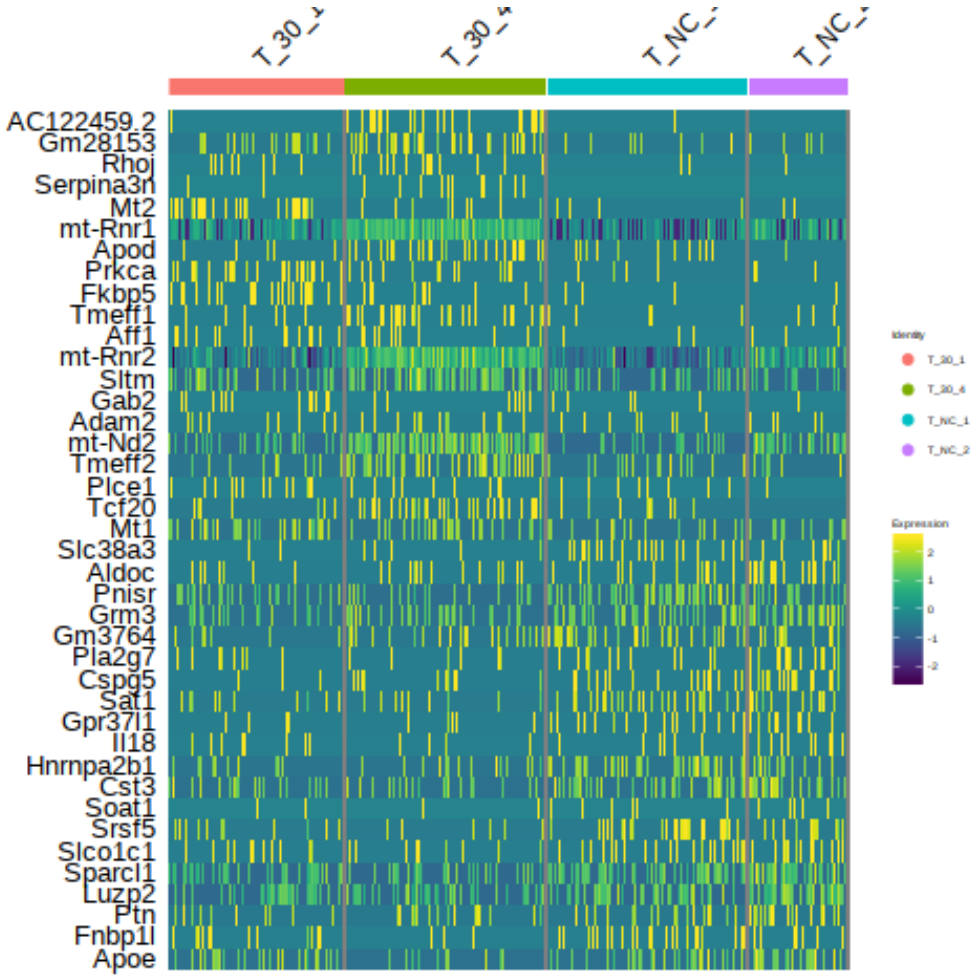
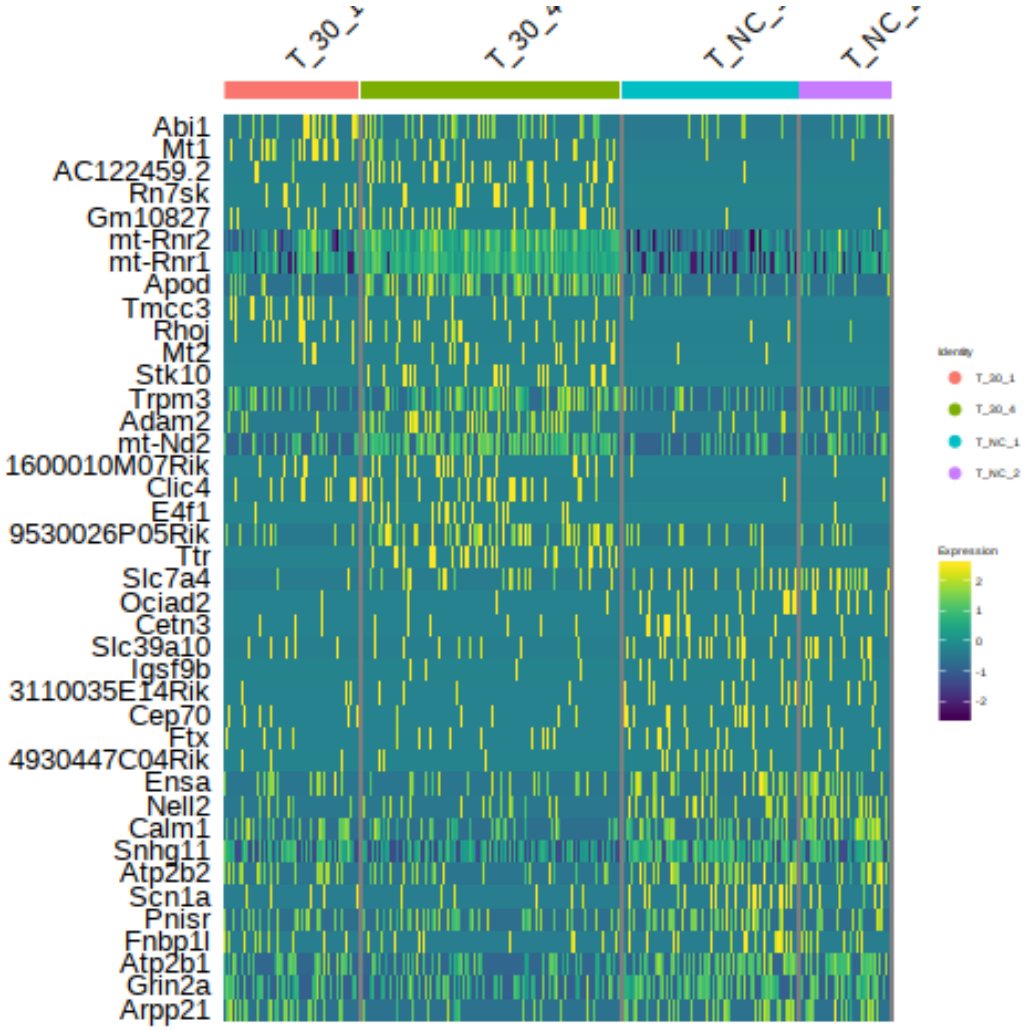
Supplementary material

Single cell sequencing reveals heterogenicity of differential gene expression and altered interactome in post-ischemic mouse brain cells

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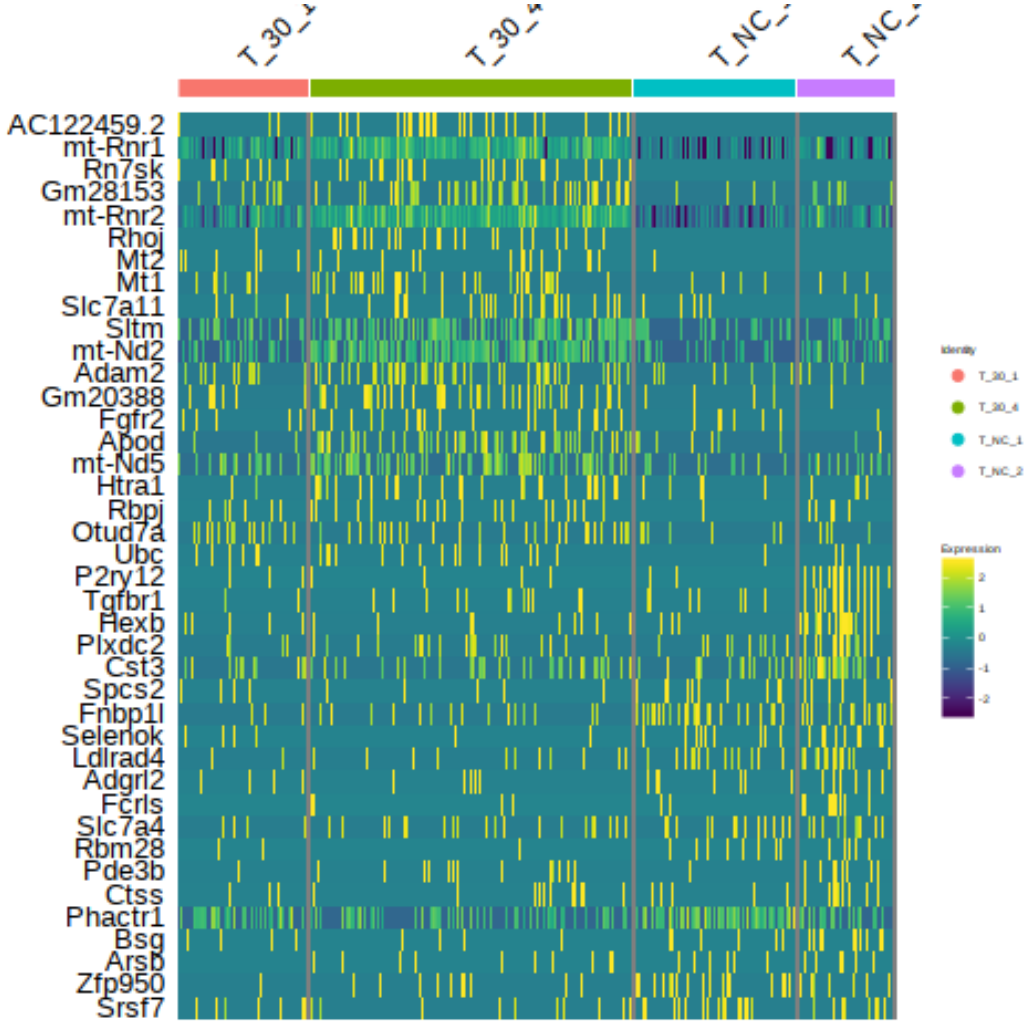
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mt-Nd2
Adam2
Gm20388
Fgfr2
Apod
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Hexb
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Spcs2
Fnbp1l
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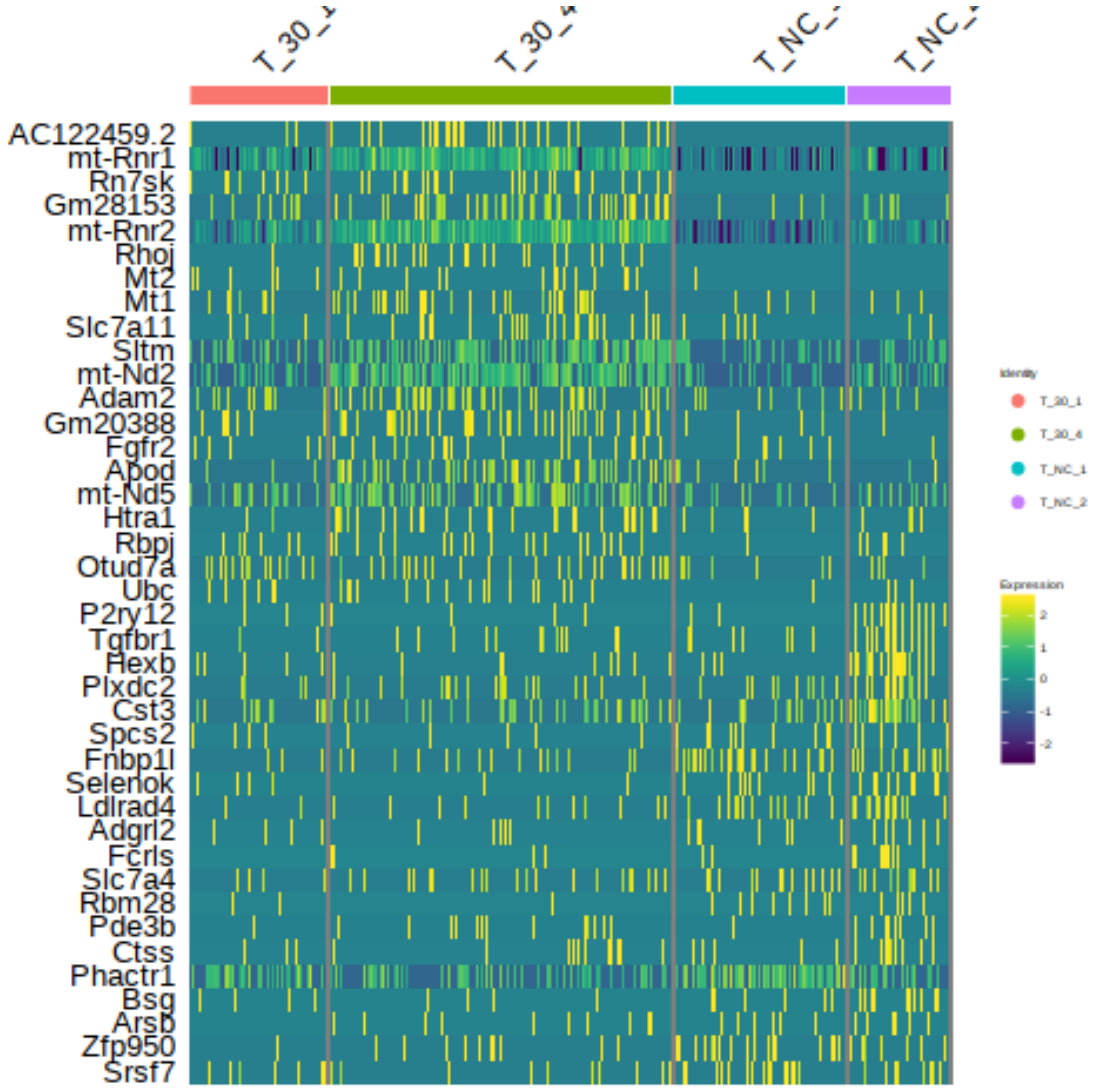
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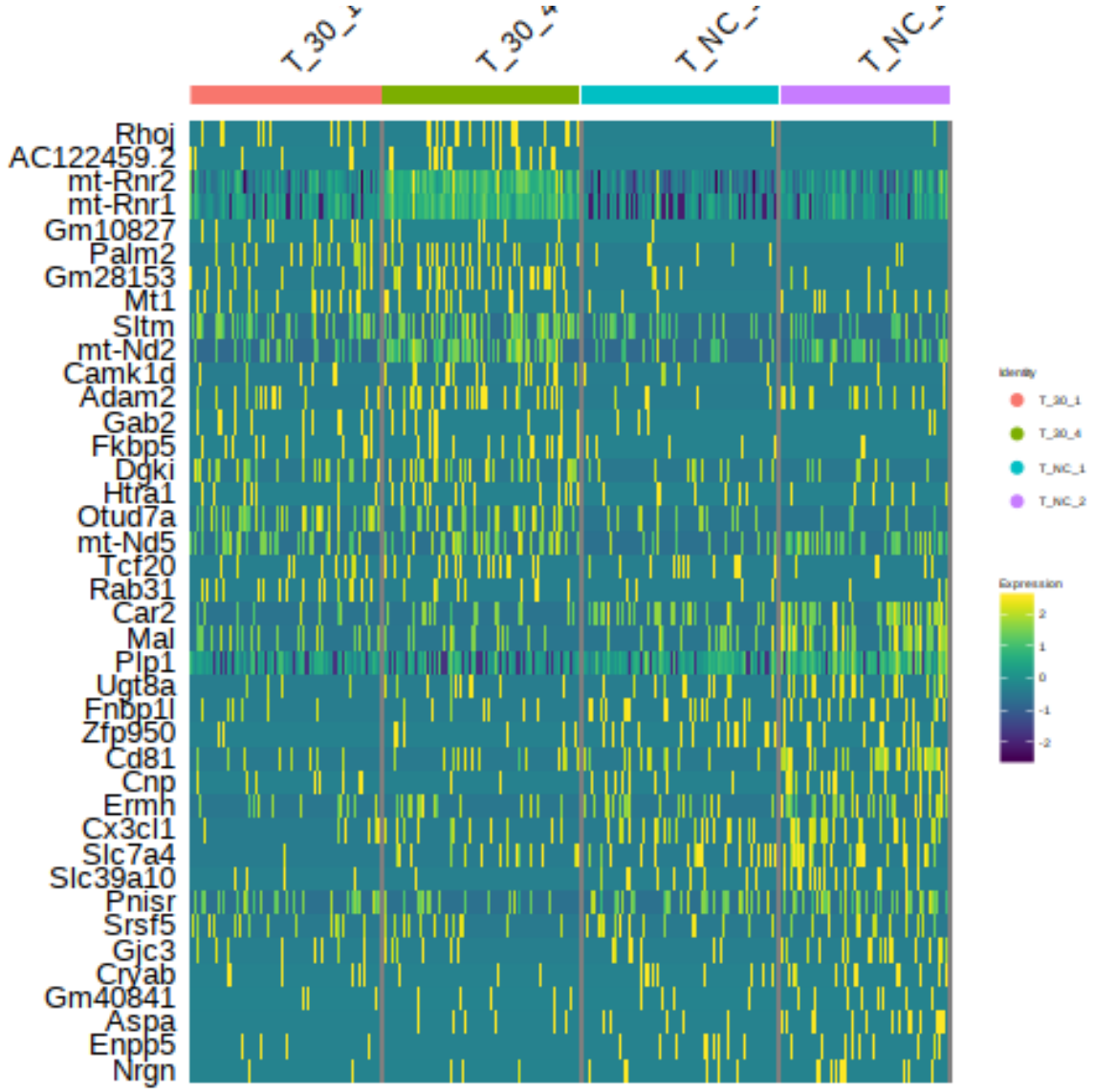
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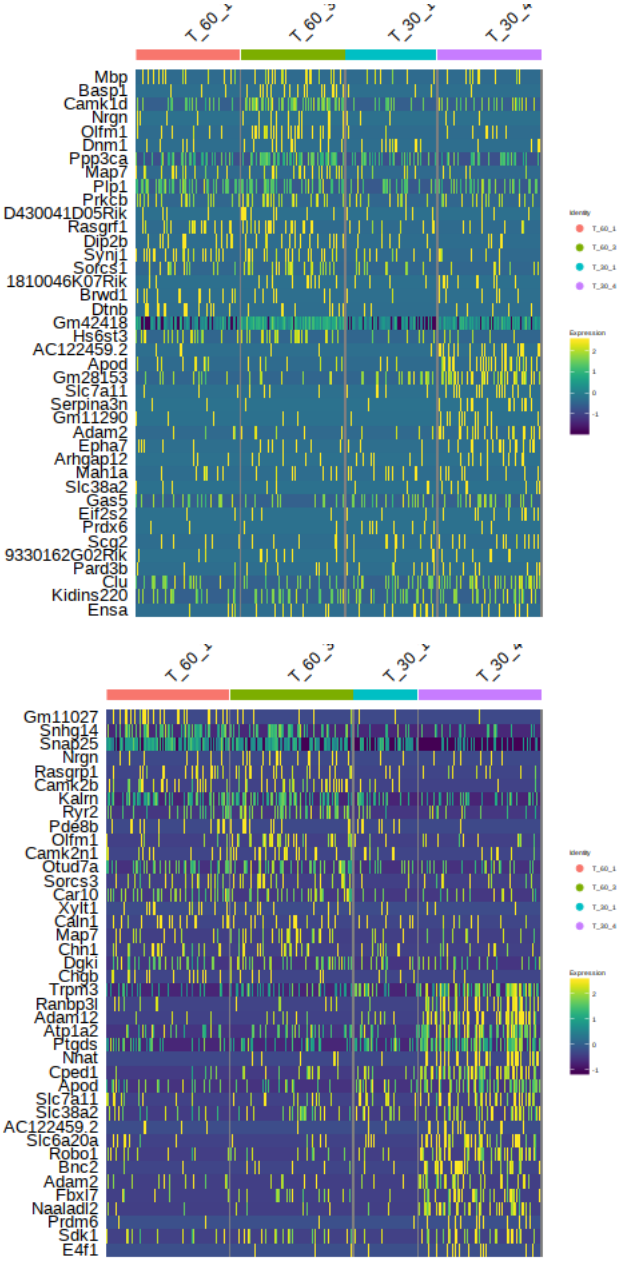
