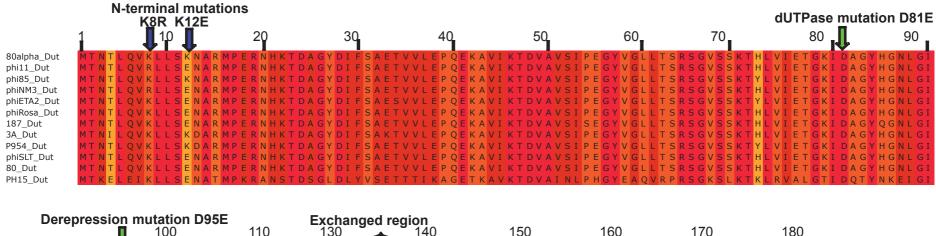
## SUPPLEMENTARY INFORMATION

S4 | **Lineup of dUTPases and dUTPases of staphylococcal phages.** Sequences were aligned by the PRALINE program, which uses the colours of the rainbow to indicate relative overall conservation at each position, with red being the most conserved, blue the least.



		100	110	130		140	150	160	170	180	
										I	I I
80alpha_Dut	NIKNDHE	<mark>)</mark>									RGEKGFGSSGV
phi11_Dut	NIKNDAI	<b>\ \</b>	<mark>S - N G Y I</mark>	TPGVFD	IKGEI	DL <mark>SD</mark>	A I R Q Y G T <mark>Y</mark> Q I I	N E G D K L A Q L V I	V P I WT P E L K	QVEEFESVSE	RGEKGFGSSGV
phi85_Dut	NIKNDEEF	R D G I P F L Y D	DIDAELE	GLISIL	DIKGN	N Y V <mark>Q D (</mark>	G R G I R R V <mark>Y</mark> Q I I	N K G D K L A Q L V I	VPI WT PELK	QVEEFESVSE	RGAKGFGSSGV
phiNM3_Dut		R D G I P F L Y D									R G A K G F G S S G V
phiETA2_Dut											R G A K G F G S S G V
phiRosa_Dut											RGAKGFGSSGV
187_Dut											R G A K G F G S S G V
3A_Dut	NIKNDNE										R G A K G F G S S G V
P954_Dut	NIKNDME	HDGITSLY-	E D L D D I	(LVNTL-	DIKGN	NYI NE (	G E G A R K V <mark>Y</mark> K I I	N K G D K L A Q L V I	VPI WT PELK	QVEEFESVSE	RGAKGFGSSGV
phiSLT_Dut	NIKNDAQ	/ Y L T T N ·	<mark>E</mark> QCFDI	QGEMEN	SFVN	N A K <mark>K K</mark> F	P F T I N D Y Y E I '	Y K G D K L A Q L V I	VPI WT PELK	QVEEFESVSE	RGAKGFGSSGV
80_Dut	NIKNDAQ	/ Y L T T N	E Q C F D I	QGEMEN	SFVN	N A K <mark>K K</mark> F	P F T I N D Y Y E I '	Y K G D K L A Q L V I	VPI WT PELK	QVEEFESVSE	RGAKGFGSSGV
PH15_Dut	ITDNIGD-	· <del>-</del>					· K D I T V I	E K G E R L A Q L V V	A P V V Y P T P K	QVDWFENE	S D R G A Y G S T G E