

The **Genomes** worksheet contains information about the genomes that were used to generate the reads.

The **Reads** worksheet contains descriptions of the input read sets for each of the seven real genomes. This includes ligation-prep and rapid-prep Nanopore reads, as well as Illumina reads. Illumina reads were evenly split into two groups: group A was paired with ligation-prep Nanopore reads and group B was paired with rapid-prep Nanopore reads.

The **Assemblies** worksheet contains basic descriptions of each of the assemblies for each genome and computational stats. Some genome-level stats are also provided here, such as the longest repeat in each genome.

The **Flye circularisation** worksheet shows the circularisation error in Flye assemblies (missing or duplicated bases at the start/end of contigs) which were manually fixed for the 'Flye (fixed circ)' assemblies.

The **Comparisons** worksheet contains chromosome identity values for each of the assemblies. These were based on aligning the chromosomal contig for each read set A assembly to the chromosomal contig in the read set B assembly. For Flye, values are given for both unaltered Flye assemblies ('Flye') and Flye assemblies where circularisation issues have been manually fixed ('Flye (fixed circ)'). Note that not all assemblies for *Serratia marcescens* 17-147-1671 produced a complete chromosomal contig, and so this genome is excluded from this and subsequent worksheets.

The **ALE scores** worksheet contains overall ALE scores for each of the assemblies of the six analysed genomes. Note that this worksheet uses the unaltered Flye assemblies.

The **ALE scores (fixed circ)** contains the same data as the previous worksheet, except that it uses the Flye assemblies with manually-fixed circularisation.

The **ALE z-scores** worksheet contains the same data as the ALE scores worksheet, except that each score has been converted into a z-score (mean of 0 and stdev of 1) on a per-genome basis.

The **ALE z-scores (fixed circ)** worksheet contains the same data as the ALE scores (fixed circ) worksheet, except that each score has been converted into a z-score (mean of 0 and stdev of 1) on a per-genome basis.

The **Ideel results** worksheet contains the fraction of protein sequences in each assembly with an Ideel ratio of 95% or more. Note that this worksheet uses the unaltered Flye assemblies.

The **Ideel results (fixed circ)** contains the same data as the previous worksheet, except that it uses the Flye assemblies with manually-fixed circularisation.

The **Repeat identities** worksheet contains the sequence identities of all assemblies for both repeat and non-repeat regions of the genome. Identities are expressed both as percentages and a Q-scores.

The **Medaka order** worksheet contains results (same format as the Comparisons worksheet) for a few different orders of running Trycycler and Medaka.

Genomes

Sample	Genome size	Replicons	Longest repeat	
			From Unicycler	From MUMmer
<i>Acinetobacter baumannii</i> J9	3,949,783	3	10,246	5,842
<i>Citrobacter koseri</i> MINF_9D	4,833,163	3	29,556	28,824
<i>Enterobacter kobei</i> MSB1_1B	5,093,569	6	14,947	12,473
<i>Haemophilus</i> M1C132_1	2,124,989	6	7,322	7,896
<i>Klebsiella oxytoca</i> MSB1_2C	5,995,634	5	10,787	5,622
<i>Klebsiella variicola</i> INF345	5,952,932	6	5,656	5,582
<i>Serratia marcescens</i> 17-147-1671	5,883,278	5	39,060	39,051

