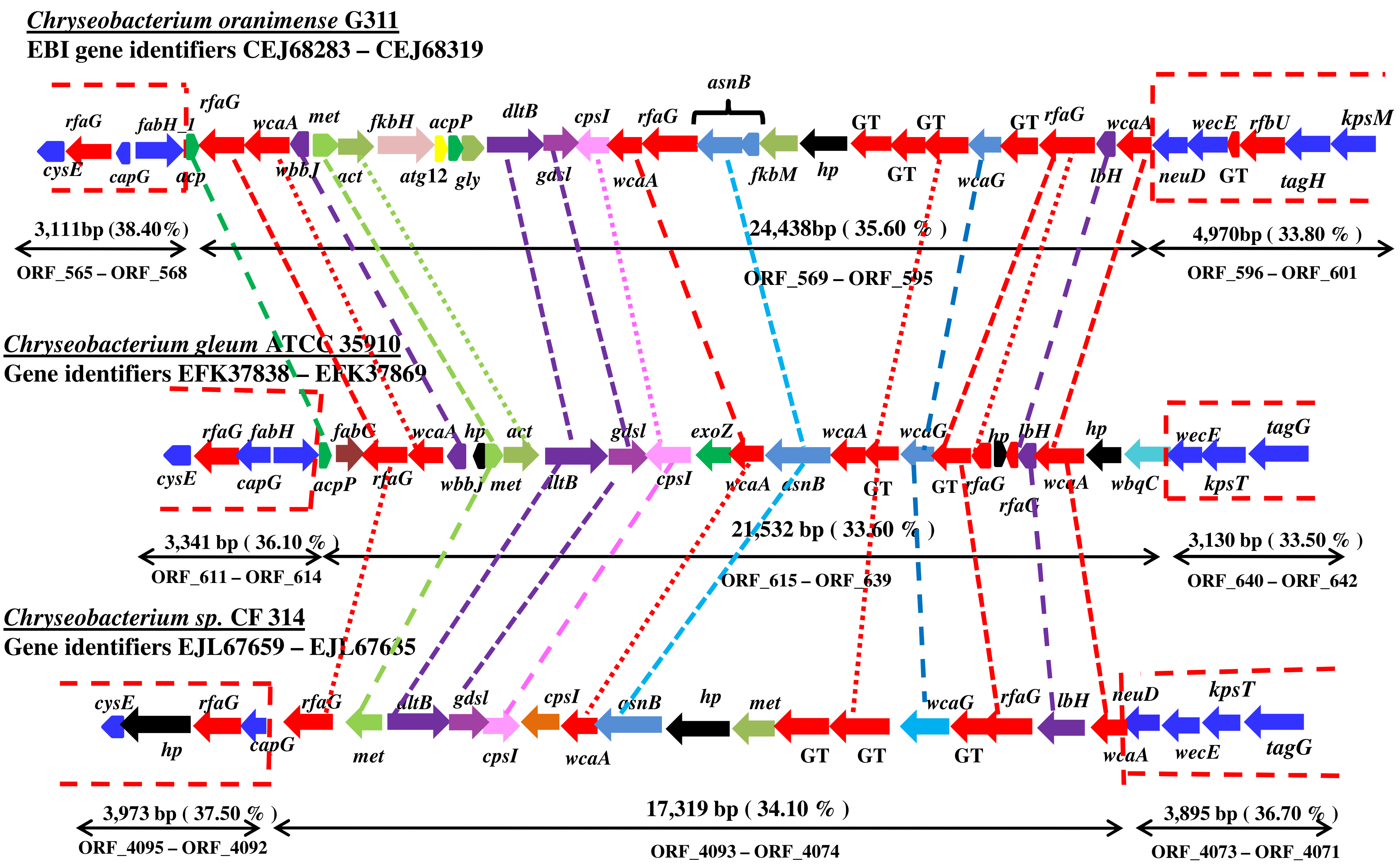
