

Supplementary Materials

Table S1. The resistance phenotypes of the *K. oxytoca* isolates used in this study.

<i>K. oxytoca</i> Strain	Source	Resistance to Antibiotic	Tolerance to Heavy Metal	16S rRNA Gene (GenBank accession no.)
7-7-27	<i>Mytilus edulis</i>	CHL/SXT/TET	Pb	OP722748
8-1-12-7	<i>Procambarus clarkii</i>		Cu/Hg/Pb/Zn	OP722749
8-2-3-6	<i>Sinonovacula constricta</i>		Cr/Cu/Hg/Pb/Zn	OP722753
8-2-11	<i>Scapharca subcrenata</i>	GEN/SXT	Cr/Cu/Hg/Mn/Pb/Zn/	OP740971
8-3-38	<i>Arca granosa</i>	SXT	Cr/Cu/Hg/Zn	OP722750
8-6-19	<i>Neptunea cumingi</i> Crosse	CHL/KAN//SXTTET	Pb	OP740972
8-8-40	<i>Anodonta woodiana</i>		Cd/Cr/Cu//Hg/Pb/Zn	OP722747
8-11-1	<i>Carassius auratus</i>	CIP/NOR/SXT	Cd/Cr/Cu/Hg/Zn	OP722744

Note: AMP, ampicillin; CHL, chloroamphenicol; KAN, kanamycin; GEN, gentamicin; SXT, sulphamethoxazole-trimethoprim; TET, tetracycline; NOR, norfloxacin; and CIP, ciprofloxacin

Table S2. The identified GIs in the *K. oxytoca* genomes.

<i>K. oxytoca</i> Isolate	GI ID	Location	Scaffold Size	Island Start (bp)	Island End (bp)	Length (bp)	CDS Gene
7-7-27	GI 01	Scaffold1	520,094	347,892	386,219	38,327	57
	GI 02	Scaffold2	473,959	193,052	241,637	48,585	59
	GI 03	Scaffold2	473,959	305,451	318,466	13,015	12
	GI 04	Scaffold3	451,111	398,914	412,552	13,638	13
	GI 05	Scaffold6	239,044	255,657	283,351	27,694	48
	GI 06	Scaffold10	292,463	149,099	167,899	18,800	14
	GI 07	Scaffold11	180,279	3706	9614	5908	7
	GI 08	Scaffold11	180,279	87,051	98,465	11,414	12
	GI09	Scaffold14	145,961	104,637	108,364	3727	7
	GI 10	Scaffold19	102,153	43,753	52,587	8834	10
	GI 11	Scaffold30	62,905	18,464	32,198	13,734	20
8-1-12-7	GI 01	Scaffold1	1,054,441	386,400	482,611	96,211	93
	GI 02	Scaffold1	1,054,441	821,835	834,966	13,131	12
	GI 03	Scaffold2	733,568	333,286	355,565	22,279	23
	GI 04	Scaffold2	733,568	39,225	57,588	18,363	14
	GI 05	Scaffold2	733,568	710,009	720,968	10,959	9
	GI 06	Scaffold3	547,020	482,515	523,827	41,312	43
	GI 07	Scaffold4	535,593	79,051	119,667	40,616	45
	GI 08	Scaffold6	388,884	205,364	236,681	31,317	39
	GI 09	Scaffold8	269,899	164,054	167,405	3351	7
	GI 10	Scaffold10	249,141	199,441	210,603	11,162	12
	GI 11	Scaffold10	249,141	33,813	38,101	4288	7
	GI 12	Scaffold10	249,141	48,260	61,666	13,406	17
8-2-3-6	GI 01	Scaffold1	807,024	146,049	159,616	13,567	13
	GI 02	Scaffold1	807,024	753,988	764,532	10,544	7
	GI 03	Scaffold2	788,961	447,903	456,152	8249	9
	GI 04	Scaffold2	788,961	670,367	712,904	42,537	39
	GI 05	Scaffold3	510,677	439,667	458,030	18,363	13
	GI 06	Scaffold4	429,785	197,125	254,844	57,719	70
	GI 07	Scaffold4	429,785	38,699	50,285	11,586	13
	GI 08	Scaffold5	417,408	22,049	75,953	53,904	52
	GI 09	Scaffold6	341,364	299,981	323,746	23,765	22
	GI 10	Scaffold11	147,734	39,007	50,124	11,117	18
	GI 11	Scaffold15	118,225	87,117	96,226	9109	12
	GI 12	Scaffold22	73,600	27,618	43,327	15,709	20
8-2-11	GI 01	Scaffold1	987,476	870,292	895,953	25,661	25
	GI 02	Scaffold3	553,027	264,164	277,450	13,286	12
	GI 03	Scaffold3	553,027	37,035	62,096	25,061	28

8-3-38	GI 04	Scaffold4	522,457	87,570	104,314	16,744	15
	GI 05	Scaffold5	462,519	396,056	458,346	62,290	74
	GI 06	Scaffold6	429,676	26,355	36,786	10,431	11
	GI 07	Scaffold7	398,542	14,771	35,584	20,813	22
	GI 08	Scaffold12	144,094	3186	9881	6695	10
	GI 09	Scaffold12	144,094	45,681	52,303	6622	8
	GI 10	Scaffold13	131,624	3317	9015	5698	9
	GI 01	Scaffold1	840,808	37,853	44,976	7123	7
	GI 02	Scaffold1	840,808	425,205	455,353	30,148	33
	GI 03	Scaffold1	840,808	753,809	773,621	19,812	15
	GI 04	Scaffold1	840,808	822,865	836,027	13,162	8
	GI 05	Scaffold2	770,426	192,865	248,409	55,544	51
	GI 06	Scaffold2	770,426	609,681	622,812	13,131	12
	GI 07	Scaffold3	553,079	221,654	226,909	5255	8
	GI 08	Scaffold3	553,079	428,412	473,124	44,712	45
	GI 09	Scaffold4	472,626	128,821	165,957	37,136	45
	GI 10	Scaffold5	446,542	106,279	110,006	3727	7
	GI 11	Scaffold5	446,542	366,286	400,142	33,856	33
	GI 12	Scaffold6	341,684	313,956	321,658	7702	7
8-6-19	GI 13	Scaffold7	323,178	222,466	231,680	9214	8
	GI 14	Scaffold9	238,027	32,328	71,686	39,358	44
	GI 15	Scaffold11	208,678	41,974	50,769	8795	10
	GI 16	Scaffold11	208,678	64,042	103,328	39,286	43
	GI 17	Scaffold13	154,967	22,394	31,641	9247	8
	GI 18	Scaffold14	135,941	107,838	115,787	7949	7
	GI 19	Scaffold21	42,879	14,209	21,303	7094	7
	GI 01	Scaffold1	1,217,762	22,388	41,107	18,719	13
	GI 02	Scaffold2	695,742	261,195	270,730	9535	10
	GI 03	Scaffold2	695,742	353,291	357,459	4168	7
	GI 04	Scaffold2	695,742	583,125	586,453	3328	7
	GI 05	Scaffold3	561,796	101,660	116,895	15,235	13
	GI 06	Scaffold4	358,056	285,623	307,827	22,204	22
	GI 07	Scaffold5	310,479	145,961	160,174	14,213	18
	GI 08	Scaffold5	310,479	166,592	171,912	5320	9
	GI 09	Scaffold5	310,479	182,312	216,334	34,022	46
	GI 10	Scaffold10	198,750	34,043	50,943	16,900	14
	GI 11	Scaffold11	181,804	160,667	167,773	7106	9
	GI 12	Scaffold13	127,030	20,780	34,910	14,130	14
8-8-40	GI 13	Scaffold14	123,506	51,048	68,320	17,272	27
	GI 14	Scaffold19	99906	55,911	65,445	9534	9
	GI 15	Scaffold22	40,571	22,240	30,258	8018	7
	GI 01	Scaffold1	1,053,471	383,413	482,649	99,236	95
	GI 02	Scaffold1	1,053,471	821,135	834,266	13,131	12
	GI 03	Scaffold2	548,207	483,759	526,036	42,277	44
	GI 04	Scaffold3	535,862	417,880	455,057	37,177	42
	GI 05	Scaffold4	468,019	110,676	144,365	33,689	32
	GI 06	Scaffold4	468,019	409,931	428,731	18,800	14
	GI 07	Scaffold6	390,032	206,278	237,595	31,317	39
	GI 08	Scaffold7	386,668	310,882	366,174	55,292	43
	GI 09	Scaffold8	271,254	103,564	107,291	3727	7
	GI 10	Scaffold10	264,208	10,504	23,597	13,093	12
8-11-1	GI 11	Scaffold11	249,017	199,425	210,587	11,162	12
	GI 12	Scaffold11	249,017	33,797	38,085	4288	7
	GI 13	Scaffold11	249,017	48,244	61,650	13,406	17
	GI 01	Scaffold1	926,696	364,156	449,647	85,491	81
	GI 02	Scaffold1	926,696	909,348	924,025	14,677	27
	GI 03	Scaffold2	821,235	20,090	90,382	70,292	70
	GI 04	Scaffold2	821,235	714,962	718,313	3351	7
	GI 05	Scaffold3	747,238	20,003	31,032	11,029	9
	GI 06	Scaffold3	747,238	383,114	402,788	19,674	20

