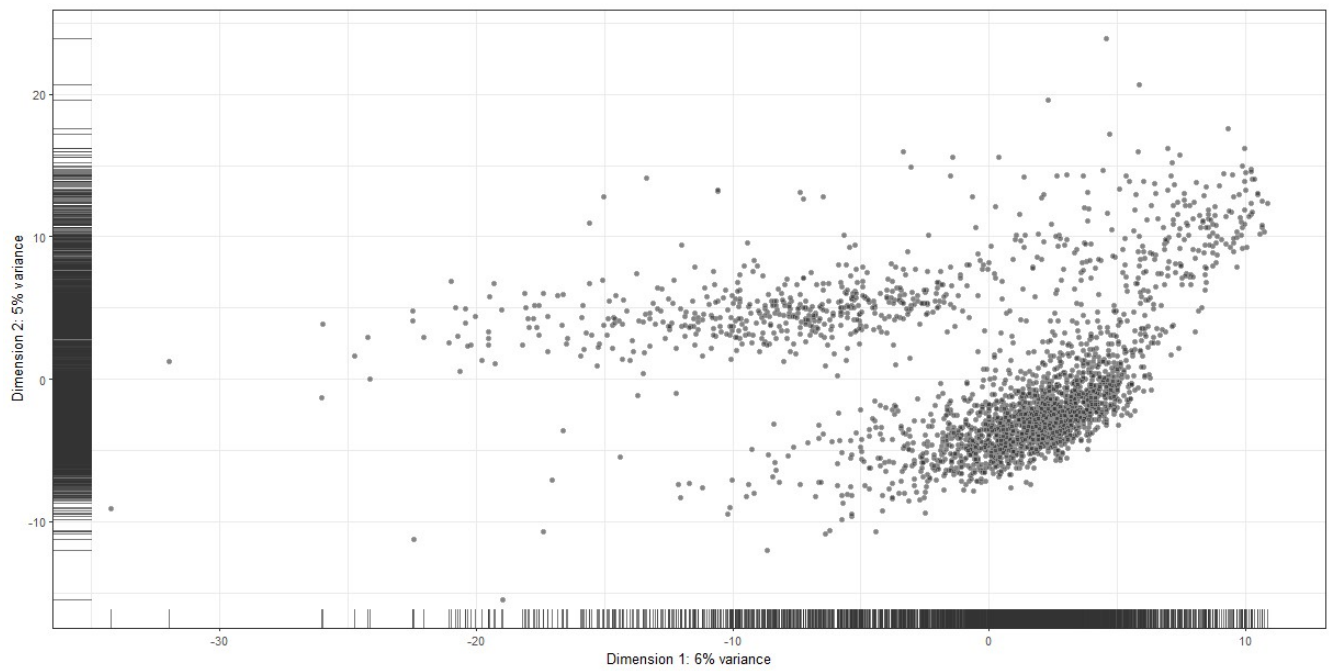
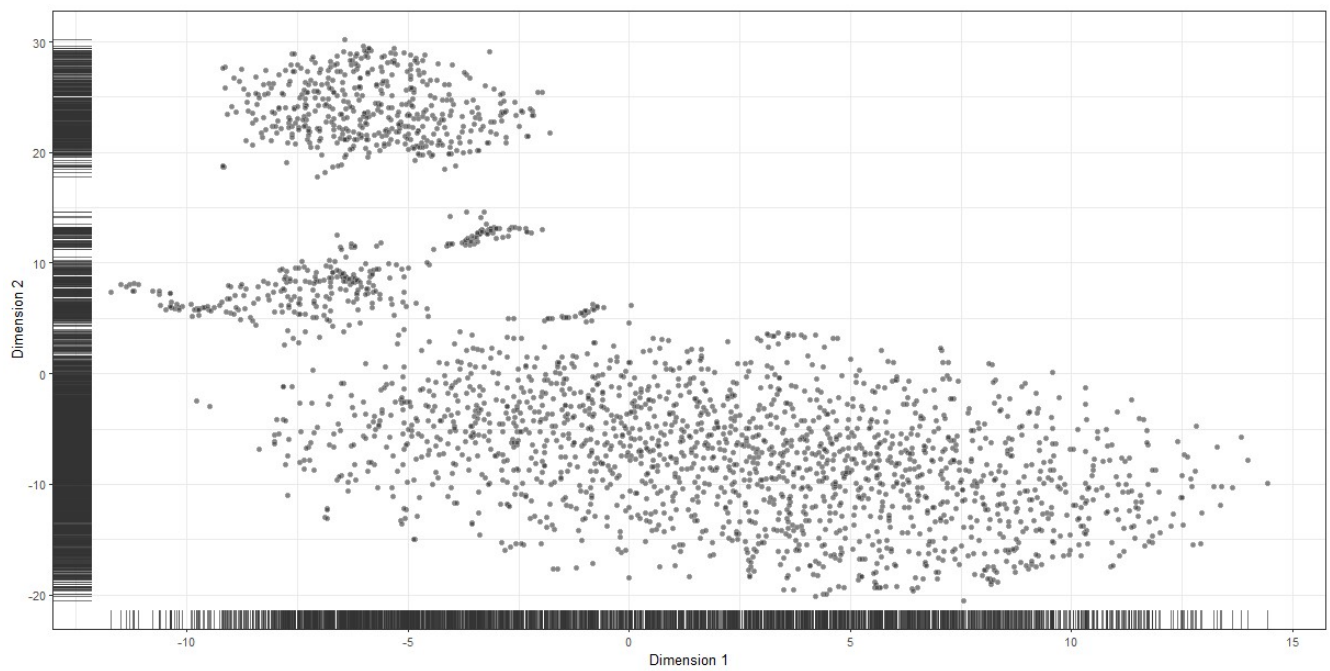


