and quantitative PCR on both the affected and non-affected body-sides before, during and after radiotherapy on a weekly basis (360 samples). Additionally, radiodermatitis severity was determined.
All patients developed radiodermatitis during the study. After five to seven weeks, four patients developed severe radiodermatitis. Strikingly, low (<5%) colonization with skin commensals (Staphylococcus epidermidis, Staphylococcus hominis, Cutibacterium acnes) at baseline was highly predictive for the development of severe radiodermatitis. Instead, different Corynebacteriaceae species were more abundant in severe cases. Corynebacteriaceae abundance was correlated positively, and commensal abundance negatively with skin pH. Strinkingly, only severe patients showed an increase in total bacterial cell numbers estimated via qPCR of the 16S rRNA copies in contrast to stable bacterial colonization in mild and moderate radiodermatitis cases prior to the onset of severe symptoms.
In summary, we have observed two logically linked phenomena exclusively in severe patients: a low baseline level of commensals, and an early increase in total bacterial load. Thus, our findings potentially show for the first time that microbes have a direct effect on the pathogenesis of radiodermatitis.

P238 | Skin microbiome dynamics as predictor and pathogenesis mechanism for severe radiodermatitis in breast cancer patients

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Radiodermatits is commonly observed during radiotherapy in post-operative breast cancer patients, severly impacting the quality of life of the patients. So far, the interindividual differences regarding radiodermatitis severity and the pathomechanism are not well understood. To understand the role of the skin microbiome and skin physiology in the development of radiodermatitis, we conducted a longitudinal pilot study with 20 female breast cancer patients undergoing radiotherapy. From each patient, the skin pH and skin microbiome were assessed via nextgeneration sequencing of the V1-V3 region of the 16S rRNA