

Table S1. List of species for each KMC

KMCG	(%)	KMCO	(%)	KMCS	(%)	KMCV	(%)
<i>Klebsiella pneumoniae</i>	20.6	<i>Staphylococcus aureus</i>	24.1	<i>Staphylococcus capitis</i>	37.0	<i>Staphylococcus aureus</i>	35.7
<i>Vibrio parahaemolyticus</i>	18.4	<i>Acinetobacter baumannii</i>	18.8	<i>Staphylococcus epidermidis</i>	16.1	<i>Haemophilus influenzae</i>	25.0
<i>Salmonella enterica</i>	15.1	<i>Streptococcus pyogenes</i>	18.4	<i>Staphylococcus aureus</i>	12.2	<i>Streptococcus agalactiae</i>	11.2
<i>Enterococcus faecium</i>	10.6	<i>Neisseria sicca</i>	16.5	<i>Klebsiella pneumoniae</i>	9.7	<i>Klebsiella pneumoniae</i>	6.3
<i>Lactaseibacillus rhamnosus</i>	10.1	<i>Klebsiella pneumoniae</i>	9.6	<i>Corynebacterium striatum</i>	8.7	<i>Listeria monocytogenes</i>	5.8
<i>Bifidobacterium longum</i>	5.9	<i>Haemophilus influenzae</i>	4.0	<i>Acinetobacter bereziniae</i>	7.1	<i>Streptococcus pneumoniae</i>	5.8
<i>Clostridium perfringens</i>	4.5	<i>Acinetobacter bereziniae</i>	4.0	<i>Enterococcus faecium</i>	5.6	<i>Lactaseibacillus rhamnosus</i>	4.0
<i>Escherichia coli</i>	3.5	<i>Acinetobacter ursingii</i>	2.6	<i>Acinetobacter ursingii</i>	3.1	<i>Escherichia coli</i>	3.7
<i>Yersinia enterocolitica</i>	3.5	<i>Escherichia coli</i>	1.2	<i>Escherichia coli</i>	0.8	<i>Gardnerella vaginalis</i>	1.7
<i>Bacteroides ovatus</i>	2.9	<i>Streptococcus pneumoniae</i>	0.0			<i>Lactaseibacillus paracasei</i>	0.7
<i>Clostridioides difficile</i>	2.5					<i>Cryptococcus neoformans</i>	0.1
<i>Lactaseibacillus paracasei</i>	2.1						

Table S2. List of species for each MC

MCG	(%)	MCO	(%)	MCS	(%)	MCV	(%)
<i>Bacteroides fragilis</i>	8.3	<i>Schaalia odontolytica</i>	16.7	<i>Acinetobacter johnsonii</i>	16.7	<i>Gardnerella vaginalis</i>	16.7
<i>Bacteroides vulgatus</i>	8.3	<i>Prevotella melaninogenica</i>	16.7	<i>Corynebacterium striatum</i>	16.7	<i>Ligilactobacillus gasseri</i>	16.7
<i>Bifidobacterium adolescentis</i>	8.3	<i>Streptococcus mitis</i>	16.7	<i>Micrococcus luteus</i>	16.7	<i>Mycoplasma hominis</i>	16.7
<i>Clostridioides difficile</i>	8.3	<i>Veillonella parvula</i>	16.7	<i>Cutibacterium acnes</i>	16.7	<i>Prevotella bivia</i>	16.7
<i>Enterococcus faecalis</i>	8.3	<i>Haemophilus parainfluenzae</i>	16.7	<i>Staphylococcus epidermidis</i>	16.7	<i>Streptococcus agalactiae</i>	16.7
<i>Lactiplantibacillus plantarum</i>	8.3	<i>Fusobacterium nucleatum</i>	16.7	<i>Streptococcus mitis</i>	16.7	<i>Ligilactobacillus jensenii</i>	16.7
<i>Enterobacter cloacae</i>	8.3						
<i>Escherichia coli</i>	8.3						
<i>Helicobacter pylori</i>	8.3						
<i>Yersinia enterocolitica</i>	8.3						
<i>Salmonellae enterica</i>	8.3						
<i>Fusobacterium nucleatum</i>	8.3						

