Annotated Example 2. **Clear parallels between messages between mediums.** The text, graph, and styling all work to highlight the main message.
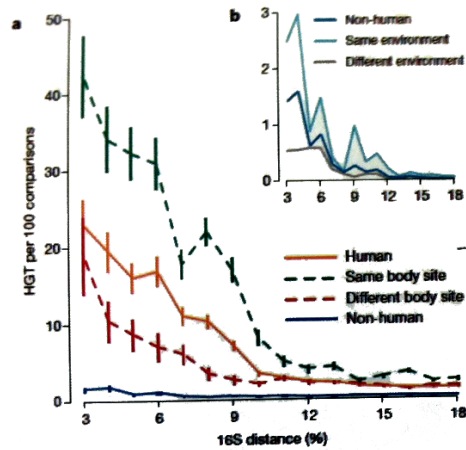

Figure 1 | Recent HGT is enriched in the human microbiome across all phylogenetic distances. HGT frequency is plotted as a function of the phylogenetic divergence between species for human-associated bacteria (a) and non-human-associated bacteria (b). We define species as clusters of genomes separated by less than 2% 16S rRNA divergence. HGT frequency is calculated in bins of 1% 16S rRNA divergence. Error bars indicate s.d. (see Supplementary Methods), with sample sizes described in Supplementary Table 8. These trends are also observed after controlling for the potential effects of sequencing centre contamination (Supplementary Fig. 4) and cosmopolitan strains (Supplementary Fig. 6).

Handwritten annotations:

cLearly sHows a Higher freq of HGT when Limiting comparison to more tightly defined ecological Locations.

soLid lines compare a Large ecological dif

dasHed lines compare a finer ecological difference

Highlighted messages represent matching message within figure Legend & plot itself.