## Mean sequencing coverage by sample input per amplicon region\_1 region\_10 region\_11 region\_12 region\_13 region\_14 region\_15 region\_16 region\_17 100 10 1 99 0 08 **99** 68 o 666 region\_18 region\_19 region\_20 region\_21 region\_22 region\_23 region\_24 region\_25 region\_26 100 10 9 · 96 90 0 000 0 00 9000 69 . Page 19 region\_28 region\_29 region\_30 region\_31 region\_32 region\_27 region\_3 region\_33 region\_34 0 0000 0 6800 0 0 g 99 o 960**0 9** 100 region\_35 region\_36 region\_37 region\_38 region\_39 region\_4 region\_41 region\_42 region\_40 100 **-**9 0 680 g 98 0 68 mg ® 0 000**0€** 0000 region\_43 region\_44 region\_45 region\_46 region\_47 region\_48 region\_49 region\_50 region\_5 100 формация< 10 region\_57 region\_52 region\_51 region\_53 region\_54 region\_55 region\_56 region\_58 region\_59 100 -68 0 68 68 0 080 ® + 68**68** 9 0 000 **9** region\_6 region\_60 region\_61 region\_62 region\_63 region\_64 region\_65 region\_66 region\_67 B 0 6860 B 0 0000 8 100 B 0 0000 10 region\_7 region\_70 region\_72 region\_68 region\_69 region\_71 region\_73 region\_8 region\_9 100 10 40 0 0000 0 00 99 0 0 0 0 ® 0 000**0€** 99 0 0000 g rRNA\_23S 100 -

per amplicon

Mean Coverage (X)

1×16 18 30 31

qPCR Ct