

Table 1. Final sets of primers and probes by our strategy on different species or subspecies of coronaviridae.

Species/ Subspecies	Gene	Forward Primer Sequence	Reference ID	Forward Primer Position	Forward Primer Conservation	Reverse Primer Sequence	Reference ID	Reverse Primer Position	Reverse Primer Conservation	Probe Sequence	Reference ID	Probe Position	Probe Conservation
HKU1	ORF1ab	CTGTGAATTAGAA CTTATTTGTGA	DQ415907	5649	33.30%	CAGTCTTTGCT AATGTACCA	DQ415907	5743	100.00%	AACAGCATCAACA CCAACACGACTT	DQ415907	5715	100.00%
OC43	S	TGGTGTTAATTTT AATGTAGA	KX344031	26278	70.60%	GCAGATCTACT GGARGC	KX344031	26367	98.20%	TACTACATTCGCT GCCTAGACAACCT	KX344031	26348	100%
NL63	replicase polyprotein 1ab	GCTGGTTTATGTG TTGTTTG	JQ765564	15138	81.70%	GTACCAAATAC ATGATCATATG C	JQ765564	15244	100.00%	TAGGCTTACGCAG ACAATCACCACAA	JQ765564	15204	98.30%
229E	replicase polyprotein 1ab	TGGTGTTGTGTGY TAYA	KT253325	14653	80.00%	CACCATTCTGA TAATATAAAGT RG	KT253325	14744	56.70%	ATCAGCAATGTAA CCAAGTTCAGCAT	KT253325	14704	100%
MERS-CoV	S	GGCTAAAGATAA AGTCAAYGAG	MF598714	31517	98.70%	GGGCATTTACA ACAAARG	MF598714	31614	98.50%	TCAAGGCACAATC CAAGCGTTCTG	MF598714	31543	98.70%
SARS-CoV	ORF1ab	CCTCAGGCTGAAG TAGA	AY394986	18941	100%	CCTCTATTTTGT AAGCTTTGTC	AY394986	19010	100%	CATGGCTGAGCAT CGTAGAACTTCC	AY394986	18984	100%
COVID-19	ORF1ab	GTGTCAACCTATA CTGTTACTA	EPI_ISL_40 2124	7959	100%	GCATCAAACAT TTTAACTGC	EPI_ISL_40 2124	8043	100%	ACTTCGCACTAT CACCAACATCAGA	EPI_ISL_4 02124	8022	100%

Notes: **HKU1** represents Human coronavirus HKU1; **OC43** represents Human coronavirus OC43; **NL63** represents Human coronavirus NL63; **229E** represents Human coronavirus 229E; **MERS** represents Middle East respiratory syndrome coronavirus; **SARS-CoV** represents severe acute respiratory syndrome coronavirus; **SARS-CoV-2** represents severe acute respiratory syndrome coronavirus 2.

Degenerate bases: R=A/G, Y=C/T, M=A/C, K=G/T, S=C/G, W= A/T, H= A/C/T, B= C/G/T, V=A/C/G, D=A/G /T,N=A/C/G/T.

**Table 2. The performance of our strategy on reducing false negative rate
for sample sets of identified multi-copy regions compared with known 16S rRNA genes.**

Target Organisms	Known rRNA Genes	Known Copy Numbers	Alignment of sequences between De Novo Biomarkers and known rRNA Genes	Distribution of Copy Numbers of De Novo Biomarkers
<i>Mycobacterium tuberculosis</i>	IS6110	10,15	GCA_001652545.1 -----tgaaccgccccgggtgagtcgggagactctctgatctgagacctca AJ242908.1 tggcgcgtagtagtagtgaaccgccccgggtgagtcgggagactctctgatctgagacctca *****	
<i>Mycobacterium Africanum</i>		20	GCA_001652545.1 gccggcggtggtctctggccttgagcgtagtaggcagcctcgagttcgaccggcggggac AJ242908.1 gccggcggtggtctctggccttgagcgtagtaggcagcctcgagttcgaccggcggggac *****	
