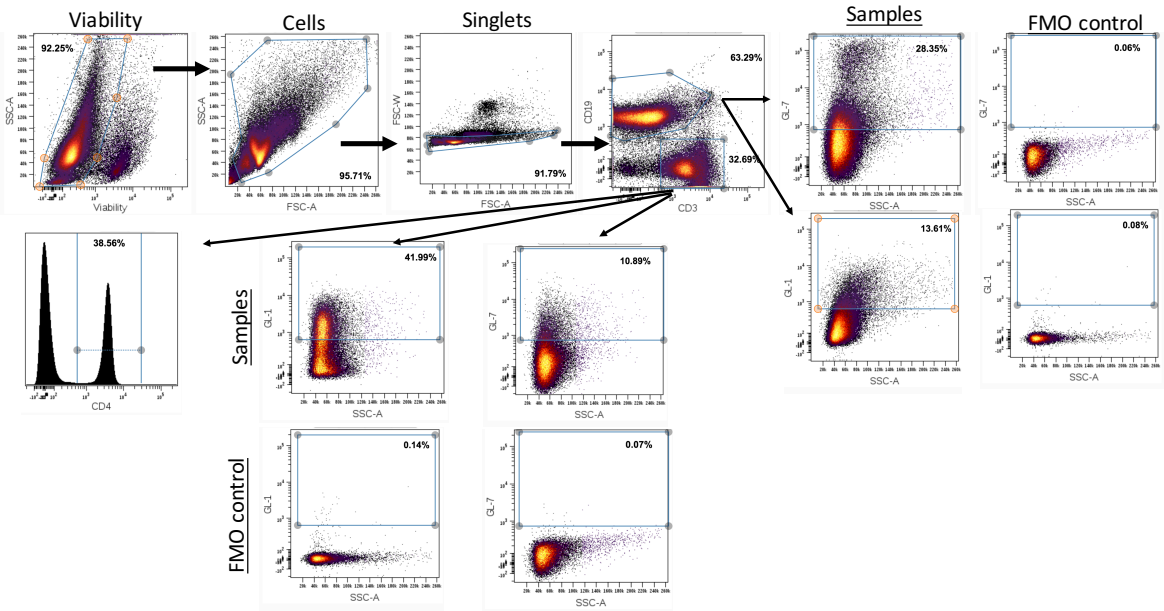

Supplemental Figure 1 B and T Lymphocyte Gating Strategy

Representative gating strategy used to distinguish activated B and T cells or germinal center T cells and B cells. Also shown are fluorescent minus one controls demonstrating how positive staining was confirmed.