Table S3. WMS QC summary by MC

MC	Input DNA Amount (ng)	Total Bases(bp)	Total Reads	GC Content (%)	Q30 (%)
MCS	1	23,555,096,416	155,994,016	51.7	92.7
MCO		2,429,394,002	16,088,702	44	92.8
MCG		40,302,789,390	266,905,890	46.9	92.9
MCV		1,520,262,262	10,067,962	43.2	92.7
MCS	10	2,010,476,514	13,314,414	51.8	92.7
MCO		25,774,300,532	170,690,732	44.5	92.5
MCG		1,477,976,222	9,787,922	43.3	92.9
MCV		43,453,019,642	287,768,342	43.3	93
MCS	100	44,499,966,666	294,701,766	51.5	92.2
MCO		2,701,527,108	17,890,908	46	93.1
MCG		19,061,845,588	126,237,388	44	92.3
MCV		2,044,804,250	13,541,750	42.9	92.5
KMCS	1	2,333,958,982	15,456,682	50.7	92.7
KMCO		47,494,702,554	314,534,454	42.8	92.5
KMCG		2,090,406,250	13,843,750	44.9	92.4
KMCV		44,328,968,528	293,569,328	44.6	92.8
KMCS	10	56,880,274,258	376,690,558	50.4	92.6
KMCO		1,921,940,382	12,728,082	44.8	92.8
KMCG		37,928,253,990	251,180,490	44.9	92
KMCV		1,644,677,806	10,891,906	37.1	92.8
KMCS	100	5,252,457,084	34,784,484	47.1	93.1
KMCO		26,534,279,908	175,723,708	44.9	92.7
KMCG		2,381,116,886	15,768,986	44.8	92.9
KMCV		36,397,040,906	241,040,006	37.1	92.9

Table S4. Expected and observed species identified by the sequencing approaches.

		Expected Genura	Observed Genura			Expected Species	Observed Species		
			WMS	16F	16P		WMS	16F	16P
KMC									
KMCG	12	12	12	8	12	12	18	0	
KMCO	8	8	11	7	10	10	12	1	
KMCS	6	6	7	6	9	9	12	1	
KMCV	9	9	9	7	11	11	11	1	
MC									
MCG	11	11	15	7	12	12	14	3	
MCO	6	6	7	7	6	6	7	2	
MCS	6	6	7	7	6	6	7	2	
MCV	6	6	7	5	6	6	7	3	

