Region	From	Ent638_	to	Ent638_	size	ORFs	int	tnp	Repeat on ext.	prophage	tRNA	alternat. codon matrix	Synteny with K12	Synteny with 342	Synteny with 568	Gene content
1	37506	0034	83855	0066	46349	35	-	+	+	-	tRNA-Sec	+	-	+/- (*)	+/- (*)	transporter for sugar uptake (PTS lactose family), Beta-glucosidase (conversion of cellobiose into glucose or glucoside into glucose), filamentous haemagglutinin, transporter (MFS family), Predicted Zn-dependent hydrolases, ORFs of unknown function
2	93676	0074	103614	0086	9938	13	-	-	-	-	-	-	-	-	-	Fimbriae biosynthesis
3	124182	0108	132857	0114	8675	7	-	-	-	-	-	-	-	-	-	Putative membrane-associated metal-dependent hydrolase, Glycosyltransferase
4	166537	0147	169882	0148	3345	3	-	-	-	-	-	-	-	-	-	Hemolysin activation/secretion protein
5	205544	0179	212385	0183	6841	8	-	-	+	-	tRNA-Pro	-	-	-	-	Rhs, peptidoglycan-binding (LysM), several partial duplication
6	332190	283	335579	286	3389	18	-	-	-	-	-	-	-	+	+	Fructokinase, fructose biphoasphate aldolase
7	364148	0317	373015	0321	8867	5	-	-	+	-	tRNA-Phe	-	-	-	-	Nickel chelation for upake or usage as cofactor, Outer membrane autotransporter with Pectin lyase fold/virulence factor (adhesin)
8	436726	0385	441897	0391	5171	7	-	-	-	-	-	-	-	-	-	Regulator, FMN-dependent NADH-azoreductase 2, Protein of unknown function, Antibiotic resistance
9	454627	0401	464073	0410	9446	11	-	-	-	-	-	-	+/-	-	+	Fimbriae biosynthesis for adhesion/virulence, genes duplicated
10	477929	0423	487952	0435	10023	12	-	-	-	-	-	-	-	+	+	Cytochrome, regulator, unknown function, dihydroorotase (peptidase), putative selenocysteine synthase L-seryl-tRNA(Ser) selenium transferase (Pyridoxal phosphate-dependent)
11	523760	0463	573310	0506	49550	43	+	-	-	-	tRNA-Leu	+	-	-	-	Integrase, phage protein, DNA repair (Dnd proteins), plasmid stabilization system, pectate lyase, oligogalacturonate-specific porin (KdgM), protease, possible anti-oxydant, regulators, autotransporter/filamentous haemagglutinin/adhesin, regulator, trancriptionnal regulator involved in virulence, system de secretion, possibly secretion of virulence factor
12	642565	572	648283	576	5718	5	-	-	-	-	-	-	-	+	+/-	Iron-hydroxymate transporter (MFS and ABC family)
13	852653	0750	860429	0756	7776	7	-	-	-	-	tRNA-Asp	-	-	-	-	Regulator, ABC transporter for amino acids
14a	875620	0770	912564	820	59647	50	+	-	+	Phage 1	tRNA-Thr	+	-	-	-	Integrase, phage proteins
14b	912987	821	935267	0837		10					-		-	-	-	Transduction with Phage 1: alpha/beta hydrolase, fimbrial protein, amino acid transporter, methylatransferase, two component sensor/regulator, permease, S-methylmethionine transporter, S-methylmethionine: homocysteine methyltransferase, haemolysin co-regulated protein (HCP), ferric ABC transporter (syntenic with K12), integrase