Reads

Sample	Read set A											Read set B														
	Nanopore ligation reads						Illumina reads - group A					Nanopore rapid reads						Illumina reads - group B								
	All			After Filtrng			All		After fastp			Insert size		All			After Filtrng			All		After fastp			Insert size	
	Read count	Total size	N50 length	Read count	Total size	N50 length	Read count	Total size	Read count	Total size	Min	Max	Read count	Total size	N50 length	Read count	Total size	N50 length	Read count	Total size	Read count	Total size	Min	Max		
<i>Acinetobacter baumannii</i> J9	85,484	1,070,356,827	21,638	60,765	1,016,840,396	22,623	3,115,226	454,925,397	3,073,586	448,907,913	157	712	101,526	780,286,224	14,351	69,135	741,274,205	15,130	3,115,226	454,886,971	3,073,051	448,801,170	157	713		
<i>Citrobacter koseri</i> MINF_9D	139,899	1,009,600,962	18,781	79,387	959,121,239	19,909	2,284,300	332,880,816	2,247,899	327,687,679	159	721	213,402	1,666,038,163	14,142	143,774	1,582,736,706	14,924	2,284,300	332,916,017	2,247,656	327,668,697	159	721		
<i>Enterobacter kobei</i> MSB1_1B	45,191	625,579,715	21,856	34,327	594,322,331	22,638	2,046,868	298,913,783	2,016,063	294,505,747	160	719	128,031	987,293,009	15,407	80,886	937,930,249	16,234	2,046,866	298,849,729	2,016,193	294,466,039	160	717		
<i>Haemophilus</i> M1C132_1	220,304	1,342,021,782	16,260	127,998	1,274,921,933	17,502	1,983,498	290,238,947	1,953,677	285,707,813	160	758	271,823	1,704,343,789	10,276	185,001	1,619,105,604	10,569	1,983,498	290,147,888	1,953,695	285,623,168	160	757		
<i>Klebsiella oxytoca</i> MSB1_2C	36,750	483,128,849	24,765	25,498	458,972,442	25,971	3,637,684	530,737,946	3,586,483	523,267,046	157	716	105,226	808,961,843	14,406	69,978	768,514,620	15,181	3,637,682	530,767,101	3,587,102	523,390,295	157	716		
<i>Klebsiella variicola</i> INF345	167,862	1,452,069,004	25,814	80,509	1,379,466,058	27,115	1,666,578	242,275,969	1,640,587	238,549,905	156	704	132,640	998,133,789	14,587	85,440	948,228,758	15,364	1,666,578	242,310,384	1,640,733	238,588,432	156	705		
<i>Serratia marcescens</i> 17-147-1671	139,058	1,091,695,992	20,731	81,121	1,037,111,473	22,098	1,585,894	232,121,118	1,556,040	227,792,294	158	734	138,974	699,122,054	9,898	94,341	664,166,169	10,457	1,585,894	232,065,297	1,556,079	227,754,139	158	755		

Flye circularisation

Assembly	Circ error size	Extra bases	Missing bases
<i>Acinetobacter baumannii</i> J9 A	-1		T
<i>Acinetobacter baumannii</i> J9 B	-2		AA
<i>Citrobacter koseri</i> MINF_9D A	0		
<i>Citrobacter koseri</i> MINF_9D B	-4		TAAT
<i>Enterobacter kobei</i> MSB1_1B A	1	T	
<i>Enterobacter kobei</i> MSB1_1B B	-4		AGTT
<i>Haemophilus</i> M1C132_1 A	0		
<i>Haemophilus</i> M1C132_1 B	4	TTTA	
<i>Klebsiella oxytoca</i> MSB1_2C A	-9		ATAGGGAGT
<i>Klebsiella oxytoca</i> MSB1_2C B	-1		C
<i>Klebsiella variicola</i> INF345 A	-4		AAAT
<i>Klebsiella variicola</i> INF345 B	-13		CCAGGCATCAAAT

