

Annotation	Start - End	Phage Name	Alignment
tRNA-Asn-GTT-2-1	52 - 82	FSL SP-029, SE5, vB_SnwM_CGG4-1*	CACUGGUUCGAGUCCAGU CACUGGUUCGAGUCCAGU
tRNA-Asp-GTC-2-1	40 - 73	38, BSP101, Mutine, PhiSH19, S8, S115, SE5, SE14, SeSz-1, SP1, SPAsTU*, vB_SalM_PM10, vB_SalM_SJ2	GGGGGUCGCGGGUUCGAGUCCCGUCCGUUCCGCC GGAGGUUCGCGGGUUCGAGUCCCGUCCGUUCCGCC
tRNA-Gln-CTG-1-1	24 - 60	SE131*, SPN3US	CAUCCGAGGUUCGAAUCCUCG CAGUACGAGGUUCGAAUCCUCG
tRNA-Gln-TTG-1-1	44 - 74	SPAsTU*	AUUCCUGGUUCGAAUCCAGGUACCCAGCC AUGCCUGGUUCGAAUCCAGGUCCACUGCC
tRNA-Glu-TTC-2-1	37 - 72	FSL SP-010, Vi01*	GGGGUUCGAAUCCCUA GGGGUUCGAAUCCCUA
tRNA-Leu-CAA-2-1	39 - 60	38, BSP101, GG32, Matapan, Melville, Mooltan, Mutine, PS5, S8, S117, S118, SenALZ1, SenASZ3, SeSz-1, SFP10, SJ46, SS3, SS9, STML-13-1, STML-198*, STP07, STP4-a, vB_SenM-2, Vi01	GUUCAAGUCCAGCAGGGGCCAC GUUCAAGUCCAGCAGGGGCCAC
tRNA-Leu-GAG-1-1	1 - 25	SHP1*	GAGGUGGUGGAAUUGGUAGA GAGGUGGUGGAAUGGUAGA
tRNA-Lys-CTT-1-1	2 - 25	SPAsTU*	GGUAUCGCCAAGCGGUAAGGC GGUAUAGCCAAGCGGUAAGGC
tRNA-Lys-TTT-2-1	51 - 75	7t3, Munch*, S113, S147, Stp1,	AGGUUCGAAUCCUGCAGC AGGUUCGAAUCCUGCAGC
tRNA-Met-CAT-1-1	1 - 21	FSL SP-029, FSL SP-058, FSL SP-076, SPAsTU*	AGCUCAGUUGGUAGAGC AGCUCAGUUGGUAGAGC
tRNA-Pro-TGG-2-1	1 - 28	41, SJ46*	GCUCAGUUGGUAGAGCGC GCUCAGUUGGUAGAGCGC
tRNA-Ser-CGA-1-1	1 - 25	FSL SP-029, SPAsTU*	CGUAGCUCAGUUGGUUAGAG CGUAGCUCAGUUGGUUAGAG
tRNA-Lys-TTT-2-1	51 - 75	3-29, 19, 41, 100268_sal2, 118970_sal2, epsilon34, LVR16A, Meda, OSY-STA, S114, S124, S133, SE8, SE11(x2), Seabear, Seafire, SEN22*, SKML-39, SP01, SP1a, SP3, SPAsTU, SPC32H, SPC32N, SPN1S, SPN9TCW, STG2, Stitch, Sw2, Th1, vB_SenS_PHB06, vB_SenS_SB6	AGGUUCGGAUCCUGCA AGGUUCGGAUCCUGCA
tRNA-Ser-CGA-2-1	71 - 93	epsilon34, SEN22*	GUUCGAAUCCUGCAGGGCGCGCC GUUCGAAUCCUGCAGGGCGCGCC
tRNA-Ser-GGA-2-1	34 - 69	7t3, Munch, PVP-SE1*	AUCGGGGGUUCGAAUCCC AUCGGGGGUUCGAAUCCC
tRNA-Thr-CGT-1-1	44 - 73	22, 25, 34, 64795_sal4, 101962B_sal5, 118970_sal4, 146851_sal5, 103203_sal4, 103203_sal5, 146851_sal4, Bp96115, FSL SP-010, GE vB TR, P22, S107, S135, S137, S149, SE10, SE16(x2), SE21, SE22, SF3, SF11, SI23, SE1 (in:p22virus)(x2), SPN9CC*, ST160, vB SalP PM43	AGGUCGUAGGUUCGACUCCUAUUAUCGGCA AGGUCGUAGGUUCGACUCCUAUUAUCGGCA
tRNA-Tyr-GTA-4-1	39 - 68	RE-2010(x2), SEN8*	UCGGACGCGGGUUC AACUCCGCCAGCUCC UCGGACGCGGGUUC AACUCCGCCAGCUCC

1.(x2): Alignments at 2 positions

2.(*): Indicates best alignment

3. The tRf extensively studied in this manuscript (tRNA-Thr-CGT-1-1, 44-73) is bolded.