Supplementary Tables for Roth et al., PyClone: Statistical inference of clonal population structure in cancer

Supplementary Table 1: Allelic counts, IBBMM and PyClone PCN cellular prevalence estimates for mutations in high grade serous ovarian cancer case 2. Copy number predictions where inferred using PICNIC as described in the **Online Methods**. Cellular prevalences where computed by taking the mean of the post burnin trace for the cellular prevalences for the respective methods. The standard deviation of the cellular prevalence parameter estimated from the post burnin trace is also included. Cluster ids (last two columns) were predicted from the post burnin trace using the MPEAR clustering criteria as described in the **Online Methods** and **Online Note**. Mutation ids list gene name, chromosome and chromosome coordinate. All coordinates are in the hg19 coordinate system.

Supplementary Table 2: Allelic counts, IBBMM and PyClone PCN cellular prevalence estimates for mutations in high grade serous ovarian cancer case 1. Copy number predictions where inferred using PICNIC as described in the **Online Methods**. Cellular prevalences where computed by taking the mean of the post burnin trace for the cellular prevalences for the respective methods. The standard deviation of the cellular prevalence parameter estimated from the post burnin trace is also included. Cluster ids (last two columns) were predicted from the post burnin trace using the MPEAR clustering criteria as described in the **Online Methods** and **Online Note**. Mutation ids list gene name, chromosome and chromosome coordinate. All coordinates are in the hg19 coordinate system.