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QUALITY CONTROL for MOLECULAR DIAGNOSTICS

Supplement to Final Report

QCMD 2010
ENVA

HIV Drug Resistance Typing EQA Programme

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on behalf of QCMD and its Scientific Council
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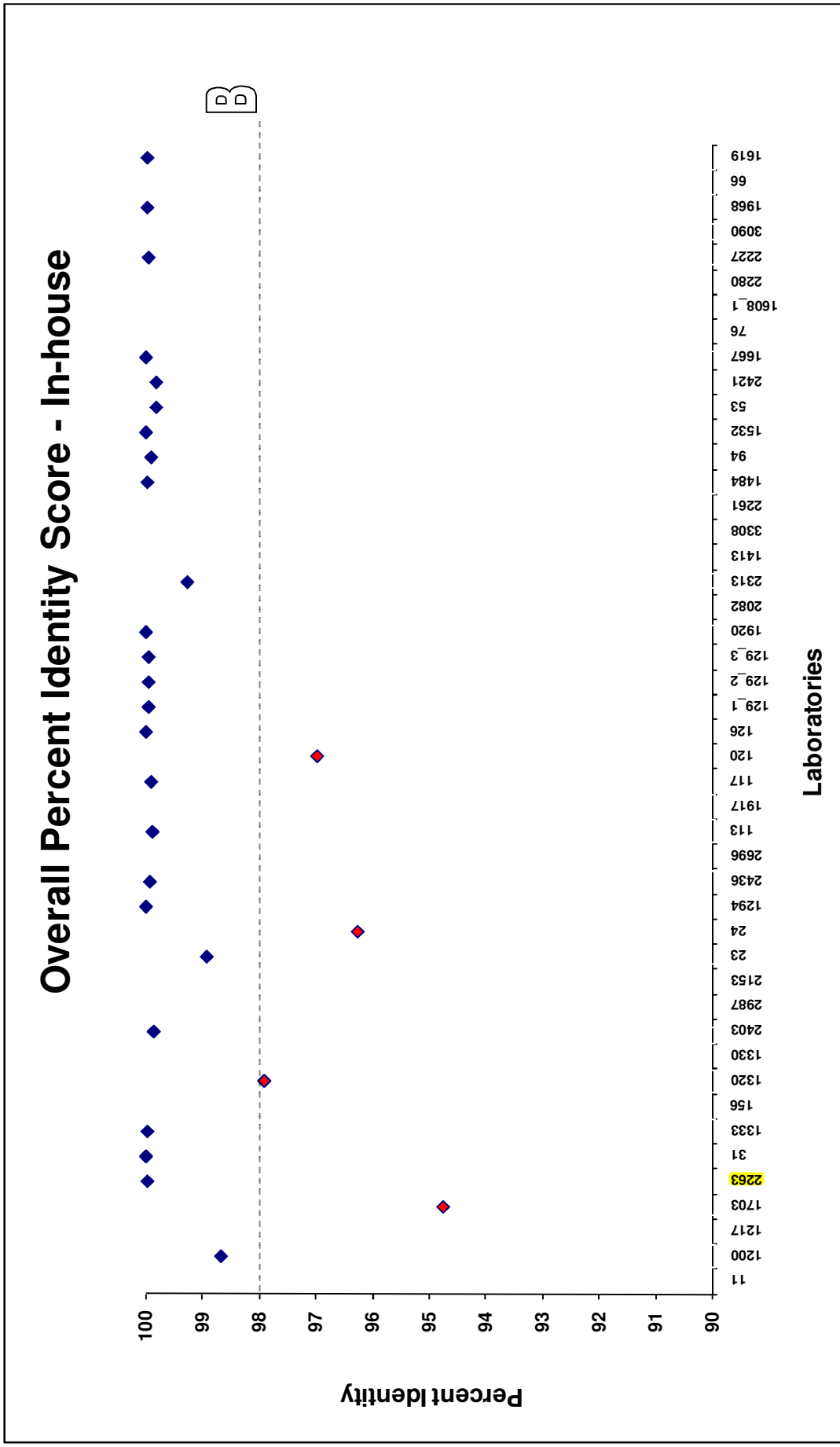
The QCMD programme is organised
in collaboration with the European
Society for Clinical Virology and the
European Society for Clinical
Microbiology & Infectious Diseases.



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Figure 1: Summary of the overall concordance for the sequences submitted by participants using In-house technologies.