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15	1027052	0924	1042473	0937	15421	15	-	-	-	-	+	-	**+/-**	+	-	Regulator, lactose degradation (syntenic with K12), signal transduction (domain EAL), transporter (beta-glucoside PTS family)
16a	1107864	0996	1154361	1055	46497	59	+	-	-	Phage 2	tRNA-Arg	+	**-**	-	-	Phage integrase, phage proteins
16b	1154789	1056	1223024	1114	68235	58					-		**-**	+	+/-	Transduction with Phage 2: Putative TonB-dependent siderophore receptor, phenylalanine transporter, Nucleoside:H+ symporter, Transcriptional regulator (LacI, XRE, TetR, LysR, GntR), permease (MFS family), fimbriae, dihydropteridine reductase, metallo-hydrolase/oxidoreductase, Ferrichrysobactin TonB dependent siderophore receptor, Enterochelin esterase, P-type ATPase transporter, RND transporter, Ribosomal large subunit pseudouridine synthase A, Putative cold-shock DNA-binding domain protein, TonB-dependent receptor, ABC transporter for amino acids, GCN5-related N-acetyltransferase, ABC transporter for chelated iron (SitABCD)
17	1248443	1135	1258304	1143	9861	8	-	-	-	-	-	-	**+/-**	+	+	ABC transporter Ribose uptake, ribose kinase, Methionine metabolism
18	1386002	1260	1392280	1264	6278	5	-	-	-	-	-	-	**-**	+	+	Histidine degradation (*hutIGCUH*)
19	1433737	1306	1438417	1309	4680	5	-	-	-	-	-	-	**-**	+	-	Aldoketo-oxidoreductase, Glycoside hydrolase (family 1), Transporter (PTS lactose/cellobiose family, IIC subunit), Transcriptional regulator (GntR)
20	1441382	1312	1446428	1314	5046	3	-	-	-	-	-	-	**-**	+	+	Alpha-glucosidases (glycosyl hydrolases family 31), Hexuronate transporter, Periplasmic binding protein/LacI transcriptional regulator
21	1472316	1338	1492323	1361	20007	23	+	-	-	Phage 3	tRNA (rybB)	+	**-**	-	-	Putative Fucose 4-O-acetylase and related acetyltransferases, phage proteins, putative TonB-dependent siderophore receptor
22	1533390	1400	1544126	1406	10736	7	-	-	+	-	-	+	**-**	-	-	Crispr associated protein
23	1639354	1484	1691939	1538	52585	29	-	-	+	-	tRNA-Ser	+/-	**-**	+/- (*)	-	Cyclopropane-fatty-acyl-phospholipid synthase, Amine oxidase, transporter (MFS), transcriptional regulator, Glycosyltransferase, Methionine aminopeptidase (MAP) (Peptidase M), arylsulfatase : sulfur metabolism, alternative pyrimidine degradation pathway, autotransporter/Filamentous haemagglutinin/Adhesin (fragments), IS transposase (family IS110), Chloramphenicol acetyltransferase (CAT), alternative pyrimidine degradation pathway
24	1804662	1650	1812852	1661	8190	12	+	-		Phage 4	-	+	**-**	-	- (*)	Phage proteins

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25	1886255	1737	1892165	1742	5910	6	-	-	-	-	-	-	**-**	+	+	TonB-dependent heme/hemoglobin receptor family protein for iron uptake
26	1929035	1775	1937050	1781	8015	7	-	-	-	-	tRNA-Val	-	**-**	+/- (*)	+/- (*)	Autotransporter for adhesion, ABC transporter system for amino acid/glutamine uptake, Putative metal-dependent RNase, consists of a metallo-beta-lactamase domain and an RNA-binding KH domain, carbonic anhydrase
27	2000083	1841	2001815	1843	1732	4	+	-	-	-	-	+	**-**	-	-	Phage integrase (fragment), incomplete phage inserted into a two component sensor/regulator (RstAB)
28	2015509	1858	2072420	1909	56911	51	-	-	-	-	-	+	**-**	-	-	Chemotaxis/mobility?, Autotransporter adhesin/invasin-like protein (YadA), Antibiotic biosynthesis, RND efflux system nodulation?, RND efflux system drug resistance, Unknown function but small possible legume lectin, beta domain for attachement, MFS transporter, lysophospholipase, coagulase/fibrinolysin, Phage regulator, SOS response
29	2115297	1949	2225046	2051	109749	103	-	-	+	-	-	-	**+/-**	+	+/-	RND transporter, Pectin acetylesterase, Many gene involved in amino acid transport, Many transcriptional regulator, Putative IAA acetyltransferase, sucrose/fructose utilisation with PTS from the beta-glc family, synthesis of acetoin periplasmic disulfide isomerase/thiol-disulphide oxidase (DsbG), depolymerisation of alginates, many transporters and many regulators
30	2260061	2081	2272628	2096	12567	16	-	-	+	-	-	-	**+/-**	+	+/-	Glutamate ABC transporter, Amino acid ABC transporter, Chemiotaxis : aerotaxis
31	2285577	2108	2302826	2119	17249	12	-	-	-	-	-	-	**-**	-	+/- (*)	Virulence proteins SrfA, methionine synthase, Polygalacturonase, pectate lyase (secreted), chondroitin AC/alginate lyase, together with pectate lyase important for colonisation (secreted), putative hydrolase (secreted), Transcriptional regulator, Chemiotaxis : aerotaxis
32a	2405497	2214	2451788	2269	65162	55	+	-	-	Phage 5	-	+	**-**	-	-	Phage, phage integrase
32b	2451959	2270	2470659	2294		24					-		**-**	-	-	Transduction with Phage 6: GCN5-related N-acetyltransferase, Transcriptional regulator (TetR), N-ethylmaleimide reductase, Oxidoreductase, permease/transporter, dehydrogenase, putative intracellular septation protein involved in cell division, hydrolase, membrane spanning TonB, 2-dehydropantoate, Putative drug/metabolite exporter (DMT family),

