Comparing polysaccharide decomposition among the type strains *Gramella echinicola* KMM 6050^T (DSM 19838^T) and *Gramella portivictoriae* UST040801-001^T (DSM 23547^T), and emended description of *Gramella echinicola* Nedashkovskaya et al. 2005 emend. Shahina et al. 2014 and *Gramella portivictoriae* Lau et al. 2005

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Additional file 2 – Supporting Information – Figures

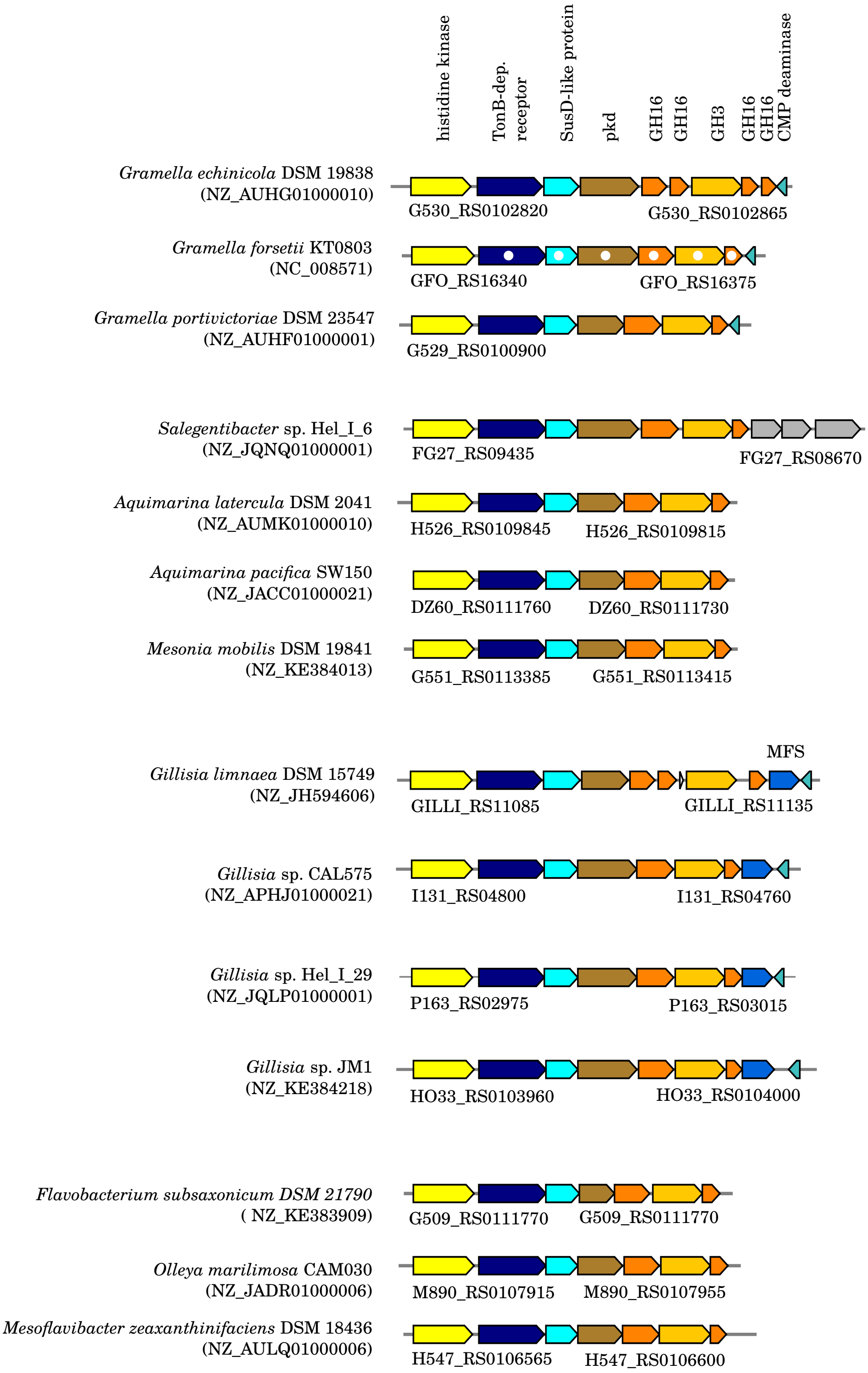

Figure S1: A laminarin-like PUL greatly conserved among *Gramella* and other closely related *Flavobacteriaceae* genera. Open circles indicate genes which were specifically expressed by '*Gramella forsetii*' KT0803 when grown on laminarin, as shown by Kabisch et al. [3]. Locus tags are given below both the first and last gene of the loci. Accession numbers in brackets are GenBank accession numbers of the corresponding contig. Investigation of syntenic loci was done using MultiGeneBlast [5]. A description of glycoside hydrolase (GH), polysaccharide lyase (PL) and carbohydrate esterase (CE) families can be seen at the CAZy homepage [1, 4]. SusD, SusD-like protein; PKD, pkd domain containing protein.

