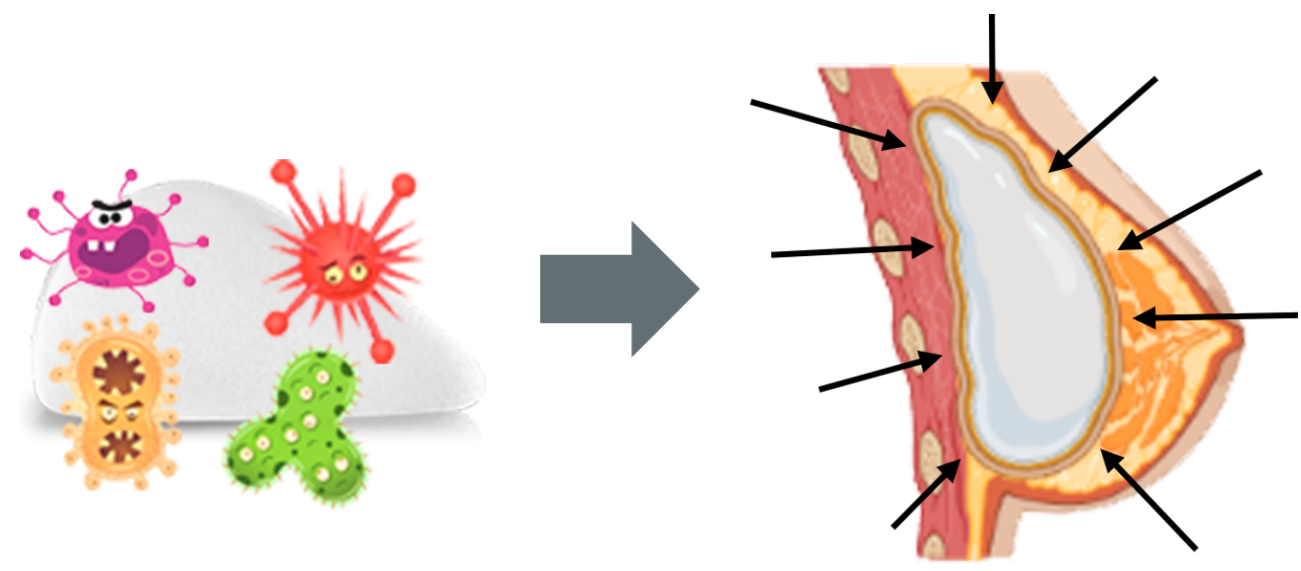


Identifying Traits in the Breast Implant Microbiome that Leads to Capsular Contracture after Breast Augmentation: A Case-Control Study of 141 Implants using Next Generation Sequencing

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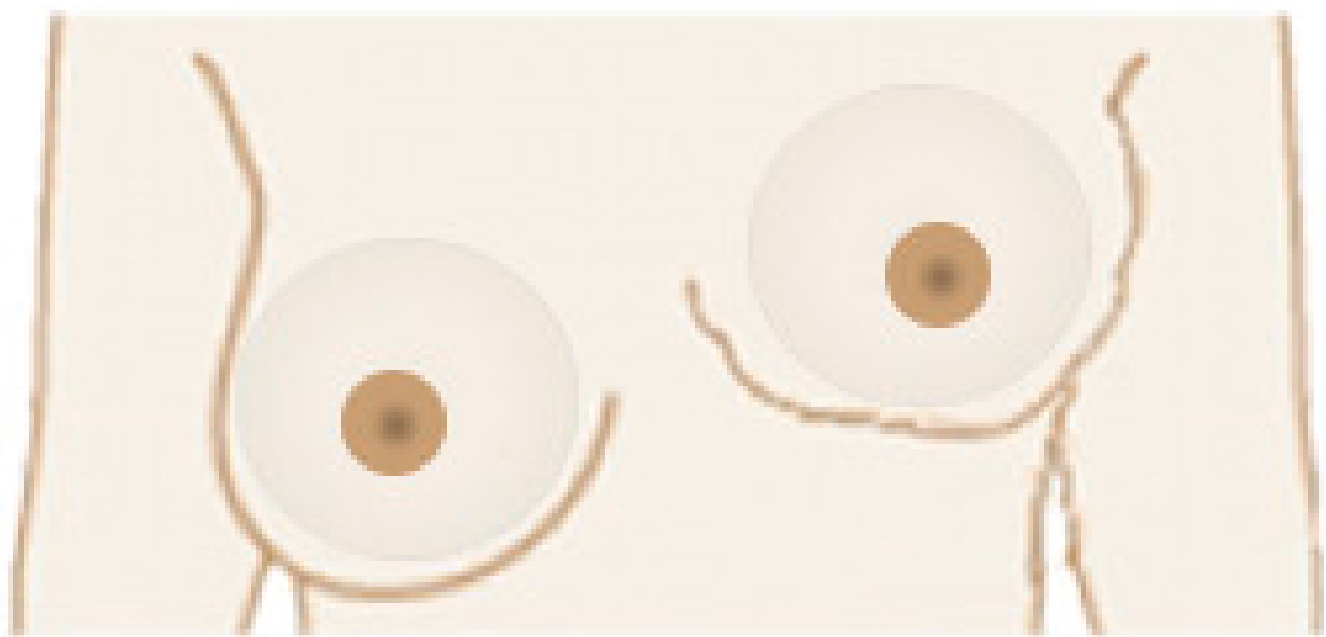
BACKGROUND