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33	2504012	2320	2519110	2329	15098	10	+	-	+	-	-	-	-	+	+	Integrase, nitrate reductase (NasA), nitrate reductase (NasB), nitrate transport (NrtCBA), region flanked by the *nar* operon involved in nitrate reduction and nitrate/nitrite transport
34	2534142	2346	2547263	2356	13121	11	-	-	-	-	-	-	-	-	-	oxidoreductase, Amino acid ABC transporter, purine ribonuclease efflux, trehalase (trehalose degradation), tonB-dependent siderophore
35	2652901	2458	2661174	2464	8273	7	+	-	+	-	-	-	-	-	+	integrase, fimbria/pili (located next to chemotaxis genes and fimbria genes)
36	2706828	2510	2720695	2521	13867	12	-	-	-	-	-	-	-	-	-	Acyl-CoA reductase (LuxC) and Acyl-protein synthetase (LuxE) which are substrat for light production by luciferase, Transketolase, fatty acid biosynthesis
37a	2747355	2553	2783747	2578	36392	25							-	+	-	Transduction with Phage 7: Outer membrane protein N, N-acetylmuramic acid 6-phosphate etherase, Two-component sensor/regulator, Thiamine biosynthesis lipoprotein, Putative NADH:flavin oxidoreductase, Tartrate transporter, anaerobic class I fumarate hydratase, regulators (for cysteine biosynthesis and nitrogen assimilation), P1-type ATPase, Universal stress protein G, transporter (RND), Putative acyltransferases, palmitoyl transferase for Lipid A, shikimate transporter, AMP nucleosidase, Aminopeptidase P, four tRNA-Asn locus, DNA gyrase inhibitor D-alanyl-D-alanine carboxypeptidase
37b	2784850	2579	2824258	2626	39408	49	+	-	-	Phage 6	tRNA-Asn	+	-	-	-	Phage integrase, phage proteins
38	2847062	2647	2851589	2650	4527	4	-	-	-	-	-	-	-	-	-	LPS biosynthesis
39	2902726	2690	2935856	2719	33130	30	-	-	-	-	-	+	-	+/- (*)	+/- (*)	glutathione peroxidase, phosphorilation of lipid, amino acid ABC transporter, diaminobutyrate catabolism, tyrosine kinase, phosphatase
40	3125655	2887	3162212	2916	36557	30	+	-	-	-	tRNA-Arg	+	-	+	-	Putative integrated plasmid: phage integrase, plasmid function, phage integrase, surface reorganisation resulting in increased adherence and increased conjugation frequency
41	3236067	2980	3241398	2983	5331	4	-	+	-	-	-	-	-	-	-	Transposase (IS481), Transporter (PTS Lactose family), Asparaginase, leucyl amidopeptidase
42	3253890	2994	3259362	2997	5472	4	-	-	-	-	-	-	-	+	-	Transcriptional regulator, MFS transporter, beta-xylosidase, Xyloside transporter