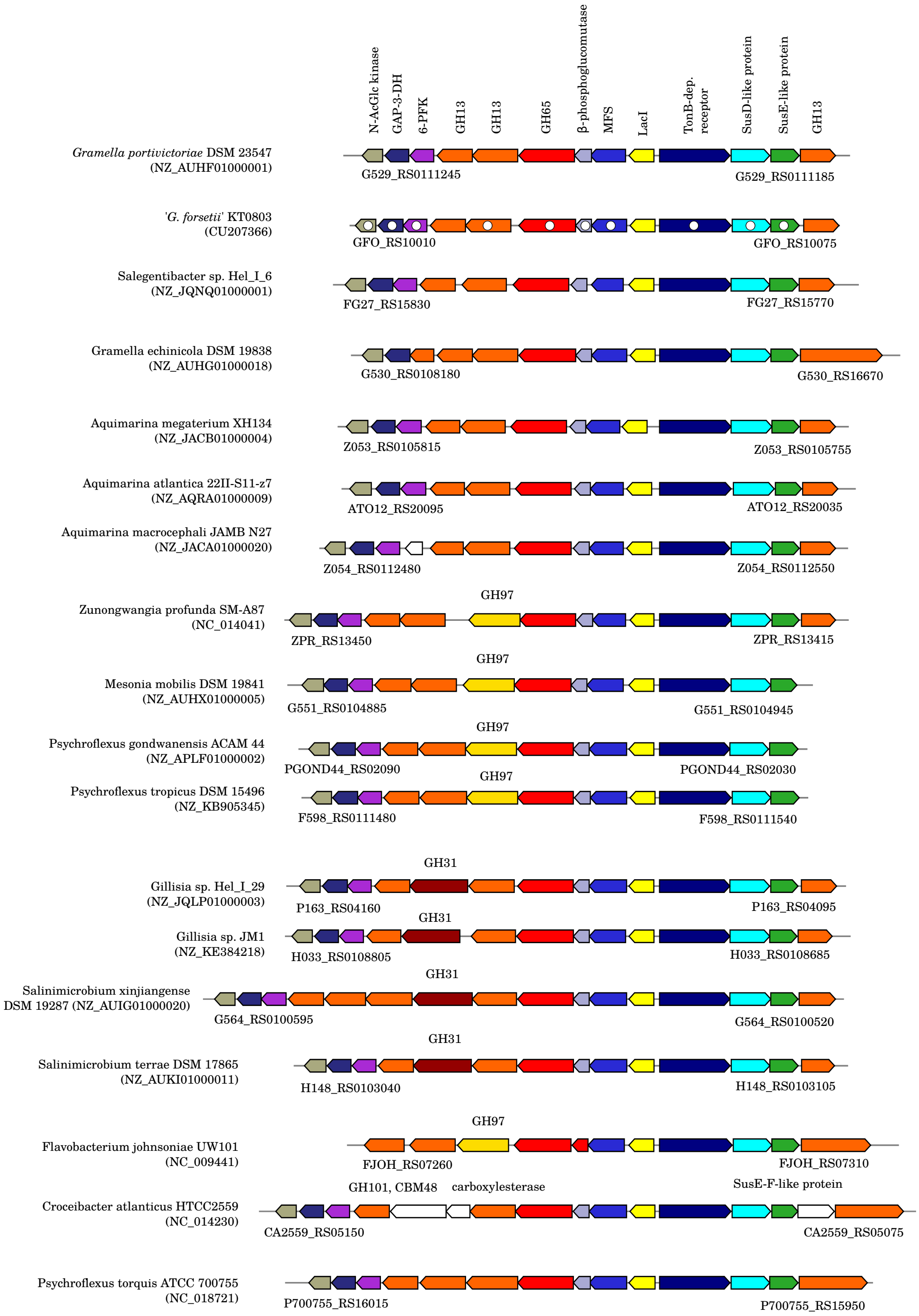

Figure S2: An 1,4-linked glucose-polymer-like PUL greatly conserved among *Gramella* and other closely related *Flavobacteriaceae* genera. Open circles indicate genes which were specifically expressed by '*Gramella forsetii*' KT0803 when grown on laminarin, as shown by Kabisch et al. [3]. Locus tags are given below both the first and last gene of the loci. Accession numbers in brackets are GenBank accession numbers of the corresponding contig. Investigation of syntenic loci was done using MultiGeneBlast [5]. A description of glycoside hydrolase (GH), polysaccharide lyase (PL) and carbohydrate esterase (CE) families can be seen at the CAZy homepage [1, 4]. LacI, LacI family transcriptional regulator; MFS, major facilitator superfamily transporter; 6-PFK, 6-phosphofructokinase; GAP-3-DH, glyceraldehyde 3-phosphate dehydrogenase; N-AcGlc, N-acetylglucosamine.

