Sequence analysis

Dragon PolyA Spotter: predictor of poly(A) motifs within human genomic DNA sequences

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We found that the data we provided (cbrc.kaust.edu.sa/dps) contained some duplicate entries that have since been removed. The repeated analysis confirms that the original qualitative conclusions stand. Accordingly, Supplementary Table S1 should be replaced with an amended Supplementary Erratum Table S1. The updated performance results based on the unchanged original protocol are given in Supplementary Erratum Table S2. In the table in Supplementary Material 2, for features 195–232 and 233–270, the description text ‘extracted from positive samples’ and ‘extracted from negative samples’, respectively, should be deleted. The corrected table is provided in Supplementary Erratum Table S3.

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Conflict of Interest: none declared.