

1 **Title: Novel phages of healthy skin metaviromes from South Africa**

2 **Running title: Phages from skin metavirome**

3
4
5 Leonardo Joaquim van Zyl^{1*}, Yoonus Abrahams¹, Emily Amor Stander¹, Bronwyn Michelle Kirby-
6 McCollough¹, Roland Jourdain², Cécile Clavaud², Lionel Breton², Marla Trindade¹

7
8 ¹ Institute for Microbial Biotechnology and Metagenomics (IMBM), University of the Western Cape,
9 Robert Sobukwe Road, Bellville, Cape Town, South Africa.

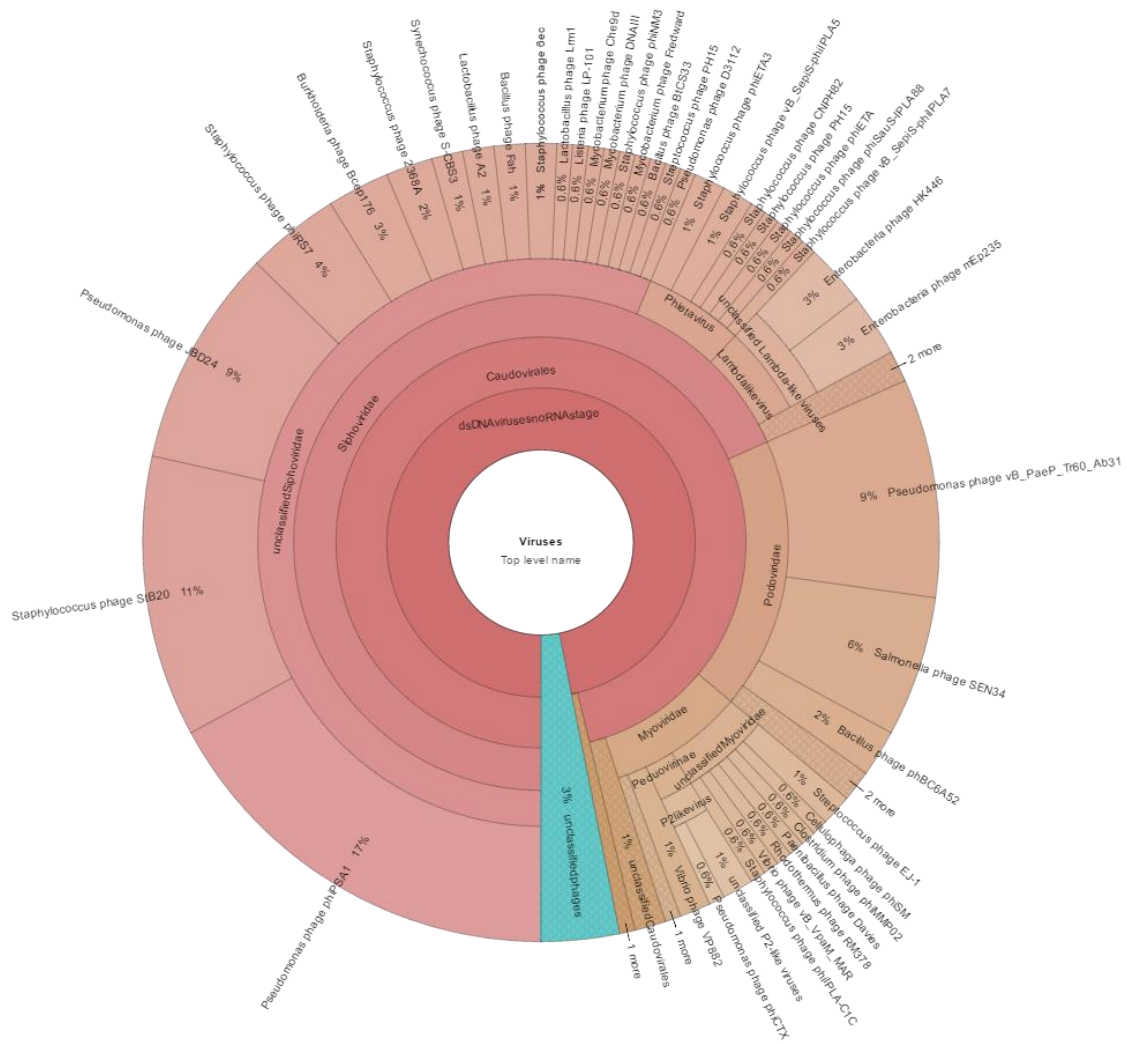
10
11 ² L'Oréal Research and Innovation, 1 Avenue Eugène Schueller, 93600 Aulnay sous Bois, France

