

Supplementary data

Table S1: A list of all phage genomes used for in-silico analysis and their identity to phage AV101.

Genus*	Phages	Query cover	Percent identity	Accession
Unclassified Aglimvirinae	Enterobacter phage fGh-Ecl02	87%	97.54%	ON212266.1
	Escherichia phage PH4	85%	97.83%	ON184126.1
	Escherichia phage PC3	85%	97.83%	ON184125.1
	Escherichia phage vB_EcoM-RPN242	88%	97.74%	OL656110.1
	Escherichia phage vB_EcoM-ZQ1	85%	97.57%	MW650886.1
Agtrevirus	Shigella phage phiSboM-AG3	85%	92.25%	NC_013693.1
	Salmonella phage P46FS4	85%	92.08%	NC_049509.1
	Salmonella phage SKML-39	85%	91.76%	JX181829.1
	Shigella phage vB_SboS_Gloob	85%	92%	OL615011.1
	Shigella phage vB_SboM_ChubbyThor	85%	93.03%	OL615013.1
	Shigella phage MK-13	84%	91.94%	NC_049455.1
	Enterobacter phage EspM4VN	83%	90.23%	NC_049384.1
	Salmonella phage pSal-SNUABM-02	82%	90.52%	MT857002.1

Table S2: overview of genes marked in Figure 1. The genes that are highlighted in Figure 1 are listed below in the order seen in the figure (right to left).

Phage SNUAMB-02	Gene product	Function	Position	Colour on Fig 1
	105	hypothetical protein	2620..3789	Blue
	106	Putative tail spike protein	3842..6877	Blue
	107	Putative tail spike protein	6930..9353	Blue
	128	hypothetical protein	29730..31052	Orange
	202	putative ribonucleoside-diphosphate reductase subunit alpha	79811..80470	Red
	203	putative ribonucleotide-diphosphate reductase subunit beta	80638..82812	Red
	5	Putative thymidylate synthase	97785..98357	Red
	6	putative dNMP kinase	98374..99423	Red
	7	putative dCTP pyrophosphatase	99423..99989	Red
	84	putative homing endonuclease	144086..144283	Orange
Phage EspM4VN	Gene product	Function	Position	Colour on Fig. 1
	213	hypothetical protein	2620..3831	Blue
	214	hypothetical protein	3884..7213	Blue
	215	hypothetical protein	7259..9055	Blue
	216	hypothetical protein	9110..11674	Blue
	165	ribose-phosphate pyrophosphokinase	50312..51106	Green
	164	nicotinamide phosphoribosyltransferase	51217..52071	Green
	119	ribonucleoside-diphosphate reductase	80789..81631	Red
	118	NrdB ribonucleotide reductase subunit beta	81717..83996	Red
	97	part of thymidylate synthase	97641..98027	Red
	96	part of thymidylate synthase	98268..98534	Red
	95	part of thymidylate synthase	98492..98833	Red
	94	hypothetical protein	98817..98978	Red
	1	putative dUTP diphosphatase	99231..99611	Red