GI 07	Scaffold3	747,238	673,912	707,930	34,018	27
GI 08	Scaffold4	614,239	305,147	314,560	9413	9
GI 09	Scaffold4	614,239	76,978	121,355	44,377	39
GI 10	Scaffold5	483,960	431,854	447,111	15,257	16
GI 11	Scaffold6	352,655	18111	44,631	26,520	28
GI 12	Scaffold9	215,320	636	8357	7721	10
GI 13	Scaffold11	167,733	150,991	165,277	14,286	23

Table S3. The predicted genes in the identified Gis in the *K. oxytoca* genomes. (see a single EXCEL Table S3)

Table S4. The identified prophages in the *K. oxytoca* genomes.

<i>K. oxytoca</i> Isolate	Prophage ID	Location	Scaffold Size	Start (bp)	End (bp)	Length(bp)	Possible Phage	NCBI Accession No.
7-7-27	Ph 01	Scaffold24	81,635	11,731	55,626	43,896	<i>Burkholderia</i> _phage_BcepC6B	NC_005887
	Ph 02	Scaffold2	473,959	197,230	231,478	34,249	<i>Enterobacteria</i> _phage_HK97	NC_002167
	Ph 03	Scaffold30	62,905	15,654	49,317	33,664	<i>Enterobacteria</i> _phage_PsP3	NC_005340
	Ph 04	Scaffold10	216,741	150,094	169,091	18,998	<i>Klebsiella</i> _phage_phiKO2	NC_005857
	Ph 05	Scaffold1	520,094	208,127	251,227	43,101	Phage_phiO18P	NC_009542
	Ph 06	Scaffold1	520,094	353,529	385,948	32,420	<i>Haemophilus</i> _phage_Aaphi23	NC_004827
8-1-12-7	Ph 01	Scaffold2	733,568	38,037	57,030	18,994	<i>Klebsiella</i> _phage_phiKO2	NC_005857
	Ph 02	Scaffold6	388,884	207,207	234,256	27,050	<i>Enterobacteria</i> _phage_ES18	NC_006949
	Ph 03	Scaffold10	249,141	35,090	82,597	47,508	<i>Pseudomonas</i> _phage_phiCTX	NC_003278
8-2-3-6	Ph 01	Scaffold3	510,677	440,225	459,222	18,998	<i>Klebsiella</i> _phage_phiKO2	NC_005857
8-2-11	Ph 01	Scaffold3	553,027	37,035	70,410	33,376	<i>Enterobacteria</i> _phage_P2	NC_001895
8-3-38	Ph 01	Scaffold11	208,678	73,113	128,625	55,513	<i>Pseudomonas</i> _phage_D3	NC_002484
	Ph 02	Scaffold9	238,027	36,939	71,686	34,748	<i>Pseudomonas</i> _phage_phiCTX	NC_003278
	Ph 03	Scaffold1	840,808	756,564	803,173	46,610	<i>Klebsiella</i> _phage_phiKO2	NC_005857
	Ph 04	Scaffold4	472,626	135,942	176,177	40,236	<i>Enterobacteria</i> _phage_ST64B	NC_004313
8-6-19	Ph 01	Scaffold5	310,479	145,961	173,799	27,839	Phage_phiO18P	NC_009542
	Ph 02	Scaffold14	123,506	40,596	98,895	58,300	<i>Enterobacteria</i> _phage_HK022	NC_002166
8-8-40	Ph 01	Scaffold6	390,032	208,121	235,170	27,050	<i>Enterobacteria</i> _phage_ES18	NC_006949
	Ph 02	Scaffold11	249,017	35,074	82,581	47,508	<i>Pseudomonas</i> _phage_phiCTX	NC_003278
	Ph 03	Scaffold4	468,019	410,926	429,919	18,994	<i>Klebsiella</i> _phage_phiKO2	NC_005857
8-11-1	Ph 01	Scaffold2	821,235	27,366	68,685	41,320	<i>Enterobacteria</i> _phage_SfV	NC_003444
	Ph 02	Scaffold11	167,733	150,991	167,656	16,666	<i>Pseudomonas</i> _phage_F10	NC_007805
	Ph 03	Scaffold1	926,696	910,697	926,694	15,998	<i>Enterobacteria</i> _phage_phiP27	NC_003356
	Ph 04	Scaffold3	747,238	676,512	709,118	32,607	<i>Klebsiella</i> _phage_phiKO2	NC_005857

Table S5. The predicted genes in the identified prophages in the *K. oxytoca* genomes. (see a single EXCEL Table S5).

Table S6. The identified INs in the *K. oxytoca* genomes.

<i>K. oxytoca</i> Isolate	IN ID	Location	Scaffold Size (bp)	Length (bp)	Start (bp)	End (bp)	CDS Gene
7-7-27	IN 01	Scaffold66	2227	1809	1	1810	1
8-6-19	IN 01	Scaffold37	3040	3365	2905	6270	4

Table S7. The identified ISs in the *K. oxytoca* genomes.

<i>K. oxytoca</i> Isolate	IS ID	Location	Scaffold Size (bp)	Start (bp)	End (bp)	IS Family
7-7-27	IS1	Scaffold1	520,094	236,156	237,574	IS91
	IS2	Scaffold1	520,094	496,787	497,702	IS91
	IS3	Scaffold42	16,375	15,002	15,765	IS1
	IS4	Scaffold44	15,984	3477	4604	IS5
	IS5	Scaffold44	15,984	8054	8823	IS1
	IS6	Scaffold51	8452	177	1422	IS30
	IS7	Scaffold55	6457	175	1395	IS3
8-2-11	IS1	Scaffold7	398,542	393,390	394,504	IS91
	IS2	Scaffold7	398,542	394,705	395,687	IS91
8-1-12-7	IS1	Scaffold2	733,568	712,518	713,434	IS91
8-3-38	IS1	Scaffold8	240,513	47,690	48804	IS5
8-6-19	IS1	Scaffold2	695,742	260,796	261,964	IS91
	IS2	Scaffold5	310,479	172,739	173,813	IS91
	IS3	Scaffold32	7741	6499	7262	IS1
	IS4	Scaffold43	1464	28	1268	IS110
8-8-40	IS1	Scaffold7	386,668	356,988	357,582	IS66

Table S8. The putative virulence-related genes identified in the *K. oxytoca* genomes.

