

Supplementary data

Figure S1 Transcriptional profiling of canine B cell lymphoma patients stratified by median time to progression (mTTP). **A.** volcano plot and **B.** gene clustering depicted by heatmap (Data derived from NanoString canine IO panel and analyzed using the ROSALIND platform, colors of the heatmap represent log₂ normalized gene expression after subtracting the mean on a per-gene basis, blue dots on volcano plot corresponds to blue horizontal bar at the top of heat map and depict genes enriched in dogs with responses above mTTP, orange dots on volcano plot corresponds to orange horizontal bar at the top of heat map and depicts genes enriched in dogs with responses below mTTP).

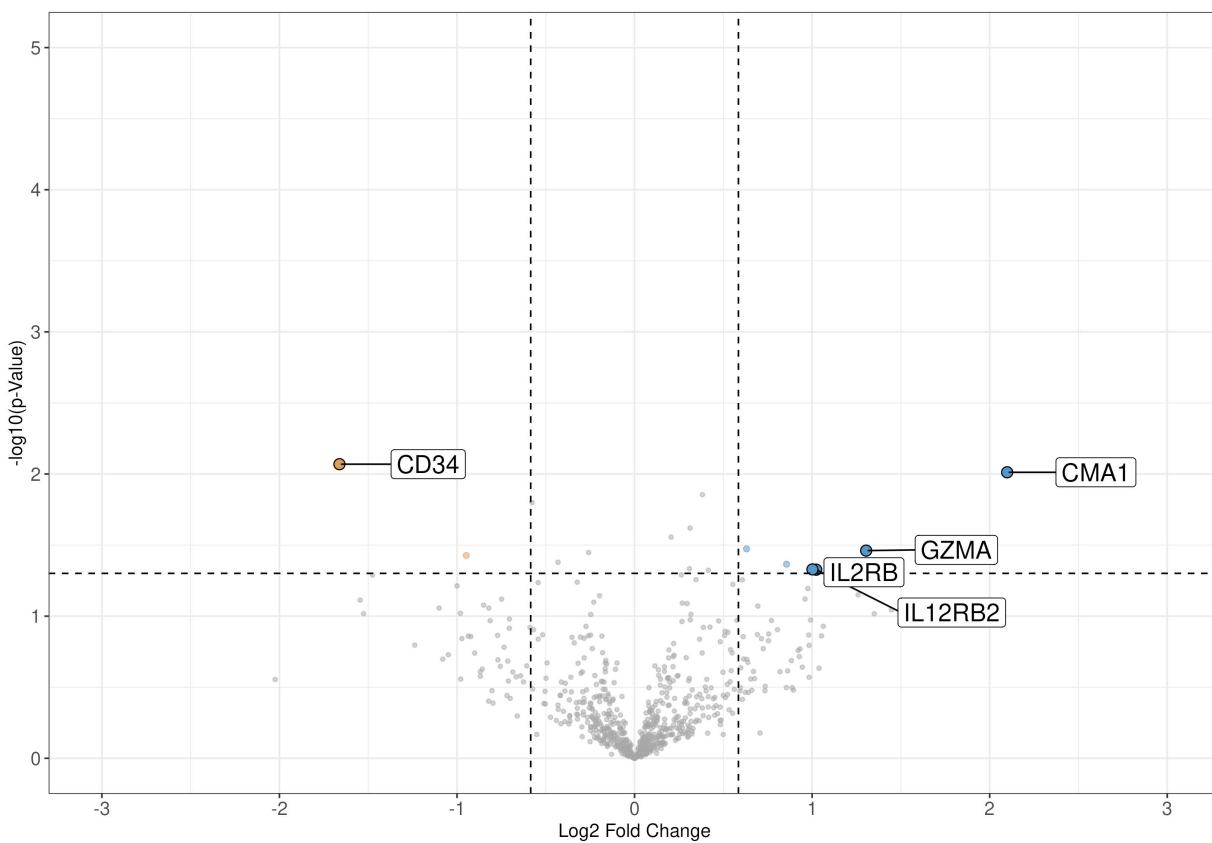
Figure S2 Transcriptional profiling of canine B cell lymphoma patients comparing naive and relapsed samples. **A.** volcano plot and **B.** gene clustering depicted by heatmap (Data derived from NanoString canine IO panel and analyzed using the ROSALIND platform, colors of the heatmap represent log₂ normalized gene expression after subtracting the mean on a per-gene basis, blue dots on volcano plot corresponds to blue horizontal bar at the top of heat map and depict genes enriched in relapses samples, orange dots on volcano plot corresponds to orange horizontal bar at the top of heat map and depicts genes enriched in naive samples).

