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task in the analysis of count data from rna seq is the detection of differentially expressed
genes the count data are presented as a table which reports for each sample the number of
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pink was estimated to be 1 10 gb and the heterozygosity was found to be 1 7 using 87 45 gb
of mgi seq 2000 survey data supplementary figs 1 3 4 and table 1 this is slightly higher than
the reported genome size of 998 5 mb estimated

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applications kraken 2 improves upon kraken 1 by reducing memory usage by 85 allowing
greater amounts of reference genomic data to be used while maintaining

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diseases for the most part they protect the host against infection but they can also have
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bioinformatics history the original fasta program was designed for protein sequence

similarity searching because of the exponentially expanding genetic information and the

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aligning a query sequence to

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that offers scientific researchers sequence any dna rna fragment length from short to ultra

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