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	76	hypothetical protein	143742..143939	Orange
Phage fGh-Ecl02	Protein Id	Function	Position	Colour on Fig 1
	USL85809.1	hypothetical protein	3857..6853	Blue
	USL85810.1	hypothetical protein	6932..9034	Blue
	USL85811.1	hypothetical protein	9114..11777	Blue
	USL85812.1	hypothetical protein	11835..14468	Blue
	USL85832.1	putative homing endonuclease	34301..35827	Orange
	USL85896.1	ribonucleoside-diphosphate reductase subunit alpha	79932..82214	Red
	USL85897.1	ribonucleotide reductase beta subunit	82285..83388	Red
	USL85921.1	putative dUTP diphosphatase	97956..98510	Red
	USL85922.1	hypothetical protein	98510..99055	Red
	USL85923.1	RecA-like recombination protein	99040..100125	Red
	USL85792.1	putative homing endonuclease	138315..139913	Orange
Phage AV101	Gene product	Function	Position	Colour on Fig x
	Peg 193	Tail spike protein 4	3884..7162	Blue
	Peg 192	Tail spike protein 3	7466..9412	Blue
	Peg 191	Hypothetical protein	9445..9600	Blue
	Peg 190	Tail spike protein 2	9952..12240	Blue
	Peg 189	Tail spike protein 1	12288..14489	Blue
	Peg 188	Hypothetical protein	14832..14957	Blue
	Peg 169	hypothetical protein	34502..35974	Orange
	Peg 141	Ribose-phosphate pyrophosphokinase	53586..54440	Green
	Peg 140	Nicotinamide phosphoribosyltransferase	54437..56101	Green
	Peg 101	ribonucleotide reductase of class Ia (aerobic) alpha subunit	83581..85863	Red
	Peg 100	ribonucleotide reductase of class Ia (aerobic) beta subunit	85934..87037	Red
	Peg 78	Putative thymidylate synthase	99997..101043	Red
	Peg 77	Hypothetical protein	101040..101609	Red
	Peg 76	putative dUTP diphosphatase	101606..102160	Red
	Peg 14	putative homing endonuclease	141564..142481	Orange

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	Peg 13	putative homing endonuclease	142474..143160	Orange
Phage ZQ1	Protein id	Function	Position	Colour on Fig. 1
	QVW27043.1	Tail fibers protein	3884..7006	Blue
	QVW27042.1	Tail spike protein	7106..9001	Blue
	QVW27222.1	Hypothetical protein	9221..9685	Blue
	QVW27221.1	hypothetical protein	9756..10157	Blue
	QVW27209.1	Putative homing endonuclease	22741..24525	Orange
	QVW27201.1	Putative homing endonuclease	30520..31992	Orange
	QVW27144.1	ribonucleotide reductase of class Ia (aerobic) alpha subunit	75315..77597	Red
	QVW27143.1	ribonucleotide reductase of class Ia (aerobic) beta subunit	77668..78771	Red
	QVW27122.1	Putative thymidylate synthase	91465..92511	Red
	QVW27121.1	putative deoxynucleotide monophosphate kinase	92508..93077	Red
	QVW27120.1	putative dUTP diphosphatase	93074..93628	Red
	QVW27062.1	putative homing endonuclease	133656..135254	Orange
Phage PC3	Gene product	Function	Position	Colour on Fig. 1
	1	hypothetical protein	3875..7036	Blue
	2	Tail spike protein 3	7136..9685	Blue
	3	Tail spike protein 2	9961..12384	Blue
	4	Tail spike protein	12703..14928	Blue
	16	homing endonuclease	28584..30272	Orange
	25	homing endonuclease	36488..38353	Orange
	88	ribonucleotide reductase of class Ia (aerobic) alpha subunit	81541..83823	Red
	89	Hypothetical protein	83893..84186	Red
	90	ribonucleotide reductase of class Ia (aerobic) beta subunit	84188..85291	Red
	112	thymidylate synthase	98260..99306	Red
	113	hypothetical protein	99303..99872	Red
	114	putative dUTP diphosphatase	99869..100423	Red
Phage PH4	Gene product	Function	Position	Colour on Fig. 1
	1	hypothetical protein	3875..7036	Blue
	2	Tail spike protein 3	7136..9685	Blue

