KLK9, 10, 11, and 15 may represent potential cancer biomarkers for evaluating ovarian cancer prognosis. In the present study, we selected a homogeneous cohort including 139 patients of advanced high-grade serous ovarian cancer (FIGO stage III/IV) and assessed the mRNA levels of KLK9, 10, 11, and 15 in tumor tissue by quantitative PCR. No significant associations of KLK9, 10, 11, and 15 mRNA with established clinical parameters (residual tumor mass, ascitic fluid volume) were found. Pronounced correlations between KLK10/KLK11 (rs = 0.647) and between KLK9/KLK15 (rs = 0.716) mRNA, but not between other combinations, indicate coordinate expression of distinct pairs of peptidases. In univariate Cox regression analysis, elevated KLK11 mRNA levels were significantly linked with prolonged overall survival (OS; p = 0.021) and progression-free survival (PFS; p = 0.008). KLK15 mRNA levels showed a trend towards significance in case of OS (p = 0.06); KLK9 and KLK10 mRNA expression levels were not associated with patients' outcome. In multivariable Cox analysis, KLK11 mRNA expression levels, apart from residual tumor mass, remained an independent predictive marker for OS (p = 0.007) and PFS (p = 0.015). Here, elevated KLK15 mRNA expression levels turned out to be significantly related to prolonged OS
(p = 0.025) as well. High KLK11 but not the other KLK mRNA levels can be considered as strong independent favorable prognostic factor in this major ovarian cancer subtype.