

S1 Fig. Genes specifically expressed between L-DC and CD8⁺ cDC.

Gene Symbol	Fold-Change (L-DC vs. CD8 ⁺ cDC) ⁺	L-DC		CD8 ⁺ cDC	
		Mean*	Standard Error	Mean*	Standard Error
<i>Zeb2</i>	14.837	548.052	67.119	36.668	0.693
<i>Ifitm6</i>	14.407	646.978	112.504	44.228	0.583
<i>Gm9733</i>	14.262	508.325	16.090	35.626	0.282
<i>Gzmb</i>	13.854	451.871	24.728	33.097	5.901
<i>Ms4a4a</i>	13.817	511.336	80.421	36.838	4.618
<i>Atp1a3</i>	13.665	528.196	5.192	38.733	2.487
<i>Llcam</i>	13.556	448.746	22.570	33.109	1.794
<i>Gda</i>	12.573	385.173	7.133	30.667	1.525
<i>Sqrdl</i>	12.326	328.967	23.265	27.184	5.500
<i>Pltp</i>	12.081	485.865	58.788	39.922	0.244
<i>Lrp1</i>	11.975	375.113	16.648	31.303	0.711
<i>Lilra5</i>	11.826	442.285	10.181	37.485	2.662
<i>Ncr1</i>	11.540	393.951	22.797	34.091	0.864
<i>C3</i>	11.306	425.896	13.786	37.653	0.302
<i>Pla2g7</i>	11.213	510.647	32.392	45.452	0.237
<i>Tlr8</i>	11.029	361.373	32.602	32.676	1.666
<i>Abcd2</i>	10.848	260.523	7.352	24.036	1.217
<i>Nupr1</i>	10.478	481.366	36.486	45.904	2.918
<i>Hgf</i>	10.139	278.901	5.863	27.518	0.972
<i>Ikzf3</i>	9.856	290.713	35.031	29.362	2.181
<i>Fam46a</i>	9.784	378.418	16.911	38.660	1.309
<i>Krt80</i>	9.635	423.455	0.465	43.950	0.235
<i>Sepp1</i>	9.454	326.572	47.610	34.184	0.839
<i>Gm5150</i>	9.449	367.228	82.481	37.895	1.292
<i>A630033H20Rik</i>	9.332	320.050	30.498	34.168	1.417
<i>Irak3</i>	9.060	264.136	8.938	29.259	2.663
<i>Pparg</i>	8.974	421.427	17.184	46.938	1.276
<i>Abca9</i>	8.492	234.244	11.094	27.566	0.790
<i>Klra8</i>	8.341	236.170	3.963	28.324	0.895
<i>Fcgr3</i>	8.200	300.711	28.094	36.512	0.215
<i>Zfyve9</i>	8.196	308.588	0.476	37.663	0.892
<i>Fam55d</i>	8.157	251.301	1.203	30.864	1.892
<i>Arhgef3</i>	7.919	387.354	66.081	48.211	1.141
<i>Mgst1</i>	7.917	166.937	11.405	21.039	0.326
<i>Slpr5</i>	7.904	303.395	4.288	38.477	2.729
<i>Plxnb2</i>	7.784	287.536	21.735	36.948	2.883
<i>Mdm1</i>	7.713	260.629	0.366	33.795	0.634
<i>Ccl9</i>	7.643	328.078	28.768	42.763	0.557
<i>Gimap4</i>	7.342	289.814	26.903	39.306	0.373
<i>Svil</i>	7.290	256.716	10.133	35.245	2.054
<i>Trem3</i>	7.262	357.258	13.473	49.163	0.101
<i>Cd300lb</i>	7.242	218.947	2.567	30.237	0.582
<i>Ccdc125</i>	6.898	197.052	2.197	28.629	1.895
<i>Trem1</i>	6.609	211.974	11.743	32.028	0.462
<i>Gstm1</i>	6.574	212.010	26.095	32.115	2.644
<i>Rhoq</i>	6.467	256.344	4.777	39.630	0.193
<i>Tmem26</i>	6.400	244.988	24.831	38.142	2.108
<i>Xylt1</i>	6.398	273.414	24.012	42.585	1.186
<i>Rtp4</i>	6.380	197.046	9.031	30.881	1.326
<i>Pros1</i>	6.351	179.988	24.135	28.108	1.130
<i>Apoc2</i>	6.340	240.037	11.321	37.820	0.295
<i>Hp</i>	6.313	182.405	43.577	28.123	1.913

