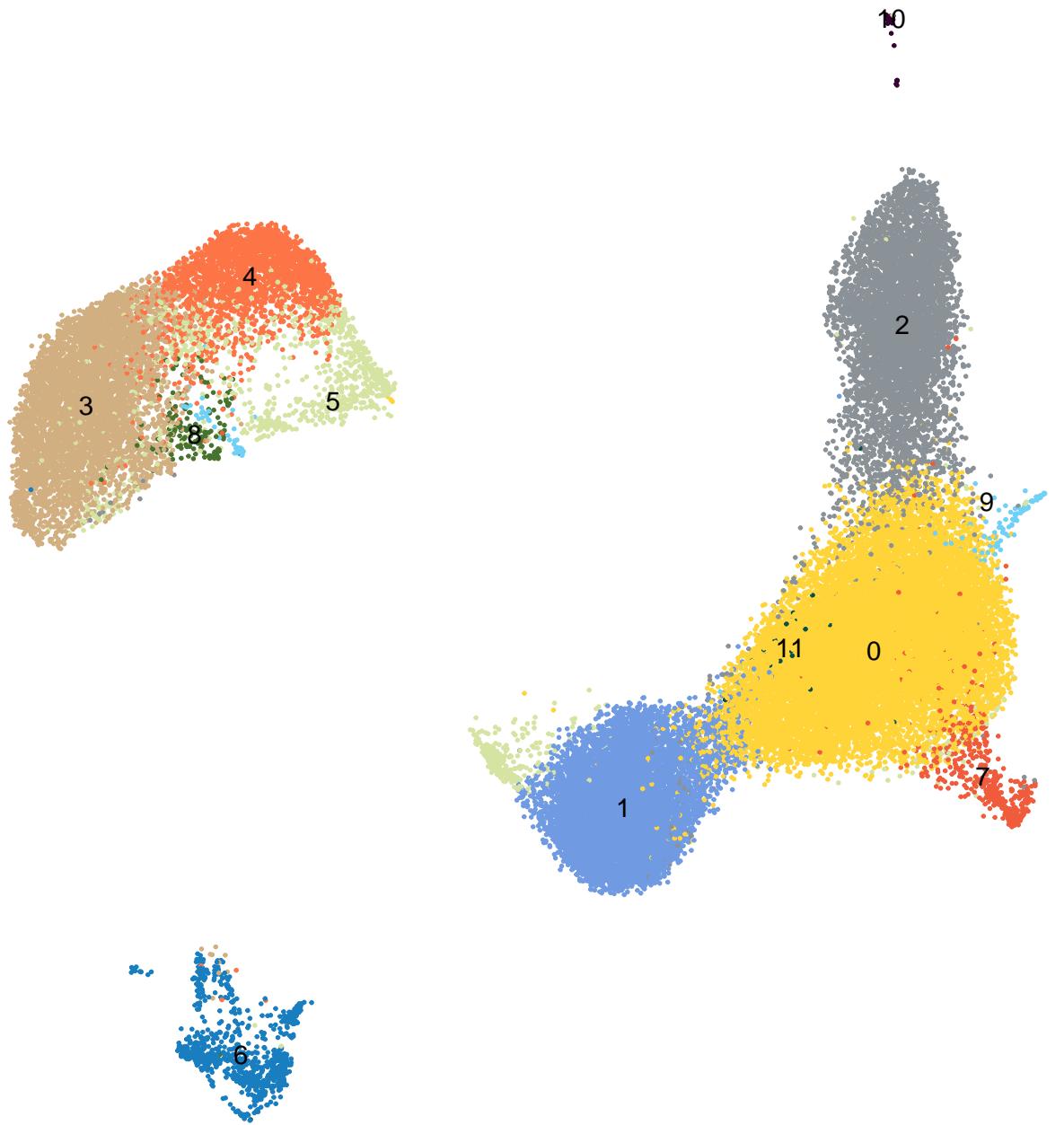
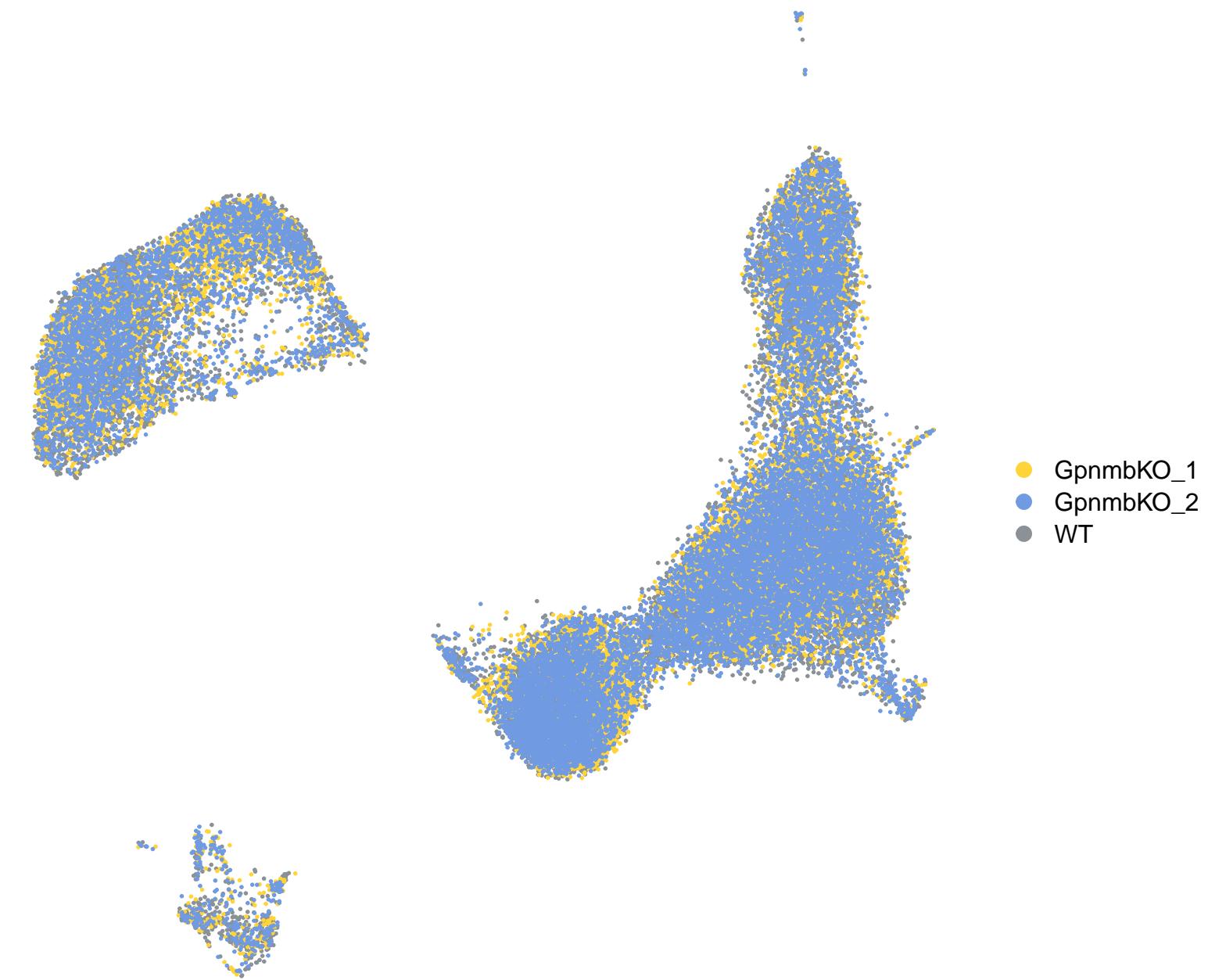