12
13 * Author to whom correspondence should be addressed; Leonardo Joaquim van Zyl, e-mail:
14 vanzylj@gmail.com; Tel.: +27 21 959 2325

15
16 Email: Leonardo Joaquim van Zyl: vanzylj@gmail.com; Cécile Clavaud: cclavaud@rd.loreal.com;
17 Roland Jourdain: rjourdain@rd.loreal.com; Lionel Breton: lbreton@rd.loreal.com; Marla I. Trindade:
18 prof.marlatt@gmail.com

19
20
21 Keywords: Bacteriophage, skin, Stb20, metagenomics

22
23
24
25
26
27
28
29



31

32

33 **Figure S1.** Taxonomic profile of contigs recovered from the combined skin metaviromes

34

35

36

37

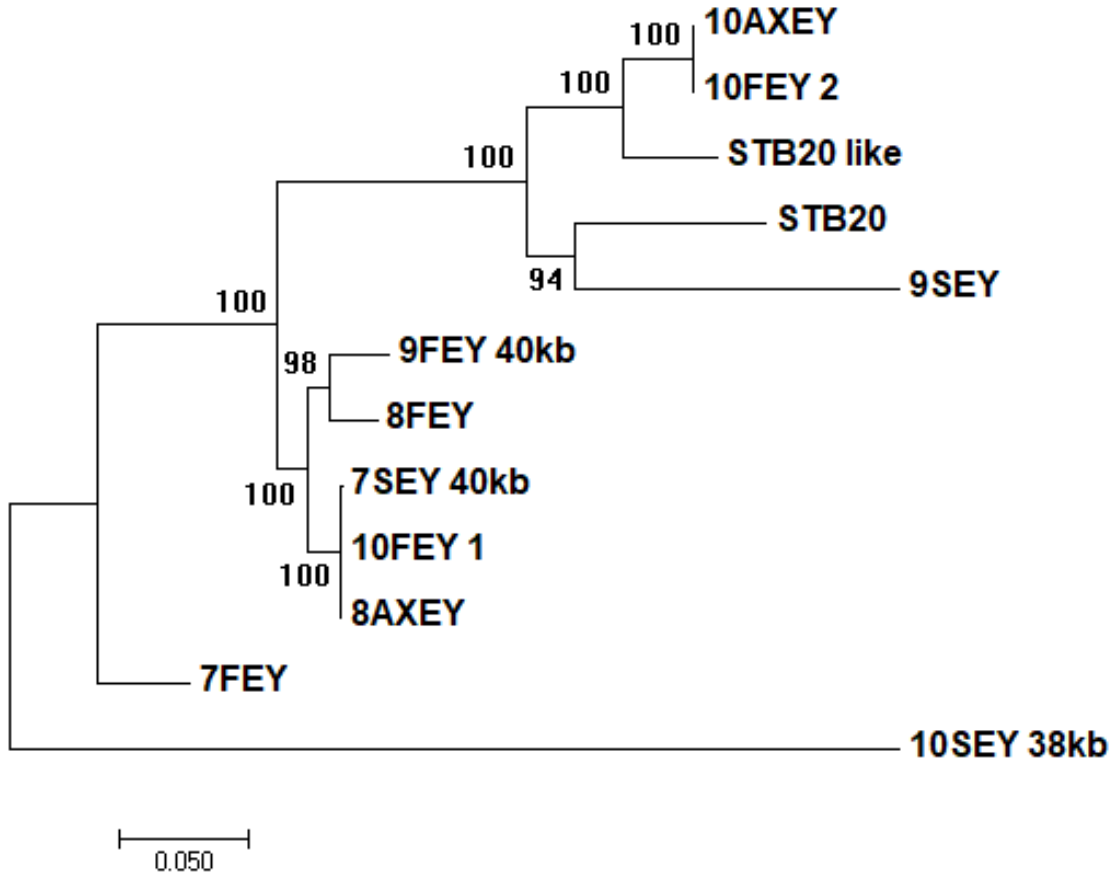
38

39

40

41

42



44

45

46 **Figure S2.** The evolutionary history of Stb20-like phages was inferred using the Neighbor-Joining
47 method. Branch lengths in the same units as those of the evolutionary distances used to infer the
48 phylogenetic tree.