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	3	Tail spike protein 2	9961..12384	Blue
	4	Tail spike protein	12703..14928	Blue
	16	homing endonuclease	28584..30272	Orange
	25	homing endonuclease	36488..38353	Orange
	88	ribonucleotide reductase of class Ia (aerobic) alpha subunit	81541..83823	Red
	89	Hypothetical protein	83893..84186	Red
	90	ribonucleotide reductase of class Ia (aerobic) beta subunit	84188..85291	Red
	112	thymidylate synthase	98260..99306	Red
	113	hypothetical protein	99303..99872	Red
	114	putative dUTP diphosphatase	99869..100423	Red
Phage RPN242	Gene product	Function	Position	Colour on Fig x
	164	Tail fibers protein	2620..3810	Blue
	163	Tail fiber protein	3863..7024	Blue
	162	Tail spike protein	7124..9673	Blue
	161	hypothetical protein	9792..12200	Blue
	142	homing endonuclease	33187..34509	Orange
	76	ribonucleoside-diphosphate reductase subunit alpha	79585..80427	Red
	75	Hypothetical protein	80511..82793	Red
	74	ribonucleotide-diphosphate reductase subunit beta	82863..83156	Red
	52	thymidylate synthase	96571..97230	Red
	51	Hypothetical protein	97230..98276	
	50	2-deoxyuridine 5-triphosphate nucleotidohydrolase	98273..98842	Red
	184	putative homing endonuclease	138680..138877	Orange
	183	homing endonuclease	138880..139785	Orange
Phage SKML-39	Gene product	Function	Position	Colour on Fig x
	207	hypothetical protein	3884..6943	Blue
	208	hypothetical protein	6991..8916	Blue
	1	Hypothetical protein	9543..11813	Blue
	2	hypothetical protein	11863..14001	Blue

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	48	ribose-phosphate pyrophosphokinase	52051..52905	Green
	49	nicotinamide phosphoribosyltransferase	52902..54566	Green
	90	ribonucleotide reductase of class Ia (aerobic) alpha subunit	81930..84212	Red
	91	Hypothetical protein	84283..84576	
	92	ribonucleotide reductase of class Ia (aerobic) beta subunit	84578..85681	Red
	115	Hypothetical protein	99516..100562	Red
	116	Hypothetical protein	100562..101128	Red
	117	Hypothetical protein	101125..101679	Red
	186	Hypothetical protein	143031..143948	Orange
Phage Gloop	Gene product	Function	Position	Colour on Fig. 1
	169	putative right handed beta helix region family	2635..3846	Blue
	168	Putative tail spike protein	3869..6901	Blue
	167	Putative tail spike protein	6931..8979	Blue
	166	putative right-handed parallel beta- helix	9164..11386	Blue
	121	putative ribose-phosphate pyrophosphokinase	49301..49540	Green
	120	putative nicotinamide	49801..50655	Green
	79	putative ribonucleoside-diphosphate	79633..80508	Red
	78	hypothetical protein	80594..82873	Red
	77	putative ribonucleotide reductase subunit	82944..83237	Red
	55	putative thymidylate synthase	97367..98413	Red
	54	putative P-loop containing nucleoside	97367..98413	Red
	53	putative dUTP diphosphatase	98410..98979	Red
	195	putative homing endonuclease	141345..141548	Orange
Phage ChubbyThor	Gene product	Function	Position	Colour on Fig. 1

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	3	putative right handed beta helix region family	2635..3846	Blue
	2	putative head binding protein	3869..6793	Blue
	1	putative tail fibers protein	6875..9007	Blue
	208	putative tail protein	9138..11843	Blue
	189	Putative HNH endonuclease	31758..33089	Orange
	163	putative ribose-phosphate pyrophosphokinase	51049..51843	Green
	162	putative nicotinamide	51954..52808	Green
	118	putative ribonucleotide diphosphate reductase	82796..83455	Red
	117	putative ribonucleotide-diphosphate reductase	83515..85803	Red
	95	Putative thymidylate synthase	99046..99720	Red
	94	putative dNMP kinase	99717..100766	Red
	93	putative dUTP diphosphatase	100763..101332	Red
	27	Hypothetical proteins	143610..143813	Orange
	26	putative endonuclease	143810..144727	Orange
Phage Ag3	Gene product	Function	Position	Colour on Fig. 1
	178	hypothetical protein	2620..3831	Blue
	177	Tailspike protein	3884..6943	Blue
	176	Tailspike protein	6990..9011	Blue
	175	hypothetical protein	9212..11473	Blue
	130	putative nicotinamide phosphoribosyl transferase	49705..51348	Green
	83	NrdA ribonucleoside-diphosphate reductase alpha subunit	80026..82305	Red
	82	Hypothetical protein	82376..82669	Red
	81	NrdB ribonucleotide reductase subunit beta	82671..83774	Red
	59	Putative thymidylate synthase	96118..96780	Red
	58	Hypothetical protein	96780..97826	Red
	57	putative dUTP diphosphatase	97823..98392	Red
	201	Hypothetical protein	141295..141492	Orange
	200	SegD-like protein	141495..142412	Orange

