Criteria	Ratings							
Section 1:	Excellent	Good	Acceptable	Needs	Not Done			
E. coli				Improvement				
assembly	Correctly identifies	Correctly identifies	Correctly identifies	Does not correctly	Does not answer at			
	the large section in	the large section in	the large section in	identify the large	least 4 of these			
	the middle of the	the middle of the	the middle of the	section in the	questions.			
	graph as the	graph as the	graph as the	middle of the graph				
	genome.	genome.	genome.	as the genome.				
	Identifies the	Identifies the	Identifies the	Identifies the				
	sections around	sections around	sections around	sections around				
	node 4 and 18 as	node 4 and 18 as	node 4 and 18 as	node 4 and 18 as				
	plasmid and phage	plasmid and phage	plasmid and phage	plasmid and phage				
	DNA, respectively.	DNA, respectively.	DNA, respectively.	DNA, respectively.				
	Explains how they	Explains how they	Explains how they	Provides no				
	identified this	identified this	identified this	explanation for how				
	(probably with	(probably with	(probably with	they identified this				
	BLAST).	BLAST).	BLAST).	(probably with				
	Identifies the	Does NOT identify	Does NOT identify	BLAST).				
	plasmid as <i>E. coli</i>	the plasmid as <i>E.</i>	the plasmid as <i>E.</i>	Does NOT identify				
	plasmid F.	<i>coli</i> plasmid F.	coli plasmid F. Does not indicate	the plasmid as <i>E.</i>				
	Describes the most			<i>coli</i> plasmid F.				
	common path for	common path for	the loops, and describes the most	Does not indicate				
		the plasmid as one the plasmid as one		the loops, and				
	of:	of:		describes the most				
	4, 199, 200, 201,	4, 199, 200, 201,	the plasmid as:	common path for				
	206, 207, 200, 201,	206, 207, 200, 201,	4, 199, 200, 201,	the plasmid as:				
	61, 62, 201, 206, 65,	61, 62, 201, 206, 65,	206, 65, 156, 40,	4, 199, 200, 201,				
	156, 40, 158, 41,	156, 40, 158, 41,	158, 41, 259, 63, 35,	206, 65, 156, 40,				
	259, 63, 35, 17, 198,	259, 63, 35, 17, 198,	(4)	158, 41, 259, 63, 35,				
	20, 35, (4)	20, 35, (4)	Identifies that the	(4)				
	OR	OR	less common paths	Does not identify				
	4, 199, 200, 201, 61,	4, 199, 200, 201, 61,	are sections with	that the less				
	62, 201, 206, 207,	62, 201, 206, 207,	mutations in these	common paths are				

200, 201, 206, 65, 200, 201, 206, 65, plasmids. sections with Does not indicate 156, 40, 158, 41, 156, 40, 158, 41, mutations in these 259, 63, 35, 17, 198, plasmids. 259, 63, 35, 17, 198, that they can not resolve the loops. Does not indicate 20, 35, (4) 20, 35, (4) Identifies that the Identifies that the Does not provide a that they can not less common paths less common paths way to resolve resolve the loops. are sections with are sections with these that would Does not provide a mutations in these way to resolve mutations in these work in sequenced plasmids. these that would plasmids. or unsequenced Should identify that Should identify that data. work in sequenced Indicates that the they can not they can not or unsequenced determine which determine which small, unconnected data. Indicates that the loop (206, 207, 200, loop (206, 207, 200, pieces are likely small, unconnected 201 or 201, 61, 62) 201 or 201, 61, 62) contamination or comes first from regions of poor pieces are likely comes first from this data. sequencing quality. this data. contamination or They should Does not provide a regions of poor indicate that that way to resolve sequencing quality. these that would might be able to resolve this with work. BLAST. Or another If previously suggestion that unsequenced, they would work. would need to get If previously long reads from Pac Bio or ONT or mate unsequenced, they would need to get pair library to long reads from Pac resolve. Bio or ONT or mate Indicates that the pair library to small. unconnected resolve. pieces are likely Indicate that the contamination or small, unconnected regions of poor pieces are likely sequencing quality.

