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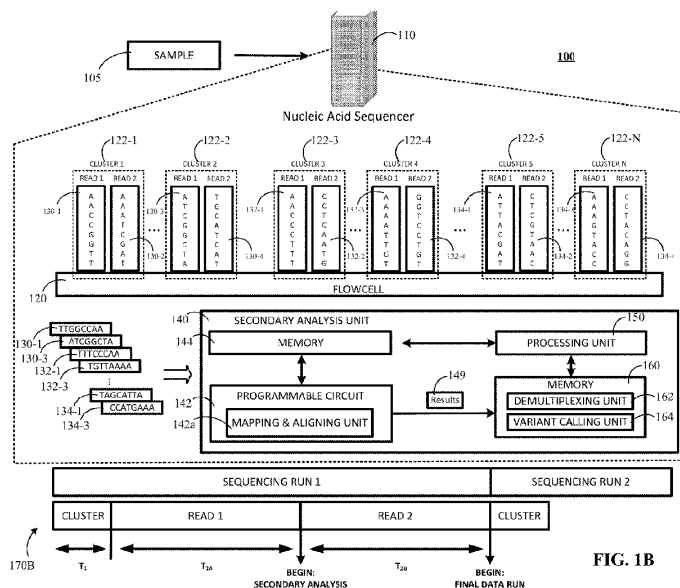


FIG. 1B

- (57) Abstract: Methods, systems, and apparatuses, including computer programs, for performing incremental secondary analysis of nucleic acid sequence reads. The method can include (i) obtaining first data describing a plurality of first reads generated by a nucleic acid sequencing device during a first read interval, (ii) obtaining second data describing a plurality of second reads generated by the nucleic acid sequencing device during a second read interval that is performed after the first read interval, wherein while the second data is being obtained: (a) providing, by the nucleic acid sequencing device, the first data as an input to a mapping and alignment unit, (b) receiving, from the mapping and alignment unit, alignment results, and (c) storing the received alignment results, and, thereafter (iii) instructing the mapping and alignment unit to begin alignment of the second data representing the second plurality of reads to the reference sequence.

[Continued on next page]

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