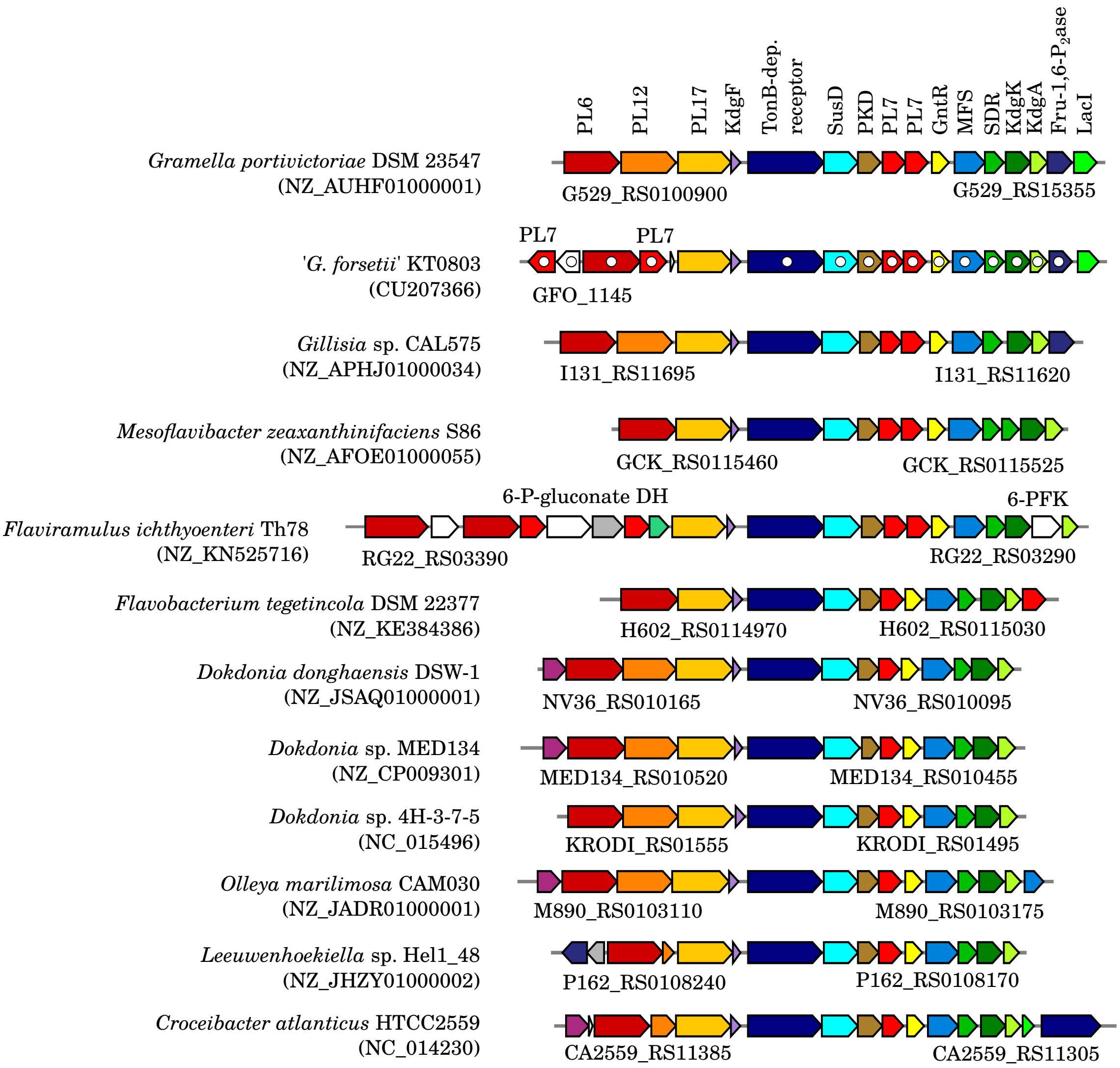

Figure S3: An alginate-like PUL of *G. portivictoriae* DSM 23547^{T}, ’*Gramella forsetii*’ KT0803 and other *Flavobacteriaceae*. Open circles indicate genes which were specifically expressed by ’*Gramella forsetii*’ KT0803 when grown on laminarin, as shown by Kabisch et al. [3]. Locus tags are given below both the first and last gene of the loci. Accession numbers in brackets are GenBank accession numbers of the corresponding contig. Investigation of syntenic loci was done using MultiGeneBlast [5]. A description of glycoside hydrolase (GH), polysaccharide lyase (PL) and carbohydrate esterase (CE) families can be seen at the CAZy homepage [1, 4]. PKD, pkd domain containing protein; SusD, SusD-like protein; GntR, GntR family transcriptional regulator; LacI, LacI family transcriptional regulator; MFS, major facilitator superfamily transporter; SDR, short-chain dehydrogenases/reductases; KdgF, pectin degradation protein; KdgK, 2-dehydro-3-deoxygluconokinase; KdgA, keto-deoxy-phosphogluconate aldolase; Fru-1,6-P2ase.