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Xylt1
Caln1
Map7
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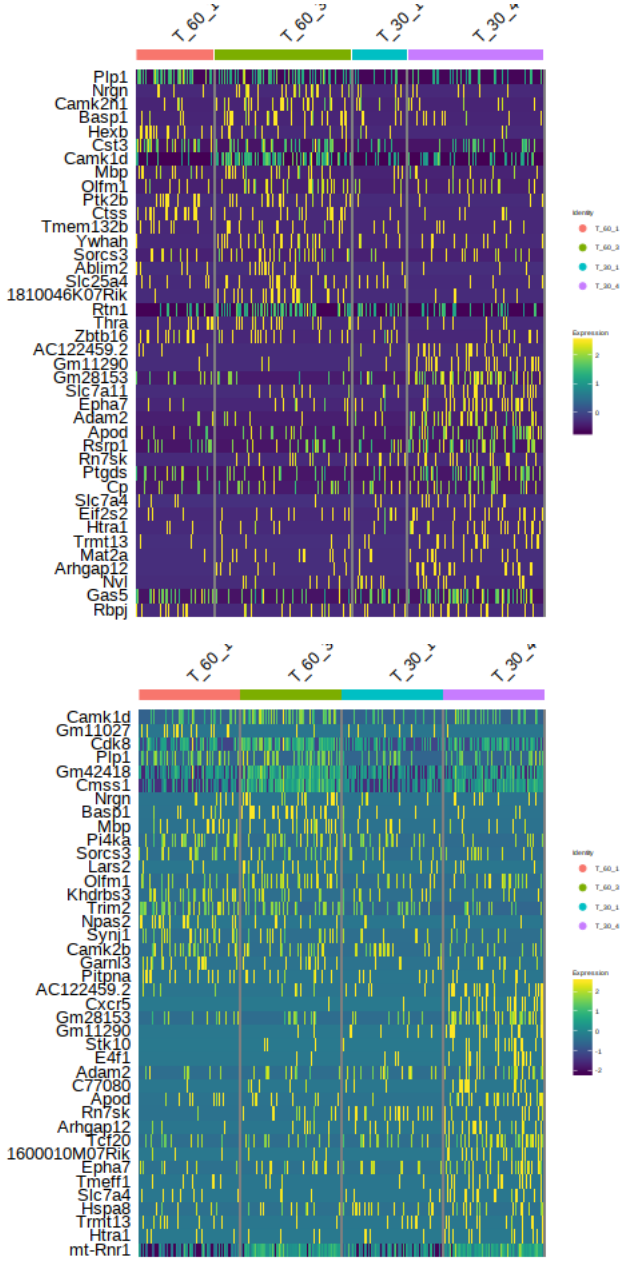
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Adam2
Apod
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Cp
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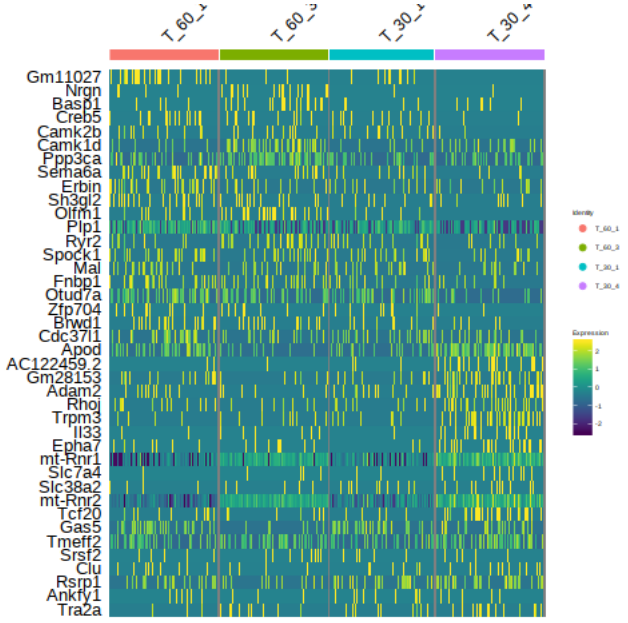
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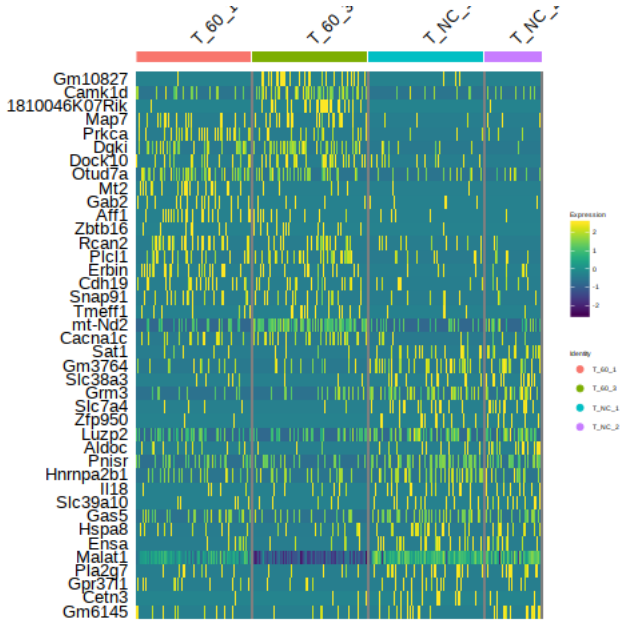
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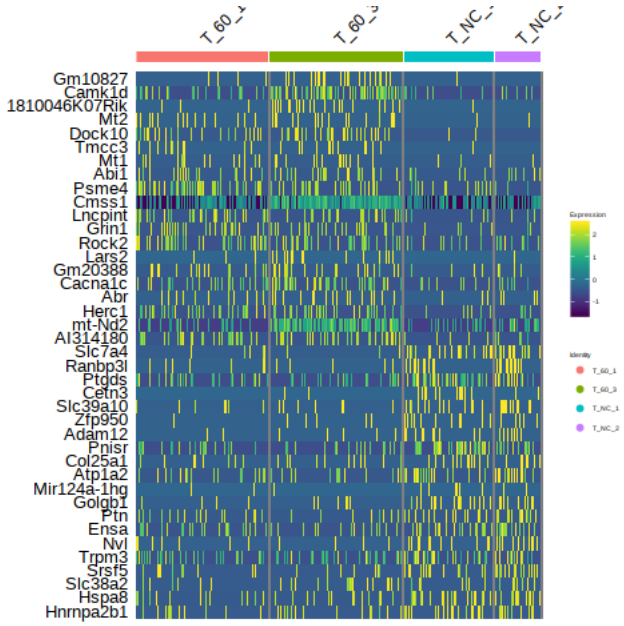
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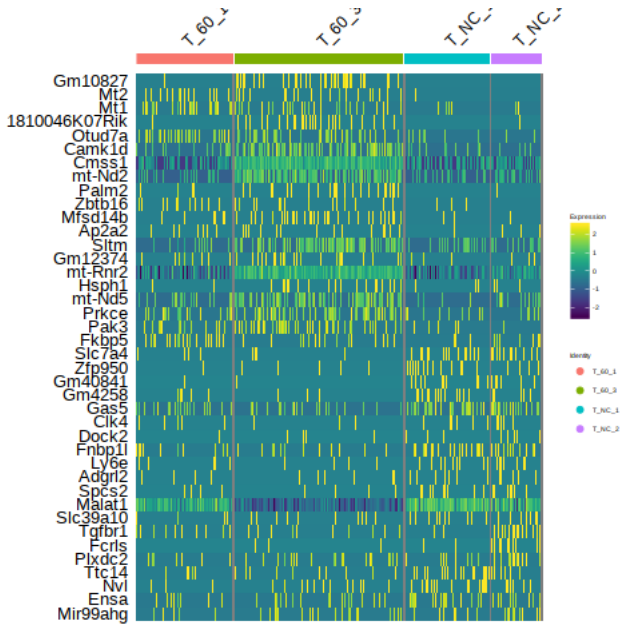
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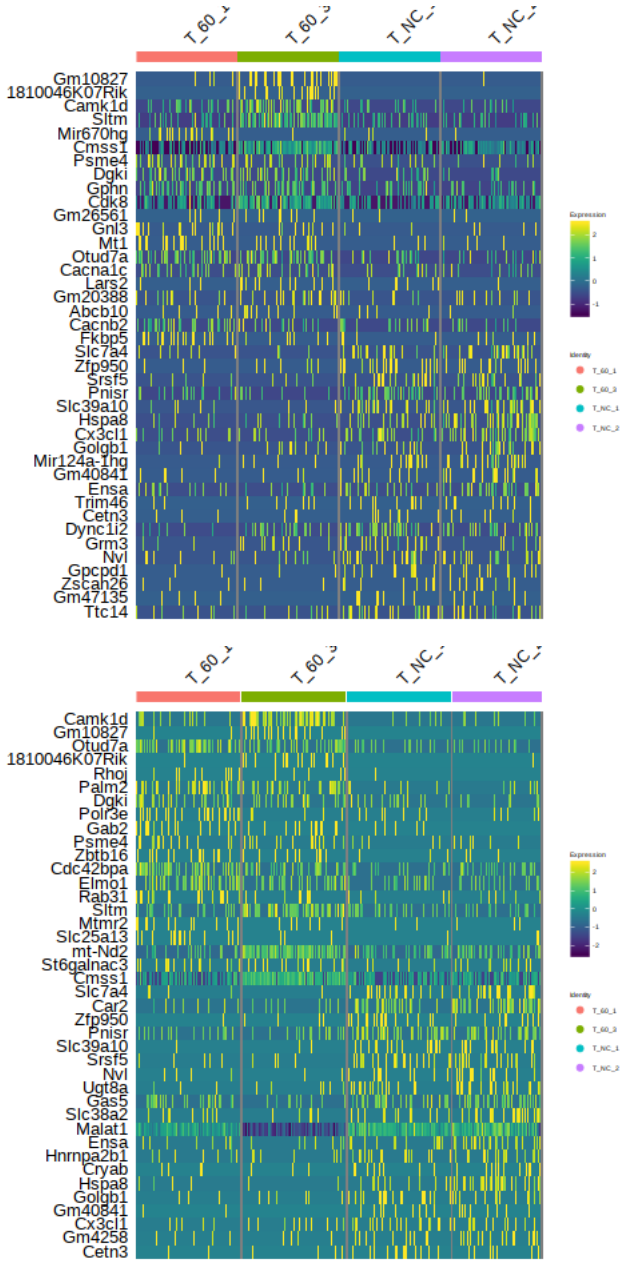

Supplementary Figure S1. Differential gene expression – cell groups

Supplementary Table SI. Network analysis – data

