

Supplementary information

Table S1. Primers used to amplify the non-toxic and toxic control genes.

Primer	Sequence (restriction site underlined)	Description	Size
Non-toxic control genes amplification			
RTg121F	GCAGCGGCCGCATGAAAACCTATAATGA ATTATC	For the amplification of the ϕR1-RT g121 gene encoding the IplI internal head protein	273 bp
RTg121R	GGTCCATGGTTAGGAAGCTTTTTTAAGC		
RTg150F	GCAGCGGCCGCATGATTAAAGTTAATGA GC	For the amplification of the ϕR1-RT g150 gene encoding the phage DNA end protector	1728 bp
RTg150R	GGTGCTAGCCTATCCAATATCAATTCGTG AA		
RTg178F	GCAGCGGCCGCATGAGCAATATTAACCA GC	For the amplification of the ϕR1-RT g178 gene encoding the phage capsid vertex	1275 bp
RTg178R	GGTCCATGGTTATCCTGCTATTAGTTTAG G		
RTg119F	GCAGCGGCCGCATGAAAACGTATAAAGA ATTTTTG	For the amplification of the ϕR1-RT g119 gene encoding the IplII internal head protein	591 bp
RTg119R	GGTCCATGGTTAACGAACGTTAGTGCCA		
RTg246F	GCAGCGGCCGCATGTCTTTAAATGAAAT G	For the amplification of the ϕR1-RT g246 gene encoding Phage ribonuclease H	939 bp
RTg246R	GGTCCATGGTTAAAAATCATTTGCATG		
Toxic control genes amplification			
NregBF	GATCGCGGCCGCCATGACTATCAATAC AGAAG	For the amplification of the T4 regB gene encoding the T4 Reg B protein	491 bp
NregBR	GGCCGCTAGCTTACCTCATTGAGTTTTAA TTAC		
IyE174F	GCAGCGGCCGCATGGTACGCTGGACTTT GTG	For the amplification of the ϕ174 lytic gene E	276 bp
IyE174R	GGTCCATGGTCACTCCTTCCGCACGTAA		
NddF	GCAGCGGCCGCATGAAATATATGACTGT TACTG	For the amplification of the T4 ndd gene encoding the nuclear disruption protein (Ndd)	456 bp
NddR	GGTCCATGGTTAATATGCCTGTAAAACAA A		

dcd1IF	GCAG <u>CGGCCGC</u> AGCCTGCTGGAAAAAGG C	For the amplification of the dcd-1l gene on pETSmt3- DCD1L	144 bp
dcd1IR	GGT <u>CCATGG</u> TTACAGCACGCTATCCAGCA C		
ⓈR1-RT phage holins and lysins			
RTg122F	GCAGCGGCCGCATGAATTTATTTGAAATG CTAC	For the amplification of the ϕR1-RT g122 gene encoding the lysozyme	489 bp
RTg122R	GGTCCATGGTTATTTGTAGGCATCCATCG		
RTg252F	GCAGCGGCCGCATGCAGACTTATAAAGA GTCTC	For the amplification of the ϕR1-RT g252 gene encoding the holin	162 bp
RTg252R	GGTCCATGGTCAGCTTTTAGGTCTAAATG		
RTg253F	GCAGCGGCCGCATGAGTTCGCCACGTGTT AC	For the amplification of the ϕR1-RT g253 gene encoding the holin	657 bp
RTg253R	GGTCCATGGTTATCTTGATCTGCCTAACG		

Table S2. Primers used to amplify the HPUF genes from ϕ R1-RT phage.

Gene	Forward Primer (restriction site underlined)	Reverse Primer (restriction site underlined)	Size
g002	GCAG <u>CGGCCG</u> CATGAAAATGTATGCTTA TAAAAAT	GGT <u>CCATGG</u> TCACGGAATACTATTCAAC	258 bp
g004	GCAG <u>CGGCCG</u> CATGATTCATTCAATGAG AATTTC	GGT <u>CCATGG</u> TCAGGAGTTAAATCCTTCAC	306 bp
g011	GCAG <u>CGGCCG</u> CATGGATATTCTTACTGTG GG	GGT <u>CCATGG</u> TTATTCAAAAACCTTACGAAC	378 bp
g012	GCAG <u>CGGCCG</u> CATGAATAAGTCTGTAA TGATATCG	GGT <u>CCATGG</u> TTAGTCCTCAAAAATAATTCTG	393 bp
g014	GCAG <u>CGGCCG</u> CATGTCTATTGTAAAGTT GG	GGT <u>CCATGG</u> TTATAATCCAAATTCAGATTTA AG	381 bp
g016	GCAG <u>CGGCCG</u> CATGAAATTTCAATTGG G	GGT <u>CCATGG</u> TTATTTAGAACTAAGTTCATCT TCG	357 bp
g017	GCAG <u>CGGCCG</u> CATGGGTGCAAAGAATAT C	GGT <u>CCATGG</u> TTATTTAGAAGATTTAGGTAAT GG	291 bp
g019	GCAG <u>CGGCCG</u> CATGCAAAATAATCGTGT G	GGT <u>GCTAGC</u> TTATTGAATAATACCATTAGG G	270 bp
g022	GCAG <u>CGGCCG</u> CATGCTAAAAATTGATAA ACACAAT	GGT <u>CCATGG</u> TCATCGTAATGCCCTG	231 bp
g023	GCAG <u>CGGCCG</u> CATGTATAAATTGAATCC AGACC	GGT <u>CCATGG</u> TTAGCATAATAAGTTCTTCAAT TT	231 bp
g028	GCAG <u>CGGCCG</u> CATGATTATGTATAAAAT TAAATTTAG	GGT <u>CCATGG</u> TCATACAAAAGGCCACTGTG	474 bp
g030	GCAG <u>CGGCCG</u> CATGTATAAAGGAATCAT GAGC	GGT <u>CCATGG</u> CTACAAAATATAATCCATAGC AATTTT	270 bp
g033	GCAG <u>CGGCCG</u> CATGGCTGTTGGATTTACT AAAG	GGTCCATGGTCACCACAATCTAAACAATTC	132 bp
g043	GCAG <u>CGGCCG</u> CATGAAACTTAAAGTTTA CCGAG	GGT <u>CCATGG</u> TCATTTTACAAGTTCAACTTCT G	177 bp
g044	GCAG <u>CGGCCG</u> CATGAACTATTTAAAAAT TTCAATCC	GGT <u>CCATGG</u> TTATTTTCTCATGCAATTATTA AATTT	462 bp
g045	GCAG <u>CGGCCG</u> CATGGCACGACTAATTCT TATC	GGT <u>CCATGG</u> TTAAGATCTAGGGGCCAC	561 bp
g049	GCAG <u>CGGCCG</u> CATGTCTATTTCACACC AGAAC	GGT <u>CCATGG</u> CTAGTCAGATAATTCATTAGA AGC	198 bp
g061	GCAG <u>CGGCCG</u> CATGAAAATCGATTCAAA TCAG	GGT <u>CCATGG</u> TTATTTGTAAAATAATCTTCA AGG	201 bp

