Background
• Cancers of the vulva are a rare gynecologic cancer, mostly squamous in histology, and approximately 50% are HPV-induced.
• NCCN guidelines have just been added (Jan. 2016) for squamous vulvar cancers, with the incorporation of therapies used for other HPV-induced cancers, including mitomycin-C, cisplatin, 5-fluorouracil, vincristine, and paclitaxel.
• Despite the NCCN compendium addition of treatment options for squamous vulvar cancers, targeted therapies are lacking from their recommendation and for this disease.

Methods
Profiling results for 150 vulvar cancer patients were included in this retrospective analysis. Testing was completed centrally at a CLIA laboratory (Caris Life Sciences, Phoenix, AZ). Specific testing was performed for each patient and included at least one of the following methodologies: mutational analysis by next-generation sequencing (NGS) or Sanger sequencing, protein expression by immunohistochemistry (IHC) and gene amplifications by in situ hybridization (ISH).

Results
• Squamous cell carcinoma of the vulva comprise the majority of vulvar cancers included in this analysis. The most frequently overexpressed proteins are EGFR (95%), TP53 (33%), PIK3CA (8%), BRCA2 (7%) and HRAS (6%) are the most frequently mutated genes.
• The rate of PDL1 expression is lower in metastatic specimens, whereas PD1+ TILs stays consistent in primary and metastatic specimens, as well, further establishing the immune evasion mechanism as cancer progresses.

Conclusions
• Molecularly-guided precision medicine could provide vulvar cancer patients alternative, targeted treatment options especially due to easy accessibility for repetitive biopsy.

References