Figure S3 Circulating biomarker profiling for aggressive canine B cell lymphoma patients stratified by median time to progression (mTTP). **A.** plasma VEGFA concentrations, **B.** plasma IL-6 concentrations, and **C.** neutrophil-to-lymphocyte ratio. (Comparisons between two groups

performed using two-tailed Mann-Whitney tests, $p < *0.05$, $**0.01$, ns = not significant. Dotted lines represent limit of detection).

Figure S4 Circulating biomarker profiling for aggressive canine B cell lymphoma patients comparing naive and relapsed samples. **A.** plasma VEGFA concentrations, **B.** plasma KC-like concentrations, **C.** plasma IL-10, and **D.** plasmaMCP-1. (Comparisons between two groups performed using two-tailed paired Wilcoxon tests, $p < *0.05$, $**0.01$. Dotted lines represent limit of detection).

A



B

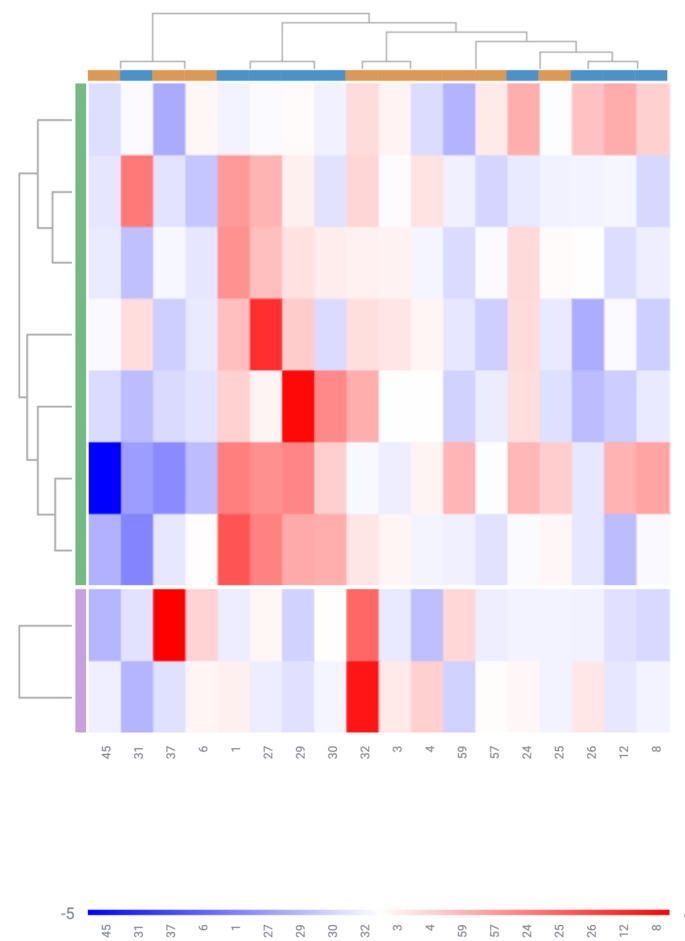
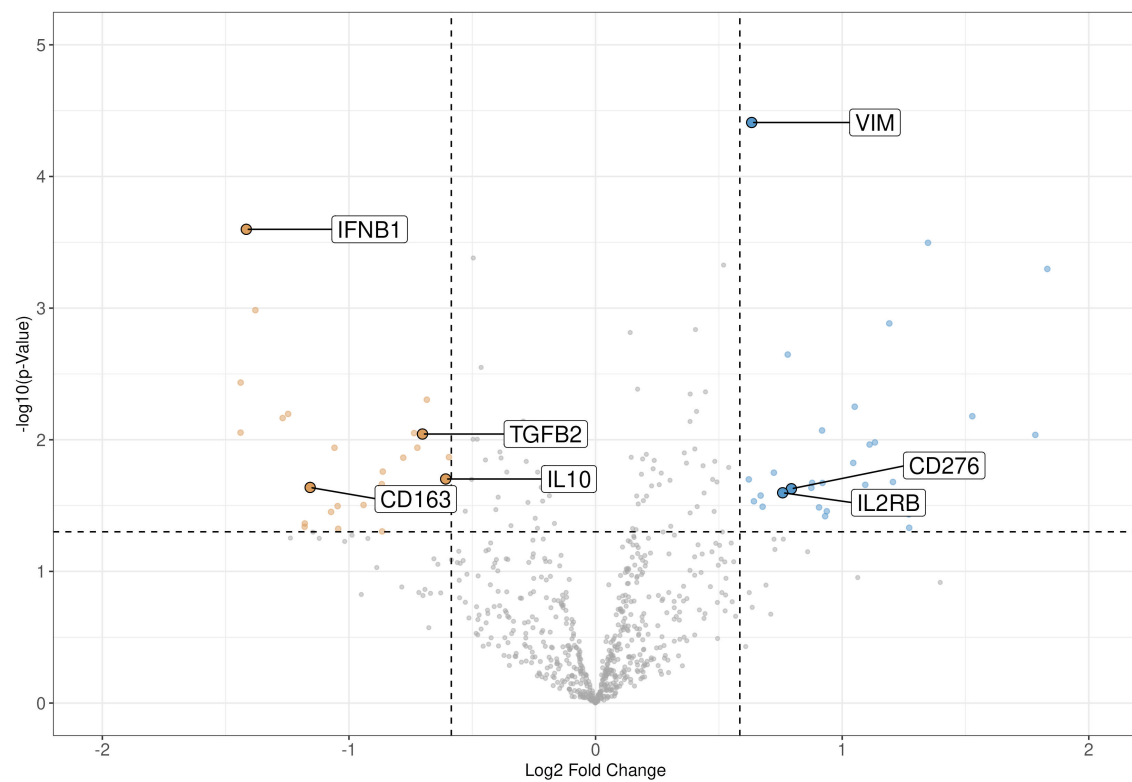