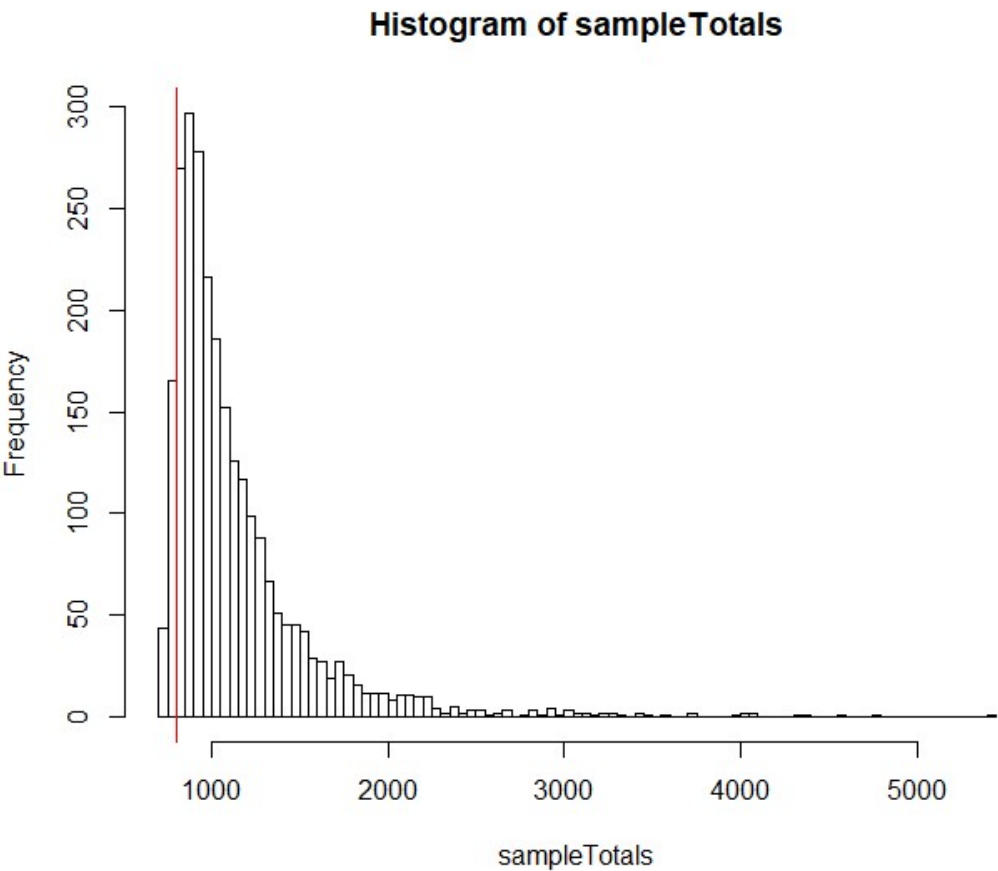
Microglia PCA pre-QC



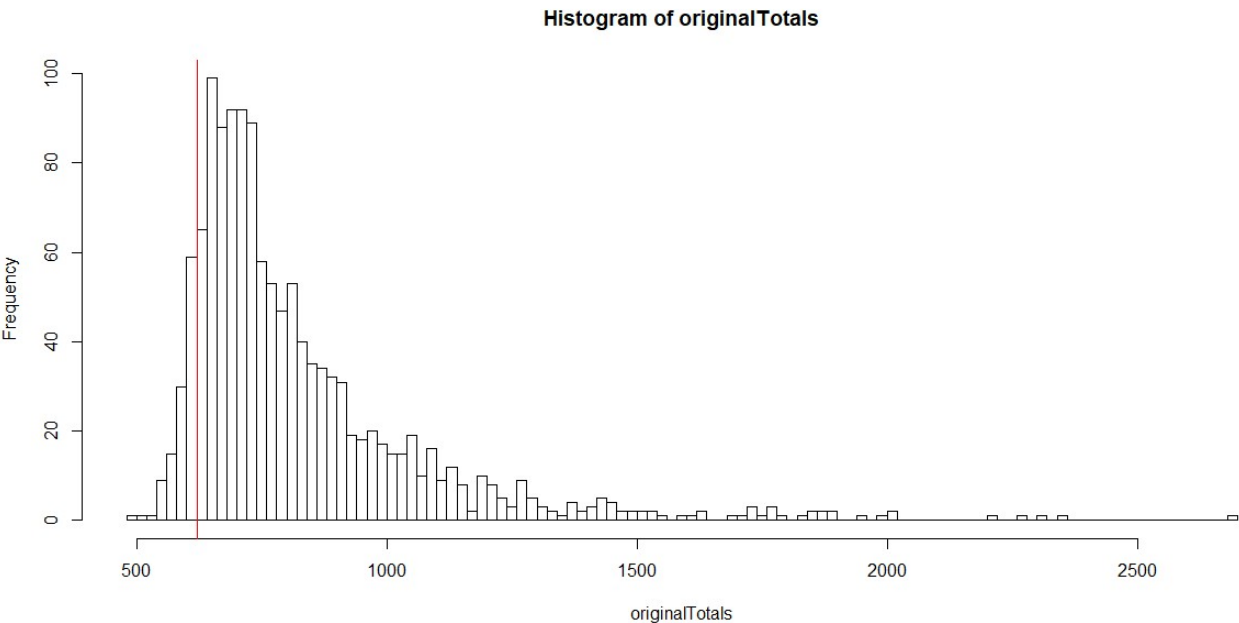
Microglia TSNE pre-QC



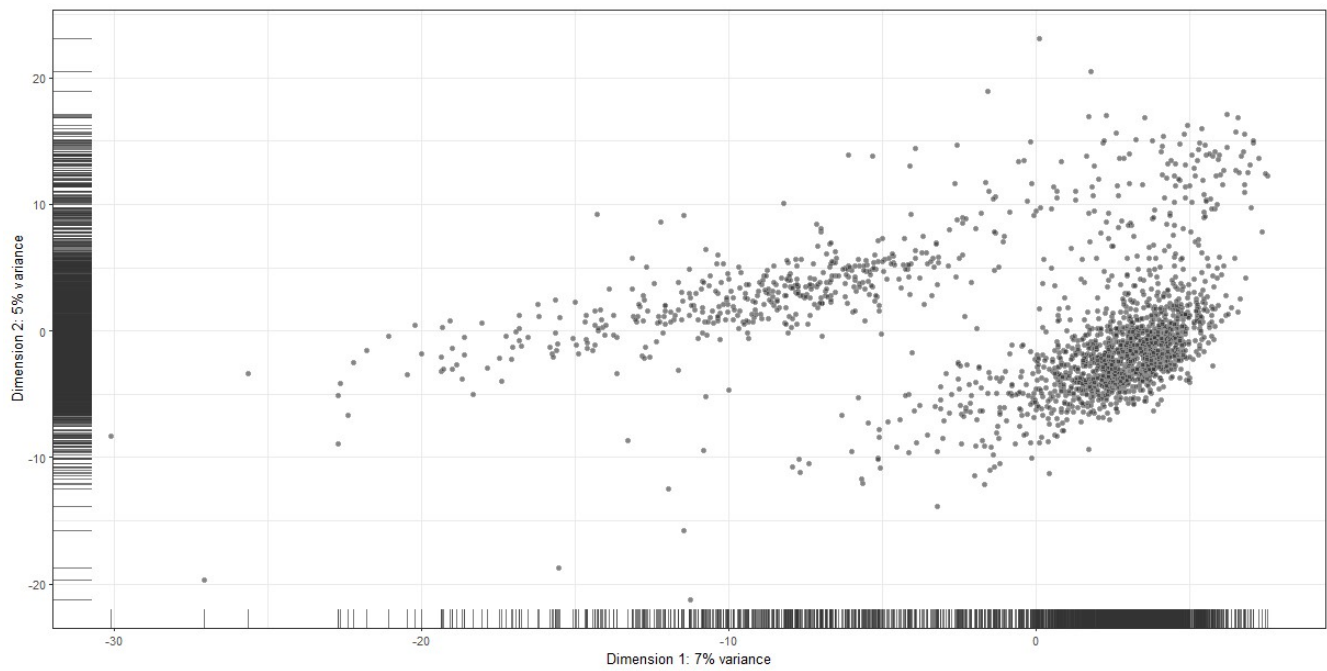
Microglia count totals, abline=800



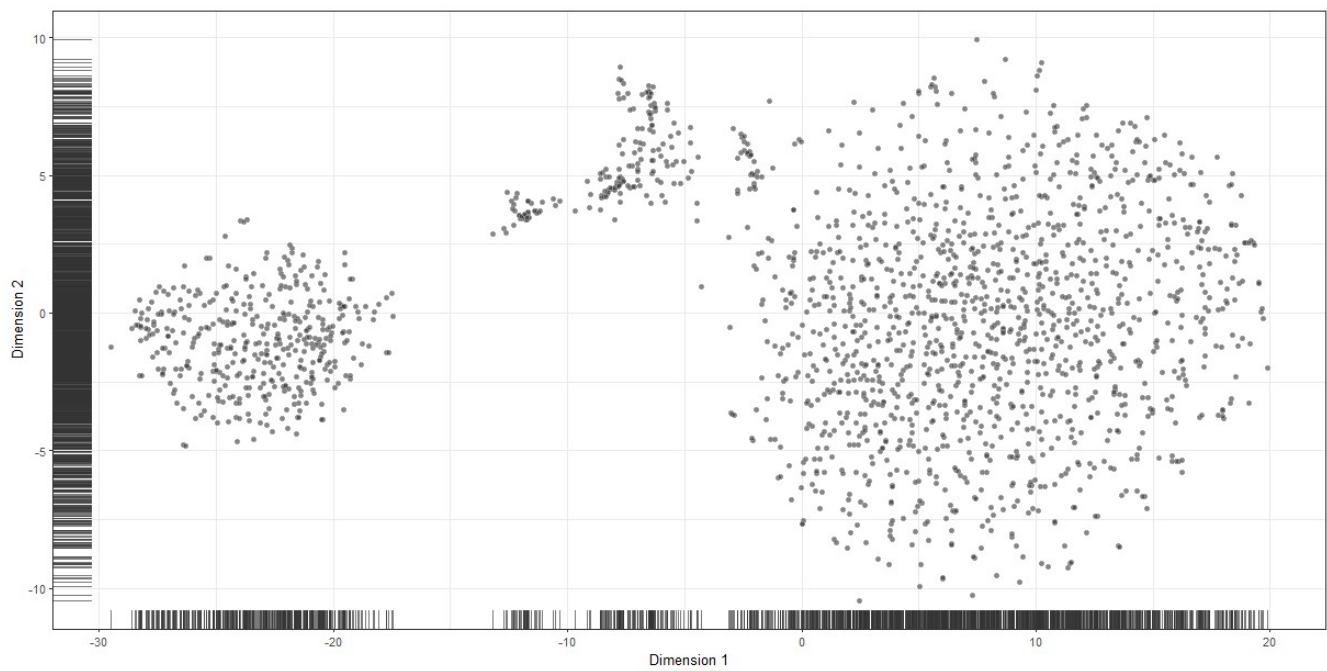
Microglia distribution, abline=520



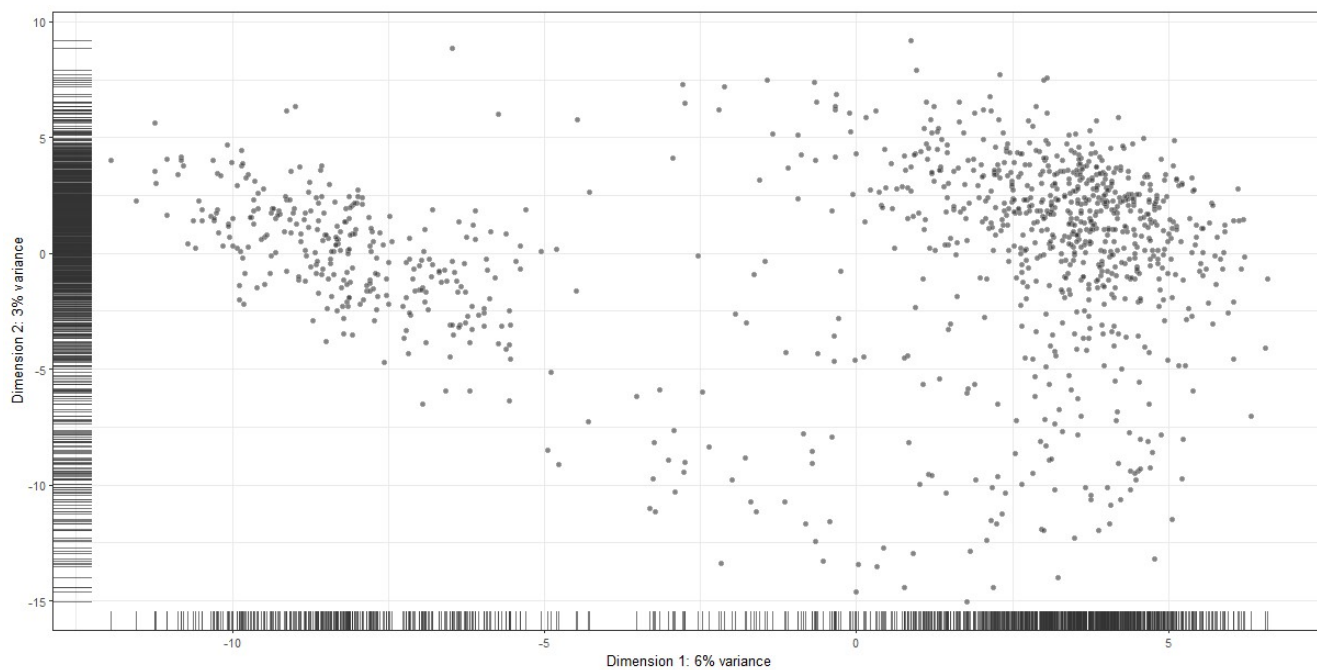