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Phage P46FS4	Gene product	Function	Position	Colour on Fig.
	1	hypothetical protein	3884..6943	Blue
	2	Tail spike protein	6990..7469	Blue
	3	Hypothetical protein	7450..8997	Blue
	4	Tail spike protein	9053..11476	Blue
	5	Tail fibers protein	11639..14101	Blue
	50	ribose-phosphate pyrophosphokinase	50468..51322	Green
	51	nicotinamide phosphoribosyltransferase	51319..52983	Green
	94	ribonucleotide reductase of class Ia (aerobic) alpha subunit	81226..83505	Red
	95	Hypothetical protein	83576..83869	Red
	96	ribonucleotide reductase of class Ia (aerobic) beta subunit	83871..84974	Red
	118	Putative thymidylate synthase	97995..99041	Red
	119	Hypothetical protein	99038..99607	Red
	120	putative dUTP diphosphatase	99604..100158	Red
	190	SegD-like protein	142956..143642	Orange
Phage MK-13	Gene product	Function	Position	Colour on Fig. 1
	202	hypothetical protein	2620..3831	Blue
	201	hypothetical protein	3884..6778	Blue
	200	Hypothetical protein	6860..8962	Blue
	199	hypothetical protein	9040..11820	Blue
	154	hypothetical protein	49429..50223	Green
	153	hypothetical protein	50334..51188	Green
	110	ribonucleoside-diphosphate reductase large subunit	80661..81503	Red
	109	hypothetical protein	81589..83868	Red
	6	hypothetical protein	98258..98920	Red
	7	hypothetical protein	98920..99966	Red
	8	hypothetical protein	99963..100532	Red
	75	hypothetical protein	141787..141984	Orange

Table S3: In-silico analysis of TSP1-4. TSP1 and TSP3 show sequence similarity to *E. coli* genomes suggesting similarity to prophages. TSP2 and TSP4 show similarity to other phages.

	Hit	Organism	Accession number genome	Query cover	Percentage identity	Protein ID
TSP1	Phage head-binding domain-containing protein	Escherichia coli H001 contig 1.26	ADIW01000026	78%	66.49%	OSK75853.1
	Phage tailspike protein	Escherichia coli strain 89 contig 15	JAIZTL010000015	78%	66.32%	MCA8532455.1
	Phage head-binding domain-containing protein	Escherichia coli CHS 77 contig 1.1.C4	JMVO01000004	78%	65.97%	KDG58944.1
TSP2	Hypothetical protein	<i>E. coli</i> phage A221	ON862890.1	100%	100%	UTQ72550.1
	Hypothetical protein	Escherichia coli isolate CP21	DADPIP010000000	68%	91.73%	HAZ7467268.1
	Tail spike protein	Salmonella phage UAB_1	OL656106.1	68%	92.12%	UIS31512.1
TSP3	Hypothetical protein	Escherichia coli strain 705003 MRSN705003_contig00003	JAKYFG010000003	85%	83.63%	MCN8021000.1
	Hypothetical protein	Escherichia coli strain 767377 MRSN767377_contig00056	JAMEID010000056	85%	83.63%	MCN3003243.1
	Hypothetical protein	Escherichia coli strain VRES0635	UDHQ01000018	85%	83.45%	MCY6644629.1
TSP4	Tail fiber protein	phage SaIM-LPST94	MH523359.1	68%	90.91%	AXF41694.1
	Tail spike protein	phage vB_EcoM-Ro121c4YLVW	MH051333.1	61%	70.49%	YP_009984889.1
	Tail fiber protein	phage ST31	KY962008.1	60%	68.86%	YP_009790654.1

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Table S4: Prophage identified in the *E. coli* sequences. PHASTER analysis of the *E. coli* genomes that carried proteins with similarity towards the TSPs of AV101.