49

50

51

52

53

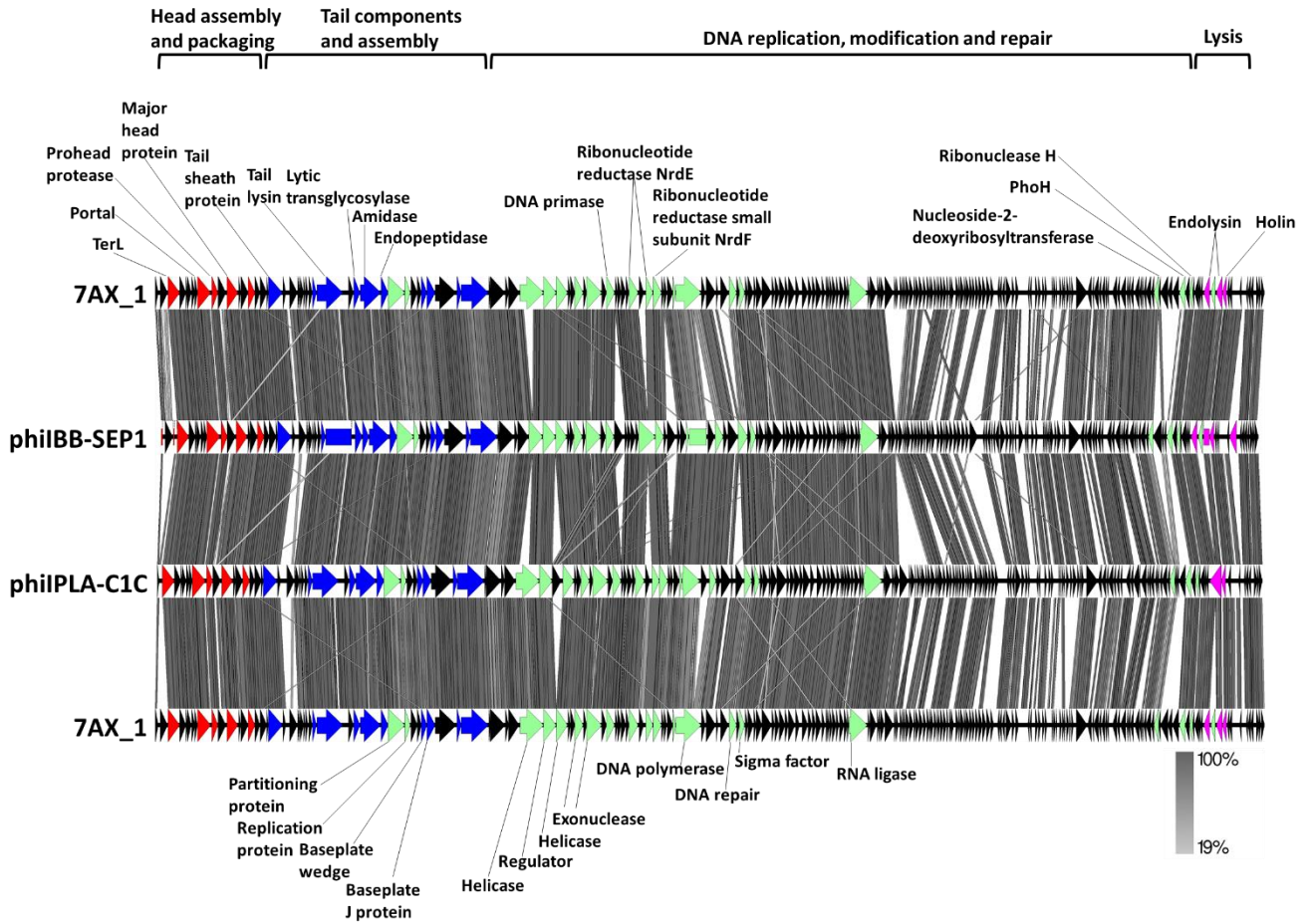
54

55

56

57

58



60 **Figure S3.** Comparison of the genomic structure of phiIPLA-C1C, phiIBB-SEP1 and a related phage
61 from 7AX

