the other hand, which is the alignment score in the lower right-hand corner of table 150.

[00158] Table 152 in Figure 1E shows the alignment scores for query sequence Q and reference sequence S2 (CGCTTCG). The highest alignment score in the rightmost column and the bottom row is in cell 153, having a value of 4. It is the glocal alignment score between Q and S2, or g(Q,S2). The Levenshtein distance between Q and S2 is identical to the Levenshtein distance between Q and S1, because there are two mismatches between the two sequences in both comparisons. However, g(Q,S2) is larger than g(Q,S1), because there are more matching nucleotides between Q and S2 than between Q and S1. Namely, the glocal alignment scores account for not only edits of nucleotides (as Levenshtein distance does), but also matches of nucleotides between sequences.

[00159] Figure 1E illustrates that the glocal alignment score can provide better error correction than Levenshtein distance or edit distance, because Levenshtein distance accounts for only number of edits in the sequence, while the glocal alignment score accounts for both number of edits and number of matches between the sequences. Figure 1F provides an example illustrating that the glocal alignment score can provide better error suppression than the global alignment score, because the glocal alignment score does not over-penalize mismatches due to insertion, deletion, or substitution at the end of the sequence.

[00160] The example in Figure 1F uses a different set of vNRUMI sequences, γ = {S1,S2} = {TTGTGAC,GGCCAT}. In the sample processing process S1 is used to label a DNA molecule. This molecule's sequence is $\boldsymbol{m_0 = TTGTGACTNNNNN}$ (SEQ ID NO: 1). During sequencing, a single insertion error occurs and the sequence GCA is inserted into $\boldsymbol{m_0}$, creating $\boldsymbol{m_1 = TTGGCATGACTNNNNN}$ (SEQ ID NO: 2). To correct for this error and recover the proper UMI for this sequence, a process takes the first 7 base pairs as the query sequence, $\boldsymbol{Q = TTGGCAT}$. The process compares $\boldsymbol{Q}$ with each sequence in $\boldsymbol{\gamma}$.

[00161] An alignment score table 160 for $\mathbf{g(Q,\ S1)}$ is obtained and shown in Figure 1F. And similarly, an alignment score table 163 is obtained for $\mathbf{g(Q, S2)}$.

[00162] If a global alignment scheme instead of a glocal alignment score is used, the score at the bottom right corner in cells 161 and 164 would be used, which