Clusters

seurat_clusters

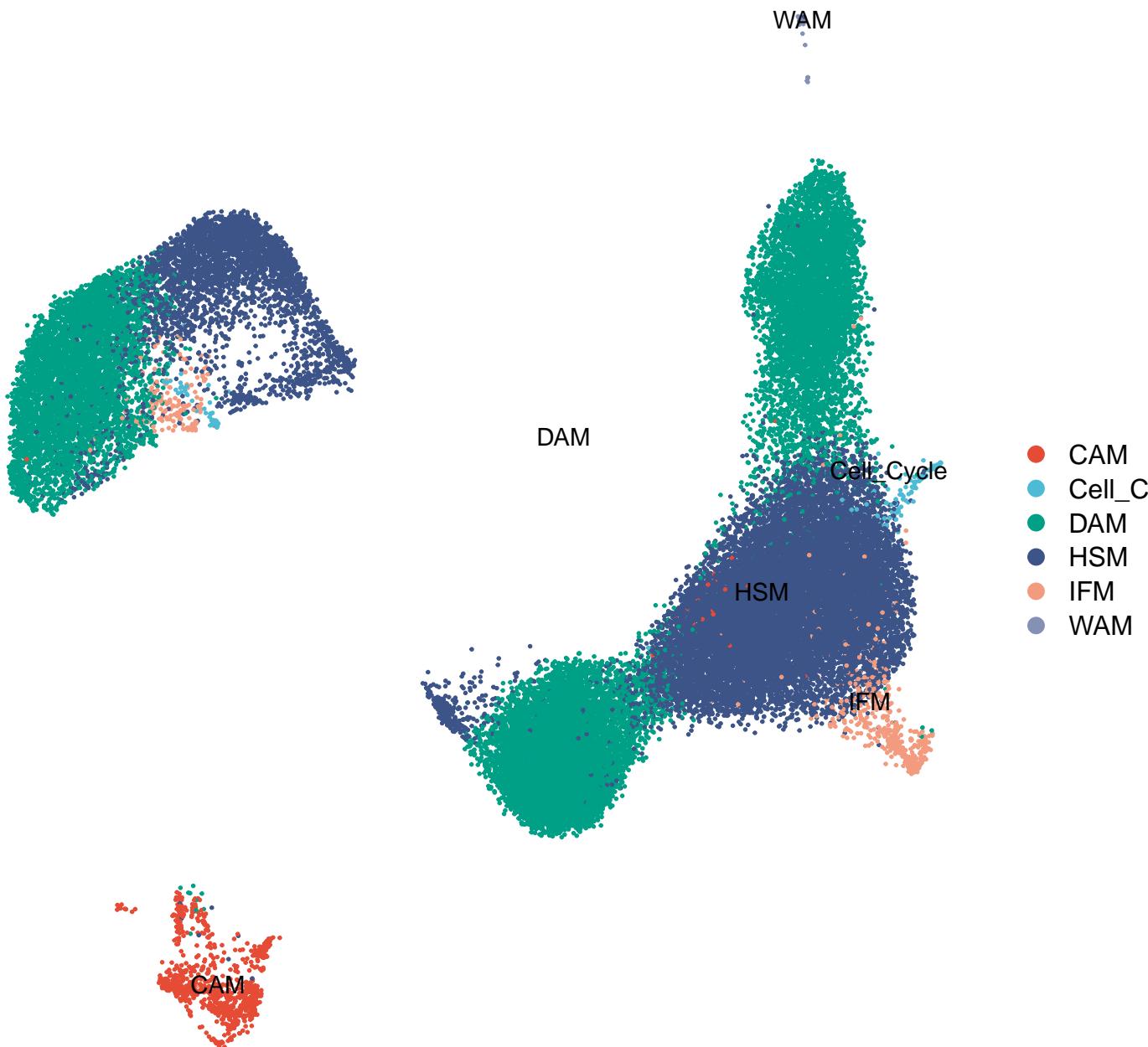


orig.ident

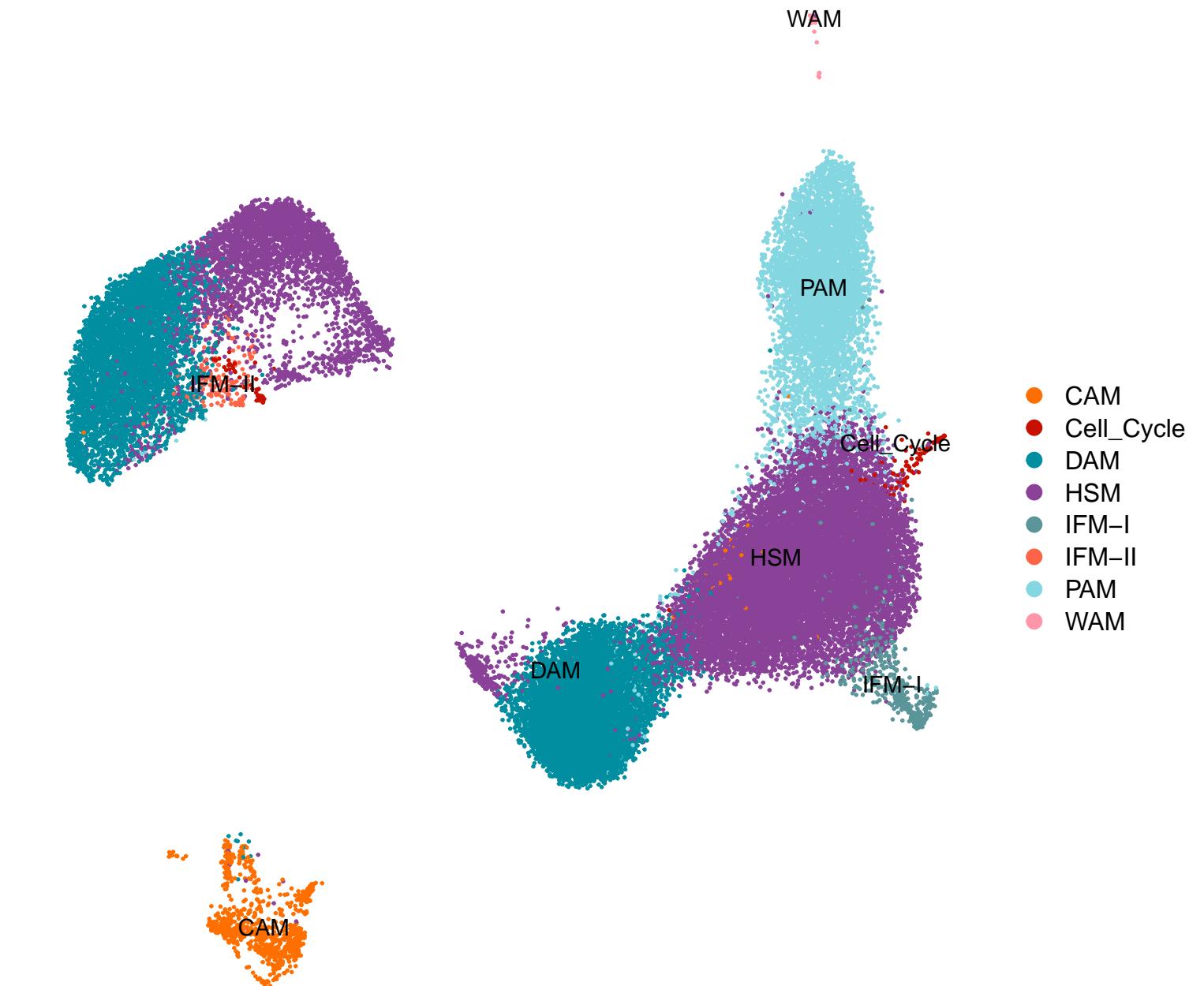


