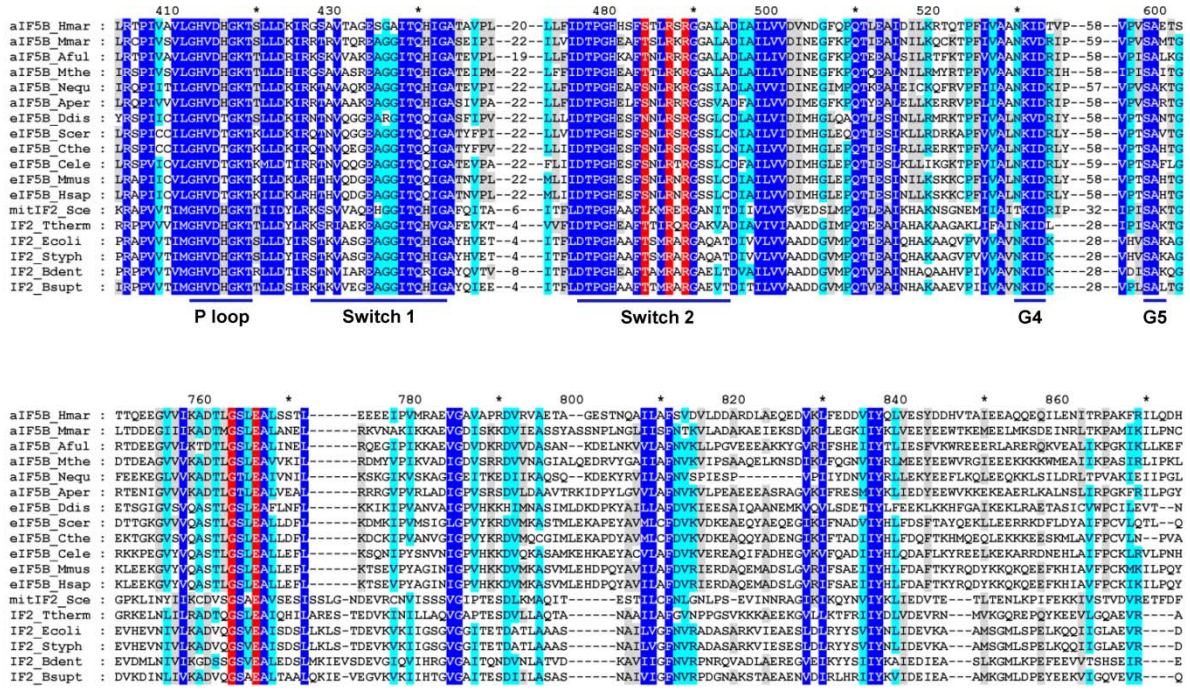

Figure S3. Sequence alignment of the G domains (upper panel) and domains III (lower panel) from different aIF5B, eIF5B and IF2 homologues. Highly conserved residues are highlighted in blue; conserved residues that are directly involved in the stable contacts between switch 2 and domain III in inactive (apo and GDP-bound) eIF5B are highlighted in red. P-loop (G1 motif), switch 1 (with the G2 motif containing Thr439), switch 2 (with the G3 motif "DTPG") and motifs G4 and G5 in the G domain are indicated. The numbering above the sequences is according to the eIF5B homologue from *Saccharomyces cerevisiae*. Residues within the G domain that are implicated in nucleotide binding and the GTP-dependent molecular switch in eIF5B are universally conserved among all three orthologs. Domain III is significantly less well conserved than the G domain; however, the N-terminal part of helix α9 (residues 763-768 in eIF5B) is highly conserved, particularly in those residues involved in the interactions with switch 2. Species names are abbreviated as follows: Hmar, *Haloarcula marismortui*; Mmar, *Methanococcus maripaludis*; Aful, *Archaeoglobus fulgidus*; Mthe, *Methanothermobacter thermoautotrophicum*; Nequi, *Nanoarchaeum equitans*; Aper, *Aeropyrum pernix*; Ddis, *Dictyostelium discoideum*; Scer, *Saccharomyces cerevisiae*; Cter, *Chaetomium thermophilum*; Cele, *Caenorhabditis elegans*; Mmus, *Mus musculus*; Hsap, *Homo sapiens*; Ttherm, *Thermus thermophilus*; Ecoli, *Escherichia coli*; Styph, *Salmonella typhimurium*; Bdent, *Bifidobacterium dentium*; Bsupt, *Bacillus subtilis*; mitIF2_Sce, mitochondrial IF2 from *S. cerevisiae*.