

## Supplementary information

### Functionally significant metabolic differences between B and T lymphocyte lineages (Khalsa et al)

#### Supplementary Tables

**Table S1:** List of genes differentially expressed between splenic follicular B cells and splenic naive T cells.

**Table S2:** List of KEGG pathways related to this study.

**Table S3:** List of genes associated with pathways listed in Table S2.

**Table S4:** Enrichment score of the differentially expressed genes for the KEGG pathways in Table S2.

**Table S5:** List of microarray data sets downloaded from the immunological genome project for developmental stage comparison.

**Table S6:** PCA analysis results shown in Figure 3.

**Table S7:** Results of the pairwise analysis of developmental stage specific gene expression.

**Table S8:** Enrichment scores for gene sets between developmental stages.

**Table S9:** Ribosome profiling differential expression results.

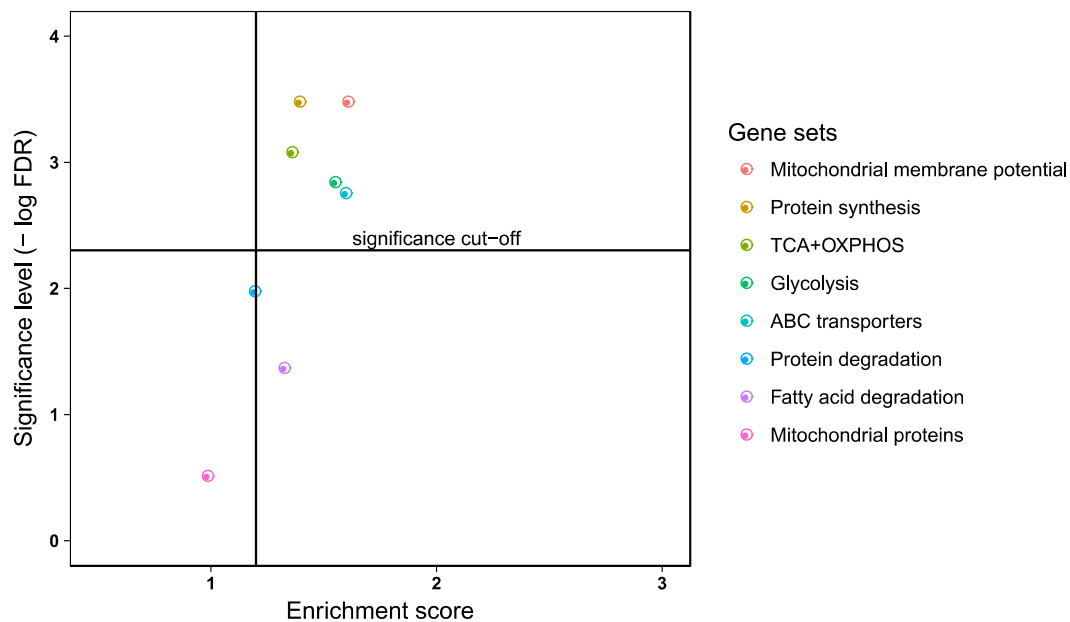
**Table S10:** Translation efficiencies calculated by Ribodiff package.

All supplementary tables are available at:

[https://github.com/savitprabhu/Immunometabolism\\_MS/tree/master/Supplementary](https://github.com/savitprabhu/Immunometabolism_MS/tree/master/Supplementary)