Automated vs. Calibrated cell type annotation

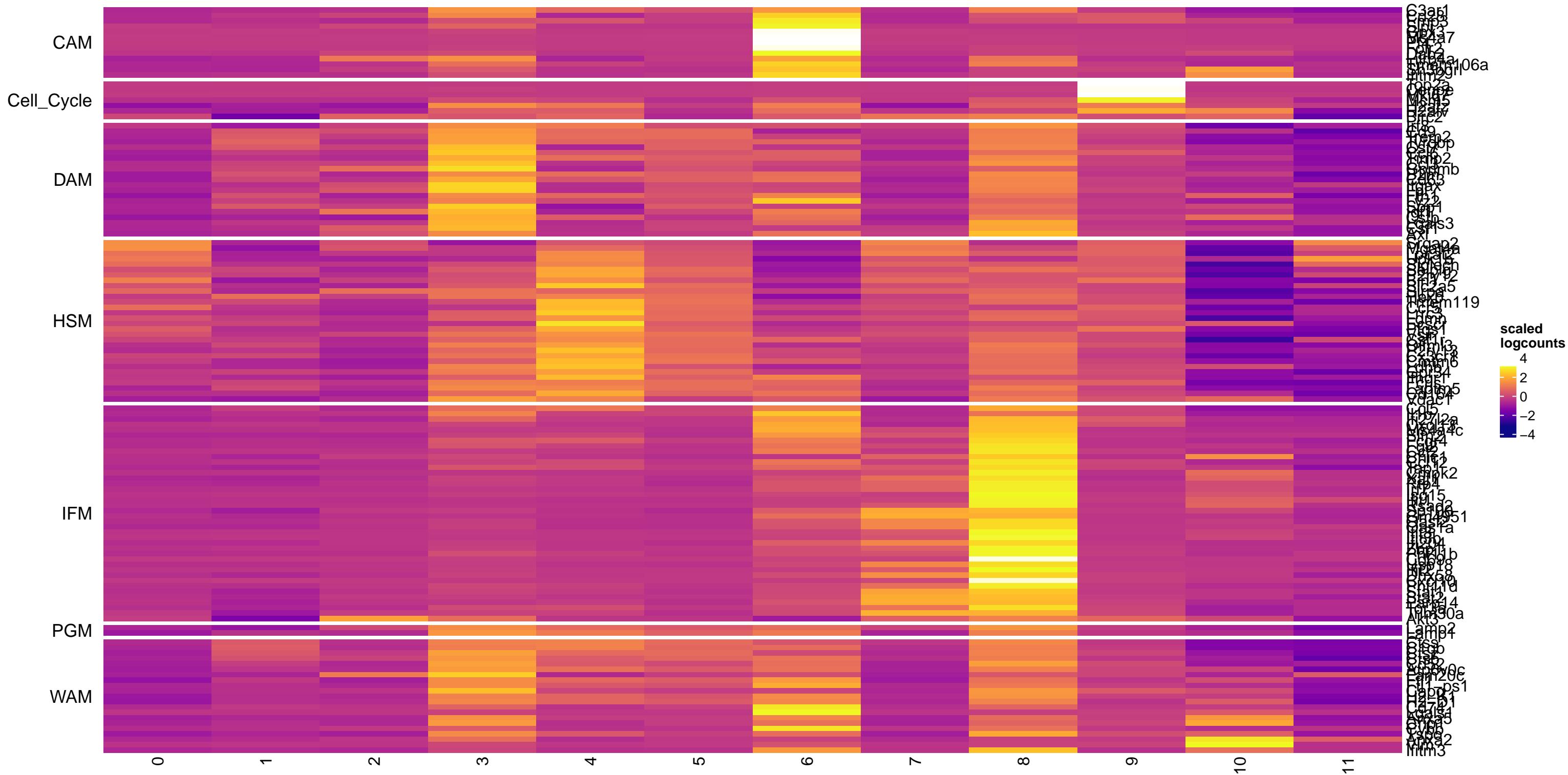
