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Table 5: Comparison of different tools for detection of antimicrobial resistance genes. We applied RGI2, Abricate (3) (with the CARD database), AMRFinderPlus (4) and Resfinder (5) to the hybrid assemblies of 82 isolates of *V. cholerae*. RGI can detect the highest amount of genes and is uniquely able to use protein variant models to find gene variants. Abricate can detect gene loci at a higher completeness, being able to merge adjacent hits that were split in the underlying BLAST alignment. CholerAegon uses a combined approach, harnessing both RGI's and Abricate's advantages. RGI – Resistance Gene Identifier; COV – mean coverage of the reference gene sequence; EC parE – Escherichia coli parE conferring resistance to fluoroquinolones.

	RGI		Abricate		AMRFinderPlus		Resfinder	
AMR gene	# found	COV	# found	COV	# found	COV	# found	COV
APH(3")-lb	74	97.08	74	100.00	74	99.11	74	100.00
APH(6)-Id	74	100.00	74	100.00	74	100.00	74	100.00
CRP	82	100.00	82	99.68	0	_	0	_
Vibrio cholerae varG	79	95.90	79	100.00	79	100.00	0	-
almG	82	100.00	82	100.00	0	-	0	-
catB9	79	100.00	79	100.00	79	100.00	79	100.00
dfrA1	79	100.00	79	100.00	79	100.00	79	100.00
floR	74	99.94	74	100.00	74	99.96	74	99.92
rsmA	82	106.56	0	-	0	-	0	-
sul2	74	99.48	74	100.00	74	99.61	74	100.00
EC parE	82	99.37	0	_	0	_	0	_

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