Subclinical infection of breast implants has been suggested to trigger capsular contracture.

PATIENTS

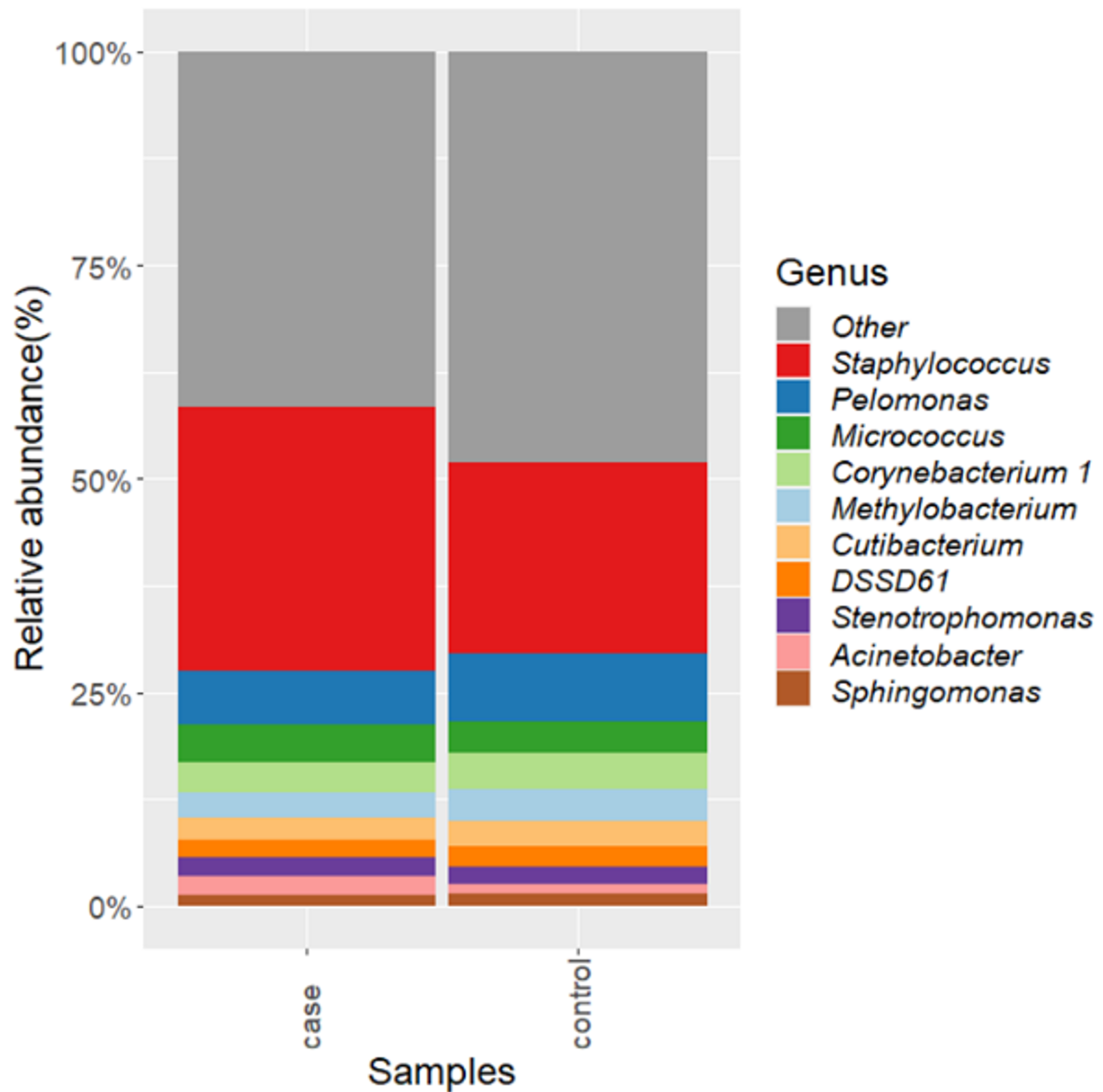
We included 141 implants from 72 healthy women undergoing implant exchange with and without capsular contracture. They were matched for time of implantation, implant brand and surface texture.