g064	GCAGCGGCCGCATGAAGAAAATTGGGGT G	GGTCCATGGCTAGGGTCCATTTGTTTTG	276 bp
g065	GCAGCGGCCGCATGCTAATTCAAACAAA ATTTAAG	GGTCCATGGTTACCATAATCGTTTCCAC	201 bp
g067	GCAGCGGCCGCATGAGCCTGAAGATTAA CC	GGTCCATGGTCATAATTCCTCGAAAGG	237 bp
g069	GCAGCGGCCGCATGATTAAAGTTAATTC TTTAAACC	GGTCCATGGTTAAAATGTTTCAAGTTCTTTA AG	369 bp
g070	GCAGCGGCCGCATGAAAAATCTTGCTCG AG	GGTCCATGGTCATGATAAATCCTTAGCAG	228 bp
g071	GCAGCGGCCGCATGAAATATATTCTTTAT ACTAAATCC	GGTCCATGGTTATTTTATTTCTGGATGTAAT	207 bp
g073	GCAGCGGCCGCATGATTGTATCTTCTAAA GCAAAC	GGTCCATGGTTATTTAATTTAGAGGCAATA ACC	225 bp
g074	GCAGCGGCCGCATGAAATATAAATTCAA AAGTTTTTAC	GGTCCATGGTTAGTGCCCTAATTTAAGTTTA AC	378 bp
g076	GCAGCGGCCGCGTGATTAATAAATTTTTT GCAC	GGTCCATGGTCAGATAGACGCATTTTTTAG	243 bp
g081	GCAGCGGCCGCATGAAAGGCCGCG	GGTCCATGGTCATTTTTTATATTTCTCTTCTA GG	345 bp
g083	GCAGCGGCCGCATGGAAATTAAAGTCGA TGAAATATA	GGTCCATGGTTAATCCTTATATTCTATATAA ATGTCTG	225 bp
g084	GCAGCGGCCGCATGAAAAATCAATTAAA TGAAG	GGTCCATGGTTAATTTCCATCAATAACTACC	204 bp
g085	GCAGCGGCCGCATGAATCCACTTGATATT ACTTAC	GGTCCATGGTCATAAAATTACCCAGCC	243 bp
g086	GCAGCGGCCGCATGGCTCGTAAATCATT G	GGTCCATGGTTAAGTAAAGTAACTGATGG TTTTC	234 bp
g087	GCAGCGGCCGCATGAGTTTATTCACTGA GTTAAAATATT	GGTCCATGGTCATTTTAGAGTTCTCAATGAT TC	879 bp
g089	GCAGCGGCCGCATGTCTACATCAAAGA TATTTTAG	GGTCCATGGTTAGATAACCTTAATCTGAGA AGG	792 bp
g090	GCAGCGGCCGCATGGCTACGCATACATT TG	GGTCCATGGCTATATTTTTCCACGATTGAG	120 bp
g091	GCAGCGGCCGCATGAATAACTGGGTGA GAATAC	GGTCCATGGTCATAAATCCTTCCATTTTAAG	447 bp
g092	GCAGCGGCCGCATGTTATATAGAATTAA ATATCGTCG	GGTCCATGGTTATTCATGAGAATCATATGG AC	438 bp

g093	GCAGCGGCCGCATGGAAATCGGCG	GGTCCATGGTTACCTCAGAAATTTAGATTTA ACTAC	135 bp
g094	GCAGCGGCCGCATGTCTTATATCTCTTAT GTATATCAAG	GGTCCATGGTCATTTAAGTTCTAAGGATTCA C	231 bp
g095	GCAGCGGCCGCATGCGTATTA AAAAGAT GTTATC	GGTCCATGGTTAAATTGTCACTGAATCATC	216 bp
g096	GCAGCGGCCGCATGCTTATGTTAGAGTCA TACAC	GGTCCATGGTCAATTTTCTAGAATAAAAGG TTC	117 bp
g098	GCAGCGGCCGCATGATTAATTTATCAAAT AGTAAAAAAA	GGTCCATGGTTAGACATTTATGTCTTTTAAC G	987 bp
g099	GCAGCGGCCGCATGAAACTAGAAATAGT TGATGTG	GGTCCATGGTTAATCATAATTTTCTCCATT TTAA	198 bp
g100	GCAGCGGCCGCATGGCTATCAAATCAGT GTC	GGTCCATGGTCACCACTTAAAGCTAACAT C	390 bp
g101	GCAGCGGCCGCATGAACGAAGGTTATAA TATTACATTTT	GGTCCATGGCTAGATATCAAATTTAGTAAA AGAAAAAG	396 bp
g102	GCAGCGGCCGCATGAGCATAAGCAAAG AAG	GGTCCATGGTTAATCAAAACGTACAGCG	168 bp
g104	GCAGCGGCCGCATGGAAATTGAGCTGAT TAG	GGTCCATGGTCATAGATAAATATGCGTCC	408 bp
g105	GCAGCGGCCGCATGATAGGGTTCACTAT ACTTAAATC	GGTCCATGGTTATTCAATCTCAATAAGTGGA C	273 bp
g106	GCAGCGGCCGCATGAGTTTACTGACTTGG GC	GGTCCATGGTTATTGACCCTTATTCATAGTT G	225 bp
g111	GCAGCGGCCGCATGAGAGAACATCTTAT TTCTAAAATAG	GGTCCATGGTCATTTGTCTTCCATTCC	174 bp
g112	GCAGCGGCCGCATGAAATTATTAGTGAG TATATTATTATGTG	GGTCCATGGTCATGAAATATCCTTAAATGAT AAAC	438 bp
g117	GCAGCGGCCGCATGGGAACACAAGCAA C	GGTCCATGGTCAATCATTCAAATGTTCC	204 bp
g124	GCAGCGGCCGCATGAGCGTAGCAATTTT TTTG	GGTCCATGGTTAATAGTCTTCAGAACTTTCA TAGTC	264 bp
g126	GCAGCGGCCGCATGTCTGTACTATTAGA AATTTCAATC	GGTCCATGGCTAGCAATCTGAACTTGATG	213 bp
g127	GCAGCGGCCGCATGGTCTATACTCCAGA ACAAATAG	GGTCCATGGTTAACACATATCACTTGATGA CAC	261 bp
g128	GCAGCGGCCGCATGAGTCGTTCAACTGA ATTG	GGTCCATGGTTAGCAAGAAGATGATTCCC	222 bp