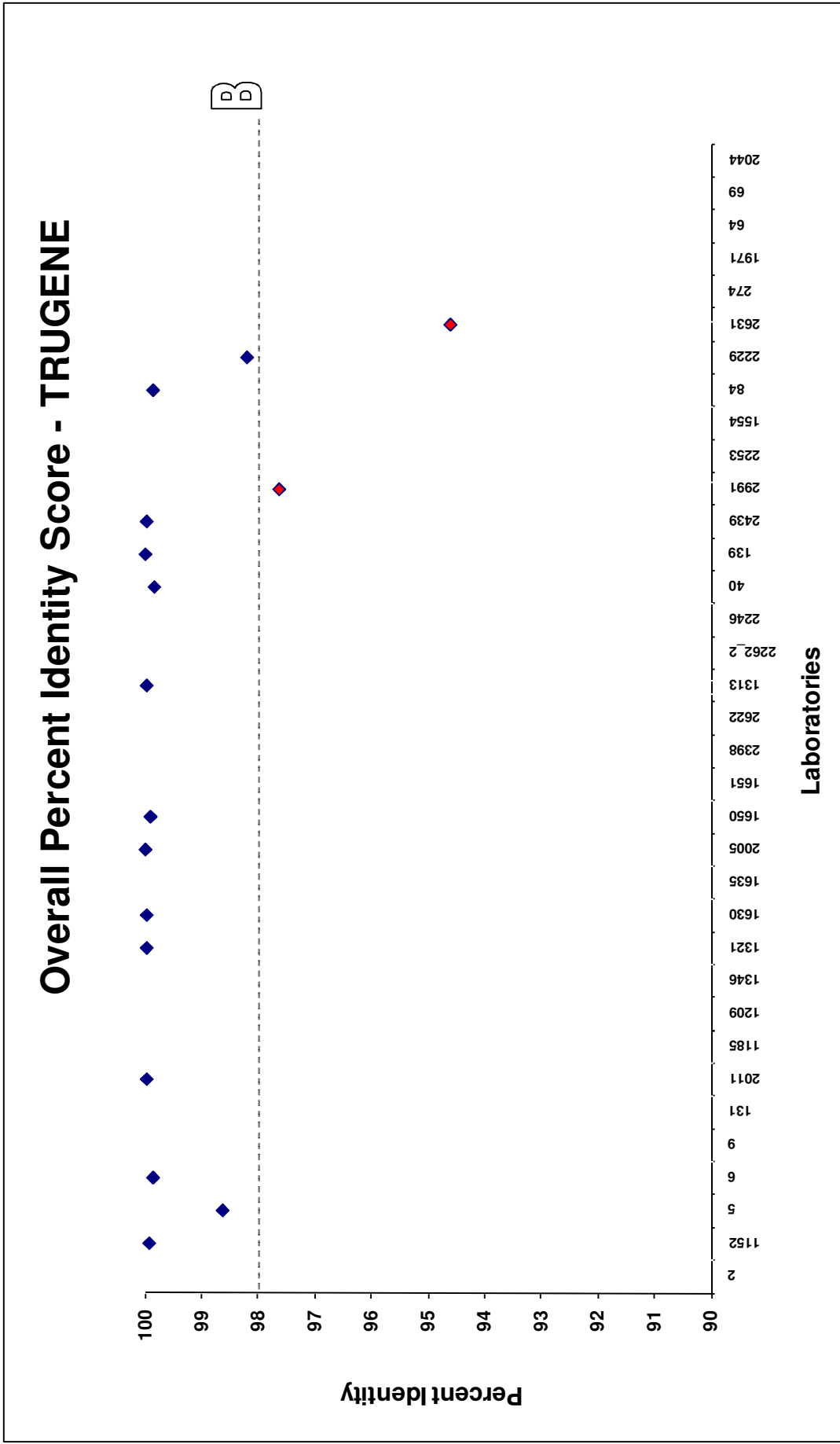


1. Alignment score is calculated by aligning each individual sequence to the consensus sequence by pairwise local alignment. While calculating the alignment score, a match is scored 1, while a mismatch is scored 0.

2. B: 98% of maximum achievable percent identity.

3. *: An overall percent identity score was only awarded to those participants who had submitted complete datasets.

Figure 2: Summary of the overall concordance for the sequences submitted by participants using TRUGENE technology.

