* Work on the output of overlapping CDR3s so that its easier to make comparisons between groups and tissues and just in general not having the repeated outputs for shared sequences
* Run the previous analysis you had done on describing the general nature of the CDR3s in terms of CDR3 length and nature of AA usage (charged vs. hydrophobic etc) between groups and tissues.  I was thinking maybe this would also be interesting to test for particular gamma chains to see if maybe certain AA are not compatible for a CDR3 with a given Vgamma or visa versa.
* Run the non-germline amino acid sequences through an alignment process for both the gamma and delta once you have those worked out
  + We decided to just run everybody for the V delta and just add the various V alphas to the iteration
  + You would write the code so that it would start iterating after the first amino acid on the V side and the last backwards on the J side
* We had the idea of testing how the H compares to other AA in that position across the data set by compiling the AAs that sit right after the J segment breaks
* Another idea was we observe there is no charge in V gamma 4 and V gamma 9 in the germline CDR1,2,3.  What about the rest of the CDR3?  Is there a pattern of AA usage in those particular gamma chains relative to others.  Here we will run into issue if we try and compare across groups because the CDR3 properties could be disease specific.  That being said, the best bet is to probably to compare the PBL and IEL of controls and ask that since you don’t have many gamma chains represented in the IEL of controls to compare.
* Another thing we could test is also how the CDR3 of Vg4 we find in Active and GFD compare to those we find in Control?  Is there evidence that its more about the CDR3 even in those Vg4 in Active?  This I guess would require an internal comparison with other Active gamma chain CDR3s.