Virulence-Related Gene	<i>K. oxytoca</i> Genome	Reference
<i>acpXL</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[1]
<i>acrAB</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[2]
<i>adeG</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[3]
<i>algU</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[4]
<i>allABCDRS</i>	8-2-11, 8-6-19	[5]
<i>chuS</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[6]
<i>clpP</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[7]
<i>clpV/tssH</i>	7-7-27, 8-1-12-7, 8-3-38, 8-6-19, 8-8-40	[8]
<i>csrA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[9]
<i>dotU/tssL</i>	8-3-38	[10]
<i>entABCDEFs</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[11]
<i>exeDEG</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[12]
<i>fepABCDG</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[11]
<i>fimABCDEFGHl</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[13]
<i>fur</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[14]
<i>fyuA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[15]
<i>galFU</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[16, 17]
<i>gmhA/lpcA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[18]
<i>gndA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[19]
<i>hcp/tssD</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[20]
<i>htpB</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[21]

<i>icmF/tssM</i>	7-7-27, 8-1-12-7, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[22]
<i>IlpA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[23]
<i>impA/tssA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[22]
<i>irp12</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[24]
<i>iutA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[25]
<i>katA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[26]
<i>kdsA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[27]
<i>lpxABCD</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[28]
<i>luxS</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[29]
<i>mgtBC</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[30]
<i>mrkABCDHFJ</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[31]
<i>msbA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[32]
<i>ompA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[33]
<i>phoPQ</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[34]
<i>rcsAB</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[35]
<i>rfaDEF</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[36]
<i>rfbABDK1</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-8-40, 8-11-1	[37]
<i>rffG</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[38]
<i>rpoS</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[39]
<i>sciN/tssJ</i>	8-3-38, 8-11-1	[40]
<i>sodB</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[41]
<i>tssFG</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[42]
<i>tufA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[43]
<i>ureA</i>	8-2-11	[44]
<i>ureBG</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[44]
<i>vasE/tssK</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[22]
<i>vfr</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[45]
<i>vgrG/tssI</i>	8-1-12-7, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[20]
<i>vipA/tssB</i>	7-7-27, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[46]
<i>vipB/tssC</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-8-38, 8-6-19, 8-8-40, 8-11-1	[46]
<i>wbtL</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[47]
<i>yagV/lecP</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[48]
<i>yagW/lecP</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[49]
<i>yagY/lecP</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[50]
<i>yagZ/lecP</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[51]
<i>ybtAEPQSTUX</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[52]
<i>ykgK/lecP</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[53]

Table S9. The putative antibiotic and heavy metal resistance-related genes identified in the *K. oxytoca* genomes.

Antimicrobial Agent	Resistance-Related Genes	<i>K. oxytoca</i> Genome	Reference
Aminoglycoside	<i>aada</i>	8-6-19	[54]
Aminoglycoside	<i>aph3-I</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[55]
Aminoglycoside	<i>msbA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[56]
Aminoglycoside	<i>strA</i>	7-7-27	[57]
Aminoglycoside	<i>strB</i>	7-7-27, 8-6-19	[58]
Aminoglycoside	<i>tuf</i>	7-7-27, 8-2-11, 8-1-12-7, 8-11-1	[59]
Aminoglycosides	<i>sdiA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[60]
Carbapenem	<i>lamB</i>	7-7-27, 8-2-11, 8-1-12-7, 8-11-1	[61]
Carbapenem	<i>phoE</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[62]
Carbapenem	<i>ptsI</i>	7-7-27, 8-2-11, 8-1-12-7, 8-11-1	[63]
Fosfomycin			
Cephalosporin	<i>ebr</i>	8-6-19	[64]
Carbapenem			
Cephalosporin	<i>ftsI</i>	7-7-27, 8-2-11, 8-1-12-7, 8-11-1	[65]

β-lactam			
Cephalosporin	<i>ompF</i>	8-2-11,8-1-12-7,8-11-1	[66]
β-lactam			
Quinolone			
Colistin	<i>eptA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[67]
Colistin	<i>eptB</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[67]
Colistin	<i>mldDF</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[68]
Colistin	<i>phoPQ</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[69]
Colistin	<i>ugd</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[70]
Fosfomycin	<i>fosA5</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[71]
Fosfomycin	<i>glpT</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[72]
Fosfomycin	<i>murA</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[73]
β-lactam	<i>lptD</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[74]
Macrolide	<i>mdfA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[75]
Nitrofurantoin	<i>marR</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[76]
Nitrofurantoin	<i>nfsA</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[77]
PAS	<i>thyA</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[78]
Polymyxin	<i>arnT</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[79]
Quinolone	<i>acrR</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[80]
Quinolone	<i>csrA</i>	7-7-27,8-2-11,8-1-12-7,,8-11-1	[81]
Rifamycin			
Aminoglycoside			
Nitrofurantoin			
Quinolone	<i>gyrAB</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[82]
Quinolone	<i>marA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[83]
Quinolone	<i>mcbG</i>	7-7-27,8-6-19	[84]
Quinolone	<i>oqxAB</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[85]
Quinolone	<i>parCE</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[86]
Rifamycin	<i>mipA</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[87]
Rifamycin	<i>rpoB</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[88]
streptomycin	<i>rpsJL</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[89]
Sulfonamide	<i>dfrA1</i>	7-7-27	[90]
Sulfonamide	<i>folP</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[91]
Sulfonamide	<i>leuO</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[92]
tetracycline	<i>bacA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[93]
Tetracycline	<i>tetA</i>	7-7-27,8-6-19	[94]
Tigecycline	<i>ramA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[95]
Tigecycline	<i>soxS</i>	7-7-27,8-2-11,8-1-12-7,8-11-1	[96]
Colistin			
Trimethoprim	<i>dfrA12</i>	8-6-19	[97]
β-lactam	<i>acrABDEF</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[98]
β-lactam	<i>ampH</i>	8-2-3-6,8-3-38,8-6-19,8-8-40	[99]
β-lactam	<i>baeRS</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[100]
β-lactam	<i>blaOXY</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[101]
β-lactam	<i>blaTEM</i>	7-7-27	[102]
β-lactam	<i>cmlA</i>	7-7-27, 8-6-19	[103]
β-lactam	<i>cpxA</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[104]
β-lactam	<i>ompCN</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[105]
β-lactam	<i>tolC</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[106]
Aminoglycoside			
Tetracycline			
Quinolone			
Phenicol			
Macrolide			
Lincosamide			
Heavy metal	<i>kdpE</i>	7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, 8-11-1	[107]

Table S10. The thirty-four *K. oxytoca* strains with complete genomes used in the phylogenetic tree.

<i>K. oxytoca</i> Strain	Host	Collected Date	Serotype	ST	Location	GenBank Accession No.
P620	Environment	2016	K58	-	China	NZ_CP046115.1
KONIH4	Environment	2015	K68	202	USA	NZ_CP026269.1
AR380	Host missing	-	O5	257	-	NZ_CP029128.1
FDAARGOS_1332	Homo sapiens	-	O5	176	USA	NZ_CP069943.1
FDAARGOS_1331	Homo sapiens	-	O5	176	USA	NZ_CP070144.1
KoPF10	Homo sapiens	2018	O5	48	USA	NZ_CP072914.1
C-21-18	Homo sapiens	2021	O5	176	Japan	NZ_CP093271.1
2022CK-00498	Homo sapiens	2022	K74	285	USA	NZ_CP114305.1
328	Homo sapiens	2018	O5	328	Spain	NZ_OW969781.1
CAV1099	Homo sapiens	2009	K68	199	USA	NZ_CP011597.1
CAV1335	Homo sapiens	2010	K68	199	USA	NZ_CP011618.1
CAV1015	Homo sapiens	2007	K68	199	USA	NZ_CP017928.1
AHC-6	Homo sapiens	2004	K68	1	-	NZ_CP098757.1
2022CK-00499	Homo sapiens	2022	K74	-	USA	NZ_CP114308.1
FDAARGOS_1336	Homo sapiens	-	K68	199	USA	NZ_JAFFQV010000001.1
325	Homo sapiens	2018	K68	325	Spain	NZ_OW849470.1
36	Homo sapiens	2018	K68	36	Spain	NZ_OW969659.1
FDAARGOS_335	Homo sapiens	2015	O3	222	USA	NZ_CP027426.1
RHBSTW-00373	Environment	2017	K68	37	United Kingdom	NZ_CP056567.1
RHB30-C02	Environment	2017	O3	145	United Kingdom	NZ_CP057330.1
FDAARGOS_1334	Homo sapiens	-	O3	201	USA	NZ_CP069911.1
KONSF-1	Homo sapiens	2021	O3	245	Unknown	NZ_CP090245.1
NMI2990_17	Homo sapiens	2017	O3	145	Poland	NZ_CP129616.1
145	Homo sapiens	2018	O3	145	Spain	NZ_OW967374.1
FDAARGOS_500	Homo sapiens	2018	O3	59	USA	NZ_CP033844.1
IR5392	Homo sapiens	2015	K74	34	China	NZ_CP064108.1
FDAARGOS_1333	Homo sapiens	-	O3	302	USA	NZ_CP070020.1
TYL-T1	Host missing	2020	K74	2	China	NZ_CP107040.1
NCTC11356	Host missing	1980	K74	101	United Kingdom	NZ_LR133932.1
NCTC13727	Homo sapiens	2018	K29	-	USA	NZ_LR134333.1
MSB1_10D	Homo sapiens	2014	K74	266	Australia	NZ_LR890312.1
2	Homo sapiens	2018	K74	2	Spain	NZ_OW967518.1
101	Homo sapiens	2018	K74	101	Spain	NZ_OW968280.1
101	Homo sapiens	2018	K74	101	Spain	NZ_OW968347.1

-: unknown.