Microglia PCA post-QC



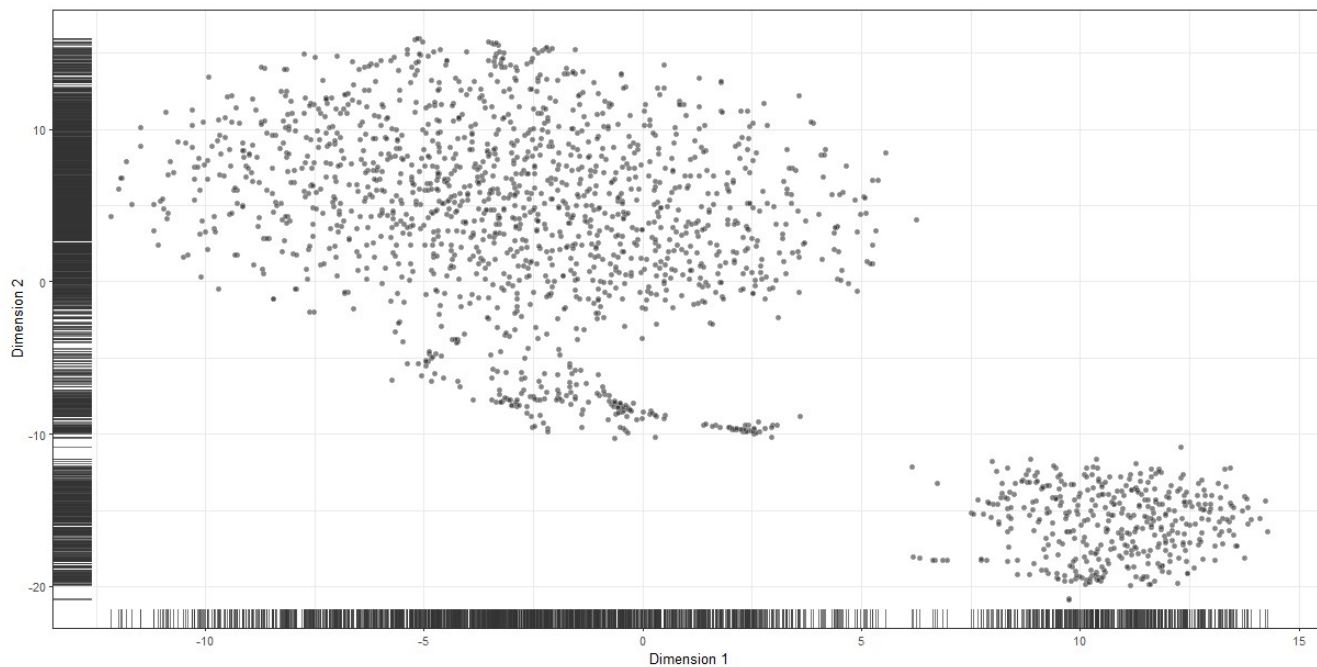
Microglia TSNE post-QC



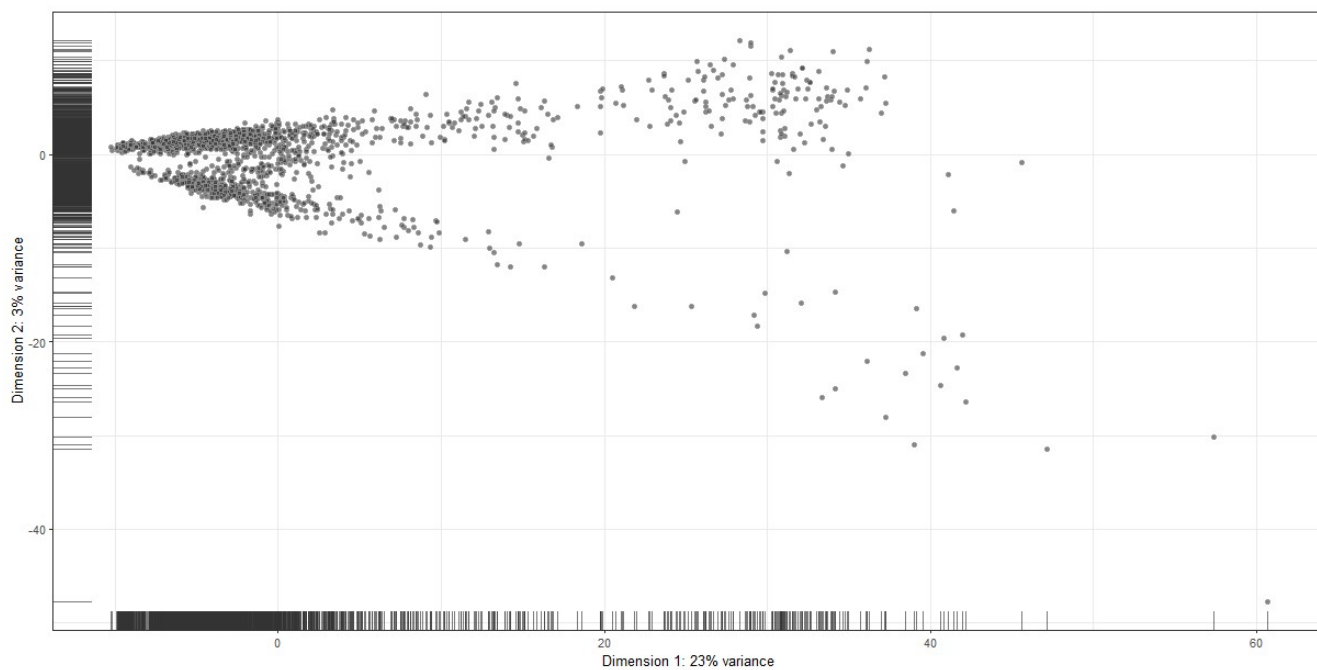
Microglia PCA post cpm normalization



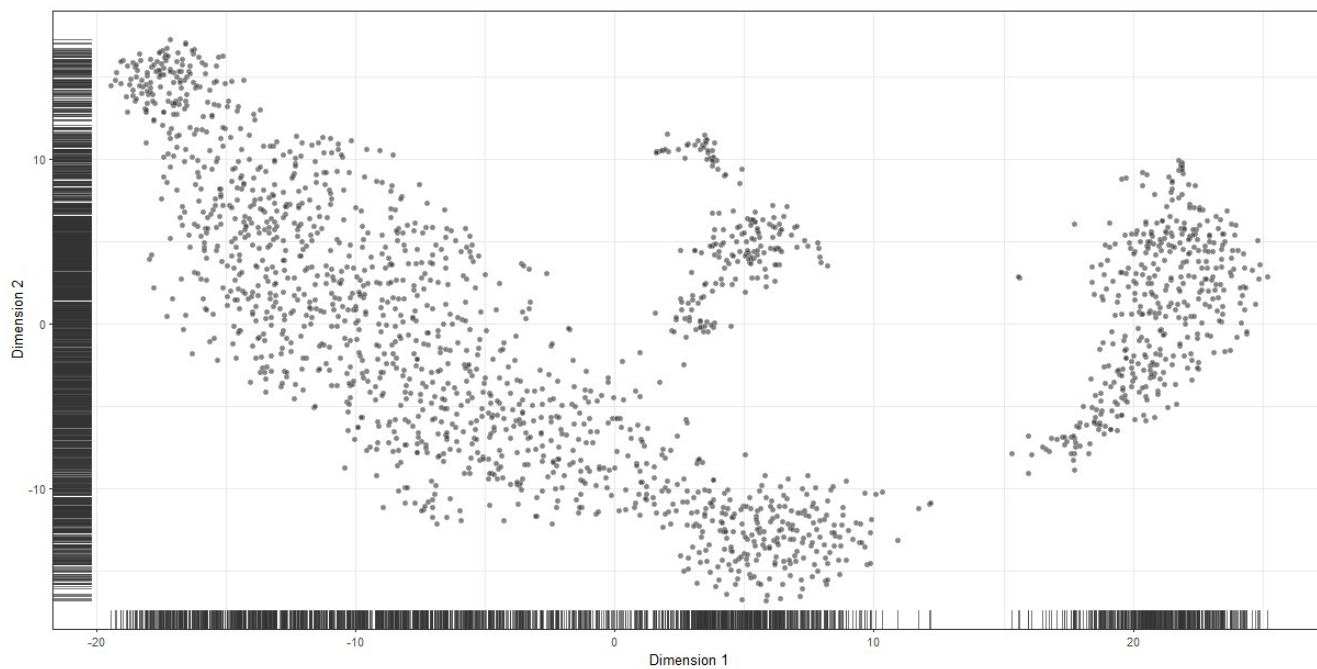
Microglia TSNE post cpm normalization



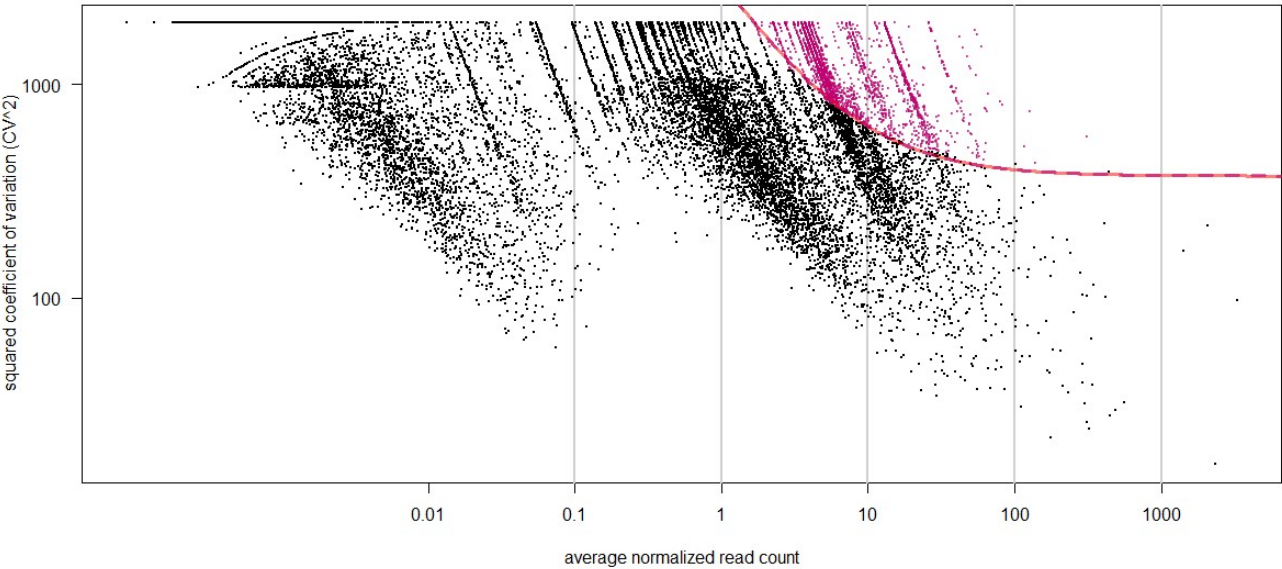
Microglia PCA post pool normalization