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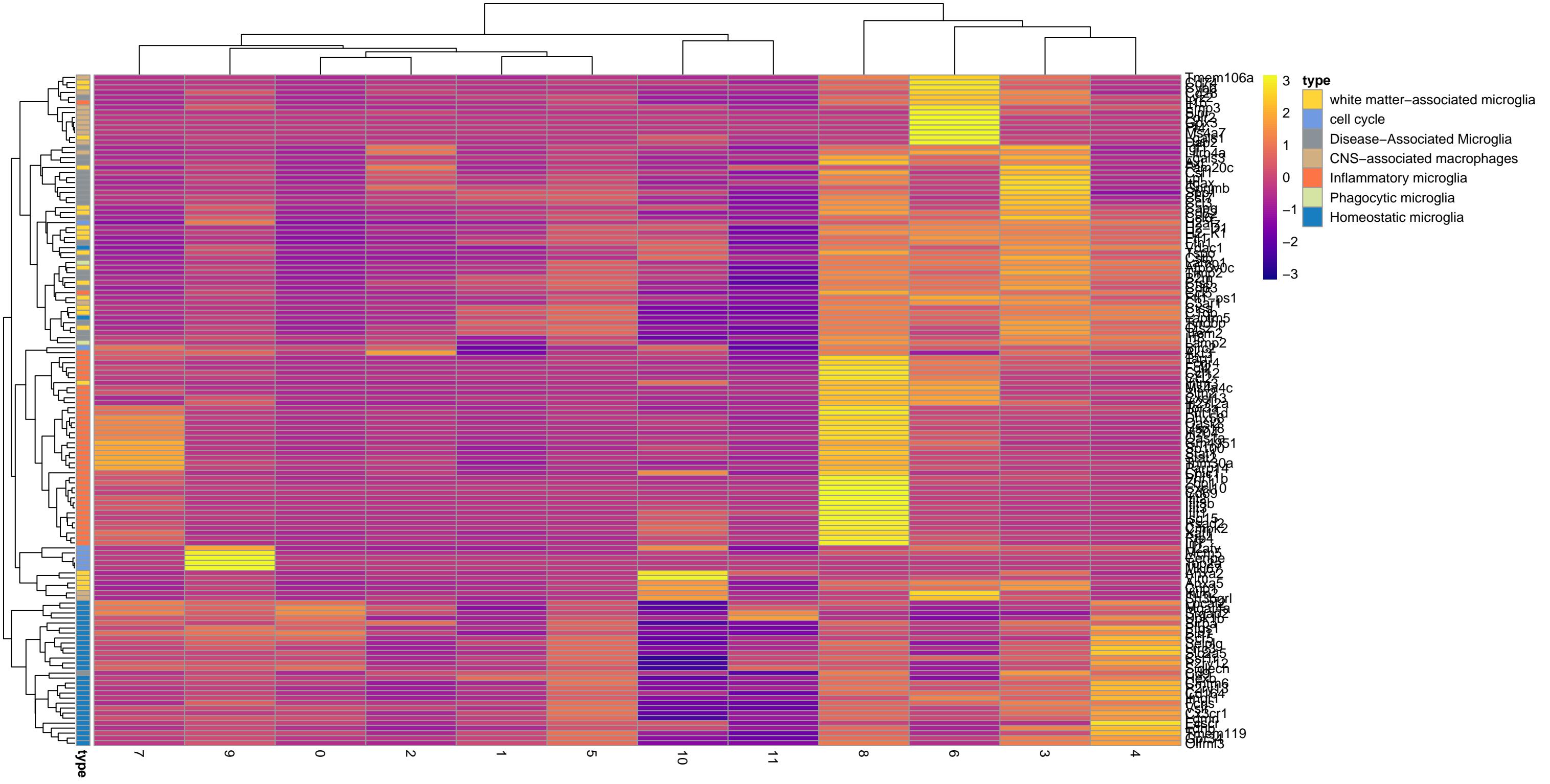