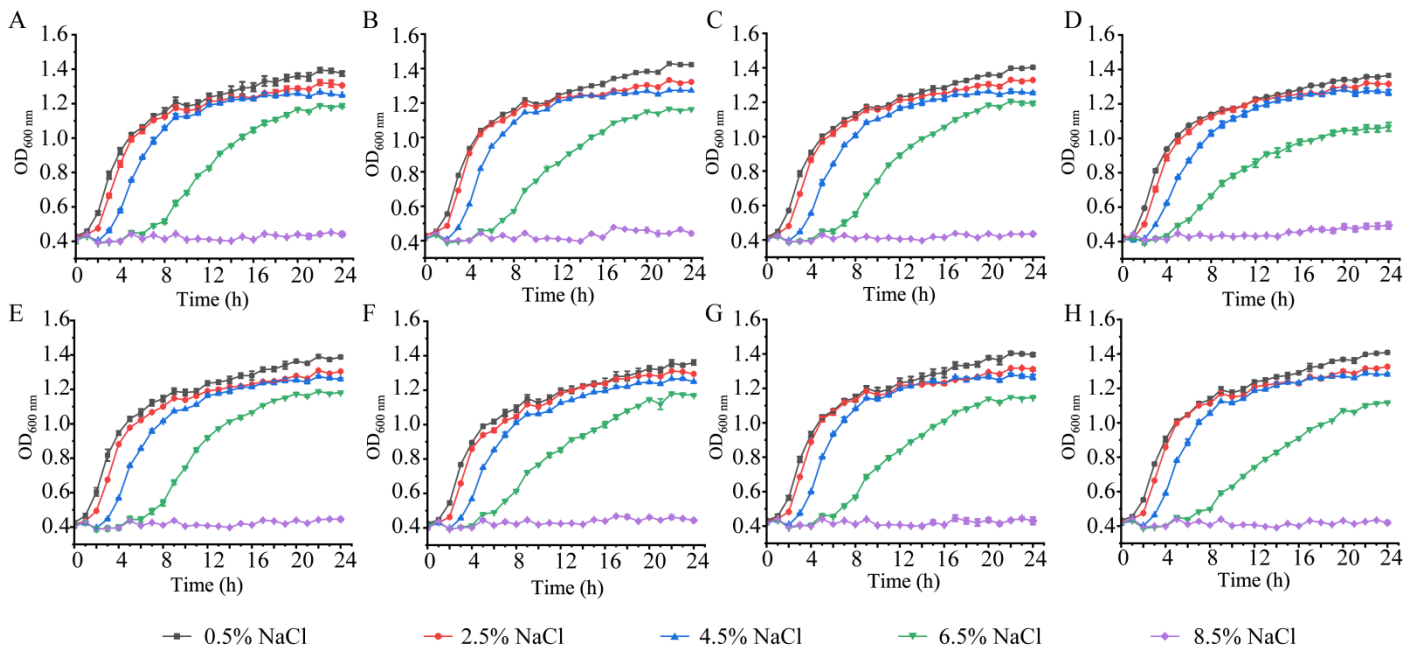


Figure S1. Growth curves of the *K. oxytoca* isolates of aquatic animal origins under different concentrations of NaCl conditions. A-H: *K. oxytoca* 7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40 and 8-11-1 isolates were incubated in the TSB (pH 7.2, 0.5–8.5% NaCl) at 37 °C for 24 h, respectively.

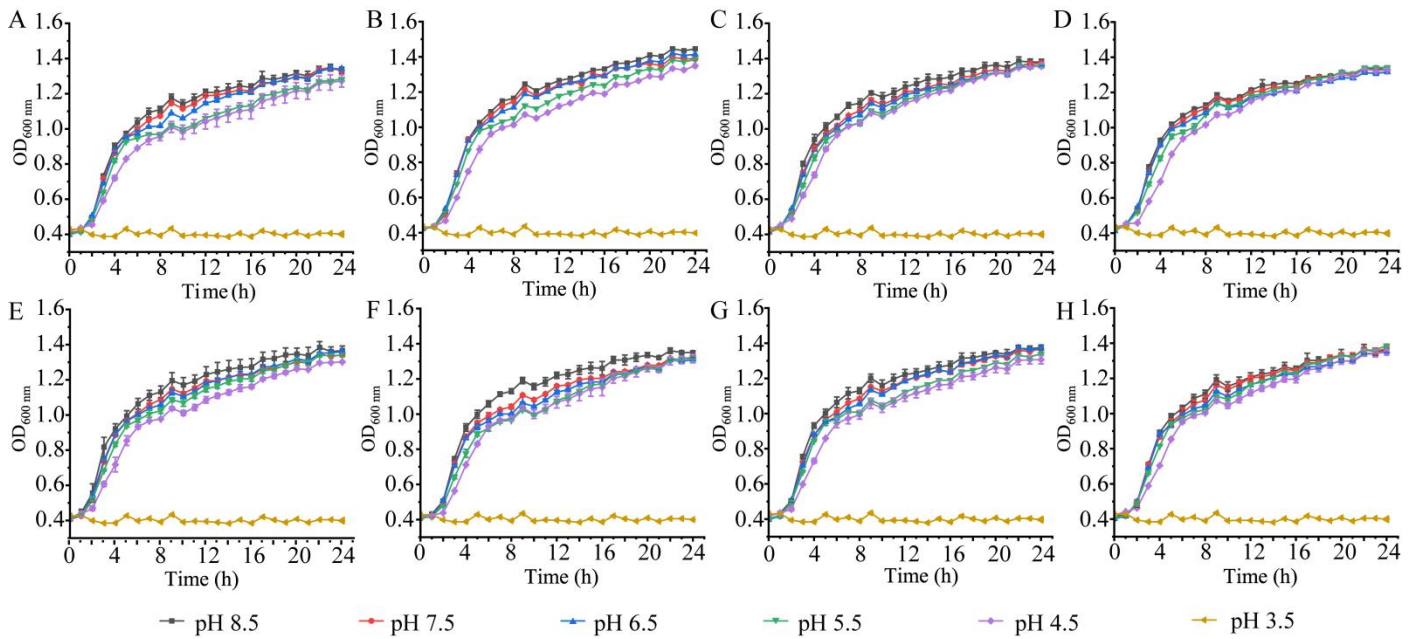


Figure S2. Growth curves of the *K. oxytoca* isolates of aquatic animal origins under different pH conditions. A-H: *K. oxytoca* 7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, and 8-11-1 isolates were incubated in the TSB (0.5% NaCl, pH 3.5–8.5) at 37 °C for 24 h, respectively.