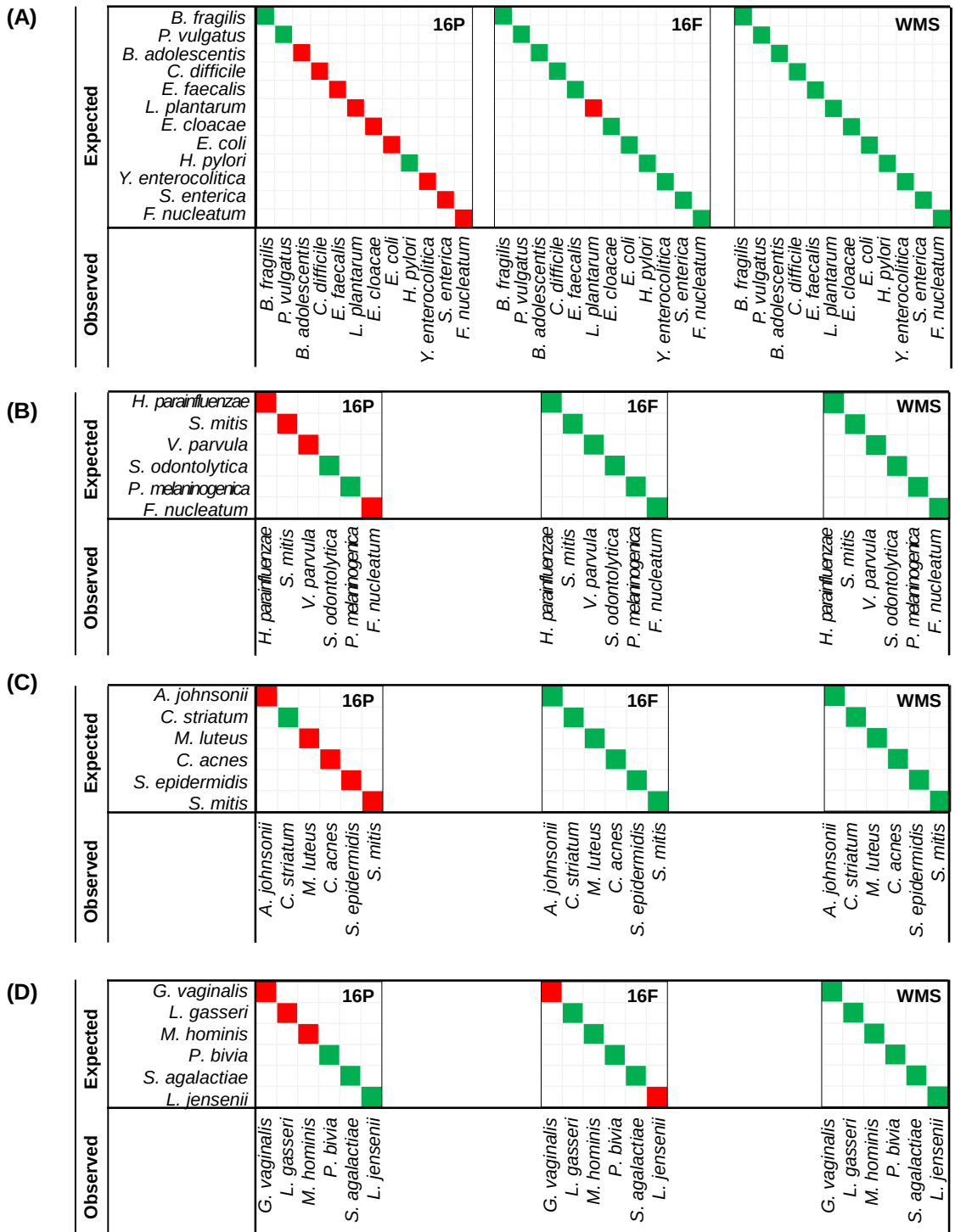


Figure S1. Matching heatmaps of qualitative taxon detection across sequencing platforms based on MC

