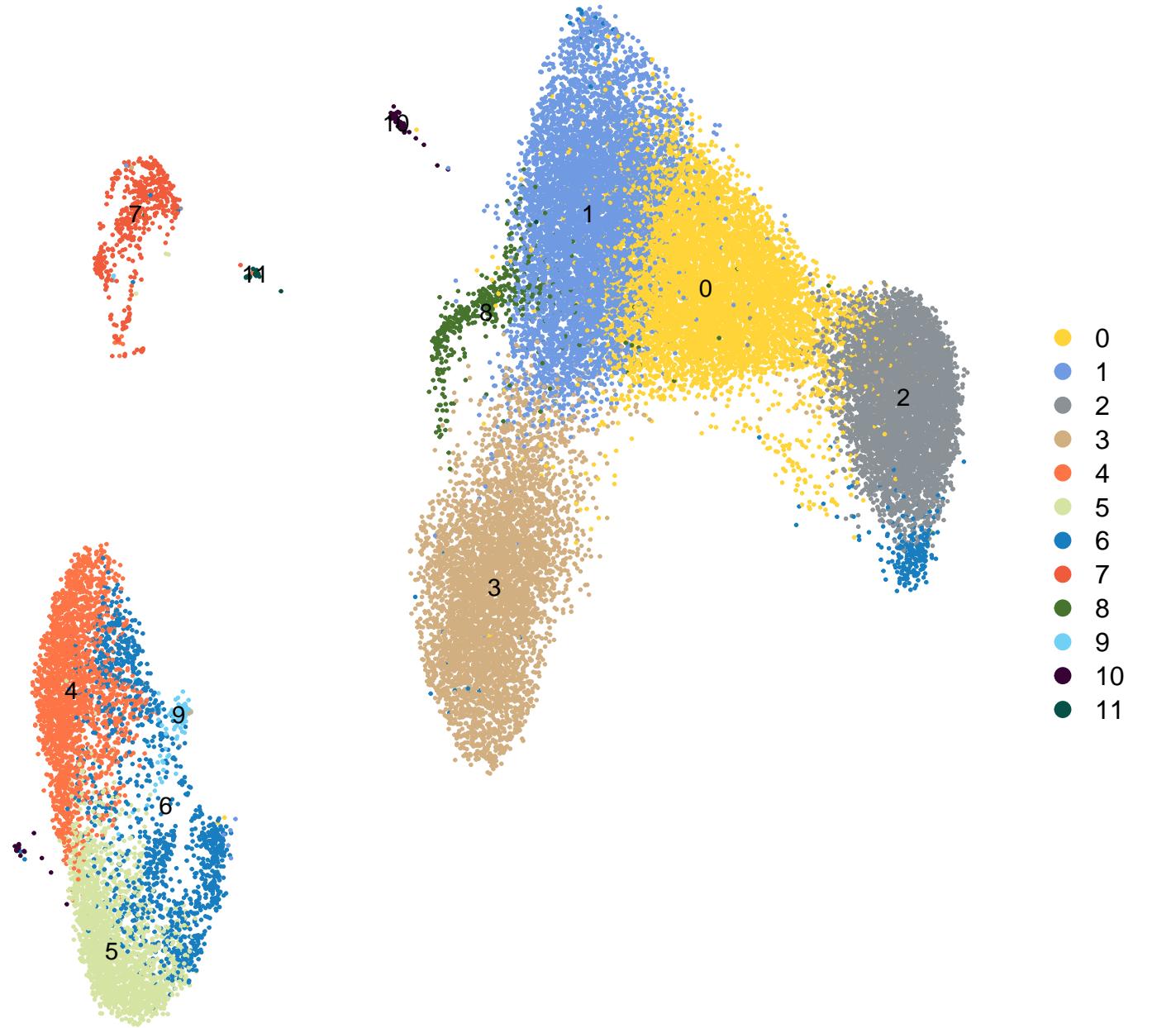
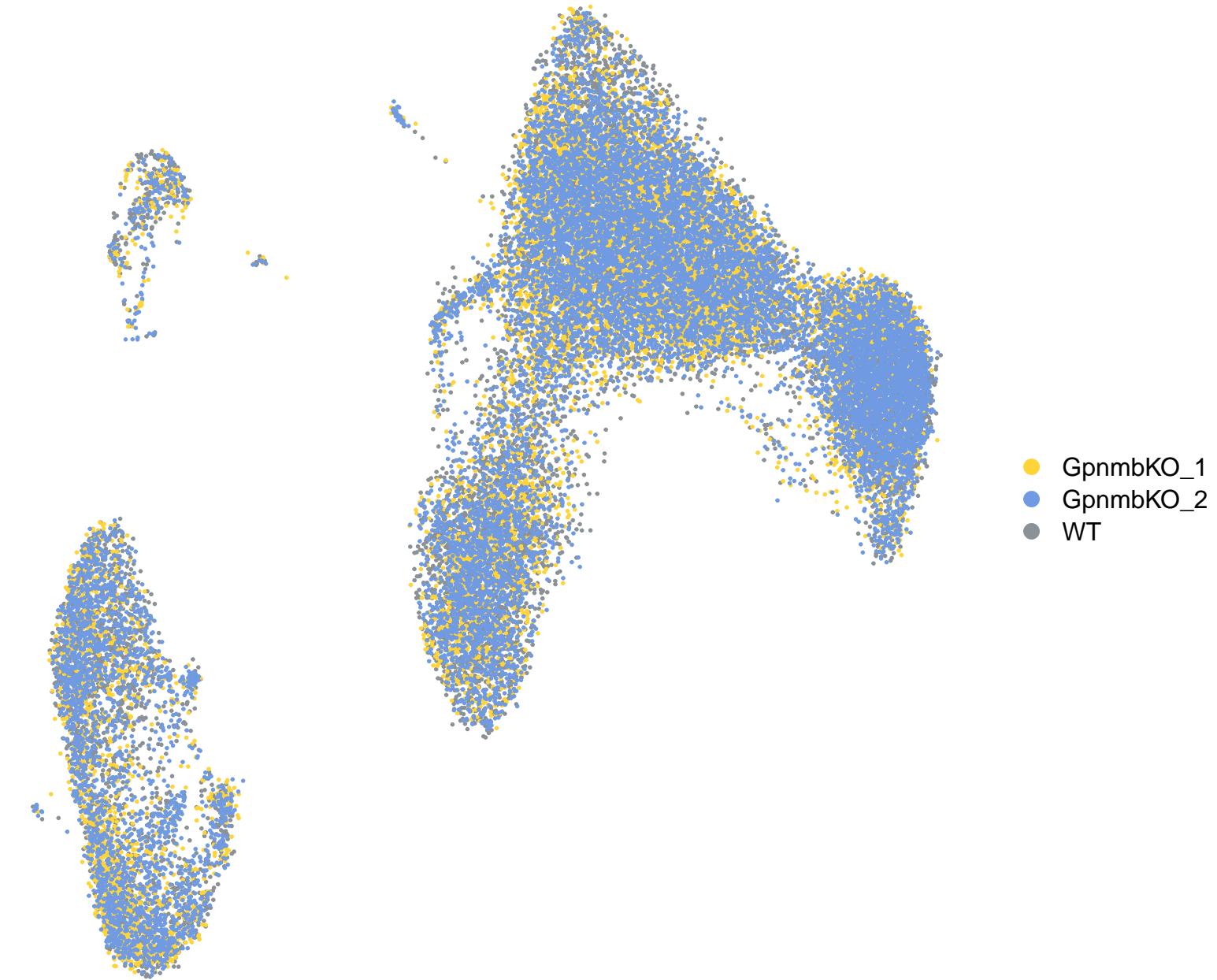


