

```
candidate_taxon_level = "species"
best_hit = $top_species_hit_PE

### First check
if ($top_species_hit_PE != $top_species_hit_SE) {
  "WARNING: Proceeding with PE top hit"
}

### Next check
if ($top_species_hit_PE_reads >= 50%) {
  candidate_taxon_level = "species"
  best_hit = $top_species_hit_PE
}

else if ( $top_species_hit_PE_reads < 50%
  AND $sec_species_hit_PE belongs to different genera) {
  candidate_taxon_level = "species"
  best_hit = $top_species_hit_PE
}

else ($sec_species_hit_PE belongs to same genera) {
  candidate_taxon_level = "genus"
  best_hit = $top_genus_hit_PE
}

### Check if refseq assembly available
if (candidate_taxon_level == "species" AND num_refseq_genomes == 0) {
  candidate_taxon_level = "genus"
  best_hit = $top_genus_hit_PE
}

### If no RefSeq Genome for genus
QUIT!
```