g129	GCAGCGGCCGCATGATATATTATTTCCG GCC	GGTCCATGGTCATTTATTACCTCTACAATAA GTTATG	150 bp
g130	GCAGCGGCCGCATGATTATACGACAAA AGATTATAAC	GGTCCATGGTTATACAACACGATAATCACC	288 bp
g132	GCAGCGGCCGCATGACTACTTTCAATAC CGTAAC	GGTCCATGGTTAAATTAAATTGTACAACCA ATTATG	201 bp
g135	GCAGCGGCCGCATGGATTTTGGTCAAAA G	GGTCCATGGTTAAGCTTTATCTTTGATAATA GG	552 bp
g136	GCAGCGGCCGCATGGGTTATATTTTAGGT TTG	GGTCCATGGTCAGAAAAAGTATATAGGTTT TACTTC	336 bp
g137	GCAGCGGCCGCATGAAAATTGCTGAACT AATTC	GGTCCATGGCTATGAGGACTTAGAAATTGT ATTC	183 bp
g138	5'GCAGCGGCCGCATGGATTATACTCATTT ACAAGTG	GGTCCATGGTTATGAAACTTGGCATTTAGG	318 bp
g141	GCAGCGGCCGCATGAATACGCATCAAAA ACG	GGTCCATGGTTATTTACCCGTCCAAGAAGC	195 bp
g167	GCAGCGGCCGCATGCGAAAGAATAAGA ACG	GGTCCATGGCTAAAAATTGCATAAGAAGTC C	600 bp
g177	GCAGCGGCCGCATGGATATATCTATTTAT AAAGATAAAAAATG	GGTCCATGGTTAAATAGATTCAAATACTAA ATTACCTG	1515 bp
g181	GCAGCGGCCGCATGAATAAATCAGTTGA AGTAC	GGTCCATGGTTATAAAGCAAATAACATCTG C	234 bp
g199	GCAGCGGCCGCATGGCTATTTTGCCTTTT AAG	GGTCCATGGTTAGTGACCTACAAAAGCAAG	273 bp
g202	GCAGCGGCCGCATGGATGTATTTGCAAA GC	GGTCCATGGTCAATAATTCGTGCCATAATA AG	177 bp
g204	GCAGCGGCCGCATGGTAGTTAAAATTGT AAGTATGTC	GGTCCATGGTCATTTAGTTTCTCGCTTTTTAG	189 bp
g205	GCAGCGGCCGCATGAATAAATTTATGGA TGGTG	GGTCCATGGTTACTTAGATAATTCGGATTCA ATG	198 bp
g206	GCAGCGGCCGCATGGACTTCTTTAAAGA AAATACC	GGTCCATGGTCAATCAGGATATTTAGTTTCA AG	570 bp
g208	GCAGCGGCCGCATGGATTTCTTCAAAGA AAAC	GGTCCATGGTTATACCTCGGTTTTGTTTAATT TATA TTG	525 bp
g209	GCAGCGGCCGCATGAACTACATTAAC TTT GAACG	GGTCCATGGTTAAAAAGTAAATTCATTAGA AACTATATC	360 bp
g210	GCAGCGGCCGCATGTCCAAAAATAAAGC TAAAG	GGTCCATGGTTATACACGTGGCTTACC	174 bp

g214	GCAGCGGCCGCATGATTGATTTAATGAA ACCTG	GGTCCATGGTCAACTGATAAGCTCATAGTT AATC	315 bp
g217	GCAGCGGCCGCATGATTACTAATAAAAC ATTTACAGAAG	GGTCCATGGTTAGTATTCCATAATTGTTTCG	231 bp
g218	GCAGCGGCCGCATGACTATTAGAACTAT TGAGCTAGATG	GGTCCATGGTCATTCTAAAATCACTCTAACA AATAG	279 bp
g219	GCAGCGGCCGCATGGTAACTGTTACGA G	GGTCCATGGTTAATGCAAAGTACGAACAG	213 bp
g221	GCAGCGGCCGCATGAAAGAGTTATTAGA AAATTATATTAAG	GGTCCATGGTTAAATCCCTAAGAAGTTTTTA AG	288 bp
g222	GCAGCGGCCGCCTTGACTCAACAGGCTAA TG	GGTCCATGGTCATTCTACTAAGCCTTGAAC	132 bp
g224	GCAGCGGCCGCATGAACGAATTAAACTG G	GGTCCATGGTTAAGACTTAGGAATATTAAG GTATG	222 bp
g232	GCAGCGGCCGCATGTTTGATAATATTTTT AAAAATGG	GGTCCATGGTTAATTCCTATATACCAGATTG C	1560 bp
g236	GCAGCGGCCGCATGTTCAAATTAATTCA AGAAGATG	GGTCCATGGTTAAGAATCACTTAGTTCAAAT AGAATTT	363 bp
g240	GCAGCGGCCGCATGAAACGTAAAACAAT TGAAC	GGTCCATGGTTAAACAAAACCTTTATCTTCG	246 bp
g241	GCAGCGGCCGCATGACCACAACTACTCA AATTG	GGTCCATGGTTATGCATCCTCTACCATATC	243 bp
g255	GCAGCGGCCGCATGAGTCATAATCTAGA ACAAGTTATAG	GGTCCATGGTCACTTTGTGGGAGTATTG	168 bp
g256	GCAGCGGCCGCATGAACAATTATGTAGC TAAAAATG	GGTCCATGGTTATGACTCATAAAATTCACC	120 bp
g257	GCAGCGGCCGCATGAAAGAATTACCTTA TGTAATAAAG	GGTCCATGGTTACTGACCTTGCATTTTAC	315 bp
g258	GCAGCGGCCGCATGACTGATATTACTAA GCAGG	GGTCCATGGTTAAAGCTTCTTTTCGCG	264 bp
g259	GCAGCGGCCGCATGTGTTTGACAGTAATT GATATG	GGTCCATGGTTAGCCAATAATGATGGTTTTT TTAG	180 bp
g261	GCAGCGGCCGCATGAATTTATTAGAACG TGTAATAAAAAA	GGTCCATGGTTATCTTGATTCACACAATTC	636 bp
g029	GCAGCGGCCGCATGCATGCAGTAAATAT TTC	GGTCCATGGTTATTTTCCTTTTGGCAC	198 bp
g052	GCAGCGGCCGCATGAAACTTTGTTTTGTT TTGATATCG	GGTCCATGGTCATAAGTTTAGTTTGATGAT TT	366 bp

Table S3. ϕ R1-RT structural proteins identified by LC-MS/MS analysis.

