

Diverse sensory repertoire of paralogous chemoreceptors Tlp2, Tlp3 and Tlp4 in *Campylobacter jejuni*

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SUPPORTING INFORMATION

Figure S1. Protein sequence alignment showing 30% identity and signalling domain completely identical across Tlp2, Tlp3 and Tlp4.

Figure S2. Phylogenetic tree containing dCache_1 containing chemoreceptors from representative genomes of *Campylobacterota* phylum. Chemoreceptors from *C. jejuni* 11168-O used throughout this study are shown in bold. This figure is also available as a scalable pdf.

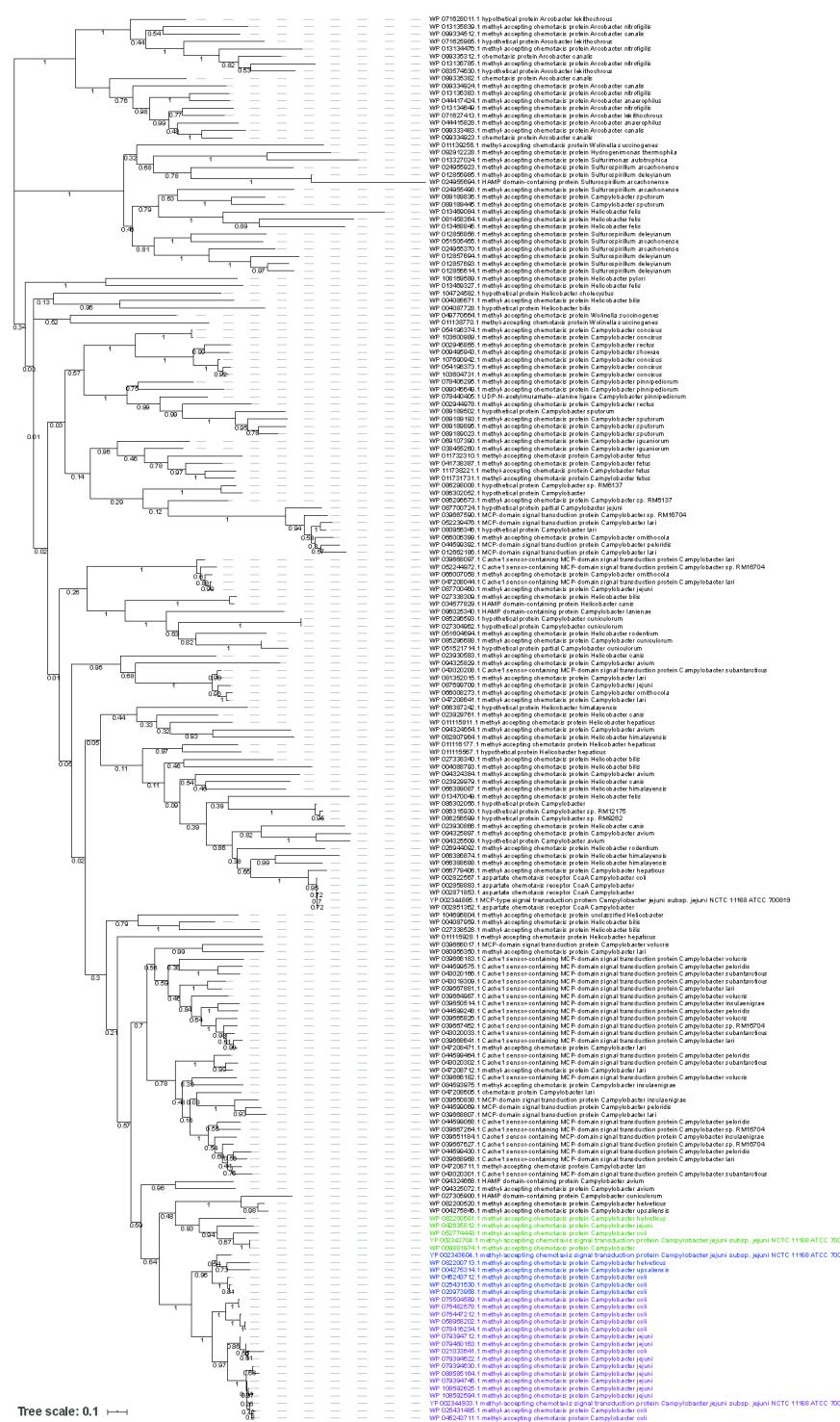


Figure S3. Relationship between dCache_1 domains from *Campylobacterota* chemoreceptors. *C. jejuni* 11168-O chemoreceptors are shown in bold. Clades containing Tlp2, Tlp3 and Tlp4 colored in blue, purple and green, respectively. Tlp1-like clade is shown in orange. Conserved amino acid recognition motif is highlighted in grey. Amino acid numeration is based on the Tlp3 protein sequence. Bootstrap support values greater than 50% are shown. This figure is also available as a scalable pdf.

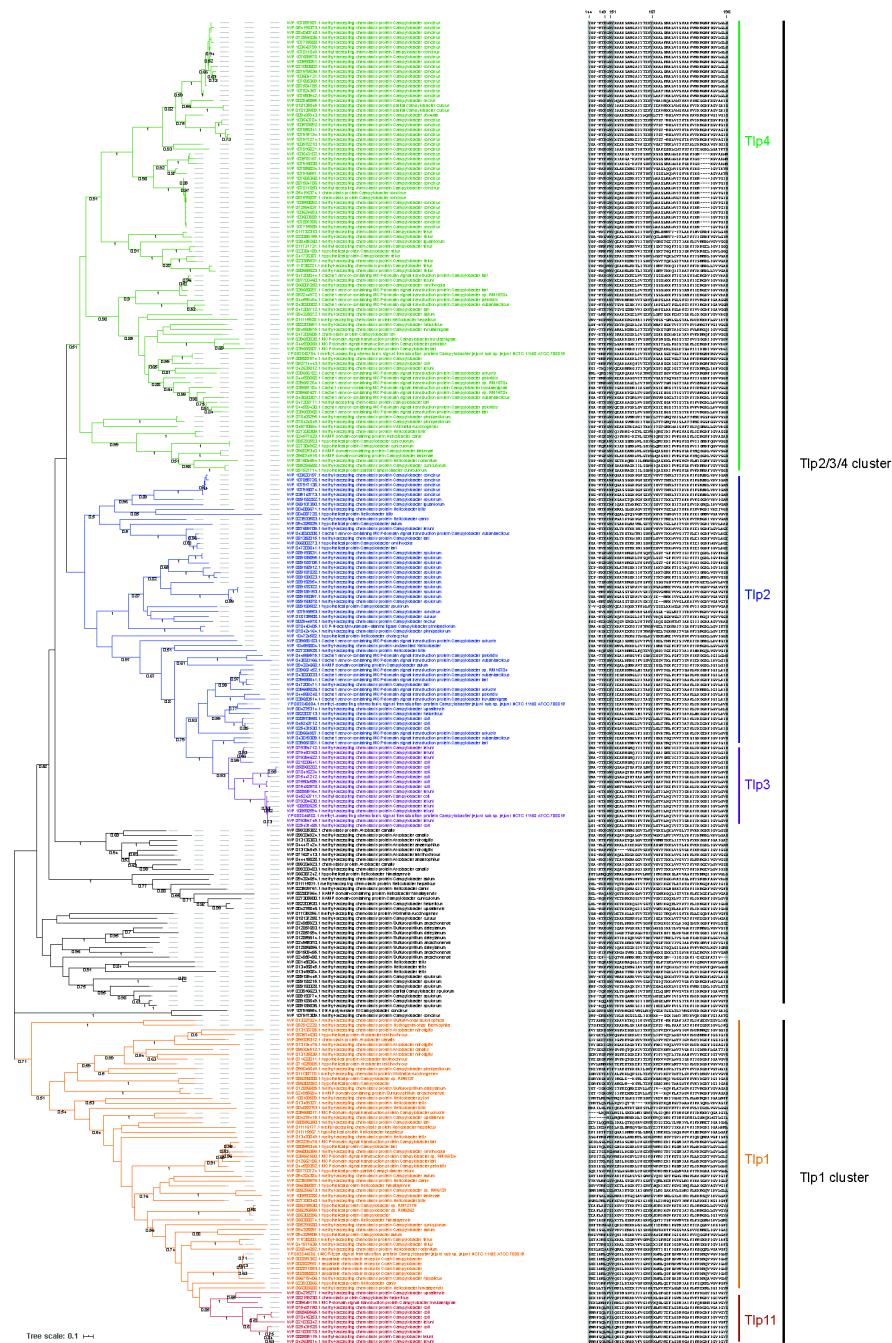


Figure S4. Phylogenetic tree of MCP signal domains from dCache_1 containing chemoreceptors. *C. jejuni* 11168-O chemoreceptors are shown in bold. Sequences are coloured according to clustering of the respective sensing domain on dCache_1 domain phylogenetic tree (Figure S3). Bootstrap percentage values greater than 40 are shown. This figure is also available as a scalable pdf.

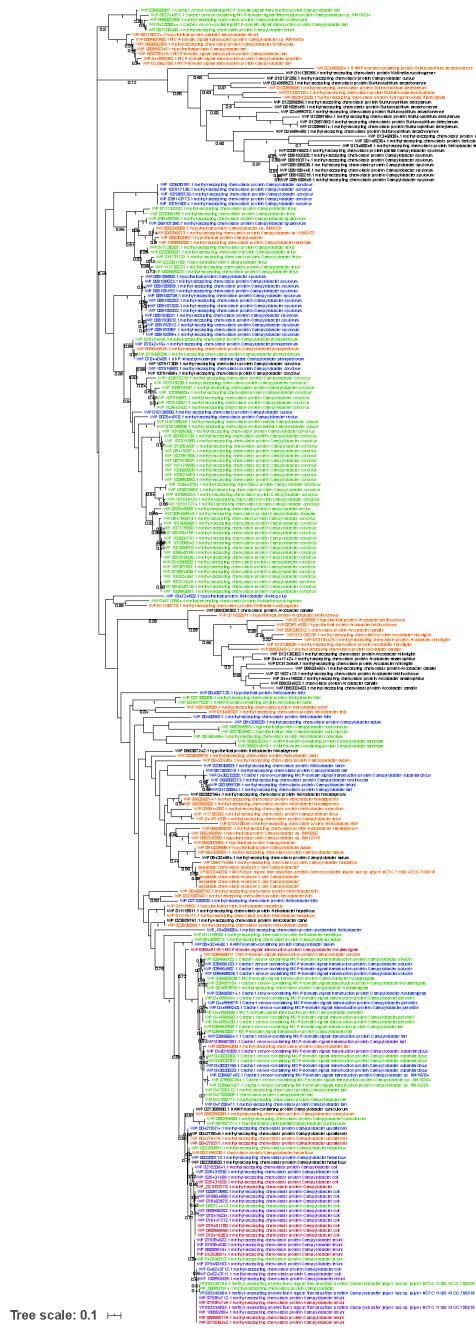


Figure S5. Surface Plasmon Resonance (SPR) sensograms for Tlp3^{peri}, Tlp2^{peri} and Tlp4^{peri}. Single cycle SPR plots are shown as concentration dependent interactions between proteins and monosaccharides as illustrated.

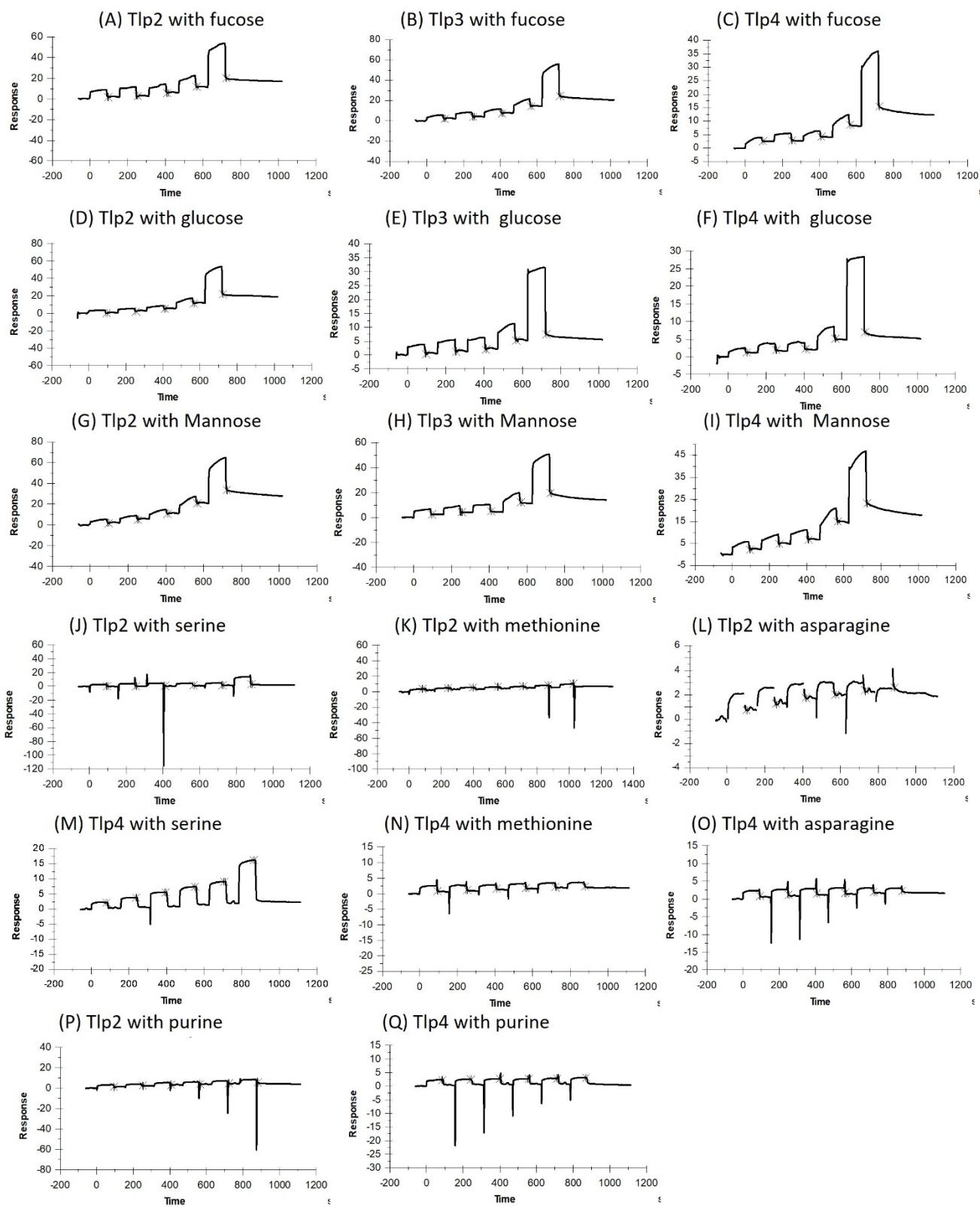


Figure S6. Competition between glucose and fucose /glucose and malic acid binding to Tlp3. **A)** Injections are indicated as injection-A (PBS or glucose at 300 μ M for 30 seconds) and injection-B (glucose at 300 μ M or fucose at 300 μ M for 60 seconds). Final responses units (RU) of injections are recorded (indicated by dashed vertical line and label), with the response of glucose equalling $5.07\text{RU} \pm 0.81$ at 15 seconds after injection-B and 1 fucose equalling $9.86 \text{ RU} \pm 1.14$ at 15 seconds after injection-B. The response 15 seconds after injection-B when glucose and fucose were competed was $4.4 \text{ RU} \pm 0.46$. As this value sits below 5 RU, it indicates direct competition for the same site where glucose replacing and blocking the bound fucose during the 60 second injection-B. **B)** A) Injections are indicated as injection-A (PBS or glucose at 500 μ M for 30 seconds) and injection-B (glucose at 300 μ M or malic acid at 200 μ M for 60 seconds). Final responses units (RU) of injections are recorded (indicated by dashed vertical line and label), with the response of glucose equalling $5.07\text{RU} \pm 0.81$ at 15 seconds after injection-B and 1 malic acid equalling $13.5 \text{ RU} \pm 2.4$ at 15 seconds after injection-B. The response 15 seconds after injection-B when glucose and malic acid were competed was $10.04 \text{ RU} \pm 0.66$. As this value sits between 5.07-13.5 RU, it indicates direct competition for the same site with glucose replacing some of the bound malic acid during the 60 second injection-B.