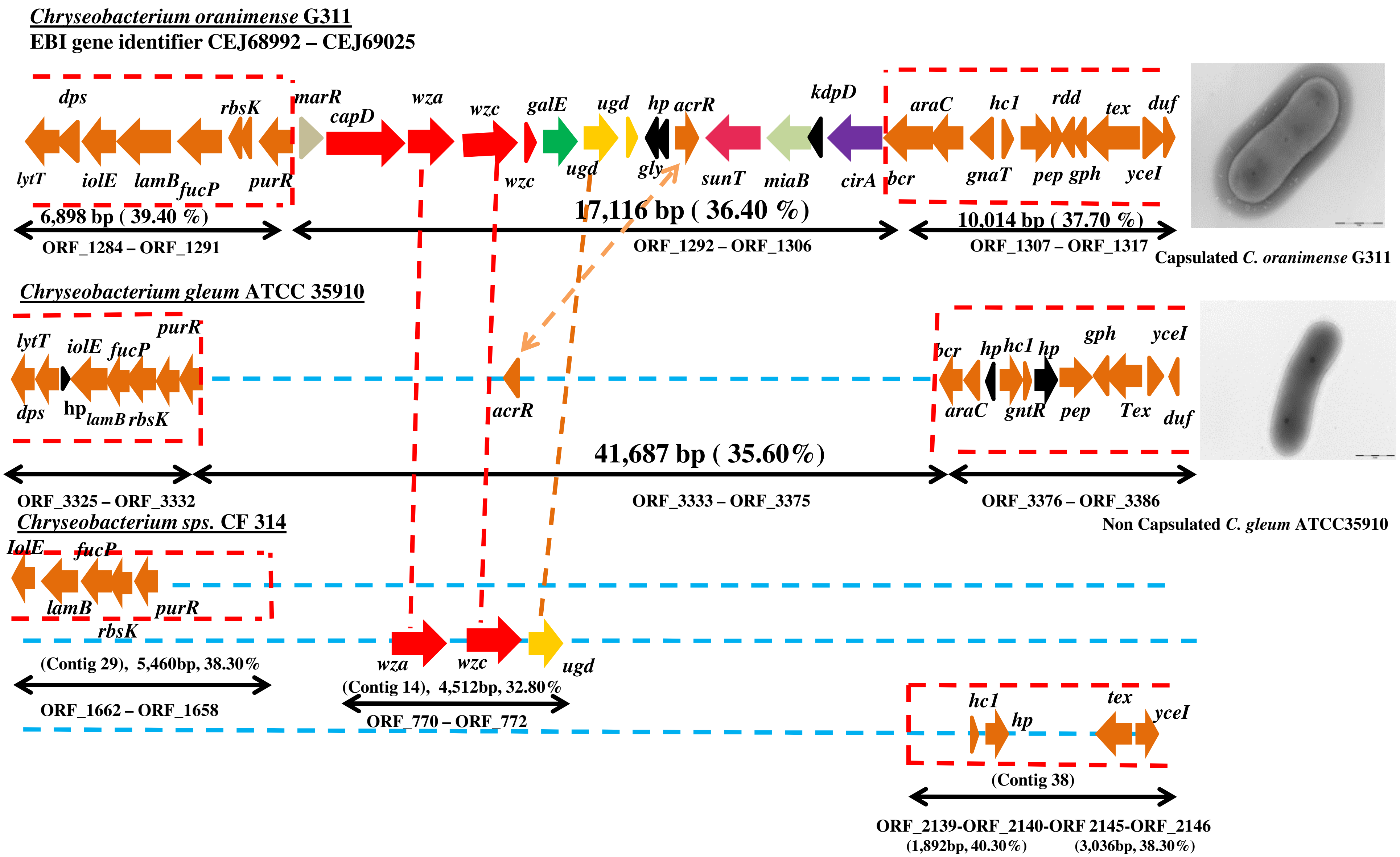