	Assesion number	Prophage length	Completeness (Score)	No. of proteins	Region position	Most common phage	GC %
TSP1:							
Escherichia coli H001 contig 1.26	ADIW01000026	27 Kb	Questionable (70)	33	413-27507	PHAGE_Enterо_Sf101	46.03
Escherichia coli strain 89 contig 15	JAIZTL010000015	44.2 Kb	Intact (150)	60	39194-83481	PHAGE_Enterо_Sf101	47.85
Escherichia coli CHS 77 contig 1.1.C4	JMVO01000004	41.9 Kb	Intact (120)	57	25895-67861	PHAGE_Enterо_IME10	47.29
TSP2:							
Escherichia coli isolate CP21	DADPIP010000000	145.9 Kb	Intact (133)	236	326-146309	PHAGE_Enterо_phi92	37.48
TSP3:							
Escherichia coli strain 705003 MRSN705003_contig00003	JAKYFG010000003	43.6 Kb	Intact (150)	60	280671-324348	PHAGE_Enterо_mEp390	47.16
Escherichia coli strain 767377 MRSN767377_contig00056	JAMEID010000056	43.7 Kb	Intact (150)	61	19221-62927	PHAGE_Enterо_mEp390	47.17
Escherichia coli strain VRES0635, contig: ERS792374SCcontig000018	UDHQ01000018	14.1 Kb	Questionable (80)	21	11789-25952	PHAGE_Enterо_HK140	44.15

Table S5: List of bacteria used in the study.

Genus	Species or serovar	KU ID	Serotype	Origin	Reference
<i>Escherichia</i>	coli	BL21(DE3)	ND	Invitrogen	Protein expression
<i>Escherichia</i>	coli	Stellar cells	ND	Takara Bio	Plasmid propagation strain
<i>Salmonella</i>	Typhimurium	LT2c	O4	(54)	Host range analysis
<i>Salmonella</i>	Derby	EGS1	O4	JEO	Host range analysis
<i>Salmonella</i>	Enteritidis	EGS48	O9	JEO	Host range analysis
<i>Salmonella</i>	Seftenberg	EGS381	O3	JEO	Host range analysis
<i>Salmonella</i>	Anatum	EGS388	O3,10	JEO	Host range analysis
<i>Salmonella</i>	Onderstepoort	EGS391	O6	JEO	Host range analysis
<i>Salmonella</i>	Minnesota	JEO3	O21	JEO	Host range analysis
<i>Escherichia</i>	coli	ESBL038	O8	In prep.	Host range analysis
<i>Escherichia</i>	coli	ESBL040	O8	In prep.	Host range analysis
<i>Escherichia</i>	coli	ESBL048	O82	In prep.	Host range analysis
<i>Escherichia</i>	coli	ESBL079	O82	In prep.	Host range analysis
<i>Escherichia</i>	coli	ESBL082	O82	In prep.	Host range analysis
<i>Escherichia</i>	coli	ESBL058	O153	In prep.	Host range analysis
<i>Escherichia</i>	coli	ESBL078	O153	In prep.	Host range analysis
<i>Escherichia</i>	coli	ESBL089	O153	In prep.	Host range analysis
<i>Escherichia</i>	coli	ESBL144	O159	In prep.	Host range analysis
<i>Escherichia</i>	coli	ECOR1	O144:H4	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR2	O48:H32	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR3	O1:H32	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR4	OR:H?	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR5	O?:H6	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR6	O173:H?	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR7	O8:H45	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR8	O86:H2	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR9	O167:H-	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR10	O6:H10	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR11	O10:H-	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR12	O?:H32	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR13	OR:H25	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR14	O71:H4	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR15	O25:H30	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR16	O9:H10	(57)	Host range analysis