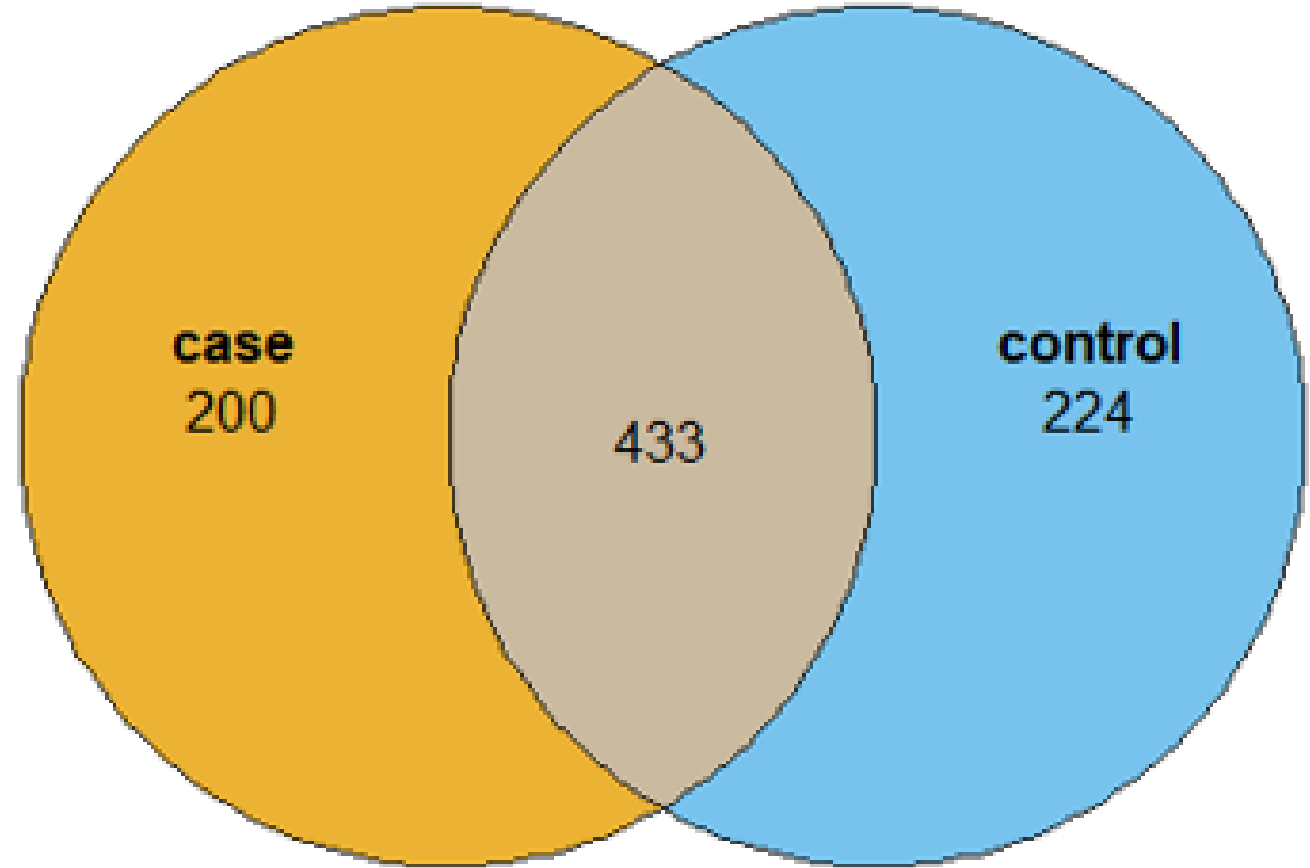
Thirty-eight patients acted as their own control contributing with one breast with capsular contracture (Baker III/IV) and a healthy contralateral breast (Baker I). Sixteen patients were Baker I bilaterally, 15 patients were Baker III/IV bilaterally and three patients contributed with one breast with Baker III/IV.