Supplementary Figure S1. Organization of the O-antigen gene cluster in the *Chryseobacterium oranimense* G311, *Chryseobacterium gleum* ATCC35910 and *Chryseobacterium sp.* CF314 genomes



Supplementary Figure S2. Organization of the capsular biosynthetic machinery (K-antigen) of *C. oranimense* G311 in comparison to the *Chryseobacterium gleum* ATCC35910 and *Chryseobacterium sp.* CF 314 genomes along with Gram staining image (Chryseobacterium sp. CF 314 strain – not available)

Supplementary Table S1: Distribution of Cluster of Orthologous Genes (COG) categories in *Chryseobacterium oranimense* G311 genome

COG Code	Colour	Description	Value	Total
A	🟦	RNA processing and modification	1	0.032
B	🟪	Chromatin structure and dynamics	0	0
C	🟪	Energy production and conversion	153	4.982
D	🟪	Cell cycle control, mitosis and meiosis	20	0.651
E	⬛	Amino acid transport and metabolism	245	7.977
F	🟥	Nucleotide transport and metabolism	71	2.311
G	⬜	Carbohydrate transport and metabolism	174	5.665
H	🟥	Coenzyme transport and metabolism	144	4.689
I	🟥	Lipid transport and metabolism	143	4.656
J	⬛	Translation	171	5.568
K	🟦	Transcription	243	7.912
L	🟦	Replication, recombination and repair	150	4.884
M	🟦	Cell wall/membrane biogenesis	239	7.782
N	🟩	Cell motility	12	0.390
O	🟫	Posttranslational modification, protein turnover, chaperones	108	3.516
P	🟪	Inorganic ion transport and metabolism	180	5.861
Q		Secondary metabolites biosynthesis, transport and catabolism	76	2.474
R	🟦	General function prediction only	414	13.481
S	🟨	No functional prediction	257	8.368
T	🟩	Signal transduction mechanisms	157	5.112
U	🟧	Intracellular trafficking and secretion	49	1.595
V	🟨	Defense mechanisms	63	2.051
W	🟪	Extracellular structures	0	0
Y	⬛	Nuclear structure	0	0
Z	🟦	Cytoskeleton	1	0.032

Supplementary Table S 2: List of the genes of the chromosomal O-antigen-like cluster in *Chryseobacterium oranimense* G311, *Chryseobacterium gleum* ATCC 35910 and *Chryseobacterium sp.* CF314 and the K-antigen chromosomal cluster of *Chryseobacterium oranimense* G311 and *Chryseobacterium gleum* ATCC 35910

Gene	ORF/EBI Gene identifier	Gene Name	Length (aa)	Function
O - antigen chromosomal cluster of *Chryseobacterium oranimense* G311				
Gene_1	565/CEJ68283	*cysE*	121	Serine acetyltransferase-like protein
Gene_2	566/CEJ68284	*rfaG*	383	Glycosyl transferase, group 1
Gene_3	567/CEJ68285	*capG*	187	Acetyltransferase
Gene_4	568/CEJ68286	*fabH*	324	3-Oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.41)
Gene_5	569/CEJ68287	*acp*	77	Acyl-carrier-protein
Gene_6	570/CEJ68288	*rfaG*	389	Glycosyl transferase, group 1
Gene_7	571/CEJ68289	*wcaA*	279	Glycosyl transferase, family 2
Gene_8	572/CEJ68290	*wbbJ*	180	Maltose O-acetyltransferase
Gene_9	573/CEJ68291	*met*	256	O-Methyltransferase
Gene_10	574//CEJ68292	*act*	342	Acyltransferase 3
Gene_11	575/CEJ68293	*fkbH*	575	Methoxymalonyl-ACP-acid phosphatases

