Table 4. Genes unique to fer1 and fer1(env). fer1 ANNOTATION FA01 hypothetical protein FA02 hypothetical protein FA03c

transposase

conserved hypothetical protein predicted to be involved in DNA repair uncharacterized protein predicted to be involved in DNA repair RecB family exonuclease predicted helicase

FA04c

FA05c

FA06c

FA07c FA08c

FA09c

FA10c

FA11c

FA12

FA13

FA14 FA15

FA36

FA37

FA61

FA77

FA119c

FA120

FA128c

FA187

FA437

FA438c

FA465c

FA466c FA477c

FA569c

FA570c

FA571

FA572 FA573

FA579

FA580

FA581c

FA582c

FA583c FA584c

FA585c

FA586c

FA589c

FA590

FA596c

FA597c

conserved hypothetical protein uncharacterized protein predicted to be involved in DNA repair hypothetical protein

uncharacterized protein predicted to be involved in DNA repair (RAMP superfamily) superfamily I DNA/RNA helicase DNA or RNA helicase of superfamily II

ATPase involved in DNA repair/chromosome segregation

hypothetical protein

conserved hypothetical protein hypothetical protein transposase

transposase transposase

transposon-encoded protein tranposase transposase transposase

transposase hypothetical protein (MazF growth inhibitor-related) conserved hypothetical protein transposase (DDE domain) predicted nucleic acid-binding protein (PIN domain)

conserved hypothetical protein integrase/recombinase hypothetical protein hypothetical protein hypothetical protein

FA578c integrase/recombinase

conserved hypothetical protein galactose mutarotase-related protein probable selenocysteine synthase (seryl-tRNASer selenium transferase)

short-chain alcohol dehydrogenase amino acid transporter

predicted DNA-binding protein N-carbamoyl-L-amino acid amidohydrolase

hypothetical protein

hypothetical protein

hypothetical protein

possible inactivated transposase

hypothetical protein

hypothetical protein

FA591 permease (major facilitator superfamily)

FA592 FA593 dihydroorotase-related cyclic amidohydrolase FA594 benzoylformate decarboxylase-related thiamine pyrophosphate-requiring enzyme FA595

FA598c	conserved hypothetical protein
FA677c	transposase
FA678c	transposase
FA750c	possible inactivated transposase
FA751c	transposase
FA772	transposase
FA774	hypothetical membrane protein
FA791	probable transposase
FA792	transposase
FA793	transposase
FA794	transposase (DDE domain)
FA797	conserved hypothetical protein (possible nucleic acid-binding protein)
FA872c	transposase
FA876c	inactivated transposase
FA877c	transposase
FA878c	hypothetical membrane protein; possible permease
FA879c	transposase
FA880c	transposase
FA1094c	transposase
FA1194	hypothetical membrane protein
FA1195	hypothetical protein
FA1196	hypothetical protein
FA1197	hypothetical membrane protein
FA1198	hypothetical membrane protein
FA1207c	metabolite transporter
FA1209c	predicted metal-dependent hydrolase related to alanyl-tRNA synthetase
FA1210c	tRNA-pseudouridine synthase I-related protein
FA1211	possible transcriptional regulator
FA1220	conserved hypothetical protein
FA1221	conserved hypothetical protein possibly involved in DNA repair
FA1222	conserved hypothetical protein possibly involved in DNA repair
FA1223	predicted helicase
FA1224	predicted RecB family exonuclease (truncated by transposon insertion)
FA1225c	transposon-encoded protein
FA1226	transposase
FA1227	predicted RecB family exonuclease (truncated by transposon insertion)
FA1228	uncharacterized protein predicted to be involved in DNA repair
FA1229	conserved hypothetical protein possibly involved in DNA repair
FA1230	hypothetical protein
FA1231c	probable inactivated transposase
FA1232c	probable inactivated transposase
FA1233c	conserved hypothetical protein
FA1234	predicted membrane-associated protease with chaperone function
FA1239c	transposase
FA1240	transposon-encoded protein
FA1242c	type I restriction-modification enzyme, M subunit
FA1243c	Co/Zn/Cd efflux system component
FA1244c	hypothetical membrane protein
FA1245c	hypothetical protein
FA1246c	hypothetical protein
FA1247c	hypothetical protein
FA1248c	transposase
FA1249	possible multi-drug efflux permease transposase/integrase
FA1283c	transposase/integrase

