

Table S1. Genetic location, molecular functions and drug class resistance induced by antibiotic resistance genes found in *Str.agalactiae* genome.

| Gene | Location in genome | Molecular function | Drug class |
|---|--|------------------------------|---|
| <i>tetM</i> | Mobile element (transposon Tn916 family) | Antibiotic target protection | Tetracycline |
| <i>tetW</i> | Mobile element (conjugative and non conjugative plasmid) | | |
| <i>tetO¹</i> | Chromosome | | |
| <i>tetS</i> | Chromosome | | |
| <i>tet(44)</i> | Mobile element | | |
| <i>tetK</i> | Mobile element (conjugative plasmid) | | |
| <i>tetL</i> | Chromosome | Antibiotic efflux | |
| <i>ermA, ermB¹, ermT</i> | Mobile element (conjugative plasmid pIP501 or ICESag37, or transposon Tn917) | Ribosomal alteration | Macrolides, lincosamides and streptogramin B (MLS _B) ² |
| <i>ant(6')la, aadE</i> | Chromosome/plasmid | Antibiotic inactivation | Aminoglycosides |
| <i>aac(6')-ie-aph(2'')-Ia</i> | Plasmid/transposon | | |
| <i>Aph(3')-Ia</i> | Chromosome | | |
| <i>sat-4</i> | Mobile element (plasmid) | | |
| <i>spw</i> | Mobile element (plasmids and transposons) | | |
| <i>mefA³, msrD</i> | Mobile element (Conjugative transposons Tn1207.1 or Tn1207.3) | Antibiotic efflux | Macrolides |
| <i>catA16, catTC</i> | Mobile element (conjugative plasmid pIP501 or transposon) | Antibiotic inactivation | Phenicol |
| <i>catP</i> | Chromosome and transposon | | |
| <i>lnuB</i> | Chromosome | Antibiotic inactivation | Lincosamides (L phenotype) |
| <i>Isa, IsaC, IsaE</i> | Mobile element (transposon) | Antibiotic efflux | Lincosamides, streptogramin A, pleuromutilins (LSA and LSAP phenotypes) |
| <i>blaTEM, blaTEM116</i> | Mobile element (plasmid) | Antibiotic inactivation | β-lactam |
| <i>PBP2x, pbp2x_Q557E</i> | Chromosome | Antibiotic target alteration | |
| <i>bleSh</i> | Transposon | Antibiotic target alteration | |
| <i>vanG, vanRG⁴, vanTG⁴, vanUG⁴, vanWG⁴, vanYG1⁴</i> | Chromosome | Glycopeptide | |
| <i>vanR⁵</i> | Chromosome | | |
| <i>vanXY</i> | Chromosome | | |
| <i>vanW⁶</i> | unknown | | unknown |

| | | | |
|--------------|----------------|-------------------------------|-------------------------|
| <i>dfrF</i> | Chromosome | Antibiotic target replacement | Diaminopyrimidine |
| <i>optrA</i> | Plasmid | antibiotic target protection | Oxazolidinone, phenicol |
| <i>vat</i> | Mobile element | Antibiotic inactivation | Streptogramin |

¹ Tetracycline resistance genes are often found on the same mobile element as erythromycin resistance genes. ² This resistance can be constitutive (cMLSB) resistance, or (iMLSB) resistance; iMLSB is mediated by *mef* gene. ³ Confers resistance to 15-membered ring macrolides (M phenotype) only, while *erm(B)* determines cross-resistance to all macrolides, lincosamides, and streptogramins B. ⁴ are all variant found in the *vanG* gene cluster. ⁵ Is a OmpR-family transcriptional activator in the VanSR regulatory system, after activation by *VanS*, it promotes cotranscription of *VanA*, *VanH*, and *VanX*. ⁶Found in vancomycin resistance gene clusters *vanB* and *vanG*.