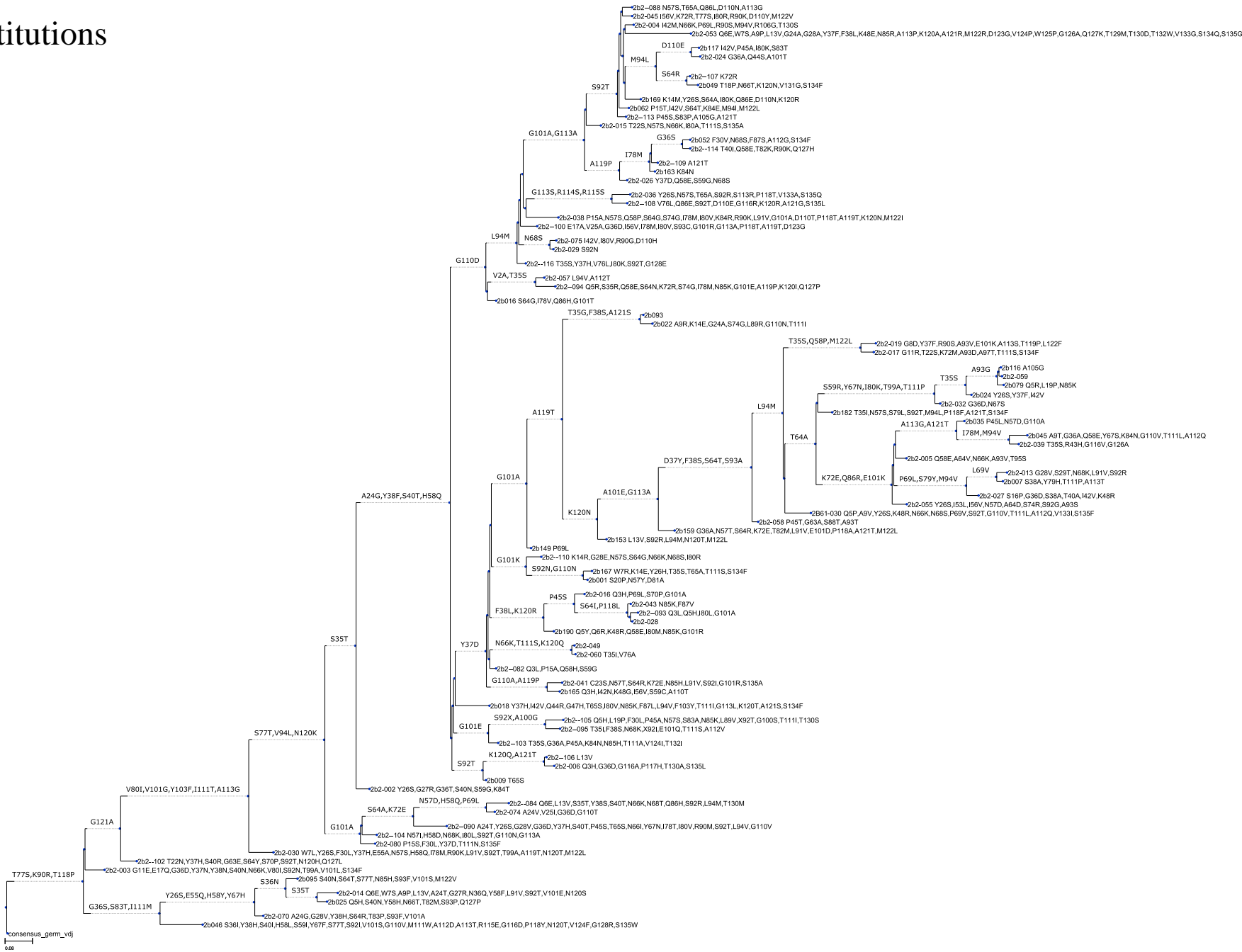


# Utilities For High-Throughput Analysis of B-Cell Clonal Lineages Supplementary Information

Graphical Output from Case Studies

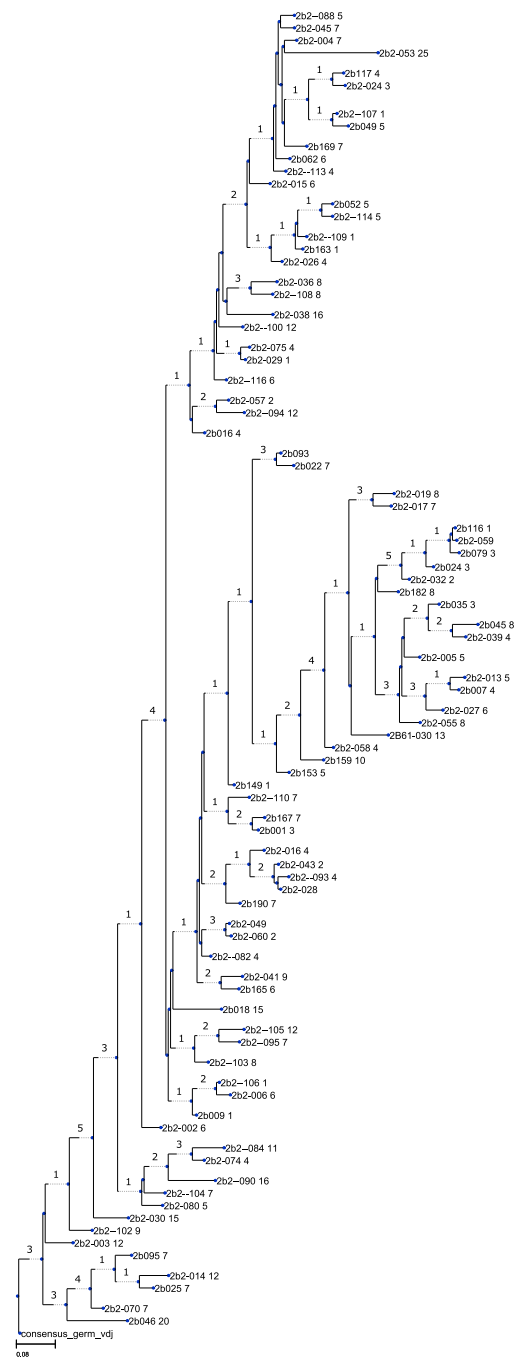
VH4-34 lineage in the human tonsil