<i>Mycobacterium bovis</i>		1,20	GCA_001652545.1 gtcgccgcagtagtaggagggcgatggtgaaccagtcgaccagcgcggtggc AJ242908.1 gtcgccgcagtagtaggagggcgatggtgaaccagtcgaccagcgcggtggc ***** GCA_001652545.1 caactcgacatcctcgatggaccgccaggccttgccgggttgatcagctcggtcttgta AJ242908.1 caactcgacatcctcgatggaccgccaggccttgccgggttgatcagctcggtcttgta ***** GCA_001652545.1 taggcggtgatcgctcggctagtgcatgtaggagcttcgaccgctccgaccga AJ242908.1 taggcggtgatcgctcggctagtgcatgtaggagcttcgaccgctccgaccga ***** GCA_001652545.1 cggttgatgcctgcctcggcgagccgctcgctgaaccggatcgatgtgtactgagatcc AJ242908.1 cggttgatgcctgcctcggcgagccgctcgctgaaccggatcgatgtgtactgagatcc ***** GCA_001652545.1 cctatccgtatgggtgataaacgtctttcagggtcagtagcgcttcttggtggcggtcca AJ242908.1 cctatccgtatgggtgataaacgtctttcagggtcagtagcgcttcttggtggcggtcca ***** GCA_001652545.1 gatggcttgctcgatcgctcgaggaccatggaggtggccatcggtgga----- AJ242908.1 gatggcttgctcgatcgctcgaggaccatggaggtggccatcggtggaagcgaccgcca *****	GCA_001652545.1_246_copy:8(8-10) 0(7) 1(63) 2(43) 3(23) 4(25) 5(4) 6(3) 7(6) 8(5) 9(11) 10(7) 11(11) 12(14) 13(17) 14(14) 15(23) 16(17) 17(13) 18(8) 19(4) 20(1) 21(9) 22(2) 23(3) 24(4) 25(2) * 97.9%[332/339] 8.37463126843658

<i>Mycobacterium tuberculosis</i>	IS1081	5,6	GCA_000658535.1 -----cgcgggccttaagccagctt X84741.1 ccgaaggatcacgcgaggaaaccttactcgtacaccacgtccctggccttgccctgggtgt * * * * * *	GCA_000658535.1_410_copy:5(2-5) 0(1) 1(2) 2(6) 3(28) 4(65) 5(236) 7(1) * 99.7%[338/339] 4.55752212389381
<i>Mycobacterium Africanum</i>		5,6	GCA_000658535.1 tagggcccagctggagccgacggcgctgtcggtttgtgccatgttgtgcccgcagcctgc X84741.1 caggcccagctggagccgacggcgctgtcggtttgtgccatgttgtgcccgcagcctgc *****	
<i>Mycobacterium bovis</i>		5,6	GCA_000658535.1 accttctgcccgctggcgcttgccctgctcgtagatcacctggaagttacggcccagctgg X84741.1 accttctgcccgctggcgcttgccctgctcgtagatcacctggaagttacggcccagctgg ***** GCA_000658535.1 gtaatgaaccctggcaggccgccaaccggcgccgccccaaaagtactcgcggtcaac X84741.1 gtaatgaaccctggcaggccgccaaccggcgccgccccaaaagtactcgcggtcaac ***** GCA_000658535.1 acatcagaaatgatggcctgatgctcggcctccagcaaccggccagagcgcggatcatg X84741.1 acatcacgaatgatggcctgatgctcggcctccagcaaccggcctgagcgcggatcatg ***** GCA_000658535.1 gcgccat----- X84741.1 gcgccatgctcgacatcccgaattgatgttgatgggtcatgaaacctgttctcctt *****	
<i>Tuberculosis complex</i>	PGRS	26,30	Cluster12423 -----tggt Z34263.1 atgcggaccacggtatctacagactcggatgaatccggactcagccggggttgccgttggt *** Cluster12423 gcctttgccgccggtggcaccgtcgaggcccttggcgccgtcgccgccggtggcgccgtt Z34263.1 gcctttgccgccggtggcaccgtcgaggcccttggcgccgtcgccgccggtggcgccgtt ***** Cluster12423 gacgccgccgctaccgccggcccgctttcccgccggccgacccggtcccgcgaacacc Z34263.1 gacgccgccgctaccgccggcccgctttcccgccggccgacccggtcccgcgaacacc ***** Cluster12423 gccgtcaccgcccggtgccggcgccgggggtaccggcattgaaaatggccccaccgtt Z34263.1 gccgtcaccg-cggtgccggcgccgggggtaccggcattgaaaatggccccaccgtt ***** Cluster12423 gccg-cgccgccgccggtcccgccagccccggcgccgcccgcctccggcaccac Z34263.1 gccgcccgcgccggtcccgccagccccggcgccgcccgcctccggcaccac *** Cluster12423 cgggttggtcatcagggcctcaagcggat----- Z34263.1 cggccccgcc----ggccccaaactggccgaatatccgcgccaccgccgtccccgcc ** . . * * * * . . *	CP054014.1 3361564-3361841 2 copy:5(3-5) length:278 1-278