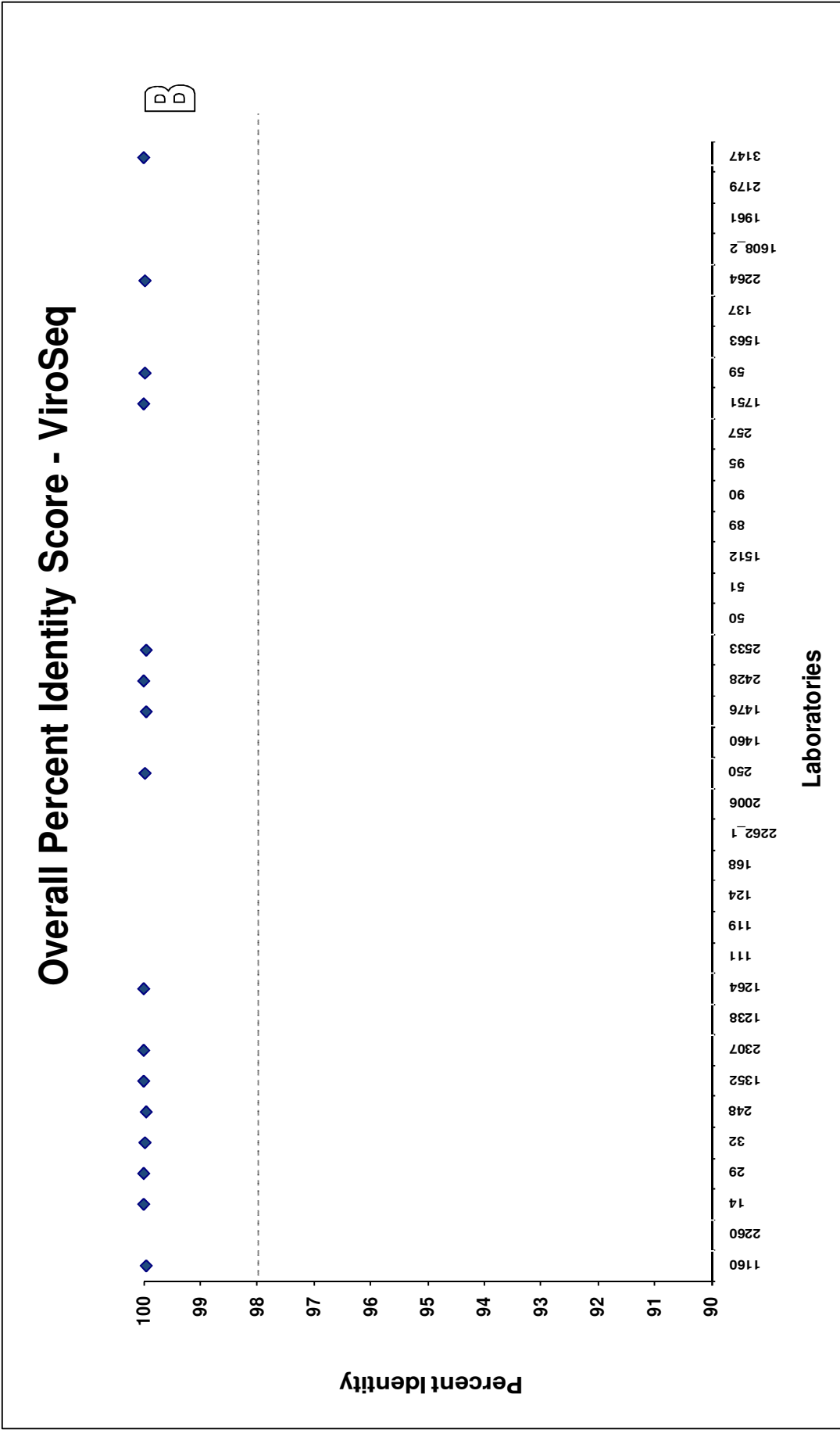


1. Alignment score is calculated by aligning each individual sequence to the consensus sequence by pairwise local alignment. While calculating the alignment score, a match is scored 1, while a mismatch is scored 0.

2. B: 98% of maximum achievable percent identity.

3. *: An overall percent identity score was only awarded to those participants who had submitted complete datasets.

Figure 3: Summary of the overall concordance for the sequences submitted by participants using ViroSeq technology.