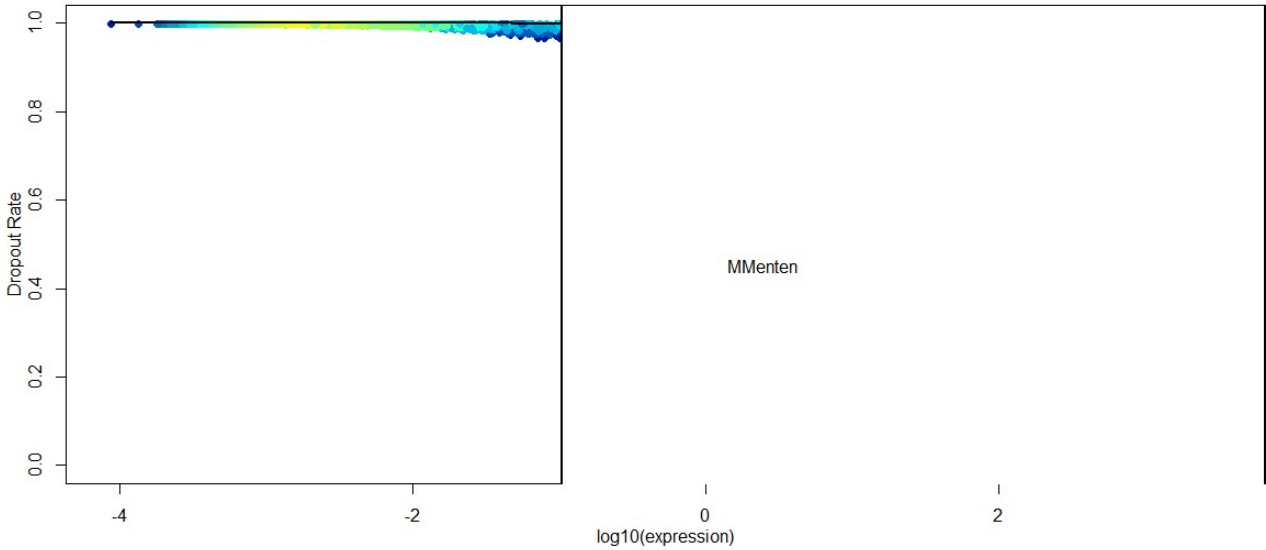
Microglia TSNE post pool normalization



BrenneckGetVariableGenes



M3Drop DifferentialExpression



Top 50 GENIE3 results

5th percentile: .05 x 7310 (interaction count) = index 366

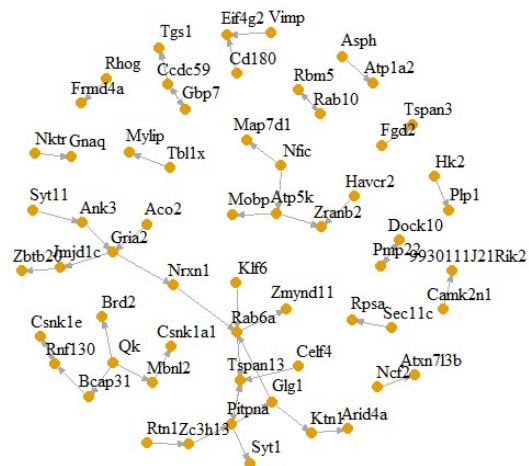
Weight value at calculated index of adjacency matrix using randomized data: 0.05633866