<i>Bordetella pertussis</i> ; <i>Bordetella parapertussis</i>	IS1002	6; 4--8; 9; 90	GCA_001509915.1 ---ctaggtcgagcccttcttgttaacagggtgatgcaacagaactggacgatgaggcag Z54268.1 ctcctaggtcgagcccttcttgttaacagggtgatgcaacagaactggacgatgaggcag ***** GCA_001509915.1 gccagccaggcggcaggggtgagcctgcgcaccggttacaagtggcttgccttcga Z54268.1 gccagccaggcggcaggggtgagcctgcgcaccggttacaagtggcttgccttcga ***** GCA_001509915.1 agcgaaggcttggaaggcctgcttgaccgagttctcggccgaccgagcccgaaggcc Z54268.1 agcgaaggcttggaaggcctgcttgaccgagttctcggccgaccgagcccgaaggcc ***** GCA_001509915.1 tgtgccccgagcaggttgagcacttcgccagcagcggccagcgtctgccgtgtgg Z54268.1 tgtgccccgagcaggttgagcacttcgccagcagcggccagcgtctgccgtgtgg ***** GCA_001509915.1 cgcatacgcgctgaaggcggccgcagcctggccaccgtggcgggtatatggaacgcatc Z54268.1 cgcatacgcgctgaaggcggccgcagcctggccaccgtggcgggtatatggaacgcatc ***** GCA_001509915.1 ggccctgagtcgactgcctcgttgaggccggcgccggcgccgggtgcggctatgaacgccc Z54268.1 ggccctgagtcgactgcctcgttgaggccggcgccggcgccgggtgcggctatg-acgcgcc ***** , ***** GCA_001509915.1 agcccaggcgagctgctgcacatcgacaccaagcggtcgggccgcatccggggcggtgggc Z54268.1 agcccaggcgagctgctgcacatcgacaccaagcggtcgggccgcatccggggcggtgggc ***** GCA_001509915.1 catcgcatcaccggcgatcgggcccagaaccgaaccggcgattggctgggacgctgtg Z54268.1 catcgcatcaccggcgatcgggcccagaaccgaaccggcgattggctgggacgctgtg ***** GCA_001509915.1 cacctggccatcgatgacttctcgcgcgtgtcctttgctcgcatcctcgacgatgaaggc Z54268.1 cacctggccatcgatgacttctcgcgcgtgtcctttgctcgcatcctcgacgatgaaggc ***** ,*** GCA_001509915.1 ggcgatcagtgcgctgagttcctgcgccaagccaccgcctactacgccagtctggcgctg Z54268.1 ggcgatcagtgcgctgagttcctgcgccaagccaccgcctactacgccagtctggcgctg ***** , ***** GCA_001509915.1 cgcatacgaccgctgatgaccgacaacggcagcggctacgtctccaggaccttcgggcg Z54268.1 cgcatacgaccgctgatgaccgacaacggcagcgggttacgtctccaggaccttcgggcg ***** , ***** GCA_001509915.1 gtgtgctggagctgggaatccgtcacatccgcacccgccctacaccccaagaccaac Z54268.1 gtgtgctggagctgggaatccgtcacatccgcacccgccctacaccccaagaccaac ***** , ***** GCA_001509915.1 ggcaaggccgagcgcctcgtgcagacctgttacgggagtgggcatagccaggccctac Z54268.1 gtcaaaggccgagcgcctcgtgaagacctgttacgggagtgggcatagccaggccctac * ***** GCA_001509915.1 acgagctcagcgaacgacaggctgccttgagcccttcattgaccgctacaactgg-- Z54268.1 acgagctcagcgaacgacaggctgccttgagcccttcattgaccgctacaactgggtg *****	GCA_001509915.1_74_copy:3(3-3) 0(179) 1(144) 2(15) 3(1) 47.2%[160/339] 0.52212389380531
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<i>Bordetella pertussis</i>	IS1663	17	NZ_CP025371.1:c -----gtggctgatagcagtttgttatctgcaggaggccaagtcattttcataggt GCA_001509915.1 ggcgagtggtgctgacagcagtttgttatctgcaggaggccaagtcattttcataggt ***** NZ_CP025371.1:c attgatgtatcaaaaggccaagctggattgcacgttgcagcggctgaggctgacaagtg GCA_001509915.1 attgatgtatcaaaaggccaagctggattgcacgttgcagcggctgaggctgacaagtg ***** NZ_CP025371.1:c aagaccaaggtggtggtcaacacgccgcggcgctacaagccctgctggcgtggtgcgcc GCA_001509915.1 aagaccaaggtggtggtcaacacgccgcggcgctacaagccctgctggcgtggtgcgcc ***** NZ_CP025371.1:c aaacacggcgacacggcgagttgcacgccatcctggagcctacgggtctgtatcac GCA_001509915.1 aaacacggcgacacggcgagttgcacgccatcctggagcctacgggtctgtatcac ***** NZ_CP025371.1:c gagcaagcggcgacggcgctgccccagggtccgggtctcttttggtcaatccgccccaggcc GCA_001509915.1 gagcaagcggcgacggcgctgccccagggtccgggtctcttttggtcaatccgccccaggcc ***** NZ_CP025371.1:c cgggactttgccaaggccttggcgctgcgtccaaaaatgatgcgtcgacagctacgtg GCA_001509915.1 cgggactttgccaaggccttggcgctgcgtccaaaaatgatgcgtcgacagctacgtg ***** NZ_CP025371.1:c ctggctcgtatggacagacgtgagccggcgctggtgacccggcgcccttgcattgcg GCA_001509915.1 ctggctcgtatggacagacgtgagccggcgctggtgacccggcgcccttgcattgcg ***** NZ_CP025371.1:c cgtcaactgcgccttgttgacgcgacgcgagggcgtgagcaaggatctgtgcgtgag GCA_001509915.1 cgtcaactgcgccttgttgacgcgacgcgagggcgtgagcaaggatctgtgcgtgag ***** NZ_CP025371.1:c ctcaatcgcaaaagagaagaccagttcagccctcggcgcccttggtcgattggtccatc GCA_001509915.1 ctcaatcgcaaaagagaagaccagttcagccctcggcgcccttggtcgattggtccatc ***** NZ_CP025371.1:c gacaaggccatcggttcttgcgcaacagatcaacaatcgagcggcgatcgatcag GCA_001509915.1 gacaaggccatcggttcttgcgcaacagatcaacaatcgagcggcgatcgatcag ***** NZ_CP025371.1:c cacatcgacaaccacccgacctcaagcaagactgcgagctgctgaactccatccccgcc GCA_001509915.1 cacatcgacaaccacccgacctcaagcaagactgcgagctgctgaactccatccccgcc ***** NZ_CP025371.1:c atcgggacctcaggccggcaacgccatcctggcgctcatgcacaatcggcatatcgactcc GCA_001509915.1 atcgggacctcaggccggcaacgccatcctggcgctcatgcacaatcggcatatcgactcc ***** NZ_CP025371.1:c gcccaagacctggcgccctatctcgssgtggtccctgtgcagcgcaatccggcagcagt GCA_001509915.1 gcccaagacctggcgccctatctcgssgtggtccctgtgcagcgcaatccggcagcagt ***** NZ_CP025371.1:c ctgaacagctgcgcacgcctgtccaaagccggccctccagggtgcgcgccagttatac GCA_001509915.1 ctgaacagctgcgcacgcctgtccaaagccggccctccagggtgcgcgccagttatac ***** NZ_CP025371.1:c atggcgccctggttgggacccgccacaacccccacatccgcgccctttaccagcgctg GCA_001509915.1 atggcgccctggttgggacccgccacaacccccacatccgcgccctttaccagcgctg ***** NZ_CP025371.1:c ctcaaaagcaggaaaaagcaaaaaggccgcgctggcgcccatgagaaaaagggtcat GCA_001509915.1 ctcaaaagcaggaaaaagcaaaaaggccgcgctggcgcccatgagaaaaagggtcat ***** NZ_CP025371.1:c ctgtgcttcggggtctctcaaaaaccgcatccctaccagcccaattacgccatgaatggt GCA_001509915.1 ctgtgcttcggggtctctcaaaaaccgcatccctaccagcccaattacgccatgaatggt ***** NZ_CP025371.1:c tga----- GCA_001509915.1 tgaactccaagacggtatctgtccccggggga ***	GCA_001509915.1_17_copy:5(2-6) 0(1) 15(1) 16(82) * 98.8%[83/84] 15.797619047619
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<i>Bordetella</i> <i>parapertussis</i>; <i>Bordetella</i> <i>bronchiseptica</i>	IS1001	20; 22 1--7; 0;	X66858.1 -----ggttcatcgcaataacgtgaggggtttggcaa-ttttctattct IGCA_004008355_0 aggcaaaaaaagggttcacgcgcataacgcgtggagggtttgcaggttttcgattctt X66858.1 tgaacgcagattttgacatcaggatgcaggagatgctggatgcagttgta'ggagt IGCA_004008355_0 tgaacgcagattttgcatcaggatgcaggagatgctggatgcagttgta'ggagt X66858.1 cgctggagagctggcagggtatggcgtcgaacgcgtggaatggccgaagaccagggc IGCA_004008355_0 cgctggagagctggcagggtatggcgtcgaacgcgtggaatggccgaagaccagggc X66858.1 gcacgtgtgatctatttgaagcaacggccaaggtgatgctgtgcagcagtcagcg IGCA_004008355_0 gcacgtgtgatctatttgaagcaacggccaaggtgatgctgtgcagcagtcagcg X66858.1 cgcgatgtgccagatgcataagaccaggttcgaaggtgcgagatctgcgatattcg IGCA_004008355_0 cgcgatgtgccagatgcataagaccaggttcgaaggtgcgagatctgcgatattcg X66858.1 agtatcgagtcgttctgcacgtgcgcgcagacttatgatgagcnahtgcagacc IGCA_004008355_0 