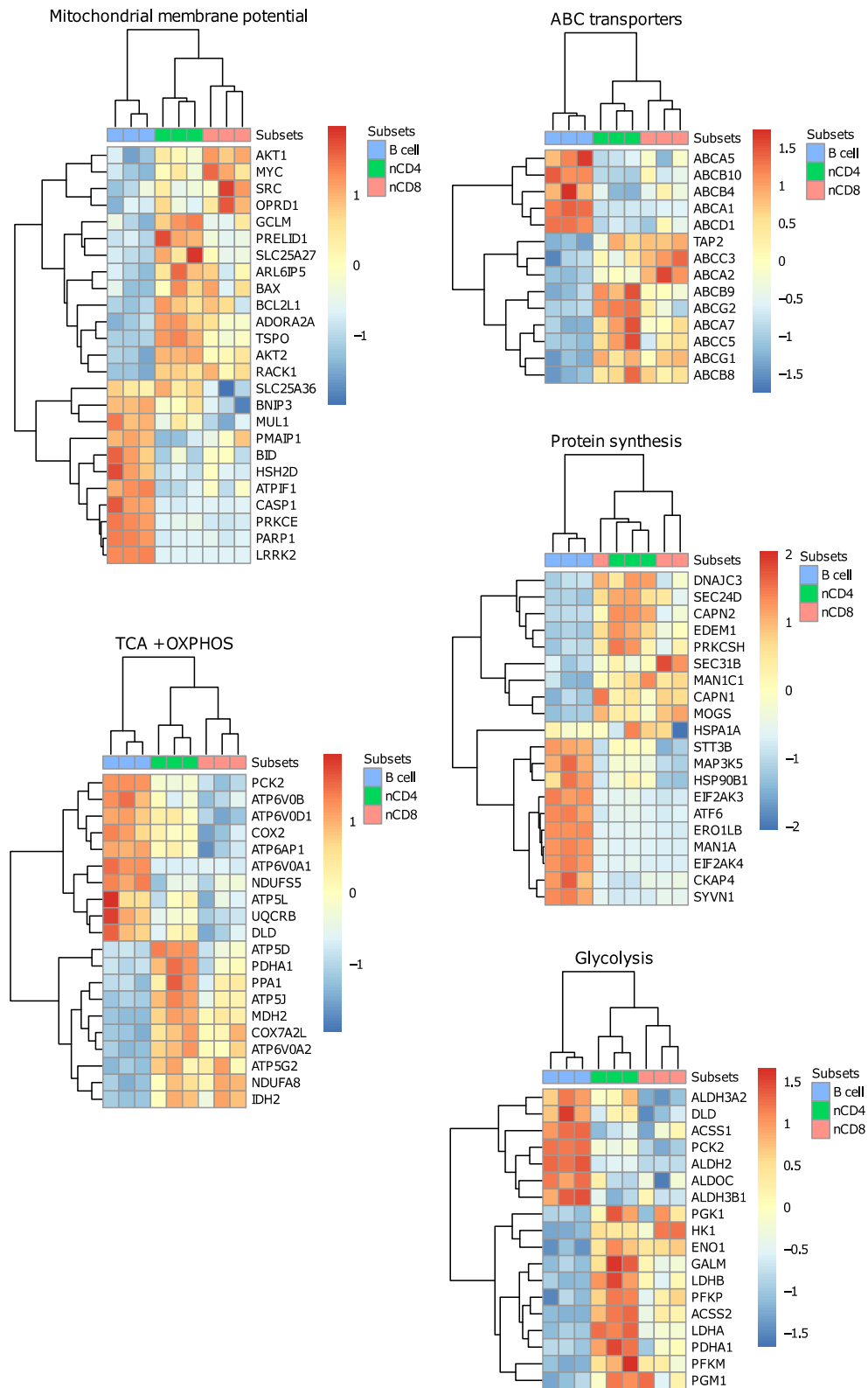
## Supplementary Figures

Figure S1



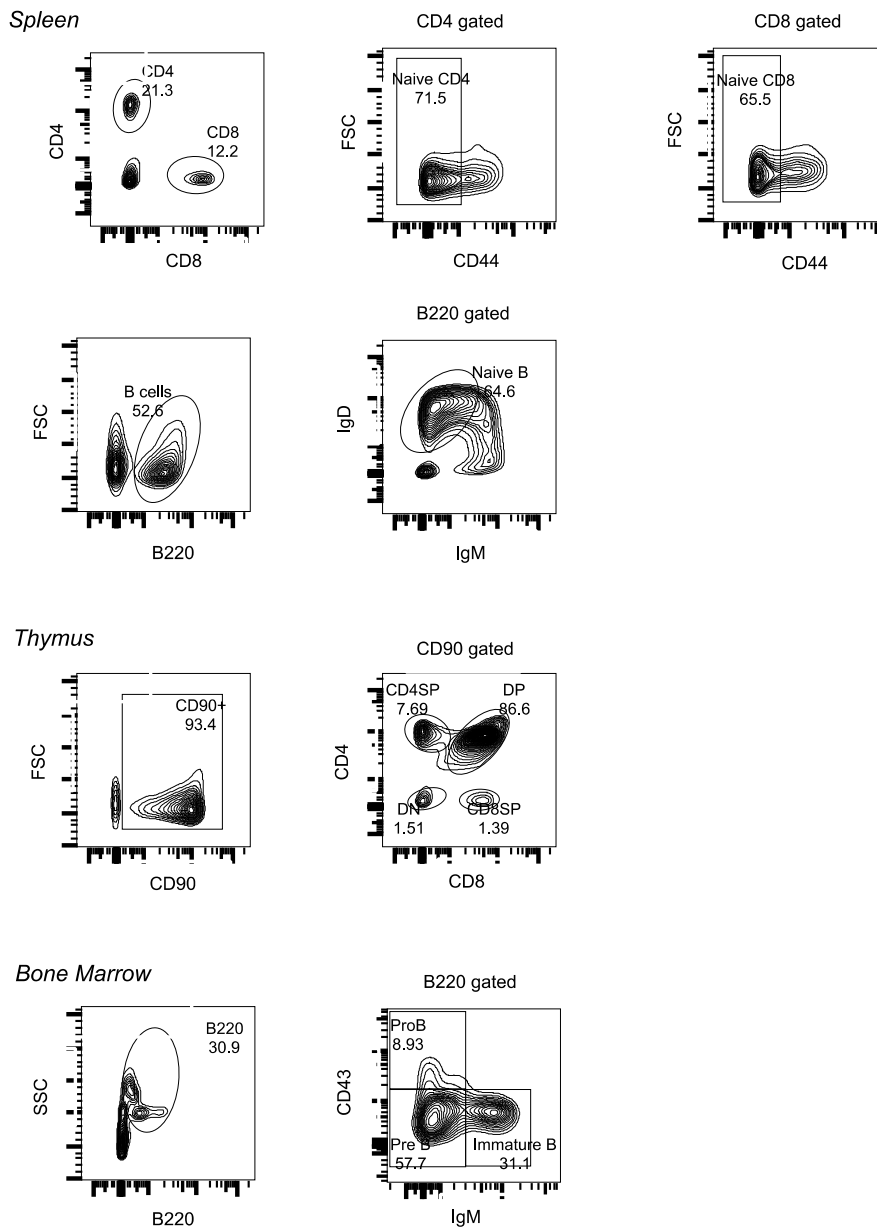
**Fig. S1.** Pathway enrichment of differentially expressed genes, plotted as enrichment score (details of calculation in methods) versus negative log p-value. Horizontal line indicates significance cutoff after multiple correction. Enrichment scores above the cutoff are significant.