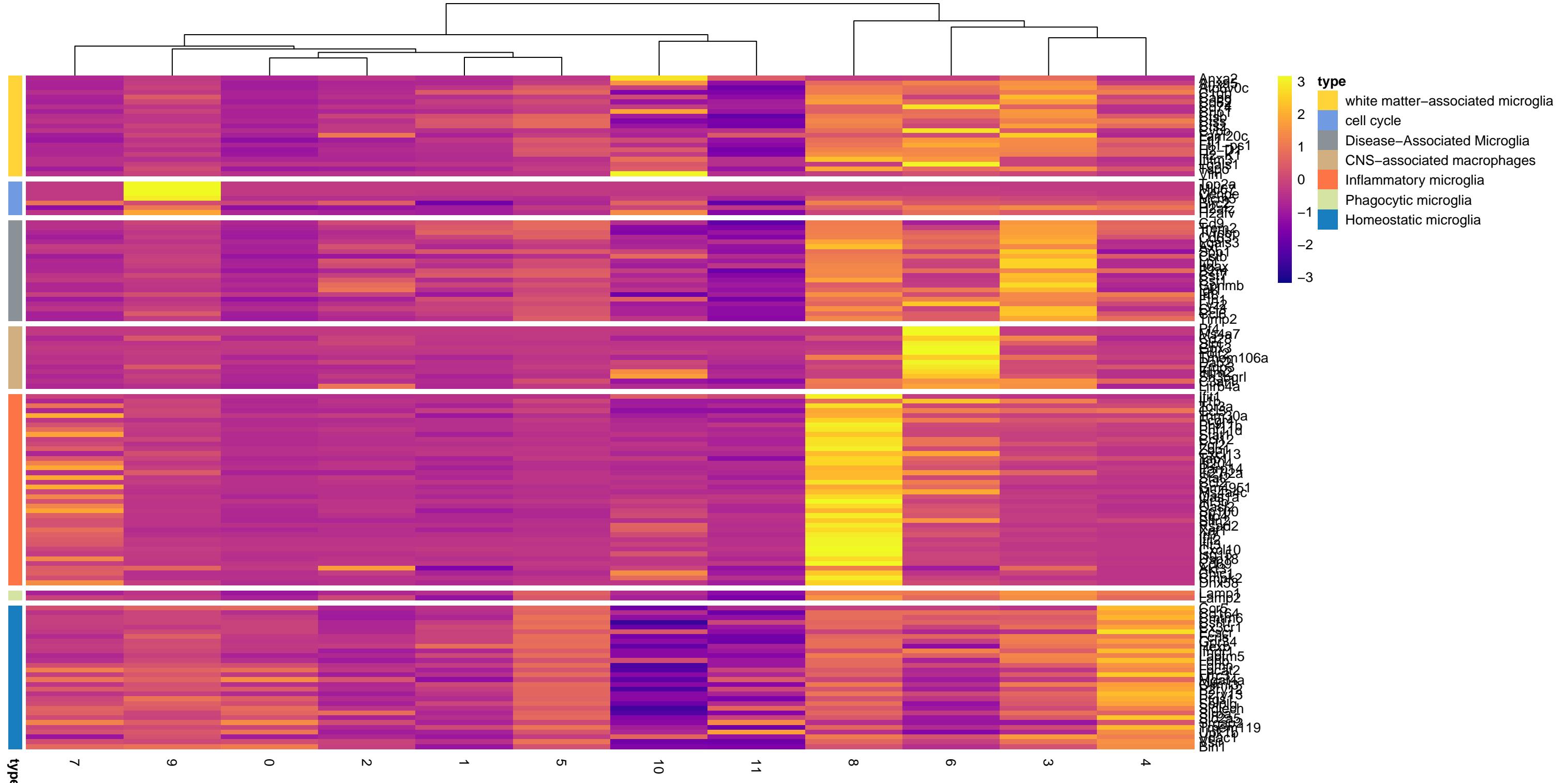
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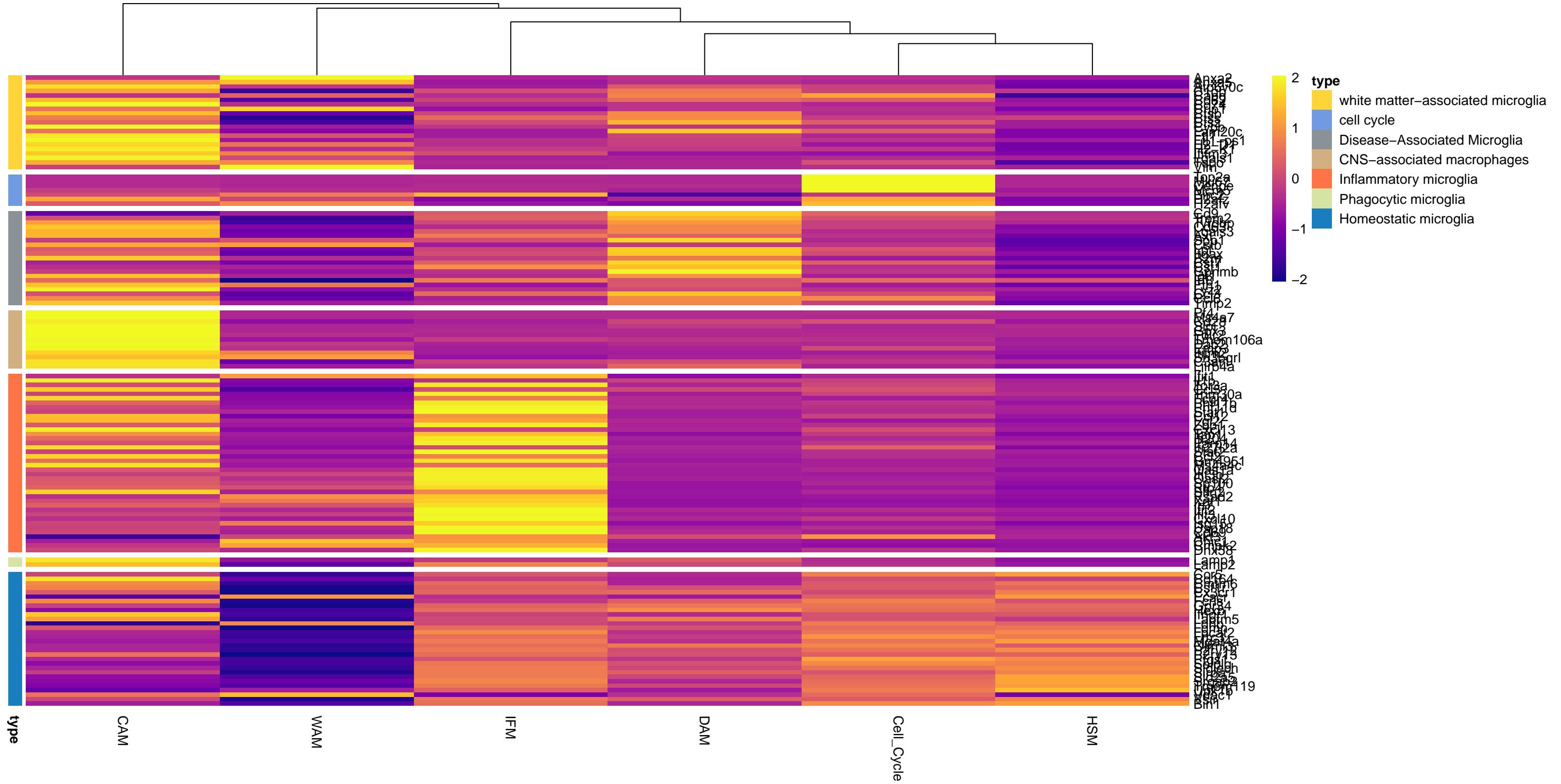