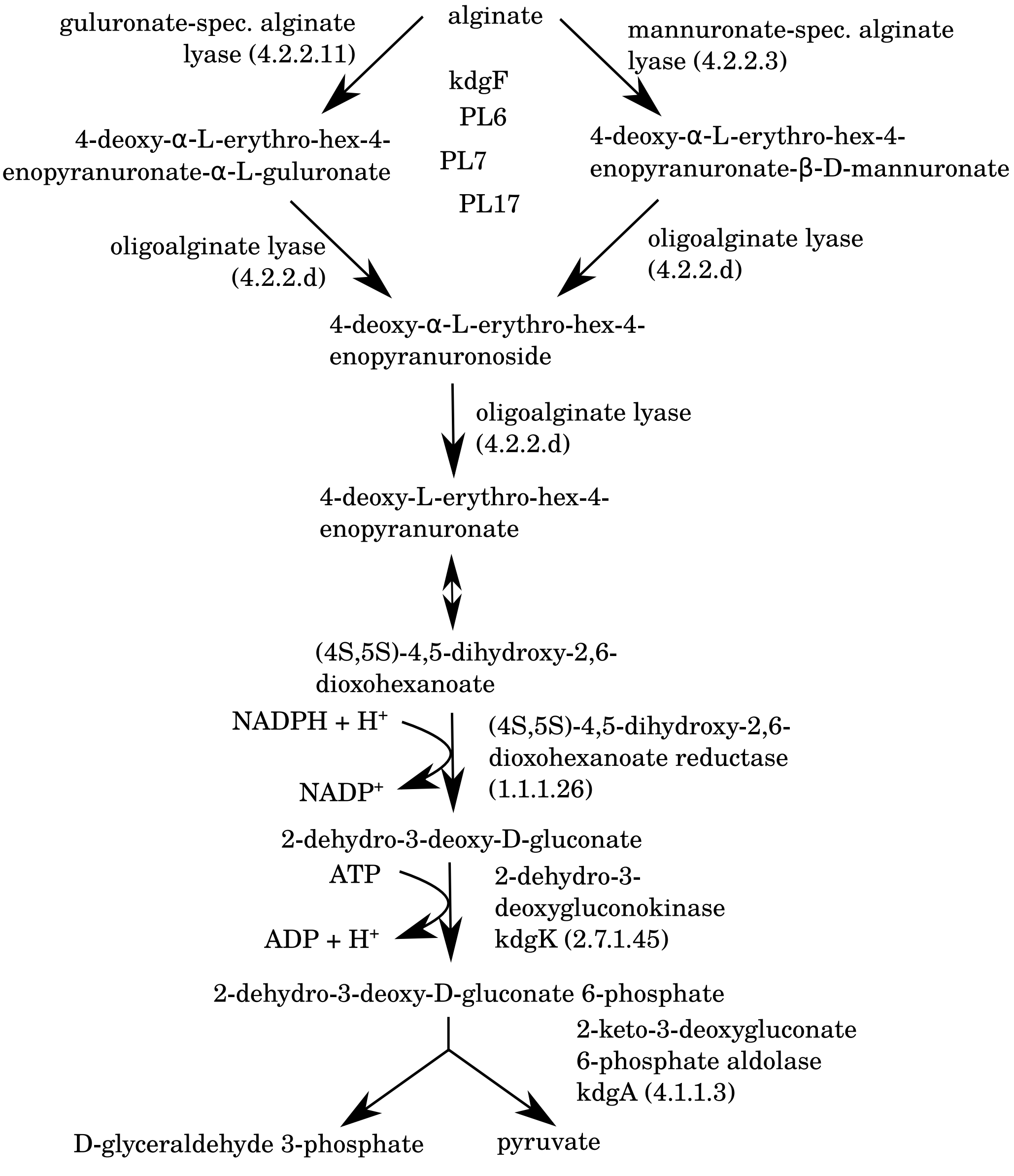

Figure S4: Part of the alginate-like polysaccharide decomposition pathway. PKD, pkd domain containing protein; SusD, SusD-like protein; GntR, GntR family transcriptional regulator; LacI, LacI family transcriptional regulator; MFS, major facilitator superfamily transporter; SDR, short-chain dehydrogenases/reductases; KdgF, pectin degradation protein; KdgK, 2-dehydro-3-deoxygluconokinase; KdgA, keto-deoxy-phosphogluconate aldolase; Fru-1,6-P2ase.