Accession	Description	Score	Coverage	Proteins	Unique Peptides	AAs	MW [kDa]
BN80_204	Gp200 RNA polymerase-ADP-ribosyltransferase Alt 126487:128613 reverse MW:79233	534.13	80.23	1	71	708	79.2
BN80_175	Gp171 phage portal vertex of the head 104925:106502 forward MW:61051	236.49	68.95	1	48	525	61.0
BN80_180	Gp176 phage major capsid protein 108684:110261 forward MW:56829	377.92	76.95	1	46	525	56.8
BN80_173	Gp169 phage tail sheath monomer 102201:104183 forward MW:71255	131.65	53.48	1	32	660	71.2
BN80_182	Gp178 phage capsid vertex 111903:113177 forward MW:45859	147.19	67.69	1	28	424	45.8
BN80_119	Gp119 IpIII internal head protein 65450:66040 reverse MW:22411	117.00	78.06	1	25	196	22.4
BN80_164	Gp160 phage fibrin (wac) protein 94120:95565 forward MW:51789	123.34	71.73	1	23	481	51.8
BN80_157	Gp153 phage baseplate wedge 83282:85234 forward MW:72610	84.77	44.46	1	22	650	72.6
BN80_251	Gp247 phage long tail fiber proximal subunit 155079:158816 forward MW:135002	69.16	26.51	1	20	1245	134.9
BN80_158	Gp154 phage baseplate wedge initiator 85240:88338 forward MW:119162	41.13	22.29	1	16	1032	119.1
BN80_121	Gp121 IpII internal head protein 66562:66834 reverse MW:10145	59.92	67.78	1	14	90	10.1
BN80_200	Gp196 phage baseplate hub 122381:124129 forward MW:63359	40.02	31.79	1	14	582	63.3

BN80_178	Gp174 phage prohead assembly (scaffolding) protein 107185:107808 forward MW:22662	61.51	52.17	1	11	207	22.6
BN80_150	Gp146 phage DNA end protector during packaging 78168:78992 reverse MW:31043	30.16	35.40	1	11	274	31.0
BN80_163	Gp159 gp12 short tail fibers 92770:94110 forward MW:47163	35.86	34.08	1	10	446	47.1
BN80_036	Gp036 gp61.1 conserved hypothetical protein 20482:20964 reverse MW:17608	44.13	61.88	1	9	160	17.6
BN80_146	Gp142 gp57B conserved hypothetical protein 76195:76656 reverse MW:17518	41.39	65.36	1	9	153	17.5
BN80_254	Gp250 phage tail fiber-like protein 160652:162163 forward MW:54271	40.31	26.04	1	9	503	54.2
BN80_192	Gp188 DNA helicase, phage-associated 117952:118182 forward MW:8743	196.72	71.05	1	8	76	8.7
BN80_246	Gp242 single stranded DNA-binding protein, phage- associated 151853:152746 reverse MW:32464	28.22	38.05	1	8	297	32.4
BN80_122	Gp122 chain A, crystal structure of T4 lysozyme mutant T152v 66844:67332 reverse MW:18227	25.42	37.04	1	8	162	18.2
BN80_161	Gp157 phage baseplate wedge 90270:92096 forward MW:67131	24.25	13.82	1	8	608	67.1
BN80_202	Gp198 phage tail assembly 125185:126123 forward MW:34155	31.70	31.73	1	8	312	34.1
BN80_154	Gp150 T4-like phage baseplate hub + tail lysozyme 80751:82478 forward MW:63803	24.40	19.30	1	8	575	63.8
P00761	Trypsin OS=Sus scrofa PE=1 SV=1 - [TRYP_PIG]	65.12	25.11	1	6	231	24.4
BN80_153	Gp149 phage baseplate wedge 80176:80754 forward MW:22194	31.01	37.50	1	6	192	22.2

BN80_198	Gp194 phage baseplate hub subunit 120749:121888 forward MW:43058	16.87	24.27	1	6	379	43.0
BN80_159	Gp155 phage baseplate wedge subunit (T4-like gp8) 88331:89335 forward MW:38139	14.43	23.05	1	6	334	38.1
BN80_253	Gp249 tail fiber protein p36 (protein Gp36) 159972:160619 forward MW:23070	19.18	40.93	1	6	215	23.1
BN80_190	Gp186 Inh inhibitor of prohead protease gp21 115594:116301 reverse MW:26921	19.86	29.79	1	5	235	26.9
BN80_179	Gp175 phage prohead assembly (scaffolding) protein 107841:108665 forward MW:30458	16.32	28.83	1	5	274	30.4
BN80_165	Gp161 T4-like phage head completion, neck hetero-dimeric protein (T4-like gp13) 95624:96556 forward MW:34703	9.54	15.48	1	5	310	34.7
BN80_006	Gp006 rIIB protector from prophage-induced early lysis 2297:3172 reverse MW:32780	21.58	21.31	1	4	291	32.8
BN80_166	Gp162 T4-like phage head completion, neck hetero-dimeric protein (T4-like gp14) 96560:97366 forward MW:30661	23.14	24.25	1	4	268	30.6
BN80_201	Gp197 phage baseplate tail tube cap (T4-like gp48) 124139:125185 forward MW:37991	15.13	16.09	1	4	348	38.0
BN80_239	Gp235 thymidylate synthase 148344:149204 reverse MW:32716	17.55	17.13	1	4	286	32.7
BN80_216	Gp212 phage head assembly chaperone protein 134388:134711 reverse MW:11631	12.45	48.60	1	4	107	11.6
BN80_252	Gp248 tail fiber protein Gp35 158816:159946 forward MW:41604	15.01	19.41	1	4	376	41.6
BN80_160	Gp156 phage baseplate wedge 89404:90270 forward MW:31166	13.74	21.18	1	3	288	31.1

BN80_177	Gp173 phage capsid and scaffold 106763:107185 forward MW:15923	7.54	8.57	1	3	140	15.9
BN80_055	Gp055 DNA polymerase, phage-associated 32894:35599 reverse MW:103949	9.71	4.44	1	3	901	103.9
BN80_003	Gp003 DenB DNA endonuclease IV 993:1550 reverse MW:20475	12.83	18.38	1	3	185	20.5
BN80_237	Gp233 ribonucleotide reductase of class Ia (aerobic), alpha subunit 145317:147566 reverse MW:84645	8.96	7.48	1	3	749	84.6
BN80_108	Gp108 rI.1 conserved hypothetical protein 60576:60788 reverse MW:8224	7.90	48.57	1	3	70	8.2
BN80_131	Gp131 Phage protein 70869:71468 reverse MW:22372	10.89	24.62	1	3	199	22.4
BN80_031	Gp031 dCTP pyrophosphatase, phage-associated 17378:17896 reverse MW:20099	6.92	27.91	1	3	172	20.1
BN80_082	Gp082 thioredoxin, phage-associated 48532:48804 reverse MW:10397	6.18	47.78	1	3	90	10.4
BN80_024	Gp024 DNA helicase, phage-associated 13006:14325 reverse MW:49468	3.36	10.93	1	3	439	49.4
BN80_042	Gp042 Phage recombination protein 23615:24793 reverse MW:43475	2.03	11.48	1	2	392	43.4
BN80_168	Gp164 proximal tail sheath stabilization protein 98021:98842 forward MW:31648	18.30	14.65	1	2	273	31.6
BN80_135	Gp134 hypothetical protein 72420:72578 reverse MW:5824	7.14	21.15	1	2	52	5.8
BN80_211	Gp207 hypothetical protein 132444:132713 reverse MW:9848	8.45	34.83	1	2	89	9.8
BN80_025	Gp025 hypothetical protein 14322:14603 reverse MW:11206	7.27	29.03	1	2	93	11.2

