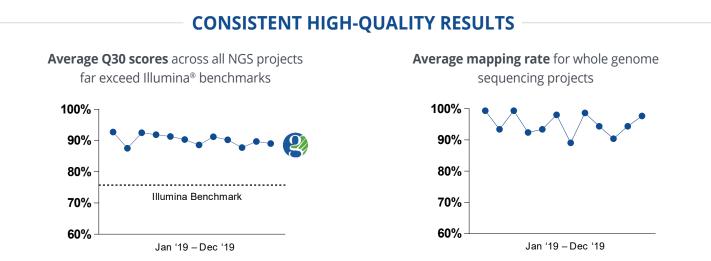


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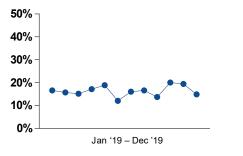
NEXT GENERATION SEQUENCING

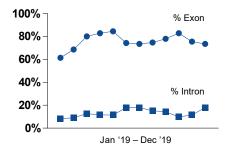
RNA SEQUENCING

Average adapter sequence percentage shows low adapter contamination, providing more useable data

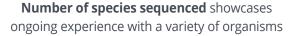
Average exon and intron mapping rates

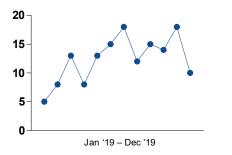
reveal high percentage of reads aligned to exons



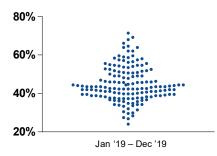


WHOLE GENOME SEQUENCING



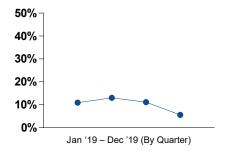




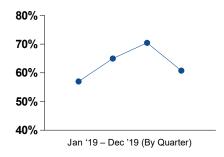


WHOLE EXOME SEQUENCING

Average adapter sequence percentage shows low adapter contamination, providing more useable data



Average on-target specificity (percent of bases on bait) indicates high precision, yielding more useful results



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