62

63

64

65

66

67

68

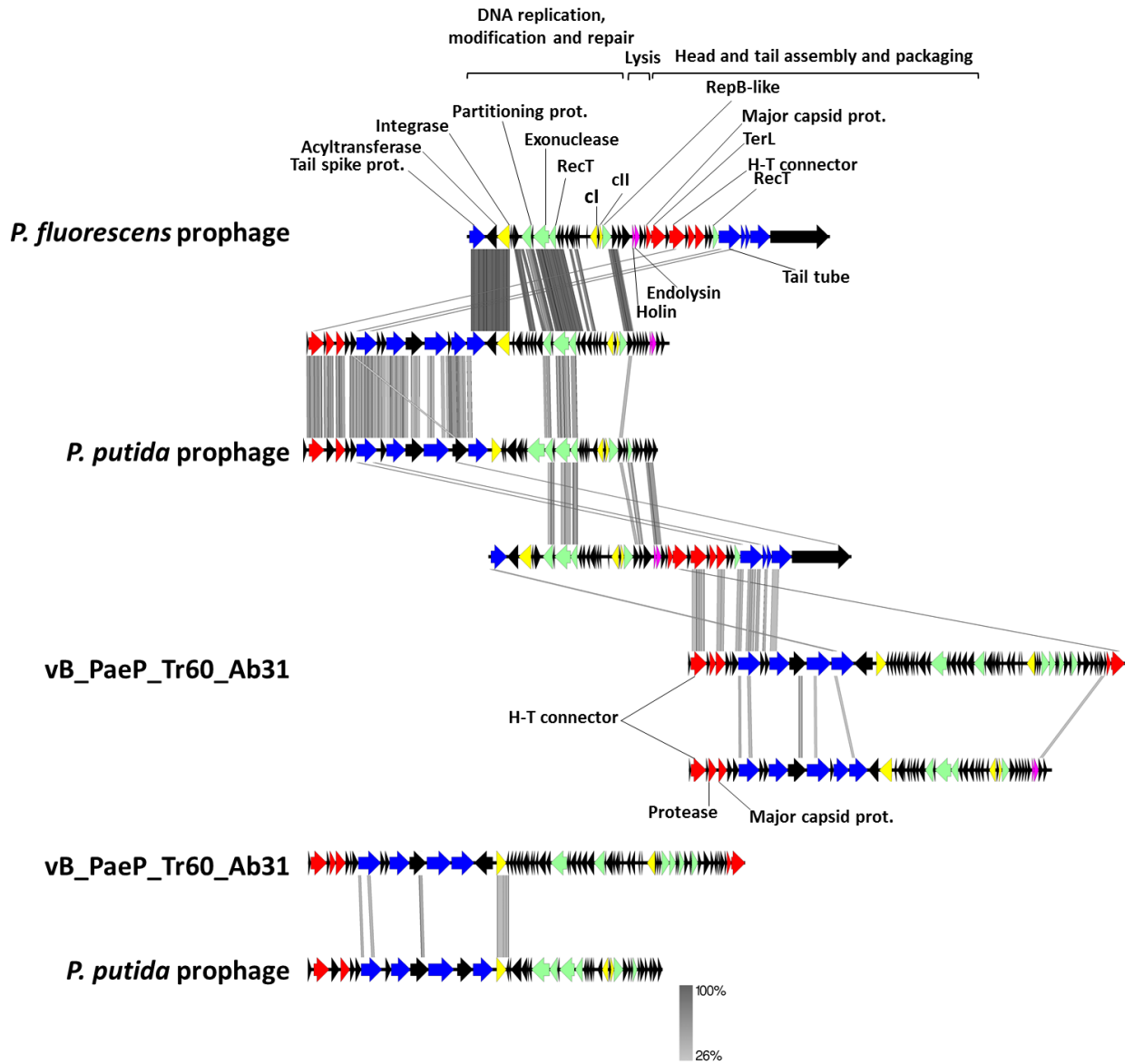
69

70

71

72

73



74

75 **Figure S4.** Comparison of the genomic structure of Ab31-like phages from 2AX, 3S, 7F, 7S, 7AX,