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<i>Escherichia</i>	coli	ECOR17	O29:H-	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR18	O?:H11	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR19	O89:H?	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR20	O121:H11	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR21	O121:H11	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR22	O150:H28	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR23	O25:H1	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR24	O15:H-	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR25	O127:H40	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR26	O104:H21	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR27	O104:H21	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR28	O104:H21	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR29	O150:H21	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR30	O113:H21	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR31	O79:H25	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR32	O25:H1	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR33	O7:H21	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR34	O88:H-	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR35	O1:H-	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR36	O1:H-	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR37	O55:H7	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR38	O7:H-	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR39	O7:H-	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR40	O7:H-	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR41	O7:H-	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR42	O87:H26	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR43	O?:H18	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR44	O17:H34	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR45	O?:H2	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR46	O1:H-	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR47	O17:H18	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR48	O23:H15	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR49	O2:H4	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR50	O2:H4	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR51	O25:H1	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR52	O25:H1	(57)	Host range analysis

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<i>Escherichia</i>	coli	ECOR53	O4:H5	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR54	O25:H1	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR55	O25:H1	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR56	O6:H10	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR57	O2:H1	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR58	O112:H8	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR59	O2:H4	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR60	O4:H5	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR61	O2:H4	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR62	O2:H4	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR63	OR:H-	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR64	O75:H-	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR65	O8:H10	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR66	O4:H40	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR67	O141:H49	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR68	O25:H21	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR69	O86:H10	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR70	O78:H-	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR71	OR:H19	(57)	Host range analysis
<i>Escherichia</i>	coli	ECOR72	O8:H30	(57)	Host range analysis
<i>Escherichia</i>	coli	NCTC12900	O157:H7	JEO	Host range analysis
<i>Escherichia</i>	coli	ATCC35150	O157:H7	JEO	Host range analysis
<i>Escherichia</i>	coli	ATCC43888	O157:H7	JEO	Host range analysis
<i>Escherichia</i>	coli	ATCC43895	O157:H7	JEO	Host range analysis
<i>Escherichia</i>	coli	JEO1894	O149:K88	JEO	Host range analysis
<i>Escherichia</i>	coli	MG1665	K12		Host range analysis

Supplementary data - Agtrevirus phage AV101 infect diverse extended spectrum β -lactamase *E. coli* by recognizing four different O-antigens

Figure S1

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Salmonella phage pSal-SNUABM-02	1		87,58	87,09	87,28	86,98	88,10	87,86	87,69	88,05	86,89	87,06	88,15	87,09
Enterobacter phage EspM4VN	2	86,64		87,67	87,76	87,65	89,40	88,95	88,68	89,18	87,81	87,86	88,89	87,67
Shigella phage vB_SboM_ChubbyThor	3	87,58	88,79		90,53	89,84	90,93	95,47	96,59	94,78	95,97	90,35	90,32	95,07
Escherichia phage PH4	4	87,09	87,67	90,53		96,82	97,24	90,87	90,80	90,61	90,91	96,77	95,85	100,00
Escherichia phage vB_EcoM-ZQ1	5	87,28	87,76	89,84	96,82		96,75	90,97	90,62	90,23	90,79	95,86	96,16	90,20
Escherichia phage vB_EcoM-RPN242	6	86,98	87,65	90,93	97,24	96,75		90,97	91,11	90,93	91,39	96,13	96,00	90,90
Salmonella phage P46FS4	7	88,10	89,40	95,47	90,87	90,97	90,97		95,91	95,19	95,93	90,76	91,02	95,51
Shigella phage Ag3	8	87,86	88,95	96,59	90,80	90,62	91,11	95,91		95,34	95,99	90,56	90,57	95,44
Salmonella phage SKML-39	9	87,69	88,68	94,78	90,61	90,23	90,93	95,19	95,34		95,58	90,01	90,39	95,46
Shigella phage MK-13	10	88,05	89,18	95,97	90,91	90,79	91,39	95,93	95,99	95,58		90,86	90,97	95,41
Enterobacter phage fGh-Ecl02	11	86,89	87,81	90,35	96,77	95,86	96,13	90,76	90,56	90,01	90,86		96,75	90,25
Escherichia phage AV101	12	87,06	87,86	90,32	95,85	96,16	96,00	91,02	90,57	90,39	90,97	96,75		90,49
Shigella phage vB_SboS_Gloob	13	88,15	88,89	95,07	90,55	90,20	90,90	95,51	95,44	95,46	95,41	90,25	90,49	
Escherichia phage PC3	14	87,09	87,67	90,52	100,00	96,82	97,24	90,87	90,80	90,61	90,91	96,77	95,84	90,55

Figure S1: Average Nucleotide Identity of the 14 Agtrevirus genomes. All 14 phages were compared and showed that they all belong to the Agtrevirus genus.

