



**Fig. S1** Number of *P. acnes* strains detected across samples (grey, right y-axis). *P. acnes* parts per million (ppm) are shown for comparison (blue, left y-axis, logarithmic scale). The bottom horizontal lines indicate enriched or shotgun-sequenced samples, and the bottom vertical ticks delimit the sample categories. The average number of strains detected is indicated below each sample category name. NTC: non-template control.

**Fig. S2** can be accessed at this link:

[http://www.cbs.dtu.dk/~txema/Supplementary/propioni\\_web/index.html](http://www.cbs.dtu.dk/~txema/Supplementary/propioni_web/index.html)

**Fig. S2** Circos plots showing BWA mapping of all human depleted reads to the 12 full *P. acnes* genomes currently present in GenBank. To facilitate visualisation the plots for each accession number is divided into several pages. The outer coverage-circle represents the accumulated coverage for all data sets, and the inner circles represent the genomic coverage in a given data set. The sample number is indicated next to the inner circles, and the corresponding sample information can be seen in the Fig. S2 sample list.