	Name of Annotator		BLAST conservation - how many other phage (or bacteria) have a highly similar gene?		NCBI BLAST alignment - does the start of this predicted gene line up with the start of other highly similar genes?		BLAST function - do other highly similar genes have an assigned function?		Glimmer - does glimmer predict the same start as genemark?		Starterator		Gap/overlap - is any existing gap or overlap between this start and the stop of the previous gene within the acceptable range?					HHPred - does hhpred data suggest a function for this gene?		Phamerator - do close relatives that have genes in the same pham predict a function for this gene?				
Direction Change Evaluation	GeneMark predicted start	Conclusions and Rationale	Results	Conclusions and Rationale	Results	Conclusions and Rationale	Results	Conclusions and Rationale	Results	Conclusions and Rationale	Results	Conclusions and Rationale	Results	Conclusions and Rationale	Gap/Overlap Length	Gap/Overlap Resolution	Which start coordinate has the strongest supporting data?	Justify your rationale for the final start site you chose.	Results	Conclusions and Rationale	Results	Conclusions and Rationale	Consider data from BLAST, HHpred, Phamerator, and phagesDB	Evaluate any putative NKF genes for the presence of transmembran	Justify the final function chosen. Be sure to only use Official
	high coding potential near 1.0 throughout most of the predicted gene, big dip around 8500 bp and small dip around 8800 bp, no cp in any other reading frame, predicted stop and start surround graph	likely a gene	Similar to SoilAssasin, e value= 1e-179, query coverage=100 %,100% identity, more than 10 similar hits	likely a gene	1:1 allignment with Gordonia Phage Soil Assasin, Mateo, Ebert, and several other phages 3.4 allignment with 2ooore phages	GL predicted start is supported by 1: 1 allignment with the start of other similar (homologous) phage	Top phage hits call Tail Assembly Chaperone	Blast data supports tail assembly chaperone	Glimmer and GeneMark both call 8361	8361 start is supported	Glimmer predicted start, 8361, start 1. It is the most annotated start site within this gene family and has 25 MAs (manual annotations). No other available start	8361 is the only supported candidate for a start site.	8361 has a gap of 4. There is only one other acceptable range. But it has no other data.	8361 is a strong candidate for a start site.	4 bp gap	No violation, smallest gap available	8361	Genemark, BLAST, Glimmer, Starterator, and Gap/Overlap all support this call	No hits with greater than 90% probability or that cover 80% or more of the query; no obvious functions present / no high quality matches. There was one gene, Phage GP 15, that had 89.4% probability, but only 23.14 percent query; the gene was a bacteriophage, however this still does not indicate a particular function being present for MrBates Gene 13.	No apparent function	When compared to Soil Assisassin and Matteo, a solid purple colored backgorund was shown around gene 13 indicating high nucleotide similarity. Both Soil Assasin and Matteo have the same pham number as MrBates, 78244, and there are approximately 26 genes in the sample.	Both comparator phage call their gene in the same pham tail assembly chaperone so phamerator data support this function	Tail Assembly Chaperone		HHpred does not suggest any function but both Blast and Phamerator evidence support that Gene 13 is a tail assembly protein or chaperone and tail assembly
Gene 91 Reverse gene	High coding potential near 1.0 from 6149-61211	likely a gene	Similar to Pureglobe_5 gene 101. It has 81 bp, Ranunculus has 82. e value is 1e-21	likely a gene	There is approximately 70-75% alignment with the 3 other pham phages Beagle, Pureglobe and Odyssey395.	Predicted start location of 61459 is supported as start site. 1:1 alignment with other phages in the pham.	All similar genes have no known function	Blast data supports No known function	Glimmer and Genemark both call 61549	61459 supported as start	Predicted start is 61459. 3 other MA from phages in the AP2 cluster.	61459 is only supported candidate for start for this gene.	Overlap of 8. The next smallest gap/overlap is a gap of 43.	61549 is strong candidate for start.	8 overlap	No violation, smallest gap/overlap available	61549	Genemark, BLAST, Glimmer, Starterator, and Gap/Overlap all support this call	No suggested function from HHPred. All probabilites are below 80%. Highest is 79.5%	No apparent function	This gene seems to align well with Beagle 103. Beagle 103 has no known function.	No apparent function for this gene.	No known function	No transmembrane domains predicted	All BLAST data supports no known function for gene 91