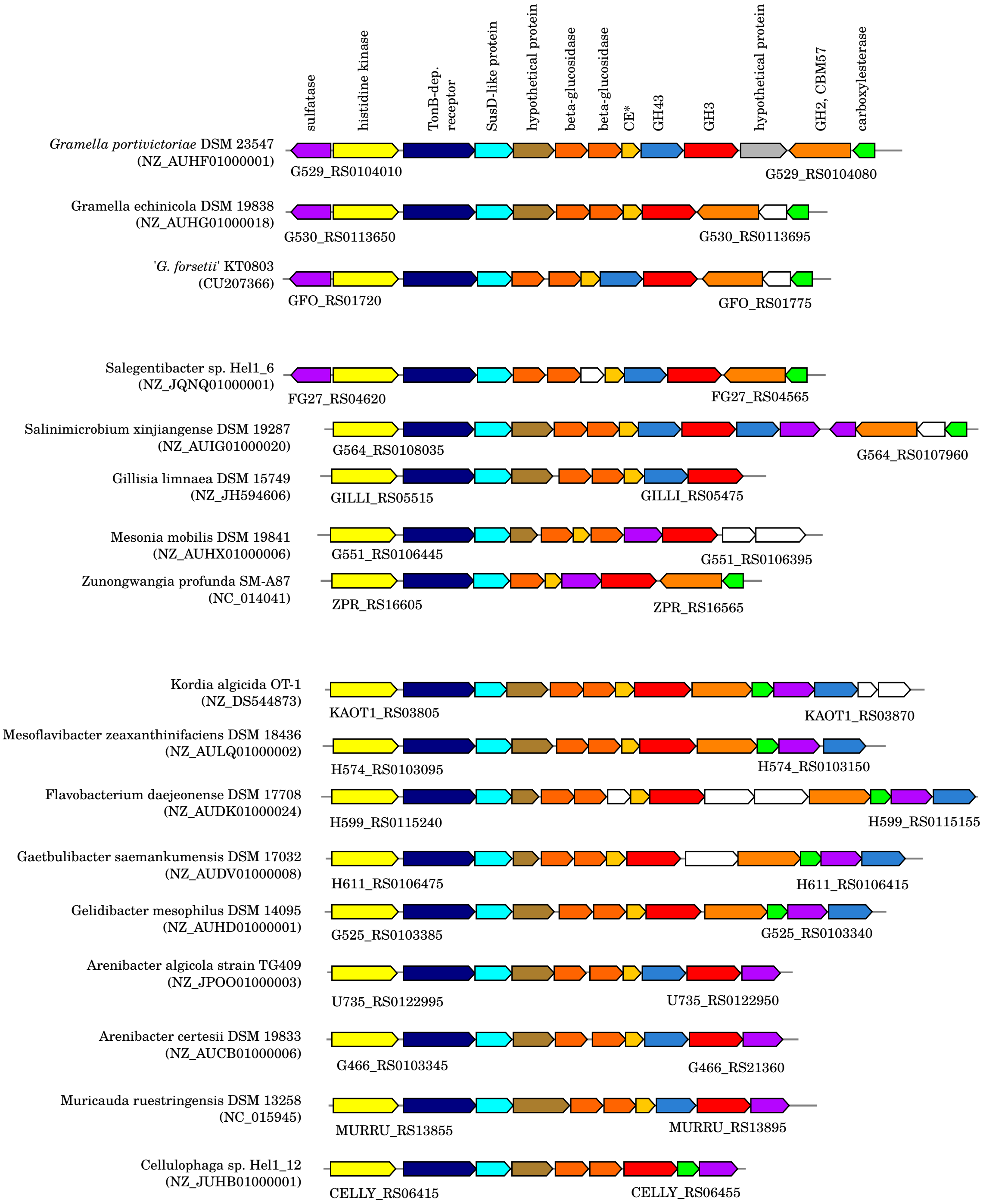

Figure S5: A sulfated β-D-glucoside PUL greatly conserved among *Gramella* and other closely related *Flavobacteriaceae* genera. Locus tags are given below both the first and last gene of the loci. Accession numbers in brackets are GenBank accession numbers of the corresponding contig. Investigation of syntenic loci was done using MultiGeneBlast [5]. A description of glycoside hydrolase (GH) and polysaccharide lyase (PL) families can be seen at the CAZy homepage [1, 4].

