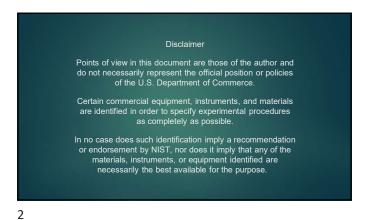
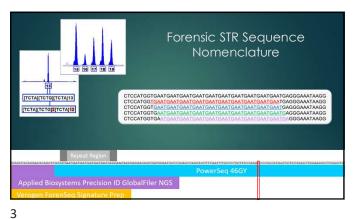
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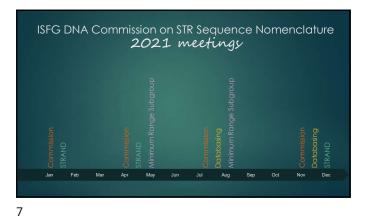






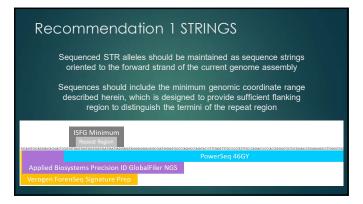


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Recommendation 1 STRINGS Minimum Reporting Range Exchange of common information Algorithmic methods for bracketing and short designators ▶ Data QC The full list of sequence strings must be submitted as Supplementary information...sequence strings should include flanking sequences and indicate the genome coordinates of the sequence read.

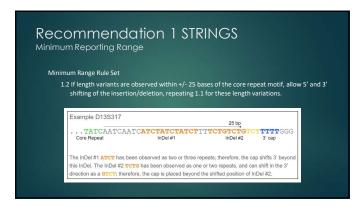
9 10

Recommendation 1 STRINGS Minimum Reporting Range 1.2 If length variants are observed within +/- 25 bases of the core repeat motif, allow 5' and 3' shifting of the insertion/deletion, repeating 1.1 for these length variations. 1.3 SNPs may be present but are not considered in determining the minimum reporting range, except when an SNP is observed which would result in a continuation of the core repeat motif. Include this SNP in the 5' and 3' shifting resulting in an expanded core repeat motif. 1.4 Add a four-base cap to each end beyond the core repeat motif.

Recommendation 1 STRINGS Minimum Reporting Range 1.1 Allow 5' and 3' shifting of the CE-counted repeat motif to determine the core repeat CTCCATGG**TGAATGAATG...AATGAA**TGAGGGAAAT - 5' shift CTCCATGGTGA**ATGAATG...AATGAATGA**GGGAAAT - 3' shift CTCCATGGTGAATGAATG. . . AATGAATGAGGGAAAT - core repeat CTCCATGCTGAATGAATG...AATGAATGAGGGAAAT - 4bp caps

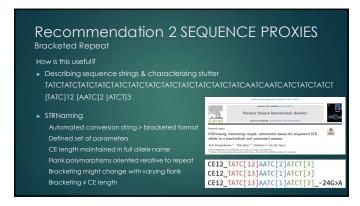
12 11

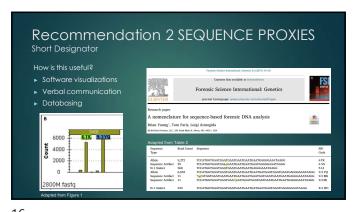
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