



Supplemental Figure 4. First 10 PCs plotted against PC 1. These 10 PCs explain 56.17% of total variance and each explains respectively: [0.270, 0.095, 0.060, 0.032, 0.025, 0.021, 0.017, 0.016, 0.014, 0.013]. There is some clustering of Chew et al. grade 0 vs grade 1, grade 2, and grade 3 in the plot of PC1 vs PC2, but the relationship appears non-linear, which is a weakness of PCA. Furthermore, PC1 and PC2 only explain 38% of total variance, and may not capture the full high-dimensional structure of MacTel disease features as learnt by the deep learning classifier.. PCA was implemented using sklearn 0.24.1 in python 3.6.12 with n_components=10 and default settings for all other parameters.