BN80_008	Gp008 hypothetical protein 5456:5608 reverse MW:5952	1.87	18.00	1	2	50	5.9
BN80_227	Gp223 hypothetical protein 138442:138948 reverse MW:19289	0.00	22.02	1	2	168	19.3
BN80_224	Gp220 3'-phosphatase, 5'-polynucleotide kinase, phage-associated 137074:137985 reverse MW:34976	2.66	7.92	1	2	303	35.0
BN80_046	Gp046 RB69ORF047c hypothetical protein 26119:27033 reverse MW:35349	2.71	9.54	1	2	304	35.3
BN80_162	Gp158 hypothetical protein 92096:92770 forward MW:23844	3.17	12.95	1	2	224	23.8
BN80_205	Gp201 DNA ligase, phage-associated 128712:130205 reverse MW:56745	5.40	4.83	1	2	497	56.7
BN80_050	Gp050 RB69ORF050c hypothetical protein 28231:29358 reverse MW:43593	2.03	6.67	1	2	375	43.6
BN80_077	Gp077 hypothetical protein 46018:46182 reverse MW:6178	4.65	25.93	1	1	54	6.2
BN80_133	Gp133 hypothetical protein 72080:72316 reverse MW:8844	7.11	20.51	1	1	78	8.8
BN80_080	Gp080 gp49.2 hypothetical protein 47873:48181 reverse MW:12202	2.80	19.61	1	1	102	12.2
BN80_048	Gp048 hypothetical protein 27721:28014 reverse MW:11383	2.60	17.53	1	1	97	11.4
BN80_176	Gp172 Gp 67 prohead core protein, precursor to internal peptides 106503:106769 forward MW:10039	3.44	17.05	1	1	88	10.0
BN80_068	Gp068 T4-like phage RNA polymerase sigma factor for late transcription 42770:43117 reverse MW:13321	2.72	16.52	1	1	115	13.3
BN80_215	Gp211 rIII lysis inhibition accessory protein, rapid lysis phenotype 134055:134303 reverse MW:9305	3.12	15.85	1	1	82	9.3

BN80_013	Gp013 hypothetical protein 8527:8967 reverse MW:17210	0.00	14.38	1	1	146	17.2
BN80_232	Gp228 Alc inhibitor of host transcription 140371:140877 reverse MW:19158	0.00	14.29	1	1	168	19.1
BN80_037	Gp037 hypothetical protein 20966:21157 reverse MW:7409	0.00	14.29	1	1	63	7.4
BN80_005	Gp005 hypothetical protein 2047:2262 reverse MW:8389	2.28	14.08	1	1	71	8.4
BN80_060	Gp060 RpbA RNA polymerase binding protein, function unknown 38375:38788 reverse MW:15518	3.74	12.41	1	1	137	15.5
BN80_149	Gp145 phage tail completion protein 77580:78158 reverse MW:21385	4.67	11.46	1	1	192	21.4
BN80_079	Gp079 hypothetical protein 47420:47863 reverse MW:16881	2.66	7.48	1	1	147	16.9
BN80_018	Gp018 hypothetical protein 10297:10788 reverse MW:18051	1.71	6.75	1	1	163	18.0
BN80_110	Gp110 Phage protein 61596:62051 reverse MW:16527	0.00	6.62	1	1	151	16.5
BN80_220	Gp216 hypothetical protein 135943:136314 reverse MW:13690	2.23	6.50	1	1	123	13.7
BN80_229	Gp225 hypothetical protein 139178:139654 reverse MW:18355	0.00	6.33	1	1	158	18.3
BN80_172	Gp168 phage terminase, large subunit 100784:102166 forward MW:52254	0.00	5.65	1	1	460	52.2

Table S4. Hypothetical proteins annotated as structural proteins from the LC-MS/MS analysis.

Accession	Description	Score	Coverage	# Proteins	# Unique Peptides	# AAs	MW [kDa]
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BN80_036	Gp036 Gp61.1 conserved hypothetical protein 20482:20964 reverse MW:17608	44.13	61.88	1	9	160	17.6
BN80_146	Gp142 Gp57B conserved hypothetical protein 76195:76656 reverse MW:17518	41.39	65.36	1	9	153	17.5
BN80_108	Gp108 rl.1 conserved hypothetical protein 60576:60788 reverse MW:8224	7.90	48.57	1	3	70	8.2
BN80_135	Gp134 hypothetical protein 72420:72578 reverse MW:5824	7.14	21.15	1	2	52	5.8
BN80_211	Gp207 hypothetical protein 132444:132713 reverse MW:9848	8.45	34.83	1	2	89	9.8
BN80_025	Gp025 hypothetical protein 14322:14603 reverse MW:11206	7.27	29.03	1	2	93	11.2
BN80_008	Gp008 hypothetical protein 5456:5608 reverse MW:5952	1.87	18.00	1	2	50	5.9
BN80_227	Gp223 hypothetical protein 138442:138948 reverse MW:19289	0.00	22.02	1	2	168	19.3
BN80_162	Gp158 hypothetical protein 92096:92770 forward MW:23844	3.17	12.95	1	2	224	23.8
BN80_050	Gp050 RB69ORF050c hypothetical protein 28231:29358 reverse MW:43593	2.03	6.67	1	2	375	43.6
BN80_077	Gp077 hypothetical protein 46018:46182 reverse MW:6178	4.65	25.93	1	1	54	6.2
BN80_133	Gp133 hypothetical protein 72080:72316 reverse MW:8844	7.11	20.51	1	1	78	8.8
BN80_080	Gp080 Gp 49.2 hypothetical protein 47873:48181 reverse MW:12202	2.80	19.61	1	1	102	12.2
BN80_048	Gp048 hypothetical protein 27721:28014 reverse MW:11383	2.60	17.53	1	1	97	11.4

BN80_013	Gp013 hypothetical protein 8527:8967 reverse MW:17210	0.00	14.38	1	1	146	17.2
BN80_037	Gp037 hypothetical protein 20966:21157 reverse MW:7409	0.00	14.29	1	1	63	7.4
BN80_005	Gp005 hypothetical protein 2047:2262 reverse MW:8389	2.28	14.08	1	1	71	8.4
BN80_079	Gp079 hypothetical protein 47420:47863 reverse MW:16881	2.66	7.48	1	1	147	16.9
BN80_018	Gp018 hypothetical protein 10297:10788 reverse MW:18051	1.71	6.75	1	1	163	18.0
BN80_220	Gp216 hypothetical protein 135943:136314 reverse MW:13690	2.23	6.50	1	1	123	13.7
BN80_229	Gp225 hypothetical protein 139178:139654 reverse MW:18355	0.00	6.33	1	1	158	18.3

Table S5. BLASTp and HHpred analysis results for the HPUFs. The results are based on the BLASTp and HHpred analysis run online during the month of January 2018.