Smallest index of results with weight below this threshold: 966

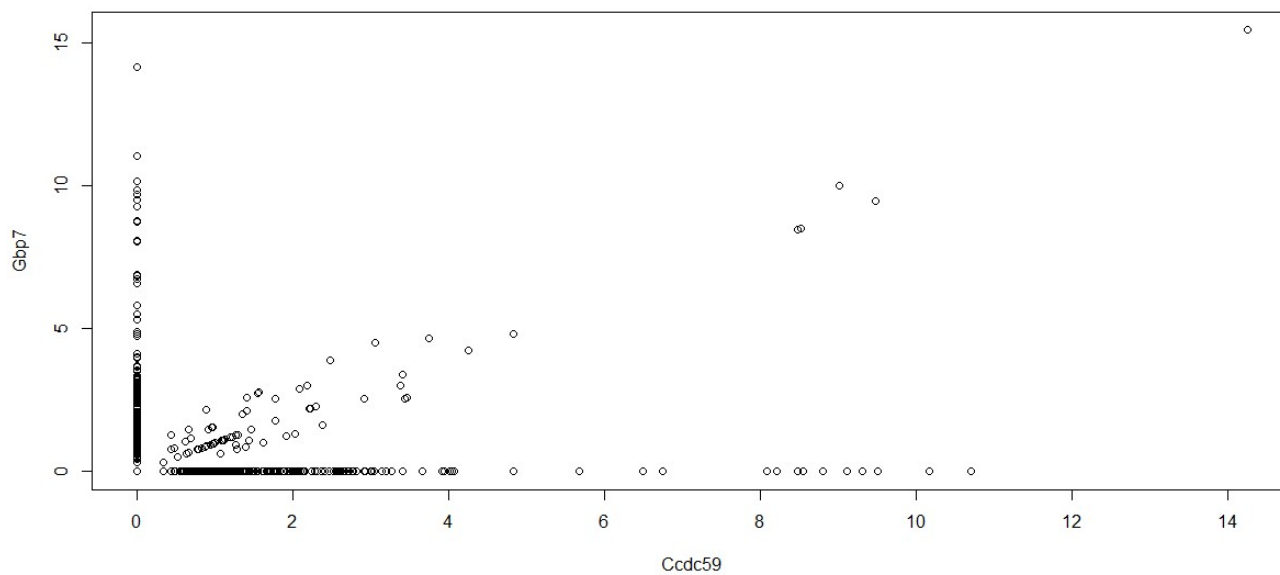
966 statistically significant interactions, (0.05 x 966) = 48 projected false positives

	regulatoryGene	targetGene	weight
1	Ccdc59	Gbp7	0.7003031
2	Ank3	Gria2	0.6319135
3	Rnf130	Csnk1e	0.5971475
4	Ktn1	Arid4a	0.5181997
5	Ccdc59	Tgs1	0.4255671
6	Jmjd1c	Zbtb20	0.4181998
7	Atp5k	Mobp	0.4114930
8	Pmp22	Dock10	0.4067408
9	Rhog	Frmd4a	0.4046124
10	Csnk1e	Rnf130	0.3974619
11	Rbm5	Rab10	0.3929946
12	Rab10	Rbm5	0.3725816
13	Pitpna	Syt1	0.3348917
14	Fgd2	Tspan3	0.3125216
15	Atp5k	Zranb2	0.3095810
16	Zc3h13	Pitpna	0.3026612
17	Tspan13	Pitpna	0.3026360
18	Nfic	Map7d1	0.3021817
19	Pitpna	Glg1	0.2989437
20	Gbp7	Ccdc59	0.2978826
21	Aco2	Gria2	0.2952948
22	Gria2	Jmjd1c	0.2930699
23	Qk	Bcap31	0.2927148
24	Nktr	Gnaq	0.2920760
25	Dock10	Pmp22	0.2875491
26	Camk2n1	9930111J21Rik2	0.2851243
27	Celf4	Tspan13	0.2835433
28	Rtn1	Zc3h13	0.2831892
29	Mbn12	Csnk1a1	0.2804449
30	Glg1	Ktn1	0.2728978
31	Gria2	Nrxn1	0.2691744
32	Bcap31	Rnf130	0.2686164
33	Asph	Atp1a2	0.2627185
34	Rab6a	Zmynd11	0.2584359
35	Ncf2	Atxn7l3b	0.2565021
36	Sec11c	Rpsa	0.2535771
37	Qk	Mbn12	0.2526582
38	Qk	Brd2	0.2465423
39	Hk2	Plp1	0.2454849
40	Havcr2	Zranb2	0.2448271
41	Nfic	Atp5k	0.2383807
42	Nrxn1	Rab6a	0.2376100
43	Klf6	Rab6a	0.2374375
44	Glg1	Rab6a	0.2372276
45	Rab6a	Tspan13	0.2367651
46	Vimp	Eif4g2	0.2366588
47	Pitpna	Tspan13	0.2364980
48	Cd180	Eif4g2	0.2358396
49	Syt11	Ank3	0.2301703
50	Tb11x	My1ip	0.2286917