	contamination or	Include a fasta file			
	regions of poor	that has the regions			
	sequencing quality.	indicated, and			
	Include a fasta file	contains the loops			
	that has the regions				
	indicated, and				
	contains the loops.				
Section 2:	Excellent	Good	Acceptable	Needs	Not Done
S. aureus				Improvement	
assembly	Explains what the	Explains what the	Explains what the	Incorrectly explains	At least 3 questions
	N50 and N75 are:	N50 and N75 are:	N50 and N75 are:	what the N50 and	not answered.
	the contig in which	the contig in which	the contig in which	N75 are: the contig	
	the assembly	the assembly	the assembly	in which the	
	reaches 50% of the	reaches 50% of the	reaches 50% of the	assembly reaches	
	length of the	length of the	length of the	50% of the length of	
	assembly and 75%,	assembly and 75%,	assembly and 75%,	the assembly and	
	respectively.	respectively.	respectively.	75%, respectively.	
	Explains that these	Explains that these	Explains that these	Does not provide a	
	are good for	are good for	are good for	correct explanation	
	comparing between	comparing between	comparing between	of why these are	
	assemblies of the	assemblies of the	assemblies of the	good for comparing	
	same genome as the	same genome as the	same genome, but	between assemblies	
	genomes are	genomes are	not why.	of the same	
	comparable, and	comparable, and	Does not, or	genome.	
	the difference is	the difference is	incorrectly,	Does not, or	
	how large the	how large the	explains that they	incorrectly,	
	contigs assembled	contigs assembled	are bad comparing	explains that they	
	are. Explains that	are.	between genomes	are bad comparing	
	they are bad	Explains that they	as different	between genomes	
	comparing between	are bad comparing	genomes are	as different	
	genomes as	between genomes	different lengths	genomes are	
	different genomes	as different	and have	different lengths	
	are different	genomes are	differences in	and have	

lengths and have different fractions of repetitive DNA, and so will present different challenges and not be comparable. N50=16, N75=31 Identified the size of a S. aureus as 2.8 Mbp. So this assembly is about the right size. They should indicate that it is similar in that it has a large central genome with small pieces of non genomic data. There are no complete assemblies of extragenomic DNA like in the *E. coli* genome assembly. They should describe that there is one large region of DNA outside the genome (213, 100, 212, 100, 230), but that a BLAST of it

different lengths. but does NOT indicate that the differences in amount of repetitive DNA will vary and make genomes not comparable. N50=16, N75=31 Identified the size of a S. aureus as 2.8 Mbp. So this assembly is about the right size. They should indicate that it is similar in that it has a large central genome with small pieces of non genomic data. There are no complete assemblies of extragenomic DNA like in the *E. coli* genome assembly. They either do NOT describe that there is one large region of DNA outside the genome (213, 100,

amount of repetitive DNA making genomes not comparable. N50=16. N75=31 Identified the size of a S. aureus as 2.8 Mbp. So this assembly is about the right size. Do not indicate similarities or differences. They both do NOT describe that there is one large region of DNA outside the genome (213, 100, 212, 100, 230), and they did not BLAST it and identify that it is found in many S. aureus, and so is probably part of the genome. They trace from 207 to a subset of the nodes: 41, 72, & 65 OR 423, 451, 42, 115, 81, 279, &, 404.

differences in amount of repetitive DNA making genomes not comparable. N50=16, N75=31 Does not identify the size of a S. aureus as 2.8 Mbp. So this assembly is about the right size. Do not indicate similarities or differences. They both do NOT describe that there is one large region of DNA outside the genome (213, 100, 212, 100, 230), and they did not BLAST it and identify that it is found in many S. aureus, and so is probably part of the genome. They do not trace from 207 the correct nodes: 41, 72, & 65 OR 423, 451, 42, 115, 81, 279, &, 404.

	indicates that is it found in many <i>S. aureus</i> , and so is probably part of the genome. They should trace from 207 to 41, 72, & 65 OR 423, 451, 42, 115, 81, 279, &, 404.	212, 100, 230 they did not E it and identify it is found in r S. aureus, and probably part genome. They trace from 207 to a subset the nodes: 41, 72, & 65 OR 423, 451, 42, 81, 279, &, 40	BLAST that many so is of the om et of				
Citations	Excellent		Acceptable		Needs Improvement		
	Cites BLAST, QUAST, and Bandage and all other sources		Cites two of the 3 tools, and all other sources.		Does not cite tools.		
Well written	Excellent		Acceptable		Needs Improvement		
and clear	Answers to each section written in paragraph form. Clearly written and easy to understand.		Answers to each section written mainly in paragraph form. Mostly clearly written and easy to understand.		Answers to each section written in bullet form. Difficult to understand.		