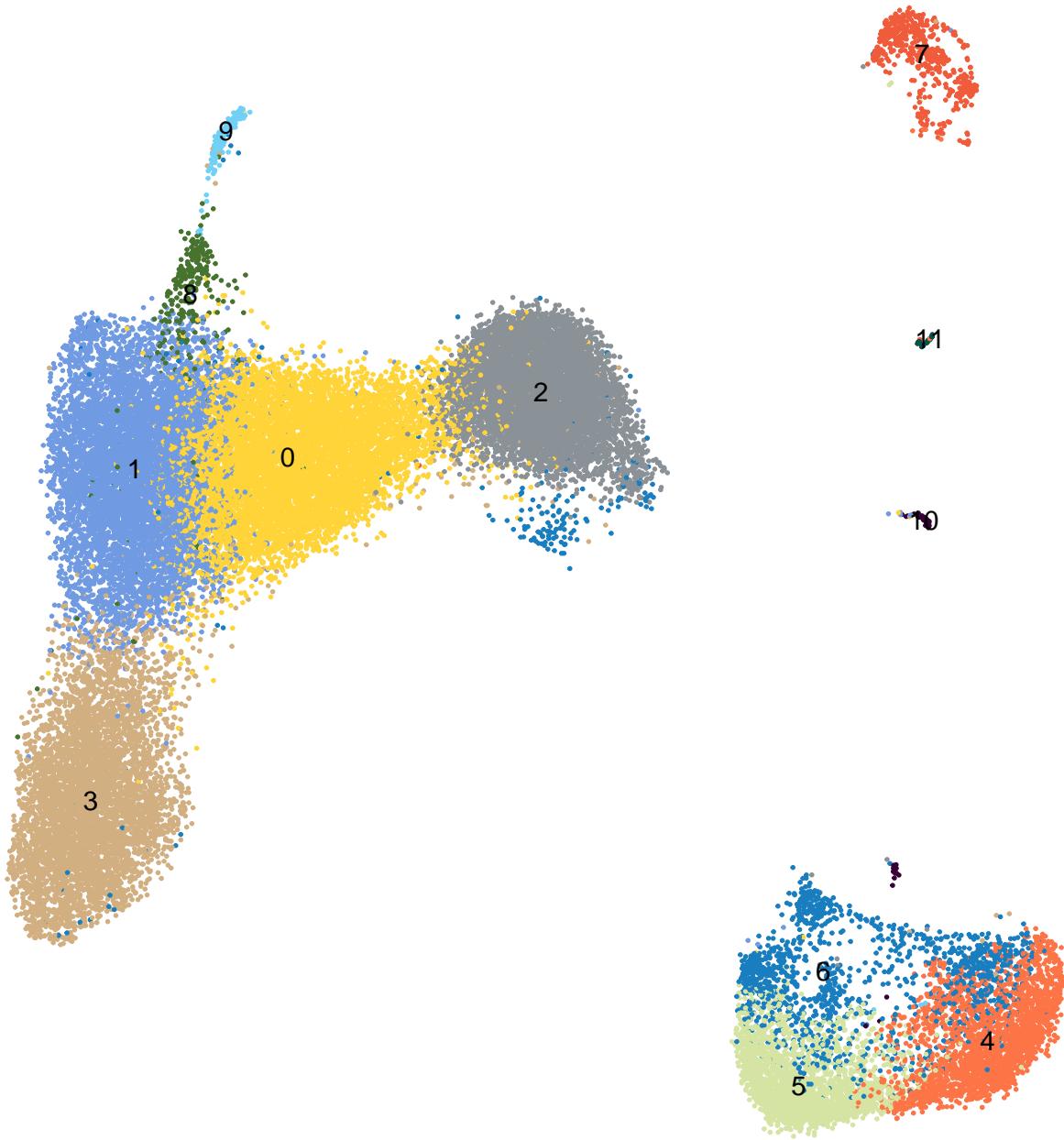
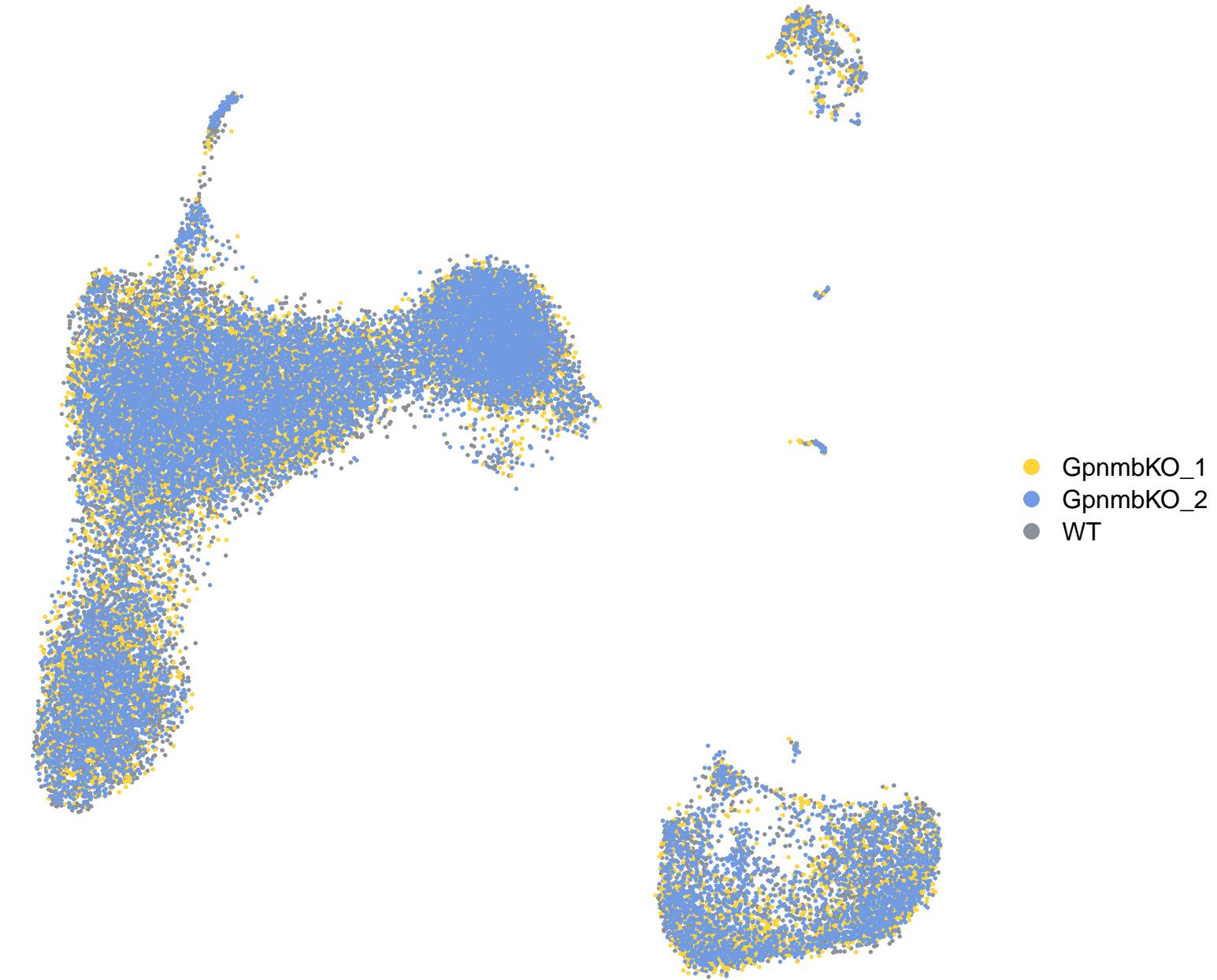


Clusters

seurat_clusters



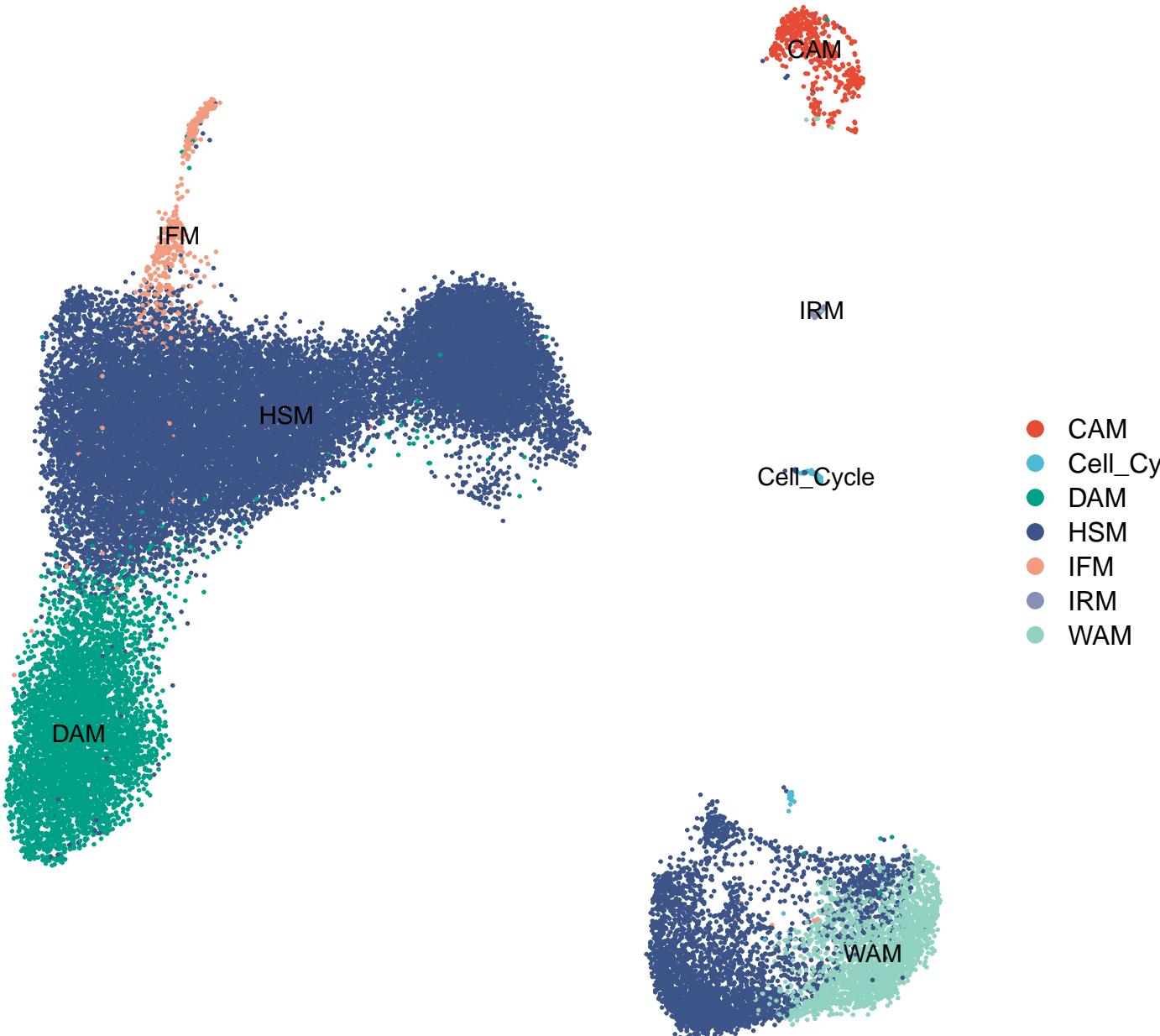
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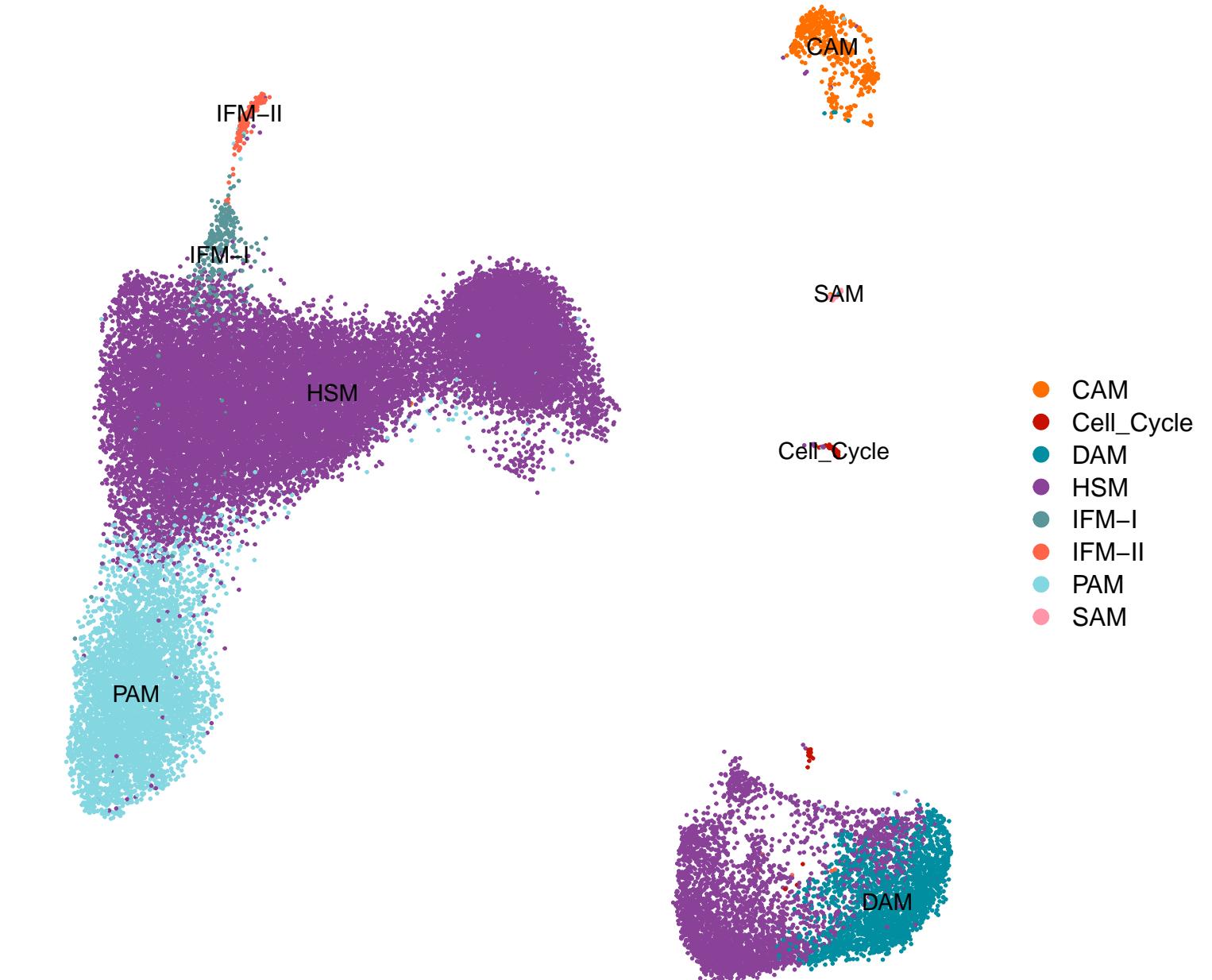
GpnmbKO_1
GpnmbKO_2
WT

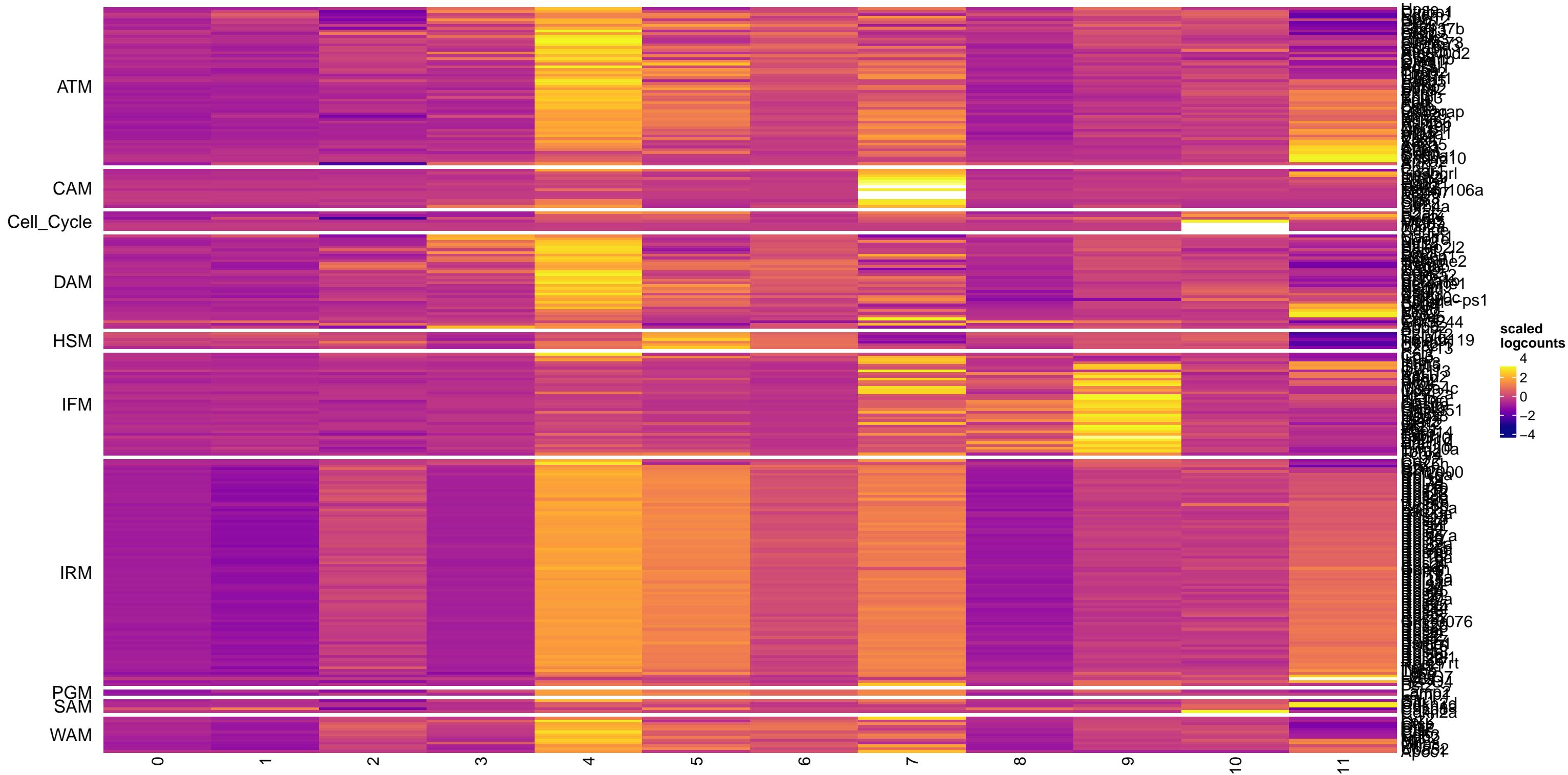
Automated vs. Calibrated cell type annotation

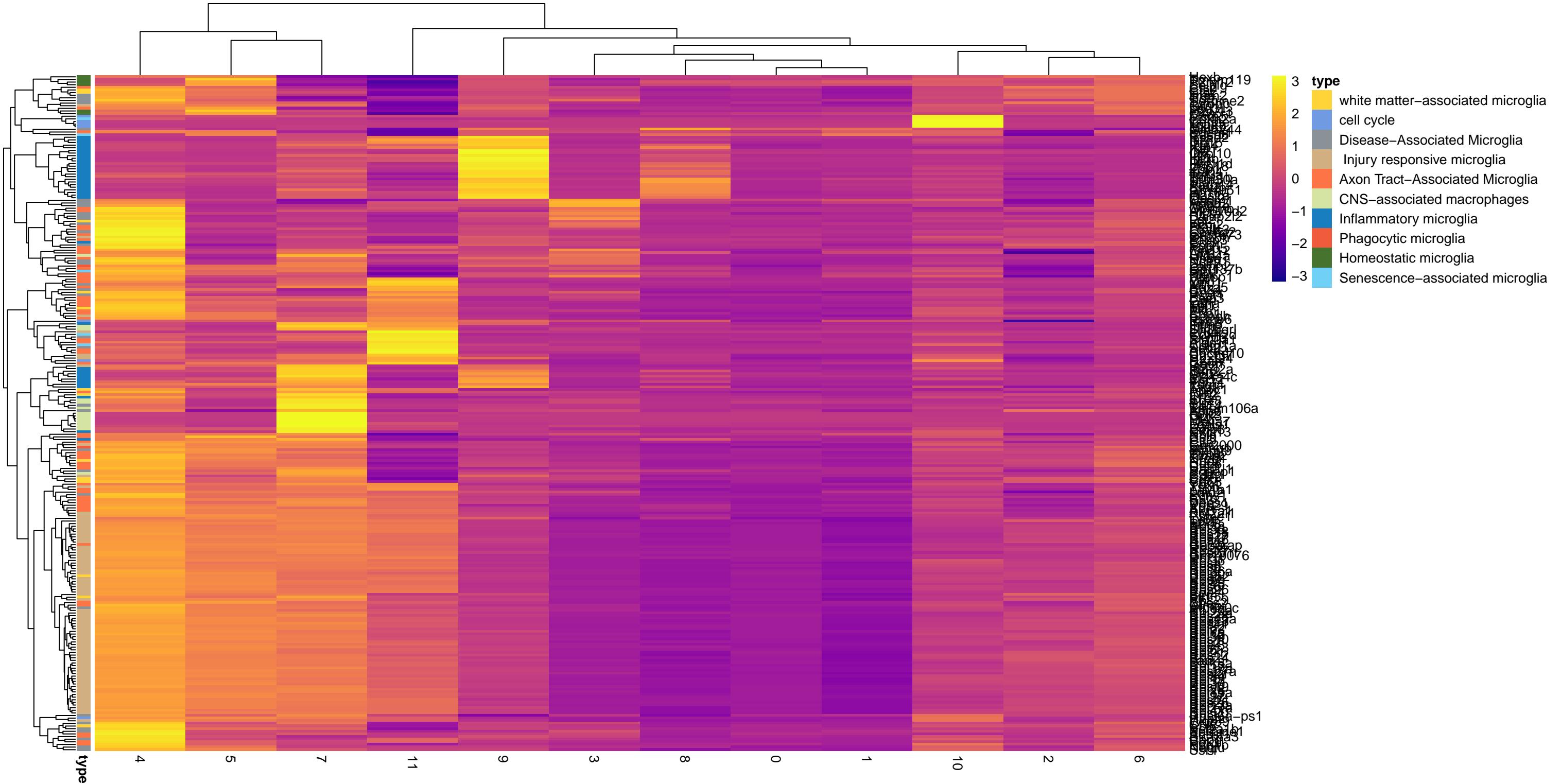