Figure S2

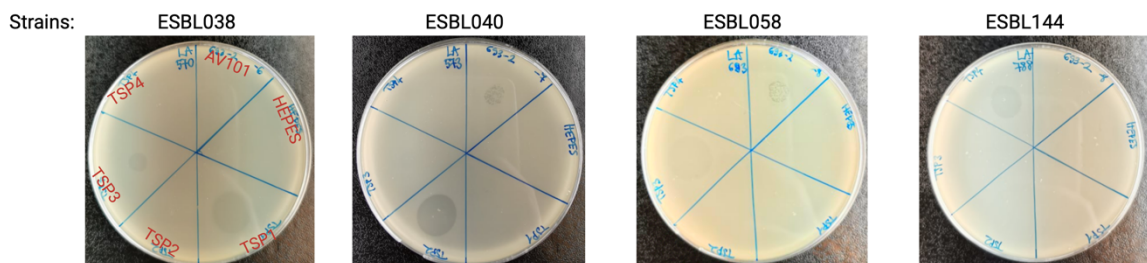


Figure S2: Each TSPs of AV101 show enzymatic activity towards different AV101 hosts. Each purified TSPs were spotted on the known AV101 phage hosts to investigate their enzymatic activity towards the O-antigen chain. The protein buffer (HEPES) was added as a negative control.