76 8AX, 8S, 9S, 9AX, 10F, 10AX to their closest relatives

77

78

79

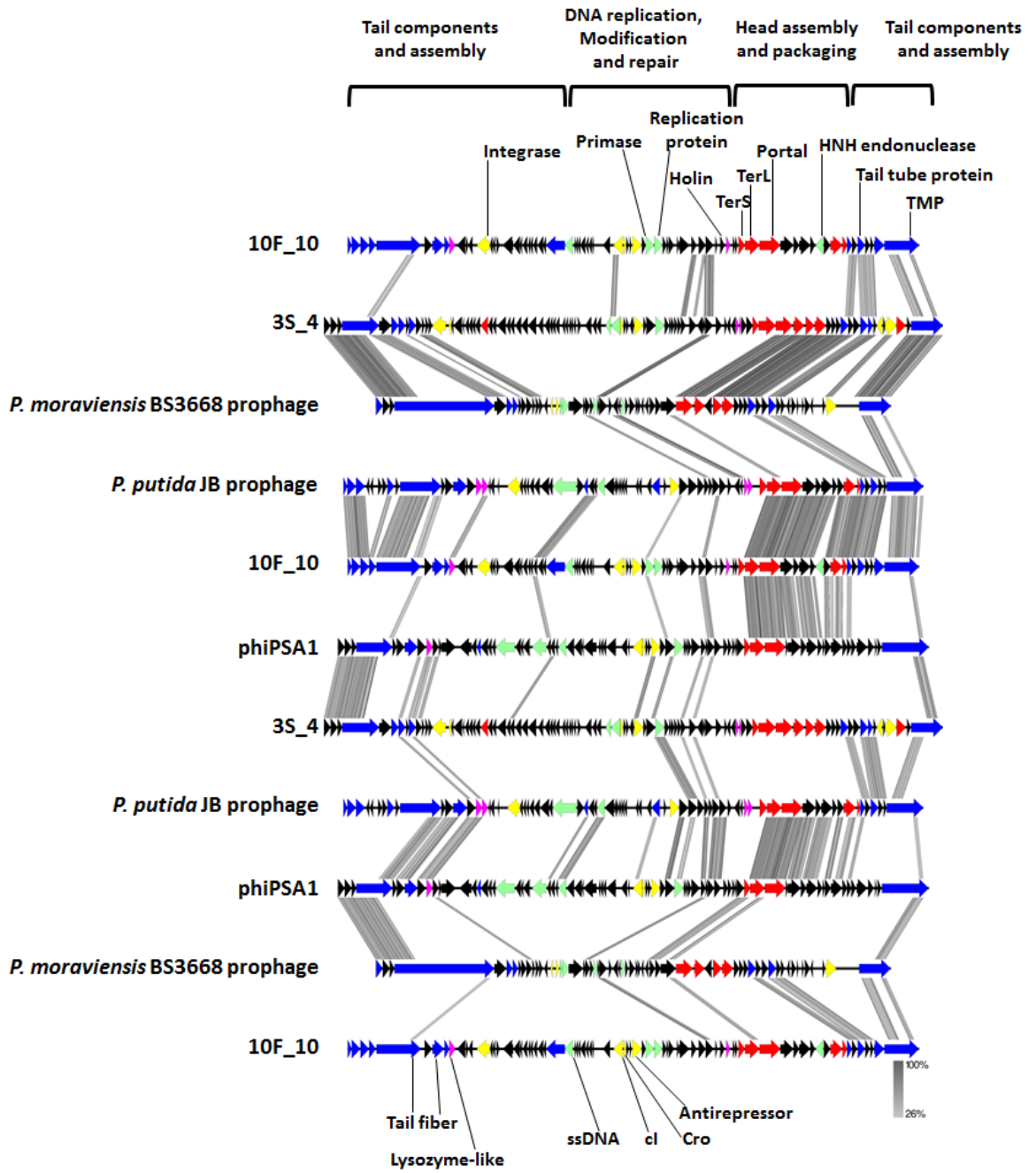
80

81

82

83

84



86

87 **Figure S5.** Comparison of the genomic structure of phiPSA1-like contigs from 10F and 8S to its
 88 closest relatives