#node 1	node 2	node1_string_id	node2_string_id	neighborhood_on_chromosome	gene_fusion	phylogenetic_cooccurrence	homology	coexpression	experimentally_determined_interaction	database_annotated	automated_textmining	combined_score
Atp2b2	Syt1	10090.ENSMUSP00000098605	10090.ENSMUSP00000100912	0	0	0	0	0.289	0	0	0.222	0.423
Calm1	Camk1d	10090.ENSMUSP00000158788	10090.ENSMUSP00000037028	0	0	0	0	0.066	0.261	0	0.208	0.405
Calm1	Sorl1	10090.ENSMUSP00000158788	10090.ENSMUSP00000058613	0	0	0	0	0.060	0	0	0.403	0.415
Cx3cl1	Cxcr5	10090.ENSMUSP00000034230	10090.ENSMUSP00000149508	0	0	0	0	0	0.041	0.650	0.590	0.850
Dync1i2	Golgb1	10090.ENSMUSP00000107768	10090.ENSMUSP00000045239	0	0	0	0	0.066	0	0.500	0.066	0.526
Fgfr2	Plcb1	10090.ENSMUSP00000112430	10090.ENSMUSP00000105743	0	0	0	0	0	0	0.650	0	0.650
Fus	Srsf5	10090.ENSMUSP00000101858	10090.ENSMUSP00000105980	0	0	0	0	0.318	0.066	0.400	0.218	0.661
