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- Precisely set speed and duration controls
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- Quickly vortex tubes with just one touch

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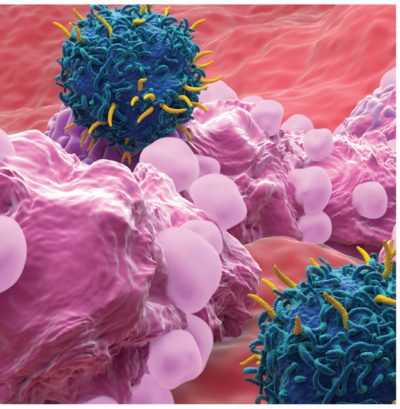

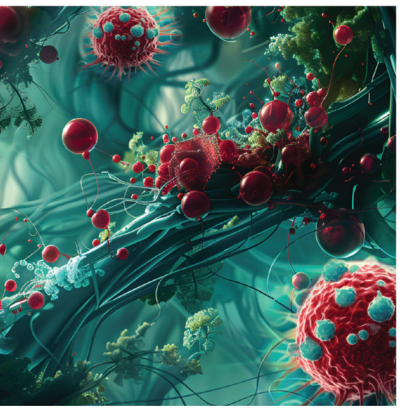

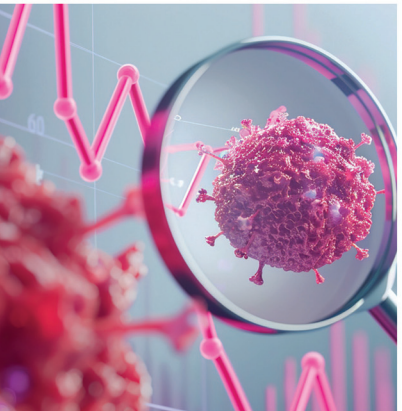

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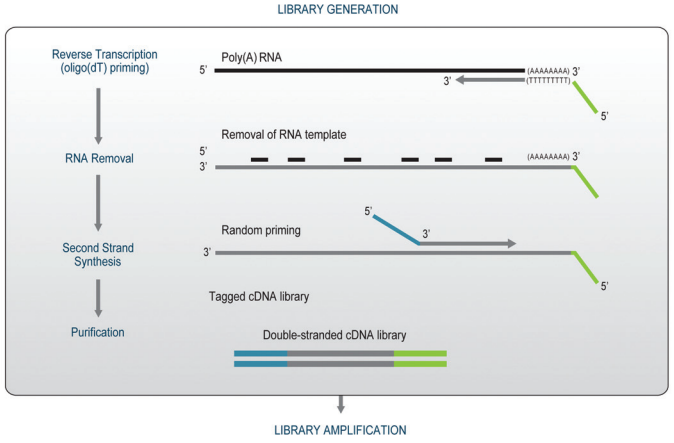

Figure 1 | QuantSeq REV V2 workflow: generate ready-to-sequence libraries in only 4.5 hours.

QuantSeq REV allows to precisely pinpoint the 3' end of poly(A) RNA following a fast and streamilned 5-step workflow: 1) oligo(dT) priming and reverse transcription to generate cDNA directly downstream of the poly(A) site, 2) RNA removal and second strand synthesis, 3) purification, 4) library amplification and indexing, and 5) final purification (Fig. 1).

Gene expression, alternative polyadenylation events, and accurate information about a transcripts' 3' UTR can be detected globally using QuantSeq REV (Fig. 2).

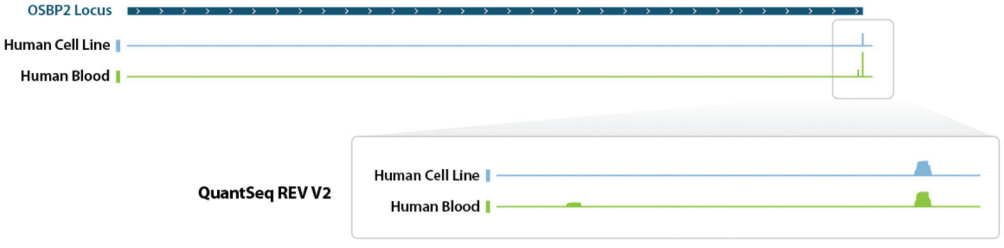

Figure 2 | Alternative polyadenylation of OSBP2 in human blood detected with QuantSeq REV V2 (with Hs Globin Block for blood sample preparation). Alternative polyadenylation site detection revealed two distinct transcript end sites for OSBP2 (human Oxysterol Binding Protein 2).

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