No	HPUF	Protein ID	BLASTP		HHpred
			Major Hit	Putative conserved domains	Major Hit
1	Gp002	CCI88576.1	Hypothetical phage protein	Not detected	No significant hits
2	Gp004	CCI88578.1	Hypothetical phage protein	Not detected	No significant hits
3	Gp011	CCI88585.1	Hypothetical phage protein	Not detected	No significant hits
4	Gp012	CCI88586.1	Hypothetical phage protein	ribonuclease Z	No significant hits
5	Gp014	CCI88588.1	Hypothetical phage protein	Not detected	No significant hits
6	Gp016	CCI88590.1	Hypothetical phage protein	Not detected	No significant hits
7	Gp017	CCI88591.1	Hypothetical phage protein, DUF551 domain-containing protein	Not detected	Protein of unknown function (DUF551)

8	Gp019	CCI88593.1	No significant hits	Not detected	No significant hits
9	Gp022	CCI88596.1	Hypothetical phage protein	Not detected	No significant hits
10	Gp023	CCI88597.1	Hypothetical phage protein	Not detected	No significant hits
11	Gp028	CCI88602.1	Hypothetical phage protein	Not detected	No significant hits
				The SMC (structural maintenance of chromosomes) superfamily proteins	
12	Gp029	CCI88603.1	Hypothetical phage protein		No significant hits
13	Gp030	CCI88604.1	Hypothetical phage protein	Not detected	No significant hits
				Not detected	Nucleoside 2- deoxyribosyltransferase like
14	Gp032	CCI88606.1	Hypothetical phage protein		
				Prokaryotic dksA/traR C4-type zinc finger	Zn finger
15	Gp033	CCI88607.1	Hypothetical phage protein		
			Hypothetical phage proteins, Spackle periplasmic protein from Enterobacter phage PG7	Not detected	Adhesin
16	Gp038	CCI88612.1			
17	Gp043	CCI88617.1	Hypothetical phage protein	Not detected	No significant hits
				Uncharacterized protein, contains a C-terminal ATPase domain (Function unknown)	
18	Gp044	CCI88618.1	Hypothetical phage protein		No significant hits
19	Gp045	CCI88619.1	Hypothetical phage protein	Not detected	Thymidylate kinase

				Thymidylate synthase and pyrimidine hydroxymethylase	
20	Gp047	CCI88621.1	Hypothetical phage protein, dCMP hydroxymethylase in phage		CMP 5-hydroxymethylase
21	Gp049	CCI88623.1	Hypothetical phage protein	Not detected	No significant hits
22	Gp052	CCI88626.1	capsule biosynthesis protein of Serratia phage CH114	Haloacid Dehalogenase-like Hydrolases	Polynucleotide kinase
23	Gp053	CCI88627.1	bifunctional protein GlmU of E. coli O157 typing phage 3	GCD1 superfamily= NDP-sugar pyrophosphorylase, includes eIF-2Bgamma, eIF-2Bepsilon, and LPS biosynthesis	MurU; Nucleotidyltransferase family protein, uridyltransferase
24	Gp061	CCI88635.1	Hypothetical phage protein	Not detected	Phage protein Gp45.2
25	Gp064	CCI88638.1	Hypothetical phage protein	Not detected	Non heme iron peroxidases
26	Gp065	CCI88639.1	Hypothetical phage protein	Not detected	No significant hits
27	Gp067	CCI88641.1	Hypothetical phage protein	Not detected	Family of unknown function (DUF5491)
28	Gp069	CCI88643.1	Hypothetical phage protein	Not detected	No significant hits
29	Gp070	CCI88644.1	Hypothetical phage protein	Not detected	Family of unknown function (DUF5495) - This is a family of unknown function found in Myoviridae.

30	Gp071	CCI88645.1	Hypothetical phage protein	Not detected	No significant hits
31	Gp073	CCI88647.1	Hypothetical phage protein	Not detected	No significant hits
32	Gp074	CCI88648.1	Hypothetical phage protein	Not detected	No significant hits
33	Gp075	CCI88649.1	Hypothetical phage protein, glutaredoxin in Pectobacterium bacteriophage PM2	Not detected	No significant hits
34	Gp076	CCI88650.1	Hypothetical phage protein	Seven-transmembrane G protein-coupled receptor superfamily	Detected 1 transmembrane helix
35	Gp081	CCI88655.1	Hypothetical phage protein	Not detected	No significant hits
36	Gp083	CCI88657.1	Hypothetical phage protein	Not detected	Translation initiation factor 2 beta
37	Gp084	CCI88658.1	Hypothetical phage protein, thioredoxin in Escherichia phage EC121	Not detected	Transposase zinc-ribbon domain
38	Gp085	CCI88659.1	Hypothetical phage protein	Not detected	No significant hits
39	Gp086	CCI88660.1	Hypothetical phage protein	Not detected	No significant hits
40	Gp087	CCI88661.1	Hypothetical phage protein	Not detected	Detected coiled-coil segments
41	Gp089	CCI88663.1	Hypothetical phage protein	Not detected	No significant hits
42	Gp090	CCI88664.1	Hypothetical phage protein	Not detected	No significant hits
43	Gp091	CCI88665.1	Hypothetical phage protein	Not detected	No significant hits
44	Gp092	CCI88666.1	Hypothetical phage protein	Not detected	No significant hits
45	Gp093	CCI88667.1	Hypothetical phage protein	Not detected	No significant hits
46	Gp094	CCI88668.1	Hypothetical phage protein	Not detected	Detected 1 transmembrane helix
47	Gp095	CCI88669.1	Hypothetical phage protein	Not detected	DNA-directed RNA polymerase II subunit