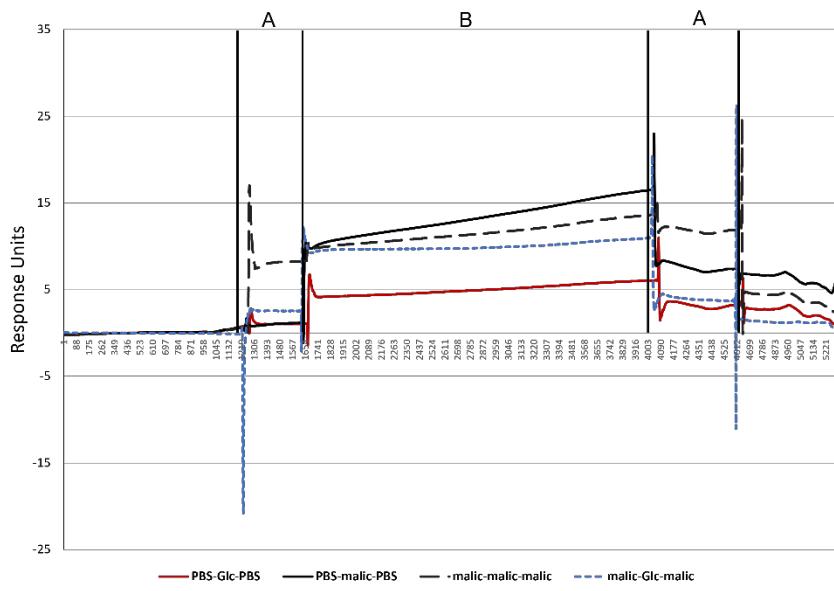
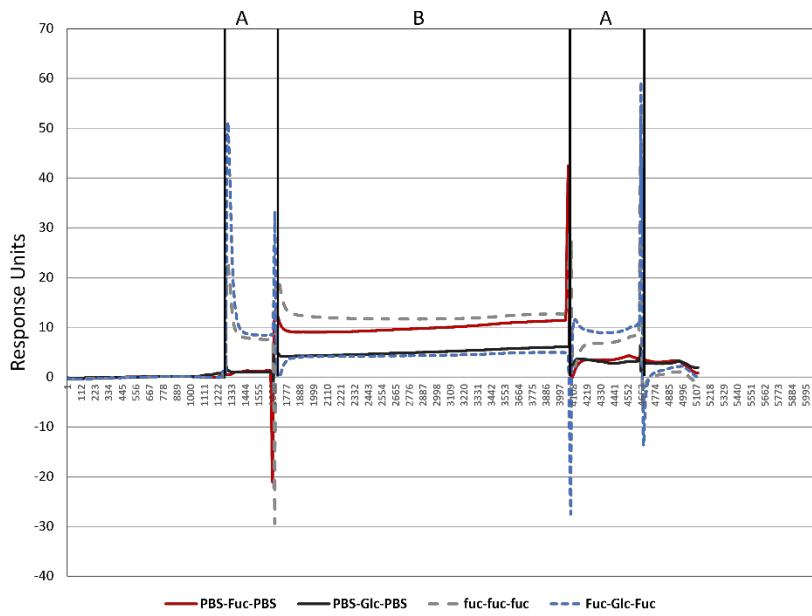


Figure S7. SPR ligand competition analysis for Tlp3. SPR competition analysis of binding of glucose (glc), α -ketoglutarate (aketo), malic acid (malic), lysine (lys), glucosamine (glcA), arginine (arg), and isoleucine (iso) to WT Tlp3^{LBD}. The experimental RU value is actual response unit (RU) values for the following: A) (glc) is responses to glucose only, (aketo) is responses to α -ketoglutarate only, and (glc+aketo) is glucose responses following saturation with α -ketoglutarate and (aketo+glc) is α -ketoglutarate following saturation with glucose. B) (glc) is responses to glucose only, (malic) is responses to malic acid only, and (glc+malic) is glucose responses following saturation with malic acid and (malic+glc) is malic acid following saturation with glucose. C) (glc) is responses to glucose only, (lys) is responses to lysine only, and (glc +lys) is glucose responses following saturation with lysine and (lys+glc) is lysine following saturation with glucose. D) (glc) responds to glucose only, (glcA) is response to glucosamine only, (glc+glcA) glucose response following saturation with glucosamine and (glcA+glc) glucosamine following saturation with glucose. E) (iso) is responses to isoleucine only, (arg) is responses to arginine only, and (iso+arg) is isoleucine responses following saturation with arginine and (arg+iso) is arginine following saturation with isoleucine. F) (iso) is responses to isoleucine only, (malic) is responses to malic acid only, and (iso+ malic) is isoleucine responses following saturation with malic acid and (malic +Iso) is malic acid following saturation with isoleucine. G) (iso) is responses to isoleucine only, (lys) is responses to lysine only, and (iso+lys) is isoleucine responses following saturation with lysine and (lys+iso) is lysine following saturation with isoleucine. The theoretical value is responses unites (RU) values based on mathematical theory. The binding status of the ligands to protein are classified as: Independent site (additive/accumulative effect); ligands binding to different binding sites, Shared site; ligands binding/sharing same binding site, Preferential Shared site; ligands binding/sharing same binding site but the protein binds to one ligand better than the other when in equilibrium. All response data was normalized 100 Da molecular weight for each analyte allowing direct comparison of responses.

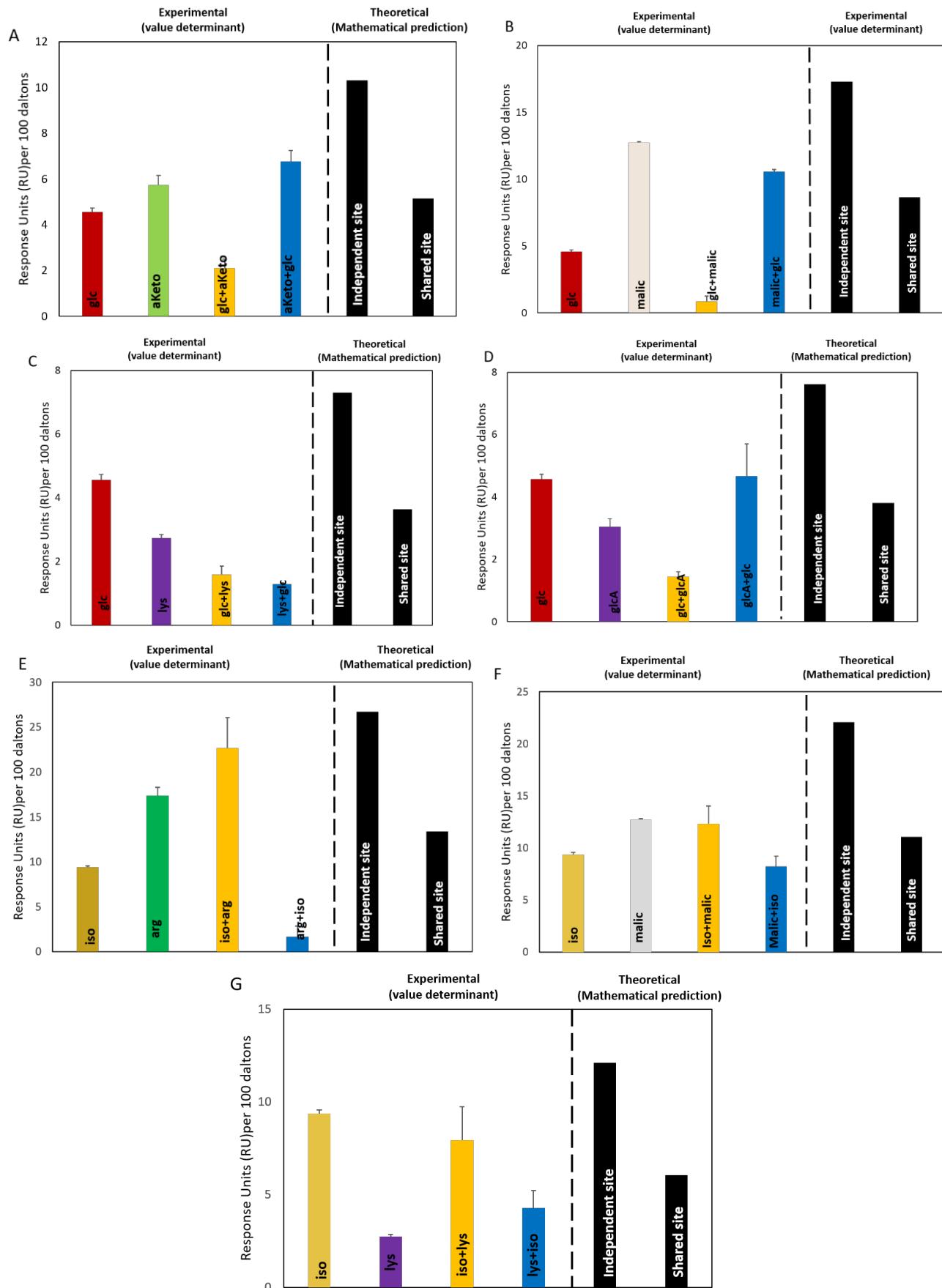


Figure S8. Modified hard plug agar assay (tHAP) chemotaxis assay quantitation. Viable counts of *C. jejuni* are shown on a log scale. The agarose plugs contained the following ligands: (A) fucose, glucose, galactose, mannose and sialic acid; (B) serine, methionine, asparagine, lysine, cysteine, purine and aspartate. *C. jejuni* 81116 *flaA*⁻/*flab*⁻ isogenic mutant was used as a non-motile, non-chemotactic control; and agar plugs containing no added ligand were used as a negative control. Standard errors are shown as bars above the mean of three replicates.

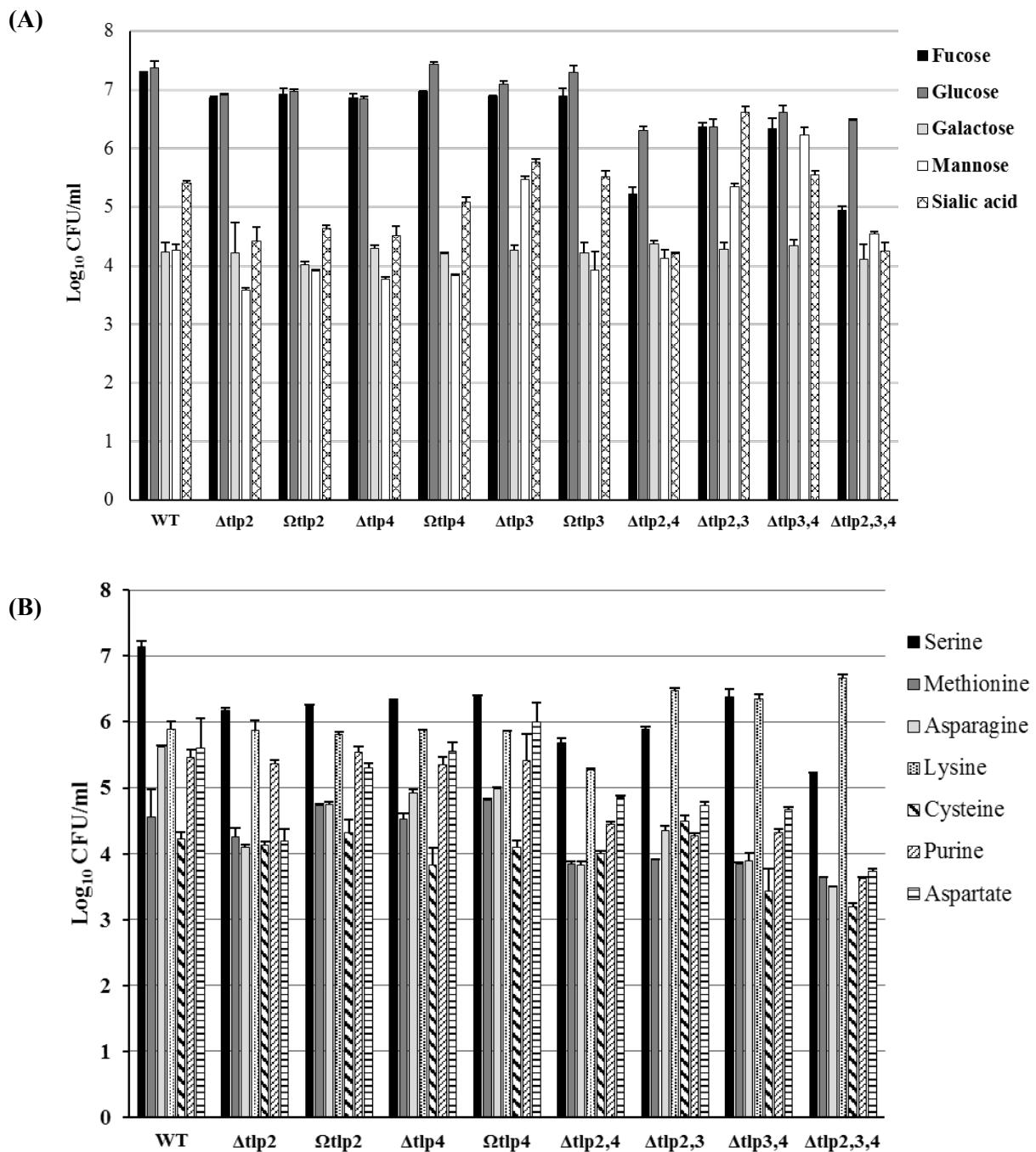
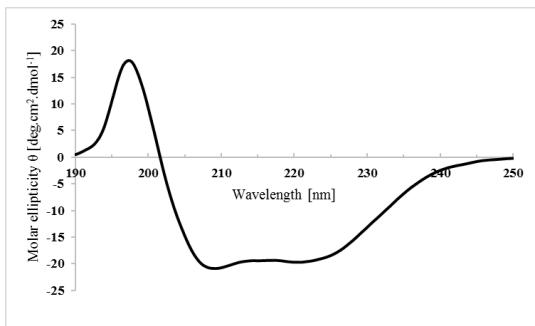
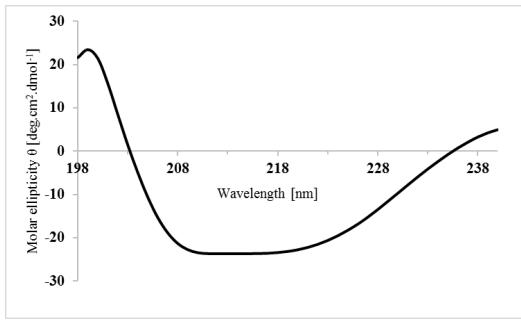


Figure S9. Circular dichroism spectrometry analyses of periplasmic domains of **(A)** Tlp2, **(B)** Tlp3 and **(C)** Tlp4. Molar ellipticity [θ] is calculated using the formula: $(\theta \times 100 \times M)/(C \times 1 \times n)$. Purified Tlp2, Tlp3 and Tlp4 were confirmed as folded proteins consisting of α -helix structures.