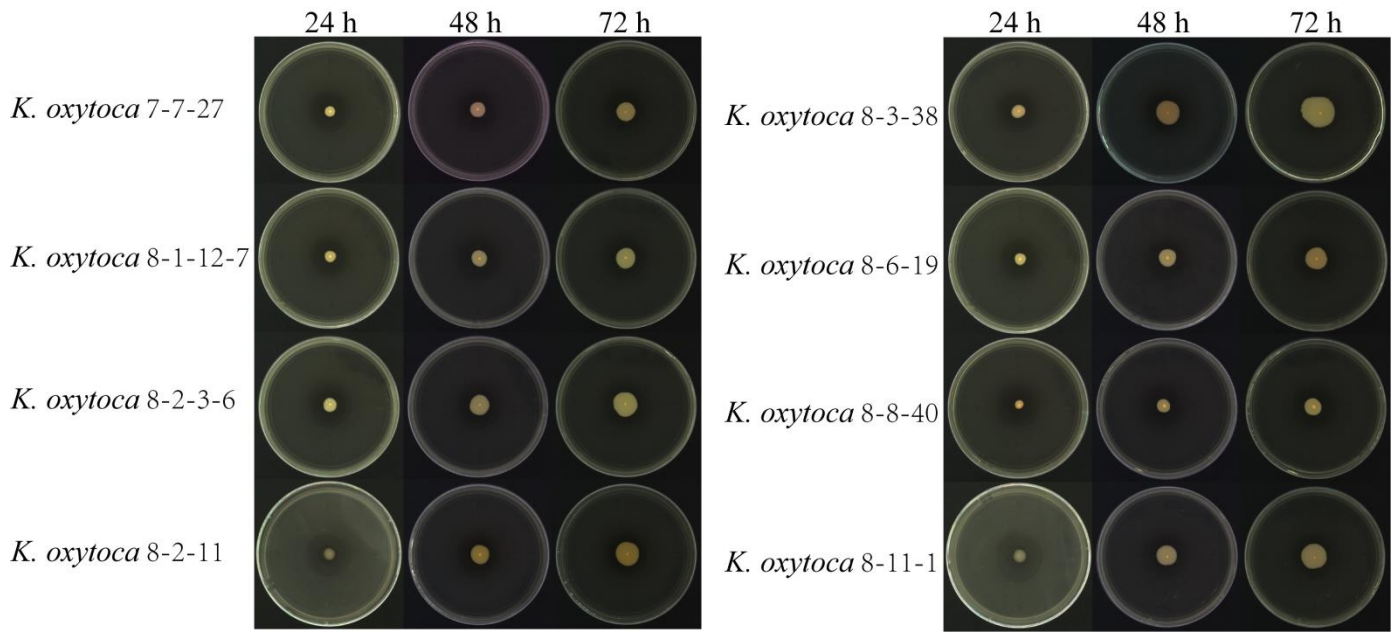
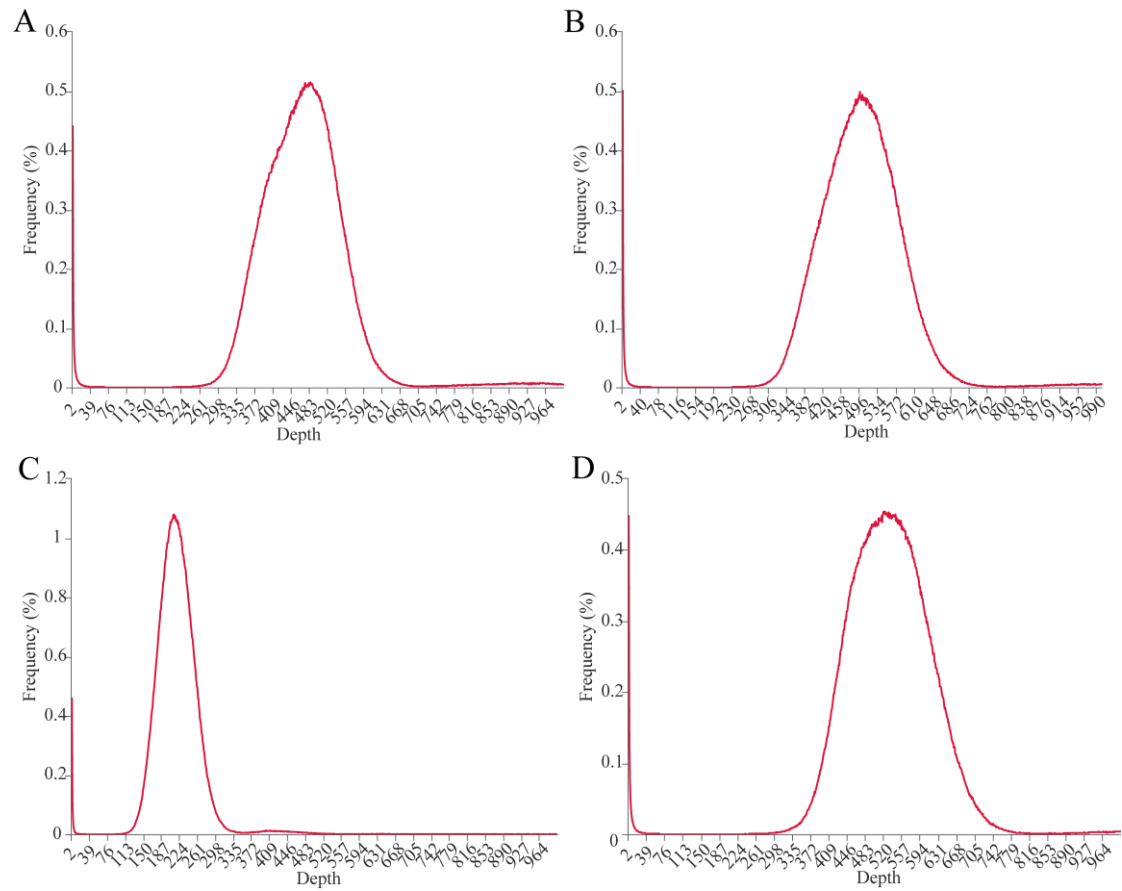


Figure S3. The swimming loops of the *K. oxytoca* isolates of aquatic animal origins. The *K. oxytoca* 7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, and 8-11-1 isolates were incubated in the TSB (0.5% NaCl, pH 8.5, 0.25% agar) at 37 °C for 72 h.



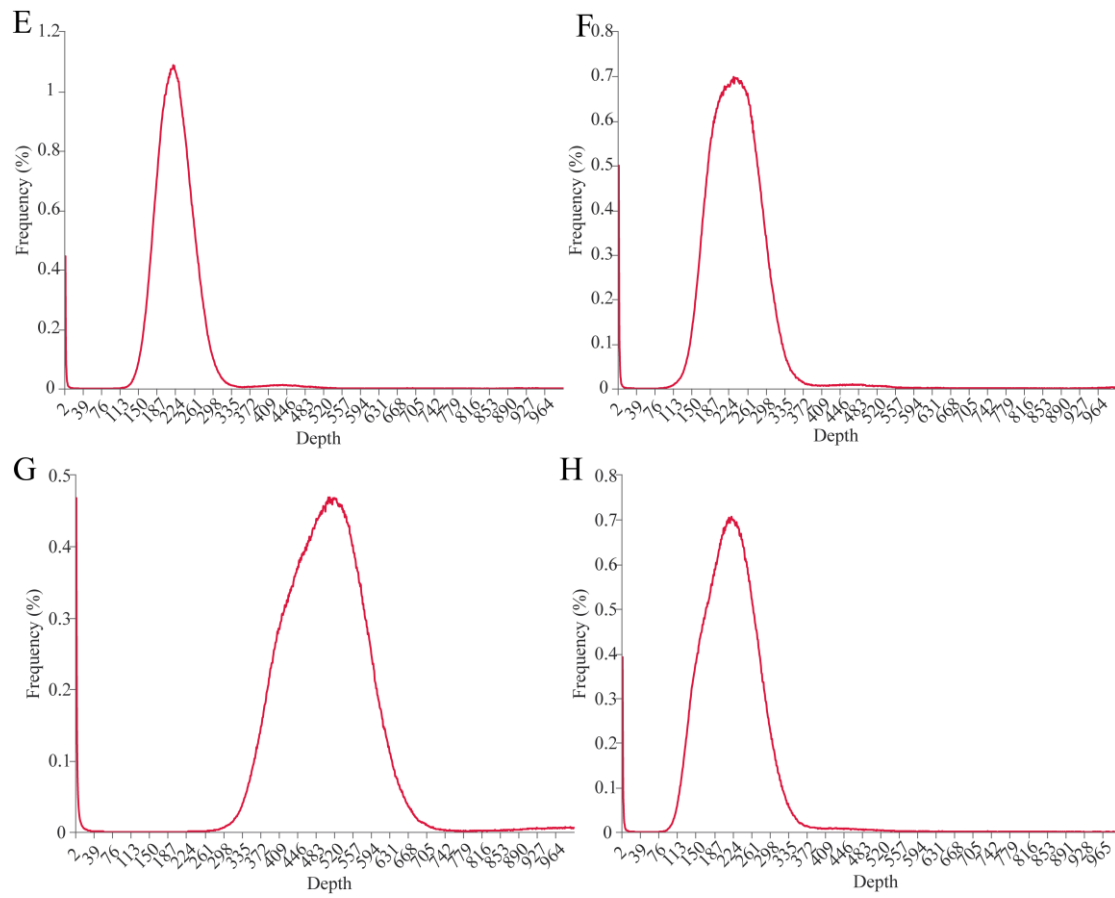
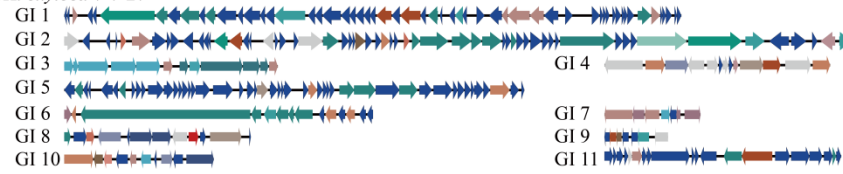
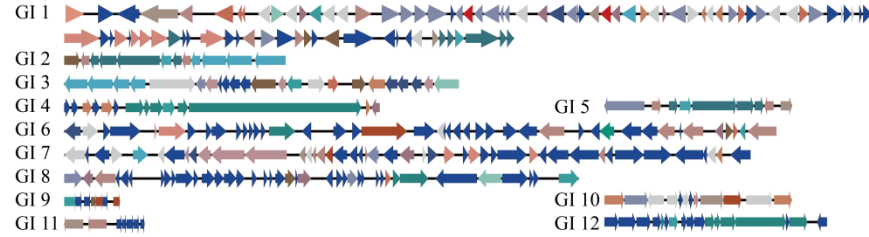