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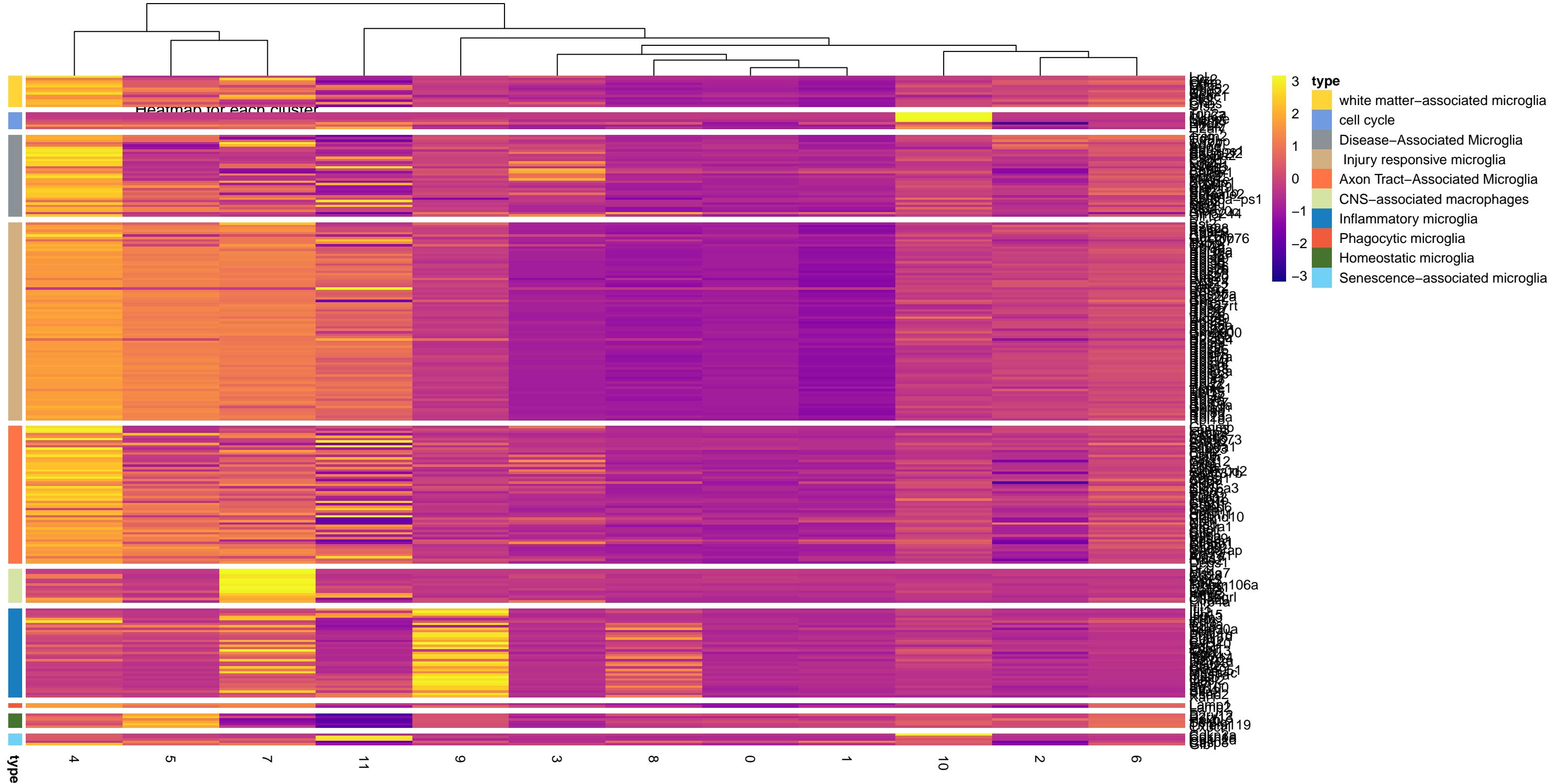


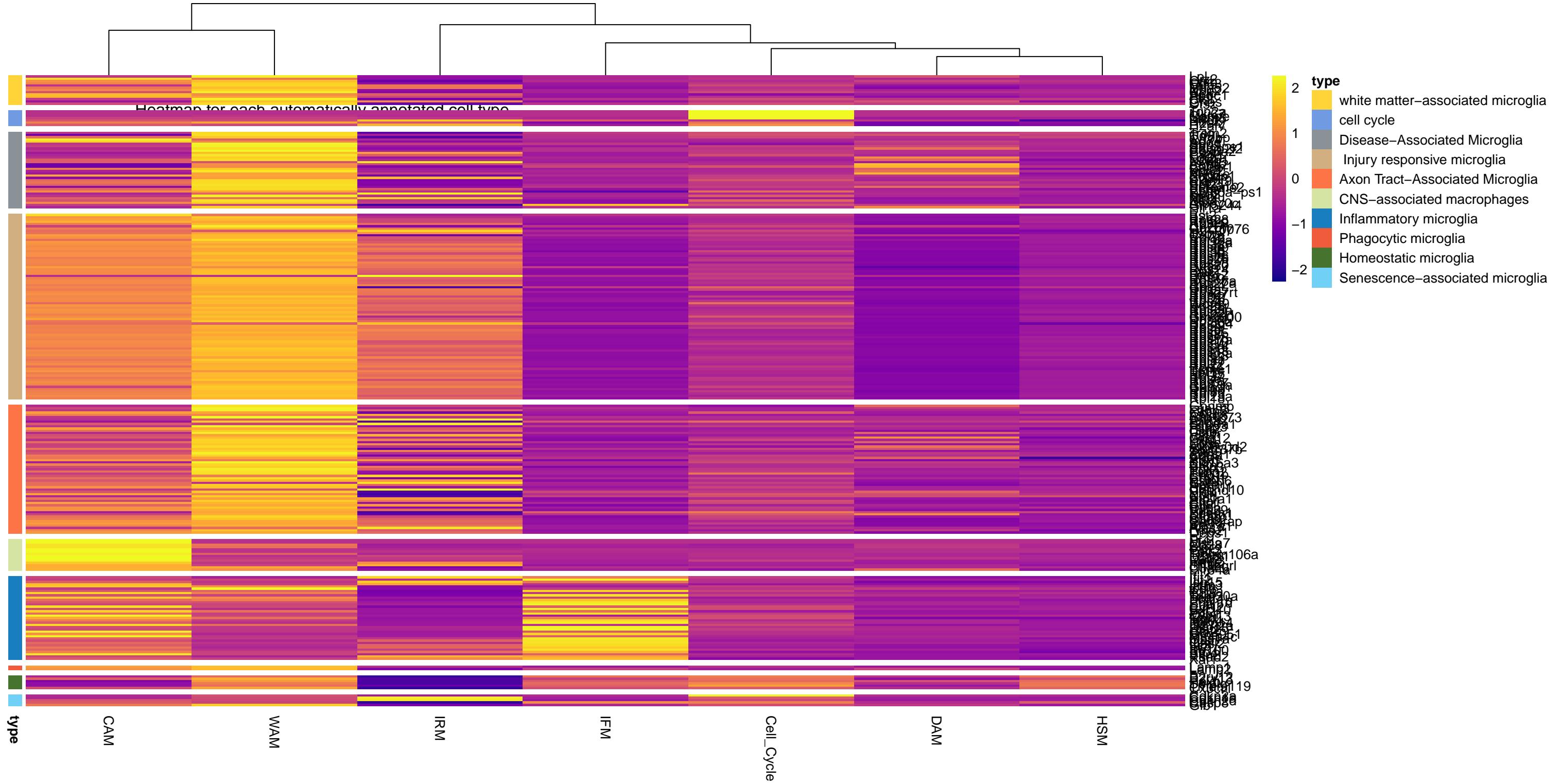
cluster_calibrated

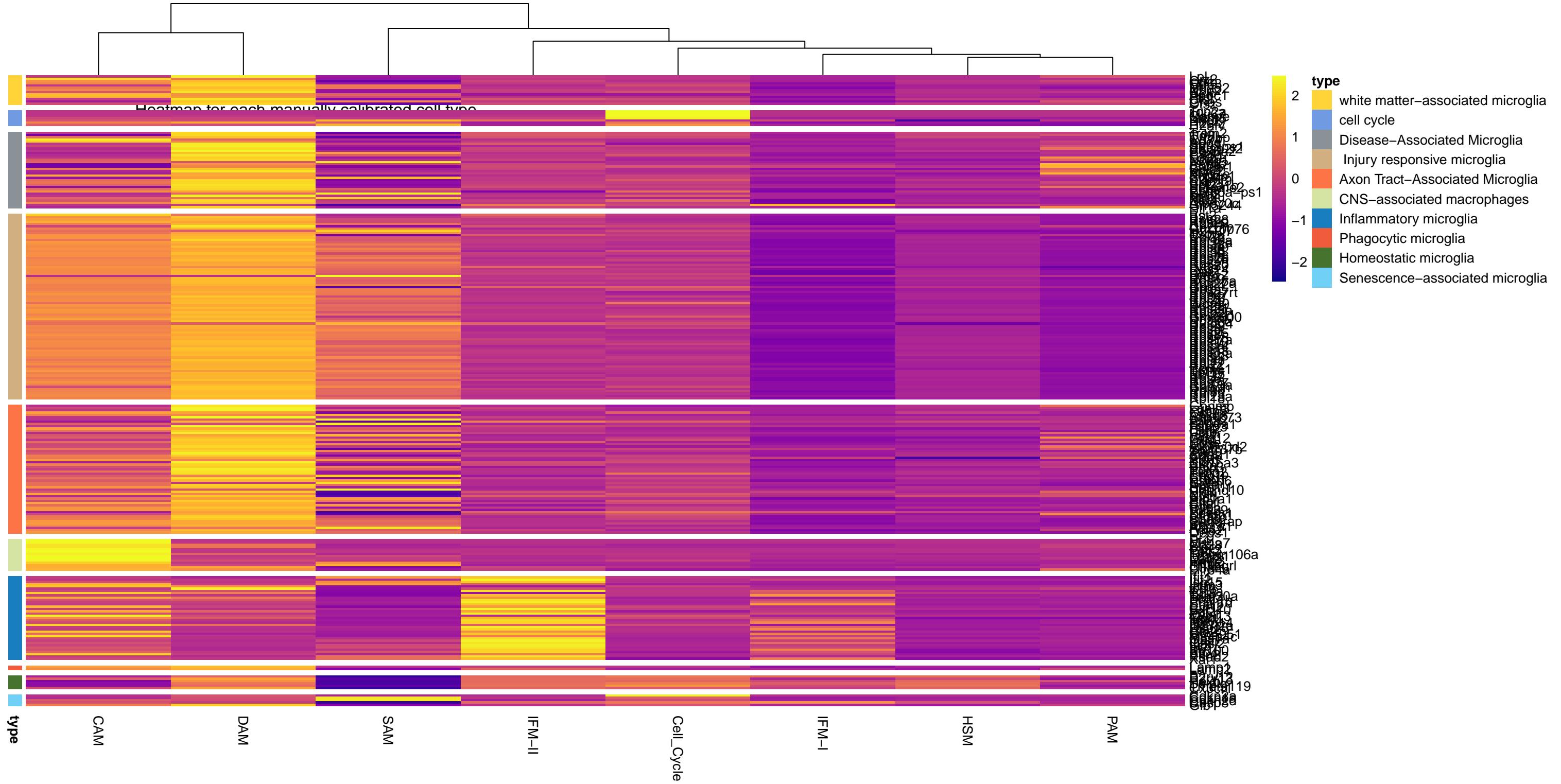




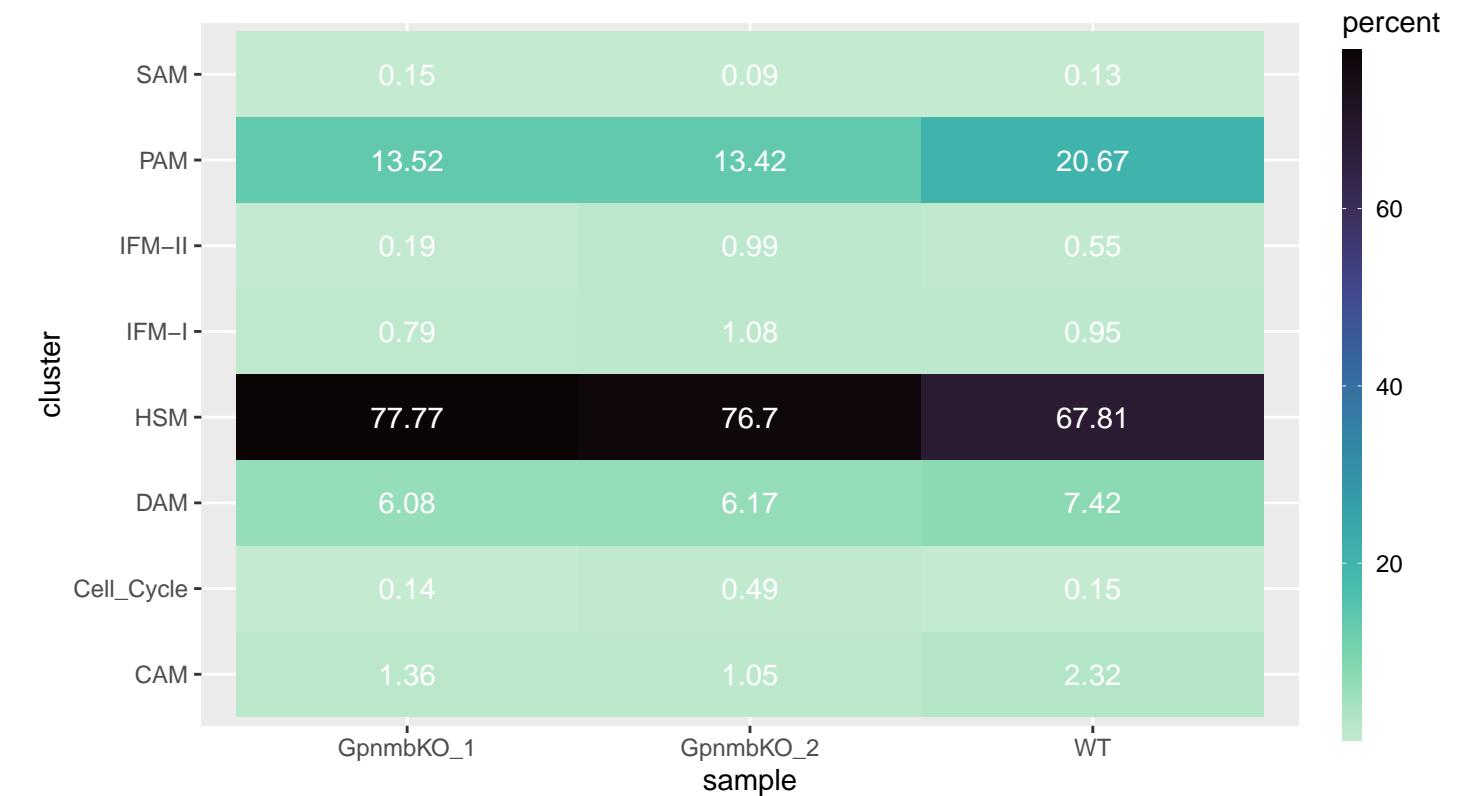
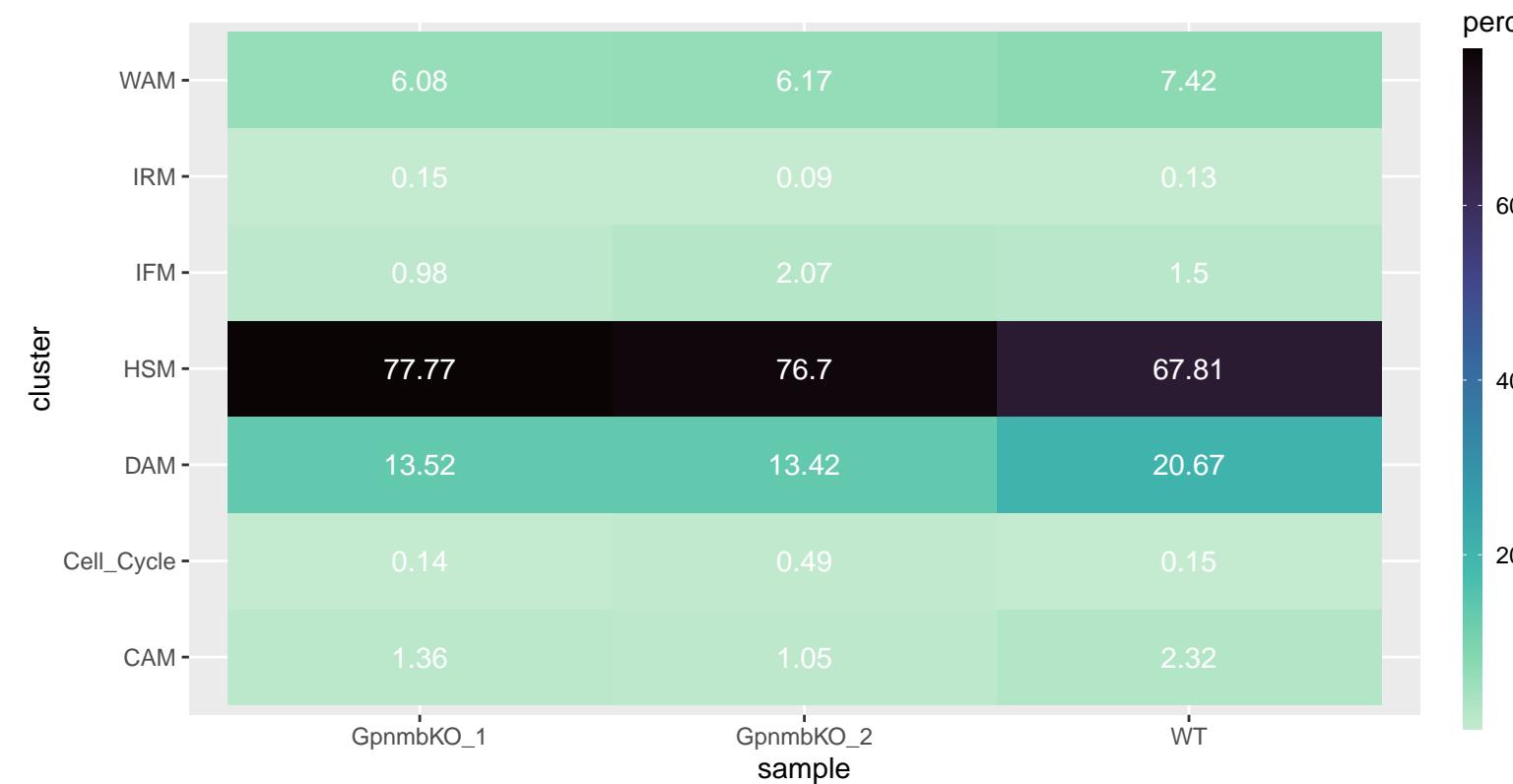








Condition composition in automated vs. calibrated cell type annotation



most likely cell type in each cluster