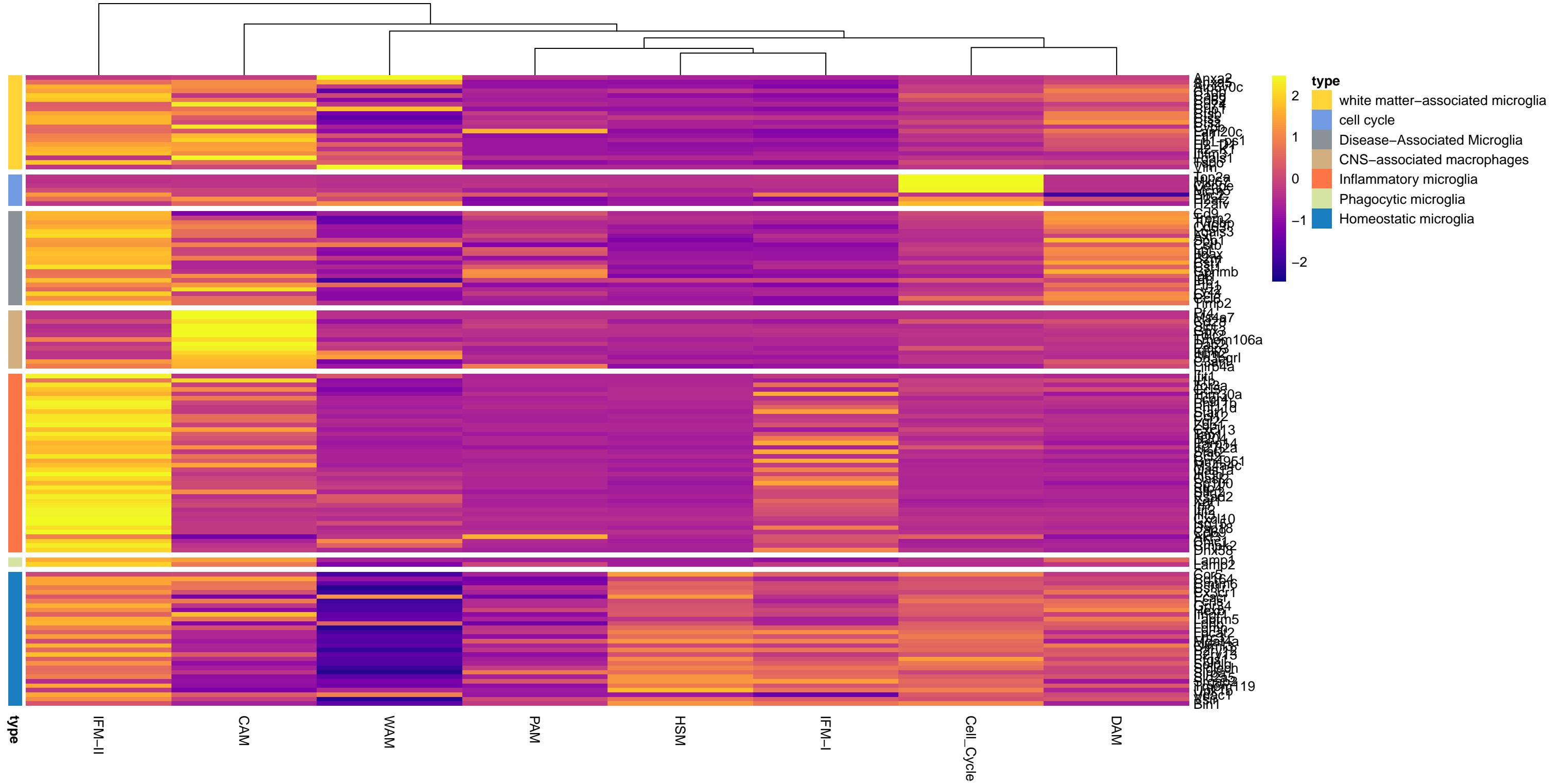
- CAM
- Cell_Cycle
- DAM
- HSM
- IFM-I
- IFM-II
- PAM
- WAM