Mean error size: 3.5833

Comparisons

Sample	Unicycler A vs B		Miniasm A vs B		Miniasm +Medaka A vs B		Miniasm +Medaka+Pilon A vs B		Raven A vs B		Raven +Medaka A vs B		Raven +Medaka+Pilon A vs B		Flye A vs B		Flye +Medaka A vs B		Flye +Medaka+Pilon A vs B		Flye (fixed circ) A vs B		Flye (fixed circ) +Medaka A vs B		Flye (fixed circ) +Medaka+Pilon A vs B		Trycycler A vs B		Trycycler +Medaka A vs B		Trycycler +Medaka+Pilon A vs B	
	Mean	Worst 100 bp identity	Mean	Worst 100 bp identity	Mean	Worst 100 bp identity	Mean	Worst 100 bp identity	Mean	Worst 100 bp identity	Mean	Worst 100 bp identity	Mean	Worst 100 bp identity	Mean	Worst 100 bp identity	Mean	Worst 100 bp identity	Mean	Worst 100 bp identity	Mean	Worst 100 bp identity	Mean	Worst 100 bp identity	Mean	Worst 100 bp identity	Mean	Worst 100 bp identity	Mean	Worst 100 bp identity	Mean	Worst 100 bp identity
	<i>Acinetobacter baumannii</i> J9	99.99871%	64%	99.65311%	16%	99.73517%	33%	99.76137%	35%	99.89528%	0%	99.92994%	0%	99.93392%	0%	99.97512%	90%	99.99689%	98%	99.9992%	98%	99.97520%	90%	99.99697%	98%	100.00000%	100%	99.98478%	97%	99.99795%	98%	100.00000%
<i>Citrobacter koseri</i> MINF_9D	99.99823%	28%													99.96541%	81%	99.99334%	96%	99.99981%	96%	99.96549%	81%	99.99342%	96%	99.99989%	99%	99.98607%	98%	99.99592%	97%	99.99998%	99%
<i>Enterobacter kobei</i> MSB1_1B	99.99731%	12%	99.93576%	49%	99.97602%	93%	99.99994%	99%	99.95272%	19%	99.97801%	19%	99.99752%	19%	99.94805%	87%	99.97336%	96%	99.99971%	96%	99.94815%	87%	99.97346%	96%	99.99981%	98%	99.97128%	96%	99.98357%	97%	99.99994%	98%
<i>Haemophilus</i> M1C132_1	99.92629%	0%							99.94055%	63%	99.99030%	78%	99.99742%	78%	99.96929%	84%	99.99186%	96%	99.99971%	96%	99.96949%	84%	99.99206%	98%	99.99990%	99%	99.98455%	96%	99.99401%	96%	99.99976%	96%
<i>Klebsiella oxytoca</i> MSB1_2C	99.85277%	11%	99.89432%	22%	99.92740%	26%	99.93321%	26%	99.96049%	19%	99.99288%	44%	99.99895%	44%	99.96640%	76%	99.99419%	91%	99.99969%	91%	99.96657%	76%	99.99437%	96%	99.99986%	96%	99.98251%	97%	99.99504%	97%	99.99998%	99%
<i>Klebsiella varicola</i> INF345	99.99500%	26%	99.93308%	0%	99.97467%	0%	99.98165%	0%	99.92892%	0%	99.96548%	0%	99.97273%	0%	99.95488%	73%	99.98680%	91%	99.99978%	91%	99.95504%	73%	99.98697%	96%	99.99994%	98%	99.97923%	96%	99.99415%	97%	99.99996%	98%

ALE scores

	Unicycler	Flye	Flye +Medaka	Flye +Medaka+Pilon	Tracycler	Tracycler +Medaka	Tracycler +Medaka+Pilon
<i>Acinetobacter baumannii</i> J9 - read set A	-68,751,495	-69,851,511	-68,764,072	-68,670,883	-69,597,973	-68,734,531	-68,669,456
<i>Acinetobacter baumannii</i> J9 - read set B	-68,820,892	-70,694,877	-68,841,011	-68,673,433	-70,307,643	-68,801,834	-68,669,456
<i>Citrobacter koseri</i> MINF_9D - read set A	-41,431,606	-43,043,830	-41,604,961	-41,322,390	-42,440,272	-41,486,711	-41,294,467
<i>Citrobacter koseri</i> MINF_9D - read set B	-41,396,907	-43,306,383	-41,615,646	-41,320,183	-42,610,011	-41,508,539	-41,302,769
<i>Enterobacter kobei</i> MSB1_1B - read set A	-68,382,308	-70,992,926	-69,702,370	-68,368,413	-70,140,607	-69,278,458	-68,332,909
<i>Enterobacter kobei</i> MSB1_1B - read set B	-68,386,694	-71,141,965	-69,570,812	-68,348,288	-70,377,882	-69,242,761	-68,338,219
<i>Haemophilus</i> M1C132_1 - read set A	-111,530,139	-112,327,531	-111,693,172	-111,483,596	-111,951,158	-111,651,146	-111,482,933
<i>Haemophilus</i> M1C132_1 - read set B	-111,606,825	-112,827,118	-111,857,505	-111,492,937	-112,332,292	-111,750,901	-111,465,398
<i>Klebsiella oxytoca</i> MSB1_2C - read set A	-134,631,858	-137,115,849	-134,747,666	-134,454,433	-136,220,774	-134,690,431	-134,411,349
<i>Klebsiella oxytoca</i> MSB1_2C - read set B	-135,327,640	-137,599,430	-134,766,778	-134,420,052	-136,585,895	-134,720,644	-134,402,870
<i>Klebsiella variicola</i> INF345 - read set A	-82,942,439	-84,400,589	-83,230,715	-82,894,952	-83,973,858	-83,012,753	-82,892,149
<i>Klebsiella variicola</i> INF345 - read set B	-82,955,365	-84,664,983	-83,151,089	-82,898,292	-84,123,419	-83,038,509	-82,891,219