agtatcgagtcgttctgcacgtgcgcgcagacttatgatgagcnahtgcagacc X66858.1 cgccctggagcagcttgcctggctggggcatatcaagggtgacggatcggtgggc IGCA_004008355_0 cgccctggagcagcttgcctggctggggcatatcaagggtgacggatcggtgggc X66858.1 aggcctgcagccaattgctgaatcgagcaacgtgcaggcggaggcaggtttctgaac IGCA_004008355_0 aggcctgcagccaattgctgaatcgagcaacgtgcaggcggaggcaggtttctgaac X66858.1 tgaattggataccgtcaagacactggacaggtcgagtcgctgctgagtgccgaac IGCA_004008355_0 tgaattggataccgtcaagacactggacaggtcgagtcgctgctgagtgccgaac X66858.1 cgagttggtccagatcgagttatggcagtgagcaggtttgcctgcccaaggcatc IGCA_004008355_0 cgagttggtccagatcgagttatggcagtgagcaggtttgcctgcccaaggcatc X66858.1 gctacgcagcagtggtgtgatccgatcgccagggcaggtgctgtgagttggccaggac IGCA_004008355_0 gctacgcagcagtggtgtgatccgatcgccagggcaggtgctgtgagttggccaggac X66858.1 gctcacgcagagcggccgggctttctgaacaattgcgcctggggcgcccaagca IGCA_004008355_0 gctcacgcagagcggccgggctttctgaacaattgcgcctggggcgcccaagca X66858.1 tcaaggcgttgccatgcagatgacacgcgcctacagttggagatccaggccacagcc IGCA_004008355_0 tcaaggcgttgccatgcagatgacacgcgcctacagttggagatccaggccacagcc X66858.1 cacagcagagatgctctatgactgttctcatgtcgtggcagatgagcagagatca IGCA_004008355_0 cacagcagagatgctctatgactgttctcatgtcgtggcagatgagcagagatca X66858.1 ttgatcgagtgccgctggatcaggccaatcaactacgccaggatgttccgcagcaggaa IGCA_004008355_0 ttgatcgagtgccgctggatcaggccaatcaactacgccaggatgttccgcagcaggaa X66858.1 ttgatcgagtgccgctggatcaggccaatcaactacgccaggatgttccgcagcaggaa IGCA_004008355_0 ttgatcgagtgccgctggatcaggccaatcaactacgccaggatgttccgcagcaggaa X66858.1 tcatcaaatcgagtcgctgactgctgcgcaacctgacaacctggatcgccnagg IGCA_004008355_0 tcatcaaatcgagtcgctgactgctgcgcaacctgacaacctggatcgccnagg X66858.1 cgctccggtcgagcaattgctgcagccaacagccgctgctgacaggtctatgtcttcg IGCA_004008355_0 cgctccggtcgagcaattgctgcagccaacagccgctgctgacaggtctatgtcttcg X66858.1 gtgacgaactcaaacgctctggtttaccaaaagacctgctggcgaagcagcctgga IGCA_004008355_0 gtgacgaactcaaacgctctggtttaccaaaagacctgctggcgaagcagcctgga X66858.1 accactggtacagcagggcgagcaaaaggaaatagccgcttgaaacacctcgctcagc IGCA_004008355_0 accactggtacagcagggcgagcaaaaggaaatagccgcttgaaacacctcgctcagc X66858.1 gcttgaaggctatctgcacggatctctggccagatgccgaatccccgaacaccgca IGCA_004008355_0 gcttgaaggctatctgcacggatctctggccagatgccgaatccccgaacaccgca X66858.1 ttgtcgaggatcaacaacactatcaaggtcatcaagcagcgcttaccgctacacg IGCA_004008355_0 ttgtcgaggatcaacaacactatcaaggtcatcaagcagcgcttaccgctacacg X66858.1 accaggaaactcttcttcaaaatcgtgcgccttccccggcaatgcgcatgaacc- IGCA_004008355_0 accaggaaactcttcttcaaaatcgtgcgccttccccggcaatgcgcatgaacc- X66858.1 ----- IGCA_004008355_0 aaaaaa	GCA_004008355_0_copy:8(2-8) 22(21) 23(1) 24(1) * 100.0%[23/23] 22.1304347826087
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<i>Mycoplasma pneumoniae</i>	RepMP 2/3	10	FJ604100.1 gctgatcaccctgggttggttgaacgccgaagacgttgtaacatcgttgcagtgg GCA_002090215.1 --tgatcaccctgggttggttgaacgccgaagacgttgtaacatcgttgcagtgg ***** FJ604100.1 caccagcttcagcttcagctcggcggttggttagttacgttcacggactttatcaaacc GCA_002090215.1 caccagcttcagcttcagctcggcggttggttagttacgttcacggactttatcaaacc ***** FJ604100.1 ccgcgctggttacctcgggctccagttaacgggtctcgtatgaagtgaaagcgaacccaaag