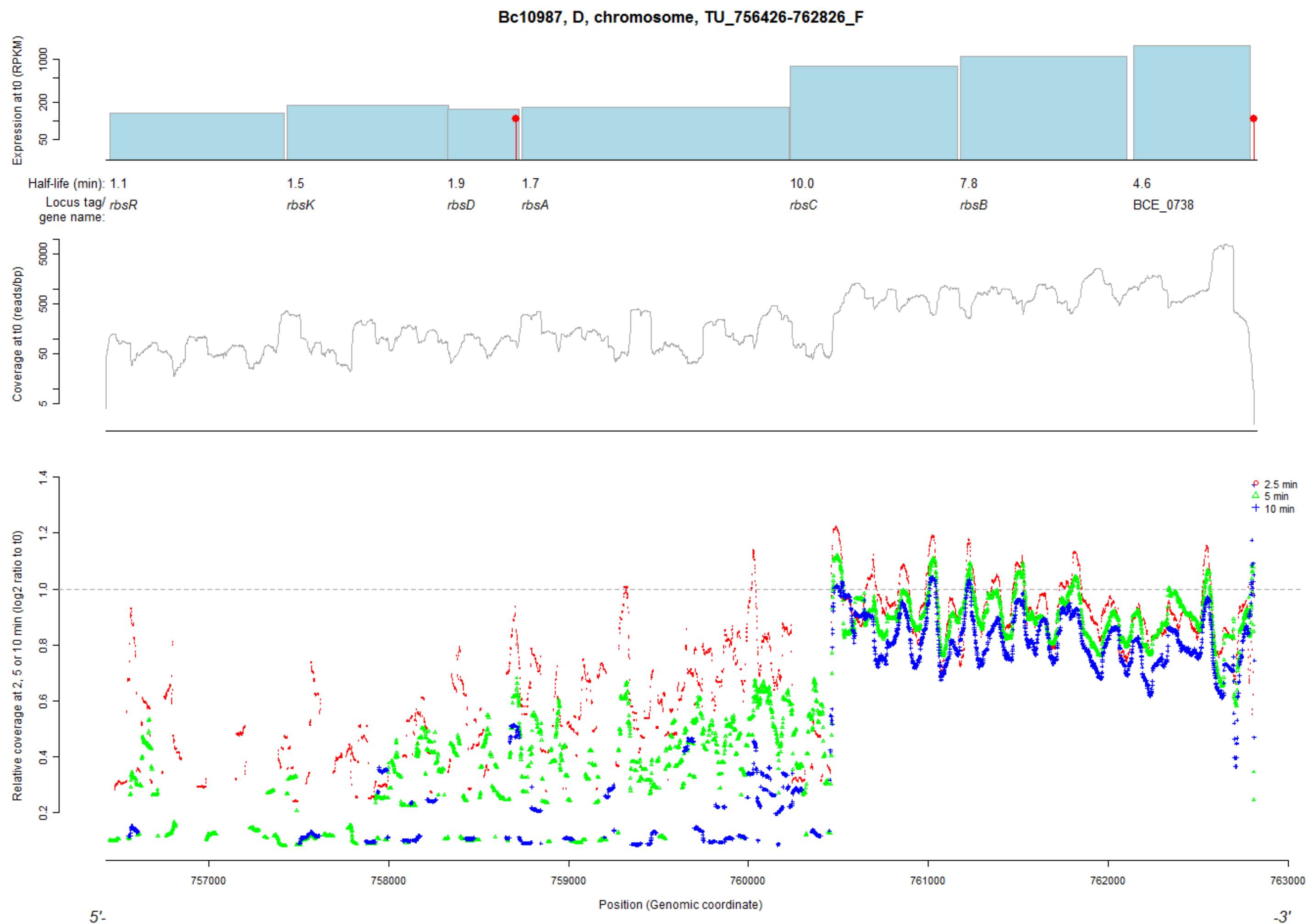




Suppl. fig. S3. Degradation patterns for the rbs (ribose utilization) operon in *B. cereus* ATCC 10987, analyzed and presented as for the gap operon in fig. 1. The first four genes, encoding a repressor (*rbsR*), a ribokinase (*rbsK*), and two subunits of an ABC transporter (including the ATP-binding subunit) (*rbsD* and *rbsA*), all had lower expression values (t0) and shorter half-lives than the three last genes of the operon, which encode the ABC transporter permease (*rbsC*) and ribose-binding (*rbsB*) subunits, and a putative transaldolase (BC0738).