ALE scores (fixed circ)

	Unicycler	Flye (fixed circ)	Flye (fixed circ) +Medaka	Flye (fixed circ) +Medaka+Pilon	Tricycler	Tricycler +Medaka	Tricycler +Medaka+Pilon
<i>Acinetobacter baumannii</i> J9 - read set A	-68,751,495	-69,850,089	-68,762,644	-68,669,456	-69,597,973	-68,734,531	-68,669,456
<i>Acinetobacter baumannii</i> J9 - read set B	-68,820,892	-70,690,752	-68,837,033	-68,669,456	-70,307,643	-68,801,834	-68,669,456
<i>Citrobacter koseri</i> MINF_9D - read set A	-41,431,606	-43,043,830	-41,604,961	-41,322,390	-42,440,272	-41,486,711	-41,294,467
<i>Citrobacter koseri</i> MINF_9D - read set B	-41,396,907	-43,303,016	-41,611,806	-41,316,343	-42,610,011	-41,508,539	-41,302,769
<i>Enterobacter kobei</i> MSB1_1B - read set A	-68,382,308	-70,992,304	-69,700,547	-68,366,580	-70,140,607	-69,278,458	-68,332,909
<i>Enterobacter kobei</i> MSB1_1B - read set B	-68,386,694	-71,138,223	-69,567,063	-68,344,539	-70,377,882	-69,242,761	-68,338,219
<i>Haemophilus</i> M1C132_1 - read set A	-111,530,139	-112,327,531	-111,693,172	-111,483,596	-111,951,158	-111,651,146	-111,482,933
<i>Haemophilus</i> M1C132_1 - read set B	-111,606,825	-112,818,648	-111,848,996	-111,484,427	-112,332,292	-111,750,901	-111,465,398
<i>Klebsiella oxytoca</i> MSB1_2C - read set A	-134,631,858	-137,101,813	-134,733,325	-134,440,092	-136,220,774	-134,690,431	-134,411,349
<i>Klebsiella oxytoca</i> MSB1_2C - read set B	-135,327,640	-137,598,249	-134,765,629	-134,418,904	-136,585,895	-134,720,644	-134,402,870
<i>Klebsiella variicola</i> INF345 - read set A	-82,942,439	-84,398,012	-83,228,161	-82,892,397	-83,973,858	-83,012,753	-82,892,149
<i>Klebsiella variicola</i> INF345 - read set B	-82,955,365	-84,657,763	-83,144,016	-82,891,219	-84,123,419	-83,038,509	-82,891,219

ALE z-scores

	Unicycler	Flye	Flye +Medaka	Flye +Medaka+Pilon	Tracycler	Tracycler +Medaka	Tracycler +Medaka+Pilon
<i>Acinetobacter baumannii</i> J9 - read set A	0.575	-1.086	0.556	0.696	-0.704	0.600	0.699
<i>Acinetobacter baumannii</i> J9 - read set B	0.470	-2.360	0.440	0.693	-1.775	0.499	0.699
<i>Citrobacter koseri</i> MINF_9D - read set A	0.597	-1.791	0.340	0.759	-0.897	0.515	0.800
<i>Citrobacter koseri</i> MINF_9D - read set B	0.648	-2.180	0.324	0.762	-1.149	0.483	0.788
<i>Enterobacter kobei</i> MSB1_1B - read set A	0.958	-1.684	-0.378	0.972	-0.822	0.051	1.008
<i>Enterobacter kobei</i> MSB1_1B - read set B	0.954	-1.835	-0.245	0.993	-1.062	0.087	1.003
<i>Haemophilus</i> M1C132_1 - read set A	0.728	-1.288	0.316	0.845	-0.336	0.422	0.847
<i>Haemophilus</i> M1C132_1 - read set B	0.534	-2.551	-0.100	0.822	-1.300	0.170	0.891
<i>Klebsiella oxytoca</i> MSB1_2C - read set A	0.620	-1.710	0.511	0.786	-0.871	0.565	0.827
<i>Klebsiella oxytoca</i> MSB1_2C - read set B	-0.033	-2.164	0.493	0.818	-1.213	0.536	0.834
<i>Klebsiella variicola</i> INF345 - read set A	0.686	-1.698	0.215	0.764	-1.000	0.571	0.769
<i>Klebsiella variicola</i> INF345 - read set B	0.665	-2.130	0.345	0.759	-1.245	0.529	0.770