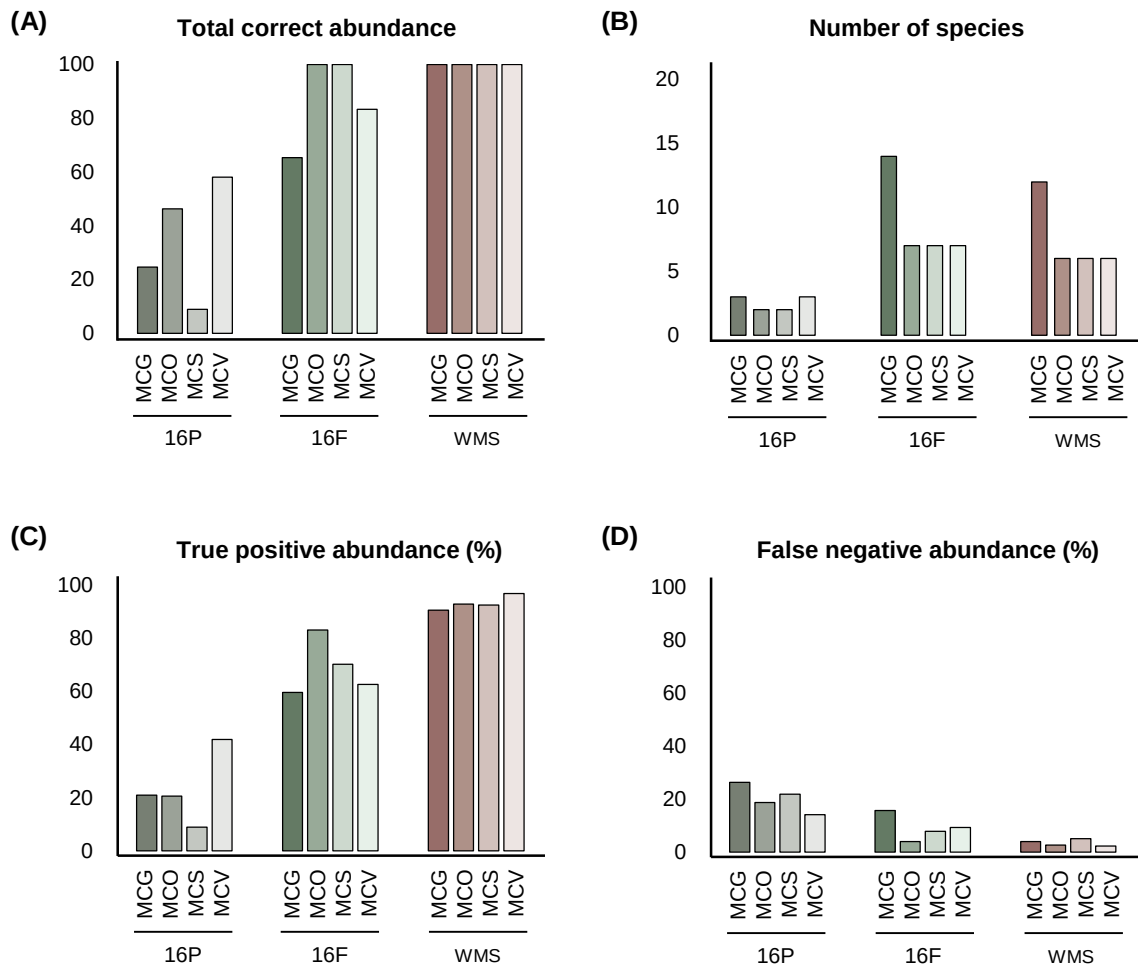


Figure S2. Quantitative evaluation of taxon detection performance across sequencing platforms using MC