# Amino Acid Substitutions





# Total Amino Acid Substitutions



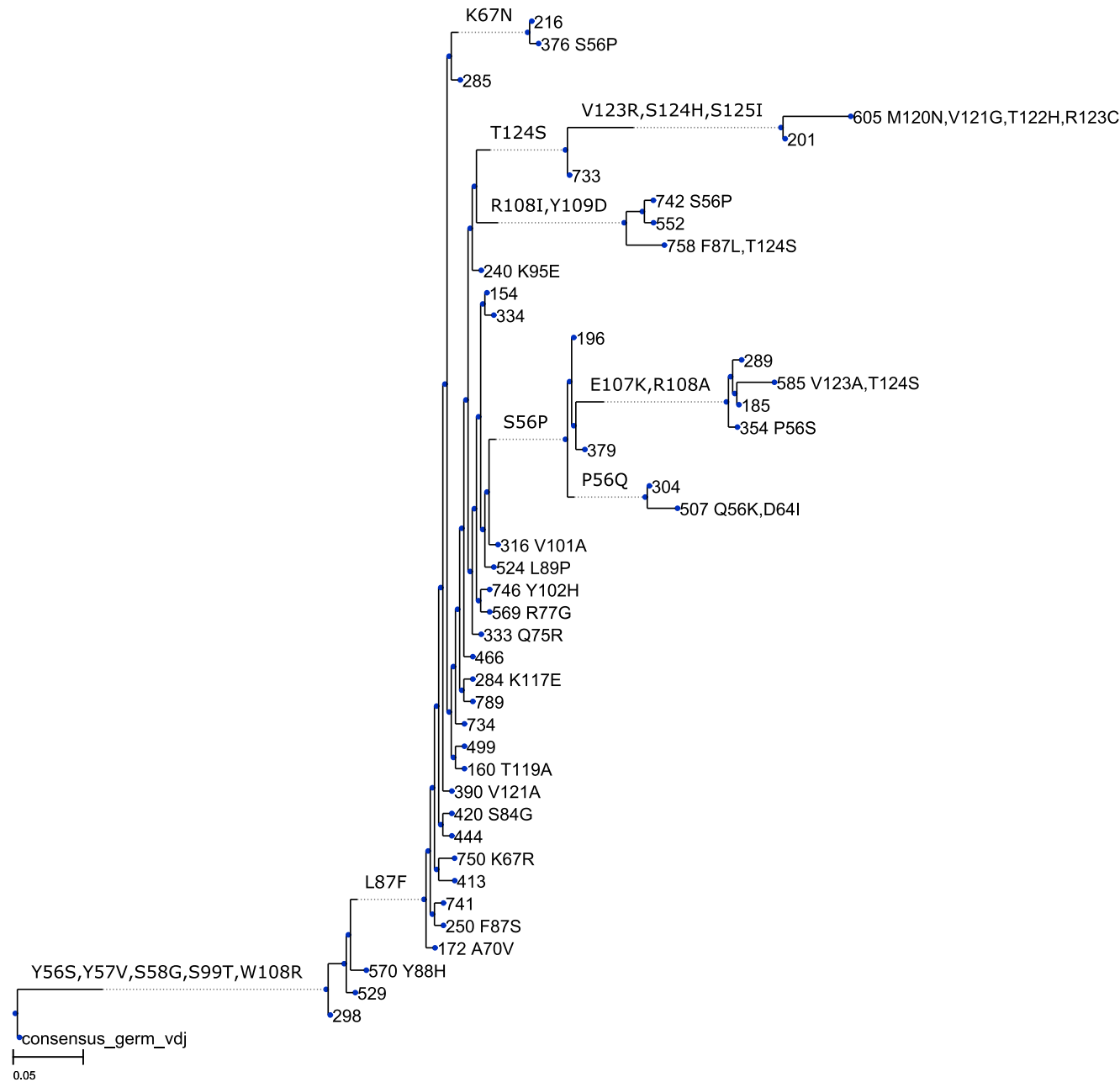


# CDR Change Analysis

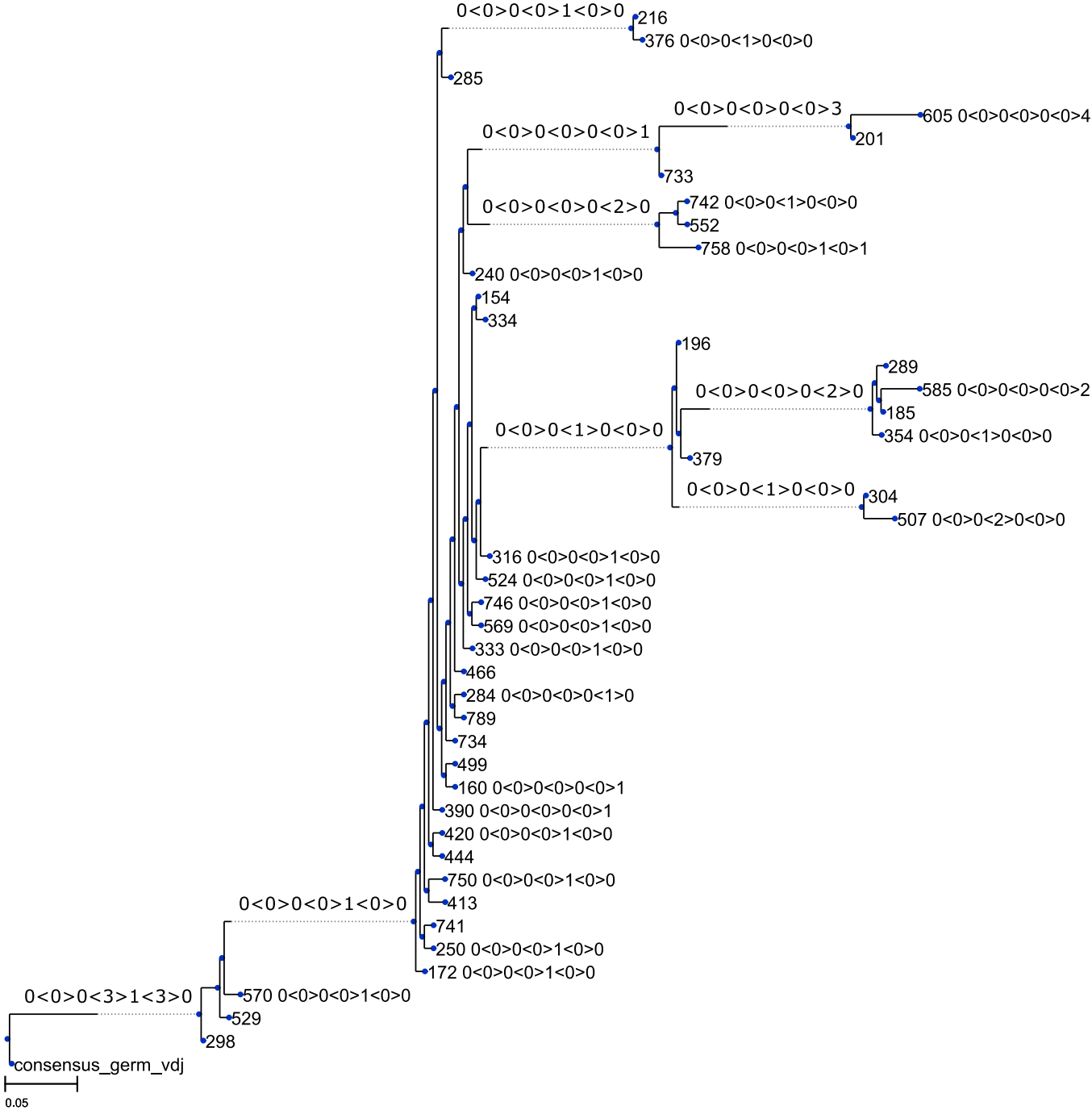
	Conserved to Germline	Common to All	Variations Across Samples
CDR1			27:GR,28:AEGV,29:ST,30:FLV,35:GIRST,36:ADGINQST,37:DFHNY,38:AFHLNSY
CDR2			56:IV,57:DINSTY,58:DEFHLPQY,59:CGIRS,63:AEG,64:ADGINRSTVY,65:AST
CDR3		107G,108L,109S	105:AG,106:GR,110:ADEGHNTVY,111:AILMNPSTW,112:ADGQTV,113:AGLPRST,114:RS,115:ERS,116:ADGRV,117:HP,118:AFLPTY,119:APT,120:AHIKNQRST,121:AGRST,122:FILMRV,123:DG,124:FIPV