48	Gp096	CCI88670.1	Hypothetical phage protein	Not detected	No significant hits
49	Gp098	CCI88672.1	Hypothetical phage protein	Not detected	Detected coiled-coil segments
50	Gp099	CCI88673.1	Hypothetical phage protein	Not detected	No significant hits
51	Gp100	CCI88674.1	Hypothetical phage protein	Not detected	No significant hits
52	Gp101	CCI88675.1	Hypothetical phage protein	Not detected	No significant hits
53	Gp102	CCI88676.1	Hypothetical phage protein	Not detected	No significant hits
54	Gp104	CCI88678.1	Hypothetical phage protein	Not detected	No significant hits
55	Gp105	CCI88679.1	Hypothetical phage protein	Not detected	Detected 2 transmembrane helices
56	Gp106	CCI88680.1	Hypothetical phage protein	Not detected	Uncharacterized protein
57	Gp107	CCI88681.1	rI lysis inhibition regulator membrane protein of Yersinia phage vB_YenM_TG1	hypothetical protein	No significant hits
58	Gp111	CCI88685.1	Hypothetical phage protein	Not detected	No significant hits
59	Gp112	CCI88686.1	Hypothetical phage protein	Not detected	No significant hits
60	Gp117	CCI88691.1	Hypothetical phage protein	Not detected	No significant hits
61	Gp124	CCI88698.1	Hypothetical phage protein	Not detected	No significant hits
62	Gp126	CCI88700.1	Hypothetical phage protein	Not detected	No significant hits
63	Gp127	CCI88701.1	Hypothetical phage protein	Sigma-70 region 3 ; Region 3 forms a discrete compact three helical domain within the sigma-factor.	No significant hits
64	Gp128	CCI88702.1	Hypothetical phage protein	cl10376, hypothetical protein	No significant hits

65	Gp129	CCI88703.1	Hypothetical phage protein	Not detected	No significant hits
66	Gp130	CCI88704.1	Hypothetical phage protein	Not detected	No significant hits
67	Gp132	CCI88706.1	Hypothetical phage protein	Not detected	No significant hits
68	Gp135	CCI88709.1	Hypothetical phage protein	Not detected	No significant hits
69	Gp136	CCI88710.1	Hypothetical phage protein	Not detected	No significant hits
70	Gp137	CCI88711.1	Hypothetical phage protein	Not detected	Detected 2 transmembrane helices
71	Gp138	CCI88712.1	No significant hits	Not detected	No significant hits
72	Gp139	CCI88713.1	Hypothetical phage protein	YadA-like C-terminal region,	Adhesin yadA
73	Gp141	CCI88715.1	Hypothetical phage protein	Not detected	No significant hits
74	Gp143	CCI88717.1	Hypothetical protein Yersinia phage fHe-Yen9-01, Yersinia phage vB_YenM_TG1	Not detected	Detected coiled-coil segments, GP57- Phage Tail fiber assembly helper protein
75	Gp167	CCI88741.1	Hypothetical phage protein	TnsA endonuclease N terminal	endodeoxyribonuclease I
76	Gp177	CCI88751.1	Hypothetical protein Yersinia phage fHe-Yen9-01, Yersinia phage vB_YenM_TG1	putative Hef-like homing endonuclease	Very short patch repair (VSR) endonuclease
77	Gp179	CCI88753.1	RNA ligase of Yersinia phage vB_YenM_TG1	Adenylation domain of proteins similar to ATP-dependent polynucleotide ligases	LYSINE ADENYLATE

				Protein of unknown function (DUF2774) ;This is a viral family of proteins with unknown function	
78	Gp181	CCI88755.1	Hypothetical phage protein	Protein of unknown function (DUF2774) ;This is a viral family of proteins with unknown function	
79	Gp183	CCI88757.1	Hypothetical phage protein	Not detected	Capsid vertex protein gp24
80	Gp184	CCI88758.1	Head outer phage capsid protein	Not detected	Capsid vertex protein gp24
81	Gp185	CCI88759.1	Head outer phage capsid protein	Not detected	Capsid vertex protein gp24
82	Gp199	CCI88773.1	Hypothetical phage protein	Not detected	No significant hits
83	Gp202	CCI88776.1	Hypothetical phage protein	Not detected	No significant hits
84	Gp204	CCI88778.1	Hypothetical phage protein	Not detected	No significant hits
85	Gp205	CCI88779.1	Hypothetical phage protein	Not detected	Protein of unknown function (DUF2945)
86	Gp206	CCI88780.1	Hypothetical phage protein	Not detected	No significant hits
87	Gp208	CCI88782.1	Hypothetical phage protein	Not detected	No significant hits
88	Gp209	CCI88783.1	Hypothetical phage protein	Phage Gp30.7 protein of unknown function	Phage Gp30.7 protein. Family members seem to be exclusively from the T4-like viruses. The function of this family is unknown.
89	Gp210	CCI88784.1	Hypothetical phage protein	Not detected	No significant hits

90	Gp213	CCI88787.1	Tail fiber protein of Enterobacteria phage RB3 and Shigella phage SHFML-11	Protein of unknown function (DUF2693)	WYL_2, Sm-like SH3 beta-barrel fold
91	Gp214	CCI88788.1	Hypothetical phage protein	Not detected	No significant hits
92	Gp217	CCI88791.1	Hypothetical phage protein	Not detected	DinI; DinI-like family
93	Gp218	CCI88792.1	Hypothetical phage protein	Not detected	no significant hits
94	Gp219	CCI88793.1	Hypothetical phage protein	Not detected	no significant hits
95	Gp221	CCI88795.1	Hypothetical phage protein	Not detected	No significant hits
96	Gp222	CCI88796.1	Hypothetical phage protein	Not detected	no significant hits
97	Gp224	CCI88798.1	Hypothetical phage protein	Protein of uncharacterised function (DUF551)	DUF551; Protein of unknown function (DUF551)
98	Gp232	CCI88806.1	Putative Hef-like homing endonuclease of Salmonella phage SG1	Not detected	No significant hits
99	Gp236	CCI88810.1	Hypothetical phage protein	Not detected	No significant hits
100	Gp240	CCI88814.1	Hypothetical phage protein	Not detected	No significant hits
101	Gp241	CCI88815.1	Hypothetical phage protein	Not detected	Bacteriophage FRD3 protein
102	Gp251	CCI88825.1	Hypothetical phage protein	Caudovirales tail fibre assembly protein	Caudovirales tail fibre assembly protein
103	Gp255	CCI88829.1	No significant hits	Not detected	No significant hits
104	Gp256	CCI88830.1	Hypothetical phage protein	Not detected	No significant hits
105	Gp257	CCI88831.1	Hypothetical phage protein	Not detected	No significant hits
106	Gp258	CCI88832.1	Hypothetical phage protein	Not detected	No significant hits
107	Gp259	CCI88833.1	Hypothetical phage protein	Not detected	No significant hits

108	Gp261	CCI88835.1	Hypothetical phage protein, sprT domain-containing protein	Protein of unknown function DUF45	SprT homologues
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Table S6. CFU counts of HPUFs and relative CFU of HPUFs to the CFU of non-toxic control genes in that batch of electroporations.