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

most expressed genes in each cluster

	0	1	2	3	4	5	6	7	8	9	10	11
1	Ctsd	Hexb	Ctsd	Ctsd	Ctsd	Hexb	Ctsd	Apoe	Ctsd	Ctsd	Ctsd	Apoe
2	Hexb	Ctsd	Apoe	Apoe	Apoe	Ctsd	Hexb	Lyz2	Hexb	Hexb	Hexb	Ctsd
3	Apoe	Apoe	Hexb	Hexb	Hexb	Cx3cr1	Apoe	Ctsd	Apoe	Apoe	Apoe	Tpt1
4	Cx3cr1	Cx3cr1	Tyrobp	Cadm1	Tyrobp	Rps29	Cx3cr1	Rps29	Cx3cr1	Cx3cr1	Cx3cr1	Hexb
5	Tyrobp	P2ry12	Trem2	Apbb2	Ctsb	Tyrobp	Ctsb	Ctsb	P2ry12	Tyrobp	Tyrobp	Rps29
6	P2ry12	Selplg	Ctsb	Ctsb	Trem2	P2ry12	Tyrobp	Ftl1	Tyrobp	Ctsb	P2ry12	Fau
7	Ctsb	Cadm1	Cx3cr1	Tyrobp	Ctsz	Selplg	Trem2	Tyrobp	Ctsb	Trem2	Trem2	Gnas
8	Selplg	Tyrobp	Rps29	Cd9	Rps29	Trem2	Ctsz	Tpt1	Trem2	B2m	Ctsz	Rps24
9	Trem2	Ctsb	Ctsz	Trem2	Cd9	Fau	Cd9	B2m	Selplg	Cd9	Ctsb	Rps21
10	Ctsz	Trem2	B2m	Cx3cr1	B2m	B2m	Rps29	Hexb	Ctsz	P2ry12	Cd9	Rpl27a