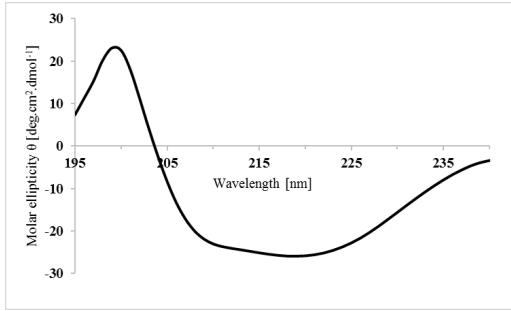
(A) Tlp2



(B) Tlp3



(C) Tlp4



Videos S1. Molecular dynamics simulations between two molecules, a monosaccharide (glucose) and an amino acid (arginine).

Videos S2. Molecular dynamics simulations between two molecules, an amino acid (arginine) and a monosaccharide (glucose).

Table S1. The presence of dCache_1 domain containing chemoreceptors in different *Campylobacterota* representatives.

Phylum	Class	Order	Family	Genus	GTDB Species name	Representative genome	NCBI name	MiST ID	NCBI ID
p_Campylobacterota									
c_Campylobacteria									
o_Campylobacteriales									
f_Arcobacteraceae									
			Aliarcobacter	<i>Arcobacter butzleri</i>	GCF_001010585.1	<i>Arcobacter butzleri</i> L348			F7 system, 36H
			Arcobacter	<i>Arcobacter nitrofigilis</i>	GCF_00009245.1-245.1	<i>Arcobacter nitrofigilis</i> <i>DSM 7299</i>	GCF_000092245.1-ARNIT_RS12945	WP_013136 383.1	F7 system, 36H
							GCF_000092245.1-ARNIT_RS10155	WP_013135 839.1	
							GCF_000092245.1-ARNIT_RS04225	WP_013134 649.1	
							GCF_000092245.1-ARNIT_RS15045	WP_013136 785.1	
							GCF_000092245.1-ARNIT_RS03330	WP_013134 476.1	
			Halarcobacter	<i>Halarcobacter anaerophilus</i>	GCF_000935065.1-065.1	<i>Arcobacter anaerophilus</i>	GCF_000935065.1-TN41_RS08535	WP_044417 424.1	F7 system, 36H
							GCF_000935065.1-TN41_RS03965	WP_044415 828.1	
			Malaciobacter	<i>Malaciobacter canalis</i>	GCF_002723485.1-485.1	<i>Arcobacter canalis</i>	GCF_002723485.1-CPG37_RS07870	WP_099334 512.1	F7 system, F9 system, 34H, 36H , 40H, 44H
							GCF_002723485.1-CPG37_RS13415	WP_099335 382.1	
							GCF_002723485.1-CPG37_RS01535	WP_099333 483.1	
							GCF_002723485.1-CPG37_RS10520	WP_099334 924.1	
							GCF_002723485.1-CPG37_RS10515	WP_099334 923.1	
							GCF_002723485.1-CPG37_RS12925	WP_099335 312.1	
			Poseidonibacter	<i>Poseidonibacter lekithochrous</i>	GCF_001878855.1-855.1	<i>Arcobacter lekithochrous</i>	GCF_001878855.1-BRO21_RS12110	WP_071627 413.1	F7 system, F8 system, 34H, 36H
							GCF_001878855.1-BRO21_RS15155	WP_071628 011.1	
							GCF_001878855.1-BRO21_RS08205	WP_083574 630.1	
							GCF_001878855.1-BRO21_RS05035	WP_071625 985.1	

f_Campylobacteraceae			-			
Campylobacter						
r						
<i>Campylobacter fetus</i>	GCF_900475935.1	<i>Campylobacter fetus</i>	GCF_900475935.1-DQN38_RS08290	WP_011732	F3 system; 24H, 28H , 40H, 44H	
			GCF_900475935.1-DQN38_RS06385	310.1		
			GCF_900475935.1-DQN38_RS06380	WP_041738		
			GCF_900475935.1-DQN38_RS06380	387.1		
			GCF_900475935.1-DQN38_RS06380	WP_111738		
			GCF_900475935.1-DQN38_RS06380	221.1		
			GCF_900475935.1-DQN38_RS0960	WP_011731		
			GCF_900475935.1-DQN38_RS0960	731.1		
<i>Campylobacter iguaniorum</i>	GCF_000736415.1	<i>Campylobacter iguaniorum</i>	GCF_000736415.1-CIG1485E_RS09305	WP_038455	F3 system; 28H , 40H	
			GCF_000736415.1-CIG1485E_RS09275	260.1		
<i>Campylobacter lanienae</i>	GCF_002139415.1	<i>Campylobacter lanienae</i>	GCF_002139415.1-CCB79_RS06750	WP_069107		
			GCF_002139415.1-CCB79_RS06750	390.1		
<i>Campylobacter sp002139855</i>	GCF_002139855.1	<i>Campylobacter sp.</i> RM6137	GCF_002139855.1-CSUIS_RS06325	WP_096025	F3 system; 28H , 40H, 44H	
			GCF_002139855.1-CSUIS_RS06325	340.1		
<i>Campylobacter sp002139875</i>	GCF_002139875.1	<i>Campylobacter sp.</i> RM12175	GCF_002139875.1-CVIC12175_RS06330	WP_086298	F3 system; 28H , 40H	
			GCF_002139875.1-CVIC12175_RS06330	008.1		
			GCF_002139875.1-CVIC12175_RS06330	WP_086296		
			GCF_002139875.1-CVIC12175_RS06330	673.1		
			GCF_002139875.1-CVIC12175_RS06330	WP_086315	F3 system; 28H , 40H, 44H	
			GCF_002139875.1-CVIC12175_RS06330	930.1		
			GCF_002139875.1-CVIC12175_RS06330	WP_086256	F3 system; 28H , 40H, 44H	
			GCF_002139875.1-CVIC12175_RS06330	599.1		
<i>Campylobacter sp002139915</i>	GCF_002139915.1	<i>Campylobacter sp.</i> NCTC 13003	GCF_002139915.1-CIGN_RS01655	WP_086302	F3 system; 28H , 40H	
			GCF_002139915.1-CIGN_RS01655	052.1		
			GCF_002139915.1-CIGN_RS01655	WP_086302		
			GCF_002139915.1-CIGN_RS01655	056.1		
Campylobacter r_A						
<i>Campylobacter A concisus</i>	GCF_001298465.1	<i>Campylobacter concisus</i>	GCF_001298465.1-CCON33237_RS03260	WP_054196	F3 system, 28H , 40H	
			GCF_001298465.1-CCON33237_RS03260	374.1		
			GCF_001298465.1-CCON33237_RS03255	WP_054196		
			GCF_001298465.1-CCON33237_RS03255	373.1		
<i>Campylobacter A concisus N</i>	GCF_002914005.1	<i>Campylobacter concisus</i>	GCF_002914005.1-CYP54_RS07185	WP_103600	F3 system, 28H , 40H	
			GCF_002914005.1-CYP54_RS07185	989.1		
			GCF_002914005.1-CYP54_RS07185	WP_103604		
			GCF_002914005.1-CYP54_RS07185	731.1		
<i>Campylobacter A concisus U</i>	GCF_003048575.1	<i>Campylobacter concisus</i>	GCF_003048575.1-CVS84_RS01985	WP_107690	F3 system, 28H , 40H	
			GCF_003048575.1-CVS84_RS01985	942.1		

<i>Campylobacter_A</i> <i>pinnipedorum</i>	GCF_002021 925.1	<i>Campylobacter</i> <i>pinnipedorum</i> <i>subsp.</i> <i>Pinnipedorum</i>	GCF_002021925.1- CPIN17260_RS08940	WP_078406 295.1	F3 system, 28H , 40H
			GCF_002021925.1- CPIN17260_RS00765	WP_099046 649.1	
			GCF_002021925.1- CPIN17260_RS00760	WP_078440 405.1	
<i>Campylobacter_A_rectus</i>	GCF_000174 175.1	<i>Campylobacter_rectus</i> <i>RM3267</i>	GCF_000174175.1- CAMRE0001_RS08300	WP_002944 978.1	F3 system, 28H , 40H
			GCF_000174175.1- CAMRE0001_RS11105	WP_002945 855.1	
<i>Campylobacter_A_showae_A</i>	GCF_000313 615.1	<i>Campylobacter_showae</i> <i>CSUNSWCD_D</i>	GCF_000313615.1- CSUNSWCD_RS08695	WP_009495 943.1	F3 system, 28H , 40H
Campylobacter_B					
<i>Campylobacter_B_sputorum</i>	GCF_002220 755.1	<i>Campylobacter_sputorum</i> <i>bv.</i> <i>paraureolyticus</i>	GCF_002220755.1- CSPARA_RS08305	WP_089189 895.1	F3 system, 28H, 40H , 44H
			GCF_002220755.1- CSPARA_RS05480	WP_089189 193.1	
			GCF_002220755.1- CSPARA_RS01695	WP_089189 023.1	
			GCF_002220755.1- CSPARA_RS05130	WP_089189 502.1	
			GCF_002220755.1- CSPARA_RS07910	WP_089189 836.1	40H
			GCF_002220755.1- CSPARA_RS04765	WP_089189 445.1	40H
Campylobacter_D					
<i>Campylobacter_D_avium</i>	GCF_002238 335.1	<i>Campylobacter_avium</i> <i>LMG 24591</i>	GCF_002238335.1- CAV_RS08355	WP_094324 384.1	F3 system, 28H , 40H, 44H
			GCF_002238335.1- CAV_RS07060	WP_094325 829.1	
			GCF_002238335.1- CAV_RS01035	WP_094324 668.1	
			GCF_002238335.1- CAV_RS00955	WP_094324 654.1	
			GCF_002238335.1- CAV_RS07455	WP_094325 897.1	
			GCF_002238335.1- CAV_RS00870	WP_094325 509.1	

	GCF_002245 935.1	<i>Campylobac ter avium</i>	GCF_002245935.1- CAV8706_RS07895	WP_094325 829.1	F3 system, 28H , 40H, 44H	
			GCF_002245935.1- CAV8706_RS01820	WP_094324 654.1		
			GCF_002245935.1- CAV8706_RS04075	WP_094325 072.1		
			GCF_002245935.1- CAV8706_RS01900	WP_094324 668.1		
			GCF_002245935.1- CAV8706_RS00375	WP_094324 384.1		
			GCF_002245935.1- CAV8706_RS01735	WP_094325 509.1		
			GCF_002245935.1- CAV8706_RS08285	WP_094325 897.1		
	<i>Campylobact er_D cuniculorum</i>	GCF_002104 335.1	RS <i>Campylobac ter cuniculorum</i> DSM 23162 = LMG 24588	GCF_002104335.1- CCUN_RS08200	WP_085296 680.1	F3 system, 28H , 40H
				GCF_002104335.1- CCUN_RS06815	WP_027305 900.1	
				GCF_002104335.1- CCUN_RS09175	WP_085296 688.1	
				GCF_002104335.1- CCUN_RS00300	WP_085296 593.1	
	GCF_000621 005.1		<i>Campylobac ter cuniculorum</i> DSM 23162 = LMG 24588	GCF_000621005.1- Q330_RS0106010	WP_027305 900.1	F3 system, 28H , 40H
				GCF_000621005.1- Q330_RS0105540	WP_051521 714.1	
				GCF_000621005.1- Q330_RS0100570	WP_027304 962.1	
	<i>Campylobact er_D helveticus</i>	GCF_002080 395.1	<i>Campylobac ter helveticus</i> ATCC 51209	GCF_002080395.1- CHELV3228_RS00050	WP_082200 713.1	F3 system, 28H , 40H, 44H
				GCF_002080395.1- CHELV3228_RS09175	WP_082200 691.1	
				GCF_002080395.1- CHELV3228_RS01550	WP_082199 230.1	
				GCF_002080395.1- CHELV3228_RS08180	WP_082200 520.1	

<i>Campylobacter_D</i> <i>upsaliensis</i>	GCF_000167 395.1	<i>Campylobac</i> <i>ter</i> <i>upsaliensis</i> <i>RM3195</i>	GCF_000167395.1- CUP_RS03190	WP_004275 314.1	F3 system, 28H , 40H, 44H
			GCF_000167395.1- CUP_RS03010	WP_004275 277.1	
			GCF_000167395.1- CUP_RS03665	WP_004275 415.1	
			GCF_000167395.1- CUP_RS05805	WP_004275 846.1	
<i>Campylobacter_D</i> <i>sp002738235</i>	GCF_002738 235.1	<i>Campylobac</i> <i>ter</i> sp. 73/13			F3 system, 40H, 44H
<i>Campylobacter_D</i> <i>hepaticus</i>	GCF_001687 475.1	<i>Campylobac</i> <i>ter</i> <i>hepaticus</i>	GCF_001687475.1- A2J15_RS07055	WP_066779 406.1	F3 system, 28H , 40H
<i>Campylobacter_D</i> <i>jejuni_B</i>	GCF_002179 165.1	<i>Campylobac</i> <i>ter</i> <i>jejuni</i> <i>W1</i>			F3 system, 28H, 40H, 44H
<i>Campylobacter_D</i> <i>coli</i>	GCF_000465 235.1	<i>Campylobac</i> <i>ter</i> <i>coli</i> <i>CVM</i> <i>N29710</i>	GCF_000465235.1- G157_RS01370	WP_002822 567.1	F3 system, 28H , 40H
			GCF_000465235.1- G157_RS01095	WP_021033 641.1	
			GCF_000465235.1- G157_RS07430	WP_021033 778.1	
	GCF_000465 235.1	<i>Campylobac</i> <i>ter</i> <i>coli</i> <i>CVM</i> <i>N29710</i>	GCF_000465235.1- G157_RS01370	WP_002822 567.1	F3 system, 28H , 40H
			GCF_000465235.1- G157_RS01095	WP_021033 641.1	
			GCF_000465235.1- G157_RS07430	WP_021033 778.1	
	GCF_000583 795.1	<i>Campylobac</i> <i>ter</i> <i>coli</i> <i>RM5611</i>	GCF_000583795.1- YSU_RS08010	WP_025431 530.1	F3 system, 28H , 40H
			GCF_000583795.1- YSU_RS01055	WP_025431 485.1	
			GCF_000583795.1- YSU_RS07490	WP_025431 528.1	
	GCF_000954 195.1	<i>Campylobac</i> <i>ter</i> <i>coli</i>	GCF_000954195.1- VC76_RS07390	WP_002822 567.1	F3 system, 28H , 40H
			GCF_000954195.1- VC76_RS07950	WP_045243 712.1	
			GCF_000954195.1- VC76_RS07680	WP_045243 711.1	
			GCF_000954195.1- VC76_RS01340	WP_021033 778.1	