**Figure S2**



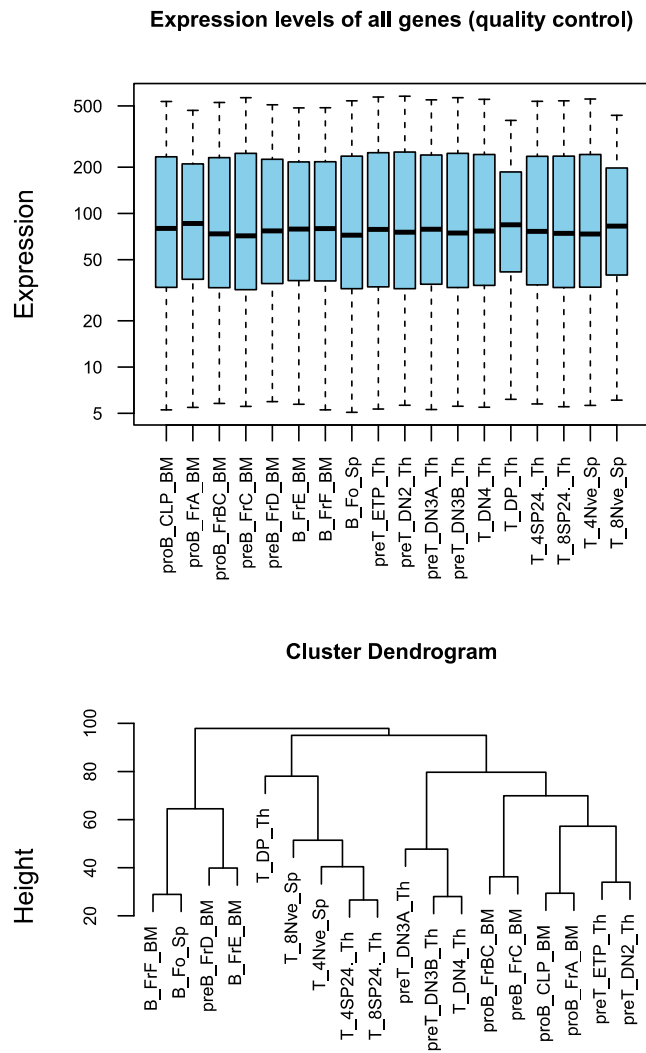
**Fig. S2.** Heatmap showing differential expression of genes from enriched pathways (from Fig. S1) in B and T cells.