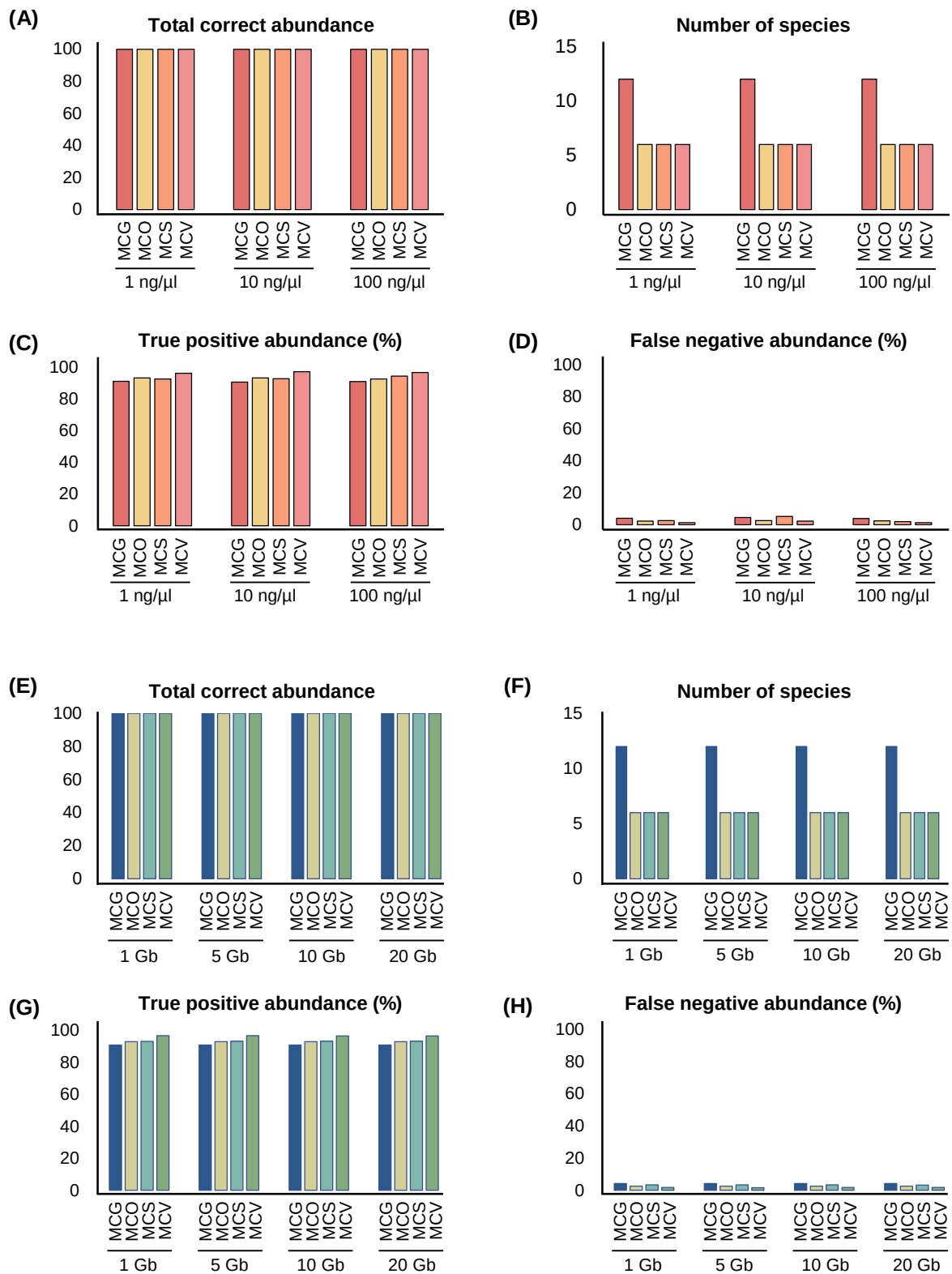


Figure S3. Comparison bar plots by WMS sequencing conditions using MC

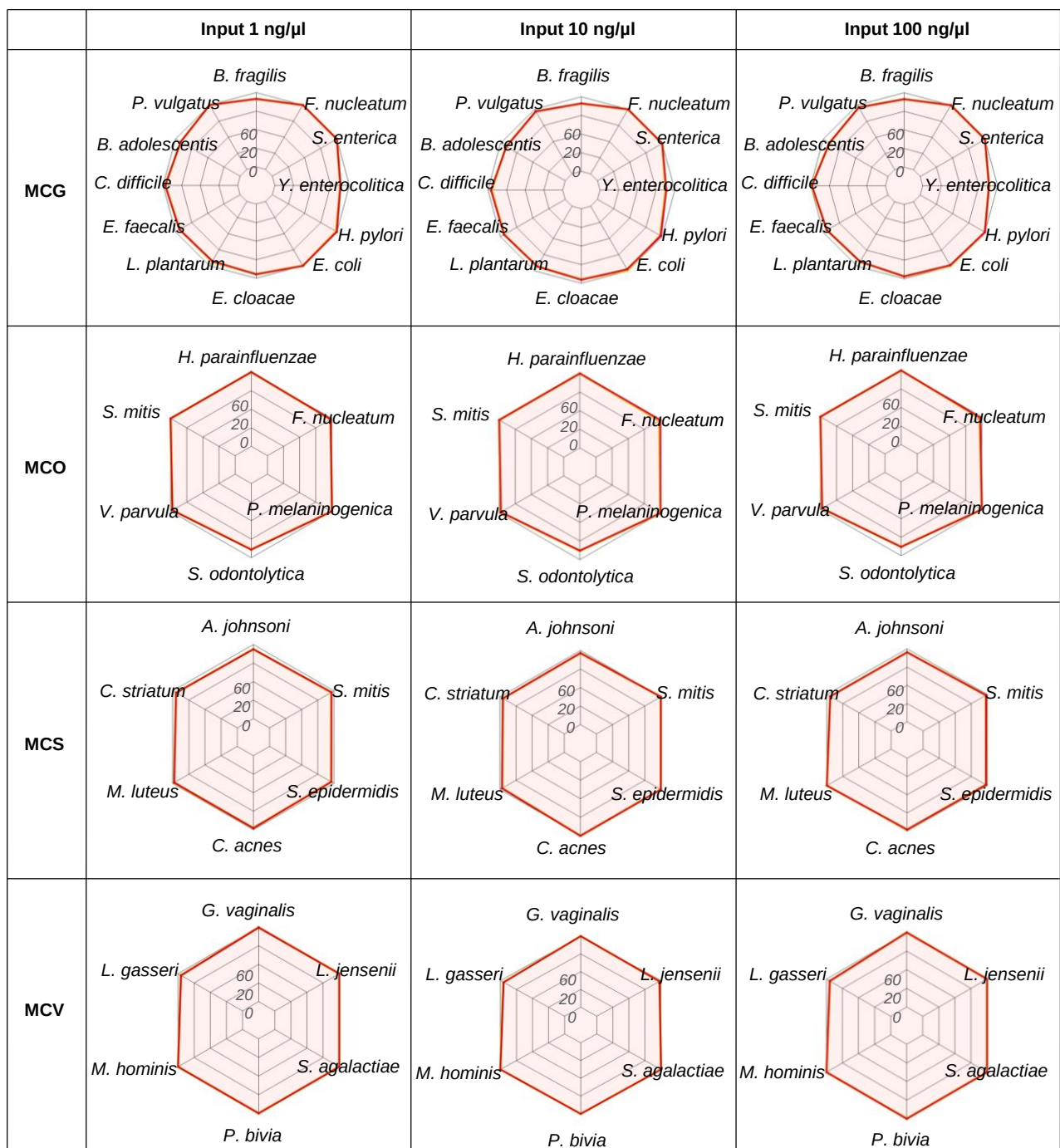
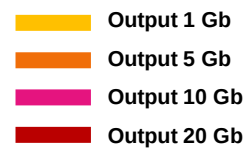