Clusters

**seurat\_clusters**



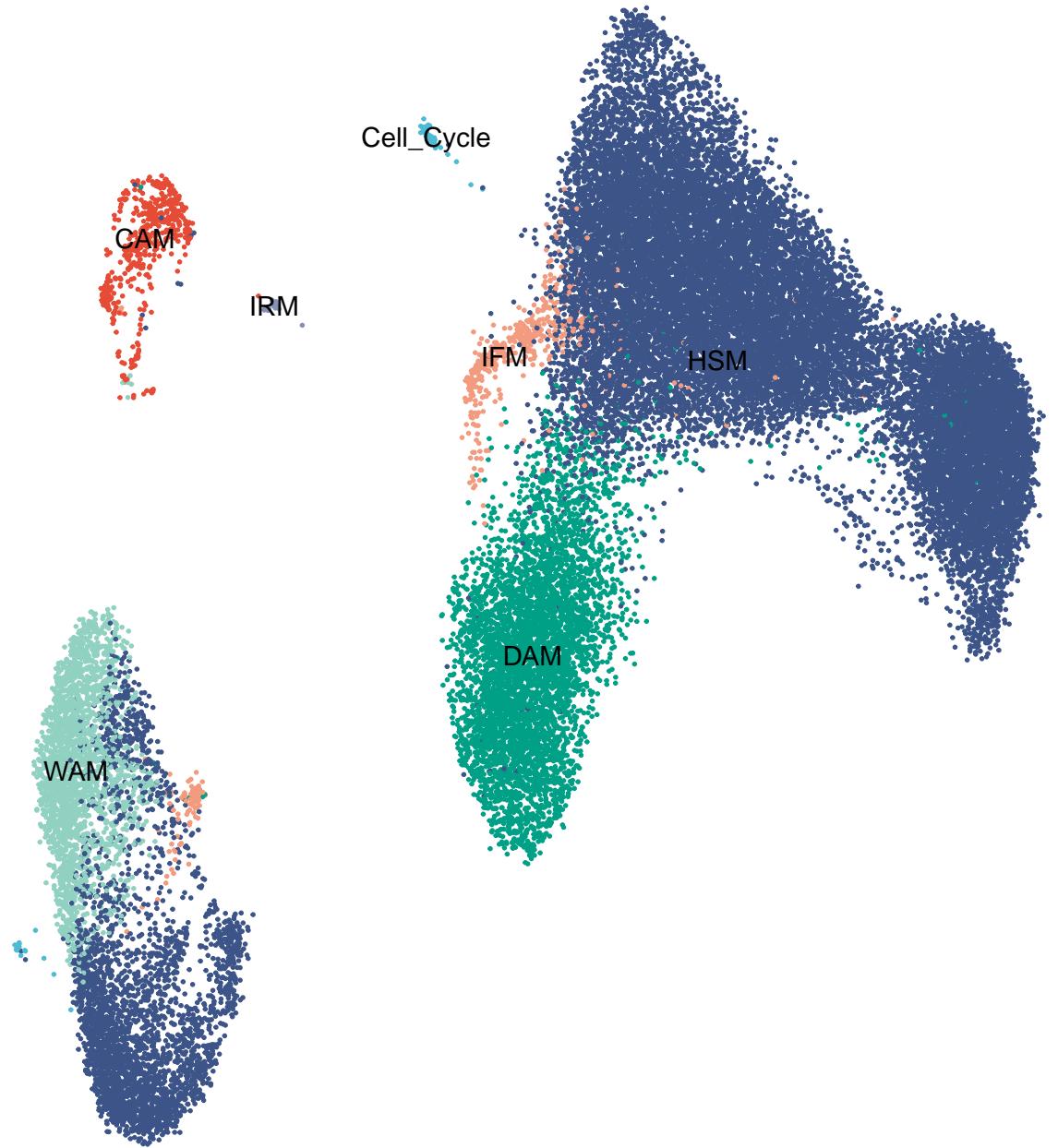
**orig.ident**



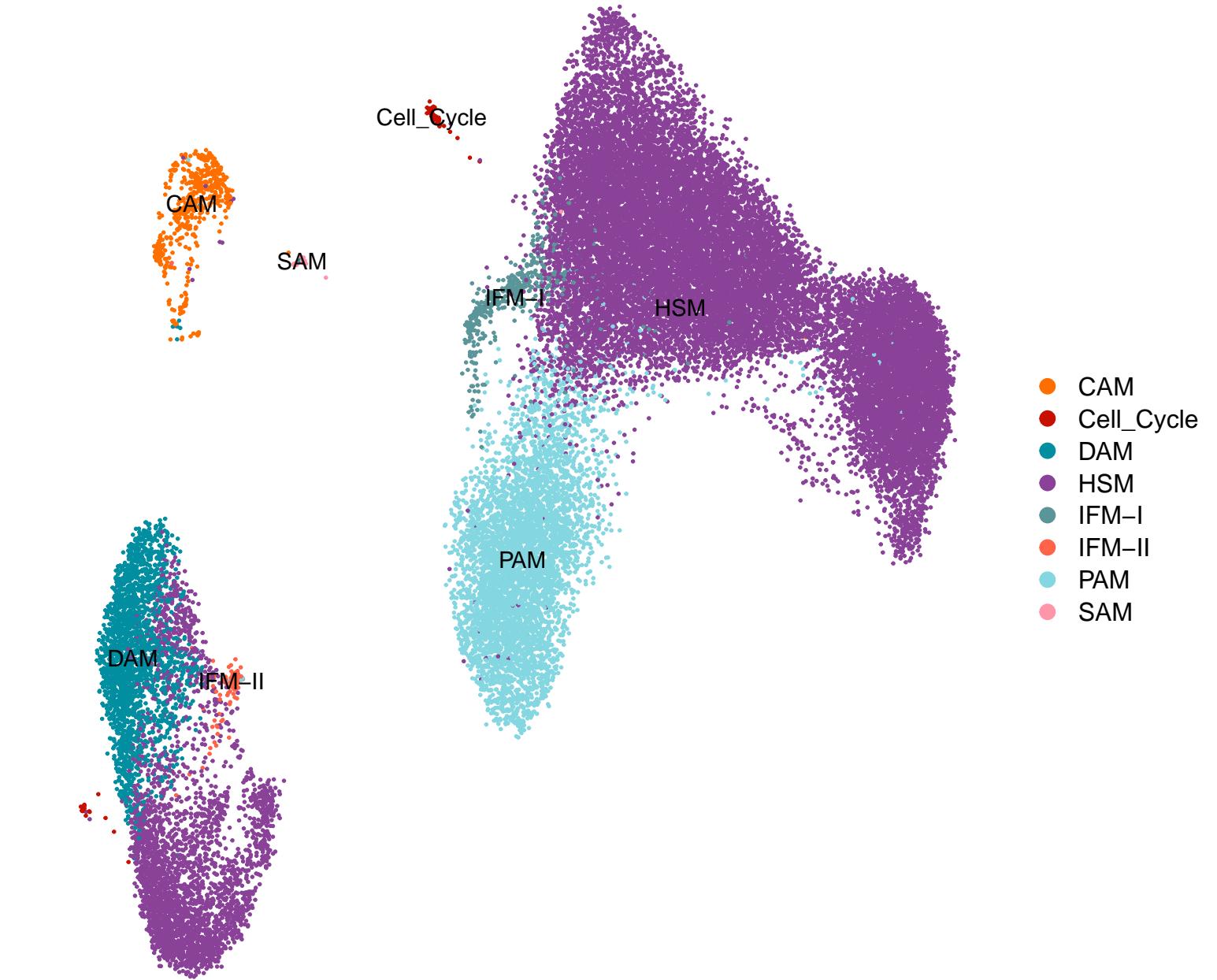