Top 200 upregulated genes

Gene	log2(fold_change)	q_value
Il17f	4.01	1.20E-02
Mki67	3.14	0.00E+00
Oxtr	2.89	1.07E-05
Gm4759	2.58	0.00E+00
Plin4	2.46	0.00E+00
Kif20b	2.44	9.77E-06
Slx4	2.24	6.55E-07
Ltf	2.15	1.49E-06
Lipf	2.14	3.59E-02
Uvssa	2.10	1.04E-05
Kif15	2.07	6.02E-04
Ankrd11	2.06	8.79E-12
Gen1	2.06	7.11E-03
Golga4	2.04	1.90E-11
Chd7	1.99	2.64E-10
Nin	1.99	8.77E-10
Gm8979	1.99	0.00E+00
Pou2f2	1.96	7.06E-08
Fcamr	1.94	9.85E-03
Ngp	1.94	3.60E-11
Rest	1.92	1.17E-07
Nipbl	1.91	1.63E-08
Camp	1.90	6.27E-08
Eppk1	1.87	7.34E-08
Kif4	1.87	5.96E-04
Trim56	1.87	3.06E-08
Ckap2l	1.85	4.19E-05
Hivep1	1.85	5.76E-11
Cep110	1.85	8.18E-05
Zfp957	1.84	7.94E-07
Gvin1	1.84	7.15E-10
Setd2	1.83	0.00E+00
Mll1	1.83	1.17E-12
Upf1	1.82	4.20E-09
Mis18bp1	1.81	1.30E-03
Lcn2	1.80	7.11E-06
Lyst	1.79	3.10E-11
Akap13	1.77	0.00E+00
Cep250	1.77	2.23E-07
Zbtb38	1.77	1.34E-06
Bod1l	1.76	1.99E-08
Rrbp1	1.76	2.37E-09
Mns1	1.76	6.38E-03
Ccdc88c	1.75	3.06E-08
Smc4	1.74	3.03E-13
Myh10	1.72	4.99E-12
Golga3	1.72	4.73E-08
Srrm2	1.72	7.75E-10
Tcf20	1.71	2.92E-07
Zfp646	1.70	1.19E-10
Myh11	1.70	1.01E-12
Zbtb16	1.69	5.91E-03
Limch1	1.68	1.25E-02
Cep350	1.68	1.59E-10
Tnrc18	1.68	1.27E-06
Gm608	1.67	4.75E-11
Chd5	1.67	1.08E-04
Iqgap3	1.66	3.49E-04
Ankrd12	1.66	8.30E-08
Dvl3	1.65	1.48E-04
Brwd3	1.65	3.76E-05
Chd3	1.65	1.73E-12
Pcnt	1.65	2.17E-07
Tcof1	1.64	6.26E-06
Plec	1.64	1.34E-07
Gm7134	1.64	2.24E-02
Fancm	1.63	3.22E-04
2810474O19R	1.63	4.03E-09
Tpr	1.62	3.08E-07
Prrc2c	1.62	8.61E-12
Syne3	1.62	1.73E-05
5830417I10Rik	1.62	9.96E-12
Spen	1.61	3.23E-06
Mest	1.59	1.29E-06
Mll5	1.59	2.88E-08
Cep135	1.59	4.74E-04
Akap9	1.58	2.69E-06
Cdk5rap2	1.58	3.46E-06
Phf3	1.57	1.00E-10
Crebbp	1.57	6.95E-08
Prr14l	1.57	2.37E-09
Adam12	1.57	1.15E-06
Gcc2	1.56	8.77E-06
Upf3b	1.56	8.18E-05
Ciita	1.56	1.60E-10
Med13l	1.56	5.44E-09
Gon4l	1.55	2.44E-06
Kif21b	1.55	3.22E-12
Myh9	1.54	0.00E+00
Ckap5	1.54	1.99E-07
Igfbp2	1.53	9.29E-03
Tph2	1.53	2.79E-03
Nktr	1.53	1.92E-07
Myh14	1.53	2.34E-07
Atp10d	1.53	1.23E-04
Cspp1	1.53	1.16E-03
Clip1	1.53	1.50E-07
Dlgap5	1.52	5.58E-03
Kat6a	1.51	2.02E-12