FA1293	hypothetical protein
FA1324c	transposase
FA1325	transposon-encoded protein
FA1425	integrase
FA1426c	hypothetical protein
FA1427c	hypothetical protein
FA1428	hypothetical protein
FA1429	hypothetical protein
FA1430	possible phage-related DNA primase/helicase (ATPase domain)
FA1431	hypothetical protein
FA1432	hypothetical protein
FA1433	hypothetical protein
FA1434	hypothetical protein
FA1435	hypothetical protein
FA1436	hypothetical protein
FA1437	hypothetical protein
FA1438	hypothetical protein
FA1439	hypothetical protein
FA1440	hypothetical protein
FA1441	hypothetical protein
FA1442	hypothetical protein (Zot-related)
FA1443	hypothetical protein
FA1444	possible phage integrase
FA1445c	conserved hypothetical membrane protein
FA1446	site-specific DNA methylase
FA1447	hypothetical protein
FA1682	transposase
FA1703	transposase
FA1704	transposase
FA1735c	probable transposon-encoded protein
FA1736	transposase
FA1783	transposase
FA1787	transposase (integrase core domain)
FA1797	probable glycosyltransferase
FA1855	transposase
FA1941c	hypothetical protein
FA1942c	hypothetical protein
FA1943	transposase
FA1944c	hypothetical protein
FA1945c	predicted ATPase (possible endonuclease)
FA1946	possible transcriptional regulator
FA1947	conserved hypothetical protein
FA1948	hypothetical protein
FA1949c	hypothetical protein
FA1950c	hypothetical protein
FA1958	hypothetical protein
FA1959	transposase

fer1(env)	ANNOTATION
env_52_2	mrr restriction system protein
env_58_28	hypothetical protein
env_63_19	conserved hypothetical membrane protein
env_65_4	hypothetical protein (possible signal peptidase)
env_65_5	hypothetical membrane protein
env_65_6	hypothetical protein
env_65_7	hypothetical protein
env_139_4	predicted phosphate transport protein
env_148_14	predicted inactivated transposase
env_149_4	hypothetical protein
env_184_16	hypothetical protein
env_243_11	hypothetical protein
env_246_10	transposase
env_246_9	transposase
env_249_13	conserved hypothetical protein
env_249_14	hypothetical protein
env_249_6	hypothetical protein
env_262_6	Type II restriction-modification methylase
env_262_7	Type II restriction-modification endonuclease
env_342_1	ABC-type sugar transport system, substrate-binding component
env_354_1	hypothetical protein
env_419_10	predicted inactivated transposase
env_442_2	integrase/recombinase
env_442_5	hypothetical protein
env_442_6	hypothetical protein
env_450_5	conserved hypothetical protein
env_450_6	hypothetical protein
env_476_1	hypothetical protein
env_476_2	hypothetical protein
env_580_5	hypothetical protein
env_588_4	hypothetical protein
env_588_6	hypothetical protein
env_636_3 env_636_4	hypothetical protein hypothetical protein
env_636_5	hypothetical protein
env_663_5	conserved hypothetical protein (possible ATPase)
env_701_2	hypothetical protein (possible ATI ase)
env_701_2 env_711_6	integrase/recombinase
env_711_0 env_722_3	hypothetical protein
env 722_5	possible glycosyltransferase
env 833 3	hypothetical protein
env 848 4	possible glycosyltransferase
env 932 3	hypothetical protein
env 986 2	ABC-type sugar transport system, substrate-binding component
env 1120 3	predicted protease
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1