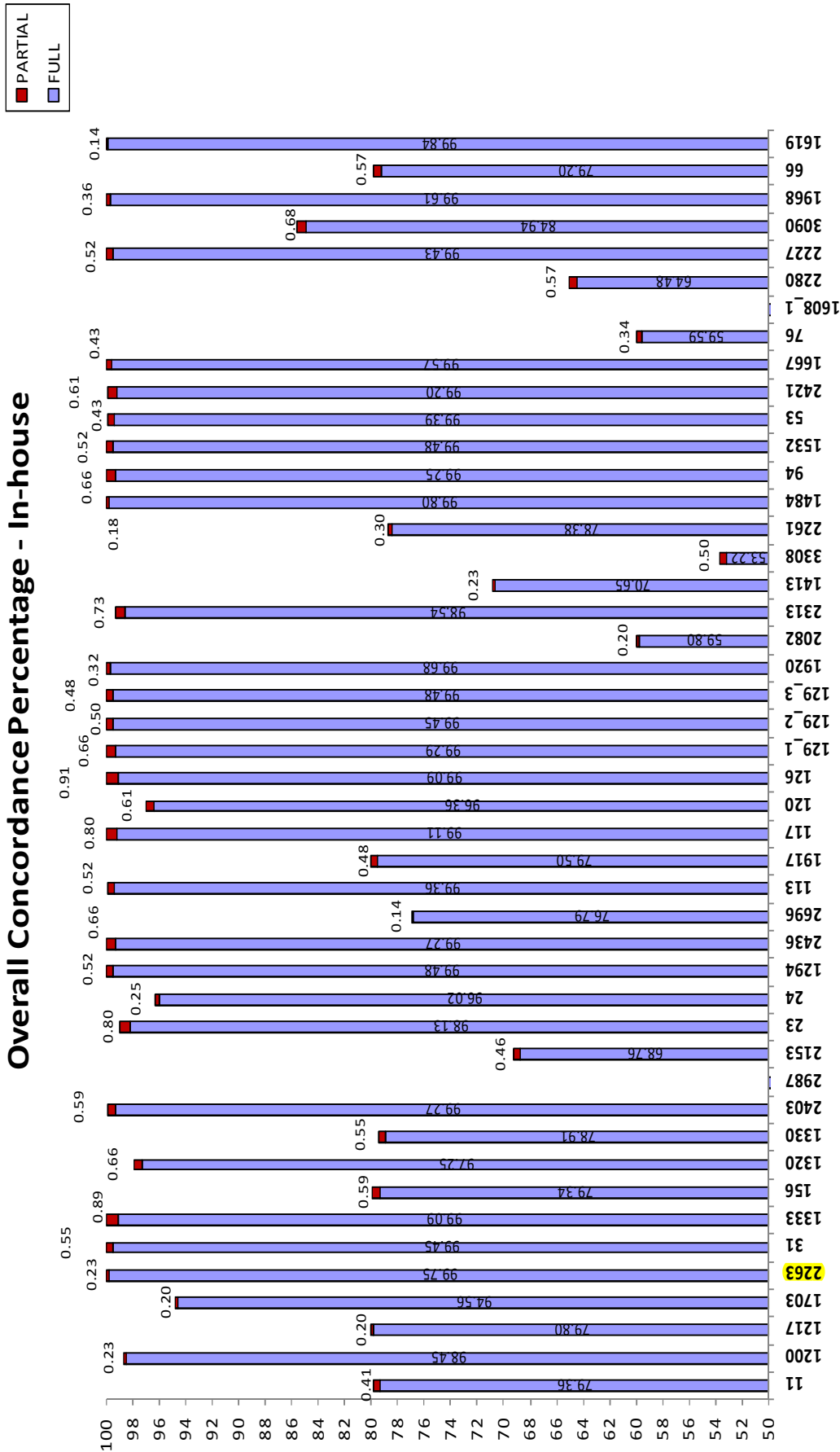


1. Alignment score is calculated by aligning each individual sequence to the consensus sequence by pairwise local alignment. While calculating the alignment score, a match is scored 1, while a mismatch is scored 0.