Gene 92 Reverse gene	High coding potential near 1.0 but has a big dip to 0 near 61580	likely a gene	Similar to Odyssey395 gene 102. It has 64 pb and Ranunculus has 61. e values is 0.000002. Score is only 50 so not using it as evidence.	Likely a gene based on coding potential, but there aren't good candidates in the pham that support this.	There is 40-50% alignment with genes of Beagle, Odyssey395 and Pureglobe5	Even though the genes don't align well, Beagle and Odyssey395 have the same start site.Start site is supported.	All similar genes have no known function.	Blast data supports No known function.	Glimmer and Genemark both support start site of 61637	61637 supported as start.	Predicted start is 61637. 2 other phages in AP2 call the same start site.	61637 is the only supported start site for this gene.	Overlap of 17. The next smallest is a gap of 44.	61637 is a strong candidate for the start site.	17 overla[	No violation; smallest gap/overlap available.	61637	Genemark, BLAST, Glimmer, Starterator, and Gap/Overlap all support this call	No suggested function from HHPred. All probabilities are bellw 65%	No apparent function	Gene appears to align with Odyssey395 gene 102.	No apparent function for this gene.	No known function	No transmembrane domains predicted	All BLAST data supports no known function for gene 92
Gene 93 Reverse gene	High coding potential near 1.0 from 62271-61621. Big dip to 0 near 61940, smaller dip to 0.85 near 62000. Dip to 0.4 near 61980	likely a gene	Similar to Odyssey395 gene 103. They are the same length (216) with e value of 1e-93.Good evidence.	likely a gene	There is about 85% alignment with Odyssey395, Pureglobe5, and Beagle, but % identity for all is less than 75%	Even though the genes don't align well, Pureglobe5, Beagle and Odyssey395 have the same start site.Start site is supported.	All similar genes have no known function.	Blast supports no known function	Yes, both predict 62271	62271 supported as start	Predicted start is 62271. 3 other phages in AP2 cluster call this a start site.	Start site of 62271 is supported	Gap of 122 seems large	Start site is still supported as this is the smallest gap available	122	Smallest gap available	62271	Genemark, BLAST, Glimmer, Starterator, and Gap/Overlap all support this call	No suggested functions from HHPred. All probabilities are under 66%	No apparent function	Gene appears to align with Odyssey395 gene 103.	No apparent function for this gene.	No known function	No transmembrane domains predicted	all BLAST data supports no known function for this gene
Gene 94 Reverse gene	High coding potential near 1.0 from 62669 to 62450. Dips to 0 at 62450. Coding capacity does not extend to the end of the gene.	likely a gene	Similar to Beagle 85, but lengths are not good match. Beagle is 85, Ranunculus is 91. But e value is 2e-21	Even though they don't match in length, this is still likely a gene.	There is about 63% alignment with Pureglobe5, Beagle and Odyssey395 genes. But % identity is less than 52%	The start site called for Ranunculus is not shared with any of these other genes.	All similar genes have no known function.	Blast supports no known function	Yes both predict 62669	Start site is likely 62669	Start position of 62669 is only called by Ranunculus. No other pham phages call this start site.	Unsure if start site is supported using Starterator data. Gap/overlap will have to be considered.	-4	Smallest gap/overlap available. Likely start site.	-4	Smallest gap available	62669	GeneMark, Glimmer and Starterator all support this start site, even though it's not shared by any other pham phage. The small overlap supports it as well.	93.9% probability of match to a gene in Enterobacter phage, but Only 61.385% coverage, so not good evidence.	No apparent function	Good match to Odyssey395 gene 104 and Beagle gene 105. Neither have a known function	No apparent function for this gene.	No known function	No transmembrane domains predicted	all BLAST data supports no known function for this gene