Figure S4. The k-mer analysis for *K. oxytoca* sequencing reads based on the number of unique 17-mers. A–H: *K. oxytoca* 7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, and 8-11-1 genomes, respectively.

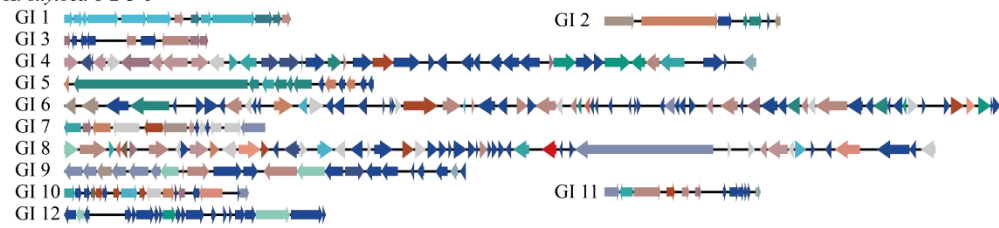
A *K. oxytoca* 7-7-27



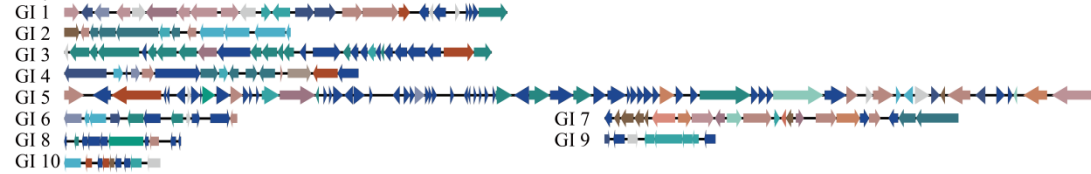
K. oxytoca 8-1-12-7



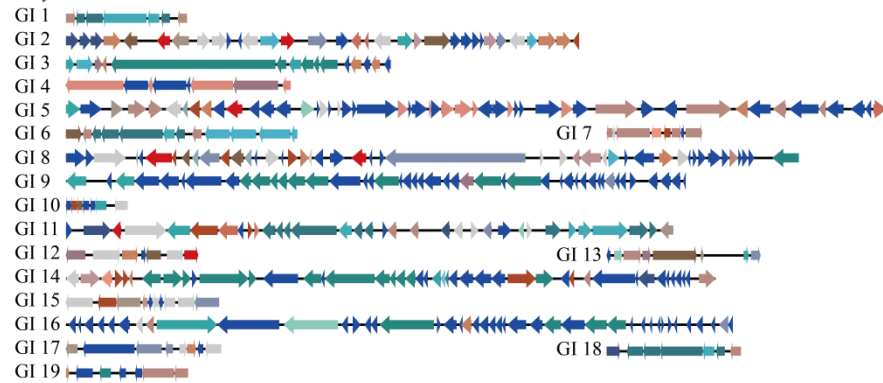
K. oxytoca 8-2-3-6



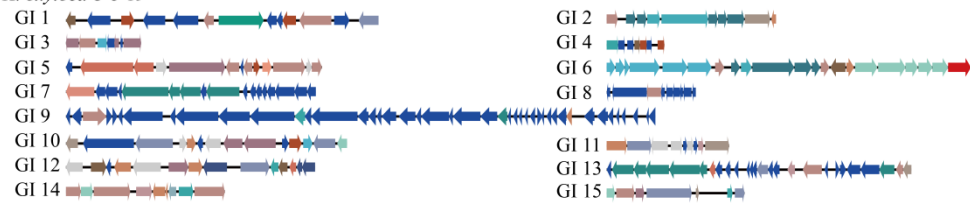
K. oxytoca 8-2-11



B *K. oxytoca* 8-3-38



K. oxytoca 8-6-19



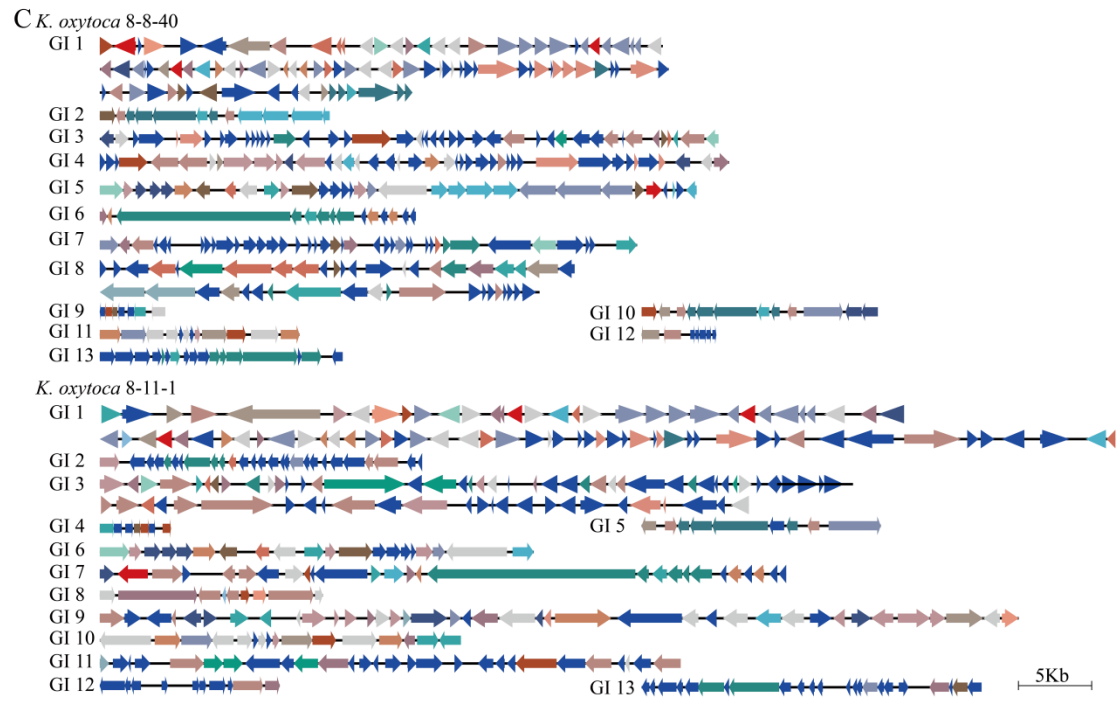