Gene	log2(fold_change)	q_value
Saa3	1.51	4.98E-03
Ncoa6	1.51	8.60E-09
Kif11	1.50	5.74E-06
Il21	1.50	4.07E-02
Rif1	1.50	4.50E-07
Mll2	1.50	1.16E-08
Myo9b	1.49	1.38E-06
Top2a	1.49	5.95E-09
Itsn2	1.49	5.45E-05
Chd6	1.49	8.15E-08
Mcm10	1.48	8.87E-03
BC018507	1.48	2.24E-08
Szt2	1.48	4.75E-03
Pik3c2b	1.47	3.13E-06
Kif18b	1.47	1.54E-03
Chd4	1.47	5.51E-13
Akna	1.47	1.24E-11
Cntln	1.47	1.52E-02
Lmtk2	1.47	4.47E-08
Apc	1.46	8.43E-09
Klf7	1.46	1.37E-02
Nlrc3	1.46	1.21E-03
Zfml	1.46	9.87E-07
Plcb4	1.46	6.91E-03
BC005561	1.46	1.18E-07
Zfp831	1.45	5.15E-08
Tnrc6b	1.44	4.35E-06
Card11	1.44	4.03E-09
Smg1	1.44	3.94E-10
Wbp7	1.44	2.92E-07
Nol8	1.43	1.85E-03
Zfp608	1.43	5.52E-06
Zfp292	1.42	9.96E-09
Stk10	1.42	2.89E-11
Golgb1	1.42	2.91E-06
Sptbn1	1.42	7.58E-12
Trrap	1.42	1.99E-07
Ppp1r12a	1.42	1.98E-07
Gm4975	1.41	3.23E-02
Adap2	1.41	3.16E-02
Sltm	1.41	6.74E-06
Fry	1.41	1.50E-05
Macf1	1.40	4.81E-07
Upf2	1.39	2.07E-06
Zcchc6	1.39	2.17E-07
Cenpj	1.39	9.47E-03
Ylpm1	1.39	3.47E-07
Arid5b	1.38	6.94E-06
Nsd1	1.38	3.60E-10
Rfc1	1.38	5.62E-07
Ankhd1	1.37	6.37E-09
Atrx	1.37	4.03E-09
Bdp1	1.37	8.20E-06
Eea1	1.37	3.65E-06
Gm13034	1.37	2.30E-06
Zfp609	1.36	9.84E-06
Zcchc11	1.36	1.23E-08
Tmie	1.36	1.96E-02
Ankrd52	1.36	2.21E-07
Zfp335	1.36	1.76E-04
Gm1995	1.36	7.89E-05
Arid1a	1.36	1.29E-10
Acin1	1.36	3.31E-03
Fbln2	1.36	8.50E-04
Znf512b	1.36	2.17E-02
Nemf	1.35	4.16E-05
Depdc5	1.35	7.23E-04
Cep164	1.35	2.72E-04
Gm5124	1.35	2.13E-06
Bcl9l	1.35	6.88E-07
Tln2	1.34	7.41E-05
Hp	1.34	1.86E-08
Rb1cc1	1.34	1.33E-06
Tln1	1.34	2.50E-11
Kdm6b	1.33	2.02E-05
Uaca	1.33	1.73E-04
Herc1	1.33	7.53E-07
Tshz3	1.33	1.50E-02
Smarca4	1.33	3.06E-08
Casp8ap2	1.33	2.79E-05
Setd5	1.33	1.67E-08
Ino80	1.32	1.01E-05
Gdf11	1.32	5.08E-03
Trip11	1.32	8.01E-05
Prdm2	1.32	9.64E-08
Clspn	1.32	1.11E-02
Bclaf1	1.31	1.71E-07
E2f8	1.31	4.14E-03
Sfswap	1.31	2.18E-04
Atad2	1.31	1.06E-05
Hivep3	1.31	5.89E-04
Dnmt1	1.31	7.29E-06
Igfbp5	1.31	4.41E-11
Zfp407	1.31	5.74E-05
Esf1	1.31	2.39E-04
Rexo1	1.31	6.78E-05
Dot1l	1.31	2.09E-04
Atp2b4	1.30	4.19E-06
Dzip1	1.30	1.27E-02
Brpf3	1.30	3.73E-05

