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Yeast Sequencing Report

The gap-filling sequence on the left arm of chromosome 2 in fission yeast *Schizosaccharomyces pombe*

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Abstract

We report a gap-filling sequence between SPBPB21E7.09 (in contig c1348) and SPBPB10D8.01 (in contig pB10D8) on the left arm of chromosome 2 in the fission yeast, *Schizosaccharomyces pombe*. The sequence was determined from a BAC clone overlapping SPBPB21E7.01c (*eno102*) (in contig c1348) and SPBC1683.07 (*malI*) (in contig pB10D8). The gap-filling sequence is 17881 bp in length and contains five putative open reading frames, which were systematically named as SPBC460.01c, SPBC460.02c, SPBC460.03, SPBC460.04c and SPBC460.05. Their deduced amino acid sequences respectively include protein motifs corresponding to amino acid permease, glutathione S-transferase C-terminal domain, taurine catabolism dioxygenase TauD TfdA family and major facilitator superfamily, whereas their functions are unknown. The sequence has been submitted to the international DNA database (DDBJ/EMBL/GenBank) under Accession No. AB325691. Copyright © 2008 John Wiley & Sons, Ltd.

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