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43a	3375316	3101	3420151	3112	3386099	11	+	-	-	Phage 7	tmRNA	+/-	-	-	-	Phage integrase, endonuclease, phage protein (uncomplete phage)
43b	3386662	3113	3429832	3146	43170	15					-		-	-	-	Transduction with Phage 8: Kinase, Sigma/anti-sigma factor, Putative hemagglutinin/hemolysin protein, Hemagglutinin transporter (outer membrane protein, ABC permease, MFP), putative 2-aminoadipate transaminase, non-haem manganese-containing catalase rpoS-dependent (KatN), Cytochrome bd ubiquinol oxidase, subunit I & II, competence damage-inducible protein A, virulence membrane protein (PagC), Transcriptional regulator (LysR), Short-chain dehydrogenase/reductase, Methyltransferase type 11, putative deaminase/amidohydrolase with metallo-dependent hydrolase domain, putative carbamate kinase, Xanthine/uracil/vitamin C permease, putative DNA-binding transcriptional regulator
44	3460156	3176	3462550	3178	2394	3	-	-	-	-	-	-	-	+	+	ABC transporter
45	3491626	3205	3495685	3208	4059	4	-	-	-	-	-	-	-	+	+/-	ABC transporter involved in Fe3+ transport (*EitABCD*)
46	3581959	3279	3586075	3282	4116	4	-	-	-	-	+	-	-	+	+	GCN4-N-acetyltransferase, trancriptionnal regulator, 6-P-beta-glucidase, Transporter (PTS lactose/cellobiose family), regulator lacI-like
47	3590526	3287	3609775	3305	19249	19	+	-	-	-	tRNA-Gly	-	-	+	+/- (*)	IS481, ABC transporter (possibly for sugar with a specialisation in pectin transport) (TogMNAB), Pectin degradation, Oligogalacturonate-specific porin precursor (product of pectin degradation),
48	3688251	3384	3715198	3408	26947	25	-	-	-	-	tRNA-Phe	-	-	-	-	Autransporter with adhesin domain, antioxidant, Molybdenum ABC transporter, Iron ABC-transport protein, periplasmic-binding component, Mechanosensitive ion channel, Chemiotaxis regulator, Autransporter with a Serine-rich
49	3738015	3433	3750557	3442	12542	10	-	-	-	-	-	-	-	+/- (*)	-	Sugar transporter (MFS), Iron compound-binding protein of ABC transporter family, periplasmic component (iron-enterobactin transporter), TonB-
50	3772076	3463	3777014	3469	4938	7	-	-	-	-	-	-	-	+	-	Urease (*ureDABCEFG*)
51a	3783633	3475	3814474	3514	30841	39	+	-	-	Phage 8	tRNA-Met	+	-	-	-(*)	Phage integrase, phage proteins (conserved in *K. pneumoniae*, *E. coli* UTI89)
51b	3814471	3516	3832226	3530	17755	24							-	-	-	Transduction with Phage 9: Phosphatidylglycerol membrane-oligosaccharide glycerophosphotransferase, Transcriptional regulators (LysR, TetR, XRE), Metallo hydrolase,
52	4069288	3771	4076336	3779	7048	9	-	-	-	-	-	-	-	+	-	Malonate (*mdc* genes), Malonate transporter (family of auxin efflux carrier) (MdcF)

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53	4192604	3882	4212209	3905	19605	24	-	-	-	-	-	-	-	-	+ (*)	Fatty acid biosynthesis
54	4255568	3936	4269242	3944	13674	9	-	-	-	-	-	-	-	+	-	Cellulose biosynthesis *(bcsZDCBA)*
55	4294762	3964	4298896	3966	4134	3	-	-	-	-	-	-	-	+	+	Transporter (Beta-glucoside PTS family)
56	4425327	4070	4437770	4081	12443	12	-	-	-	-	-	-	-	+	- (*)	Ribose ABC transporter, raffinose operon (transport/utilisation)
						495										

The coordinate given are those of the genes, not those of the repeat from phage

organism used for the comparison: K. pneumoniae MGH78578, E. coli K12, O157-H7, UTI89, C. koseri BAA-895

Compared with 568 and 342, K12 and 638 have the operons:0231-0234 porins and lipoproteins;