





Sequencing report

Table of contents

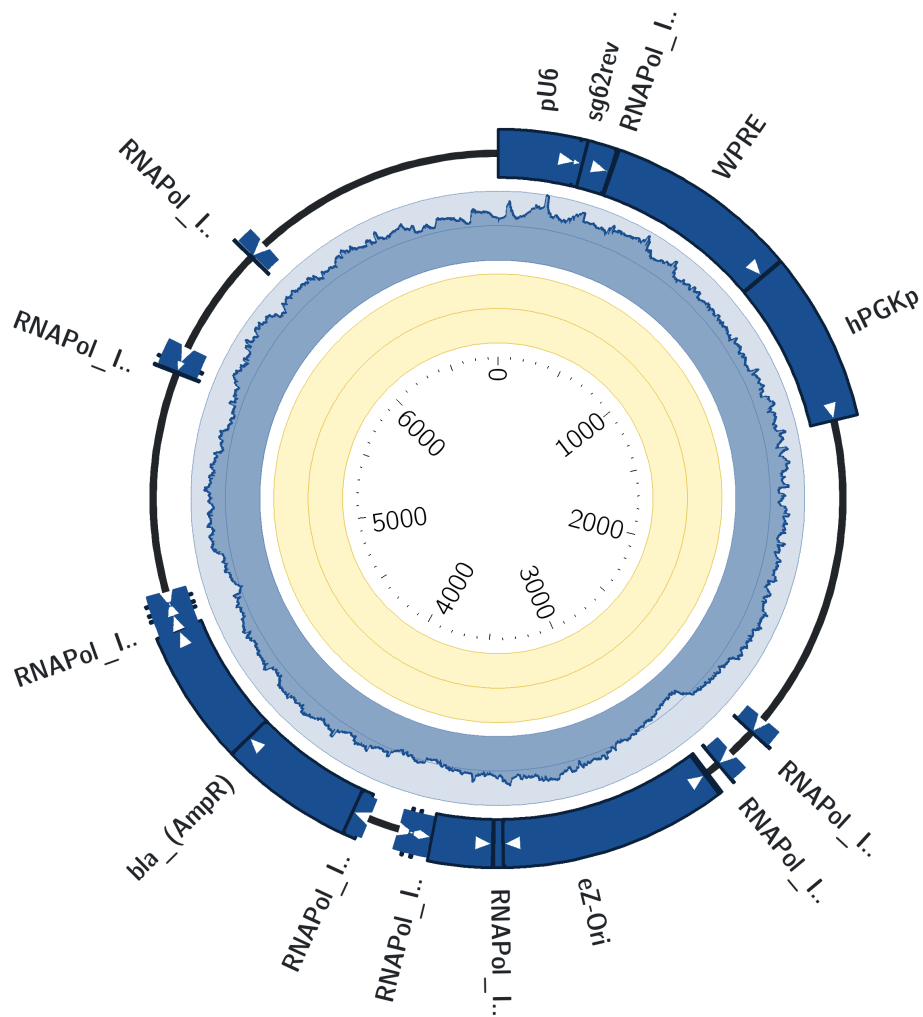
1 Sample A3062.1C	1
1.1 Overview	1
1.2 Visual representation of the sequencing results	2
1.3 Local variations (SNV and indels <30bp) from the expected sequence	3
1.4 Contamination	4

1 Sample A3062.1C

1.1 Overview

Name	A3062.1C
Type	vector (circular) 
NGS reference	20230901_C0079_ez002
Concentration (ng/μL)	491.2
Expected sequence length	6875 bp
Estimated sequencing depth	4489 X
Verified sequence	6875 base pairs  <i>download available on your account</i>
Mycoplasma contamination	 <0.1%
Comparison vs expected sequence	 100% validated

1.2 Visual representation of the sequencing results



1.3 Local variations (SNV and indels <30bp) from the expected sequence

Position	Reference	Alternative	Ratio	Feature
2062	C	T	31.81%	
2611	A	T	10.58%	
2621	A	G	17.74%	
2623	C	T	5.86%	
2626	G	C	6.53%	
2631	T	C	5.72%	
2632	A	T	10.7%	
2642	A	T	11.2%	
2652	A	T	9.39%	
2664	A	T	9.26%	
2669	T	C	5.77%	
6686	T	A	5.8%	
6751	T	A	8.77%	
6769	T	A	7.86%	

1.4 Contamination

strain U5/41	13.6475%
"Types A and B" Laidlaw and Elford 1936	0.05088%
phage phi-80	0.03414%
Enterobacteria phage mEp237	0.00488%
Enterobacteria phage HK225	0.00391%
Punavirus P1	0.00294%
Kamchatkavirus AP45	0.00188%
Tequatrovirus kaw	0.00168%
Escherichia virus mEpX1	0.00147%
Adeno-associated dependoparvovirus A	0.00146%
Lambdavirus lvO276	0.00142%
Escherichia virus DE3	0.00117%
Shigella phage SfIV	0.00098%
Pankowvirus WGPS6	0.00098%
phage lambda	0.0008%
Lambdavirus HK630	0.00076%
strain FH	0.00049%
human	0.00049%
Gemsvirus gv5004652	0.00049%
Woodchuck hepatitis virus	0.00049%
Punavirus RCS47	0.00049%
Escherichia phage TL-2011b	0.00049%