Figure S1

A



B

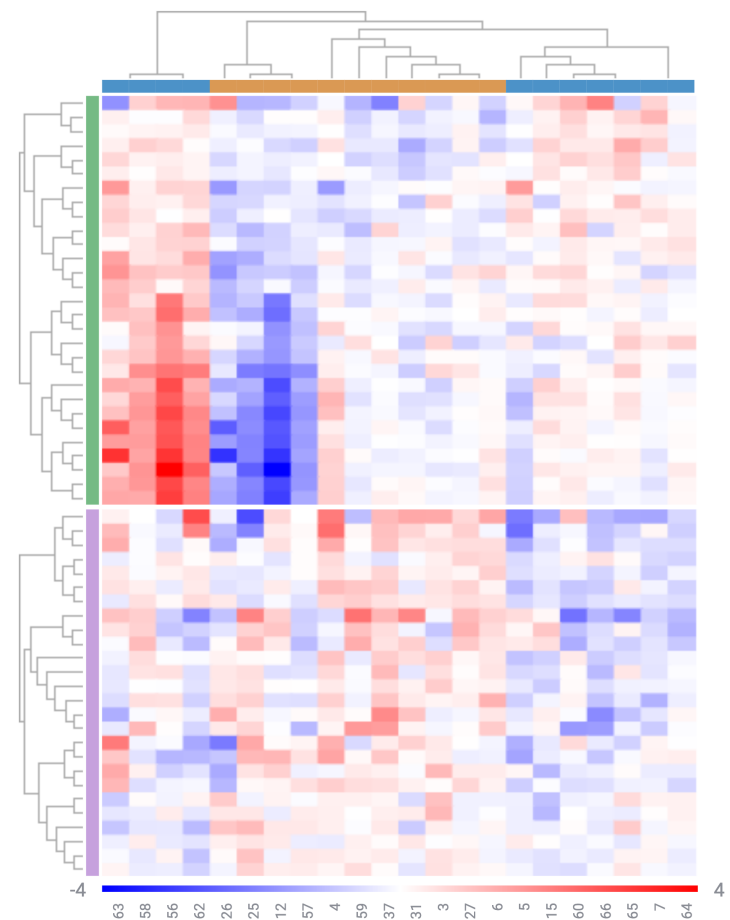


Figure S2

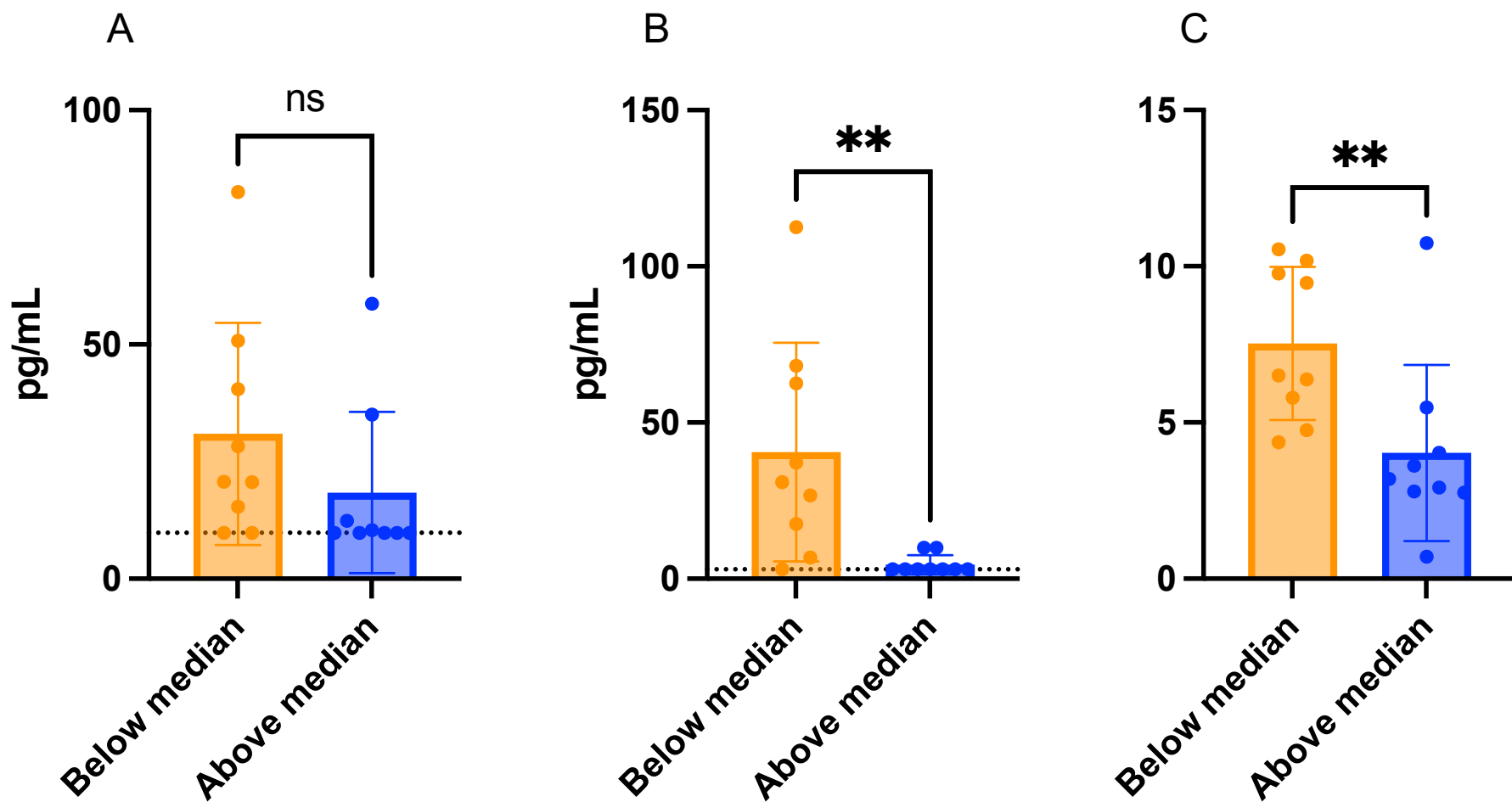


Figure S3

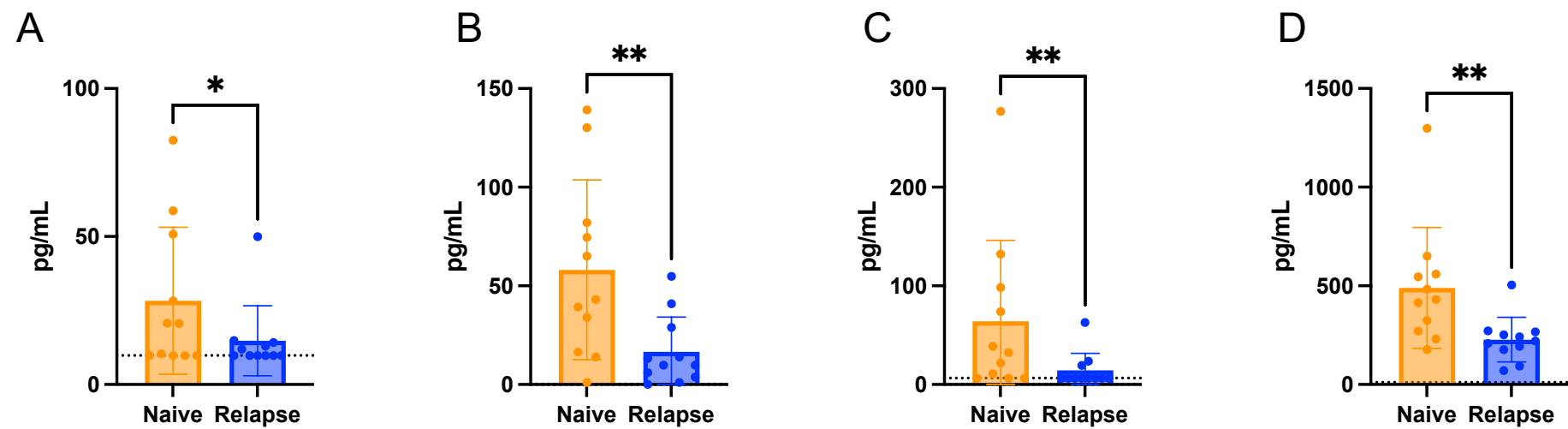


Figure S4

Table S1 CHOP protocol (IV intravenous, PO per os)

Drug	Week																			
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Vincristine 0.6-0.7 mg/m ² IV (<15 kg= 0.5 mg/m ²)	• 0.6		• 0.7			•		•			•		•			•		•		
Cyclophosphamide 250-300 mg/m ² PO + 2 mg/kg PO Furosemide		• 250					• 275					• 300					•			
Doxorubicin 30 mg/m ² IV (<15 kg=1 mg/kg)				•					•					•					•	
Prednisone 40 mg/m ² PO taper	•	•	•	•																

Dosages for vincristine and cyclophosphamide were increased as indicated depending on tolerability, nadir neutrophil and platelet count, and clinician discretion. Patients weighing less than 15 kg were dosed at 1 mg/kg doxorubicin.