<i>Campylobacter_D coli_A</i>	GCF_000470 055.1	<i>Campylobacter coli</i> 76339	GCF_000470055.1-BN865_RS01275	WP_020973 958.1	F3 system, 28H , 40H
	GCF_001498 475.1	<i>Campylobacter coli</i>	GCF_001498475.1- AV450_RS02685	WP_075504 589.1	F3 system, 28H , 40H
	GCF_001494 895.1	<i>Campylobacter coli</i>	GCF_001494895.1- AV288_RS04180	WP_075482 578.1	F3 system, 28H , 40H
<i>Campylobacter D coli_B</i>	GCF_001492 295.1	<i>Campylobacter coli</i>	GCF_001492295.1- AV154_RS00980 GCF_001492295.1- AV154_RS08260	WP_058968 202.1 WP_058969 565.1	F3 system, 28H , 40H
	GCF_002019 865.1	<i>Campylobacter coli</i>	GCF_002019865.1- BOQ00_RS06585 GCF_002019865.1- BOQ00_RS08225	WP_078416 234.1 WP_078416 353.1	F3 system, 28H , 40H
	GCF_002020 015.1	<i>Campylobacter coli VA8</i>	GCF_002020015.1- BOP99_RS05705 GCF_002020015.1- BOP99_RS05315 GCF_002020015.1- BOP99_RS00005	WP_075447 212.1 WP_052774 443.1 WP_075481 750.1	F3 system, 28H , 40H
<i>Campylobacter_D jejuni</i>	GCF_000009 085.1	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> NCTC 11168 = ATCC 700819	GCF_000009085.1-Cj1506c GCF_000009085.1-Cj0144 GCF_000009085.1-Cj1564 GCF_000009085.1-Cj0262c	YP_0023448 85.1 YP_0023436 04.1 YP_0023449 33.1 YP_0023437 04.1	F3 system, 28H , 40H
	GCF_000835 285.1	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	GCF_000835285.1- PJ17_RS07875 GCF_000835285.1- PJ17_RS00730 GCF_000835285.1- PJ17_RS08150 GCF_000835285.1- PJ17_RS01290 GCF_000835285.1- PJ17_RS01300	WP_002858 883.1 WP_079394 622.1 WP_079394 630.1 WP_042635 812.1 WP_042635 814.1	F3 system, 28H , 40H
	GCF_002209 045.1	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	GCF_002209045.1- A6J93_RS07640 GCF_002209045.1- A6J93_RS00985	WP_002871 853.1 WP_079460 163.1	F3 system, 28H , 40H

			<u>GCF_002209045.1-</u> <u>A6J93_RS07895</u>	WP_088585 164.1
			<u>GCF_002209045.1-</u> <u>A6J93_RS01525</u>	WP_088585 119.1
GCF_003060 745.1	<i>Campylobac ter jejuni</i>		<u>GCF_003060745.1-</u> <u>CJ12660_RS07665</u>	WP_002851 F3 system, 28H , 40H 362.1
			<u>GCF_003060745.1-</u> <u>CJ12660_RS07910</u>	WP_108592 625.1
			<u>GCF_003060745.1-</u> <u>CJ12660_RS00720</u>	WP_108592 594.1
			<u>GCF_003060745.1-</u> <u>CJ12660_RS01265</u>	WP_021036 342.1
GCF_000835 345.1	<i>Campylobac ter jejuni subsp. jejuni</i>		<u>GCF_000835345.1-</u> <u>PJ19_RS08250</u>	WP_002851 F3 system, 28H , 40H 362.1
			<u>GCF_000835345.1-</u> <u>PJ19_RS00730</u>	WP_079394 712.1
			<u>GCF_000835345.1-</u> <u>PJ19_RS08495</u>	WP_079394 745.1
			<u>GCF_000835345.1-</u> <u>PJ19_RS01250</u>	WP_009881 974.1
<i>Campylobact er_D insulaenigrae</i>	GCF_000816 185.1	<i>Campylobac ter insulaenigra e NCTC 12927</i>	<u>GCF_000816185.1-</u> <u>CINS_RS06385</u>	WP_039650 F3 system, 28H , 40H, 44H 838.1
			<u>GCF_000816185.1-</u> <u>CINS_RS07375</u>	WP_039651 184.1
			<u>GCF_000816185.1-</u> <u>CINS_RS00645</u>	WP_084593 975.1
			<u>GCF_000816185.1-</u> <u>CINS_RS05400</u>	WP_039650 514.1
			<u>GCF_000816185.1-</u> <u>CINS_RS01075</u>	WP_039649 119.1
<i>Campylobact er_D volucris</i>	GCF_000816 345.1	<i>Campylobac ter volucris LMG 24379</i>	<u>GCF_000816345.1-</u> <u>CVOL_RS07670</u>	WP_039666 F3 system, 28H , 40H, 44H 183.1
			<u>GCF_000816345.1-</u> <u>CVOL_RS07665</u>	WP_039666 182.1
			<u>GCF_000816345.1-</u> <u>CVOL_RS06585</u>	WP_039666 017.1
			<u>GCF_000816345.1-</u> <u>CVOL_RS05505</u>	WP_039665 826.1
			<u>GCF_000816345.1-</u> <u>CVOL_RS00675</u>	WP_039664 987.1
<i>Campylobact er_D peloridis</i>	GCF_000816 785.1	<i>Campylobac ter peloridis LMG 23910</i>	<u>GCF_000816785.1-</u> <u>CPEL_RS08275</u>	WP_044599 F3 system, 28H , 40H 430.1
			<u>GCF_000816785.1-</u> <u>CPEL_RS07205</u>	WP_044599 248.1

			GCF_000816785.1- CPEL_RS06215	WP_044599 069.1	
			GCF_000816785.1- CPEL_RS06210	WP_044599 575.1	
			GCF_000816785.1- CPEL_RS06205	WP_044599 068.1	
			GCF_000816785.1- CPEL_RS00725	WP_044599 464.1	
			GCF_000816785.1- CPEL_RS08030	WP_044599 392.1	
	<i>Campylobacter</i> <i>D</i> <i>sp000816245</i>	GCF_000816 245.1	<i>Campylobac</i> <i>ter sp.</i> <i>RM16704</i>	GCF_000816245.1- CAQ16704_RS07750 GCF_000816245.1- CAQ16704_RS06675 GCF_000816245.1- CAQ16704_RS05595 GCF_000816245.1- CAQ16704_RS02125 GCF_000816245.1- CAQ16704_RS07495	WP_039667 627.1 WP_039667 452.1 WP_039667 264.1 WP_052244 972.1 WP_039667 590.1
	<i>Campylobacter</i> <i>D</i> <i>subantarcticus</i>	GCF_000816 305.1	<i>Campylobac</i> <i>ter</i> <i>subantarcticus LMG</i> <i>24377</i>	GCF_000816305.1- CSUB8523_RS09320 GCF_000816305.1- CSUB8523_RS09315 GCF_000816305.1- CSUB8523_RS08420 GCF_000816305.1- CSUB8523_RS08075 GCF_000816305.1- CSUB8523_RS07005 GCF_000816305.1- CSUB8523_RS00730	WP_043020 302.1 WP_043020 301.1 WP_043020 208.1 WP_043020 166.1 WP_043020 033.1 WP_043019 309.1
	<i>Campylobacter</i> <i>D</i> <i>ornithocola</i>	GCF_001705 345.1	<i>Campylobac</i> <i>ter</i> <i>ornithocola WBE38</i>	GCF_001705345.1- A7X81_RS05805 GCF_001705345.1- A7X81_RS02290 GCF_001705345.1- A7X81_RS00225	WP_066008 273.1 WP_066007 058.1 WP_066006 399.1
	<i>Campylobacter</i> <i>D lari</i>	GCF_900111 465.1	<i>Campylobac</i> <i>ter lari</i> <i>subsp. Lari</i> <i>ATCC</i> <i>35221</i>	GCF_900111465.1- BMY58_RS03220 GCF_900111465.1- BMY58_RS06285	WP_081352 015.1 WP_012662 186.1

<i>Campylobacter_D lari_B</i>	GCF_000816 225.1	<i>Campylobacter lari</i> <i>subsp.</i> <i>concheus</i> <i>LMG 11760</i>	GCF_000816225.1-CONCH_RS07460	WP_039668 968.1	F3 system, 28H , 40H, 44H	
			GCF_000816225.1-CONCH_RS06405	WP_039668 807.1		
			GCF_000816225.1-CONCH_RS00695	WP_039667 881.1		
			GCF_000816225.1-CONCH_RS05400	WP_039668 641.1		
			GCF_000816225.1-CONCH_RS02065	WP_039668 097.1		
			GCF_000816225.1-CONCH_RS07215	WP_052239 476.1		
<i>Campylobacter_D lari_C</i>	GCF_001017 575.1	<i>Campylobacter lari</i>	GCF_001017575.1-CD56_RS06815	WP_047208 605.1	F3 system, 28H , 40H, 44H	
			GCF_001017575.1-CD56_RS05810	WP_047208 471.1		
			GCF_001017575.1-CD56_RS07085	WP_047208 641.1		
			GCF_001017575.1-CD56_RS07865	WP_047208 712.1		
			GCF_001017575.1-CD56_RS07860	WP_047208 711.1		
			GCF_001017575.1-CD56_RS02030	WP_047208 044.1		
			GCF_001017575.1-CD56_RS08150	WP_080956 350.1		
			GCF_001017575.1-CD56_RS07615	WP_080956 346.1		
<i>Campylobacter_D jejuni_C</i>	GCF_002179 635.1	<i>Campylobacter jejuni S4</i>	GCF_002179635.1-CAS13_RS02695	WP_087699 709.1	F3 system, 28H , 40H, 44H	
			GCF_002179635.1-CAS13_RS06905	WP_087700 724.1		
			GCF_002179635.1-CAS13_RS05225	WP_087700 460.1		
f_Helicobacteraceae						
Helicobacter	<i>Helicobacter pylori</i>	GCF_900478 295.1	<i>Helicobacter pylori</i> NCTC 11637 = CCUG 17874 = ATCC 43504	GCF_900478295.1-DQL14_RS01445	WP_108169 589.1	F3 system, 28H , 40H
Helicobacter_A	<i>Helicobacter A bilis</i>	GCF_000686 565.1	<i>Helicobacter bilis ATCC</i> 51630	GCF_000686565.1-T368_RS13380	WP_004087 959.1	F3 system, 28H , 40H, 44H

				GCF_000686565.1- T368_RS0105195	WP_027338 340.1
				GCF_000686565.1- T368_RS0103980	WP_027338 309.1
				GCF_000686565.1- T368_RS0112100	WP_027338 528.1
				GCF_000686565.1- T368_RS0111695	WP_004086 671.1
				GCF_000686565.1- T368_RS0101325	WP_004088 793.1
				GCF_000686565.1- T368_RS0104865	WP_004087 728.1
Helicobacter_B	<i>Helicobacter_B canis</i>	GCF_000507865.1	<i>Helicobacter canis</i> NCTC 12740	GCF_000507865.1- HMPREF2087_RS09205	WP_034577 829.1
				GCF_000507865.1- HMPREF2087_RS07780	WP_023930 583.1
				GCF_000507865.1- HMPREF2087_RS04115	WP_023929 761.1
				GCF_000507865.1- HMPREF2087_RS09050	WP_023930 866.1
				GCF_000507865.1- HMPREF2087_RS05180	WP_023929 979.1
Helicobacter_C	<i>Helicobacter_C hepaticus</i>	GCF_000007905.1	<i>Helicobacter hepaticus</i> ATCC 51449	GCF_000007905.1- HH_RS05325	WP_011115 928.1
				GCF_000007905.1- HH_RS04770	WP_011115 811.1
				GCF_000007905.1- HH_RS06465	WP_011116 177.1
				GCF_000007905.1- HH_RS03595	WP_011115 567.1
Helicobacter_D	<i>Helicobacter_D rodentium</i>	GCF_000687535.1	<i>Helicobacter rodentium</i> ATCC 700285	GCF_000687535.1- BS85_RS10280	WP_051604 694.1
				GCF_000687535.1- BS85_RS0106525	WP_026944 092.1
Helicobacter_E	<i>Helicobacter_E felis</i>	GCF_000200595.1	<i>Helicobacter felis</i> ATCC 49179	GCF_000200595.1- HFELIS_RS04385	WP_013469 327.1
				GCF_000200595.1- HFELIS_RS07975	WP_013470 049.1
				GCF_000200595.1- HFELIS_RS02830	WP_081458 40H 364.1
				GCF_000200595.1- HFELIS_RS03120	WP_013469 40H 084.1
				GCF_000200595.1- HFELIS_RS01885	WP_013468 40H 845.1

Helicobacter_F	<i>Helicobacter_F_himalayensis</i>	GCF_001602 095.1	<i>Helicobacter_himalayensis</i>	GCF_001602095.1-A3217_RS04305	WP_082807 964.1	F3 system, 28H , 40H, 44H
				GCF_001602095.1-A3217_RS01860	WP_066387 242.1	
				GCF_001602095.1-A3217_RS06775	WP_066389 087.1	
				GCF_001602095.1-A3217_RS00950	WP_066386 874.1	
				GCF_001602095.1-A3217_RS05205	WP_066388 688.1	
Helicobacter_G	<i>Helicobacter_G_cholecystus</i>	GCF_900198 475.1	<i>Helicobacter_cholecystus</i>	GCF_900198475.1-C6H20_RS03470	WP_104724 582.1	F3 system, 24H, 28H
Helicobacter_H	<i>Helicobacter_H_sp900199585</i>	GCF_900199 585.1	<i>Helicobacter sp. 'house sparrow 1'</i>	GCF_900199585.1-C6H31_RS00220	WP_104696 804.1	F3 system, 24H, 28H , 44H
Helicobacter_I	<i>Helicobacter_I_sp002272925</i>	GCF_002272 925.1	<i>Helicobacter sp.</i>	13S00401-1		F3 system, 24H, 28H, 44H
Helicobacter_J	<i>Helicobacter_J_sp002272795</i>	GCF_002272 795.1	<i>Helicobacter sp.</i>	13S00482-2		F3 system, 24H, 40H, no 28H
Wolinella	<i>Wolinella_succinogenes</i>	GCF_000196 135.1	<i>Wolinella succinogene s DSM 1740</i>	GCF_000196135.1-WS_RS06375	WP_049770 664.1	F3 system, 28H , 36H, 40H , 44H
				GCF_000196135.1-WS_RS04140	WP_011138 770.1	
				GCF_000196135.1-WS_RS06705	WP_011139 256.1	40H
f_Hydrogenimonadaceae						
Hydrogenimomas	<i>Hydrogenimomas_thermophila</i>	GCF_900115 615.1	<i>Hydrogenimonas_thermophila</i>	GCF_900115615.1-BM227_RS06280	WP_092912 228.1	F3, F7, and F8 systems, 28H, 34H, 36H, 40H , 44H
f_Nitratiruptoraceae						
Nitratiruptor	<i>Nitratiruptor_tergarcus</i>	GCF_900176 045.1	<i>Nitratiruptor_tergarcus DSM 16512</i>			F14, 40H, 44H
f_Sulfurimonadaceae						
Sulfuricurvum	<i>Sulfuricurvum_kuijense</i>	GCF_000183 725.1	<i>Sulfuricurvum kuijense DSM 16994</i>			F3, F7, and F8 systems, 28H, 34H, 36H, 40H , 44H
Sulfurimonas	<i>Sulfurimonas_autotrophica</i>	GCF_000147 355.1	<i>Sulfurimonas autotrophic a DSM 16294</i>	GCF_000147355.1-SAUT_RS06215	WP_013327 024.1	F3 and F8 systems, 34H, 40H

Desulfurella	<i>Desulfurella acetivorans</i>	GCF_000517 565.1	<i>Desulfurella acetivorans A63</i>	F1 system, 40H, 44H
Desulfurella	<i>Desulfurella amilsii</i>	GCF_002119 425.1	<i>Desulfurella amilsii</i>	F1 system, 40H, 44H
f_Hippeaceae				
Hippea	<i>Hippea maritima</i>	GCF_000194 135.1	<i>Hippea maritima DSM 10411</i>	F3 system, 24H, 40H, 44H
Hippea_A	<i>Hippea jasoniae</i>	GCF_000744 435.1	<i>Hippea_A jasoniae</i>	F3 system, 40H, 44H

Table S2. The presence of tlp2, tlp3 and tlp4 genes in *Campylobacter_D* species with complete and draft genomes.

