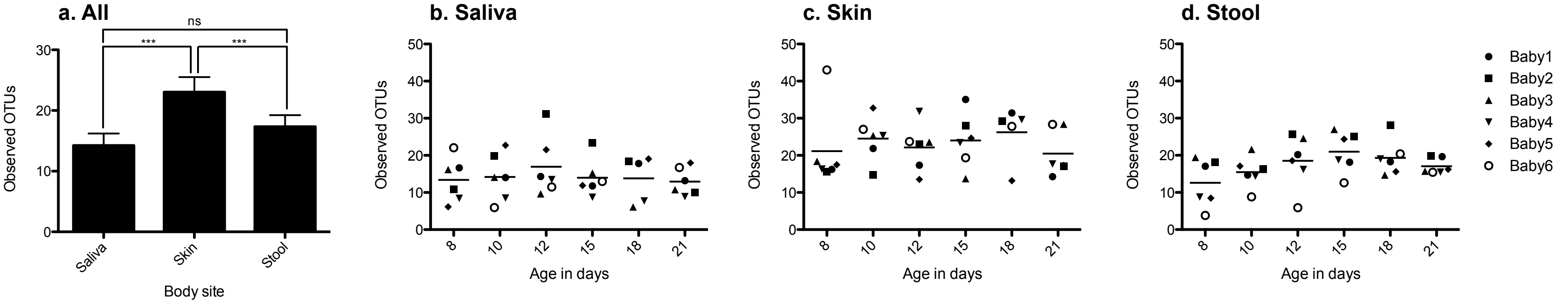

Supplemental Figure S2. Bacterial OTU richness at a depth of 200 sequences/sample. OTUs were defined at 97% sequence identity. Points and bars represent means for 50 rarefaction replicates and for the 6 LBW infants, respectively. In (a), error bars represent 95% CI. 106/108 samples yielded at least 200 sequences and were included in the analysis. On average, communities on skin were richer in bacterial OTUs than those in saliva or stool (Tukey's post-hoc tests, ***P<0.001).