Gphn	Grin2b	10090.ENSMUSP00000106018	10090.ENSMUSP00000062284	0	0	0	0	0.042	0	0	0.556	0.557
Gphn	Syt1	10090.ENSMUSP00000106018	10090.ENSMUSP00000100912	0	0	0	0	0.079	0	0	0.432	0.454
Gphn	Grin2a	10090.ENSMUSP00000106018	10090.ENSMUSP00000142900	0	0	0	0	0	0	0	0.502	0.502
Grin2a	Grm3	10090.ENSMUSP00000142900	10090.ENSMUSP00000004076	0	0	0	0	0.158	0	0	0.770	0.798
Grin2a	Grin2b	10090.ENSMUSP00000142900	10090.ENSMUSP00000062284	0	0	0	0.944	0.261	0.888	0.900	0.983	0.999
Grin2a	Syt1	10090.ENSMUSP00000142900	10090.ENSMUSP00000100912	0	0	0	0	0.176	0	0	0.387	0.473
Grin2b	Grm3	10090.ENSMUSP00000062284	10090.ENSMUSP00000004076	0	0	0	0	0.193	0	0	0.652	0.707
Grin2b	Syt1	10090.ENSMUSP00000062284	10090.ENSMUSP00000100912	0	0	0	0	0.188	0	0	0.399	0.491
Grin2b	Plcb1	10090.ENSMUSP00000062284	10090.ENSMUSP00000105743	0	0	0	0	0.135	0	0	0.492	0.541