GTDB Species	Assembly ID	Strain	Tlp2	Tlp3 paralog 1 YNxxxRxW Y x Y x D	Tlp3/CcmL	Tlp3 paralog 2	Tlp4
<i>Campylobacter_D jejuni</i>	GCF_00150 7125.1	Campylobacter jejuni CJ677CC024					
	GCF_00150 6885.1	Campylobacter jejuni CJ677CC040					
	GCF_00150 6205.1	Campylobacter jejuni CJ677CC002					
	GCF_00150 6345.1	Campylobacter jejuni CJ677CC036					
	GCF_00150 6465.1	Campylobacter jejuni CJ677CC530					
	GCF_00150 6665.1	Campylobacter jejuni CJ677CC528					
	GCF_00150 7145.1	Campylobacter jejuni CJ677CC064					
	GCF_00150 7065.1	Campylobacter jejuni CJ677CC094		WP_05911 9483.1			
	GCF_00150 6485.1	Campylobacter jejuni CJ677CC532					
	GCF_00150 6705.1	Campylobacter jejuni CJ677CC520					

GCF_00150	
7045.1	Campylobacter jejuni CJ677CC522
GCF_00150	
6225.1	Campylobacter jejuni CJ677CC534
GCF_00150	
6445.1	Campylobacter jejuni CJ677CC092
GCF_00150	
6685.1	Campylobacter jejuni CJ677CC538
GCF_00150	
6385.1	Campylobacter jejuni CJ677CC016
GCF_00150	
6425.1	Campylobacter jejuni CJ677CC535
GCF_00150	
6505.1	Campylobacter jejuni CJ677CC529
GCF_00150	
6525.1	Campylobacter jejuni CJ677CC531
GCF_00150	
6565.1	Campylobacter jejuni CJ677CC059
GCF_00150	
6625.1	Campylobacter jejuni CJ677CC537
GCF_00150	
6745.1	Campylobacter jejuni CJ677CC039
GCF_00150	
6825.1	Campylobacter jejuni CJ677CC078
GCF_00150	
6905.1	Campylobacter jejuni CJ677CC061
GCF_00150	
6965.1	Campylobacter jejuni CJ677CC047
GCF_00150	
6985.1	Campylobacter jejuni CJ677CC058
GCF_00150	
7085.1	Campylobacter jejuni CJ677CC008
GCF_00150	
6185.1	Campylobacter jejuni CJ677CC519
GCF_00150	
6545.1	Campylobacter jejuni CJ677CC062
GCF_00150	
6805.1	Campylobacter jejuni CJ677CC527
GCF_00150	
7005.1	Campylobacter jejuni CJ677CC013

WP_05911
6327.1
WP_07975
6629.1

WP_07975
6887.1

GCF_00150	
7025.1	Campylobacter jejuni CJ677CC100
GCF_00150	
7185.1	Campylobacter jejuni CJ677CC026
GCF_00150	
6305.1	Campylobacter jejuni CJ677CC526
GCF_00150	
6365.1	Campylobacter jejuni CJ677CC524
GCF_00150	
7165.1	Campylobacter jejuni CJ677CC525
GCF_00150	
6245.1	Campylobacter jejuni CJ677CC536
GCF_00150	
6285.1	Campylobacter jejuni CJ677CC521
GCF_00150	
6845.1	Campylobacter jejuni CJ677CC523
GCF_00150	
6725.1	Campylobacter jejuni CJ677CC014
GCF_00150	
7225.1	Campylobacter jejuni CJ677CC086
GCF_00150	
6945.1	Campylobacter jejuni CJ677CC533
GCF_00150	
7245.1	Campylobacter jejuni CJ677CC095
GCF_00150	
7265.1	Campylobacter jejuni CJ677CC012
GCF_00150	
6585.1	Campylobacter jejuni CJ677CC032
GCF_00150	
7105.1	Campylobacter jejuni CJ677CC541
GCF_00150	
6265.1	Campylobacter jejuni CJ677CC073
GCF_00150	
6405.1	Campylobacter jejuni CJ677CC041
GCF_00150	
6605.1	Campylobacter jejuni CJ677CC033
GCF_00150	
6645.1	Campylobacter jejuni CJ677CC542
GCF_00150	
6765.1	Campylobacter jejuni CJ677CC085

WP_07975
6629.1

WP_05911
9230.1

GCF_00150	Campylobacter jejuni CJ677CC052			
6785.1	Campylobacter jejuni CJ677CC540			
GCF_00150	Campylobacter jejuni CJ677CC539			
6865.1	Campylobacter jejuni CJ677CC034			
GCF_00150	Campylobacter jejuni CJ066CC508			
6925.1	Campylobacter jejuni subsp. Jejuni 35925			
GCF_00093	Campylobacter jejuni NCTC12662	WP_07939	WP_07900	WP_044305740.1
4305.1	Campylobacter jejuni subsp. Jejuni ATCC 35925	9331.1	5337.1	WP_044305740.1
GCF_00202	Campylobacter jejuni NCTC 12661		WP_07900	WP_044305740.1
4325.1	Campylobacter jejuni HF5-5-1	WP_03840	5337.1	WP_044305740.1
GCF_00195	Campylobacter jejuni HF5-7-1	2013.1	WP_07588	WP_075888364.1
1255.1	Campylobacter jejuni RM1246-ERRC	WP_03840	8393.1	WP_075888364.1
GCF_00195	Campylobacter jejuni 4031	2013.1	WP_07588	WP_087694997.1
1275.1	Campylobacter jejuni CJ515CC45	WP_09395	8393.1	WP_07946
GCF_00223	Campylobacter jejuni CJ513CC45	8665.1	7350.1	7350.1
4455.1	Campylobacter jejuni CJ031CC45		WP_07927	WP_07927
GCF_00049	Campylobacter jejuni subsp. jejuni 81116		9415.1	9415.1
3495.1	Campylobacter jejuni subsp. Jejuni	WP_01200	WP_07925	WP_012006635.1
GCF_00336	FDAARGOS_266	6626.1	4164.1	WP_088592094.1
8065.1	Campylobacter jejuni subsp. Jejuni	WP_01200	WP_07925	
GCF_00336	MTVDSCj20	6626.1	4164.1	
8125.1	Campylobacter jejuni CJ067CC45			
GCF_00336	Campylobacter jejuni subsp. Jejuni	WP_03840	WP_07588	
8085.1		2013.1	8393.1	
GCF_00001				WP_014516918.1
7905.1				
GCF_00220				
9065.1				
GCF_00336				
8045.1				
GCF_00073				
7085.1				

GCF_00014			WP_07588	
8705.1	Campylobacter jejuni subsp. jejuni M1		8393.1	WP_014516918.1
GCF_00141			WP_07588	
2295.1	Campylobacter jejuni CJM1cam		8393.1	WP_014516918.1
GCF_00336				
8105.1	Campylobacter jejuni CJ017CCUA	WP_05820	WP_07975	
GCF_00145			7847.1	4350.1
7695.1	Campylobacter jejuni NCTC11351	WP_05820	WP_07975	
GCF_00220	Campylobacter jejuni subsp. Jejuni	7847.1	4350.1	
9005.1	FDAARGOS_262	WP_00285	WP_07925	
GCF_00129	Campylobacter jejuni subsp. Jejuni	4643.1	4326.1	WP_002854722.1
9565.1	RM3197	WP_00285	WP_07925	
GCF_00129	Campylobacter jejuni subsp. Jejuni	4643.1	4326.1	WP_002854722.1
9595.1	RM3196	WP_00988		
GCF_00001		1803.1		WP_009881974.1
5525.1	Campylobacter jejuni subsp. jejuni 81-176	WP_00988	WP_01089	
GCF_00222		1803.1	1944.1	WP_009881974.1
4385.1	Campylobacter jejuni 81-176_G1_B0		WP_07946	WP_065453843.1
GCF_00168	Campylobacter jejuni subsp. Jejuni		1914.1	
6905.1	RM1285	WP_07036		WP_002851876.1
GCF_00176	Campylobacter jejuni subsp. jejuni str.	3962.1		
7215.1	RM3420	WP_05279		WP_002851876.1
GCF_00221		1709.1		
4785.1	Campylobacter jejuni FORC_046		WP_07946	
GCF_00171			0008.1	WP_07985
7625.1	Campylobacter jejuni subsp. Jejuni 14980A			1618.1
GCF_00336				
8205.1	Campylobacter jejuni CJ090CC1332	WP_11576		
GCF_00336		6720.1		
8225.1	Campylobacter jejuni CJ018CCUA			
GCF_00336				
8185.1	Campylobacter jejuni CJ071CC464			
GCF_00186				
5435.1	Campylobacter jejuni IF1100	WP_07939	WP_07939	
GCF_00083				WP_042635812.1
5285.1	Campylobacter jejuni subsp. Jejuni 00-1597	4622.1	4630.1	
GCF_00186		WP_07946	WP_07986	
5595.1	Campylobacter jejuni subsp. jejuni M129	7177.1	0163.1	
GCF_00186			WP_07946	
5395.1	Campylobacter jejuni FJ3124		0008.1	

GCF_00336	Campylobacter jejuni CJ088CC52		WP_07934		
8145.1			3735.1		
GCF_00017	Campylobacter jejuni CG8421		WP_07925	WP_07925	
1795.2			4342.1	4358.1	
GCF_00018	Campylobacter jejuni subsp. jejuni S3	WP_01451	WP_07925	WP_07925	WP_014517176.1
4205.1		7177.1	4358.1	4358.1	
GCF_00001	Campylobacter jejuni RM1221	WP_01104	WP_07925	WP_07925	WP_011049651.1
1865.1		9652.1	4358.1	4358.1	
GCF_00258	Campylobacter jejuni FDAARGOS_421	WP_01104	WP_07925	WP_07925	WP_011049651.1
7225.1		9652.1	4358.1	4358.1	
GCF_00336	Campylobacter jejuni CJ074CC443		WP_11576	WP_11576	
8165.1			9683.1	9683.1	
GCF_00156	Campylobacter jejuni RM3194	WP_05281	WP_07946	WP_01089	WP_061099736.1
3565.1		6913.1	0008.1	1944.1	
GCF_00172	Campylobacter jejuni subsp. Jejuni		WP_07985	WP_07985	
1965.1	MTVDSCj13		4565.1	4575.1	
GCF_00172	Campylobacter jejuni subsp. Jejuni		WP_07985	WP_07985	
1985.1	MTVDSCj16		4703.1	4727.1	
GCF_00303	Campylobacter jejuni CFSAN054107		WP_10713	WP_10713	
0185.1			1175.1	1164.1	
GCF_00186	Campylobacter jejuni TS1218		WP_07131	WP_07131	
5415.1			1218.1	1218.1	
GCF_00187	Campylobacter jejuni YQ2210				
0085.1					
GCF_00187	Campylobacter jejuni ZP3204				
0105.1					
GCF_00043	Campylobacter jejuni 32488		WP_07926	WP_07926	WP_009881974.1
0385.1			9902.1	9906.1	
GCF_00240	Campylobacter jejuni CFSAN032806	WP_09677	WP_09677	WP_09677	WP_009881974.1
7125.1		7911.1	7910.1	7910.1	
GCF_00077	Campylobacter jejuni subsp. jejuni F38011	WP_00988	WP_01089	WP_01089	WP_041160003.1
2225.1		1803.1	1944.1	1944.1	
GCF_00220	Campylobacter jejuni subsp. Jejuni		WP_07946	WP_08858	
9045.1	FDAARGOS_265		0163.1	5164.1	
GCF_00158	Campylobacter jejuni OD267			WP_06157	
7015.1				7918.1	
GCF_00158	Campylobacter jejuni WP2202				WP_061563569.1
7035.1					
GCF_00030	Campylobacter jejuni subsp. jejuni PT14	WP_07976	WP_07976	WP_07976	WP_015016423.1
2555.5		8733.1	8734.1	8734.1	

GCF_00172	Campylobacter jejuni subsp. Jejuni	WP_06935	WP_01089	
1945.1	MTVDSCj07	8644.1	1944.1	WP_015016423.1
GCF_00131			WP_01089	
4285.1	Campylobacter jejuni RM1285		1944.1	
GCF_00306			WP_10861	
0785.1	Campylobacter jejuni NCTC 12664		4575.1	
GCF_00195			WP_07591	WP_108614536.1
1235.1	Campylobacter jejuni HF5-4A-4	WP_00285	2974.1	WP_075912928.1
GCF_00258		1724.1	WP_01089	
7105.1	Campylobacter jejuni FDAARGOS_422	YP_002343	1944.1	WP_002851876.1
GCF_00000	Campylobacter jejuni subsp. jejuni NCTC	604.1	YP_002344	YP_002343704.1
9085.1	11168 = ATCC 700819		933.1	
GCF_00030	Campylobacter jejuni subsp. jejuni NCTC	WP_00988	WP_01089	
4375.1	11168-BN148	1803.1	1944.1	WP_009881974.1
GCF_00083	Campylobacter jejuni subsp. jejuni NCTC	WP_04133	WP_07939	
0775.1	11168-K12E5	7137.1	4646.1	WP_041337140.1
GCF_00083	Campylobacter jejuni subsp. jejuni NCTC	WP_04133	WP_07939	
0805.1	11168-Kf1	7137.1	4646.1	WP_041337140.1
GCF_00083	Campylobacter jejuni subsp. jejuni NCTC	WP_00988	WP_01089	
0825.1	11168-mcK12E5	1803.1	1944.1	WP_009881974.1
GCF_00083	Campylobacter jejuni subsp. jejuni NCTC	WP_00988	WP_01089	
0845.1	11168-mfK12E5	1803.1	1944.1	WP_009881974.1
GCF_00083	Campylobacter jejuni subsp. jejuni NCTC	WP_00988	WP_01089	
0865.1	11168-GSv	1803.1	1944.1	WP_009881974.1
GCF_00220	Campylobacter jejuni subsp. Jejuni	WP_00988		
9025.1	FDAARGOS_263	1803.1		WP_009881974.1
GCF_00222		WP_00988	WP_01089	
4325.1	Campylobacter jejuni 11168H/lacY	1803.1	1944.1	WP_009881974.1
GCF_00223		WP_00988	WP_01089	
8375.1	Campylobacter jejuni 11168H/araE	1803.1	1944.1	WP_009881974.1
GCF_90047		WP_00988	WP_01089	
5265.1	Campylobacter jejuni subsp. jejuni	1803.1	1944.1	WP_009881974.1
GCF_00306		WP_10859	WP_10859	
0745.1	Campylobacter jejuni NCTC 12660	2625.1	2594.1	
GCF_00195		WP_07222	WP_07586	
1295.1	Campylobacter jejuni NS4-1-1	3305.1	7322.1	
GCF_00195		WP_07222	WP_07586	
1315.1	Campylobacter jejuni NS4-5-1	3305.1	7322.1	
GCF_00195		WP_07222	WP_07586	
1335.1	Campylobacter jejuni NS4-9-1	3305.1	7322.1	