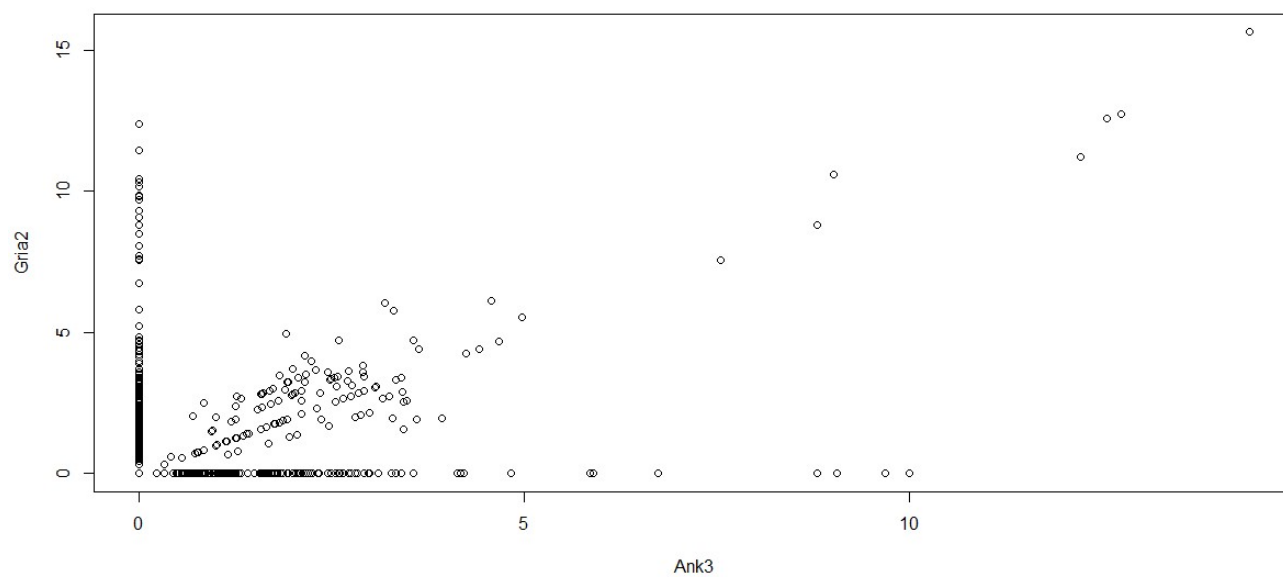
GENIE3 Network



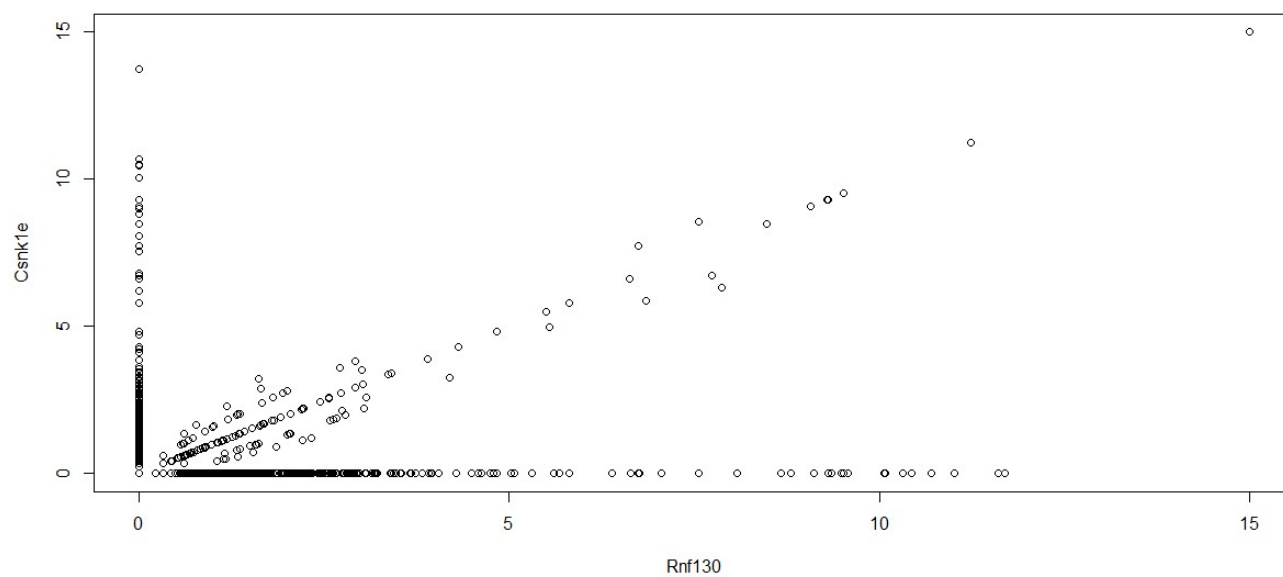
Interaction # 1



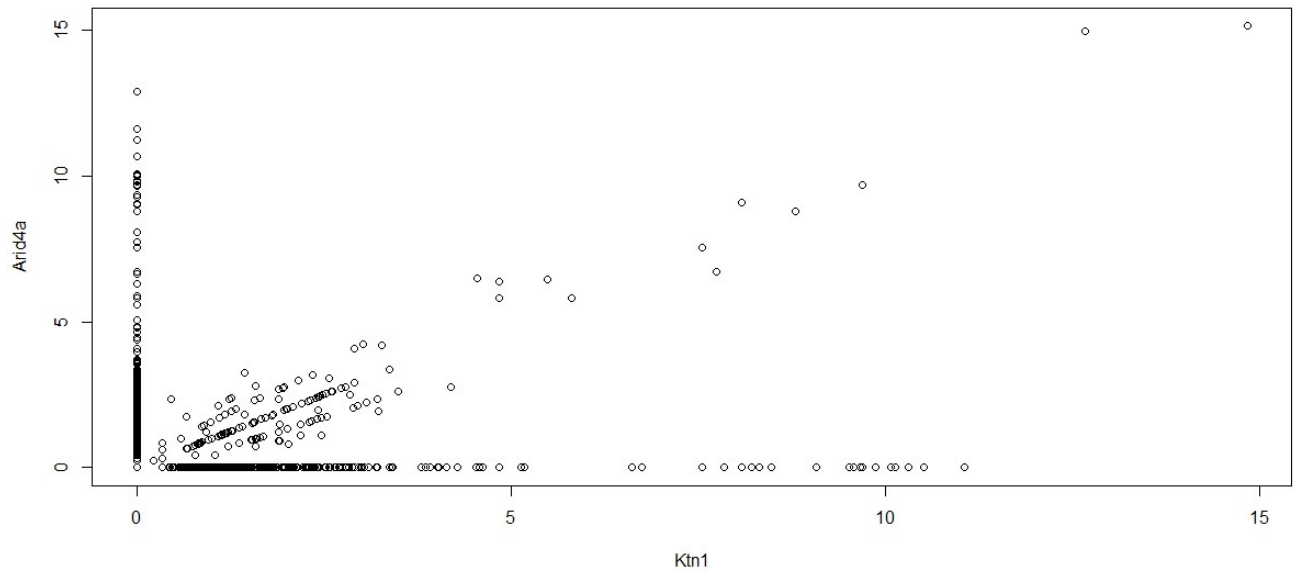
Interaction # 2



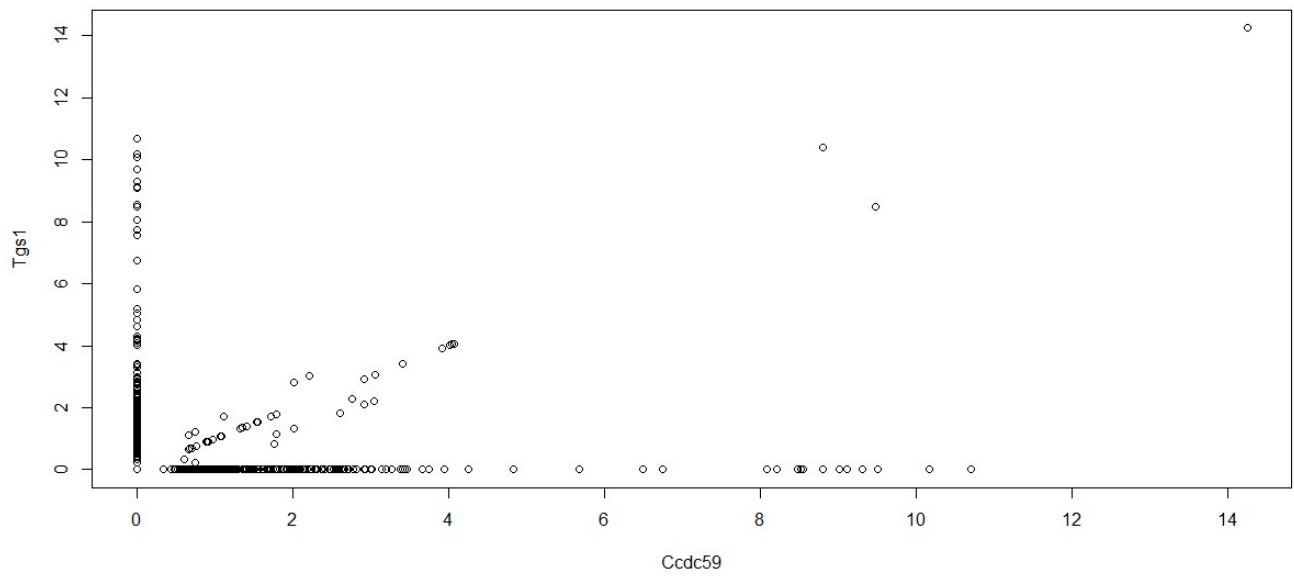
Interaction # 3



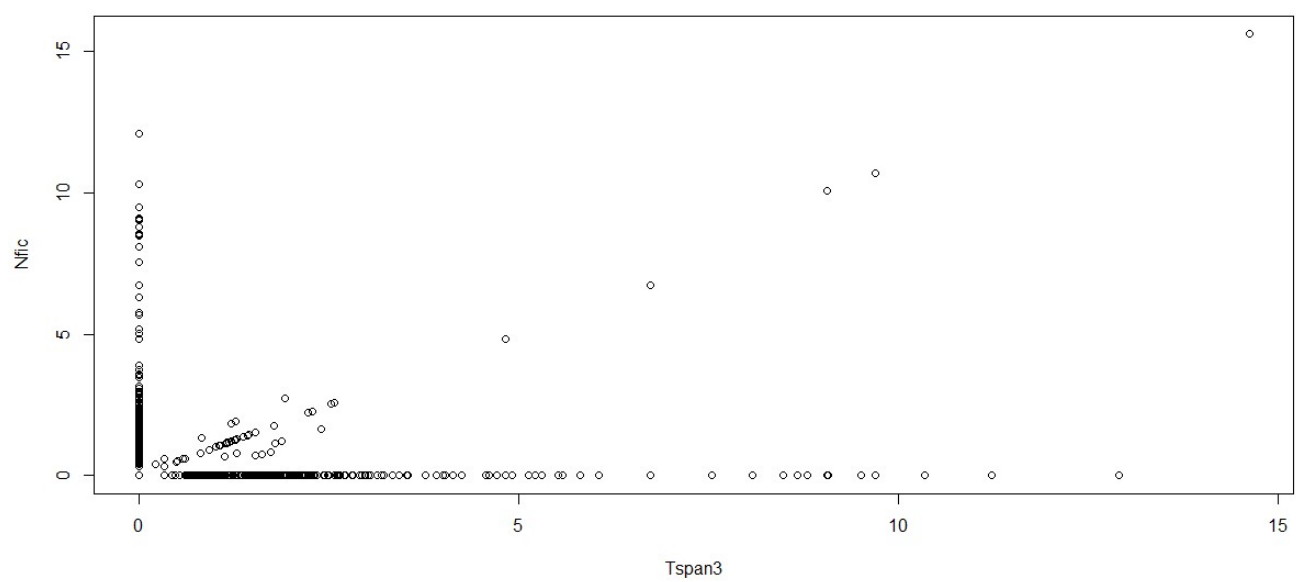
Interaction # 4



Interaction # 5



Bottom-ranked Interaction



Top 50 CLR results

5th percentile: .05 x 7310 (interaction count) = index 366

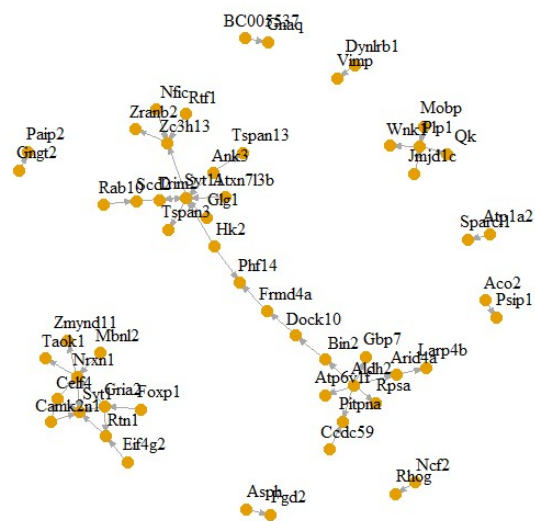
Weight value at calculated index of adjacency matrix using randomized data: 2.928638

Smallest index of results with weight below this threshold: 408

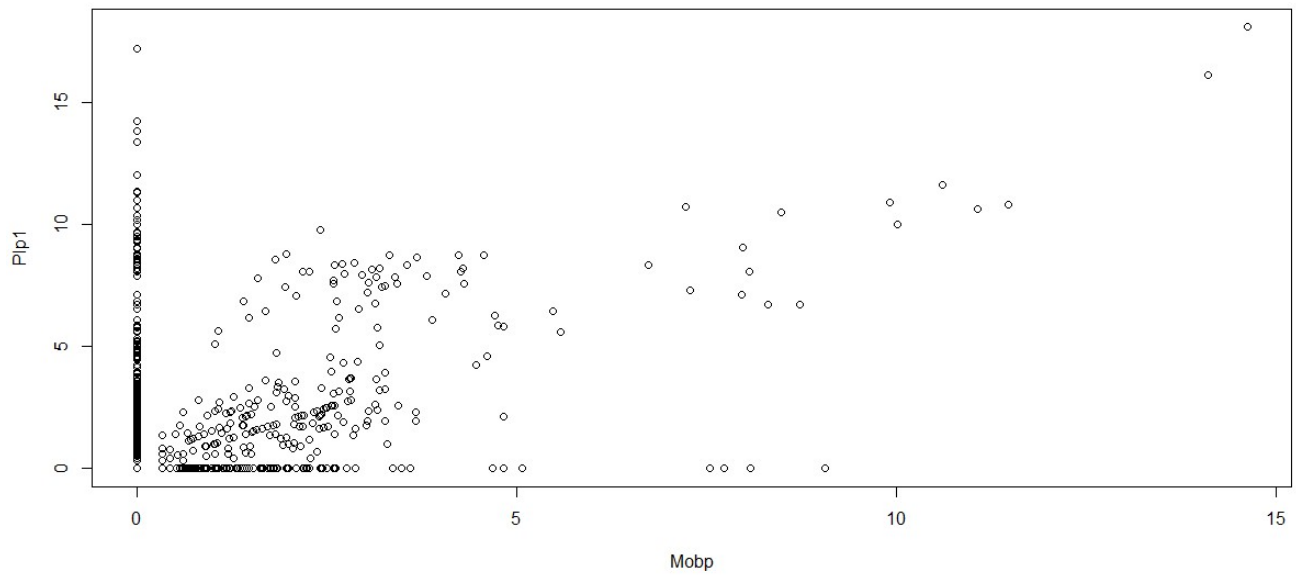
408 statistically significant interactions, (0.05 x 408) = 20 projected false positives

	regulatoryGene	targetGene	weight
1	Mobp	Plp1	12.390267
2	Aldh2	Bin2	8.157652
3	Ank3	Syt11	7.874531
4	Aldh2	Rpsa	6.602549
5	Arid4a	Larp4b	6.523280
6	Gria2	Syt1	6.462170
7	Ccdc59	Pitpna	6.412303
8	Aldh2	Pitpna	6.357327
9	Rab10	Scd2	6.298706