Heavy chain clonal family from a 2-week old zebrafish

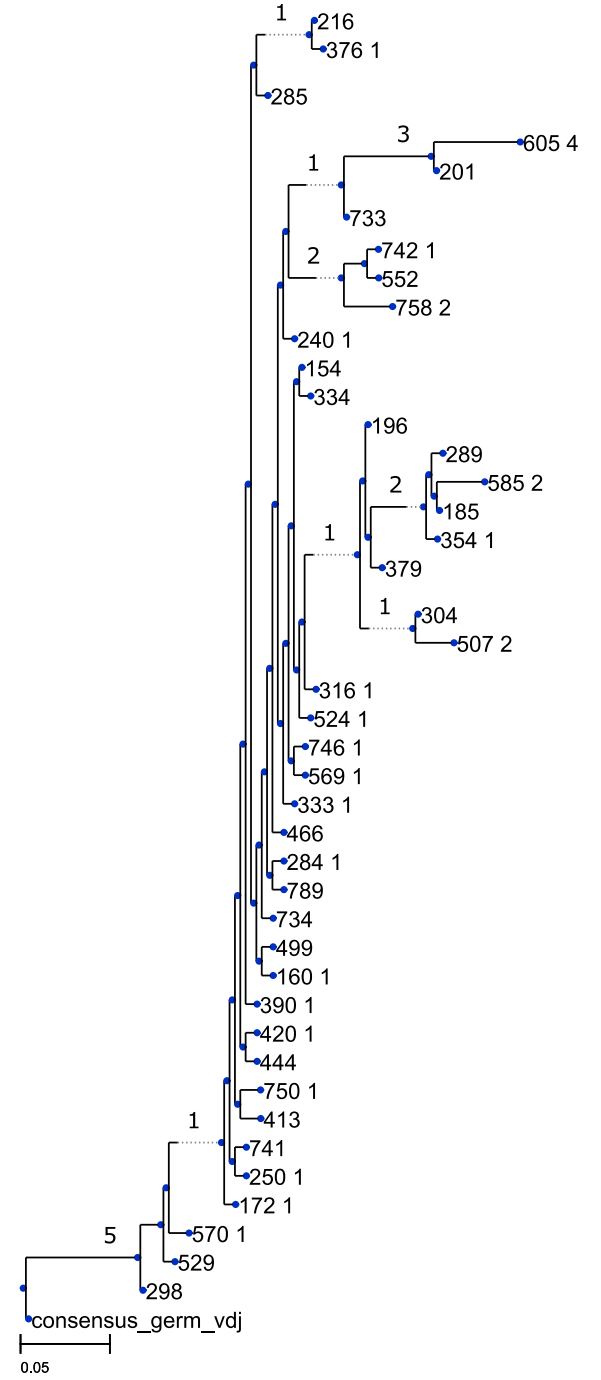
# Amino Acid Substitutions



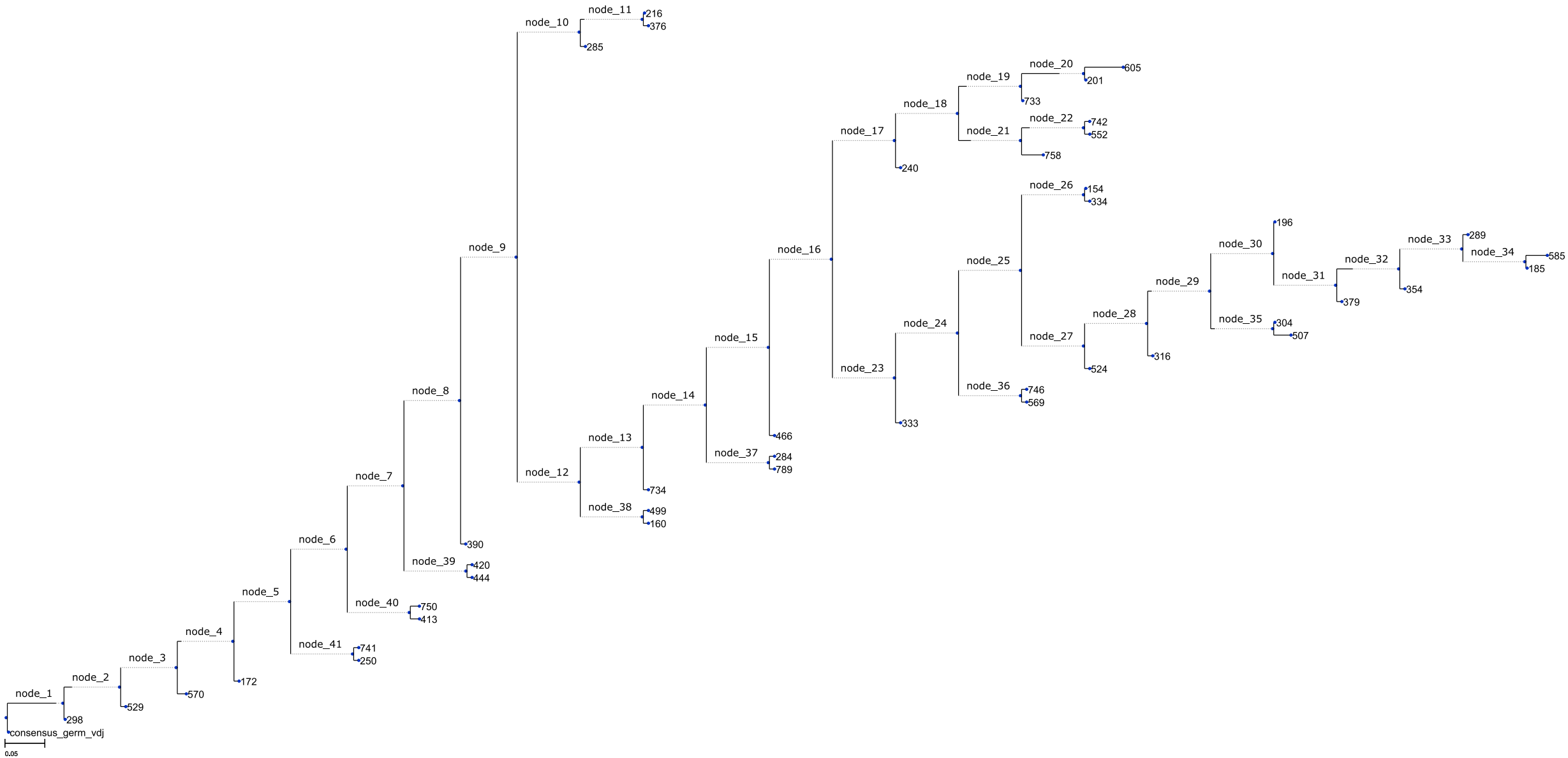