GpnmbKO\_1  
GpnmbKO\_2  
WT

Automated vs. Calibrated cell type annotation

**cluster\_auto**

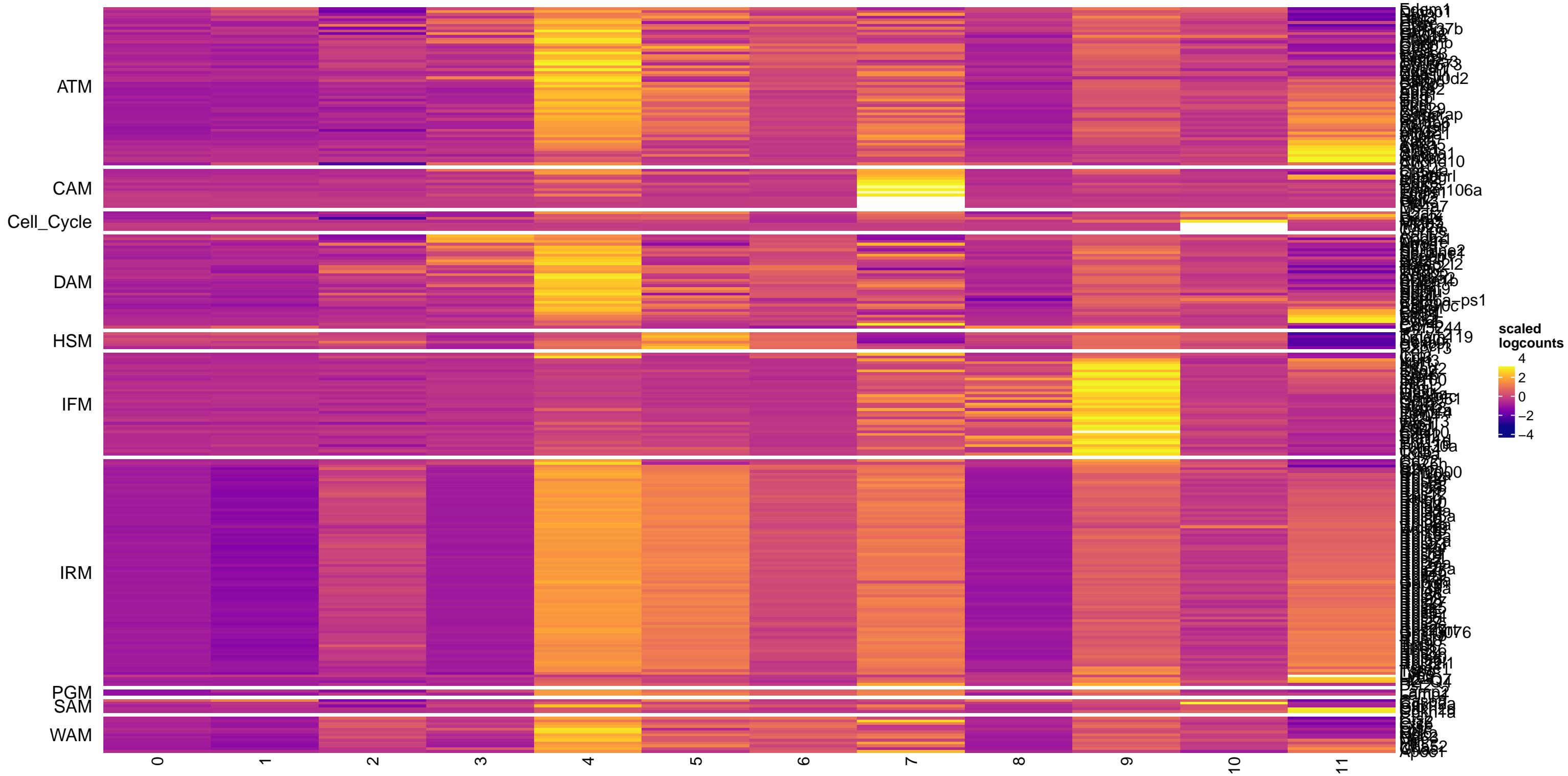


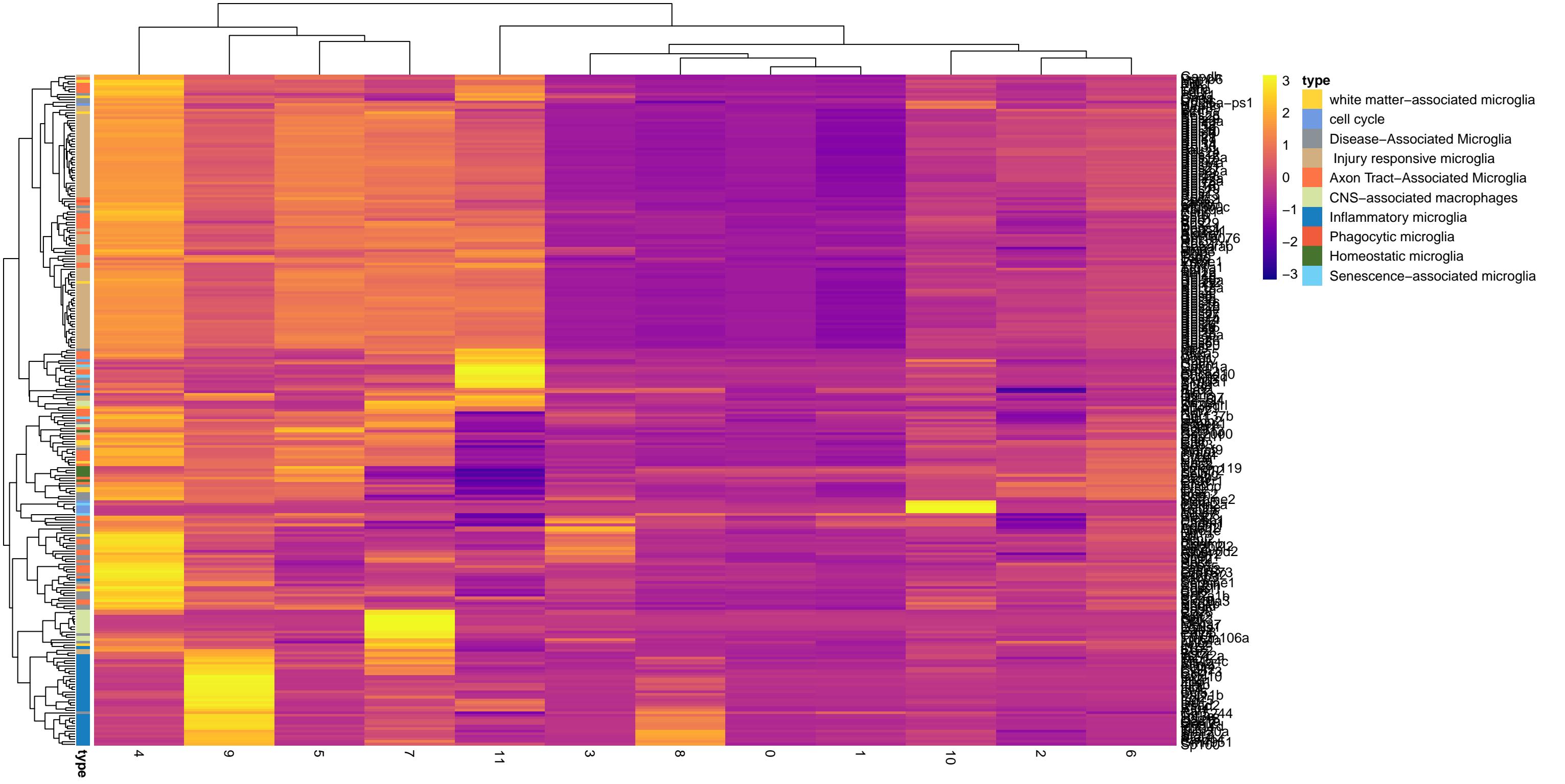
**cluster\_calibrated**