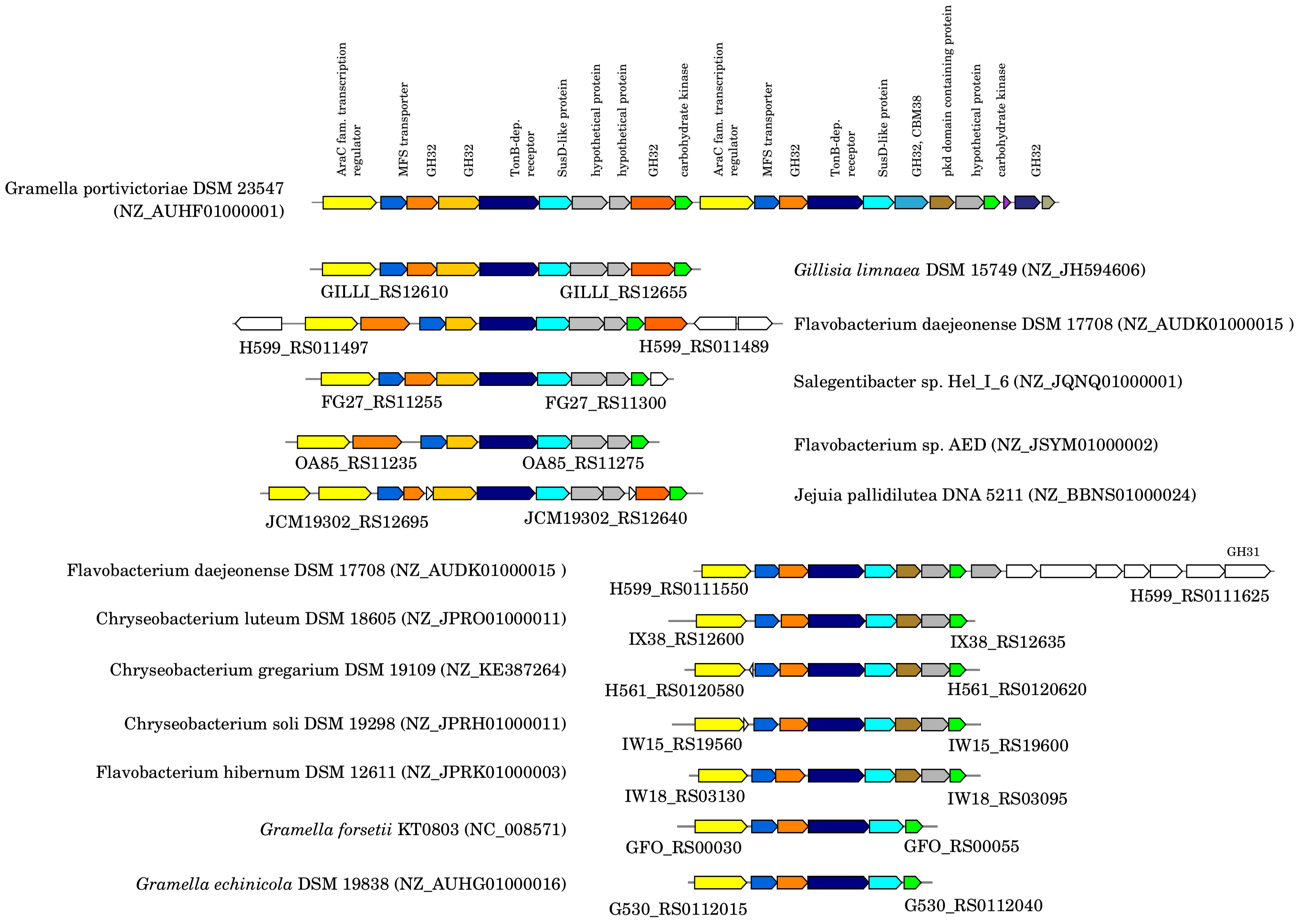

Figure S6: Two combined β-D-fructans PUL unique for *G. portivictoriae* DSM 23547^{T}. Locus tags are given below both the first and last gene of the loci. Accession numbers in brackets are GenBank accession numbers of the corresponding contig. Investigation of syntenic loci was done using MultiGeneBlast [5]. A description of glycoside hydrolase (GH) and polysaccharide lyase (PL) families can be seen at the CAZy homepage [1, 4].