10	Aldh2	Arid4a	6.116359
11	Aldh2	Atp6v1f	6.081656
12	Aldh2	Gbp7	6.004803
13	Bin2	Dock10	6.000226
14	Plp1	Qk	5.855514
15	Atp1a2	Sparcl1	5.812292
16	Dynlrb1	Vimp	5.775609
17	Syt11	Trim2	5.703418
18	Camk2n1	Syt1	5.676191
19	Nrxn1	Syt1	5.643851
20	Gngt2	Paip2	5.611886
21	Glg1	Syt11	5.549120
22	Rtn1	Syt1	5.526147
23	Nrxn1	Taok1	5.498152
24	Celf4	Syt1	5.462747
25	BC005537	Gnaq	5.366931
26	Gria2	Nrxn1	5.300977
27	Scd2	Syt11	5.268685
28	Zc3h13	Zranb2	5.251791
29	Dock10	Frmd4a	5.214845
30	Nfic	Zc3h13	5.194081
31	Plp1	wnk1	5.126669
32	Rtf1	Zc3h13	5.120360
33	Jmjd1c	Plp1	5.070019
34	Mbnl2	Nrxn1	5.045874
35	Syt11	Tspan3	5.007866
36	Gria2	Rtn1	4.980453
37	Celf4	Nrxn1	4.943868
38	Atxn7l3b	Syt11	4.912797
39	Hk2	Syt11	4.887612
40	Aco2	Psip1	4.887609
41	Ank3	Tspan13	4.887433
42	Camk2n1	Celf4	4.858768
43	Ncf2	Rhog	4.849082
44	Frmd4a	Phf14	4.845105
45	Foxp1	Gria2	4.803401
46	Hk2	Phf14	4.799668
47	Syt11	Zc3h13	4.781255
48	Eif4g2	Rtn1	4.779969
49	Nrxn1	Zmynd11	4.770691
50	Asph	Fgd2	4.770250

