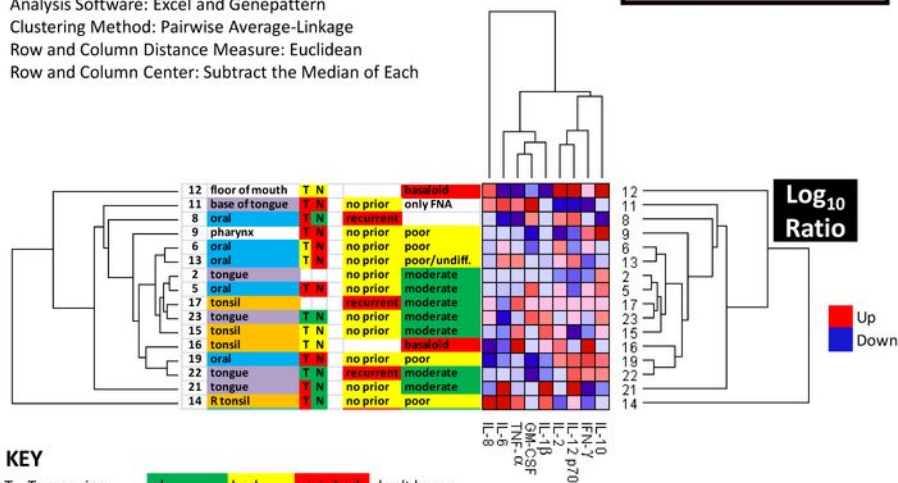


A

Normalized to Total Protein (Log₁₀)

Plate Layout Method: As suggested by Manufacturer
 Calibration Method: Standard Curve
 Analysis Software: Excel and Genepattern
 Clustering Method: Pairwise Average-Linkage
 Row and Column Distance Measure: Euclidean
 Row and Column Center: Subtract the Median of Each

Salivary
SUPERNATANT



KEY

T = Tumor size
 N = Nodes
 M = Metastasis
 Differentiation

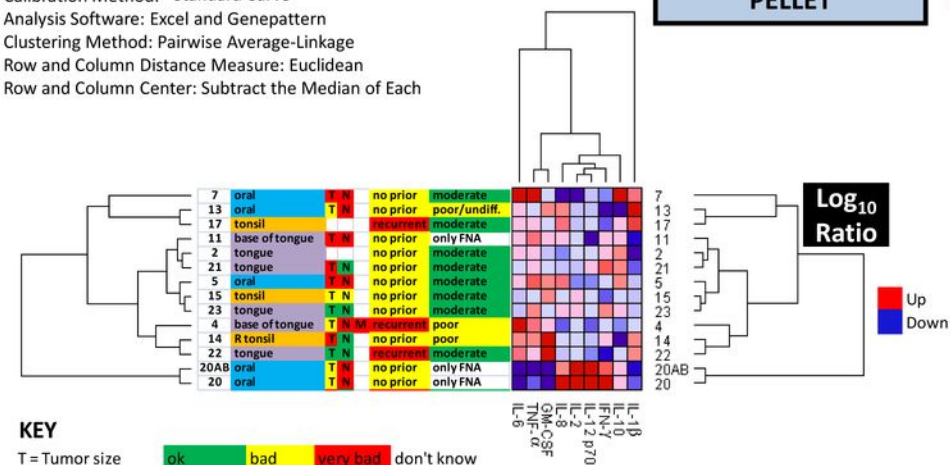
ok	bad	very bad	don't know
ok	bad	very bad	don't know
		very bad	don't know
moderate	poor	basaloid	don't know

B

Normalized to Total Protein (Log₁₀)

Plate Layout Method: As suggested by Manufacturer
 Calibration Method: Standard Curve
 Analysis Software: Excel and Genepattern
 Clustering Method: Pairwise Average-Linkage
 Row and Column Distance Measure: Euclidean
 Row and Column Center: Subtract the Median of Each

Salivary Cell
PELLET



KEY

T = Tumor size
 N = Nodes
 M = Metastasis
 Differentiation

ok	bad	very bad	don't know
ok	bad	very bad	don't know
		very bad	don't know
moderate	poor	basaloid	don't know