Mef2c	Pnisr	10090.ENSMUSP00000143401	10090.ENSMUSP00000029911	0	0	0	0	0.046	0.086	0	0.438	0.467
Mef2c	Sorl1	10090.ENSMUSP00000143401	10090.ENSMUSP00000058613	0	0	0	0	0.071	0	0	0.522	0.537
Pnisr	Sltm	10090.ENSMUSP00000029911	10090.ENSMUSP00000049112	0	0	0	0	0.502	0.051	0	0.057	0.515
Pnisr	Srsf5	10090.ENSMUSP00000029911	10090.ENSMUSP00000105980	0	0	0	0	0.341	0.102	0	0.273	0.533
mt-Co1	mt-Nd2	10090.ENSMUSP00000080993	10090.ENSMUSP00000080992	0	0	0	0	0.683	0.758	0	0.893	0.991
mt-Co1	mt-Nd5	10090.ENSMUSP00000080993	10090.ENSMUSP00000081001	0	0	0	0	0.927	0.758	0	0.899	0.998
mt-Nd2	mt-Nd5	10090.ENSMUSP00000080992	10090.ENSMUSP00000081001	0	0	0.245	0.588	0.985	0.990	0.900	0.981	0.999

#node1	node2	node1_string_id	node2_string_id	neighborhood_on_chromosome	gene_fusion	phylogenetic_cooccurrence	homology	coexpression	experimentally_determined_interaction	database_annotated	automated_textmining	combined_score
