



Supplemental Figure 2. Independent clustering of canine glioma tumor subtypes based on enrichment for immune subsets. All samples were analyzed using the advanced analysis module in nSolver (Nanostring Technologies) with patient glioma samples ($n = 22$) normalized to adjacent normal controls ($n = 3$). Samples cluster to a lesser degree into those expressing mRNA gene signatures associated with an array of immune infiltrate on the left side of the heat map versus those on the right exhibiting fewer immune cell mRNA gene signatures.