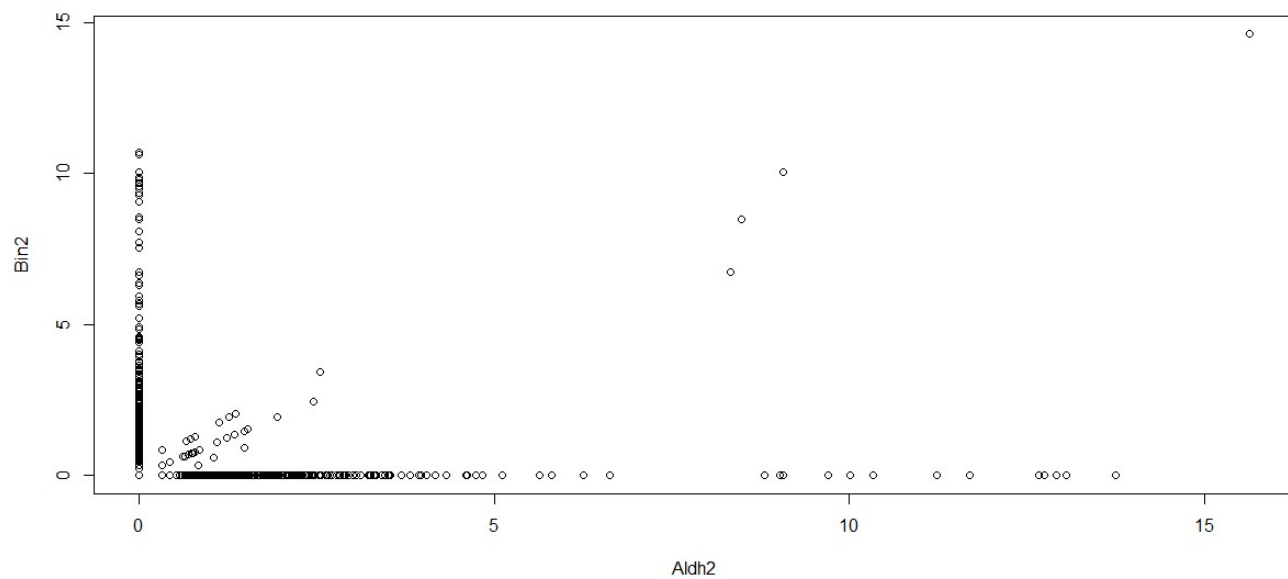
CLR Network



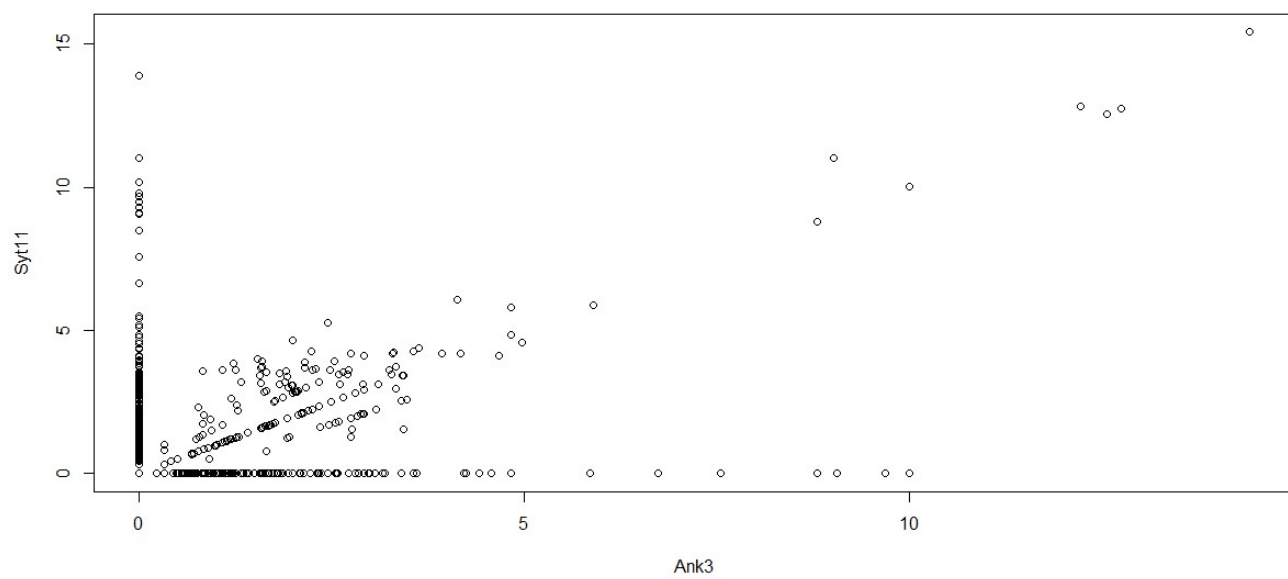
Interaction # 1



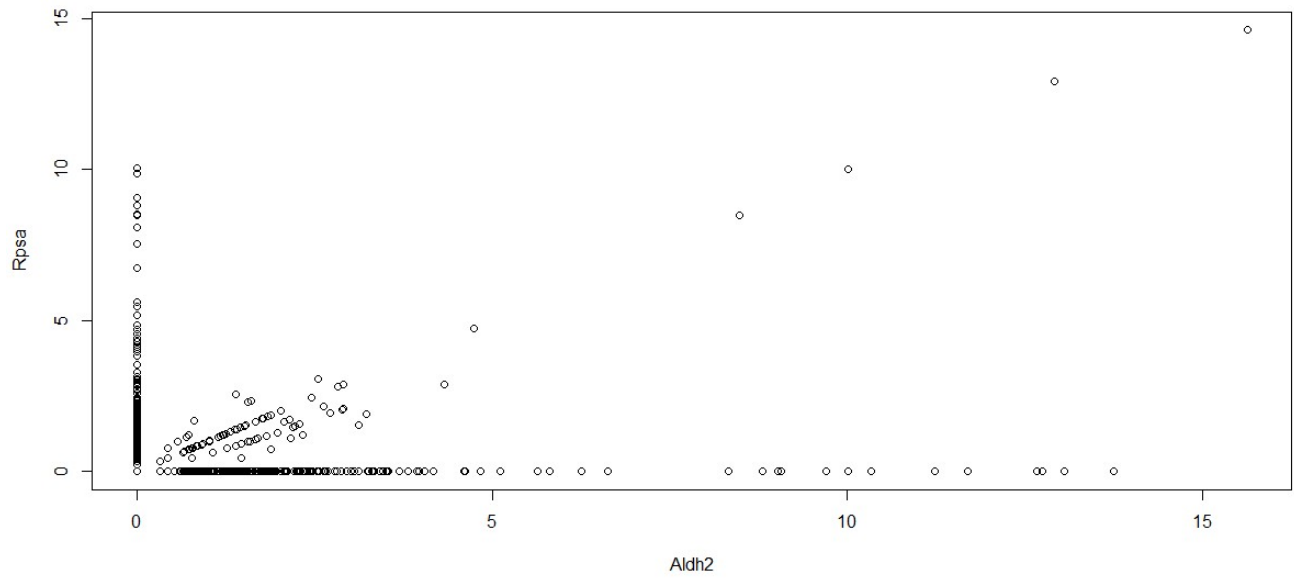
Interaction # 2



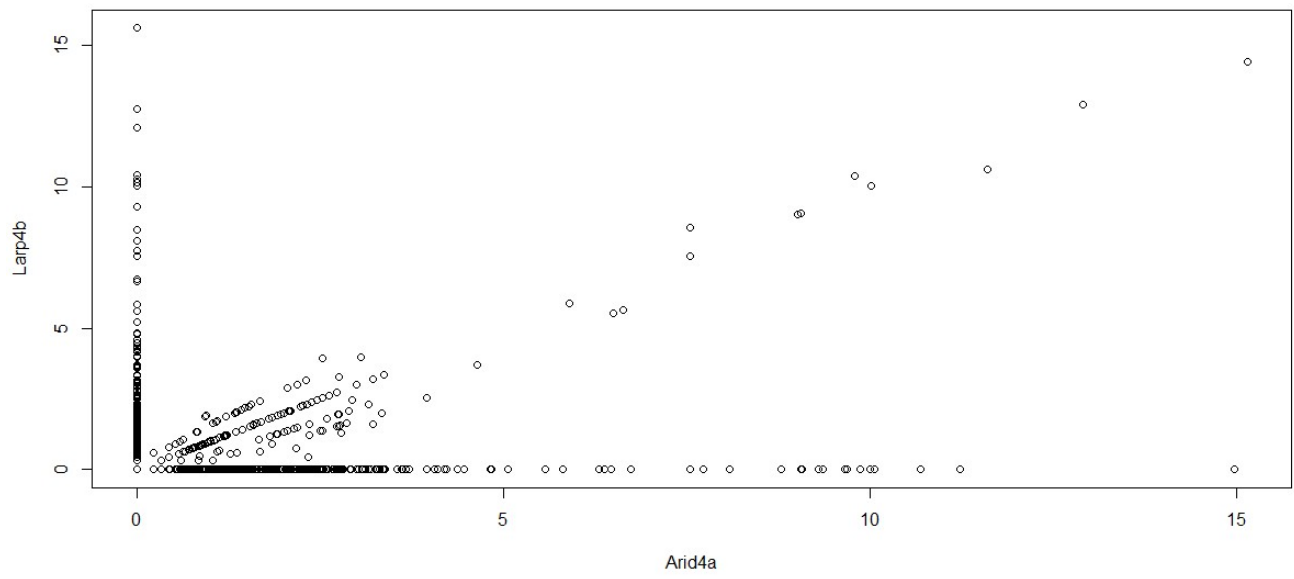
Interaction # 3



Interaction # 4



Interaction # 5



Bottom-ranked Interaction