Top 200 downregulated genes

Gene	log2(fold_change)	q_value
Laptm4a	-0.55	5.51E-03
Rpl27a	-0.55	1.01E-02
Tspan3	-0.55	7.13E-03
2010107E04R	-0.55	1.36E-02
Mgst1	-0.55	1.40E-02
Sult1a1	-0.55	3.26E-02
Ier2	-0.55	2.91E-02
Rpl35a	-0.56	8.16E-03
Angptl4	-0.56	4.74E-02
Car3	-0.56	1.75E-02
Rplp1	-0.56	9.99E-03
Itm2a	-0.56	1.93E-02
Pfdn5	-0.56	4.35E-03
S100a16	-0.56	2.01E-02
Ndufa6	-0.57	1.06E-02
Bst2	-0.57	1.62E-02
Rps15a	-0.57	8.74E-03
Churc1	-0.57	1.93E-02
Rpl37a	-0.57	4.95E-03
Bpgm	-0.57	2.58E-02
Rgs18	-0.57	4.91E-02
Rps24	-0.57	1.97E-02
Rps15a-ps6	-0.57	3.20E-02
Rps27a	-0.57	5.29E-03
Sptssa	-0.57	4.78E-03
Havcr1	-0.58	4.36E-02
Laptm4b	-0.58	1.10E-02
Mrpl52	-0.58	2.50E-02
Nenf	-0.58	3.64E-02
Rpl22	-0.58	3.46E-03
Rpl38	-0.58	3.17E-03
Rps15a-ps4	-0.58	2.52E-02
Gm4832	-0.58	3.73E-02
Gm6525	-0.58	4.96E-03
Rpl22l1	-0.58	3.12E-03
Cd209b	-0.58	4.52E-03
Rps18	-0.58	6.48E-03
Usp18	-0.58	3.86E-02
Rpl36a	-0.59	2.65E-03
Rps21	-0.59	2.85E-03
Klf10	-0.59	2.44E-02
Rps28	-0.59	2.29E-03
Gm15421	-0.59	2.83E-03
Klk8	-0.60	1.07E-02
Tmem160	-0.60	1.40E-02
Ube2l6	-0.60	5.49E-03
Cd209c	-0.60	1.79E-02
Cd209e	-0.60	2.44E-02
Lhfp	-0.60	1.45E-02
Sox18	-0.61	4.71E-02
Uqcrh	-0.61	1.52E-03
Rgs10	-0.61	2.59E-03
Siglech	-0.61	9.81E-03
Bok	-0.62	1.67E-02
Fmo1	-0.62	7.13E-03
Tspan7	-0.62	2.09E-03
Bod1	-0.62	3.04E-02
Bola3	-0.62	2.78E-02
Folr4	-0.62	2.30E-02
Rps12	-0.62	1.47E-03
Fam198b	-0.62	3.33E-02
Rpl39	-0.63	2.12E-03
Cmpk2	-0.63	3.62E-02
Camk1	-0.63	4.42E-02
Xaf1	-0.63	4.74E-02
Nt5c3	-0.63	3.36E-02
Prg3	-0.63	2.74E-02
Fcgr1	-0.63	4.09E-02
Tm4sf1	-0.65	6.08E-03
Paox	-0.65	1.90E-02
Oas1g	-0.65	2.73E-02
Oas1a	-0.66	2.42E-02
Gm13476	-0.66	4.43E-02
Tmem98	-0.67	2.58E-02
Dusp1	-0.67	8.00E-03
Tal1	-0.67	4.10E-02
2610035D17R	-0.68	1.39E-02
Mmrn1	-0.68	1.24E-02
Cma1	-0.68	5.18E-04
Wfdc18	-0.69	2.26E-02
Klhl4	-0.69	1.48E-02
Dab2	-0.69	7.66E-03
Cpa3	-0.70	5.44E-04
Irf7	-0.70	2.24E-02
Wfdc17	-0.71	4.81E-03
Gng11	-0.71	1.40E-03
Ccl12	-0.72	2.18E-02
Jam3	-0.74	3.15E-04
Mgp	-0.75	2.38E-02
Cfhr2	-0.76	3.17E-03
Aldh1l1	-0.76	2.46E-02
Efna1	-0.76	2.02E-02
Ninj1	-0.76	1.41E-04
Nrep	-0.76	4.95E-02
Fcer1a	-0.76	7.11E-03
Sepp1	-0.77	1.76E-03
Hbb-b1,Hbb-b	-0.77	4.61E-02
Ces1d	-0.77	1.49E-02
Oas3	-0.77	4.97E-02