2. B: 98% of maximum achievable percent identity.

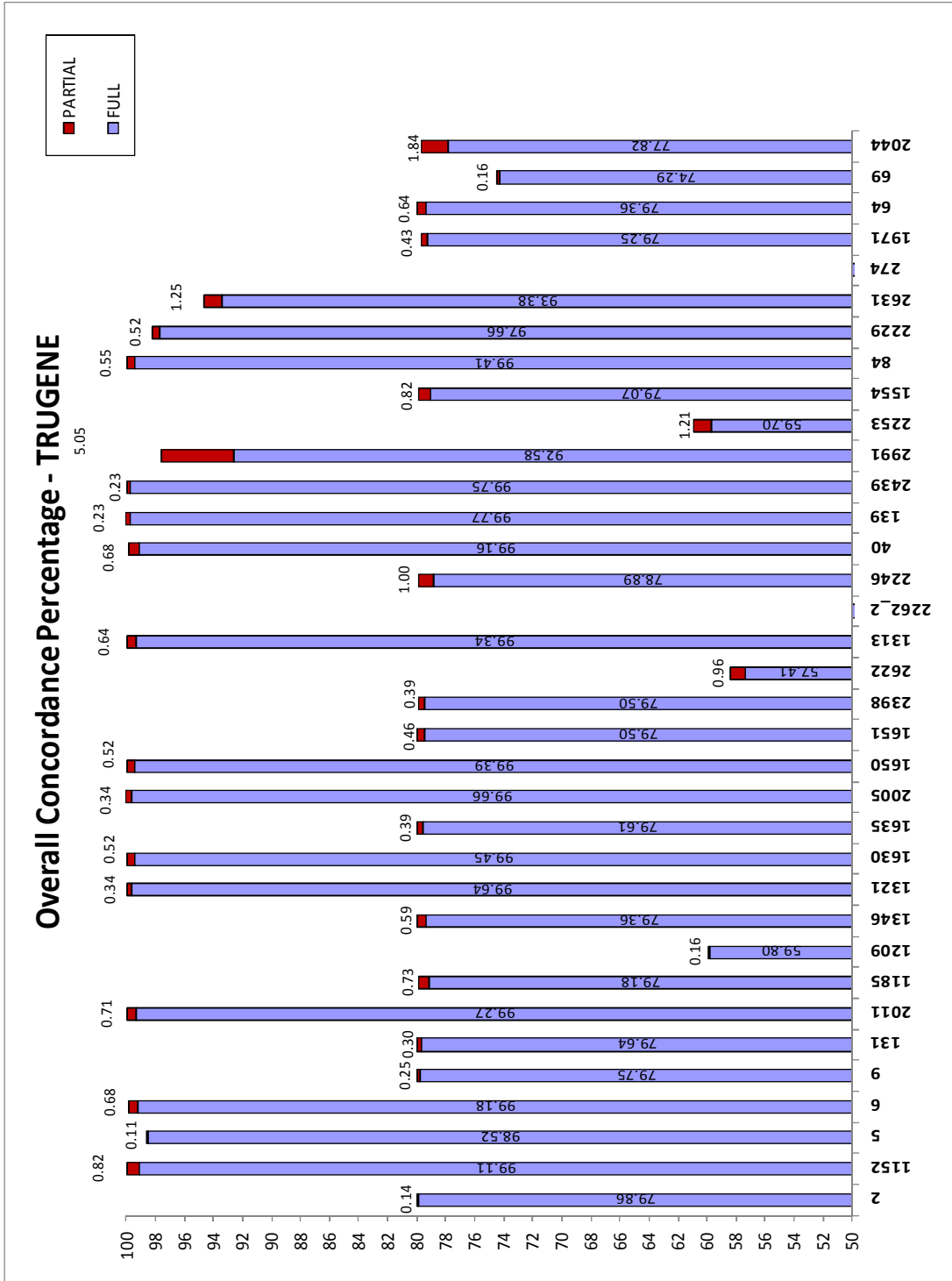
3. *: An overall percent identity score was only awarded to those participants who had submitted complete datasets.

Figure 4: Percentage overall sequence concordance for the In-house technologies.