11	Rps29	Ctsz	Cd9	Ctsz	Cx3cr1	Tpt1	B2m	Fau	Trim30a	Ctsz	Selplg	Rps8
12	B2m	Cd9	Tpt1	Myo1e	Fau	Ctsb	P2ry12	Rps24	Cadm1	Rps29	Rps29	B2m
13	Cd9	B2m	Fau	B2m	Tpt1	Ctsz	Fau	Cx3cr1	B2m	Trim30a	B2m	Rpl13
14	Cadm1	Rps29	P2ry12	P2ry12	Ctsl	Apoe	Selplg	Rps21	Cd9	Selplg	Cadm1	Rps12
15	Tpt1	Fau	Rps24	Rps29	Ftl1	Cd9	Ctsl	Rps12	Rps29	Fau	Fau	Rps27
16	Fau	Grn	Rps12	Gnas	Rps12	Rps21	Ftl1	Rpl37a	Tpt1	Grn	Tpt1	Rpl35a
17	Rps12	Tpt1	Selplg	Fau	Rps24	Rps24	Tpt1	Rpl35a	Grn	Tpt1	Grn	Ftl1
18	Rps24	Rps21	Ctsl	Ctsl	Rps21	Rps12	Grn	Dab2	Fau	Cadm1	Rps12	Rpl21
19	Rps21	Rps24	Rps21	Tpt1	Rpl21	Rpl13	Cadm1	Rpl13	Rps21	Rps12	Rps24	Rpl41
20	Grn	Rps12	Ftl1	Selplg	Rpl13	Ftl1	Rps21	Rps8	Ly6e	Rps21	Ctsl	Rps14

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	Hexb	Apoe	Ctsd
3	Ctsd	Apoe	Hexb	Apoe	Apoe	Apoe	Hexb	Tpt1