Gene	log2(fold_change)	q_value
Gpr34	-0.78	9.32E-04
Gpx6	-0.78	3.95E-02
Reln	-0.78	1.80E-02
Hspb11	-0.79	2.45E-02
Ms4a8a	-0.79	1.83E-02
Cd209d	-0.79	2.76E-04
Mrgprx2	-0.79	2.59E-03
Sh3gl3	-0.80	1.40E-02
Cfhr1	-0.81	1.98E-03
Dnahc6	-0.81	2.20E-02
Hscb	-0.81	2.43E-03
Cdo1	-0.82	9.24E-03
Gpx3	-0.82	3.50E-05
Syngr1	-0.82	2.77E-02
Il15	-0.82	9.03E-03
Ppp1r3c	-0.83	1.05E-02
Ccl8	-0.83	1.01E-05
Pck1	-0.84	3.95E-02
Hes1	-0.85	2.59E-03
Gpm6a	-0.85	4.74E-04
Id1	-0.85	4.56E-03
Khdrbs3	-0.89	2.43E-02
Tpsab1	-0.89	2.25E-04
Ccdc148	-0.90	6.81E-03
Tpsb2	-0.90	1.20E-06
Cd209a	-0.91	2.51E-04
Adh1	-0.91	8.67E-05
Hoxd10	-0.91	1.14E-02
Mrgprb1	-0.92	8.16E-05
Retn	-0.92	1.25E-02
Hist3h2ba	-0.92	4.11E-02
Rtp4	-0.93	3.71E-04
Oosp1	-0.94	1.70E-02
Nnat	-0.95	4.51E-02
Inmt	-0.95	5.74E-06
Fxyd6	-0.96	6.86E-06
Upb1	-0.96	2.18E-02
Slc6a4	-0.96	1.30E-03
Cldn5	-0.97	7.45E-07
Klrg1	-0.97	2.96E-02
Xlr3b	-0.98	1.07E-02
Rsad2	-0.98	2.31E-03
Xlr3c	-0.98	1.13E-02
Mrgprb2	-0.99	1.20E-03
Il22ra2	-1.00	2.21E-07
Klk1b9	-1.05	2.03E-02
Slc40a1	-1.08	5.46E-08
Enho	-1.08	7.02E-03
Fibin	-1.08	2.46E-02
Mylpf	-1.09	1.36E-02
Cldn11	-1.09	5.30E-05
Atp8b5	-1.11	8.97E-04
Rbp4	-1.12	6.49E-03
Klk1b24	-1.14	1.32E-02
Klk1b21	-1.14	8.94E-03
Xlr3a	-1.15	3.68E-03
Sncb	-1.15	2.53E-02
Gabra3	-1.16	1.47E-02
Slc13a3	-1.17	4.86E-02
Clec4g	-1.19	3.90E-04
Hba-x	-1.19	1.24E-02
Tm4sf20	-1.20	9.29E-03
Klk1b4	-1.20	7.68E-03
Ngb	-1.21	4.91E-02
Cbr2	-1.24	3.41E-07
Klk1b3	-1.25	2.84E-03
Ckm	-1.26	2.37E-03
Tnni2	-1.27	2.47E-04
Timp4	-1.27	9.77E-06
Klk1	-1.28	7.21E-04
Klk1b5	-1.28	1.19E-03
Gm4956	-1.32	4.33E-03
Cyp2f2	-1.35	1.71E-07
Hbb-bh2	-1.36	7.14E-06
Hbb-y	-1.38	1.70E-06
C1ql2	-1.39	5.40E-03
Hbq1a	-1.39	2.81E-03
Mpz	-1.40	1.57E-03
Alas2	-1.40	3.06E-07
Ifi44	-1.41	2.42E-05
Beta-s	-1.41	5.44E-09
Hbb-bh1	-1.42	2.45E-10
Cd209g	-1.42	4.73E-09
Cd209f	-1.44	4.30E-10
Hba-a1,Hba-a	-1.46	4.70E-08
Hbq1b	-1.46	1.32E-03
Klk1b11	-1.48	6.47E-03
Ifit3	-1.55	1.10E-09
I830012O16R	-1.56	1.07E-09
Hba-a2	-1.56	3.32E-03
Snca	-1.66	1.42E-02
Isg15	-1.67	2.82E-09
Thrsp	-1.76	2.34E-09
Fos	-1.78	0.00E+00
Smpx	-1.81	4.54E-02
Ppbp	-1.81	2.65E-03
Hbb-b2	-2.31	2.28E-04
Myoz1	-2.54	3.86E-02
Pvalb	-2.67	4.86E-06
Cyp2e1	-2.68	0.00E+00
Tnnc2	-4.20	1.04E-05

Supplementary Table 1 List of top upregulated and downregulated genes in obese lymph nodes

Popliteal lymph nodes were isolated from naïve obese/T2D and control mice and whole transcriptome analysis performed (see Fig 7 for analysis). Shown are the top 200 significantly upregulated and downregulated genes in obese/T2D mice relative to lean-fed control mice. n= 3 mice per group.