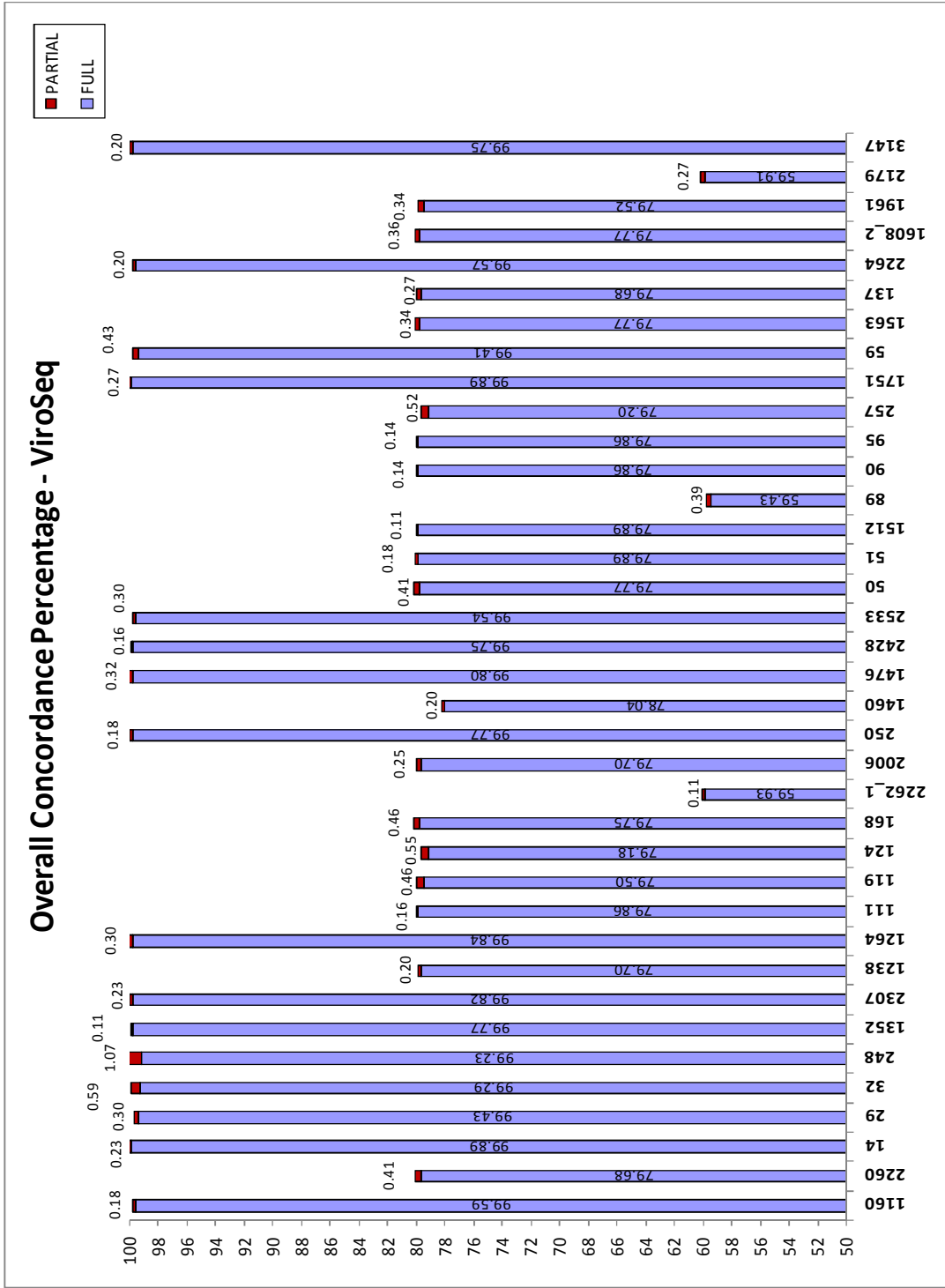
1. A full concordance was recorded if a participant reported nucleotide completely matched the result for the consensus sequence.
2. A partial concordance was recorded if a participant's reported nucleotide was :
 - a. A single nucleotide that partially matched the IUB code representing a mixed nucleotide in the consensus sequence at that position.
 - b. A mixed nucleotide represented by a IUB code that partially matched the nucleotide in the consensus sequence at that position.
3. *: An overall concordance score was only awarded to those participants who had submitted complete datasets.

Figure 5: Percentage overall sequence concordance for the TRUGENE technology.



1. A full concordance was recorded if a participant reported nucleotide completely matched the result for the consensus sequence.
2. A partial concordance was recorded if a participant's reported nucleotide was :
 - a. A single nucleotide that partially matched the IUB code representing a mixed nucleotide in the consensus sequence at that position.
 - b. A mixed nucleotide represented by a IUB code that partially matched the nucleotide in the consensus sequence at that position.
3. *: An overall concordance score was only awarded to those participants who had submitted complete datasets.

Figure 6: Percentage overall sequence concordance for the ViroSeq technology.



1. A full concordance was recorded if a participant reported nucleotide completely matched the result for the consensus sequence.
2. A partial concordance was recorded if a participant's reported nucleotide was :
 - a. A single nucleotide that partially matched the IUB code representing a mixed nucleotide in the consensus sequence at that position.
 - b. A mixed nucleotide represented by a IUB code that partially matched the nucleotide in the consensus sequence at that position.
3. *: An overall concordance score was only awarded to those participants who had submitted complete datasets.