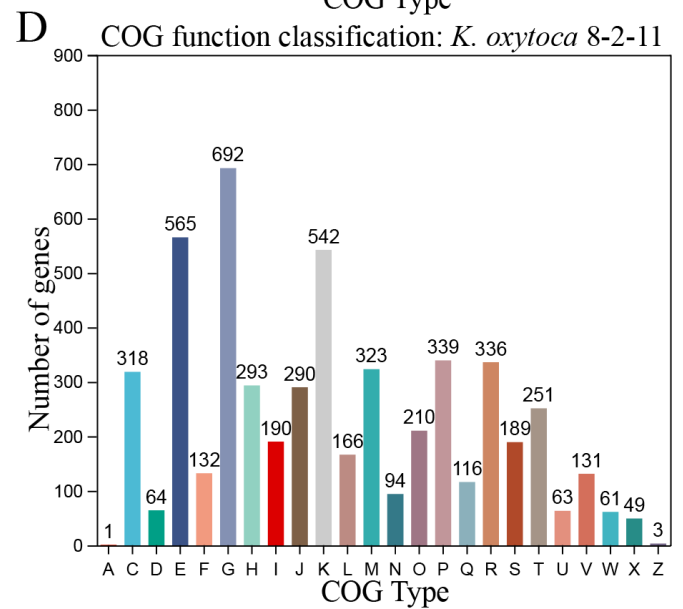
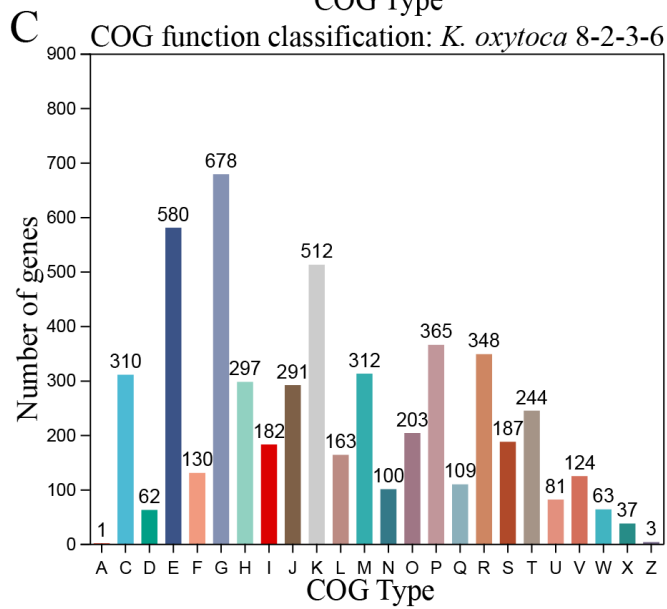
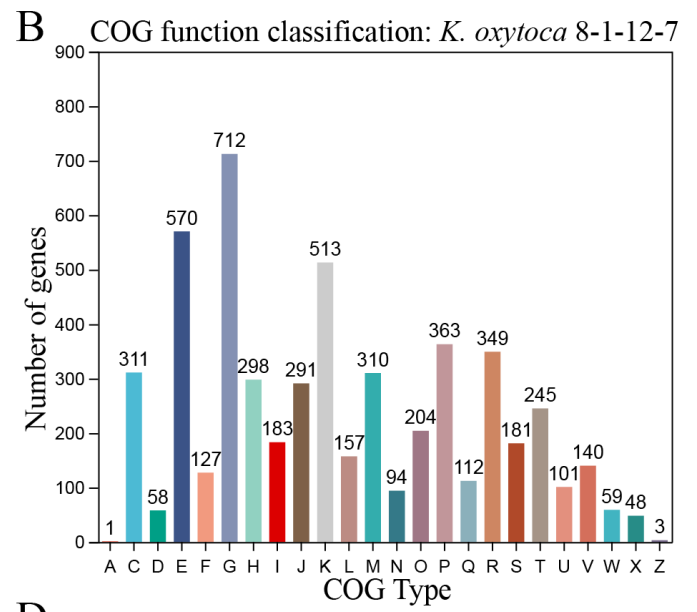
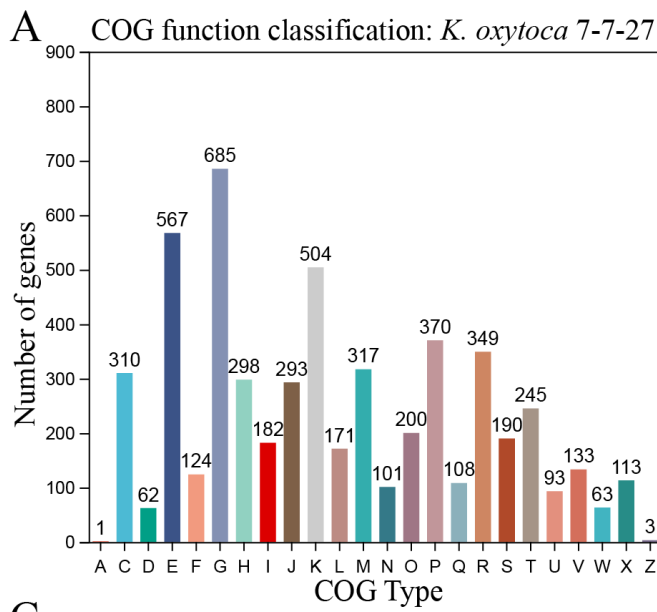


Figure S5. Gene organizations of the GIs identified in the *K. oxytoca* genomes (A-C). Different colors referred to COG classification to mark gene functions (Figure S5).



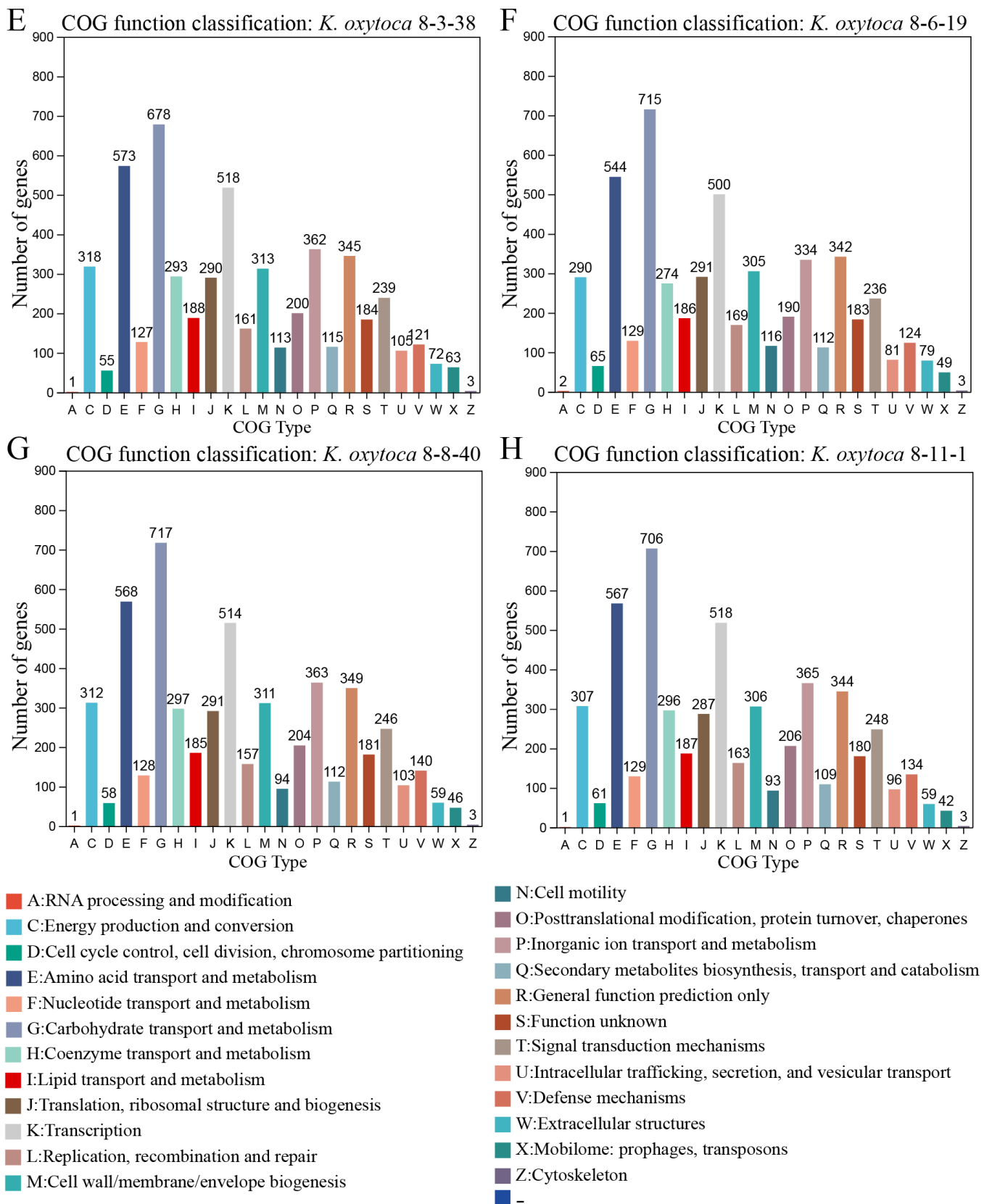


Figure S6. The COG function classification of the genes in the *K. oxytoca* genomes. A-H: *K. oxytoca* 7-7-27, 8-1-12-7, 8-2-3-6, 8-2-11, 8-3-38, 8-6-19, 8-8-40, and 8-11-1 genomes, respectively.

