**PP-45**  
**Understanding multifocality in prostate cancer and clonal origin of metastasis**  
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**Introduction:** Technology allowing for focal ablation of a portion of prostate involving cancer has improved tremendously. However, one primary concept that requires further evaluation is whether there is indeed an “index” lesion that drives cancer progression and, if so, can it be identified and differentiated from other lesions. Therefore, we studied specimens from patients who had undergone prostatectomy and were found to have positive lymph nodes and correlated these to different lesions in the prostate.

**Methods:** 20 patients were found to have positive lymph nodes and multiple distinct areas of cancer within the prostate. A minimum of 2 different foci and an area of normal prostate as well as the cancerous lymph nodes were microdissected and the DNA was purified. Epigenetic DNA methylation analysis was performed using the 450k infinium array on each foci. Correlations of the epigenetic profile from each tumor focus within the prostate was made to the metastatic lymph node.

**Results:** 8 cases were able to be successfully completed with epigenetic DNA methylation profiling. Figure 1 demonstrates a multidimensional scaling plot with clustering of normal prostate, primary prostate, and lymph node metastasis. Figure 2 is a heatmap of 5% of the most variable CPG island in one patient that demonstrates similarity among the positive lymph nodes (PL1 and PL2) and one tumor focus within the prostate (T1) but not the other tumor foci (T2 and T3) or normal prostate (AN).

**Conclusions:** A significant correlation can be seen between one specific focus of tumor within the prostate and the metastatic lymph node. This supports the notion of an “index” lesion and that DNA methylation profiling may aid in identification for subsequent targeting with ablative technologies. Further work to identify which methylation profiles are associated with greater metastatic potential is underway.