<i>Tmem71</i>	6.311	151.394	20.686	23.769	0.444
<i>Fpr1</i>	6.308	169.278	2.425	26.835	0.312
<i>Thbd</i>	6.226	211.722	25.817	33.902	3.149
<i>S100a6</i>	6.167	219.687	25.302	35.415	1.409
<i>Cd84</i>	6.158	228.672	10.700	37.366	4.491
<i>Rbpms</i>	6.026	288.010	12.871	48.001	4.910
<i>Tbc1d2b</i>	5.971	191.380	0.900	32.084	1.493
<i>Csf3r</i>	5.969	163.212	1.153	27.365	1.077
<i>Map3k15</i>	5.930	247.350	7.442	41.866	3.836
<i>B4galt5</i>	5.804	270.397	21.621	46.762	5.476
<i>Cyp4f18</i>	5.798	195.922	7.464	33.830	2.110
<i>Abi3</i>	5.691	188.720	13.844	33.098	1.328
<i>Gcnt2</i>	5.659	201.374	9.994	35.548	0.638
<i>Ms4a6d</i>	5.547	158.618	7.103	28.609	1.567
<i>Rap1gap2</i>	5.470	212.381	9.855	38.794	0.906
<i>6430548M08Rik</i>	5.397	215.089	13.036	39.859	2.514
<i>Pdlim1</i>	5.343	244.698	2.334	45.881	2.751
<i>Alox5</i>	5.338	176.833	3.283	33.130	0.641
<i>Ttc39a</i>	-5.281	41.159	1.918	217.696	15.663
<i>Amical</i>	-5.347	38.433	1.812	206.023	17.717
<i>Trpm2</i>	-5.403	44.730	0.361	244.203	35.127
<i>Frmd4b</i>	-5.486	43.374	2.417	237.666	6.732
<i>Gca</i>	-5.498	45.694	2.830	252.937	33.173
<i>Fam149a</i>	-5.810	27.369	1.392	159.397	13.597
<i>Fnip2</i>	-6.095	42.679	5.517	259.547	28.938
<i>Actn1</i>	-6.103	34.869	2.537	212.299	5.480
<i>Met</i>	-6.298	35.512	2.706	223.965	20.668
<i>Cxcl16</i>	-6.382	42.028	0.692	268.406	11.225
<i>Ppef2</i>	-6.640	32.921	0.067	218.863	10.681
<i>Fndc7</i>	-6.643	29.337	0.427	194.899	4.072
<i>Nek6</i>	-6.724	34.587	2.361	232.055	4.099
<i>H2-Oa</i>	-6.780	32.437	0.130	221.097	22.887
<i>Cdon</i>	-6.952	41.034	2.449	284.776	0.732
<i>Rab30</i>	-7.135	42.721	0.268	304.795	0.546
<i>Clec1a</i>	-7.266	29.651	0.328	215.436	2.336
<i>Itgae</i>	-7.569	29.068	0.032	221.400	24.737
<i>Rnf144b</i>	-7.821	33.829	4.037	264.515	31.007
<i>Ecel</i>	-7.880	47.285	0.344	374.364	36.515
<i>Plekha5</i>	-8.317	42.413	6.056	349.171	6.188
<i>Fam40b</i>	-8.470	30.717	1.708	262.130	35.061
<i>Ciita</i>	-8.991	43.440	2.971	391.061	33.038
<i>Gatm</i>	-9.527	32.792	2.301	311.982	14.869
<i>Kmo</i>	-10.016	47.450	3.216	474.173	1.057
<i>Adam19</i>	-10.264	40.698	1.667	418.164	25.395
<i>Gcet2</i>	-10.314	30.685	0.161	316.697	11.734
<i>Pdia5</i>	-10.391	34.510	2.207	360.117	40.376
<i>Adam8</i>	-10.538	45.131	0.709	476.002	21.794
<i>Hepacam2</i>	-11.851	23.649	1.339	280.052	11.621
<i>Kit</i>	-12.288	45.381	3.567	556.738	30.154
<i>Cacna1e</i>	-13.444	34.281	0.870	461.562	27.567
<i>Ly75</i>	-13.465	44.834	0.452	603.775	10.825
<i>Tlr3</i>	-14.975	30.232	1.223	452.356	2.728

⁺ Genes were selected which showed between 5 to 15 fold change in signal value where one subset has signal value ≤ 50 and the comparison subset has a signal value ≥ 150 , in either L-DC or CD8⁺ cDC assessed in pairwise comparison.

* Data represent mean of duplicate samples (n=2).