4	Rps29	Cx3cr1	Tyrobp	Cx3cr1	Cx3cr1	Cx3cr1	Cadm1	Hexb
5	Ctsb	Tyrobp	Ctsb	Tyrobp	P2ry12	Tyrobp	Apbb2	Rps29
6	Ftl1	P2ry12	Trem2	P2ry12	Tyrobp	Ctsb	Ctsb	Fau
7	Tyrobp	Trem2	Ctsz	Ctsb	Ctsb	Trem2	Tyrobp	Gnas
8	Tpt1	Ctsz	Rps29	Trem2	Trem2	B2m	Cd9	Rps24
9	B2m	Ctsb	Cd9	Ctsz	Selplg	Cd9	Trem2	Rps21
10	Hexb	Cd9	B2m	Selplg	Ctsz	P2ry12	Cx3cr1	Rpl27a
11	Fau	Selplg	Cx3cr1	Rps29	Trim30a	Ctsz	Ctsz	Rps8
12	Rps24	Rps29	Fau	B2m	Cadm1	Rps29	Myo1e	B2m
13	Cx3cr1	B2m	Tpt1	Cd9	B2m	Trim30a	B2m	Rpl13
14	Rps21	Cadm1	Ctsl	Fau	Cd9	Selplg	P2ry12	Rps12
15	Rps12	Fau	Ftl1	Tpt1	Rps29	Fau	Rps29	Rps27
16	Rpl37a	Tpt1	Rps12	Cadm1	Tpt1	Grn	Gnas	Rpl35a
17	Rpl35a	Grn	Rps24	Rps24	Grn	Tpt1	Fau	Ftl1
18	Dab2	Rps12	Rps21	Rps12	Fau	Cadm1	Ctsl	Rpl21
19	Rpl13	Rps24	Rpl21	Rps21	Rps21	Rps12	Tpt1	Rpl41
20	Rps8	Ctsl	Rpl13	Grn	Ly6e	Rps21	Selplg	Rps14