

**Table 2. Strategies for Reporting Vancomycin Results When Using Molecular and Phenotypic AST Methods for *Enterococcus* spp.**

Indication	Target(s)	Method	Specimen Type	Result		Suggestions for Resolution	Report as:	Footnotes*
				Genotype or Predicted Phenotype	Observed Phenotype (if tested)			
Detection of vancomycin resistant enterococci	<i>vanA</i> , <i>vanB</i>	NAAT or array hybridization technology	Blood culture broth or surveillance cultures	<i>vanA</i> and/or <i>vanB</i> detected	Vancomycin R	N/A	Report phenotypic result as found (if available), consider reporting presence of molecular target per institutional protocol	1-3
				<i>vanA</i> and/or <i>vanB</i> not detected	Vancomycin S	N/A	Report phenotypic result as found (if available), consider reporting presence of molecular target per institutional protocol	
				<i>vanA</i> and/or <i>vanB</i> detected	Vancomycin S	Confirm isolate identification to species level (e.g. <i>E. faecalis</i> ) and repeat AST. If mixed culture, test isolates individually.	If discrepancy is not resolved by suggested testing, report as vancomycin R	1-3
				<i>vanA</i> and/or <i>vanB</i> not detected	Vancomycin R	Confirm isolate identification to species level (e.g. <i>E. faecalis</i> ) and repeat AST. If mixed culture, test isolates individually.	If discrepancy is not resolved by suggested testing, report as vancomycin R	4
	<i>vanA</i>	NAAT	Surveillance cultures	<i>vanA</i> detected	Vancomycin R	N/A	Report phenotypic result as found (if available), consider reporting presence of molecular target per institutional protocol	1-2
				<i>vanA</i> not detected	Vancomycin S	N/A	Report phenotypic result as found (if available), consider reporting presence of molecular target per institutional protocol	5
				<i>vanA</i> detected	Vancomycin S	Confirm isolate identification to species level (e.g. <i>E. faecalis</i> ) and repeat AST. If mixed culture, test isolates individually.	If discrepancy is not resolved by suggested testing, report as vancomycin R	1-2
				<i>vanA</i> not detected	Vancomycin R	Confirm isolate identification to species level (e.g. <i>E. faecalis</i> ) and repeat AST. If mixed culture, test isolates individually.	If discrepancy is not resolved by suggested testing, report as vancomycin R	4-5

\*In addition to the specific possibilities referenced, genotype/phenotype discrepancies could arise as a consequence of suboptimal sampling, mixed cultures, emergence of new genotypes, or mutations and/or wild-type reversions of resistance targets.

## References

- 1 *vanA* may be present in nonenterococcal species (Patel R.2000 Apr 1;185(1):1-7).
- 2 Vancomycin-variable *E. faecium* isolates have been recently revealed in Canada. They carry wildtype *vanA*, but initially test as vancomycin-susceptible with culture based method. They are able to convert to a resistant phenotype during vancomycin treatment (Gagnon S et al. 2011. J Antimicrob Chemother 66:2758–2762.; Thaker MN et al. 2015. Antimicrob Agents Chemother 59:1405–1410).
- 3 *vanB* gene has been found in several commensal nonenterococcal bacteria which may lead to misclassification of vancomycin susceptible enterococci as resistant in surveillance cultures containing mixed bacterial species (Ballard SA et al., Antimicrob Agents Chemother 2005;49:77-81).
- 4 Constitutive low-level vancomycin resistance can be detected phenotypically (2-32µg/ml) from the presence of *vanC*, an intrinsic resistance characteristic of *E. gallinarum* (*vanC1*) and *E. casseliflavus* (*vanC2-4*) (Courvalin P. 2006. Clin Infect Dis 42:S25-34).
- 5 Targeting *vanA* only may miss regional *vanB*-carrying VRE (Nebreda T et al. J Antimicrob Chemother 2007; 59:806-7).