89

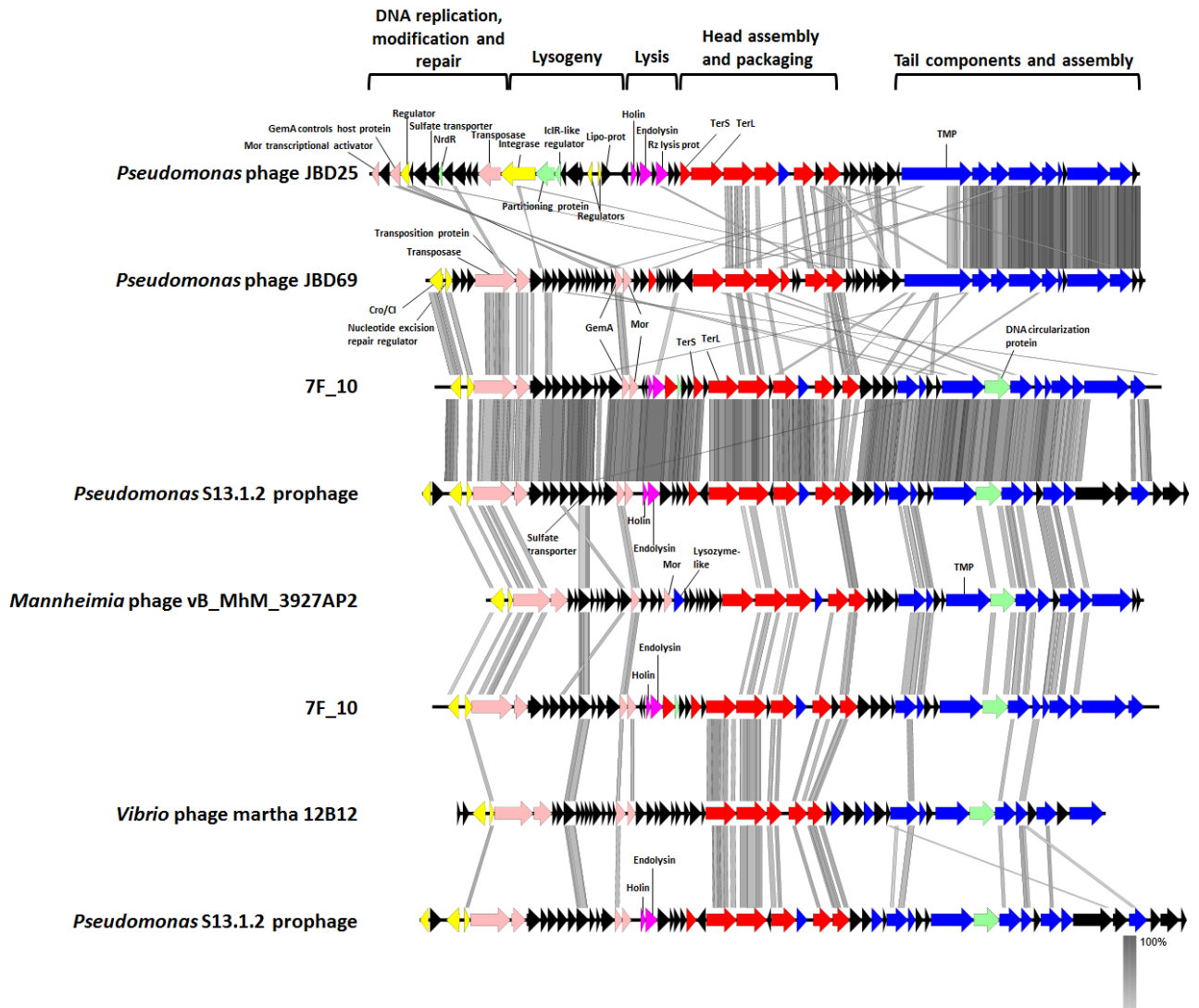
90

91

92

93

94



96

97 **Figure S6.** Comparison of the genomic structure of *Pseudomonas* infecting Mu-like phages