Figure S4. Spider chart showing resolution scores by species for different WMS sequencing conditions using KMCs

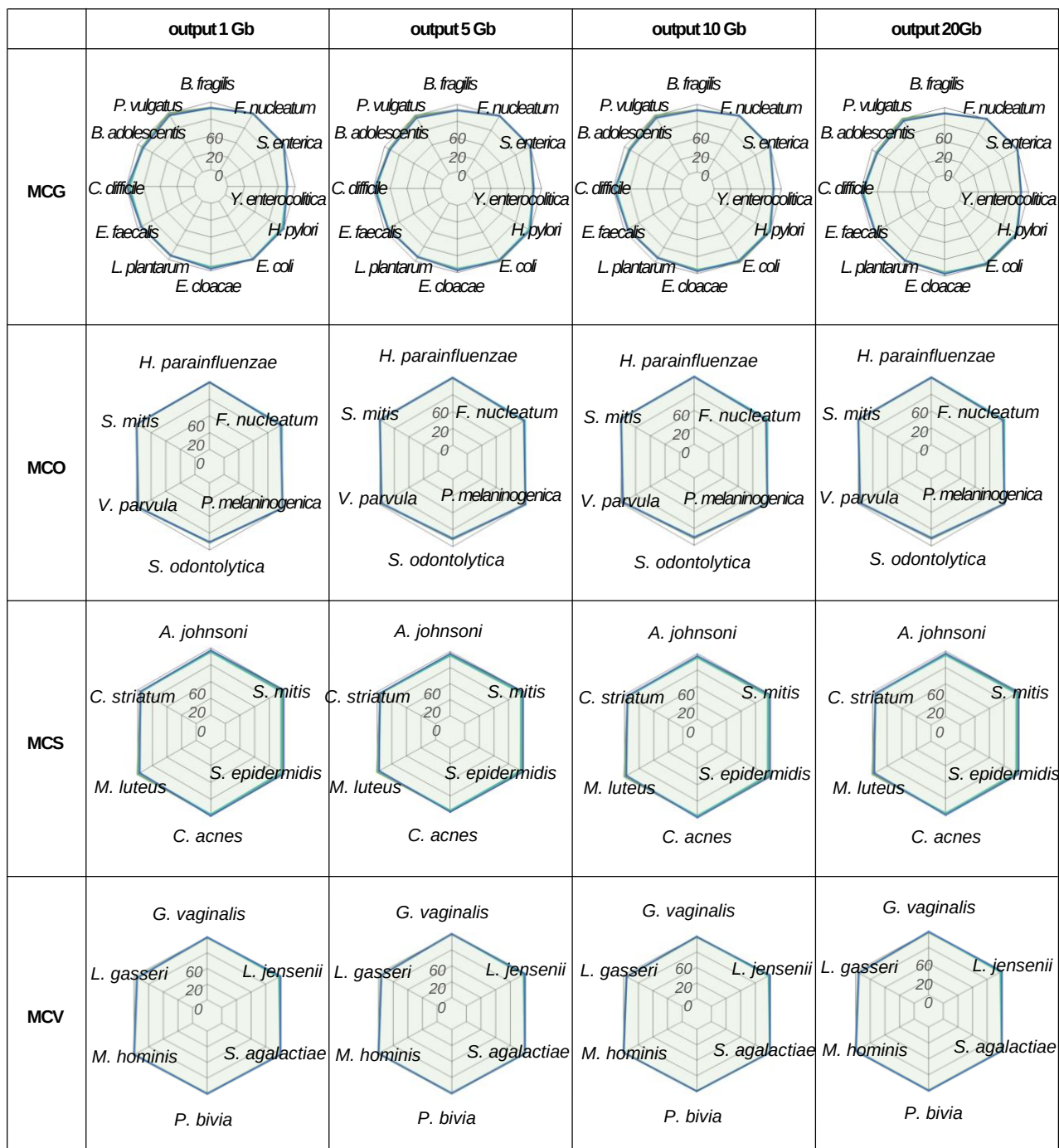
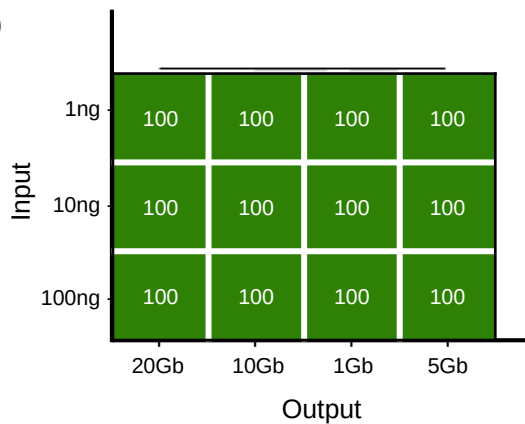
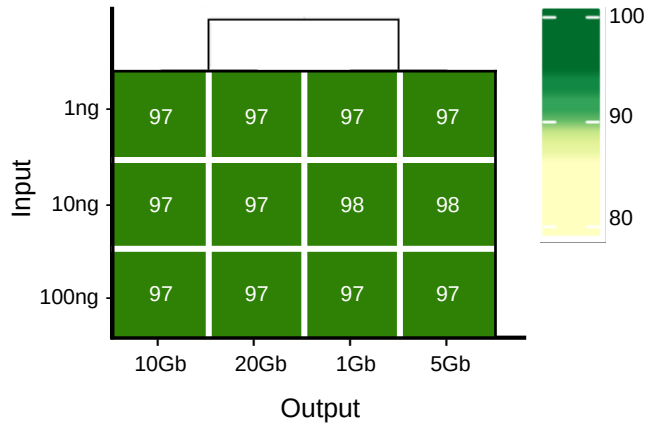