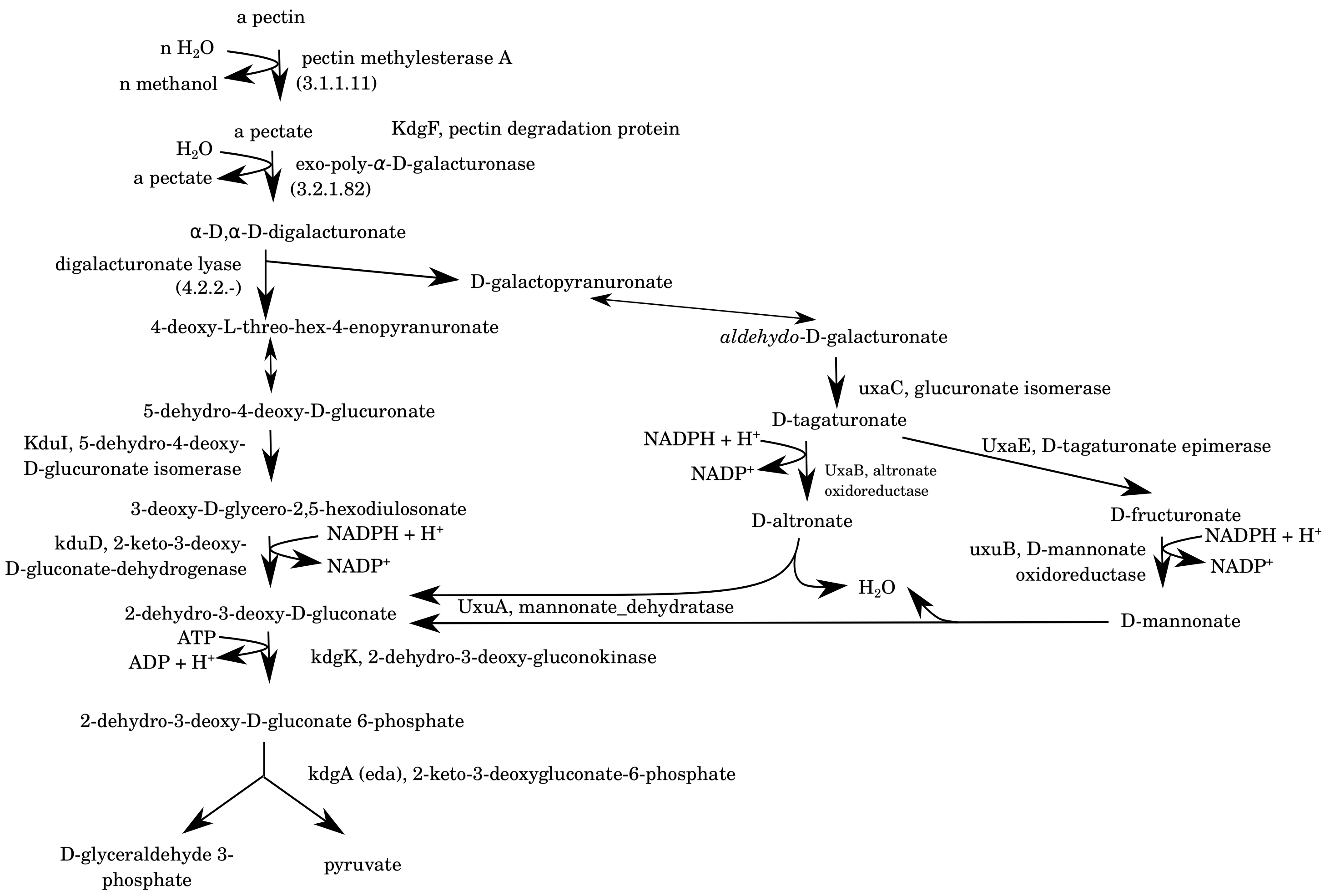

Figure S7: Part of the pectin-like polysaccharide decomposition pathway, encoded by genes of the *G. portivictoriae* DSM 23547^T genome. The full range of pathways for pectin decomposition and catabolism can be seen at MetaCyc, pathway PWY-6516 [2].

References

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[5] Medema MH, Takano E, and Breitling R. Detecting sequence homology at the gene cluster level with MultiGeneBlast. Mol. Biol. Evol. 2013; 30:1218–23.