Gene_12	576/CEJ68294	*atg*12	51	Ubiquitin-like protein *atg*12
Gene_13	577/CEJ68295	*acpP*	79	Acyl carrier protein
Gene_14	578/CEJ68296	*gly*	125	Lactoylglutathione lyase
Gene _15	579/CEJ68297	*dltB*	471	O-acetyltransferase
Gene _16	580/CEJ68298	*gdsl*	307	Lipase GDSL, hydrolase family
Gene_17	581/CEJ68299	*cpsI*	312	Capsular polysaccharide biosynthesis protein *cpsI*
Gene_18	582/CEJ68300	*wcaA*	311	Glycosyltransferase/ capsular polysaccharide biosynthesis protein *cpsI*
Gene_19	583/CEJ68301	*rfaG*	382	Glycosyltransferase, group 1
Gene_20	584/CEJ68302	*asnB*	360	Asparagine synthetase
Gene_21	585/CEJ68303	*asnB*	168	Asparagine synthetase
Gene 22	586/CEJ68304	*fkbM*	272	Methyltransferase
Gene_23	587/CEJ68305	hp	379	Hypothetical protein
Gene_24	588/CEJ68306	GT	320	Glycosyltransferase, family 1
Gene_25	589/CEJ68307	GT	262	Glycosyltransferase, family 2
Gene_26	590/CEJ68308	GT	316	Glycosyl transferase, family 2
Gene_27	591/CEJ68309	*wcaG*	222	NDP-hexose 4-ketoreductase
Gene_28	592/CEJ68310	GT	287	Glycosyltransferase, group 2

Gene_29	593/CEJ68311	*rfaG*	394	Glycosyltransferase, family 2
Gene_30	594/CEJ68312	*lbH*	198	Exopolysaccharide biosynthesis protein, acetyltransferase *lbH*_MAT like
Gene_31	595/CEJ68313	*wcaA*	292	Glycosyltransferase, family 2
Gene_32	596/CEJ68314	*neuD*	209	Putative acyltransferase
Gene_33	597/CEJ68315	*wecE*	360	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase
Gene_34	598/CEJ68316	GT	50	Glycosyltransferase, LPS biosynthesis protein
Gene_35	599/CEJ68317	*rfbU*	368	LPS biosynthesis protein
Gene_36	600/CEJ68318	*tagH*	395	ATP-binding protein
Gene_37	601/CEJ68319	*kpsM*	280	Polysialic acid transport protein

O-antigen chromosomal cluster of *Chryseobacterium gleum* ATCC 35910

Gene_1	611/EFK37838	*cysE*	185	Serine acetyltransferase-like protein
Gene_2	612/EFK37839	*rfaG*	383	Glycosyl transferase, family 1
Gene 3	613/EFK37840	*capG*	190	Capsular polysaccharide biosynthesis protein *capG*
Gene_4	614/EFK37841	*fabH*	323	3-Oxoacyl-ACP synthase
Gene_5	615/EFK37842	*acpP*	77	Acyl carrier protein
Gene_6	616/EFK37843	*fabG*	252	3-Oxoacyl-[acyl-carrier-protein] reductase

Gene_7	617/EFK37844	*rfaG*	386	Glycosyltransferase, Group 1
Gene_8	618/EFK37845	*wcaA*	278	Glycosyltransferase, Group 2
Gene_9	619/EFK37846	*wbbJ*	181	Exopolysaccharide biosynthesis protein
Gene_10	620/EFK37847	hp	43	Hypothetical protein
Gene_11	621/EFK37848	*met*	256	O-Methyltransferase
Gene_12	622/EFK37849	*act*	342	Acetyltransferase 3 COG 1835
Gene_13	623/EFK37850	*dltB*	477	O-Acetyltransferase
Gene _14	624/EFK37851	*gdsl*	305	Lipase GDSL (Hydrolase family)
Gene _15	625/EFK37852	*cpsI*	313	Capsular polysaccharide biosynthesis protein *cpsI*
Gene_16	626/EFK37853	*exoZ*	332	Acetyltransferase, exopolysaccharide biosynthesis protein *exoZ*
Gene_17	627/EFK37854	*wcaA*	312	Glycosyltransferase/ Capsular polysaccharide biosynthesis protein CpsI
Gene_18	628/EFK37855	*asnB*	598	Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4)
Gene_19	629/EFK37856	*wcaA*	307	Glycosyltransferase, family 2
Gene_20	630/EFK37857	GT	306	Glycosyl transferase, family 2
Gene_21	631/EFK37858	*wcaG*	222	NAD-dependent epimerase/dehydratase
Gene 22	632/EFK37859	GT	289	Glycosyl transferase, group 2

