Hi Zachary,

Your project objective is clearly defined and is well written. I have a few comments/suggestions.

1. Are you sure you specifically designated wolf as the Outgroup species in Raxml-NG? That is the only reason I can see why it occurs as one of the clades in the tree and not as the outgroup, if you haven't done so.

2. I would suggest that you do not include duplicate sequences just to avoid more complications for the discussion.

3. You could also try Averaging over the GTR models option and run a RJ-MCMC analysis and see if your tree topology and log likelihood values improve/ are closer to the phylogeny inferred from the SNP data.

4. I would suggest that you do not call your analysis results as abnormalities. Since you are using mtDNA as your dataset its just a question of how it 'deviates' or 'differs' from the SNP analysis.

5. You could also designate the different clades from your analysis by the different geographic regions they belong to - for example if Chinese breeds are indeed clustered together you can indicate that using arrows or colors - that is another way you can find more support for your mtDNA phylogenetic inference w.r.t geographic classification

6. Since you also did a bootstrap analysis, you can include a tree with bootstrap support values in your paper.

7. You may find some similarities and some difference between your tree and the SNP tree. You could point them out in your discussion section.

That is all. Well done!