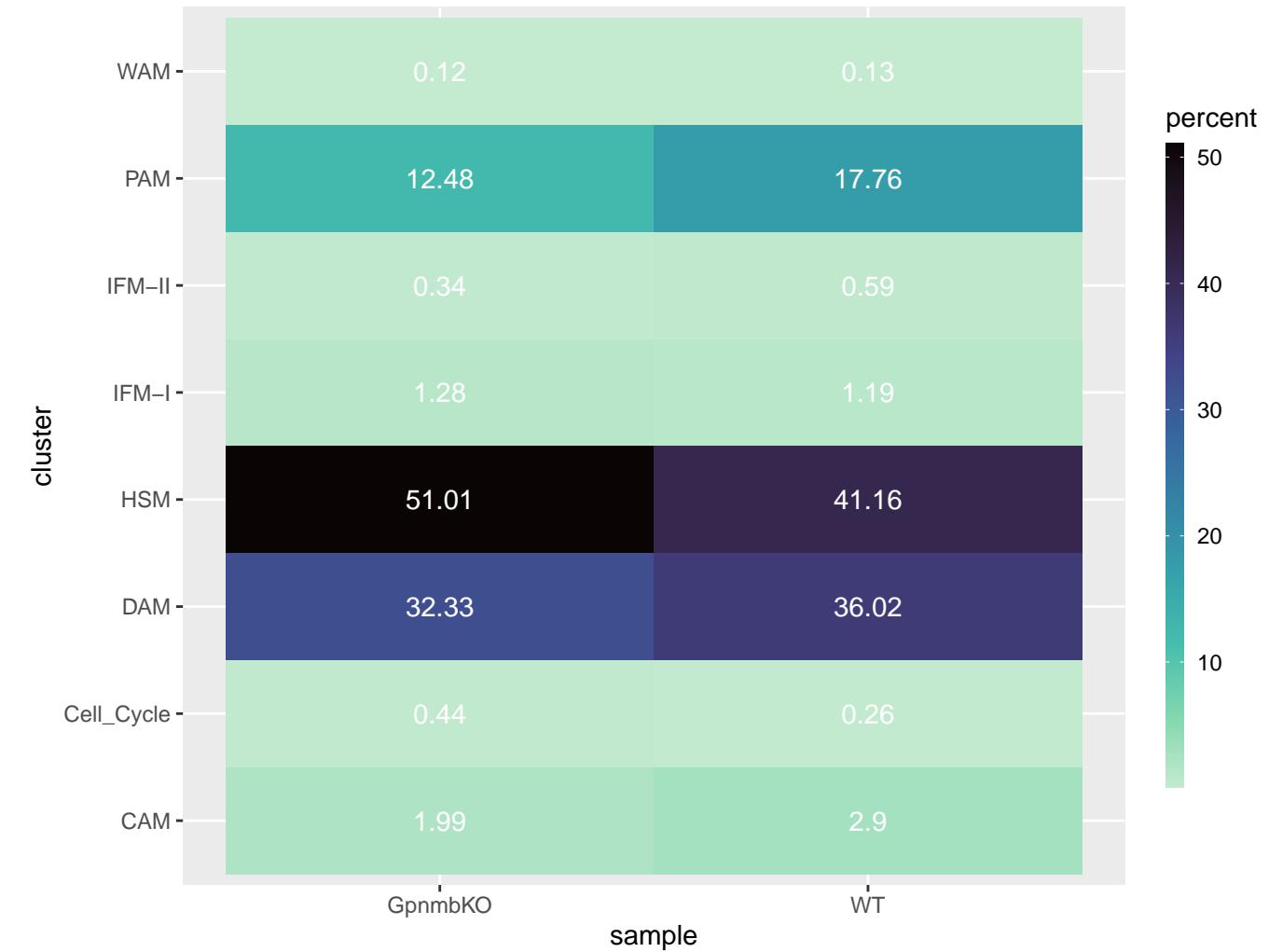
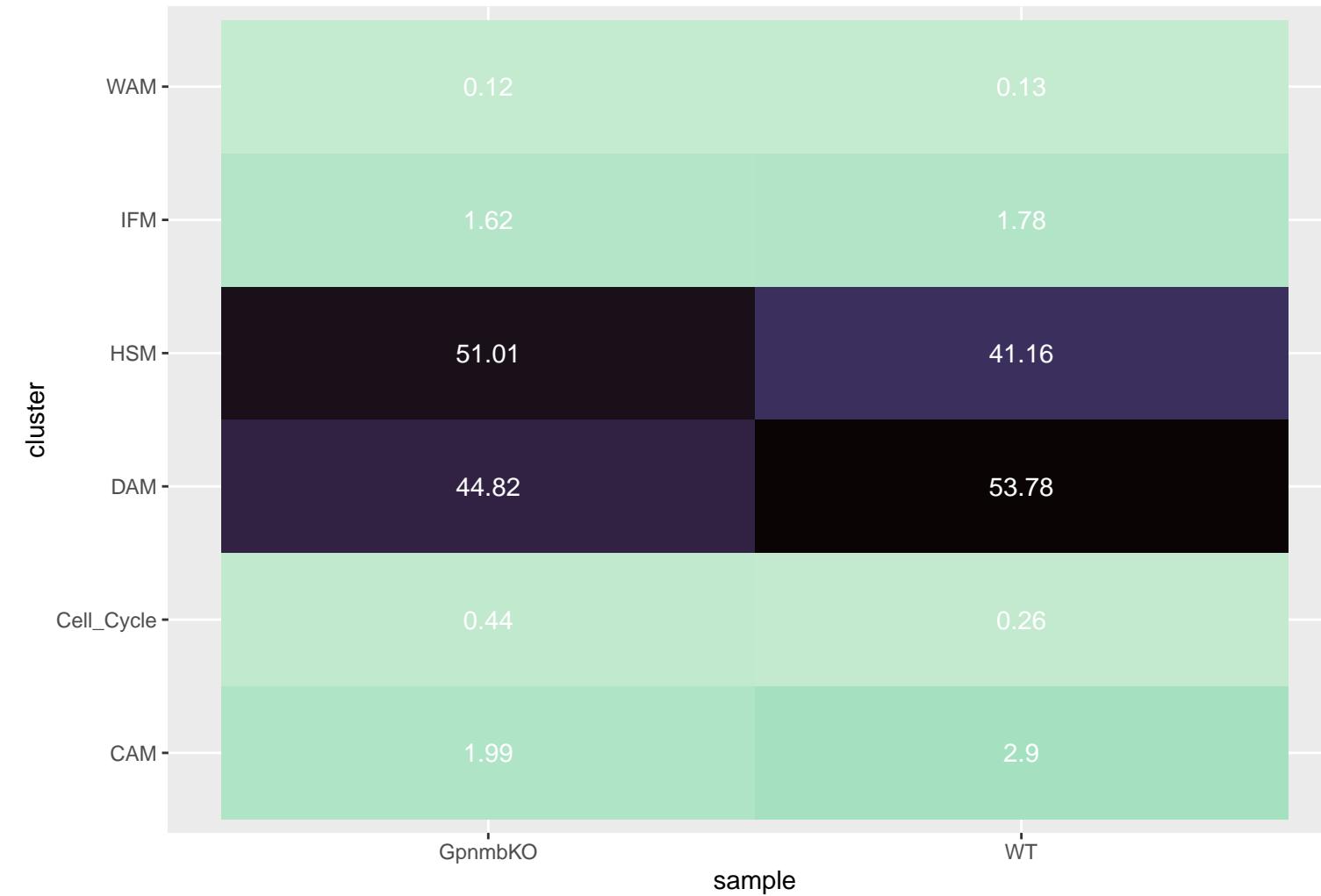








