Comparing sequencing depth among samples with at least 1 read N = 14 3 Field_BL Blanks 2 1 0 N = 14810 Blanks Lib_BL 5 0 300 N = 1391 200 Feces Baby 100 0 N = 894 100 Forearm Baby 50 0 250 N = 926 200 Mouth Baby 150 100 -50 · Number of samples 0 N = 765 90 Feces Mom 60 30 0 N = 848100 Forearm Mom 50 0 200 N = 873150 Mouth Mom 100 50 0 N = 52960 Nose 40 Mom 20 0 -150 N = 714 Right_Areola 100 -Mom 50 · 0 -200 · N = 888150 Vagina Mom 100 50 0 . 10 1000 50000 10000 Sequencing depth in log scale