GCA_002090215.1 ccgcgctggttacctcgggctccagttaacgggtctcgtatgaagtgaaagcgaacccaaag ***** FJ604100.1 ggagttaatttggccaagcggccctgagcggcctttcgtggcagttgggtcaaccggct GCA_002090215.1 ggagttaatttggccaagcggccctgagcggcctttcgtggcagttgggtcaaccggct ***** FJ604100.1 gggccgcgtggagagtgtgtgggatttcaagggggtgtggcggatcaagctcagttggc GCA_002090215.1 gggccgcgtggagagtgtgtgggatttcaagggggtgtggcggatcaagctcagttggc ***** FJ604100.1 cgcgcaagcagctacaagtagtaccaccaccacggcaacagggttaccttaccggagca GCA_002090215.1 cgcgcaagcagctacaagtagtaccaccaccacggcaacagggttaccttaccggagca ***** FJ604100.1 cccgaatgccctcgcgtaccaaatagctataccgacaaggattcgtacaaggcttcac GCA_002090215.1 cccgaatgccctcgcgtaccaaatagctataccgacaaggattcgtacaaggcttcac ***** FJ604100.1 tcaagggttcgggtcaaaccaattcccaaaacaattcgccctacctccattttattaaacc GCA_002090215.1 tcaagggttcgggtcaaaccaattcccaaaacaattcgccctacctccattttattaaacc ***** FJ604100.1 taagaaagtcgaaagcacgacccaactcgaccagggttaaaaaacctgttggacccaa GCA_002090215.1 taagaaagtcgaaagcacgacccaactcgaccagggttaaaaaacctgttggacccaa ***** FJ604100.1 ccagggttcgcaccaagctgcgccaagctttggtacagaccattccaccagccccagcc GCA_002090215.1 ccagggttcgcaccaagctgcgccaagctttggtacagaccattccaccagccccagcc ***** FJ604100.1 ccaatcgctcaaaacaacgacaccggtatttgggaggagtagtggtaacctcagtagtgt GCA_002090215.1 ccaatcgctcaaaacaacgacaccggtatttgggaggagtagtggtaacctcagtagtgt ***** FJ604100.1 gtttagtggtgggggtgctggagggggttcttcaggctcaggtcaa GCA_002090215.1 gtttagtggtgggggtgctggagggggttcttcaggctcaggtcaa *****	GCA_002090215.1_89_copy:6(3-7) 0(1) 1(9) * 90.0% 9/10 0.9
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<i>Mycoplasma pneumoniae</i>	RepMP 5	7, 9	HQ698831.1 GCA_002090215.1 aagagagcgaaagaagcagtatgccttctatcgcgattatctgctcaaccaagaaaatat aagagagcgaaagaagcagtatgccttctatcgcgattatctgctcaaccaagaaaatat ***** HQ698831.1 GCA_002090215.1 ccgaaaaatttacggagcaaatatacctttcgaaacttttcaagtaaaggatatttgtga ccgaaaaatttacggagcaaatatacctttcgaaacttttcaagtaaaggatatttgtga ***** HQ698831.1 GCA_002090215.1 aattagaagaggtcgagcgatcactaaagcgtatattaggaataatcctggagaaaatcc aattagaagaggtcgagcgatcactaaagcgtatattaggaataatcctggagaaaatcc ***** HQ698831.1 GCA_002090215.1 agtttattccgcagctaccacaaatgatggtaggttaggacgtattaaagattgcgattt agtttattccgcagctaccacaaatgatggtaggttaggacgtattaaagattgcgattt ***** HQ698831.1 GCA_002090215.1 tgatggtgaatacatcacttgaactacaaatggttatgctggagtagttttttatcgtaa tgatggtgaatacatcacttgaactacaaatggttatgctggagtagttttttatcgtaa ***** HQ698831.1 GCA_002090215.1 tggcaagtttaatgcatcacaaagattgcggtgttttaaagggttaaaaaataaaaaatctg tggcaagtttaatgcatcacaaagattgcggtgttttaaagggttaaaaaataaaaaatctg ***** HQ698831.1 GCA_002090215.1 caccaaatcctatcctttttattaaagatagaagcaccaaatcgttcataatctagc caccaaatcctatcctttttattaaagatagaagcaccaaatcgttcataatctagc ***** HQ698831.1 GCA_002090215.1 ttcaagacaaaaactaagccaaaaagtaatggctgaaatcgaactctcttttccacctct ttcaagacaaaaactaagccaaaaagtaatggctgaaatcgaactctcttttccacctct ***** HQ698831.1 GCA_002090215.1 agaaattcaagaaaagattgctgatattctctttgcctttgaaaaactttgcaatgattt agaaattcaagaaaagattgctgatattctctttgcctttgaaaaactttgcaatgattt ***** HQ698831.1 GCA_002090215.1 agtagaaggtattcctgctgaagtcgaaatgcgtaaaaagcaattggattactatcagaa agtagaaggtattcctgctgaagtcgaaatgcgtaaaaagcaattggattactatcagaa ***** HQ698831.1 GCA_002090215.1 cttcttatttaattgagtgaagaacaaaaaactcaattagagcaattatgtaatgctt cttcttatttaattgagtgaagaacaaaaaactca----- *****