Figure S3

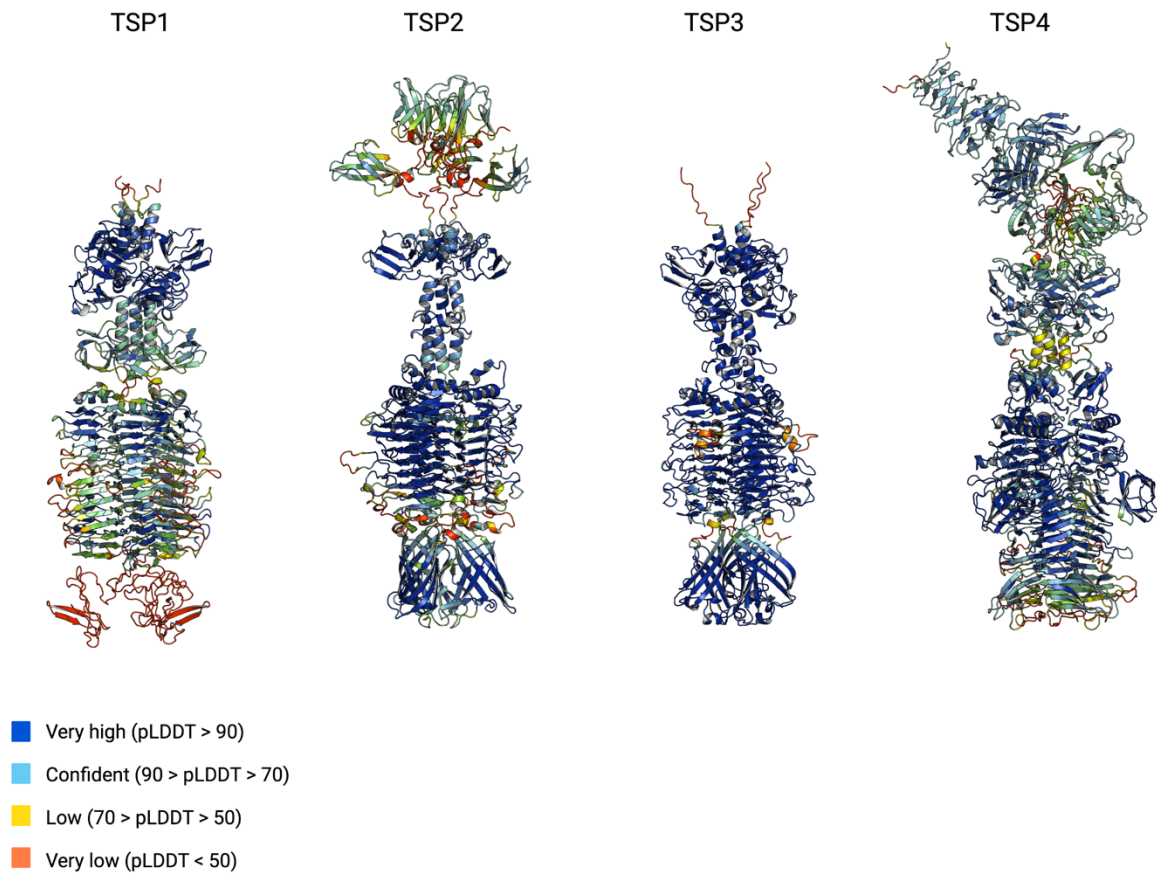


Figure S3: AlphaFold2 prediction of the four AV101 TSPs. The structures of the TSPs of AV101 have similar fold as other known TSPs. The structures are coloured after the β -score. The beta-helices, hence the receptor binding domain of the TSPs had a higher prediction score compared to the head-binding domains.

Figure S4

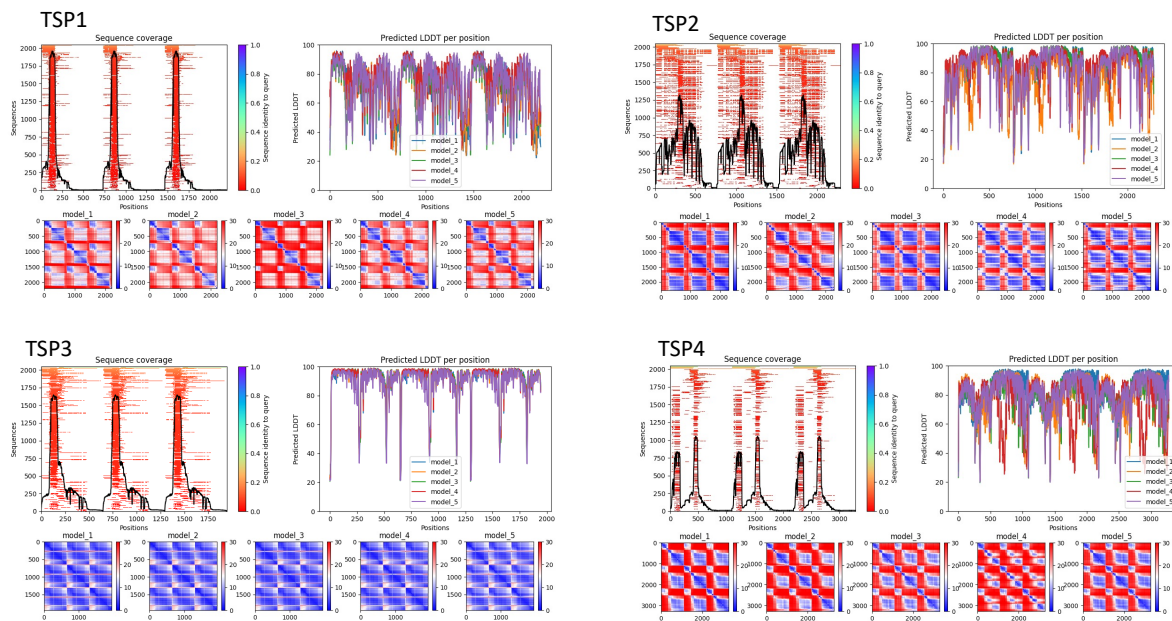


Figure S4: Prediction quality metrics plots from Alphafold2 for the four TSPs. The top-left graph represents the MSA coverage for each of the sequences. In the top-right is the pLDDT per position plot for the five final models for each TSP1. In the bottom is the Predicted Aligned Error matrix for the five final models for the four TSP1.