98

99

100

101

102

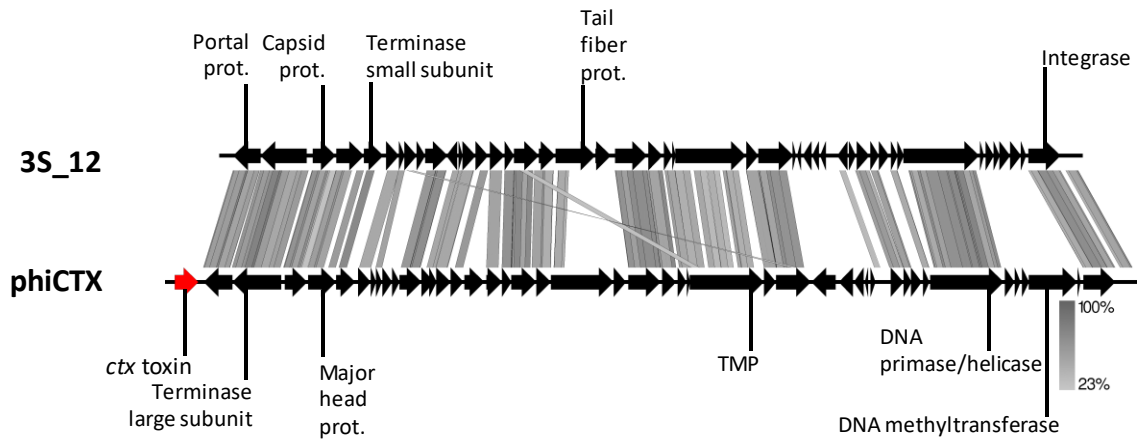
103

104

105

106

107

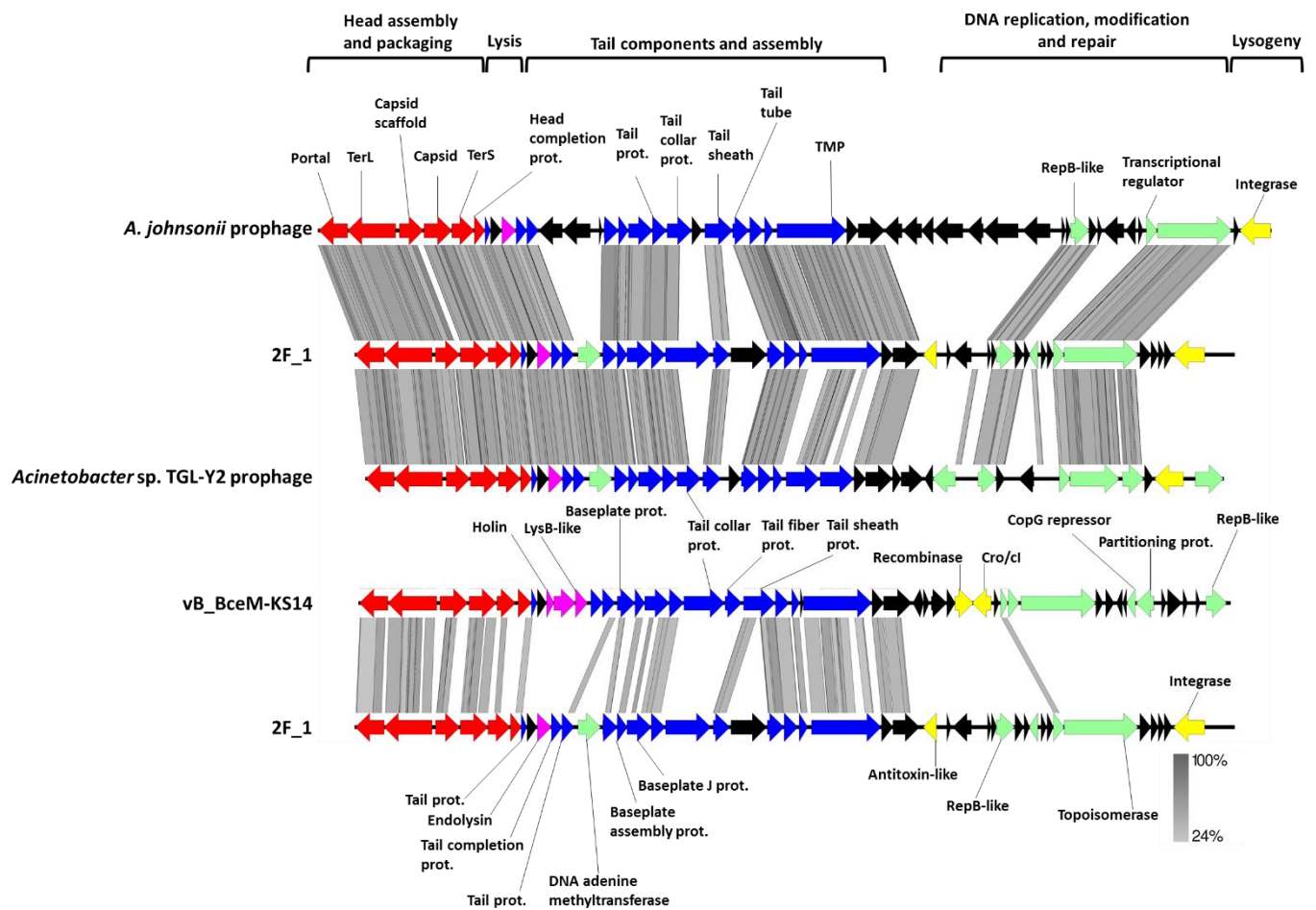


109

110 **Figure S7.** Comparison of the genomic structure of phiCTX-like contig from 3S and phiCTX. The

111 ORF highlighted in red is the *ctx* toxin

112



113

114

115 **Figure S8.** Comparison of the genomic structure of the vB_Bcem-KS14-like contig from 2F to its

116 closest relatives