Gene 95 Reverse gene	High coding potential of 1.0 from 63058 to 62666. No dips	likely a gene	Tank_82 has sequence length of 112 (Ranunculus_95 has 130). e value is 2e-8 but score is only 57, so not good evidence	Even though they don't match in length, this is still likely a gene.	Only max of 42% alignment with any genes, so not good evidence	63058 start site is shared by Tank_82 and SilentRX_76, even though they don't have good alignment, it's still likely the start site	No highly similar genes, but those that show up with any similarity have no known function	Blast supports no known function	Yes both predict 63058	Start site is likely 63058	Start position of 63058 is called by 3 genes in the pham.	Start site of 63058 is supported	Gap of 38	Start site supported as this is the smallest gap avaialble	38	Smallest gap available	63058	Genemark, BLAST, Glimmer, Starterator, and Gap/Overlap all support this call	No suggested functions from HHPred. All probabilities are under 50%	No apparent function	Good match to Tank_82	No apparent function for this gene.	No known function	No transmembrane domains predicted	all BLAST data supports no known function for this gene
Gene 96 Reverse gene	High coding potential of 1.0 from 63522 - 63097. No dips	Likely a gene	Atuin_105 has sequence length of 154 (Ranunculus_96 is 141). e value of 2e-16. Not same phage pham cluster	Even though they don't match in length, this is still likely a gene.	All % alignment is below 42%, so no gene alignment with others	Start site may still be supported, but not by NCBI BLAST data	No highly similar genes, but those that show up with any similarity have no known function	Blast supports no known function	Yes, both predict 63522	Start site is likely 63522	Suggested start site of 63522 is not called by any other genes. 0 MA. But other potential start sites are not called by any other genes.	Possible start site, but not from Starterator comparison	69 gap	start site can be supported with this gap	69	Not the smallest gap available, but the gap of 0 has start site in area with no coding potential.	63522	Genemark, Glimmer, and Gap/Overlap all support this call	There is 82.2695% coverage and probability of 91.5% match to a structural proten for Salmonella Typhi.	No apparent function, not willing to call it structural protein because it matches a bacterium, not a phage	Does not match genes with any other pham phage	No apparent function for this gene.	No known function	There is 1 transmembrane protein predicted by TmHmm. But since there is only one (minimum of 2 required), we cannot assign it as a membrane protein.	all BLAST data supports no known function for this gene. It does not match any gene with a known function.
Gene 97 Reverse gene	High coding potential at or near 1.0 from 64383 - 63592. No major dips	Likely a gene	Odyssey395_107 has a sequence length of 277 (Ranunculus_97 is 263), but e value of 1e-49 is good evidence	Even though they don't match in length, this is still likely a gene.	There is 56% alignment with Odyssey395_107, but coverage is less than 44% so no good evidence	Start site may still be supported, but not by NCBI BLAST data	No highly similar genes, but those that show up with any similarity have no known function	Blast supports no known function	Yes both call 64383	start site is likely 64383	Start of 64383 is called in 3 other genes: Beagle_109, Odyssey395_107, Pureglobe5_107. 3 MA	64383 is likely start site	Gap of 175	Start site can be supported with this gap	175	Gap seems large but the only smaller gap/overlap appears to be in a different gene. No coding potential between them	64383	Genemark, Glimmer, Starterator all support this call	All probabilities and coverage are below 70%.	No apparent function	Appears to line up with Beagle_109 and Odyssey395_107	No apparent function for this gene.	No known function	No transmembrane domains predicted	All BLAST data supports no known function for this gene
