Table S2. Calculation of sensitivity and specificity of RNAz and eQRNA independently and of the combination of the two analyses using known *S. pyogenes* RNAs

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | BLASTNa | eQRNAb | RNAzb | Overlap between QRNA and RNAzb |
| Real alignmentsc | 68/68 | 66/68 | 65/68 | 65/68 |
| Shuffled alignmentsd | 68/68 | 16/68 | 3/68 | 1/68 |

a BLAST comparisons detected 68 of the 68 known RNAs tested.

b To estimate the specificity of both methods combined, both programs scored identical shuffled windows.

c 67 tRNAs and 1 tmRNA were used in order to get the sensitivity.

d Shuffled 67 tRNAs and 1 tmRNA were used to score the number of false positive alignments, which represents the specificity of our approach.