

**Supplemental Table 1.**

Between-site similarity of the gene expression profiles of ovarian tumors sampled at three sites in five different subjects. The height of the tree encompassing the three sites for a given patient in the dendrograms shown in Figure 1, referred to as the cophenetic spanning distance, was used as a measure of similarity, with smaller distances representing more similar gene expression profiles.

Gene set	Cophenetic spanning distance					Mean spanning distance for subject
	Anti-microbials	Antigen processing and presentation	Cytokines	TGF-beta signaling	TCR signaling	
Subject						
697	2	3	2	2	3	2.4
710	2	2	2	4	2	2.4
716	5	3	2	4	2	3.2
717	5	2	2	2	3	2.8
718	4	2	2	3	4	3
Mean spanning distance for gene set	3.6	2.4	2.0	3.0	2.8	
Dendrogram max height	5	7	3	5	7	

## OS according to CD3+ TIL density and heterogeneity

