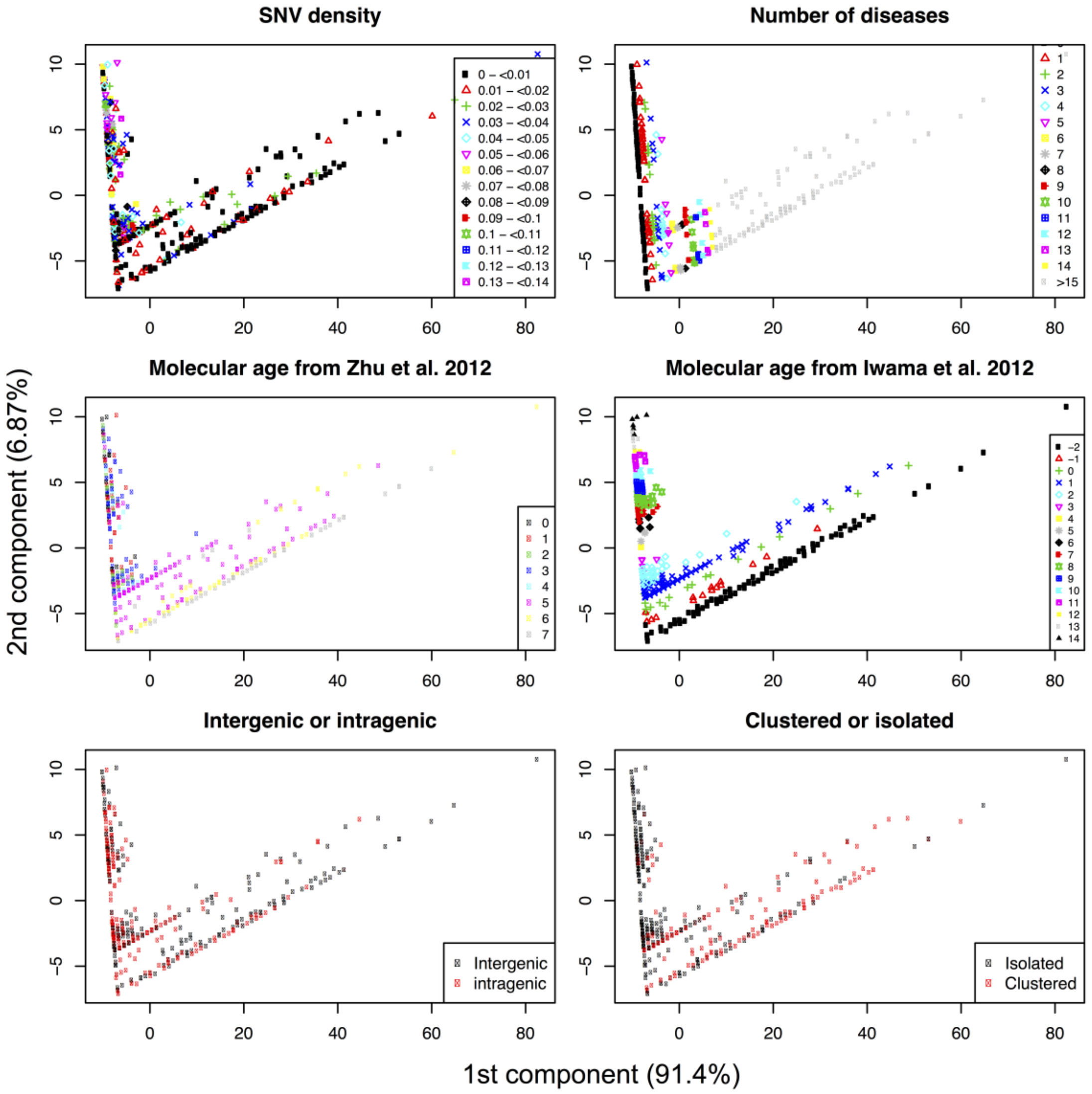
S1 Figure. Distribution of miRNAs in the PCA analysis. Each plot corresponds to one variable used on the PCA analysis. Molecular age is taken from Zhu et al. [1] and Iwama et al. [2] where each integer represents a period of origin. In [1] oldest miRNAs have the highest values while in [2] oldest miRNAs have the lowest values. Number of diseases explains the first component and molecular age the second component. Conserved miRNAs (low SNV density values) tend to be involved in a larger number of diseases, older and located in clusters.



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