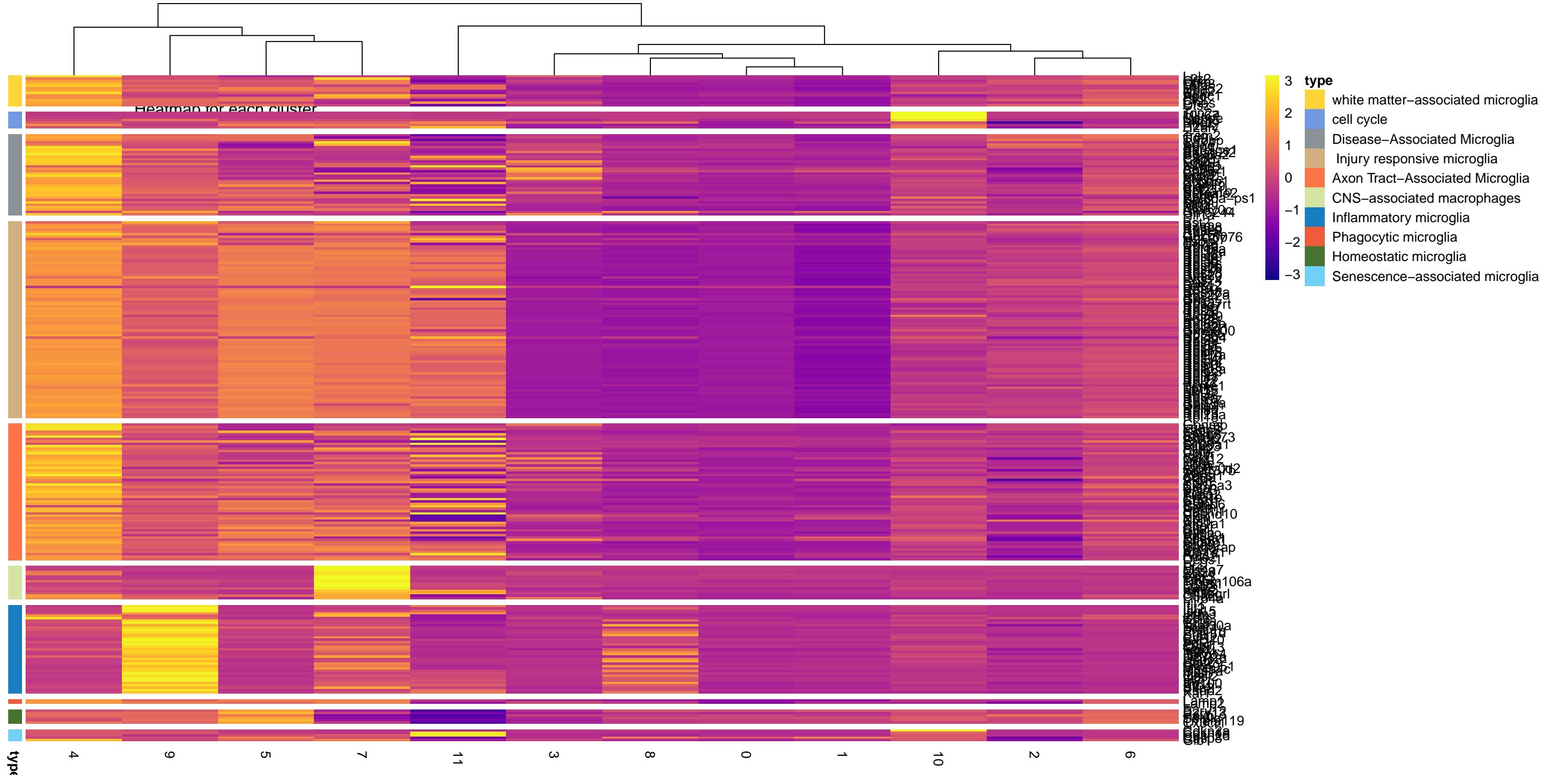


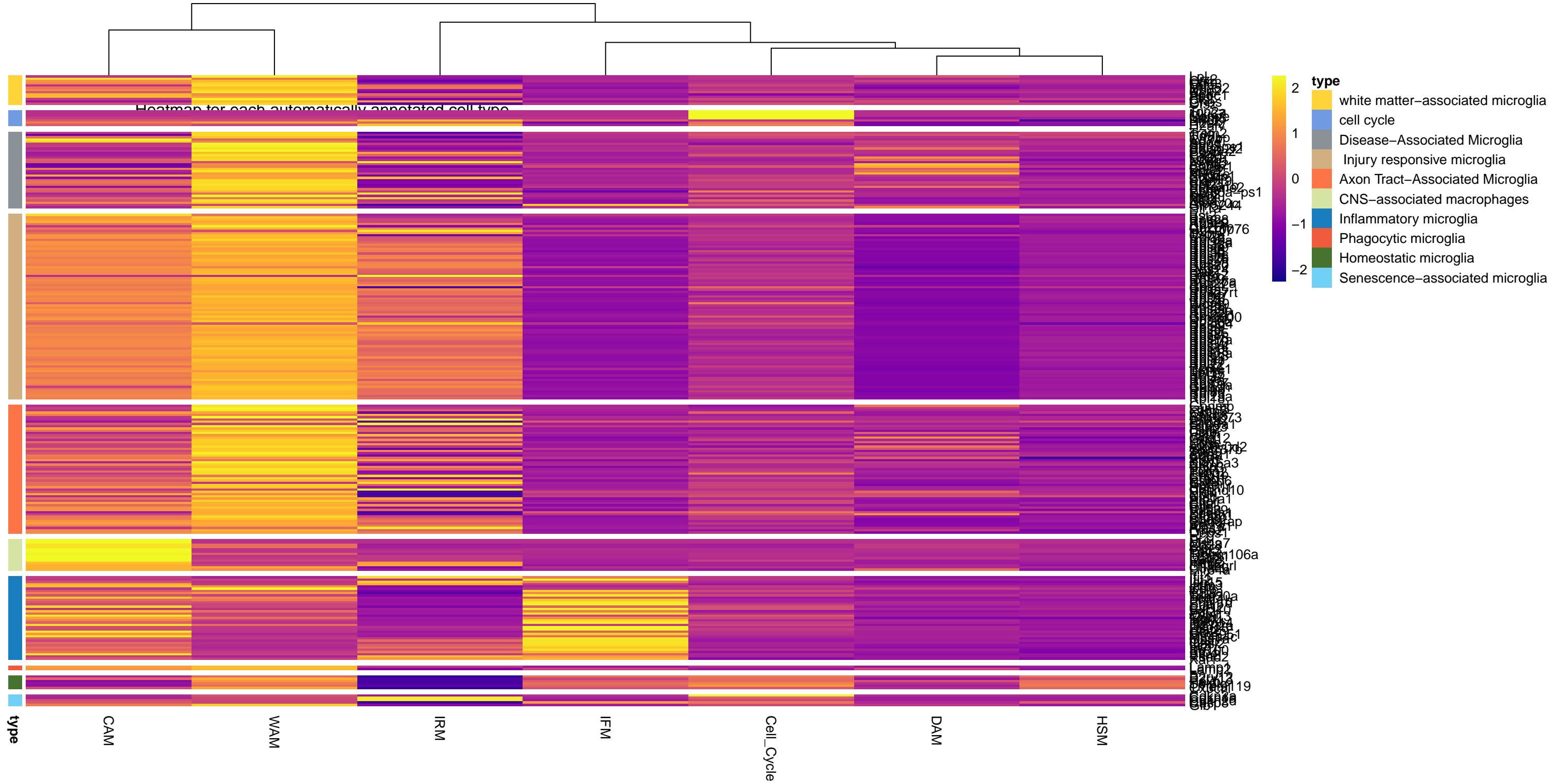
- CAM
- Cell\_Cycle
- DAM
- HSM
- IFM