Condition composition in automated vs. calibrated cell type annotation



most likely cell type in each cluster

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

most expressed genes in each cluster

	0	1	2	3	4	5	6	7	8	9	10	11
1	Srgap2	Hexb	Hexb	Hexb	Hexb	Hexb	Lyz2	Hexb	Hexb	Hexb	Fth1	Srgap2
2	Hexb	C1qb	Srgap2	C1qb	C1qb	C1qb	C1qb	Srgap2	C1qb	Srgap2	Hexb	Hexb
3	C1qb	Ctss	C1qb	Tyrobp	Ctss	Ctss	Fth1	Ctss	Ctss	C1qb	B2m	Csf1r
4	Ctss	Tyrobp	Ctss	Ctss	Cx3cr1	Tyrobp	Ftl1	C1qb	Tyrobp	Ctss	Ftl1	Siglech
5	Lgmn	Fth1	Ctsb	Fth1	Fth1	Cx3cr1	Ctss	Lgmn	Fth1	Lgmn	C1qb	P2ry12
6	Csf1r	Trem2	Tyrobp	Ctsb	Csf1r	Ctsb	Ctsb	Csf1r	Ctsb	Csf1r	Ctss	Cx3cr1
7	Cx3cr1	Ctsb	Sirpa	Trem2	Tyrobp	Fth1	Tyrobp	Cx3cr1	B2m	Tyrobp	Srgap2	C1qb
8	Siglech	Cx3cr1	Cd9	Ctsz	Lgmn	Trem2	Hexb	P2ry12	Trem2	Fth1	Ctsb	Lgmn
9	P2ry12	Ctsz	Csf1r	B2m	P2ry12	Csf1r	B2m	Siglech	Ctsz	Cx3cr1	Cd9	Tyrobp
10	Sirpa	B2m	Trem2	Cd9	Trem2	Lgmn	Csf1r	Tyrobp	Cx3cr1	Ctsz	H2-D1	Ctss
11	Tyrobp	Csf1r	Lgmn	Ftl1	Srgap2	Ctsz	Cx3cr1	Lpcat2	Cd9	Trem2	Tyrobp	Selplg
12	Lpcat2	Cd9	Cx3cr1	Cx3cr1	B2m	Srgap2	Cd74	Sirpa	Csf1r	Ctsb	Ctsz	Lpcat2
13	Selplg	Lgmn	Ctsz	Csf1r	Selplg	B2m	Lgmn	Ctsb	Lgmn	P2ry12	Cx3cr1	Fth1
14	Ctsb	Srgap2	Fth1	Laptm5	Ctsb	Cd9	Laptm5	Trem2	Laptm5	Siglech	Trem2	Trem2
15	Bin1	Laptm5	B2m	Lyz2	Laptm5	Laptm5	H2-D1	Trim30a	Ftl1	Selplg	Csf1r	Mgat4a
16	Trem2	P2ry12	P2ry12	Lgmn	Ctsz	P2ry12	Ctsz	Fth1	Srgap2	Cd9	Lgmn	Sirpa
17	Fth1	Selplg	Siglech	Cst7	Cd9	Ftl1	Trem2	Selplg	Selplg	Fcrls	Laptm5	Ctsz
18	Ctsz	Ftl1	Akt3	Cd63	Siglech	Selplg	Fcrls	Ctsz	H2-D1	B2m	H2-K1	Laptm5
19	Mgat4a	Fcrls	Laptm5	Fcrls	Ftl1	Fcrls	Srgap2	B2m	Lyz2	Laptm5	Timp2	Ftl1
20	Cd9	Siglech	Fcrls	H2-D1	Gpr34	Sirpa	Dab2	Cd9	Sirpa	Lpcat2	Lamp1	B2m

most expressed genes in each calibrated cell type

	CAM	Cell_Cycle	DAM	HSM	IFM-I	IFM-II	PAM	WAM
1	Lyz2	Hexb	Hexb	Hexb	Hexb	Hexb	Hexb	Fth1
2	C1qb	Srgap2	C1qb	Srgap2	Srgap2	C1qb	Srgap2	Hexb
3	Fth1	C1qb	Ctss	C1qb	Ctss	Ctss	C1qb	B2m
4	Ftl1	Ctss	Tyrobp	Ctss	C1qb	Tyrobp	Ctss	Ftl1
5	Ctss	Lgmn	Fth1	Cx3cr1	Lgmn	Fth1	Ctsb	C1qb
6	Tyrobp	Csf1r	Trem2	Csf1r	Csf1r	Ctsb	Tyrobp	Ctss
7	Ctsb	Tyrobp	Ctsb	Lgmn	Cx3cr1	B2m	Sirpa	Srgap2
8	Hexb	Fth1	Ctsz	P2ry12	P2ry12	Trem2	Cd9	Ctsb
9	B2m	Cx3cr1	B2m	Siglech	Siglech	Ctsz	Csf1r	Cd9
10	Csf1r	Ctsz	Cx3cr1	Tyrobp	Tyrobp	Cx3cr1	Trem2	H2-D1
11	Cx3cr1	Trem2	Cd9	Sirpa	Lpcat2	Cd9	Lgmn	Tyrobp
12	Lgmn	Ctsb	Csf1r	Fth1	Sirpa	Csf1r	Cx3cr1	Ctsz
13	Cd74	P2ry12	Lgmn	Selplg	Ctsb	Lgmn	Ctsz	Cx3cr1
14	Laptm5	Siglech	Laptm5	Ctsb	Trem2	Laptm5	Fth1	Trem2
15	Ctsz	Selplg	Ftl1	Trem2	Trim30a	Ftl1	B2m	Csf1r
16	H2-D1	Cd9	Srgap2	Lpcat2	Fth1	Srgap2	P2ry12	Lgmn
17	Trem2	Fcrls	P2ry12	Ctsz	Selplg	Selplg	Siglech	Laptm5
18	Srgap2	B2m	Lyz2	B2m	Ctsz	H2-D1	Akt3	H2-K1
19	Fcrls	Laptm5	Fcrls	Cd9	B2m	Lyz2	Laptm5	Timp2
20	Dab2	Lpcat2	Selplg	Bin1	Cd9	Sirpa	Fcrls	Lamp1