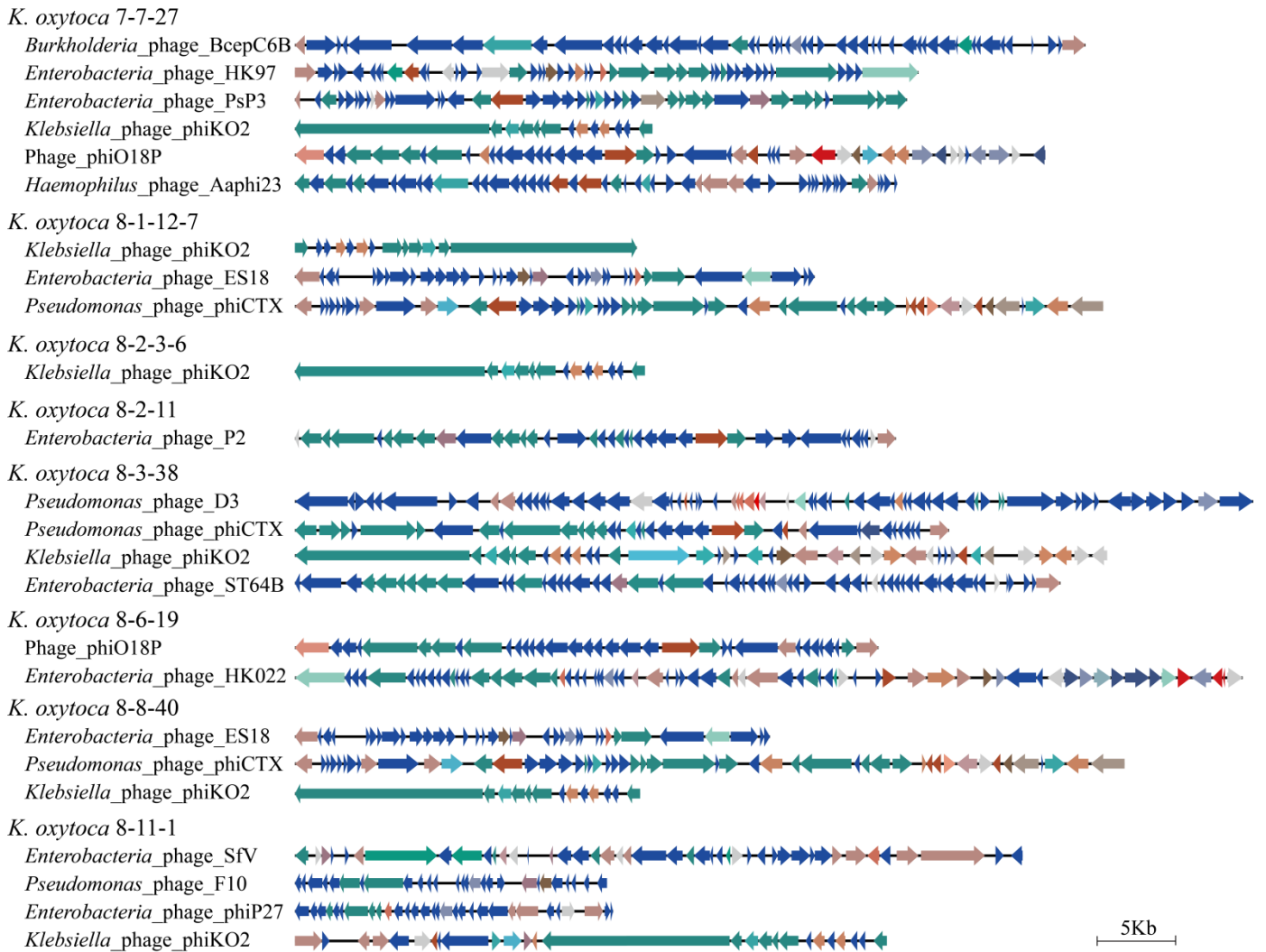


Figure S7. Gene organizations of the prophages identified in the *K. oxytoca* genomes. Different colors referred to COG classification to mark gene functions (Figure S5).

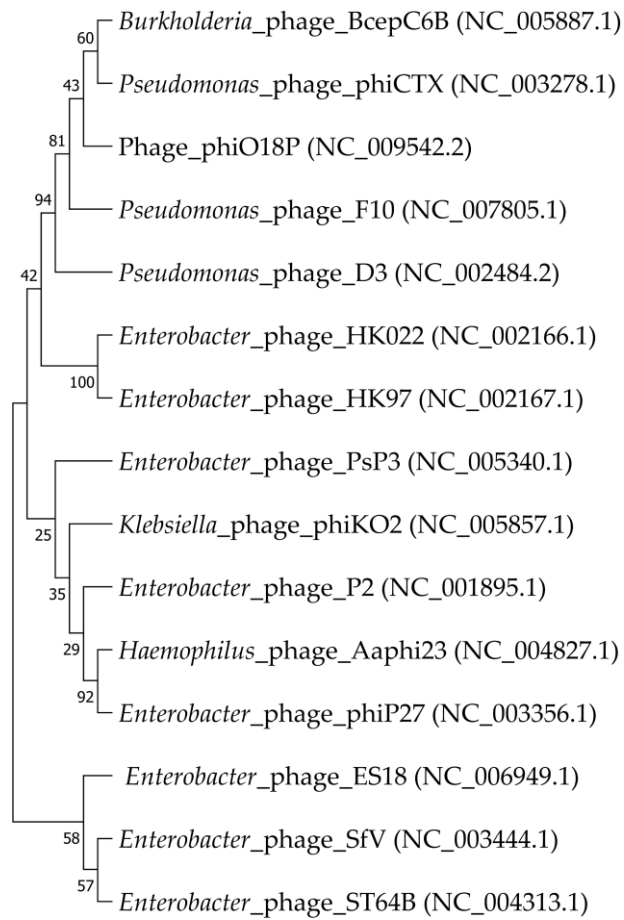


Figure S8. Phylogenetic relationship of the identified prophages in the *K. oxytoca* genomes.

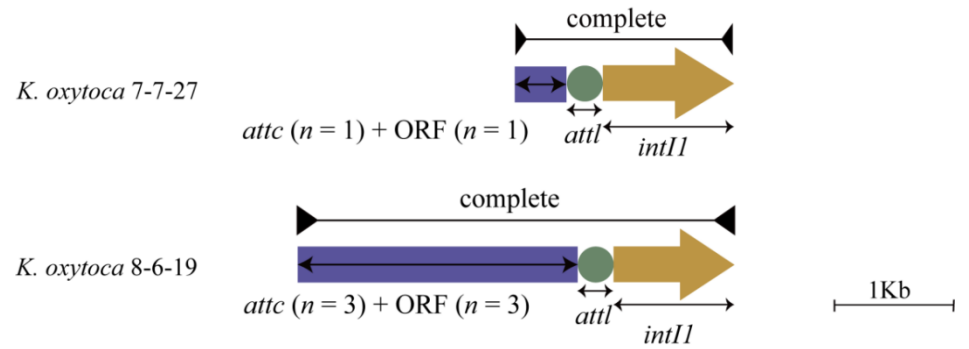


Figure S9. The structure diagram of the INs identified in the *K. oxytoca* genomes.



Figure S10. Structural features of the CRISPRs identified in the *K. oxytoca* genomes. The repeat sequences were shown by the rectangle in different colors and the spacer regions were represented by rhombuses in different colors.

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