- IRM
- WAM

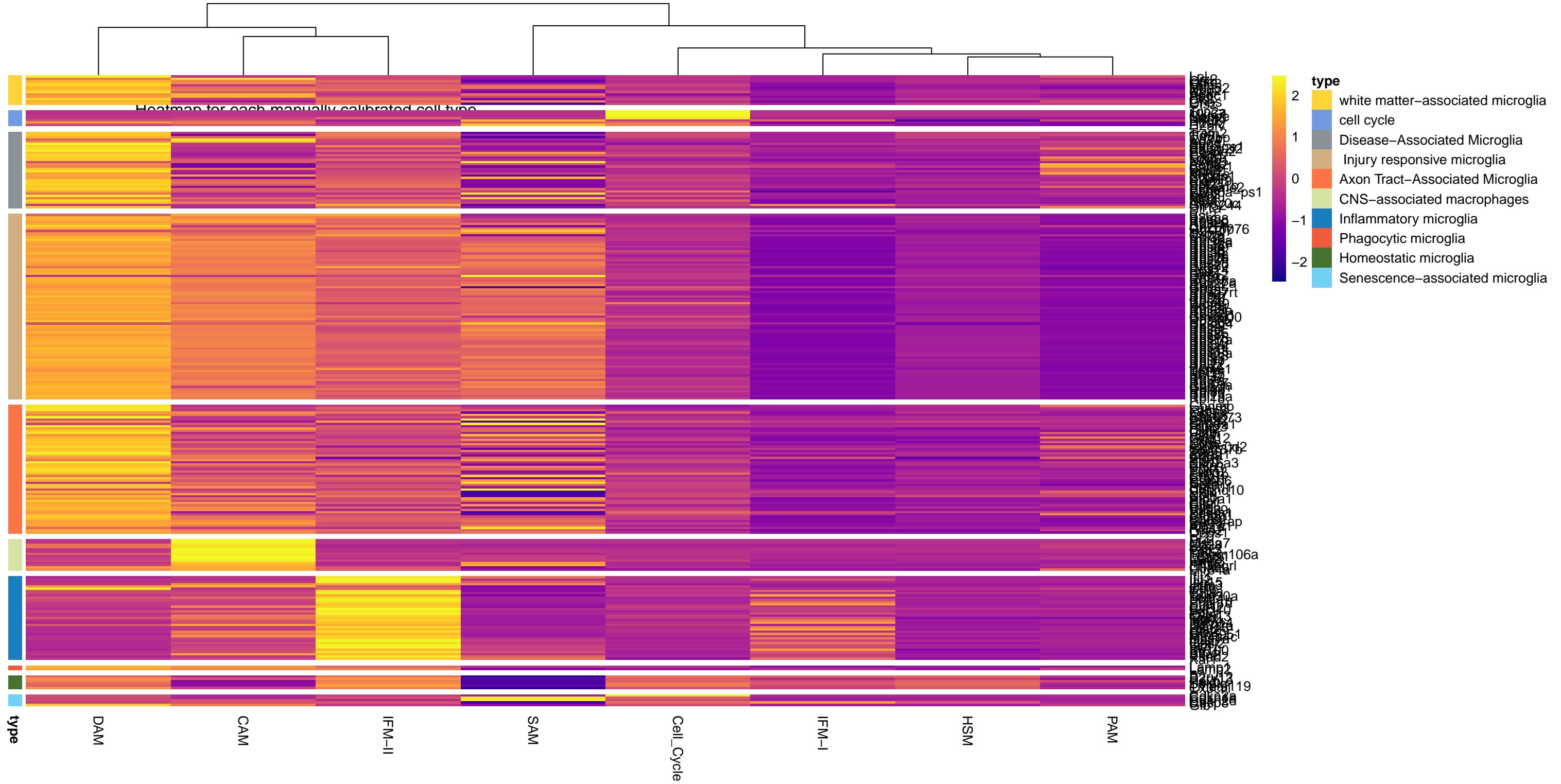
- CAM
- Cell\_Cycle
- DAM
- HSM
- IFM-I
- IFM-II
- PAM
- SAM