Table S2 Differentially expressed genes stratified by median time to progression (mTTP)

Name	Fold Change	p-Value	Name	Fold Change	p-Value
Enriched in patients above mTTP			Enriched in patients below mTTP		
<i>CMA1</i>	4.28261	0.009724	<i>CD34</i>	-3.16486	0.008528
<i>IL7</i>	1.54818	0.033622	<i>CCND3</i>	-1.9289	0.037438
<i>GZMA</i>	2.46972	0.034587			
<i>LGALS3</i>	1.80992	0.043102			
<i>IL2RB</i>	2.00266	0.046912			
<i>IL12RB2</i>	2.03225	0.047104			
<i>CD9</i>	2.22109	0.048695			

Table S3 Differentially expressed genes between naive and relapsed samples

Name	Fold Change	p-Value	Name	Fold Change	p-Value
Enriched in relapsed					
<i>VIM</i>	1.55081	0.000039	<i>CXCR3</i>	1.83829	0.021245
<i>MAPK11</i>	2.5455	0.000319	<i>EGR1</i>	1.89235	0.021278
<i>CX3CR1</i>	3.55974	0.000504	<i>ITK</i>	2.13407	0.021991
<i>DDR1</i>	2.28319	0.001307	<i>IGHG</i>	1.83408	0.02318
<i>AMICA1</i>	1.71604	0.002253	<i>CD276</i>	1.73383	0.023557
<i>NINJ2</i>	2.07174	0.005609	<i>IL2RB</i>	1.69183	0.025267
<i>CD6</i>	2.8832	0.006625	<i>ITGA1</i>	1.59033	0.026531
<i>CD8A</i>	1.88999	0.008498	<i>RORA</i>	1.56051	0.029326
<i>TRGC3</i>	3.44177	0.009186	<i>IL26</i>	1.59925	0.032257
<i>TRAT1</i>	2.19258	0.010475	<i>TRBC</i>	1.87399	0.032621
<i>CD5</i>	2.16021	0.010868	<i>ARG2</i>	1.91518	0.034918
<i>CD8B</i>	2.06314	0.014988	<i>CCL17</i>	2.41193	0.03688
<i>PVR</i>	1.65045	0.017781	<i>TRAC</i>	1.90633	0.038085
<i>TNFRSF17</i>	1.53826	0.020008	<i>CD28</i>	2.41441	0.046635
<i>TCF7</i>	2.3067	0.020923			
Enriched in naive					
<i>IFNB1</i>	-2.66902	0.000252	<i>ELANE</i>	-1.81864	0.017445
<i>ESR2</i>	-2.60176	0.001037	<i>IL10</i>	-1.52397	0.01986
<i>EBI3</i>	-2.71193	0.003676	<i>MME</i>	-1.82379	0.021736
<i>MGMT</i>	-1.6069	0.00496	<i>CD163</i>	-2.2306	0.023022
<i>C4BPA</i>	-2.37316	0.006365	<i>CD200</i>	-1.91969	0.031294
<i>CD70</i>	-2.40974	0.00684	<i>PDGFRA</i>	-2.06497	0.031907
<i>LOC477699</i>	-2.71261	0.008822	<i>CXCL13</i>	-1.54552	0.032276
<i>LOC484343</i>	-1.66527	0.008901	<i>MASP2</i>	-1.84317	0.032638
<i>TGFB2</i>	-1.6267	0.009046	<i>S100A8</i>	-2.10321	0.035321
<i>CSF2RB</i>	-1.65022	0.011495	<i>PDPN</i>	-2.26439	0.043223
<i>MEFV</i>	-2.08317	0.0115	<i>CD1B</i>	-2.26539	0.045821
<i>FCRL2</i>	-1.51	0.013555	<i>LOC102154078</i>	-2.06142	0.047483
<i>PLAU</i>	-1.71697	0.013683	<i>TNFSF18</i>	-1.82191	0.049655