Gene_23	633/EFK37860	*rfaG*	179	Glycosyltransferase, family 2
Gene_24	634/EFK37861	hp	45	Hypothetical protein
Gene_25	635/EFK37862	*rfaG*	125	Glycosyltransferase, Group 1
Gene_26	636/EFK37863	*lbH*	199	Exopolysaccharide biosynthesis protein, acetyltransferase *lbH*_MAT like
Gene_27	637/EFK37864	*wcaA*	457	Glycosyl transferase, family 2
Gene_28	638/EFK37865	hp	317	Hypothetical protein
Gene_29	639/EFK37866	*wbqC*	238	Putative glycine transferase in O-antigen biosynthesis cluster
Gene_30	640/EFK37867	*wecE*	360	Aminotransferase *degT*
Gene_31	641/EFK37868	*kpsT*	398	ABC transporter ATP-binding protein, *wzt*-like
Gene_32	642/EFK37869	*tagG*	280	ABC superfamily ATP-binding cassette transporter permease protein
O-antigen chromosomal cluster of *Chryseobacterium sp.* CF314				
Gene_1	4095/EJL67659	*cysE*	185	Serine acetyltransferase-like protein
Gene_2	4094/EJL67658	hp	403	Hypothetical protein
Gene 3	4093/EJL67657	*rfaG*	383	Glycosyltransferase, family 1
Gene_4	4092/EJL67656	*capG*	187	Capsular polysaccharide biosynthesis protein *capG*

Gene_5	4091/EJL67655	*rfaG*	385	Glycosyltransferase, family 1
Gene_6	4090/EJL67654	*met*	257	O-Methyltransferase
Gene_7	4089/EJL67653	*dltB*	477	O-Acetyltransferase
Gene_8	4088/EJL67652	*gdsl*	296	Hypothetical protein
Gene_9	4087/EJL67651	*cpsI*	315	Capsular polysaccharide biosynthesis protein *cpsI*
Gene_10	4086/EJL67650	*cpsI*	313	Capsular polysaccharide biosynthesis protein *cpsI*
Gene_11	4085/EJL67649	*wcaA*	312	Glycosyltransferase/capsular polysaccharide biosynthesis protein *cpsI*
Gene_12	4084/EJL67648	*asnB*	598	Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4)
Gene_13	4083/EJL67647	hp	531	Hypothetical protein
Gene _14	4082/EJL67646	*met*	261	Methyltransferase
Gene _15	4081/EJL67645	GT	307	Glycosyltransferase, family 2
Gene_16	4080/EJL67644	GT	306	Glycosyltransferase, family 2
Gene_17	4079/EJL67643	*wcaG*	222	NAD-dependent epimerase/Dehydratase
Gene_18	4078/EJL67642	GT	290	Glycosyl transferase, group 2
Gene_19	4077/EJL67641	*rfaG*	394	Glycosyltransferase, group 1
Gene_20	4076/EJL67640	*lbH*	196	Exopolysaccharide biosynthesis acetyltransferase *lbH*_MAT like