RESULTS

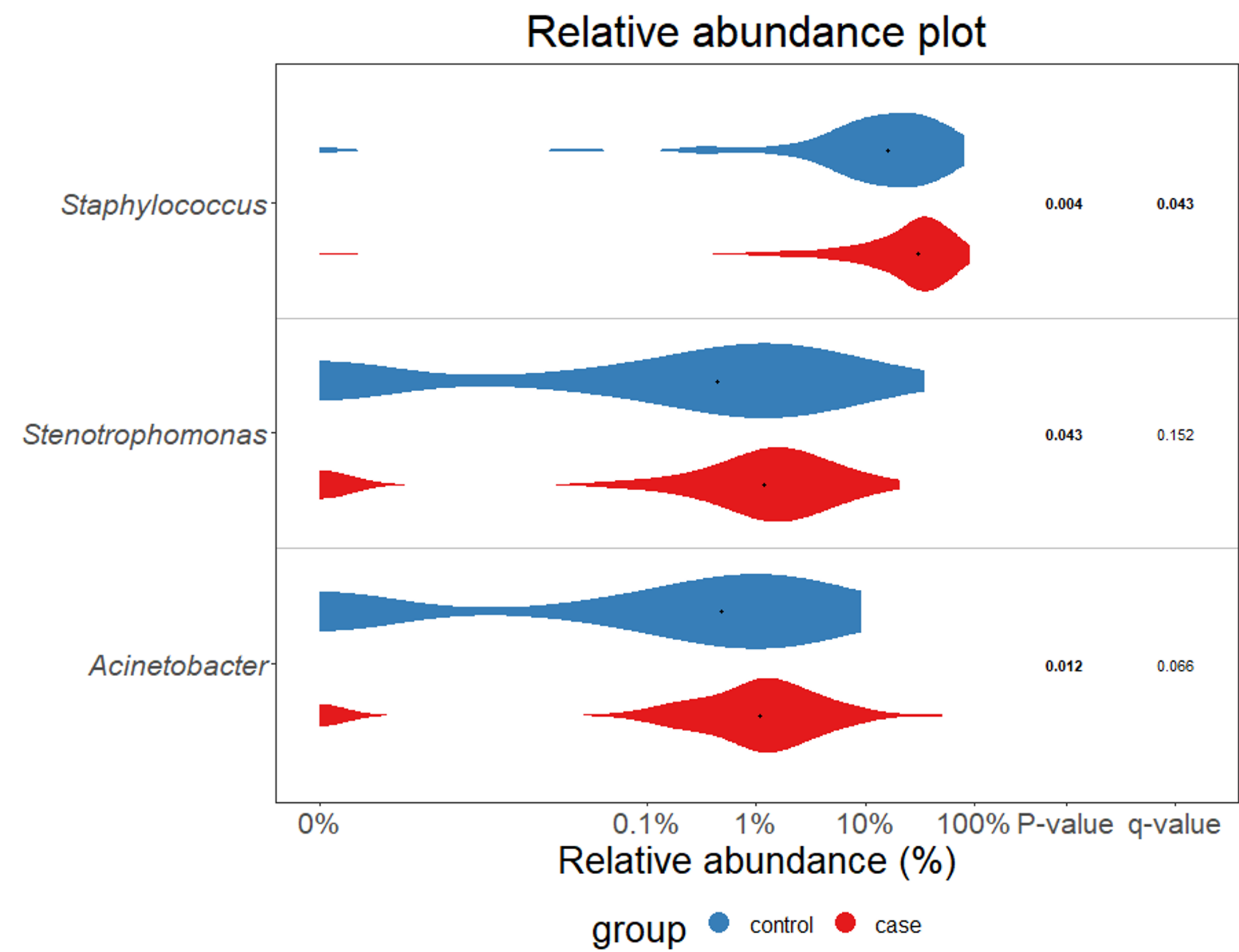
We identified a rich network of bacteria in all samples with 879 unique genera. The core implant microbiome consisted of the *Staphylococcus*, *Pelomonas* and *Micrococcus* genera.