Amph	Grin1	10090.ENSMUSP00000142766	10090.ENSMUSP00000028335	0	0	0	0	0.122	0	0	0.692	0.718
Cacna1c	Grin1	10090.ENSMUSP00000108413	10090.ENSMUSP00000028335	0	0	0	0	0.094	0	0	0.485	0.513
Cacna1c	Snap25	10090.ENSMUSP00000108413	10090.ENSMUSP00000028727	0	0	0	0	0.125	0	0	0.565	0.603
Cacna1c	Grin2a	10090.ENSMUSP00000108413	10090.ENSMUSP00000142900	0	0	0	0	0.085	0	0	0.490	0.513
Cacna1c	Cacnb2	10090.ENSMUSP00000108413	10090.ENSMUSP00000110371	0	0	0	0	0.215	0.987	0.720	0.973	0.999
Dock10	Herc1	10090.ENSMUSP00000077099	10090.ENSMUSP00000044801	0	0	0	0	0.041	0.491	0	0	0.491
Dync1i2	Golgb1	10090.ENSMUSP00000107768	10090.ENSMUSP00000045239	0	0	0	0	0.066	0	0.500	0.066	0.526
Gphn	Grin1	10090.ENSMUSP00000106018	10090.ENSMUSP00000028335	0	0	0	0	0	0	0	0.640	0.640