Gene 21	4075/EJL67639	*wcaA*	301	Glycosyltransferase, family 2
Gene_22	4074/EJL67638	*neuD*	211	Hexapeptide transferase / Sugar O-acyltransferase *nueD*
Gene_23	4073/EJL67637	*wecE*	360	Aminotransferase *degT*
Gene_24	4072/EJL67636	*kpsT*	419	ABC transporter ATP-binding protein *wztC*
Gene_25	4071/EJL67635	*tagG*	282	ABC superfamily ATP binding cassette transporter permease protein
K-antigen chromosomal cluster of *Chryseobacterium oranimense* G311				
Gene _1	1284/CEJ68992	*lytT*	231	DNA-binding response regulator
Gene_2	1285/CEJ68993	*dps*	157	Non-specific DNA-binding protein *dps* / Iron-binding ferritin-like antioxidant protein / Ferroxidase (EC 1.16.3.1)
Gene_3	1286/CEJ68994	*iolE*	279	D-tagatose 3-epimerase
Gene_4	1287/CEJ68995	*lamB*	469	Maltoporin
Gene_5	1288/CEJ68996	*fucP*	414	Fucose permease
Gene_6	1289/CEJ68997	*rbsK*	128	Fructokinase (EC 2.7.1.4)
Gene_7	1290/CEJ68998	*rbsK*	176	Fructokinase (EC 2.7.1.4)
Gene_8	1291/CEJ68999	*purR*	335	Periplasmic binding protein/*LacI* transcriptional regulator
Gene_9	1292/CEJ69000	*marR*	153	Transcriptional regulator, *marR* family
Gene_10	1293/CEJ69001	*capD*	637	UDP-N-acetylglucosamine 4,6-dehydratase

Gene_11	1294/CEJ69002	*wza*	263	Polysaccharide export outer membrane protein
Gene_12	1295/CEJ69003	*wzc*	692	Tyrosine-protein kinase Wzc (EC 2.7.10.2)
Gene_13	1296/CEJ69004	*wzc*	85	Tyrosine-protein kinase Wzc (EC 2.7.10.2)
Gene_14	1297/CEJ69005	*galE*	322	UDP-glucose 4-epimerase (EC 5.1.3.2)
Gene_15	1298/CEJ69006	*ugd*	231	UDP-glucose dehydrogenase (EC 1.1.1.22)
Gene_16	1299/CEJ69007	*ugd*	199	UDP-glucose dehydrogenase (EC 1.1.1.22)
Gene_17	1300/CEJ69008	gly	104	Glyoxalase
Gene_18	1301/CEJ69009	hp	67	Hypothetical protein
Gene_19	1302/CEJ69010	*acrR*	209	Transcriptional regulator, TetR family
Gene_20	1303/CEJ69011	*sunT*	727	ABC transporter ATP-binding protein
Gene_21	1304/CEJ69012	*miaB*	423	Putative RNA methylase
Gene_22	1305/CEJ69013	*kdpD*	50	Histidine kinase
Gene_23	1306/CEJ69014	*cirA*	792	TonB-dependent receptor
Gene_24	1307/CEJ69015	*bcr*	404	Multidrug transporter
Gene_25	1308/CEJ69016	*araC*	315	Transcriptional regulator, AraC family
Gene_26	1309/CEJ69017	*gnaT*	171	GCN5-related N acetyltransferase
Gene_27	1310/CEJ69018	*hc1*	58	Histone protein

Gene_28	1311/CEJ69019	*pep*	445	Peptidase M 28 family
Gene_29	1312/CEJ69020	*pep*	50	Peptidase M28
Gene_30	1313/CEJ69021	*rdd*	196	RDD domain-containing protein
Gene_31	1314/CEJ69022	*gph*	217	5'-methylthioadenosine nucleosidase (EC 3.2.2.16) / S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)
Gene_32	1315/CEJ69023	*tex*	707	RNA-binding domain
Gene_33	1316/CEJ69024	*yceI*	225	Rhodanese-like domain protein
Gene_34	1317/CEJ69025	*duf*	91	Protein of unknown function DUF1294 – cold shock protein