GCF_00002			WP_01451	WP_07925
5425.1	Campylobacter jejuni subsp. jejuni IA3902		6860.1	4169.1
GCF_00083		WP_07939	WP_07939	
5345.1	Campylobacter jejuni subsp. Jejuni 01-1512	4712.1	4745.1	
GCF_00083	Campylobacter jejuni subsp. Jejuni 00-	WP_07939	WP_07939	
5365.1	0949	4712.1	4721.1	
GCF_00306				
0725.1	Campylobacter jejuni 12567			
GCF_00210		WP_01451	WP_07925	
1355.1	Campylobacter jejuni YH002	6860.1	4169.1	
GCF_00083	Campylobacter jejuni subsp. Jejuni 00-	WP_01451	WP_07939	
5305.1	6200	6860.1	4740.1	
GCF_00046		WP_07937	WP_07937	
6075.2	Campylobacter jejuni subsp. jejuni 00-2544	6548.1	6546.1	
GCF_00046		WP_07937	WP_07937	
6065.2	Campylobacter jejuni subsp. jejuni 00-2538	6548.1	6546.1	
GCF_00046		WP_07937	WP_07937	
6105.2	Campylobacter jejuni subsp. jejuni 00-2426	6548.1	6546.1	
GCF_00046		WP_07937	WP_07937	
8915.2	Campylobacter jejuni subsp. jejuni 00-2425	6548.1	6546.1	
<i>Campylobacter_D_cuniculorum</i>				
GCF_00210	Campylobacter cuniculorum DSM 23162 =			
4335.1	LMG 24588			
GCF_00062	Campylobacter cuniculorum DSM 23162 =			
1005.1	LMG 24588			
<i>Campylobacter_D_helveticus</i>		WP_08220		WP_082200691.1,
GCF_00208		0713.1		WP_082200520.1
0395.1	Campylobacter helveticus			
GCF_90017				
6295.1	Campylobacter helveticus			
<i>Campylobacter_D_upsaliensis</i>				
GCF_00062		WP_00427		
0965.1	Campylobacter upsaliensis DSM 5365	5314.1		
GCF_00016				
7395.1	Campylobacter upsaliensis RM3195			
GCF_00018				
5345.1	Campylobacter upsaliensis JV21			
<i>Campylobacter_D_sp0027382</i>				
GCF_00273				
35	8235.1	Campylobacter sp. 73/13		

<i>Campylobacter_D</i>	GCF_00273 8305.1	Campylobacter sp. 251/13	
<i>hepticus</i>	GCF_00168 7475.1	Campylobacter hepaticus	
<i>Campylobacter_D</i>	GCF_00025 4135.1	Campylobacter coli LMG 9860	
<i>coli</i>	GCF_00202 4185.1	Campylobacter coli aerotolerant OR12	WP_09904 6908.1
	GCF_00046 5235.1	Campylobacter coli CVM N29710	WP_02103 3641.1
	GCF_00049 4775.1	Campylobacter coli 15-537360	WP_02336 2248.1
	GCF_00058 3755.1	Campylobacter coli RM1875	WP_02336 2235.1
	GCF_00058 3795.1	Campylobacter coli RM5611	WP_02543 1530.1
	GCF_00095 4195.1	Campylobacter coli FB1	WP_04524 3712.1
	GCF_00141 7635.1	Campylobacter coli HC2-48	WP_02543 1485.1
	GCF_00148 3845.1	Campylobacter coli OR12	WP_05891 4555.1
	GCF_00163 9125.1	Campylobacter coli YH501	WP_06365 1861.1
	GCF_00171 7605.1	Campylobacter coli 14983A	WP_05799 2610.1
	GCF_00186 5495.1	Campylobacter coli BP3183	WP_07130 4885.1
	GCF_00186 5515.1	Campylobacter coli WA333	
	GCF_00186 5555.1	Campylobacter coli BG2108	
	GCF_00193 6355.1	Campylobacter coli YH502	WP_07539 5263.1
	GCF_00240 7145.1	Campylobacter coli CFSAN032805	WP_09678 8361.1
	GCF_00284 3985.1	Campylobacter coli YH503	WP_10134 8801.1

GCF_00303		WP_10712	WP_10712
0205.1	Campylobacter coli CFSAN054106	8010.1	8017.1
GCF_00141		WP_06047	
7615.1	Campylobacter coli CO2-160	3514.1	
GCF_00141			
7655.1	Campylobacter coli CF2-75		
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<i>Campylobacter_D</i>			
<i>coli_A</i>	GCF_00047	WP_02097	
	0055.1	Campylobacter coli 76339	3958.1
	GCF_00047	WP_02097	
	0055.1	Campylobacter coli	3958.1
	GCF_00148		
	8335.1	Campylobacter coli	
	GCF_00201	WP_07839	
	9885.1	Campylobacter coli VA7	7504.1
	GCF_00149		
	5535.1	Campylobacter coli	
	GCF_00149	WP_07550	
	8475.1	Campylobacter coli	4589.1
	GCF_00149	WP_07548	
	4895.1	Campylobacter coli	2578.1
<hr/>			
<i>Campylobacter_D</i>			
<i>coli_B</i>	GCF_00149	WP_05896	
	2295.1	Campylobacter coli	8202.1
	GCF_00201	WP_07544	
	9985.1	Campylobacter coli VA46	7212.1
	GCF_00202		
	0085.1	Campylobacter coli VA37	
	GCF_00201	WP_07841	
	9865.1	Campylobacter coli VA6	6234.1
	GCF_00202	WP_07544	
	0015.1	Campylobacter coli VA8	7212.1
	GCF_00149	WP_07543	
	1515.1	Campylobacter coli	8466.1
	GCF_00149		WP_052774443.1
	0995.1	Campylobacter coli	
	GCF_00149	WP_07545	
	7615.1	Campylobacter coli	7517.1

Table S3: Glycan structures recognized by (A) Tlp2^{LBD}, (B) Tlp3^{LBD} and (C) Tlp4^{LBD}. Blood group A antigens - A (typeX), Blood group B antigens -B (typeX), Blood group H antigens -H (typeX), Lewis^a (Le^a), Lewis^b (Le^b), Lewis^c (Le^c), Lewis^x (Le^x), Lewis^y (Le^y), Ganglioside asialo GM1(Asialo-GM1), Thomsen-Friedenreich (TF) antigens, and Thomsen nouvelle (Tn) antigens. GM1(Asialo-GM1), Thomsen-Friedenreich (TF) antigens, P antigens P₁, P₂, P^k, and P and Thomsen nouvelle (Tn) antigens.

(A) Tlp2

Glycan No	Structure	Common name
240	(Glc α 1-4)3 β -sp4	TRISACCHARIDES
390	(Glc α 1-4)4 β -sp4	TRISACCHARIDES
241	(Glc α 1-6)3 β -sp4	TRISACCHARIDES
492	(Glc α 1-6)5 β -sp4	PENTA-NONA SACCHARIDES
502	(Glc α 1-6)6 β -sp4	PENTA-NONA SACCHARIDES
165	Glc α 1-3Gal β -sp3	DISACCHARIDES
164	Glc α 1-3GlcNAc β -sp3	DISACCHARIDES
166	Glc α 1-6Gal β -sp3	DISACCHARIDES
392	Fuc α 1-2(GalNAc α 1-3)Gal β 1-3GalNAc α -sp3	A (type 3)
366	Fuc α 1-2(GalNAc α 1-3)Gal β 1-3GlcNAc β -sp3	A (type 1)
368	Fuc α 1-2(GalNAc α 1-3)Gal β 1-4GlcNAc β -sp3	A (type 2)
363	Fuc α 1-2(Gal α 1-3)Gal β 1-3GalNAc β -sp3	B (type 4)
359	Fuc α 1-2(Gal α 1-3)Gal β 1-3GlcNAc β -sp3	B (type 1)
360	Fuc α 1-2(Gal α 1-3)Gal β 1-4GlcNAc β -sp3	B (type 2)
371	Fuc α 1-2Gal β 1-3(Fuc α 1-4)GlcNAc β -sp3	Le ^b
480	Fuc α 1-2Gal β 1-3GlcNAc β 1-3Gal β 1-4GlcNAc β -sp2	H (type1) penta
19L	Fuc α 1-2Gal β 1-4(Fuc α 1-3)GlcNAc β 1-3Gal	Le ^y pentaose
216	Fuc α 1-2Gal β 1-4GlcNAc β -sp3	H (type 2)
219	Fuc α 1-2Gal β 1-4Glc β -sp4	H (type 6)
71	Fuc α 1-2Gal β -sp3	H _{di}
483	Fuc α 1-3(Fuc α 1-2 (Gal α 1-3)Gal β 1-4)GlcNAc β -sp3	Ble ^y
497	Fuc α 1-3(Fuc α 1-2Gal β 1-4)GlcNAc β 1-3Gal β 1-4Glc β -sp4	Le ^y -Lac
372	Fuc α 1-3(Fuc α 1-2Gal β 1-4)GlcNAc β -sp3	Le ^y
364	Fuc α 1-3(Gal α 1-3Gal β 1-4)GlcNAc β -sp3	α Gal-Le ^x
234	Fuc α 1-3(Gal β 1-4)GlcNAc β -sp3	Le ^x
429	Fuc α 1-3(Neu5Ac α 2-3(6-O-Su)Gal β 1-4)GlcNAc β -sp3	TETRASACCHARIDES
428	Fuc α 1-3(Neu5Ac α 2-3Gal β 1-4)6-O-Su-GlcNAc β -sp3	TETRASACCHARIDES
423	Fuc α 1-3(Neu5Ac α 2-3Gal β 1-4)GlcNAc β -sp3	Sia-Le ^x
18E	GalNAc α 1-3(Fuc α 1-2)Gal β 1-4(Fuc α 1-3)Glc	Blood group A pentasaccharide
9A	Gal α 1-3(Fuc α 1-2)Gal β 1-4(Fuc α 1-3)Glc	Blood Group B pentasaccharide
233	Gal β 1-3(Fuc α 1-4)GlcNAc β -sp3	Le ^a

8C	Gal β 1-3GlcNAc β 1-3Gal β 1-4(Fuc α 1-3)GlcNAc β 1-3Gal β 1-4Glc	Fucosylated glycans
19J	Gal β 1-4(Fuc α 1-3)GlcNAc β 1-3Gal	Le ^x tetraose
8E	Gal β 1-4(Fuc α 1-3)GlcNAc β 1-6(Fuc α 1-2Gal β 1-3GlcNAc β 1-3)Gal β 1-4Glc	Fucosylated glycans
289	Gal α 1-3(Neu5Aca2-6)GalNAc α -sp3	6-Sia-TF
2A	Gal α 1-3Gal β 1-4Gal α 1-3Gal	Terminal galactose
373	Gal α 1-3Gal β 1-4GlcNAc β 1-3Gal β -sp3	Galili 4
220	Gal α 1-3Gal β 1-4Glc β -sp2	TRISACCHARIDES
375	Gal α 1-4GlcNAc β 1-3Gal β 1-4GlcNAc β -sp3	TETRASACCHARIDES
228	Gal β 1-2Gal α 1-4GlcNAc β -sp4	TRISACCHARIDES
145	Gal β 1-3(6-O-Su)GlcNAc β -sp3	6-O-Su-Le ^c
388	Gal β 1-3(Gal β 1-4GlcNAc β 1-6)GalNAc α -sp3	TETRASACCHARIDES
382	Gal β 1-3GalNAc β 1-4Gal β 1-4Glc β -sp3	Asialo-GM1
229	Gal β 1-3Gal β 1-4GlcNAc β -sp4	TRISACCHARIDES
377	Gal β 1-3GlcNAc β 1-3Gal β 1-3GlcNAc β -sp2	TETRASACCHARIDES
379	Gal β 1-3GlcNAc β 1-3Gal β 1-4GlcNAc β -sp3	TETRASACCHARIDES
376	Gal β 1-3GlcNAc β 1-3Gal β 1-4Glc β -sp4	TETRASACCHARIDES
381	Gal β 1-3GlcNAc β 1-6Gal β 1-4GlcNAc β -sp2	TETRASACCHARIDES
18M	Gal β 1-4Gal	Terminal galactose
264	Gal β 1-4Gal β 1-4GlcNAc-sp3	TRISACCHARIDES
94	Gal β 1-4Gal β -sp4	TRISACCHARIDES
488	Gal β 1-4GlcNAc β 1-3(Gal β 1-4GlcNAc β 1-6)GalNAc α -sp3	LN2-3,6-Tn
499	Gal β 1-4GlcNAc β 1-3(Gal β 1-4GlcNAc β 1-6)Gal β 1-4GlcNAc-sp2	PENTA-NONA SACCHARIDES
489	Gal β 1-4GlcNAc β 1-3(GlcNAc β 1-6)Gal β 1-4GlcNAc-sp2	PENTA-NONA SACCHARIDES
383	Gal β 1-4GlcNAc β 1-3Gal β 1-4Glc β -sp2	TETRASACCHARIDES
97	Gal β 1-4GlcNAc β -sp3	DISACCHARIDES
119	Man α 1-2Man β -sp4	DISACCHARIDES
495	Man α 1-3(Man α 1-3(Man α 1-6)Man α 1-6)Man β -sp4	PENTA-NONA SACCHARIDES
258	Man α 1-3(Man α 1-6)Man β -sp4	TRISACCHARIDES
120	Man α 1-3Man β -sp4	DISACCHARIDES
121	Man α 1-4Man β -sp4	DISACCHARIDES
5F	Man α 1-6Man	Mannosyl containing glycans
122	Man α 1-6Man β -sp4	DISACCHARIDES
123	Man β 1-4GlcNAc β -sp4	DISACCHARIDES
19F	Neu5Aca2-6Gal β 1-4GlcNAc β 1-2Man α 1-3(Neu5Aca2-6Gal β 1-4GlcNAc β 1-2Man α 1-6)Man β 1-4GlcNAc β 1-4(Fuc α 1-6)GlcNAc	Complex type X-glycan

(B) Tlp3

Glycan	Structure	Common name
12P	Δ UA-GalNAc-4S,6S	Glycosaminoglycans - high and low molecular weight
18I	GlcA	D-Glucuronic acid
12F	Neocarradecaos-41, 3, 5, 7, 9-penta-O-sulphate (Na ⁺)	Glycosaminoglycans - high and low molecular weight

