Ideas and questions:

1. Maybe we can look at the clusters of decorrelation distribution and average values in 4 locations in normal, fatty, and cirrhotic liver and if difference is seen, use that feature in a one-hot-encoding input (3 dimensions).
2. Maybe look at temperature groups of like <40, 40-60, 60-80, 80-100, >100 as well see how accurate our model can predict these ranges of temperature