

Genomic coordinates and sequence alignments for various genes including BGL13_G, BGL12_G, BGL11_G, BGL10_G, BGL9_G, BGL8_G, BGL7_G, BGL6_G, BGL5_G, BGL4_G, BGL3_G, BGL2_G, and BGL1_G. The image displays reference sequences and multiple alignments with gaps and matches indicated by dashes and dots. Annotations for each gene are provided at the end of each section, including gene names, coordinates, and other identifiers.

Genomic coordinates and sequence alignments for various regions (e.g., BG13_G, BG12_G, BG11_G, BG10_G, BG9_G, BG8_G, BG7_G, BG6_G, BG5_G, BG4_G, BG3_G, BG2_G, BG1_G, Annotated_BG0). The text shows DNA sequences with specific nucleotide changes highlighted in red and green, and corresponding gene annotations in blue and green. The sequences are organized into blocks, each representing a different genomic region or gene model.

Genomic coordinates and sequence alignments for various genes (e.g., BGL13, BGL12, BGL11, BGL10, BGL9, BGL8, BGL7, BGL6, BGL5, BGL4, BGL3, BGL2, BGL1) across different loci (B12BGL1Locus, B12BGL2Locus, B12BGL3Locus, B12BGL4Locus, B12BGL5Locus, B12BGL6Locus, B12BGL7Locus, B12BGL8Locus, B12BGL9Locus, B12BGL10Locus, B12BGL11Locus, B12BGL12Locus, B12BGL13Locus). The text shows coordinates and corresponding DNA sequences for each gene and locus, with some sequences highlighted in bold.

Genomic coordinates and sequence alignments for B12BG1.Locus. The image displays a grid of sequence alignments for various genomic regions (e.g., B613_GF, B612_GF, B611_GF) across multiple coordinates (5465 to 4938). Each alignment is represented by a horizontal line with a label on the left and a sequence of characters on the right. The labels include region identifiers and coordinates. The sequences consist of uppercase letters (A, C, G, T) and dashes representing gaps. Some sequences are highlighted in yellow. The alignments are organized into blocks, with some blocks labeled as 'Annotated_B60'.

Genomic coordinates and sequence alignments for B12BG1Locus. The image displays a grid of sequences for various genomic features (BG13_GF, BG12_GF, BG11_GF, BG10_GF, BG9_GF, BG8_GF, BG7_GF, BG6_GF, BG5_GF, BG4_GF, BG3_GF, BG2_GF) across multiple B12BG1Locus annotations (Annotated_BG0, Annotated_BG1, Annotated_BG2, Annotated_BG3, Annotated_BG4, Annotated_BG5, Annotated_BG6, Annotated_BG7, Annotated_BG8, Annotated_BG9, Annotated_BG10, Annotated_BG11, Annotated_BG12, Annotated_BG13). Each row shows a reference sequence and one or more alternative sequences, with positions indicated by dots. The sequences consist of nucleotide bases (A, C, G, T) and dashes representing gaps or missing data. The coordinates range from approximately 6024 to 938 on the top row and 6024 to 938 on the bottom row, with intermediate coordinates (6165, 5834, 6644, 6137, 6420, 5832, 6054, 5837, 5956, 6030, 5288, 4954, 4938) marking specific positions. The sequences are organized into blocks corresponding to each genomic feature and annotation, with some features having multiple alternative sequences.

Genomic coordinates and sequence alignments for various genes (BG13_GF to BG2_GF) across different loci (B12B61Locus, B12B61Locus Annotated_B60). The sequences are presented in a grid-like format with corresponding coordinates on the right side.