12J	ΔUA-2S-GlcNAc	Glycosaminoglycans - high and low molecular weight
13A	ΔUA-2S-GalNAc-4S	Glycosaminoglycans - high and low molecular weight
13M	(GlcA/IdoAβ1-3(±S)GalNAcβ1-4)n (n<250)	Glycosaminoglycans - high and low molecular weight
14E	HA 30000	Glycosaminoglycans - high and low molecular weight
13M	HA 107000	Glycosaminoglycans - high and low molecular weight
1N	Galα1-3Gal (α1-3 Galactobiose)	Terminal galactose
2B	Galβ1-6Gal (beta1-6galactobiose)	Terminal galactose
5G	Manα1-6(Manα1-3)Man(α1-3,α1-6-Mannobiose)	Mannosyl containing glycans
10E	Neu5Acα2-3Galβ1-3(Neu5Acα2-6)GalNAc	Sialylated glycans
8B	SO ₃ -3Galβ1-4(Fucα1-3)GlcNAc	Fucosylated glycans
19M	Galβ1-3(Fucα1-4)GlcNAcβ1-3Gal	Le ^a tetraose
19N	Fucα1-2Galβ1-3(Fucα1-4)GlcNAc	Le ^b tetraose
2C	GalNAcβ	Terminal galactose
20	Rhaα	MONOSACCHARIDES
19	ManNAcβ	MONOSACCHARIDES
78	Galα1-3GalNAcα-sp3	DISACCHARIDES
168	GlcNAcβ1-[HOOC(CH ₃)CH]-3-O-GlcNAcβ-L-alanyl-D-i-glutaminyl-L-lysine	DISACCHARIDES
177	Galβ1-4(6-O-Su)GlcNAcβ	DISACCHARIDES
123	Manβ1-4GlcNAcβ	DISACCHARIDES
206	Neu5Gcα2-3Gal	DISACCHARIDES
232	Galβ1-4GlcNAcβ1-6GalNAcα	TRISACCHARIDES
240	(Glcα1-4) ₃ β	TRISACCHARIDES
293	Neu5Acα2-3Galβ1-4Glcβ	TRISACCHARIDES
331	Neu5Gcα2-3Galβ1-3GlcNAcβ	3`Sia-Le ^c (Gc)
359	Fucα1-2(Galα1-3)Galβ1-3GlcNAcβ	B (type 1)
389	GalNAcβ1-3Galα1-4Galβ1-4Glcβ	P antigen
495	Manα1-3(Manα1-3(Manα1-6)Manα1-6)Manβ	PENTA-NONA SACCHARIDES
534	Neu5Acα2-3Galβ1-4GlcNAcβ1-3Galβ1-4GlcNAcβ	PENTA-NONA SACCHARIDES

(C) Tlp4

Glycan	Structure	Common name
240	(Glcα1-4) ₃ β-sp4	TRISACCHARIDES
241	(Glcα1-6) ₃ β-sp4	TRISACCHARIDES
45	GlcAβ-sp3	MONOSACCHARIDES
19P	Glcα1-4Glcα1-4Glcα1-4Glc	Terminal Glucose structures
110	Glcα1-4Glcβ-sp3	DISACCHARIDES
7	Glcα-sp3	MONOSACCHARIDES
112	Glcβ1-6Glcβ-sp4	DISACCHARIDES
9	Glcβ-sp3	MONOSACCHARIDES
287	3-O-Su-Galβ1-3(Fucα1-4)GlcNAcβ-sp3	Su-Le ^a
8J	Fucα1-2Galβ1-4(Fucα1-3)GlcNAcb1-3(Fucα1-2)Galβ1-4Glc	Fucosylated glycans

366	Fuc α 1-2(GalNAc α 1-3)Gal β 1-3GlcNAc β -sp3	A (type 1)
368	Fuc α 1-2(GalNAc α 1-3)Gal β 1-4GlcNAc β -sp3	A (type 2)
363	Fuc α 1-2(Gal α 1-3)Gal β 1-3GalNAc β -sp3	B (type 4)
359	Fuc α 1-2(Gal α 1-3)Gal β 1-3GlcNAc β -sp3	B (type 1)
226	Fuc α 1-2(Gal α 1-3)Gal β -sp3	B _{tri}
371	Fuc α 1-2Gal β 1-3(Fuc α 1-4)GlcNAc β -sp3	Le ^b
217	Fuc α 1-2Gal β 1-3GalNAc α -sp3	H (type 3)
219	Fuc α 1-2Gal β 1-4Glc β -sp4	H (type 6)
288	Fuc α 1-3(3-O-Su-Gal β 1-4)GlcNAc β -sp3	Su-Le ^x
372	Fuc α 1-3(Fuc α 1-2Gal β 1-4)GlcNAc β -sp3	Le ^y
364	Fuc α 1-3(Gal α 1-3Gal β 1-4)GlcNAc β -sp3	α Gal-Le ^x
234	Fuc α 1-3(Gal β 1-4)GlcNAc β -sp3	Le ^x
72	Fuc α 1-3GlcNAc β -sp3	DISACCHARIDES
1	Fuc α -sp3	MONOSACCHARIDES
7M	Gal β 1-3(Fuc α 1-2)Gal	Blood Group B Trisaccharide
7J	Gal β 1-3(Fuc α 1-4)GlcNAc	Le ^a
7E	Gal β 1-3(Fuc α 1-4)GlcNAc β 1-3Gal β 1-4(Fuc α 1-3)Glc	Fucosylated glycans
233	Gal β 1-3(Fuc α 1-4)GlcNAc β -sp3	Le ^a
8C	Gal β 1-3GlcNAc β 1-3Gal β 1-4(Fuc α 1-3)GlcNAc β 1-3Gal β 1-4Glc	Fucosylated glycans
7H	Gal β 1-4(Fuc α 1-3)Glc	Fucosylated glycans
7I	Gal β 1-4(Fuc α 1-3)GlcNAc	Le ^x
	Gal β 1-4(Fuc α 1-3)GlcNAc β 1-6(Fuc α 1-2Gal β 1-3(Fuc α 1-4)GlcNAc β 1-3)Gal β 1-4Glc	Fucosylated glycans
8F	Gal β 1-4(Fuc α 1-3)GlcNAc β 1-6(Gal β 1-3GlcNAc β 1-3)Gal β 1-4Glc	Fucosylated glycans
8D	Gal β 1-4(Fuc α 1-3)GlcNAc β 1-6(Gal β 1-3GlcNAc β 1-3)Gal β 1-4Glc	Fucosylated glycans
19A	Gal β 1-4GlcNAc β 1-2Man α 1-3(Gal β 1-4GlcNAc β 1-2Man α 1-6Man) β 1-4GlcNAc β 1-4(Fuc α 1-6)GlcNAc	Complex type N-glycans
8G	Gal β 1-4GlcNAc β 1-3Gal β 1-4(Fuc α 1-3)Glc	Fucosylated glycans
8E	Gal β 1-4(Fuc α 1-3)GlcNAc β 1-6(Fuc α 1-2Gal β 1-3GlcNAc β 1-3)Gal β 1-4Glc	Fucosylated glycans
75	Gal α 1-2Gal β -sp3	DISACCHARIDES
289	Gal α 1-3(Neu5Ac α 2-6)GalNAc α -sp3	TRISACCHARIDES
78	Gal α 1-3GalNAc α -sp3	DISACCHARIDES
77	Gal α 1-3GalNAc β -sp3	DISACCHARIDES
2E	Gal α 1-4Gal β 1-4GlcNAc	P1 antigen
224	Gal α 1-4Gal β 1-4Glc β -sp3	P ^k antigen
375	Gal α 1-4GlcNAc β 1-3Gal β 1-4GlcNAc β -sp3	TETRASACCHARIDES
81	Gal α 1-4GlcNAc β -sp3	DISACCHARIDES
83	Gal α 1-6Glc β -sp4	DISACCHARIDES
2	Gal α -sp3	MONOSACCHARIDES
84	Gal β 1-2Gal β -sp3	DISACCHARIDES
254	Gal β 1-3(GlcNAc β 1-6)GalNAc α -sp3	TRISACCHARIDES
1E	Gal β 1-3GalNAc	Terminal galactose
89	Gal β 1-3GalNAc α -sp3	DISACCHARIDES
88	Gal β 1-3GalNAc β -sp3	DISACCHARIDES
229	Gal β 1-3Gal β 1-4GlcNAc β -sp4	TRISACCHARIDES
87	Gal β 1-3Gal β -sp3	DISACCHARIDES
85	Gal β 1-3GlcNaAc β -sp3	DISACCHARIDES

1A	Gal β 1-3GlcNAc	Terminal galactose
378	Gal β 1-3GlcNAc α 1-3Gal β 1-4GlcNAc β -sp3	TETRASACCHARIDES
377	Gal β 1-3GlcNAc β 1-3Gal β 1-3GlcNAc β -sp2	TETRASACCHARIDES
2G	Gal β 1-3GlcNAc β 1-3Gal β 1-4GlcNAc β 1-6(Gal β 1-3GlcNAc β 1-3)Gal β 1-4Glc	Terminal galactose
1C	Gal β 1-4Gal	Terminal galactose
264	Gal β 1-4Gal β 1-4GlcNAc-sp3	TRISACCHARIDES
19B	Gal β 1-4GlcNAc β 1-2(Gal β 1-4GlcNAc β 1-4)Man α 1-3(Gal β 1-4GlcNAc β 1-2(Gal β 1-4GlcNAc β 1-6)Man α 1-6Man) β 1-4GlcNAc β 1-4GlcNAc	Complex type N-glycans
231	Gal β 1-4GlcNAc β 1-3GalNAc α -sp3	LN3-Tn
232	Gal β 1-4GlcNAc β 1-6GalNAc α -sp3	LN6-Tn
93	Gal β 1-4Glc β -sp4	Terminal galactose
2B	Gal β 1-6Gal	Terminal galactose
1D	Gal β 1-6GlcNAc	Terminal galactose
3	Gal β -sp3	MONOSACCHARIDES
119	Man α 1-2Man β -sp4	DISACCHARIDES
120	Man α 1-3Man β -sp4	DISACCHARIDES
20	Rha α -sp3	MONOSACCHARIDES

Table S4. Tlp3 docking analysis.

Kd [uM]	Arg	Asp	Fu	Gal	GlcN	Glu	Iso	Lys	Mal	Man	Pur	Sia	Thia
Cluster A (ASN 116)	143	469	109	110	98	93	145	248	376	69	399	19	11
Cluster B (ARG 69)	-	851	-	-	-	-	548	574	472	-	515	-	-
Cluster C (ASN 212)	-	-	-	-	-	-	-	-	663	-	552	-	76
Cluster D (PHE 216)	-	731	326	196	161	143	-	-	468	152	567	27	-
Cluster E (GLN 174)	-	-	-	-	250	232	-	-	-	146	608	72	34
Binding energy [kcal/mol]	Arg	Asp	Fu	Gal	GlcN	Glu	Iso	Lys	Mal	Man	Pur	Sia	Thia
Cluster A (ASN 116)	5.25	4.54	5.41	5.40	5.47	5.49	5.24	4.92	4.67	5.67	4.64	6.47	6.75
Cluster B (ARG 69)	-	4.19	-	-	-	-	4.45	4.42	4.54	-	4.49	-	-
Cluster C (ASN 212)	-	4.12	-	-	-	-	-	-	4.34	-	4.44	-	5.62
Cluster D (PHE 216)	-	4.28	4.76	5.06	5.17	5.24	-	-	4.54	5.21	4.43	6.23	-
Cluster E (GLN 174)	-	-	-	-	4.91	4.96	-	-	-	5.23	4.39	5.65	6.10
#conformers	Arg	Asp	Fu	Gal	GlcN	Glu	Iso	Lys	Mal	Man	Pur	Sia	Thia
Cluster A (ASN 116)	1000	530	780	685	550	650	950	950	350	800	400	750	650
Cluster B (ARG 69)	-	55	-	-	-	-	50	50	250	-	200	-	-
Cluster C (ASN 212)	-	-	-	-	-	-	-	-	50	-	150	-	50
Cluster D (PHE 216)	-	315	120	315	400	300	-	-	250	150	150	200	-
Cluster E (GLN 174)	-	-	-	-	50	50	-	-	-	50	50	50	300

Table S5: Summary of chemotactic responses of $\Delta tlp3$, $\Delta tlp2$, $\Delta tlp4$, $\Delta tlp2,4$, $\Delta tlp2,3$, $\Delta tlp3,4$ and $\Delta tlp2,3,4$ strains illustrated as log-changes compared to the wild type. Green indicates ligands identified as chemoattractants (down), red indicates ligands identified as chemorepellents (UP) and yellow indicates ligands that showed no significant difference compared with wild-type strain ($P<0.05$).

Ligands	$\Delta tlp3$ *	$\Delta tlp2$	$\Delta tlp4$	$\Delta tlp2,4$	$\Delta tlp2,3$	$\Delta tlp3,4$	$\Delta tlp2,3,4$
	Depletion assay*	Depletion assay					
Serine		2.0 down	1.5 down	2.7 down	2.2 down	1.5 down	3.1 down
Methionine		1.8 down	1.4 down	1.9 down	1.9 down	2.2 down	2.0 down
Asparagine		1.7 down	2.4 down	2.7 down	1.7 down	2.3 down	3.5 down
Cysteine		1	1.4 down	1.4 down	1	1.3 down	1.9 down
Lysine	1.6 UP	1.4 UP	1.8 down	1.1 down	1.8 UP	1	1.5 UP
Purine	1.2 down	1.2 down	1.1 down	1.4 down	1.4 down	1.3 down	2.6 down
Aspartate	1.9 down	1.7 down	1.1 down	1.7 down	2.3 down	1.8 down	2.9 down
Isoleucine	2.7 down						
Malic acid	2.0 down						
Fumaric acid	2.2 down						
Arginine	1.3 UP						
Glucosamine	2.1 UP						
Thiamine	1.2 UP						
Succinic acid	1.2 UP						
Glucose	1.2 down	1.6 down	1.4 down	1.7 down	1.4 down	1.2 down	2.4 down
Fucose	1.4 down	1.7 down	1.4 down	2.4 down	2.1 down	2.0 down	3.4 down
Galactose	1	1	1	1.1 down	1.1 down	1.1 down	1.4 down
Mannose	1.4 UP	1.2 down	1.0 down	1.4 down	1.2 UP	1.3 UP	1.2 UP
Sialic acid	1.2 UP	1.4 down	1.2 down	1.3 down	1.1 UP	1	1.1 down