# Substitutions by Region



# Total Amino Acid Substitutions



# Intermediate Node Names

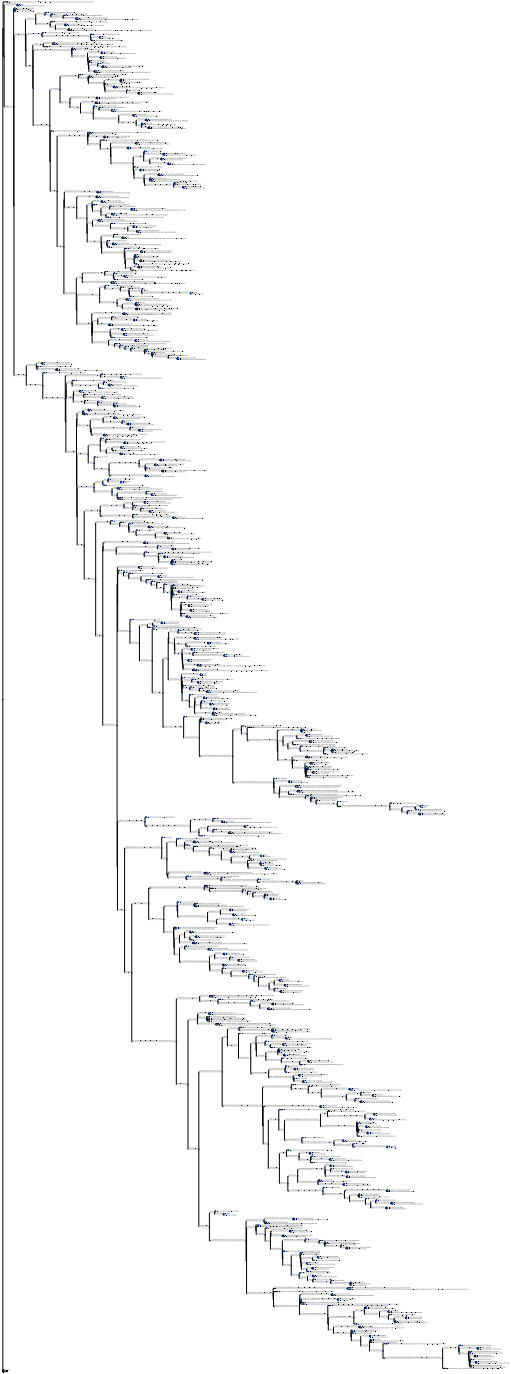


# CDR Change Analysis

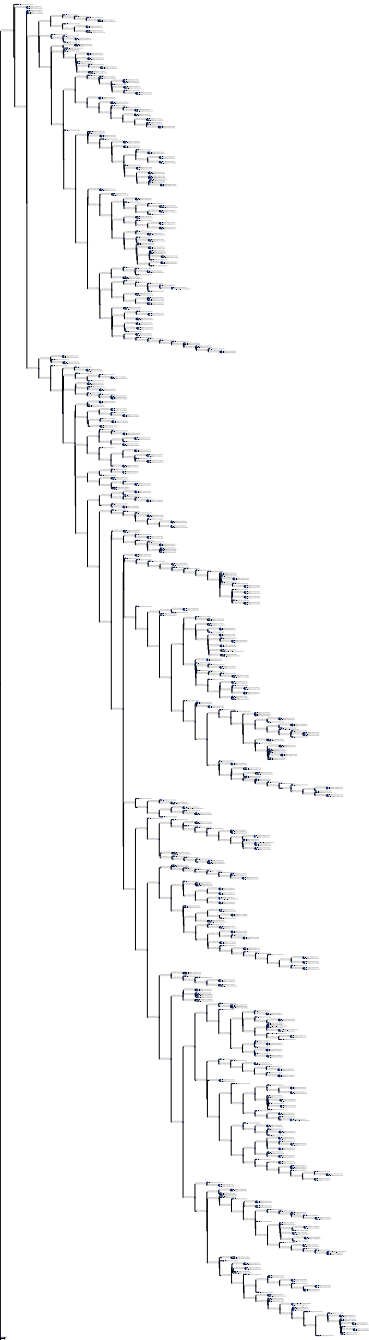
	Conserved to Germline	Common to All	Variations Across Samples
CDR1			
CDR2	65S	57V,58G	56:KPQS,64:DI
CDR3	105A,110G,111A,112F,113D,114Y,115W,116G	106R	107:EK,108:AIR,109:DY,117:EK