Gphn	Grin2a	10090.ENSMUSP00000106018	10090.ENSMUSP00000142900	0	0	0	0	0	0	0	0.502	0.502
Grin1	mt-Nd2	10090.ENSMUSP00000028335	10090.ENSMUSP00000080992	0	0	0	0	0	0.093	0	0.398	0.430
Grin1	Snap25	10090.ENSMUSP00000028335	10090.ENSMUSP00000028727	0	0	0	0	0.277	0	0	0.490	0.615
Grin1	Grin2a	10090.ENSMUSP00000028335	10090.ENSMUSP00000142900	0	0	0	0.685	0.189	0.995	0.900	0.988	0.999
Grin2a	Snap25	10090.ENSMUSP00000142900	10090.ENSMUSP00000028727	0	0	0	0	0.175	0	0	0.455	0.531
Hspa8	Snap25	10090.ENSMUSP00000015800	10090.ENSMUSP00000028727	0	0	0	0	0.061	0.292	0.500	0.746	0.904
Pnisr	Sltm	10090.ENSMUSP00000029911	10090.ENSMUSP00000049112	0	0	0	0	0.502	0.051	0	0.057	0.515
Pnisr	Srsf5	10090.ENSMUSP00000029911	10090.ENSMUSP00000105980	0	0	0	0	0.341	0.102	0	0.273	0.533