**Figure S3**



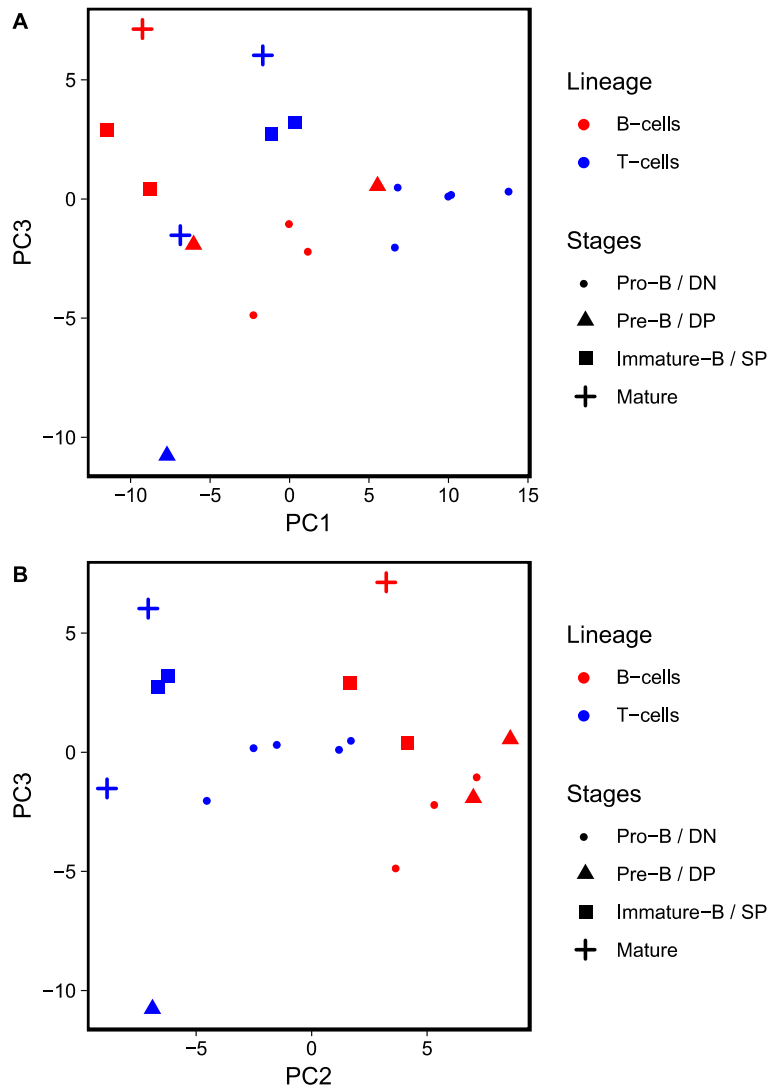
**Fig. S3.** Gating strategy for B and T cell subsets in thymus, bone marrow and spleen.

**Figure S4**



**Fig. S4.** Box plots (A) and clustering (B) of immgen subsets based on microarray data. Y axis in (A) represents the expression levels of all genes and X axis shows the samples. Box plots indicate median and interquartile ranges. Height in (B) shows hierarchical clustering dendrogram of each immune cell population based on expression values of all genes considered together.

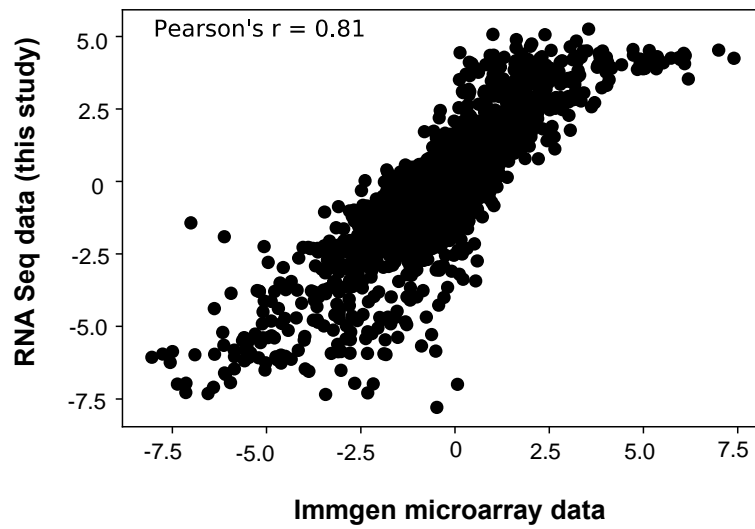
**Figure S5**



**Fig. S5.** Contribution of PC3 in separating Immature and mature B and T cell subsets.



**Figure S7**



**Fig. S7.** RNAseq data (this study) and public microarray data (from Immgen database) for resting B and T cells correlate. Log<sub>2</sub>-fold changes calculated from the RNAseq experiment and the Immgen data are plotted. Pearson correlation coefficient for these two samples is calculated (Pearson's  $r = 0.81$ ).