Gene 98 Reverse gene	High coding potential near 1.0 between 64693 and 64559	Likely a gene	Beagle_111 has a sequence length of 42 (Ranunculus_98 is 44) with evalue of 7e-8. Good evidence	Likely a gene	No data	Nothing can be concluded with no data	Beagle_111 has no known function	Blast supports no known function	NO. Glimmer has a start of 64693. GeneMark has start of 64687	We cannot determine start just from this information	Suggested start site of 64693 is not called by any other gene. But start site of 64687 is called by 3 other genes in the cluster.	Possibly Not Informative. Start site of 64693 is not supported with this comparison	64687 has overlap of -4. 64693 has an overlap of -10.	64687 is more likely start site because of smaller overlap	-4	Smallest gap available	64687	Gap/overlap, and GeneMark both support start site of 64687. BLAST also supports this as 3 other genes in the pham call the same start site	No data	No conclusion can be made for function with no data	Appears to line up with Beagle_111 and Odyssey395_108; both have no known function	No apparent function for this gene.	No known function	There is 1 transmembrane protein predicted by TmHmm. But since there is only one (minimum of 2 required), we cannot assign it as a membrane protein.	BLAST data and Phamerator data support no known function for this gene

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Direction Change Evaluation	GeneMark predicted start	Conclusions and Rationale	Results	Conclusions and Rationale	Results	Conclusions and Rationale	Results	Conclusions and Rationale	Results	Conclusions and Rationale	Results	Conclusions and Rationale	Gap/Overlap Length	Gap/Overlap Resolution	Which start coordinate has the strongest supporting data?	Justify your rationale for the final start site you chose.	Results	Conclusions and Rationale	Results	Conclusions and Rationale	Consider data from BLAST, HHpred, Phamerator, and phagesDB	Evaluate any putative NKF genes for the presence of transmembran	Justify the final function chosen. Be sure to only use Official
Gene 99 Reverse gene	High coding potential near 1.0 entire length of gene (64791-64684)	Likely a gene	No data	no conclusions can be drawn with no data	No data	Nothing can be concluded with no data	No similar genes found	no conclusions can be made	No. Glimmer does not predict a start site. GeneMark predicts 64791	We cannot determine start just from this information	No report	Nothing can be determined with no report	Overlap of 4.	Suggested start by GeneMark is likely start site because it has smallest gap/overlap	-4	Smallest gap available	64791	This is the only start site that has any support. GeneMark suggests it and it has the smallest gap/overlap	There is an 86.3% probability but only 54.2857% coverage at the highest, so no evidence for functiond.	no apparent functon	Gene 99 does not match any other pham genes	no conclusion can be drawn from lack of data	No known function	There is 1 transmembrane protein predicted by TmHmm. But since there is only one (minimum of 2 required), we cannot assign it as a membrane protein.	There is minimal data for this gene. So we can only conclude no known function.
Gene 100 Reverse gene	High coding potential near 1.0 from 64967 to 64788	Likely a gene	BeatusComedenti_84 has same length of gene and evalue of 7e-16	likely a gene	74% aligned and 62.7119% identity with BeatusComedenti_84, but that's the best match. Hypothetical protein	Start site supported as this gene calls same start of 64967	BeatusComedenti_84 has no known function	Blast supports no known function	Yes, both predict start site of 64967	Start site is likely 64967	Suggested start site of 64967 is called in 2 other genes; BeatusComedenti_87 and Kitkat_85.	64967 is likely start site	Start site of 64967 has Gap of -1	64967 is likely start site	-1	Smallest gap available	64967	Genemark, BLAST, Glimmer, Starterator, and Gap/Overlap all support this call	Probability of 88.1% and Coverage of 81.3% suggests a subfamily of peptidase enzyme in bacteria.	Cannot conclude a function based on this because it's not a phage. No known function.	Does not match genes with any other pham phage	No function can be suggested with no pham matches	No known function	No transmembrane domains predicted	BLAST data does not match well to any known protein, so No known function is supported