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The Number Of Mismatches Per Half-site (0, 1 Or 2) Is Inputted Into The Last Box. Use 0 To Scan Only For Sites Exactly Matching The Half-sites. This Mode Is Useful For Verifying The Location Of Target Sites In One Or More Gen-omes. The Number Of Off-target Sites Returned Can Be Greatly Increased By Allowing 1 Or 2 Mismatches Per Half-site. Mar 1th, 2024

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C. Sakazakii Genomes Was 4393kb, With An Average Of 4055 Protein Coding Genes, And An Average Genome G+C Content Of 56.9%. The Genomes Contained Genes Related To Carbohydrate Transport And Metabolism, Amino Acid Transport And Metabolism, And Cell Wall/membrane Biogenesis. In Addition, We Identified Genes Encoding Proteins May 1th, 2024

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Data Against A Reference Wolf Mitochondrial Genome (DQ480508, Bj€ornerfeldt Et Al., 2006). We Took Advantage Of The Circularity Of MtDNA In Order To Increase The Number Of Captured Reads At The Extremes Of The Assembly. With This Goal In Mind, We Applied A Second Round Of Mapping And A Jan 3th, 2024

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