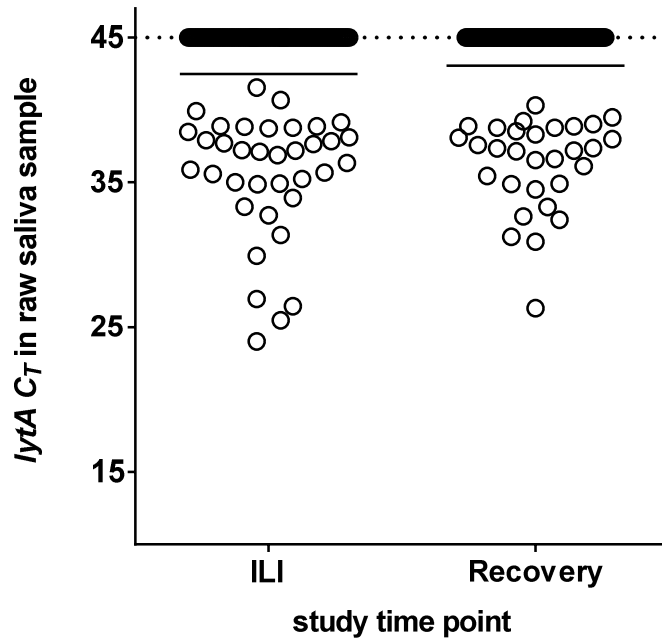


Figure S2. Absolute abundance of *Streptococcus pneumoniae* in saliva samples collected at ILI onset and after recovery from ILI.



Each dot represents an individual sample. The position of symbols corresponds to C_T values for *lytA*-specific signals in DNA extracted from raw sample of saliva at ILI onset or after recovery, as marked on X-axis. Horizontal lines represent mean C_T value. There was no significant difference between quantities of *lytA* detected in samples collected at ILI (n=135) versus the post-recovery sampling time point (n=135; Mann-Whitney, p=0.36), neither for the subset of samples considered in the study as positive for *S. pneumoniae* by qPCR at ILI (n=42) versus post-recovery (n=34; p=0.26).