ROC 10-fold cross-validation methylation classification (Accuracy = 93.38%) 1.00 -0.75 -Methylation class Classic-like (N = 118, AUC = 1.00) Codel (N = 122, AUC = 1.00) True positive rate Cortex (N = 16, AUC = 1.00)-G-CIMP-high (N = 135, AUC = 1.00)G-CIMP-low (N = 19, AUC = 1.00)0.50 -Granulation (N = 8, AUC = 1.00) Inflammatory-TME (N = 24, AUC = 1.00) LGm6-PA (N = 33, AUC = 0.99)Mesenchymal-like (N = 128, AUC = 0.97) Reactive-TME (N = 16, AUC = 1.00) 0.25 -0.00 -0.50 0.25 0.75 0.00 1.00 False positive rate