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<i>Mycoplasma pneumoniae</i>	RepMP 1	14	X13093.1 cagttcggacgactgctgcaagtagtagttttctcaacctctttcagaaggagttattg GCA_002090215.1 --gttggcagcactgctgcaagtagtagttttctcaacctctttcagaaggagttattg ***** X13093.1 cttaatgaagaaaaaactccctttaaaaacgaaaaagaattccatgacatgggtgaaaaa GCA_002090215.1 cttaatgaagaaaaaactccctttaaaaacgaaaaagaattccatgacatgggtgaaaaa ***** X13093.1 gacccaaaagggcactttttcagggtgatacatcgttaatccagagaacaacagtggtgga GCA_002090215.1 gacccaaaagggcactttttcagggtgatacatcgttaatccagagaacaacagtggtgga ***** X13093.1 attctctggcaatttcaatagacaattttaaacttaacaaannnnntataccagtgaaacac GCA_002090215.1 attctctggcaatttcaatagacaattttaaacttaacaaacgggttataccagtgaaacac ***** X13093.1 ggaatacgtaacgcgtaagagttcaacgagtacaagactcaaacgaccaacgactcat GCA_002090215.1 ggaatacgtaacgcgtaagagttcaacgagtacaagactcaaacgaccaacgactcat ***** X13093.1 aaagattgaaccacttttgctgcccaagggtgaacaataagaatccagggtgagcaaat GCA_002090215.1 aaagattgaaa----- *****	GCA_002090215.1_182_copy:8(3-8) 10(2) 11(8) * 100.0%[10/10] 10.8
<i>Streptococcus agalactiae</i>	GBSi1	2	AJ292930.1 ggttcagacccaatcgctcctgcgaacagccattgttcagctacttgagtatttaacg GCA_002073795.1 -----gctacttgagtatttaacg ***** AJ292930.1 atggctacgagtgattgtggacattgacttggaaaagttcttcgatactgttccgcaag GCA_002073795.1 atggctacgagtgattgtggacattgacttggaaaagttcttcgatactgttccgcaag ***** AJ292930.1 acagattgatgtccctgggttcataatcattcaagatggcgatacggagtcactgattc GCA_002073795.1 acagattgatgtccctgggttcataatcattcaagatggcgatacggagtcactgattc ***** AJ292930.1 gtaagtacttccattcgggagttgttattaacggacagcgacataagacttttagtcggga GCA_002073795.1 gtaagtacttccattcgggagttgttattaacggacagcgacataagacttttagtcggga ***** AJ292930.1 cacctcaaggcgggaatctatcacccctcctatctaattattatgcttaagagtttagaca GCA_002073795.1 cacctcaaggcgggaatctatcacccctcctatctaattattatgcttaagagtttagaca ***** AJ292930.1 aagggttgaaaaagcgaggtcttcgctttgtcgttacgccgatgactgtgtcatcactg GCA_002073795.1 aagggttgaaaaagcgaggtcttcgctttgtcgttacgccgatgactgtgtcatcactg ***** AJ292930.1 tcggaagcgaagcagctgctaagcgggtcatgcattcggtcagtagctatattgagaagc GCA_002073795.1 tcggaagcgaagcagctgctaagcgggtcatgcattcggtcagtagctatattgagaagc ***** AJ292930.1 gattagggttgaaagtcacatgactaagaccaagattgtcagaccgaacaaactcaaat GCA_002073795.1 gattagggttgaaagtcacatgactaagac----- *****	GCA_002073795.1_71_copy:3(3-3) 0(5) 3(1) 20(1) 28.6%[2/7] 3.28571428571429

1.4-3.7

[illegible]

FR666836.1_ copy:2

FR666836.1 copy:2(2-2)

Table 3. The performance of our strategy on reducing false positive rate for sample sets of identified newly discovered species or subspecies specific multi-copy regions.

Target Organisms	Distribution of Copy Numbers of De Novo Biomarkers	Sequences of identified newly discovered species or subspecies specific multi-copy regions.