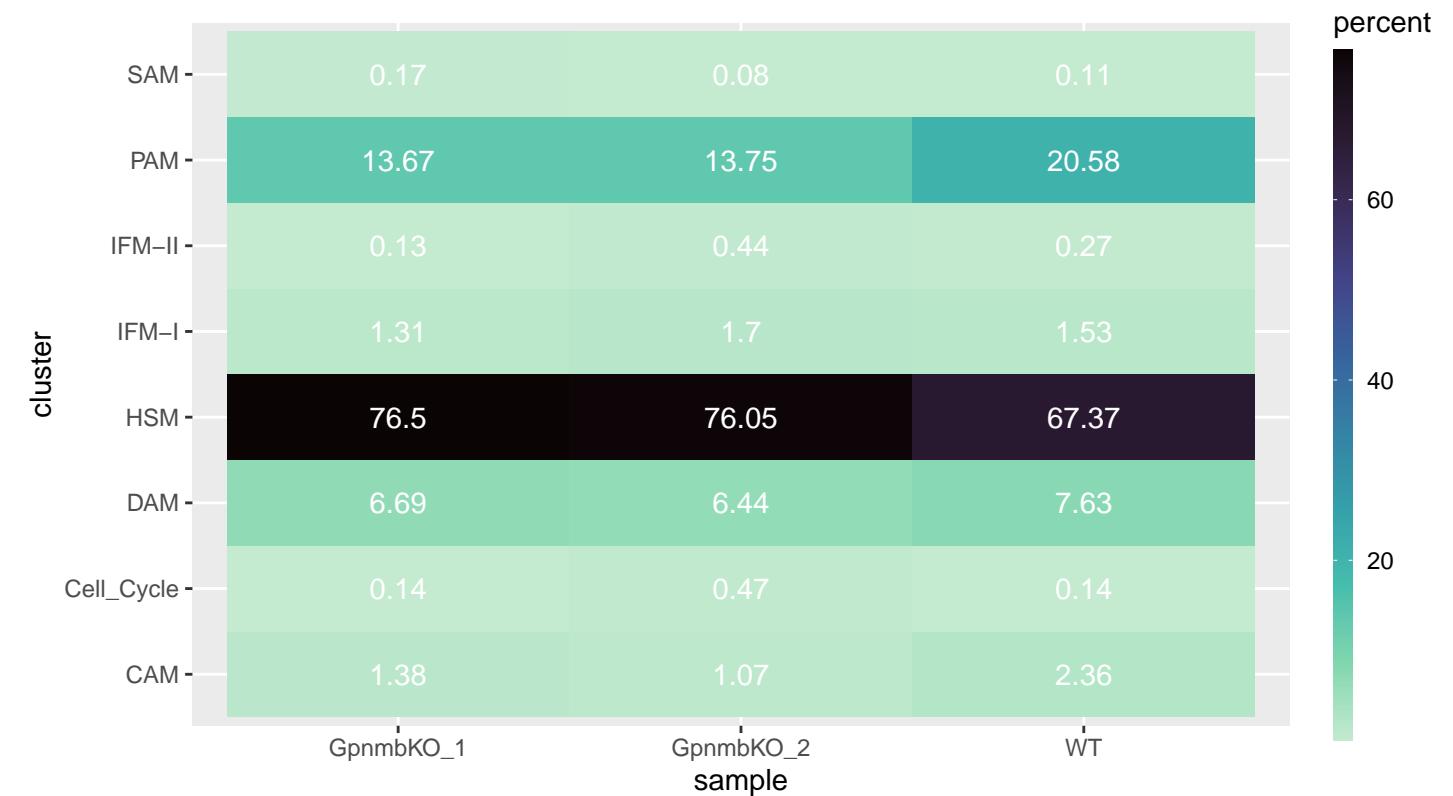








Condition composition in automated vs. calibrated cell type annotation



most likely cell type in each cluster

	<b>0</b>	<b>1</b>	<b>2</b>	<b>3</b>	<b>4</b>	<b>5</b>	<b>6</b>	<b>7</b>	<b>8</b>	<b>9</b>	<b>10</b>	<b>11</b>
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	IFM	CAM	DAM	PGM	PGM	ATM	DAM	WAM	Cell_Cycle	IRM	DAM	ATM