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#node1	node2	node1_string_id	node2_string_id	neighborhood_on_chromosome	gene_fusion	phylogenetic_cooccurrence	homology	coexpression	experimentally_determined_interaction	database_annotated	automated_textmining	combined_score
Apod	Plp1	10090.ENSMUSP00000119827	10090.ENSMUSP00000033800	0	0	0	0	0.284	0	0	0.240	0.433
Hspa8	Pi4ka	10090.ENSMUSP00000015800	10090.ENSMUSP00000156049	0	0	0	0	0.068	0.096	0	0.403	0.453
Hspa8	Synj1	10090.ENSMUSP00000015800	10090.ENSMUSP00000113308	0	0	0	0	0	0	0	0.633	0.633
Mbp	Plp1	10090.ENSMUSP00000046185	10090.ENSMUSP00000033800	0	0	0	0	0.585	0.289	0	0.918	0.973
Pi4ka	Synj1	10090.ENSMUSP00000156049	10090.ENSMUSP00000113308	0	0	0	0	0.124	0	0.650	0.376	0.792
Pi4ka	Pitpna	10090.ENSMUSP00000156049	10090.ENSMUSP00000115723	0	0	0	0	0.079	0.222	0	0.274	0.435
Pi4ka	Slc7a4	10090.ENSMUSP00000156049	10090.ENSMUSP00000127280	0	0	0	0	0	0	0	0.513	0.513