

Table S2. Transposons related to TnXax1**A) TnPa43 :19,903 bp – Source: ISfinder**

Locus Tag	Element ID	Coordinates	Length	Orientation	Predicted Product
n/d	ISPa43_00001	43..1,824	1,782	-	Methyltransferase domain protein
n/d	ISPa43_00002	2,224..2,451	228	-	hypothetical protein
n/d	ISPa43_00003	2,769..3,629	861	+	ectoine hydroxylase
n/d	ISPa43_00004	3,654..4,550	897	+	Phosphate-import protein PhnD precursor
n/d	ISPa43_00005	4,674..5,522	849	+	Phosphate-import permease protein PhnE
n/d	ISPa43_00006	5,556..6,368	813	+	Phosphate-import ATP-binding protein PhnC
n/d	ISPa43_00007	6,380..6,925	546	+	phosphonate ABC transporter, permease protein PhnE
n/d	ISPa43_00008	7,011..7,412	402	+	Phosphate-import permease protein PhnE
n/d	ISPa43_00009	7,439..7,918	480	+	phosphonate C-P lyase system protein PhnG
n/d	ISPa43_00010	7,911..8,495	585	+	Alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnH
n/d	ISPa43_00011	8,495..9,616	1,122	+	Alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnI
n/d	ISPa43_00012	9,613..10,518	906	+	Alpha-D-ribose 1-methylphosphonate 5-phosphate C-P lyase
n/d	ISPa43_00013	10,744..11,316	573	+	Putative phosphonates utilization ATP-binding protein PhnK
n/d	ISPa43_00014	11,330..12,055	726	+	Alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnL
n/d	ISPa43_00015	12,052..13,206	1,155	+	Alpha-D-ribose 1-methylphosphonate 5-triphosphate diphosphatase
n/d	ISPa43_00016	13,220..13,789	570	+	Ribose 1,5-bisphosphate phosphokinase PhnN
n/d	ISPa43_00017	13,780..14,547	768	+	Phosphoribosyl 1,2-cyclic phosphodiesterase
n/d	ISPa43_00018	14,544..15,353	810	+	phosphonate utilization associated putative membrane protein
n/d	ISPa43_00019	15,471..16,805	1,335	+	site-specific tyrosine recombinase XerD (TnpI)
n/d	ISPa43_00020	16,862..19,849	2,988	+	Transposase, TnpA family (DDE domain)

B) TnStma1: 28,714 bp from Stenotrophomonas maltophilia D457 - NC_017671

Locus Tag	Element ID	Coordinates	Length	Orientation	Predicted Product
SMD_2129	ISSStma18_00001	84..1,142	1,059	-	chromosome segregation protein SMC
SMD_2130	ISSStma18_00002	1,465..1,857	393	+	hypothetical protein
SMD_2131	ISSStma18_00003	1,929..3,233	1,305	+	type I secretion outer membrane protein, TolC family
SMD_2132	ISSStma18_00004	3,230..4,726	1,497	+	Cation efflux system protein CusB precursor
SMD_2133	ISSStma18_00005	4,723..7,884	3,162	+	Cation efflux system protein CusA
SMD_2134	ISSStma18_00006	7,930..8,286	357	+	hypothetical protein
SMD_2135	ISSStma18_00007	8,379..8,780	402	+	Cation efflux system protein CusF precursor
SMD_2136	ISSStma18_00008	9,152..9,661	510	-	Lipoprotein signal peptidase
SMD_2137	ISSStma18_00009	9,654..10,901	1,248	+	Sodium/calcium exchanger protein
SMD_2138	ISSStma18_00010	10,924..11,244	321	-	Nitrogen regulatory protein P-II
SMD_2139	ISSStma18_00011	11,244..14,369	3,126	-	Cation efflux system protein CzcA
SMD_2140	ISSStma18_00012	14,407..15,597	1,191	-	Nickel and cobalt resistance protein CnrB
SMD_2141	ISSStma18_00013	15,594..16,871	1,278	-	Cation efflux system protein CzcC
n/d	ISSStma18_00014	17,170..17,337	168	+	hypothetical protein
SMD_2142	ISSStma18_00015	17,575..19,971	2,397	-	putative cadmium-transporting ATPase
SMD_2143	ISSStma18_00016	19,968..21,938	1,971	-	Ferrous iron uptake protein
SMD_2144	ISSStma18_00017	22,127..22,567	441	+	Copper export regulator
SMD_2145	ISSStma18_00018	22,605..24,251	1,647	+	Glutamine-dependent NAD(+) synthetase
SMD_2146	ISSStma18_00019	24,226..25,527	1,302	+	site-specific tyrosine recombinase XerD (TnpI)
SMD_2147	ISSStma18_00020	25,566..28,550	2,985	+	Transposase, TnpA family (DDE domain)

C) TnXca1: 11,523 bp from X. campestris pv. vesicatoria str. 85-10 plasmid pXCV183 - NC_007507

Locus Tag	Element ID	Coordinates	Length	Orientation	Predicted Product
XCVd0093	ISXca_00001	352..1,389	1,038	+	hypothetical protein
XCVd0094	ISXca_00002	1,377..2,444	1,068	-	chromosome segregation protein SMC
XCVd0095	ISXca_00003	2,635..2,838	204	+	hypothetical protein
XCVd0096	ISXca_00004	2,890..3,603	714	+	Site-specific recombinase XerD
XCVd0097	ISXca_00005	3,612..6,575	2,964	+	Transposase, TnpA family
XCVd0098	ISXca_00006	6,906..8,132	1,227	-	Plasmid encoded RepA protein
XCVd0099	ISXca_00007	8,412..9,599	1,188	-	UDP-N-acetylglucosamine kinase
XCVd0100	ISXca_00008	9,606..9,869	264	-	hypothetical protein
XCVd0101	ISXca_00009	9,894..10,295	402	-	tRNA(fMet)-specific endonuclease VapC
XCVd0102	ISXca_00010	10,292..10,552	261	-	Virulence-associated protein
XCVd0103	ISXca_00011	10,742..11,308	567	+	DNA-invertase hin

D) Tn*Tin1*: 6,123 bp from *Thiomonas intermedia* K12 - CP002021 - Only Transposition related genes

Locus Tag	Element ID	Coordinates	Length	Orientation	Predicted Product
Tint_1402	ISTin1_00001	49..2,268	2,219	-	Transposase, TnpA family
Tint_1403	ISTin1_00002	2,265..3,083	818	-	recombinase
Tint_1404	ISTin1_00003	3,076..4,596	1,520	-	Integrase
Tint_1405	ISTin1_00004	4,981..6,081	1,100	+	chromosome segregation protein SMC