ALE z-scores (fixed circ)

	Unicycler	Flye (fixed circ)	Flye (fixed circ) +Medaka	Flye (fixed circ) +Medaka+Pilon	Tracycler	Tracycler +Medaka	Tracycler +Medaka+Pilon
<i>Acinetobacter baumannii</i> J9 - read set A	0.573	-1.087	0.556	0.697	-0.706	0.599	0.697
<i>Acinetobacter baumannii</i> J9 - read set B	0.468	-2.357	0.444	0.697	-1.778	0.497	0.697
<i>Citrobacter koseri</i> MINF_9D - read set A	0.596	-1.793	0.339	0.758	-0.899	0.514	0.799
<i>Citrobacter koseri</i> MINF_9D - read set B	0.647	-2.177	0.329	0.767	-1.150	0.482	0.787
<i>Enterobacter kobei</i> MSB1_1B - read set A	0.957	-1.685	-0.377	0.973	-0.823	0.050	1.007
<i>Enterobacter kobei</i> MSB1_1B - read set B	0.953	-1.833	-0.242	0.996	-1.063	0.086	1.002
<i>Haemophilus</i> M1C132_1 - read set A	0.725	-1.296	0.312	0.843	-0.342	0.418	0.845
<i>Haemophilus</i> M1C132_1 - read set B	0.531	-2.541	-0.083	0.841	-1.308	0.166	0.889
<i>Klebsiella oxytoca</i> MSB1_2C - read set A	0.617	-1.701	0.522	0.797	-0.874	0.562	0.824
<i>Klebsiella oxytoca</i> MSB1_2C - read set B	-0.036	-2.167	0.491	0.817	-1.217	0.534	0.832
<i>Klebsiella variicola</i> INF345 - read set A	0.684	-1.699	0.216	0.766	-1.005	0.569	0.766
<i>Klebsiella variicola</i> INF345 - read set B	0.663	-2.124	0.354	0.768	-1.250	0.526	0.768

IDEEL results

	Unicycler	Flye	Flye +Medaka	Flye +Medaka +Pilon	Tracycler	Tracycler +Medaka	Tracycler +Medaka +Pilon
<i>Acinetobacter baumannii</i> J9 - read set A	0.98074	0.83440	0.96771	0.98074	0.86345	0.97167	0.98075
<i>Acinetobacter baumannii</i> J9 - read set B	0.98074	0.74877	0.95873	0.98074	0.78676	0.96461	0.98075
<i>Citrobacter koseri</i> MINF_9D - read set A	0.97408	0.74287	0.92229	0.97363	0.79542	0.93346	0.97408
<i>Citrobacter koseri</i> MINF_9D - read set B	0.97385	0.70504	0.91679	0.97408	0.77871	0.93698	0.97386
<i>Enterobacter kobei</i> MSB1_1B - read set A	0.97649	0.71420	0.88853	0.97582	0.78683	0.93793	0.97626
<i>Enterobacter kobei</i> MSB1_1B - read set B	0.97649	0.67523	0.90247	0.97605	0.75682	0.93183	0.97626
<i>Haemophilus</i> M1C132_1 - read set A	0.95781	0.73555	0.88579	0.95829	0.83422	0.90540	0.95829
<i>Haemophilus</i> M1C132_1 - read set B	0.95734	0.66005	0.85060	0.95882	0.74362	0.86836	0.95833
<i>Klebsiella oxytoca</i> MSB1_2C - read set A	0.98601	0.74720	0.95105	0.98564	0.78714	0.95338	0.98564
<i>Klebsiella oxytoca</i> MSB1_2C - read set B	0.98526	0.69549	0.94823	0.98526	0.75922	0.95041	0.98583
<i>Klebsiella variicola</i> INF345 - read set A	0.98153	0.72098	0.90015	0.98193	0.76292	0.95594	0.98193
<i>Klebsiella variicola</i> INF345 - read set B	0.98193	0.69127	0.92822	0.98154	0.73622	0.94877	0.98174