Table S6. Microbial strains and plasmids

Strain/plasmid	Description	Reference/source
Bacterial strains/ plasmids		
<i>C. jejuni</i> 11168-O	Wild type (human isolated strain) originally strain 5636/77	[1])
<i>C. jejuni</i> 81116 Δ <i>flaA</i> / <i>flab</i> ⁻	Isogenic mutant of <i>flaA</i> / <i>flab</i>	J.M. Ketley
<i>C. jejuni</i> 11168-O Δ <i>tlp3</i> :: <i>aphA3</i>	Isogenic mutant of <i>tlp3</i>	[2]
<i>C. jejuni</i> 11168-O Δ <i>tlp2</i> :: <i>Er</i> ^R	Isogenic mutant of <i>tlp2</i>	This study
<i>C. jejuni</i> 11168-O Δ <i>tlp4</i> :: <i>Cm</i> ^R	Isogenic mutant of <i>tlp4</i>	This study
<i>C. jejuni</i> 11168- O Δ <i>tlp2</i> :: <i>Er</i> ^R Δ <i>tlp4</i> :: <i>Cm</i> ^R	Isogenic mutant of <i>tlp2</i> and <i>tlp4</i>	This study
<i>C. jejuni</i> 11168- O Δ <i>tlp2</i> :: <i>Er</i> ^R Δ <i>tlp3</i> :: <i>Km</i> ^R	Isogenic mutant of <i>tlp2</i> and <i>tlp3</i>	This study
<i>C. jejuni</i> 11168- O Δ <i>tlp3</i> :: <i>Km</i> ^R Δ <i>tlp4</i> :: <i>Cm</i> ^R	Isogenic mutant of <i>tlp3</i> and <i>tlp4</i>	This study
<i>C. jejuni</i> 11168- O Δ <i>tlp2</i> :: <i>Er</i> ^R Δ <i>tlp3</i> :: <i>Km</i> ^R Δ <i>tlp4</i> :: <i>Cm</i> ^R	Isogenic mutant of <i>tlp2</i> , <i>tlp3</i> and <i>tlp4</i>	This study
<i>C. jejuni</i> 11168- O Δ <i>tlp2</i> :: <i>Er</i> ^R Ω <i>tlp2</i> :: <i>Km</i>	Complemented <i>tlp2</i> ^{+/+} mutant in <i>C. jejuni</i> 11168- O Δ <i>tlp2</i> :: <i>Er</i> ^R	This study
<i>C. jejuni</i> 11168- O Δ <i>tlp4</i> :: <i>Cm</i> ^R Ω <i>tlp4</i> :: <i>Km</i>	Complemented <i>tlp4</i> ^{+/+} mutant in <i>C. jejuni</i> 11168- O Δ <i>tlp4</i> :: <i>Cm</i> ^R	This study
<i>C. jejuni</i> 11168-O Δ <i>tlp3</i> :: <i>aphA3</i> Ω <i>tlp3</i> :: <i>cat</i>	Complemented <i>tlp3</i> ^{+/+} mutant in <i>C. jejuni</i> 11168- O Δ <i>tlp3</i> :: <i>Km</i>	[2,3]
<i>E. coli</i> BL21(DE3)	F ⁻ <i>ompT hsdS_B</i> (r _B ⁻ m _B ⁻) <i>gal dcm</i> (DE3)	Novagen
<i>E. coli</i> DH5α	F ⁻ , ø80dlacZΔM15, Δ(<i>lacZYA-argF</i>)U169, <i>deoR</i> , <i>recA1</i> , <i>endA1</i> , <i>hsdR17</i> (rK ⁻ , mK ⁺), <i>phoA</i> , <i>supE44</i> , λ-, <i>thi-1</i> , <i>gyrA96</i> , <i>relA1</i>	[3]
pGEM-T Easy	Cloning vector	Promega
pET-19b	His-tag expression vector	Novagen
pGU0504	<i>tlp2</i> ^{peri} cloned into pGEM-T Easy	This study
pGU0706	<i>tlp4</i> ^{peri} cloned into pGEM-T Easy	This study
pGU0505	<i>tlp2</i> ^{peri} cloned into pET-19b	This study
pGU0707	<i>tlp4</i> ^{peri} cloned into pET-19b	This study
pGU0816	<i>tlp3</i> ^{peri} cloned into pET-19b	[2]
pGU0817	Tlp3 ^{LBD} K149A	This study
pGU0818	Tlp3 ^{LBD} W151A	This study
pGU0819	Tlp3 ^{LBD} D169A	This study
pGU0820	Tlp3 ^{LBD} T170A	This study
pGU0821	Tlp3 ^{LBD} D196A	This study
pGU0510	Δ <i>tlp2</i> :: <i>Er</i> ^R cloned into pGEM-T Easy	This study

pGU0720	$\Delta tlp4::Cm^R$ cloned into pGEM-T Easy	This study
pGU0817	$\Delta tlp3::Km^R$ cloned into pGEM-T Easy	[2]
pK46 $tlp2$	pK46: $tlp2^{peri}$	This study
pK46 $tlp4$	pK46: $tlp4^{peri}$	This study
pK46	<i>C. jejuni</i> cj0046 pseudogene integration vector; Km ^R	[2,4]

Table S7. Primers used in this study.

Primer name	Sequence 5'-3'	Restriction Site	Reference
Tlp2 ^{LBD} Forward	<u>CATATGCAAGCAATTTCATGAAGTTGTGA</u>	NdeI	This study
Tlp2 ^{LBD} Reverse	<u>CTCGAGTTATAAACTGGAGCTTCTATTGTT</u>	XhoI	This study
Tlp2 Forward	<u>CATATGAAAAGCGTAAAATTG</u>	NdeI	This study
Tlp2 Reverse	<u>CTCGAGTTAAAACCTCTTCTAACATC</u>	XhoI	This study
Tlp2_invMUT Forward	<u>AGATCTCTGCAGCAGCTTAGAAGAG</u>	BglII	This study
Tlp2_invMUT Reverse	<u>AGATCTGCCGCAAGAATATCTACAGC</u>	BglII	This study
Tlp4 ^{LBD} Forward	<u>CTCGAGGATTCGAGAAACAATACATATGAATT</u>	XhoI	This study
Tlp4 ^{LBD} Reverse	<u>CTCGAGTTGTTCATTAATAGAACATACAGC</u>	XhoI	This study
Tlp4 Forward	<u>GGTACCCAATCAATAAATTCAAGG</u>	KpnI	This study
Tlp4 Reverse	<u>CTCGAGTTAAAACCTCTTCTTCTAACATC</u>	XhoI	This study
Tlp4_invMUT Forward	<u>AGATCTCACCAAGGCGTAGATTATGC</u>	BglII	This study
Tlp4_invMUT Reverse	<u>AGATCTTCCAACCCATAGCGTAAGC</u>	BglII	This study
Tlp2Com Forward	<u>ACTCGTCTCATGAAAAGCGTAAAATTG</u>	BsmBI	This study
Tlp2Com Reverse	<u>GTCCGTCTCTTAAACCTCTTCTTCTTAAC</u>	BsmBI	This study
Tlp3 Forward	<u>ATGCTAAAAATAACAAAGATTAAAAG</u>	-	This study
Tlp3 Reverse	<u>AAACCTCTTCTTCTTCTAACATC</u>	-	This study
Tlp4Com Forward	<u>ACTCGTCTCATGCAATCAATAAATTCAAGG</u>	BsmBI	This study
Tlp4Com Reverse	<u>GTCCGTCTCTTAAACCTCTTCTTCTTAACATC</u>	BsmBI	This study
cj0046 Forward	<u>CTCTCTCCGCTAGAAATTAAATCC</u>	-	This study
Ery_ Forward (ErmCBgIII-F)	<u>AGATCTATGAACGAGAAAAATATAAAACACAG</u>	BglII	This study
Ery Reverse (ErmCBgIII-R)	<u>AGATCTTACTTATTAAATAATTATAGCTA</u>	BglII	This study
Chlr Forward	<u>AGATCTATGATGCAATTACAAAGATT</u>	BglII	This study
Chlr Reverse	<u>AGATCTTATTATTCAAGTCTTG</u>	BglII	This study
Kan Forward	<u>AATGGCTAAAATGAGAATATC</u>	-	This study
Kan Reverse	<u>AAACAATTCCAGTAAAAT</u>	-	This study
pC46 Cat Forward	<u>ATGATGCAATTACAAAGATT</u>	-	[2]
pC46 Cat Reverse	<u>TTATTATTCAAGTCTTG</u>	-	[2]
pK46 Kan Forward	<u>AATGGCTAAAATGAGAATATC</u>	-	[2]
pK46 Kan Reverse	<u>AAACAATTCCAGTAAAAT</u>	-	[2]

Table S8 - Supplementary glycan microarray document based on MIRAGE guidelines. DOI:
10.1093/glycob/cww118.

Classification	Guidelines
1. Sample: Glycan Binding Sample	
Description of Sample	<p><u>Sample names:</u> Tlp2,3, and 4 proteins <u>Origin:</u> <i>Helicobacter pylori</i> SS1; produced as a recombinant His -tagged protein in <i>E. coli</i>.</p> <p><u>Method of preparation:</u> The preparation of Tlp2,3, and 4 is explained in the Materials and Methods section: Expression and purification of the periplasmic domain of Tlp2,3, and 4.</p>
Sample modifications	Sample is a His Tagged protein containing only the periplasmic receptor domain of the full length Tlp2,3, and 4 transmembrane protein.
Assay protocol	<p><i>Please see Materials and Methods: Tlps 2/3/4 bind to a range of ligands, including glycans and amino acids</i></p> <p>Proteins were complexed with mouse anti-his antibody, with secondary and tertiary AlexaFluor555 antibodies (rabbit anti-mouse, goat anti-rabbit) at a molar ratio of 4:2:1. The protein/antibody complex was incubated on ice for 10 mins prior to placing on the array. Arrays were performed with 1 µg of complexed protein incubated on the array for 20 min. Arrays were then washed 3 times in Array PBS (PBS + 2mM MgCl₂ + 2mM CaCl₂) then dried by centrifugation for 3 min at 300 x g. Scanning was performed using an Innopsys InnoScan 1100AL and analyzed using Mapix (Innopsys). Yes/no binding was determined by six positive replicate spots in three replicate experiments. Positive binding was determined by spots being significantly greater than negative control spots by two-tailed <i>t</i> test.</p>
2.1 Glycan Library	
Glycan description for defined glycans	Glycans in this study are listed in Table S2 and is a published library in doi: 10.1371/journal.pntd.0004120.
Glycan description for undefined glycans	N/A.
Glycan modifications	<p>Glycans were prepared in one of two ways for printing:</p> <p>1. Glycans (with IDs in number/letter format; e.g. 1A, 4C, 7K) were sourced commercially from Dextra Laboratories, Elicityl and CarboSynth and were made into glycoamines using the protocol published in Day et al 2009 (doi: 10.1371/journal.pone.0004927).</p>

	2. Glycans (with IDs in number only format) were obtained from Prof Nicolai Bovin and were modified with spacers as per DOI: 10.1073/pnas.0407902101. The library of these glycans was first published in DOI: 10.1016/j.molimm.2009.06.010
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2.2 Small molecule Library

Sample description for defined compounds	Compounds printed in the amino acid/small molecule array for this study are listed in Table1 and Table S5.
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3. Printing Surface; e.g., Microarray Slide

Description of surface	Epoxy activated glass microarray slides.
Manufacturer	ArrayIt SuperEpoxy 3 (SME3).
Custom preparation of surface	N/A.
Non-covalent Immobilisation	N/A.

4. Arrayer (Printer)

Description of Arrayer	Glycan array: SpotBot® Extreme Protein Microarray Spotter (ArrayIt, California, USA). Small molecule array: ArrayJet Argus Marathon non-contact printer.
Dispensing mechanism	Glycan array: Contact printing using 946NS6 pins with a 6 pin in a 3 columns x 2 rows configuration. Small molecule array: Non-contact jet printing
Glycan and small molecule deposition	Glycan array: Approximately 1.8 nl per spot is printed according to manufacturers guidelines. Glycan were at 500 µM in 50:50 DMF:DMSO. Small molecule array: Approximately 320 nl per spot is printed according to manufacturers guidelines. Samples were at 1000 µM in PBS with 2% glycerol
Printing conditions	Glycan array: Array were printed with dehumidification at a maximum humidity of 60% relative humidity (Standard laboratory starting humidity of 75-90%) at 22°C. Glycans were left to react with the slide for at least 8 hours after the print was completed. Small molecule array: Array were printed with dehumidification at a maximum humidity of 60% relative humidity (Standard laboratory starting humidity of 75-90%) at 22°C. Samples were left to react with the slide for at least 15 hours after the print was completed.

5.1 Glycan array with “Map”

Array layout	The array consists of a single array of glycans split between 6 pins (3 columns x 2 rows) with 4500µm row and column spacing. Each pin printed a 20 columns x 16 rows with 200µm spot spacing (centre to centre) with a minimum spot size of 100µm. Each sample is printed in quadruplicate with each of the 6 print areas including at least three negative control samples (print solution only) and two positive control samples consisting of one sample of fluorosciename and one sample of a mixture of rabbit anti-mouse antibody labeled with Alexa 555 and Alexa 647. Positive controls provide proof of successful immobilization of the amine reagents and provides for orientation for analysis. The antibodies also can provide controls for secondary antibodies used in experiments (if applicable).
Glycan identification and quality control	Arrays are quality controlled by a range of measures. 1. Each printed array is post print scanned to confirm deposition of the glycans on the array surface prior to neutralization of the remaining slide surface. 2. Post neutralized slides are scanned again to monitor for remaining autofluorescence. 3. Slides are assayed with fluorescently labeled lectins: WGA-Texas Red (EY Laboratories) and ConA-FITC (EY Laboratories).

5.2 Small molecule array with “Map”

Array layout	The array consists of triplicate sub-arrays of amino acids and small molecules (24 rows x 10 columns) with 400µm spot spacing (centre to centre) with a minimum spot size of 100µm. Each sample is printed six times, with each of the 3 sub-arrays including at least six negative control samples (print solution only) and a positive control samples consisting of one a mixture of rabbit anti-mouse antibody labeled with Alexa 555 and Alexa 647. Positive controls provide proof of successful immobilization of the amine reagents and provides for orientation for analysis.
Sample identification and quality control	Arrays are quality controlled by a range of measures. 1. Each printed array is post print scanned to confirm deposition of the samples on the array surface prior to neutralization of the remaining slide surface. 2. Post neutralized slides are scanned again to monitor for remaining autofluorescence.

6. Detector and Data Processing

Scanning hardware	Innopsys InnoScan 1100AL (Lasers: 488 nM, 532 nM with two filter sets for analysis at 532 and 595 nM), 635 nM) scanner.
Scanner settings	Scanning resolution: 10µM Laser channel: 532nM operating 595nM excitation / 625nM emission filter set. PMT: 20% gain Scan powers: Low laser power.
Image analysis software	Innopsys MAPIX.
Data processing	Data was exported as a CSV file and exported to Microsoft Excel.

7. Glycan Microarray Data Presentation

Data presentation	Glycan array: Data is presented as yes/no binding in Table 1. The full list of glycans is shown in Table S5.
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8. Interpretation and Conclusion from Microarray Data

Data interpretation	<p>Glycan arrays: We only use glycan arrays as a yes/no binding tool. Due to this we look only at binding that is unambiguously above background vs lack of binding above background. Average background + 3x standard deviation of the background of 20 sets of 4 spots of DMF:DMSO only spots is applied to determine if binding observed is significantly above background. Only spots with values equal to or greater than this value were considered as binding from data of any tested slide. These values are slide dependent.</p> <p>Small molecule arrays: We only use amino acid arrays as a yes/no binding tool. Due to this we look only at binding that is unambiguously above background vs lack of binding above background. Average background + 3x standard deviation of the background of 6 spots of PBS + 2% glycerol only spots is applied to determine if binding observed is significantly above background. Only spots with values equal to or greater than this value were considered as binding from data of any tested slide. These values are slide dependent.</p>
Conclusions	Tlp2, Tlp3 and Tlp4 are a parologue family of dCache_1 chemoreceptors which capable of responding to carbohydrates including complex glycans as well as to organic and amino acids

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