**SI Table 1:** List of all used primer systems with their corresponding target gene, expected amplicon size, accuracy and efficiency of the used calibration curves.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Organism** | **Target Gene** | **Primer** | **Sequence** | **Amplicon** | **Accuracy (R²)** | **Efficency [%]** | **Reference** |
| **Antibiotic resistance genes** | |  |  |  |  |  |  |
| *E. coli* pNorm\* | *sul1* | sul1-FW | CGCACCGGAAACATCGCTGCAC | 163 bp | 0.999 | 97.6 | ([Rocha et al., 2018](#_ENREF_4)) |
|  |  | sul1-RV | TGAAGTTCCGCCGCAAGGCTCG |  |  |  |  |
| *E. coli* pNorm\* | *intI1* | intI.1-LC1 | GCCTTGATGTTACCCGAGAG | 196 bp | 1.0 | 94.1 | ([Rocha et al., 2018](#_ENREF_4)) |
|  |  | intI.1-LC5 | GATCGGTCGAATGCGTGT |  |  |  |  |
| *S. aureus+* | *mecA* | mecA1 FP | CGCAACGTTCAATTTAATTTTGTTAA | 91 bp | 1.0 | 99.8 | ([Volkmann et al., 2004](#_ENREF_5)) |
| *CNS* |  | mecA1 RP | TGGTCTTTCTGCATTCCTGGA |  |  |  |  |
| *E. coli* pNorm\* | *ctx-M-32* | ctxm32-F | CGTCACGCTGTTGTTAGGAA | 155 bp | 1.0 | 92.5 | ([Rocha et al., 2018](#_ENREF_4)) |
|  |  | ctxm32-R | CGCTCATCAGCACGATAAAG |  |  |  |  |
| *S. hyointestinales* | *ermB* | ermB-F | TGAATCGAGACTTGAGTGTGCAA | 71 bp | 1.0 | 99.7 | ([Alexander et al., 2015](#_ENREF_1)) |
|  |  | ermB-R | GGATTCTACAAGCGTACCTT |  |  |  |  |
| *E. coli* pNorm\* | *blaTEM* | qblaTEM-F | TTCCTGTTTTTGCTCACCCAG | 112 bp | 0.999 | 100.8 | ([Rocha et al., 2018](#_ENREF_4)) |
|  |  | qblaTEM-R | CTCAAGGATCTTACCGCTGTTG |  |  |  |  |
|  | *vanA* | vanA-For | TCTGCAATAGAGATAGCCGC | 376 bp | 1.0 | 91,6 | ([Klein et al., 1998](#_ENREF_3)) |
|  |  | vanA Rev | GGAGTAGCTATCCCAGCATT |  |  |  |  |
| **Taxonomic marker genes** | |  |  |  |  |  |  |
| *E. coli* | *yccT* | yccTFP | GCATCGTGACCACCTTGA | 59 bp | 0.994 | 98.4 | ([Clifford et al., 2012](#_ENREF_2)) |
|  |  | yccTRP | CAGCGTGGTGGCAAAA |  |  |  |  |
| *P. aeruginosa* | *ecfX* | ecfXRT-F | AGCGTTCGTCCTGCACAAGT | 81 bp | 0.999 | 101.7 | ([Clifford et al., 2012](#_ENREF_2)) |
|  |  | ecfXRT-R | TCCACCATGCTCAGGGAGAT |  |  |  |  |
| *Enterococcus* spp. | 23S rRNA | ECST784F | AGAAATTCCAAACGAACTTG | 93 bp | 1.0 | 90.1 | ([Volkmann et al., 2004](#_ENREF_5)) |
|  |  | ENC854R | CAGTGCTCTACCTCCATCATT |  |  |  |  |
| Eubacteria;  *E. coli* pNorm\* | 16S rRNA | 331-F | TCCTACGGGAGGCAGCAGT | 195 bp | 1.0 | 96.6 | ([Rocha et al., 2018](#_ENREF_4)) |
|  |  | 518-R | ATTACCGCGGCTGCTGG |  |  |  |  |

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