IDEEL results (fixed circ)

	Unicycler	Flye (fixed circ)	Flye (fixed circ) +Medaka	Flye (fixed circ) +Medaka +Pilon	Tracycler	Tracycler +Medaka	Tracycler +Medaka +Pilon
<i>Acinetobacter baumannii</i> J9 - read set A	0.98074	0.83463	0.96771	0.98075	0.86345	0.97167	0.98075
<i>Acinetobacter baumannii</i> J9 - read set B	0.98074	0.74877	0.95873	0.98075	0.78676	0.96461	0.98075
<i>Citrobacter koseri</i> MINF_9D - read set A	0.97408	0.74287	0.92229	0.97363	0.79542	0.93346	0.97408
<i>Citrobacter koseri</i> MINF_9D - read set B	0.97385	0.70439	0.91659	0.97408	0.77871	0.93698	0.97386
<i>Enterobacter kobei</i> MSB1_1B - read set A	0.97649	0.71406	0.88926	0.97582	0.78683	0.93793	0.97626
<i>Enterobacter kobei</i> MSB1_1B - read set B	0.97649	0.67503	0.90247	0.97605	0.75682	0.93183	0.97626
<i>Haemophilus</i> M1C132_1 - read set A	0.95781	0.73555	0.88579	0.95829	0.83422	0.90540	0.95829
<i>Haemophilus</i> M1C132_1 - read set B	0.95734	0.65990	0.85060	0.95829	0.74362	0.86836	0.95833
<i>Klebsiella oxytoca</i> MSB1_2C - read set A	0.98601	0.74720	0.95105	0.98564	0.78714	0.95338	0.98564
<i>Klebsiella oxytoca</i> MSB1_2C - read set B	0.98526	0.69509	0.94840	0.98564	0.75922	0.95041	0.98583
<i>Klebsiella variicola</i> INF345 - read set A	0.98153	0.72086	0.89996	0.98193	0.76292	0.95594	0.98193
<i>Klebsiella variicola</i> INF345 - read set B	0.98193	0.69144	0.92825	0.98174	0.73622	0.94877	0.98174

