Retrieval of coding sequence information for 45 APP genes for all available mammals (primates for CTSL1 and CTSL2)

- Multiple sequence alignment using RevTrans
- Hand inspection and editing of alignments
- Screen for recombination using GARD and split alignments on the basis of recombination breakpoints

Run PAML site models (M1a vs M2a and M7 vs M8) using the F3x4 model of codon frequency: BLMH, CD1D, CD207, CTSG, CTSL2, CTSG, CYBB, ERAP2, LNPEP, TAPBP, TAPBPL, and TAP1 show a significant better fit using both selection models.

The F61 model of codon frequency confirms selection for: BLMH, CD207, CD1D, CTSG, CTSL2, CYBB, ERAP2, LNPEP, TAPBP, TAPBPL, and TAP1.

- Identify positively selected sites with BEB (from M8)
- Identify positively selected sites with MEME

Intersection the two methods: a total of 51 positively selected sites are identified.

Run BS-REL to analyse lineage-specific selection: CD207, CTSG, and CYBB. show evidences positive selection for the primate or murid lineages.

Cross-validate branches using the PAML branch-site models (MA vs MA1)

At least one branch is validated for CD207 and CTSG

Identify lineage-specific positively selected sites with BEB (from MA)

Intersection the two methods: one site postively selected in simians is identified.