## Internal Cluster validation measures Table

Clustering Method	Average Silhouette Width
PAM PRAD_miRNASeqGene	0.008
PAM PRAD_RNASeq2Gene	0.006
PAM PRAD_RPPAArray	0.008
PAM average integration	0.004
PAM SNF integration	0.002
PAM NEMO integration	0.003
Spectral NEMO integration	0.004
Spectral SNF integration	0.002