RESULTS



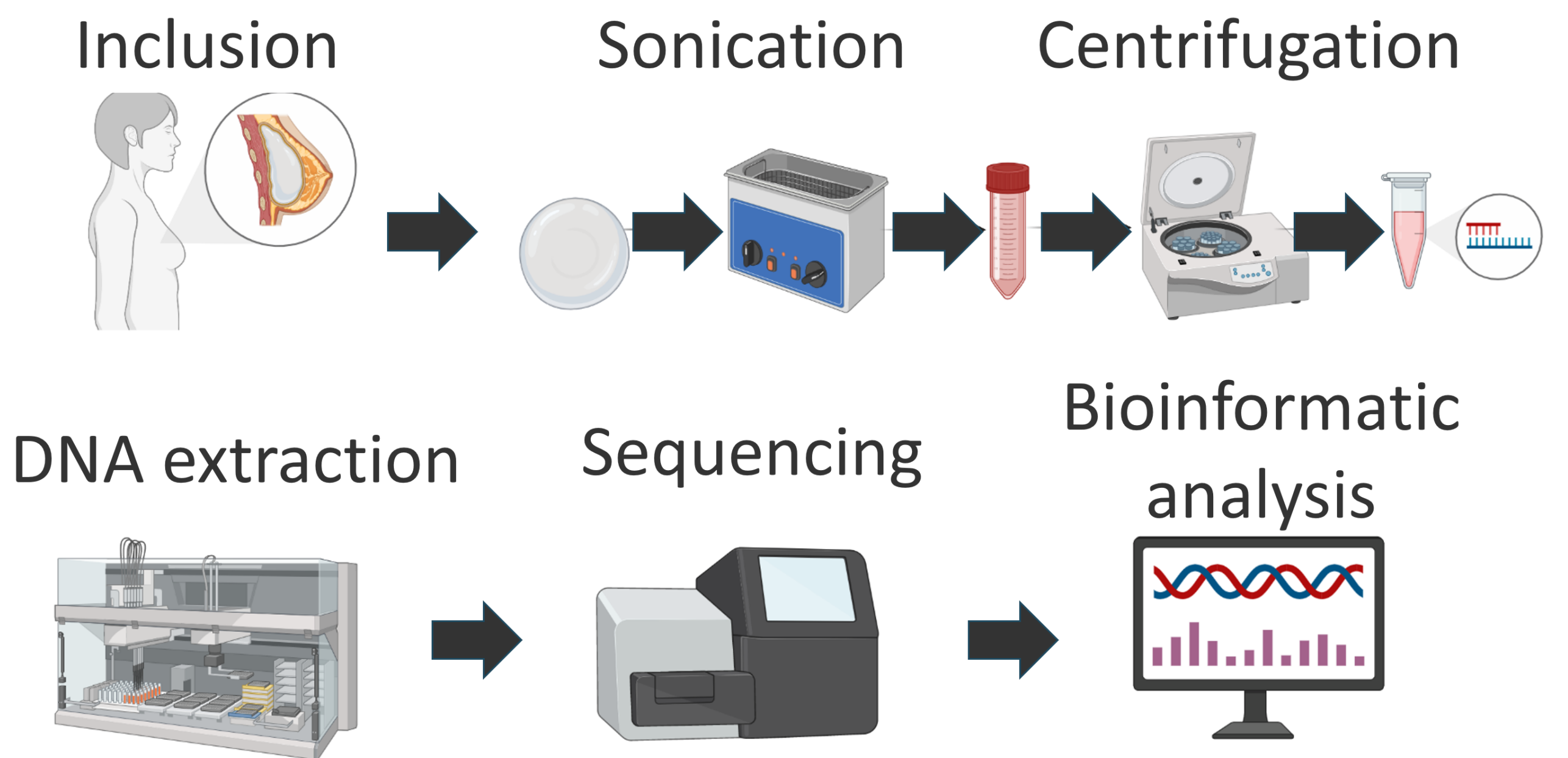
Venn diagram Cases 71 | Controls 70



The relative abundance of *Staphylococcus* was significantly higher on implants with capsular contracture compared with the control group of Baker I implants (p=0.004).

METHODS

The entire implant was sonicated for isolation of bacteria before extraction of bacterial DNA and analyzed with amplicon sequencing of the hypervariable V3-V4 region of the bacterial 16S rRNA gene on the Illumina MiSeq Platform.



CONCLUSION

We identified a unique implant microbiome in healthy patients. Implants with capsular contracture had a higher relative abundance of the *Staphylococcus* genus compared with Baker I implants supporting the hypothesis that traits of the implant microbiome may cause capsular contracture.