Repeat identities

Sample	Unicycler A vs B				Flye A vs B				Flye +Medaka A vs B				Flye +Medaka+Pilon A vs B				Flye (fixed circ) A vs B				Flye (fixed circ) +Medaka A vs B				Flye (fixed circ) +Medaka+Pilon A vs B				Tricycler A vs B				Tricycler +Medaka A vs B				Tricycler +Medaka+Pilon A vs B			
	Non-repeat identity	Non-repeat Qscore	Repeat identity	Repeat Qscore	Non-repeat identity	Non-repeat Qscore	Repeat identity	Repeat Qscore	Non-repeat identity	Non-repeat Qscore	Repeat identity	Repeat Qscore	Non-repeat identity	Non-repeat Qscore	Repeat identity	Repeat Qscore	Non-repeat identity	Non-repeat Qscore	Repeat identity	Repeat Qscore	Non-repeat identity	Non-repeat Qscore	Repeat identity	Repeat Qscore	Non-repeat identity	Non-repeat Qscore	Repeat identity	Repeat Qscore	Non-repeat identity	Non-repeat Qscore	Repeat identity	Repeat Qscore	Non-repeat identity	Non-repeat Qscore	Repeat identity	Repeat Qscore				
<i>Acinetobacter baumannii</i> J9	99.99903%	50.1	99.98396%	37.9	99.97506%	36.0	99.97779%	36.5	99.99699%	45.2	99.99260%	41.3	100.00000%	inf	99.99630%	44.3	99.97506%	36.0	99.98149%	37.3	99.99699%	45.2	99.99630%	44.3	100.00000%	inf	100.00000%	inf	99.98491%	38.2	99.97903%	36.8	99.99793%	46.8	99.99877%	49.1	100.00000%	inf	100.00000%	inf
<i>Citrobacter koseri</i> MNV1_30	99.99833%	48.0	99.98941%	39.9	99.96494%	34.6	99.98652%	38.7	99.99311%	41.8	99.99037%	40.2	100.00000%	inf	99.99133%	40.6	99.96494%	34.6	99.99037%	40.2	99.99241%	41.8	99.99422%	42.4	100.00000%	inf	99.99519%	43.2	99.98597%	38.5	99.99037%	40.2	99.99588%	43.8	99.99807%	47.2	100.00000%	inf	99.99904%	50.2
<i>Enterobacter kobei</i> MSB1_1B	99.99746%	46.0	99.99088%	40.4	99.94742%	32.8	99.97537%	36.1	99.97302%	35.7	99.98814%	39.3	99.99989%	59.8	99.99179%	40.9	99.94750%	32.8	99.97628%	36.2	99.97310%	35.7	99.98906%	39.6	99.99998%	66.7	99.99270%	41.4	99.97089%	35.4	99.98814%	39.3	99.98336%	37.8	99.99270%	41.4	100.00000%	inf	99.99726%	45.6
<i>Haemophilus M1C132_1</i>	99.98826%	35.0	98.02041%	17.0	99.96911%	35.1	99.97743%	36.5	99.99203%	41.0	99.98420%	38.0	100.00000%	inf	99.98646%	38.7	99.96911%	35.1	99.98646%	38.7	99.99203%	41.0	99.99323%	41.7	100.00000%	inf	99.99549%	43.5	99.98426%	38.0	99.99774%	46.5	99.99397%	42.2	99.99549%	43.5	99.99980%	57.0	99.99774%	46.5
<i>Klebsiella oxytoca</i> MSB1_2C	99.85205%	28.3	99.90528%	30.2	99.96762%	34.9	99.87616%	29.1	99.99452%	42.6	99.97034%	35.3	100.00000%	inf	99.97679%	36.3	99.96762%	34.9	99.89906%	29.5	99.99452%	42.6	99.98323%	37.8	100.00000%	inf	99.98968%	39.9	99.98254%	37.6	99.98053%	37.1	99.95502%	43.0	99.99613%	44.1	100.00000%	inf	99.99871%	48.9
<i>Klebsiella variicola</i> INF345	99.99552%	43.5	99.94877%	37.2	99.99476%	33.4	99.99530%	34.6	99.98662%	38.8	99.98513%	38.3	99.99919%	61.3	99.98678%	38.8	99.95478%	33.4	99.97823%	36.7	99.98648%	38.8	99.99855%	47.8	99.99948%	62.5	100.00000%	inf	99.97909%	36.8	99.99174%	40.8	99.99417%	42.3	99.99670%	44.8	99.99966%	64.3	100.00000%	inf
Average (mean)	99.96305%	34.3	99.97799%	23.7	99.96483%	34.5	99.95865%	33.8	99.98999%	40.0	99.98513%	38.3	99.99998%	66.7	99.98853%	39.4	99.96485%	34.5	99.96473%	34.5	99.99001%	40.0	99.99121%	40.6	100.00000%	73.7	99.99461%	42.7	99.98171%	37.4	99.98718%	38.9	99.99323%	41.7	99.99623%	44.2	99.99966%	64.0	99.99855%	48.4

Medaka order

Sample	Trycycler +Medaka A vs B			Medaka +Trycycler A vs B			Medaka +Trycycler +Medaka A vs B		
	Mean identity	Qscore	Worst 100 bp identity	Mean identity	Qscore	Worst 100 bp identity	Mean identity	Qscore	Worst 100 bp identity
<i>Acinetobacter baumannii</i> J9	99.99795%	46.88	98%	99.99710%	45.38	98%	99.99789%	46.76	98%
<i>Citrobacter koseri</i> MINF_9D	99.99592%	43.89	97%	99.99422%	42.38	98%	99.99523%	43.21	98%
<i>Enterobacter kobei</i> MSB1_1B	99.98357%	37.84	97%	99.98284%	37.65	97%	99.98334%	37.78	97%
<i>Haemophilus</i> M1C132_1	99.99401%	42.23	96%	99.99264%	41.33	96%	99.99381%	42.08	96%
<i>Klebsiella oxytoca</i> MSB1_2C	99.99504%	43.05	97%	99.99395%	42.18	98%	99.99450%	42.60	98%
<i>Klebsiella variicola</i> INF345	99.99415%	42.33	97%	99.99413%	42.31	97%	99.99406%	42.26	97%