

Table S1: Clinicopathological features of two clusters classified by consensus clustering based on cellular response to IL-4-related gene set in CGGA dataset.

Features	Cluster 1 (n=124)	Cluster 2 (n=201)	<i>P</i> value
Age			< 0.0001
Median	38	46	
Gender			0.3513
Female	51	71	
Male	73	130	
TCGA subtype			< 0.0001
Classical	10	64	
Mesenchymal	7	61	
Neural	33	48	
Proneural	74	28	
WHO Tumor grade			< 0.0001
II	67	42	
III	30	42	
IV	27	117	
IDH status			< 0.0001
Mutation	108	59	
Wildtype	16	142	
1p/19q status			< 0.0001
Codeletion	35	20	
Non-codeletion	84	166	
NA	5	15	