Developmental lineage of the HIV bnAb CAP256-VRC26 over 8 timepoints

Amino Acid Substitutions

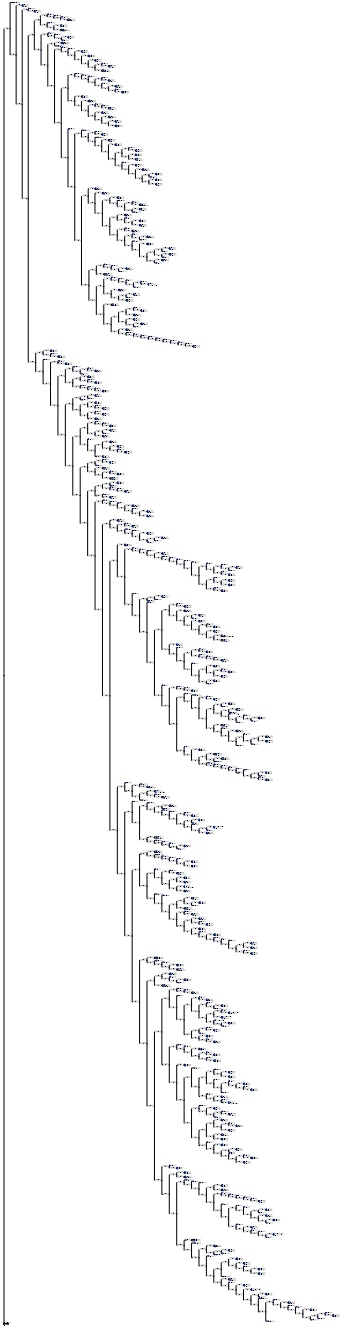


# Substitutions by Region



### Total Amino Acid Substitutions

Intermediate Node Names



# CDR Change Analysis

	Conserved to Germline	Common to All	Variations Across Samples
CDR1			27:-ADEGHKQRVXY,28:-FILV,29:-AEGIKMNPRSTY,30:-FILSVY,35:ACDEGIKNRSTVXY,36:ADEFGHIKNPQRSTVXY,37:ACFHNSTVY,38:ACDEFGHIPSTVWXY
CDR2			56:-EILMTVX,57:-AGHLNPRSTWX,58:-DFGHKLN PSTXY,59:-ADEGHNPRSV,62:-ADEGRS,63:-ADGHIKNPQRSTVXY,64:-ADEFGHIKLNQRSTXY,65:*-DEFIKMNQRSTXY
CDR3		112.11Y	105:ATV,106:KR,107:DE,108:AEHILMPQRSVX,109:ADGHQRX,110:ADEFGHIKLQVY,111:ADEFGHIKLMNRSTVWY,111.1:ADEKQS,111.2:CDEIKNPRSTV,111.3:-EIMVX,111.4:-D,111.5:DEGLM,111.6:AELQRTVY,111.7:RW,111.8:-AEGKPQRSTW,111.9:ALST,111.10:-P,111.11:DEHNTY,111.12:-NXY,112.10:CEY,112.9:-ADEGNSV,112.8:-FILMW,112.7:-W,112.6:-AGRSWY,112.5:-DEIKNRSTVY,112.4:-ADEGHKNPQRSVWX,112.3:-DN,112.2:ACDFGHILQRSVY,112.1:LPT,112:ACGILVY,113:AEHIKLPQRTV,114:ADEGHKNQSTV,115:AFPQRSTVWY,116:GHKPQRT,117:-GT