most expressed genes in each cluster

	<b>0</b>	<b>1</b>	<b>2</b>	<b>3</b>	<b>4</b>	<b>5</b>	<b>6</b>	<b>7</b>	<b>8</b>	<b>9</b>	<b>10</b>	<b>11</b>
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	Tpt1
3	Apoe	Apoe	Hexb	Hexb	Hexb	Cx3cr1	Apoe	Ctsd	Apoe	Apoe	Apoe	Ctsd
4	Cx3cr1	Cx3cr1	Tyrobp	Cadm1	Tyrobp	Rps29	Cx3cr1	Rps29	Cx3cr1	Tyrobp	Cx3cr1	Fau
5	Tyrobp	P2ry12	Trem2	Apbb2	Ctsb	Tyrobp	Tyrobp	Ctsb	P2ry12	Cx3cr1	Tyrobp	Rps29
6	P2ry12	Selplg	Ctsb	Ctsb	Trem2	P2ry12	Ctsb	Ftl1	Tyrobp	Ctsb	P2ry12	Hexb
7	Ctsb	Cadm1	Cx3cr1	Tyrobp	Ctsz	Selplg	Trem2	Tyrobp	Ctsb	B2m	Trem2	Gnas
8	Selplg	Tyrobp	Ctsz	Cd9	Rps29	Trem2	Ctsz	Tpt1	Trem2	Trem2	Ctsz	Rps8
9	Trem2	Ctsb	Rps29	Trem2	Cd9	Fau	Cd9	B2m	Selplg	Rps29	Ctsb	Rps21
10	Ctsz	Trem2	B2m	Cx3cr1	Cx3cr1	B2m	B2m	Hexb	Trim30a	Ctsz	Cd9	Rps24
11	Rps29	Ctsz	Cd9	Ctsz	B2m	Tpt1	Rps29	Fau	Cadm1	Cd9	Selplg	Rpl13
12	Cd9	Cd9	Tpt1	Myo1e	Fau	Ctsb	P2ry12	Rps24	B2m	Fau	Rps29	Rpl27a
13	B2m	B2m	Fau	B2m	Tpt1	Ctsz	Fau	Cx3cr1	Ctsz	Ly6e	B2m	B2m
14	Cadm1	Rps29	Rps12	P2ry12	Ctsl	Apoe	Selplg	Rps21	Cd9	P2ry12	Cadm1	Rpl35a
15	Tpt1	Fau	P2ry12	Gnas	Ftl1	Cd9	Ctsl	Rps12	Rps29	Tpt1	Grn	Rps12
16	Fau	Grn	Rps24	Rps29	Rps12	Rps21	Tpt1	Rpl37a	Grn	Selplg	Fau	Rpl41
17	Rps24	Tpt1	Ctsl	Fau	Rps24	Rps24	Ftl1	Dab2	Tpt1	Grn	Tpt1	Rps14
18	Rps12	Rps21	Selplg	Ctsl	Rps21	Rps12	Grn	Rpl35a	Fau	Ctsl	Rps12	Rps16
19	Rps21	Apbb2	Rps21	Selplg	Rpl21	Rpl13	Rps21	Rpl13	Ly6e	Rps12	Rps24	Rpl37a
20	Grn	Rps24	Ftl1	Tpt1	Rpl13	Ftl1	Rpl13	Rps8	Rps24	Rps24	Rps21	Rps27

most expressed genes in each calibrated cell type

	<b>CAM</b>	<b>Cell_Cycle</b>	<b>DAM</b>	<b>HSM</b>	<b>IFM-I</b>	<b>IFM-II</b>	<b>PAM</b>	<b>SAM</b>
1	Apoe	Ctsd	Ctsd	Ctsd	Ctsd	Ctsd	Ctsd	Apoe
2	Lyz2	Hexb	Apoe	Hexb	Hexb	Hexb	Apoe	Tpt1
3	Ctsd	Apoe	Hexb	Apoe	Apoe	Apoe	Hexb	Ctsd
4	Rps29	Cx3cr1	Tyrobp	Cx3cr1	Cx3cr1	Tyrobp	Cadm1	Fau
5	Ctsb	Tyrobp	Ctsb	Tyrobp	P2ry12	Cx3cr1	Apbb2	Rps29
6	Ftl1	P2ry12	Trem2	P2ry12	Tyrobp	Ctsb	Ctsb	Hexb
7	Tyrobp	Trem2	Ctsz	Ctsb	Ctsb	B2m	Tyrobp	Gnas
8	Tpt1	Ctsz	Rps29	Trem2	Trem2	Trem2	Cd9	Rps8
9	B2m	Ctsb	Cd9	Ctsz	Selplg	Rps29	Trem2	Rps21
10	Hexb	Cd9	Cx3cr1	Selplg	Trim30a	Ctsz	Cx3cr1	Rps24
11	Fau	Selplg	B2m	Rps29	Cadm1	Cd9	Ctsz	Rpl13
12	Rps24	Rps29	Fau	B2m	B2m	Fau	Myo1e	Rpl27a
13	Cx3cr1	B2m	Tpt1	Cd9	Ctsz	Ly6e	B2m	B2m
14	Rps21	Cadm1	Ctsl	Fau	Cd9	P2ry12	P2ry12	Rpl35a
15	Rps12	Grn	Ftl1	Tpt1	Rps29	Tpt1	Gnas	Rps12
16	Rpl37a	Fau	Rps12	Cadm1	Grn	Selplg	Rps29	Rpl41
17	Dab2	Tpt1	Rps24	Rps12	Tpt1	Grn	Fau	Rps14
18	Rpl35a	Rps12	Rps21	Rps24	Fau	Ctsl	Ctsl	Rps16
19	Rpl13	Rps24	Rpl21	Rps21	Ly6e	Rps12	Selplg	Rpl37a
20	Rps8	Rps21	Rpl13	Grn	Rps24	Rps24	Tpt1	Rps27