

**Supplementary Figure 1. Phylogenetic history of bacterial diversity across age.** An animation showing the phylogenetic history of the human fecal (**A**), oral (**B**), and skin (**C**) microbiomes from childhood to old age measured in the American Gut Project dataset, citizen science project containing 21,919 fecal, 1,920 oral, and 998 skin microbiome samples with 16S rRNA gene amplicon sequencing <sup>1</sup>. The phylogeny of the microorganisms found at each stage of life, is produced through SEPP insertion <sup>2</sup> of the Greengenes phylogeny <sup>3</sup>.

1. Palmer, C., Bik, E. M., DiGiulio, D. B., Relman, D. A. & Brown, P. O. Development of the human infant intestinal microbiota. *PLoS Biol.* 5, e177 (2007).
2. Janssen, S. et al. Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. *mSystems* 3, (2018).
3. McDonald, D. et al. An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. *ISME J.* 6, 610–618 (2012).