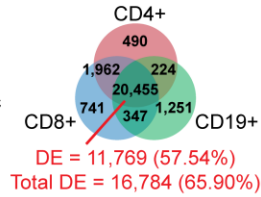


Autoimmune candidate genes

T1D candidate genes

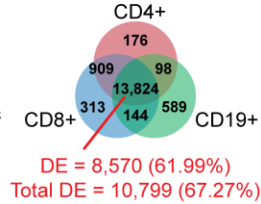
Total splicing events

25,470 events
9.74% cell type specific
80.31% common



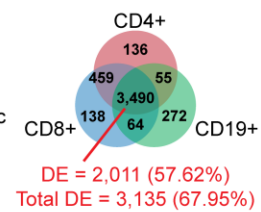
Junctions annotated to a transcript

16,053 events
6.72% cell type specific
86.11% common



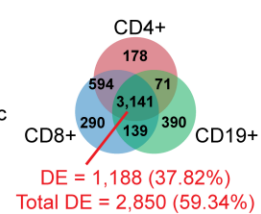
Junctions not annotated to a transcript

4,614 events
11.83% cell type specific
75.64% common



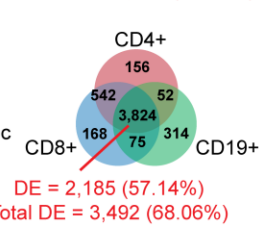
Retained introns

4,803 events
17.86% cell type specific
65.40% common



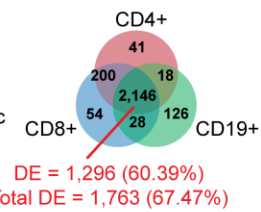
Exon skipping junctions

5,131 events
12.43% cell type specific
74.53% common



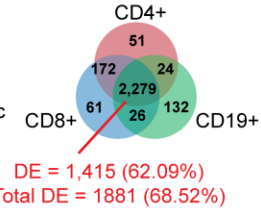
Alternative donor junctions

2,613 events
8.46% cell type specific
82.13% common



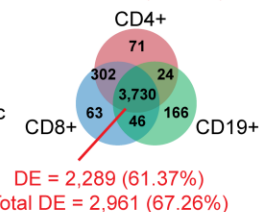
Alternative acceptor junctions

2,745 events
8.89% cell type specific
83.02% common

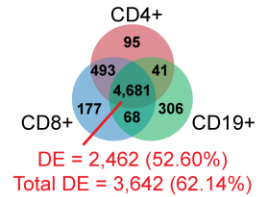


Alternative donor and acceptor junctions

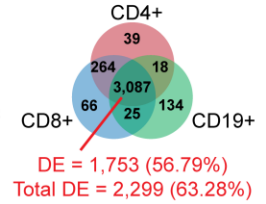
4,402 events
6.82% cell type specific
84.73% common



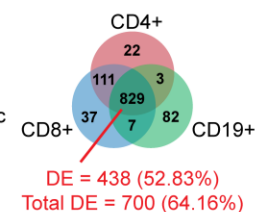
5,861 events
9.86% cell type specific
79.87% common



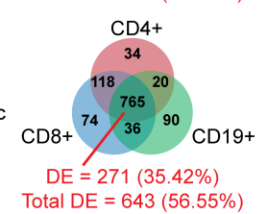
3,633 events
6.58% cell type specific
84.97% common



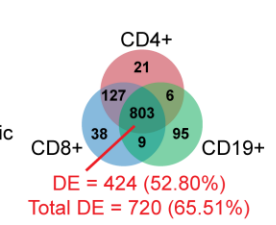
1,091 events
12.92% cell type specific
75.99% common



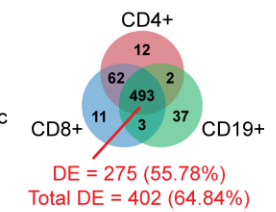
1,137 events
17.41% cell type specific
67.28% common



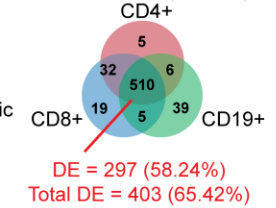
1,099 events
14.01% cell type specific
73.07% common



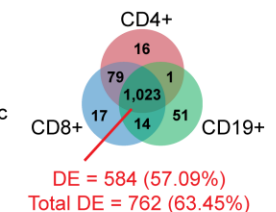
620 events
9.68% cell type specific
79.52% common



616 events
10.23% cell type specific
82.79% common



1,201 events
6.99% cell type specific
85.18% common



Supplemental Figure S3. Splicing events in autoimmune disease and T1D candidate genes detected in the three lymphocyte classes. Splicing events amongst expressed autoimmune and T1D candidate genes from ImmunoBase in CD4⁺ T (red), CD8⁺ T (blue) and CD19⁺ B (green) lymphocytes. Counts reported are the number of splicing events detected in each tissue (tissue-specific and shared between two or more tissues). Tissue-specific events for each splicing event type are reported as percentage of all detected splicing events of that event type. Common events are the percentage of splicing events detected in all three tissues, differentially-expressed splicing events (red text) are reported as a proportion of these common events. “Total DE” is the total number of differentially expressed splicing events defined as the sum of splicing events detected in one or two tissues and the number of splicing events detected in all three tissues that are DE.