Assay	Gene	Transformation efficiency (CFU/ng)	Relative CFU
1	g073	7518,66	1,501
	g083	6841,98	1,366
	g081	3705,96	0,740
	g074	2896,41	0,578
	g076	2525,25	0,504
	g121	5010,07	1,000
2	g084	11437,68	4,752
	g086	8582,75	3,566
	g087	5257,05	2,184
	g089	3828,97	1,591
	g085	3742,34	1,555
	g121	2407,12	1,000
3	g090	8220,83	2,583
	g091	8173,69	2,568
	g121	3182,29	1,000
4	g135	2782,33	0,545
	g138	4376,30	0,858
	g178	5101,29	1,000
5	g181	4108,41	2,738
	g199	3378,13	2,251
	g141	1924,77	1,283
	g167	1840,05	1,226
	g177	1274,59	0,849
	g178	1500,70	1,000
6	g209	4001,06	1,833
	g208	3716,65	1,703
	g205	2074,28	0,950
	g204	1981,72	0,908
	g206	1897,88	0,870
	g178	2182,34	1,000

7	g221	7703,72	2,863
	g219	6983,61	2,595
	g214	5973,63	2,220
	g217	3265,12	1,213
	g210	3025,35	1,124
	g218	2912,75	1,082
	g246	2691,12	1,000
8	g224	8934,64	1,278
	g241	4330,18	0,619
	g222	3826,52	0,547
	g236	2807,18	0,401
	g240	1231,91	0,176
	g232	5,04	0,001
	g246	6993,21	1,000
9	g258	9596,13	5,165
	g259	5674,18	3,054
	g255	3507,08	1,888
	g261	1693,78	0,912
	g256	1612,45	0,868
	g246	1857,86	1,000
10	g202	5655,88	0,779
	g111	3136,76	0,432
	g246	7258,62	1,000
11	g104	7950,78	1,259
	g098	4998,45	0,792
	g095	3248,04	0,514
	g012	5753,53	0,911
	g150	6313,72	1,000
12	g257	11115,59	1,458
	g019	8301,81	1,089
	g150	7626,28	1,000
13	g017	7927,71	2,188
	g022	7196,60	1,986
	g023	6796,79	1,876
	g028	5815,51	1,605
	g030	4788,25	1,322
	g121	3622,92	1,000
14	g094	3898,16	0,729
	g043	4278,43	0,801
	g137	2354,55	0,441
	g121	5344,62	1,000
15	g093	2255,86	0,518
	g105	3443,40	0,790

	g124	4826,75	1,108
	g121	4357,29	1,000
16	g033	350,31	0,314
	g044	463,52	0,415
	g045	709,08	0,635
	g049	448,72	0,402
	g061	1006,06	0,902
	g064	195,54	0,175
	g065	2587,00	2,318
	g178	1115,91	1,000
17	g067	1436,74	1,428
	g069	2113,21	2,101
	g070	450,43	0,448
	g071	1711,08	1,701
	g002	1298,55	1,291
	g004	2168,49	2,156
	g011	3028,42	3,010
	g178	1005,96	1,000
18	g014	4094,60	1,432
	g016	3238,41	1,133
	g092	196,48	0,069
	g096	1367,99	0,479
	g099	1828,75	0,640
	g100	316,63	0,111
	g101	2402,88	0,841
	g178	2858,48	1,000
19	g106	718,45	0,684
	g112	1076,88	1,026
	g117	1118,44	1,065
	g126	987,45	0,940
	g127	726,34	0,692
	g178	1049,94	1,000
20	g132	1196,28	0,607
	g130	1344,71	0,682
	g129	2372,85	1,204
	g178	1970,70	1,000
21	g052	2041,84	2,041
	g029	1024,44	1,024
	g102	2471,80	2,471
	g128	1079,21	1,079
	g178	1000,47	1,000
22	g136	3658,43	0,396
	g178	9248,83	1,000

Table S7. CFU values for ϕ R1-RT encoded holins and endolysin relative to CFU of **control non-toxic gene g119**.

Assay	Gene	Length (bp)	Predicted function	Transformation efficiency (CFU/ng)	Relative CFU
1	g122	489	lysin	2053,97	1,215
	g252	162	holin	2267,63	1,342
	g253	657	holin	1658,58	0,981
	g119	591	structural protein	1690,36	1,000

Figure S1. Map of the plasmid construct pU11L4 with KpnI-PstI linker and luxAB. All the control genes and the HPUF genes were cloned in the linker region.

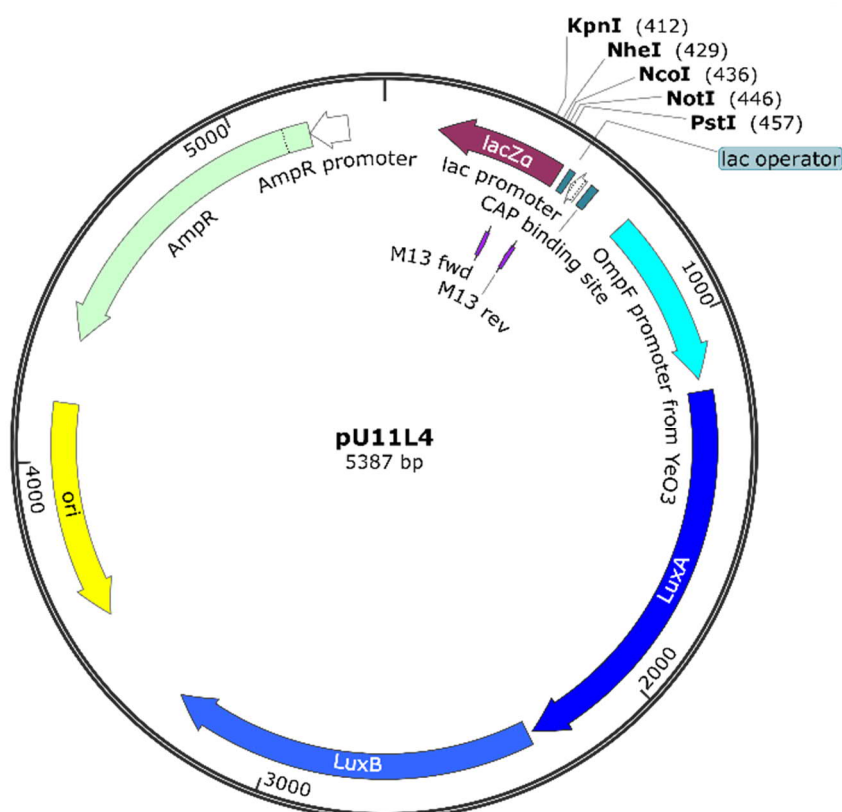


Figure S2. Inter-assay variability of the screening assay. In order to calculate the inter-assay variability of the relative CFU values of toxic hits with respect to the control gene g178, two separate ligations of the genes to the pU11I4 was carried out and each ligation mix was electroporated and plated in replicates of three.