Figure S5. Spider chart showing resolution scores by species for different WMS sequencing conditions using KMCs

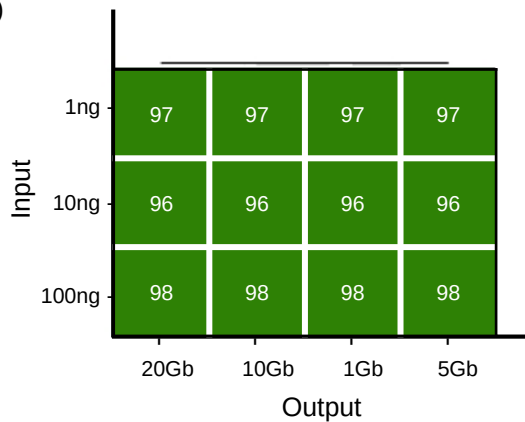
(A)



(B)



(C)



(D)

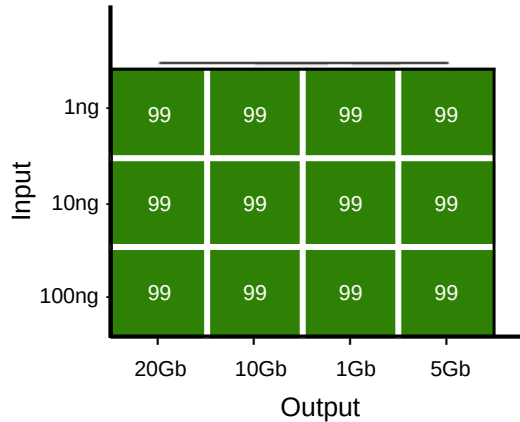


Figure S6. Heatmaps summarizing species-level resolution scores across WMS conditions using MC