<i>Mycobacterium tuberculosis</i>	Outlier0 Distribution Outlier1 Outlier2 Outlier3 Outlier4 Outlier5 Outlier6 Outlier7 Outlier8 Outlier9 Outlier10 Outlier11 Outlier12 Outlier13 Outlier14 Outlier15 Outlier16 Outlier17 Outlier18 Outlier19 Outlier20 Outlier21 Outlier22 Outlier23 Outlier24 Outlier25 Outlier26 Outlier27 Outlier28 Outlier29 Outlier30 Outlier31 Outlier32 Outlier33 Outlier34 Outlier35 Outlier36 Outlier37 Outlier38 Outlier39 Outlier40 Outlier41 Outlier42 Outlier43 Outlier44 Outlier45 Outlier46 Outlier47 Outlier48 Outlier49 Outlier50 Outlier51 Outlier52 Outlier53 Outlier54 Outlier55 Outlier56 Outlier57 Outlier58 Outlier59 Outlier60 Outlier61 Outlier62 Outlier63 Outlier64 Outlier65 Outlier66 Outlier67 Outlier68 Outlier69 Outlier70 Outlier71 Outlier72 Outlier73 Outlier74 Outlier75 Outlier76 Outlier77 Outlier78 Outlier79 Outlier80 Outlier81 Outlier82 Outlier83 Outlier84 Outlier85 Outlier86 Outlier87 Outlier88 Outlier89 Outlier90 Outlier91 Outlier92 Outlier93 Outlier94 Outlier95 Outlier96 Outlier97 Outlier98 Outlier99 Outlier100 Outlier101 Outlier102 Outlier103 Outlier104 Outlier105 Outlier106 Outlier107 Outlier108 Outlier109 Outlier110 Outlier111 Outlier112 Outlier113 Outlier114 Outlier115 Outlier116 Outlier117 Outlier118 Outlier119 Outlier120 Outlier121 Outlier122 Outlier123 Outlier124 Outlier125 Outlier126 Outlier127 Outlier128 Outlier129 Outlier130 Outlier131 Outlier132 Outlier133 Outlier134 Outlier135 Outlier136 Outlier137 Outlier138 Outlier139 Outlier140 Outlier141 Outlier142 Outlier143 Outlier144 Outlier145 Outlier146 Outlier147 Outlier148 Outlier149 Outlier150 Outlier151 Outlier152 Outlier153 Outlier154 Outlier155 Outlier156 Outlier157 Outlier158 Outlier159 Outlier160 Outlier161 Outlier162 Outlier163 Outlier164 Outlier165 Outlier166 Outlier167 Outlier168 Outlier169 Outlier170 Outlier171 Outlier172 Outlier173 Outlier174 Outlier175 Outlier176 Outlier177 Outlier178 Outlier179 Outlier180 Outlier181 Outlier182 Outlier183 Outlier184 Outlier185 Outlier186 Outlier187 Outlier188 Outlier189 Outlier190 Outlier191 Outlier192 Outlier193 Outlier194 Outlier195 Outlier196 Outlier197 Outlier198 Outlier199 Outlier200 Outlier201 Outlier202 Outlier203 Outlier204 Outlier205 Outlier206 Outlier207 Outlier208 Outlier209 Outlier210 Outlier211 Outlier212 Outlier213 Outlier214 Outlier215 Outlier216 Outlier217 Outlier218 Outlier219 Outlier220 Outlier221 Outlier222 Outlier223 Outlier224 Outlier225 Outlier226 Outlier227 Outlier228 Outlier229 Outlier230 Outlier231 Outlier232 Outlier233 Outlier234 Outlier235 Outlier236 Outlier237 Outlier238 Outlier239 Outlier240 Outlier241 Outlier242 Outlier243 Outlier244 Outlier245 Outlier246 Outlier247 Outlier248 Outlier249 Outlier250 Outlier251 Outlier252 Outlier253 Outlier254 Outlier255 Outlier256 Outlier257 Outlier258 Outlier259 Outlier260 Outlier261 Outlier262 Outlier263 Outlier264 Outlier265 Outlier266 Outlier267 Outlier268 Outlier269 Outlier270 Outlier271 Outlier272 Outlier273 Outlier274 Outlier275 Outlier276 Outlier277 Outlier278 Outlier279 Outlier280 Outlier281 Outlier282 Outlier283 Outlier284 Outlier285 Outlier286 Outlier287 Outlier288 Outlier289 Outlier290 Outlier291 Outlier292 Outlier293 Outlier294 Outlier295 Outlier296 Outlier297 Outlier298 Outlier299 Outlier300 Outlier301 Outlier302 Outlier303 Outlier304 Outlier305 Outlier306 Outlier307 Outlier308 Outlier309 Outlier310 Outlier311 Outlier312 Outlier313 Outlier314 Outlier315 Outlier316 Outlier317 Outlier318 Outlier319 Outlier320 Outlier321 Outlier322 Outlier323 Outlier324 Outlier325 Outlier326 Outlier327 Outlier328 Outlier329 Outlier330 Outlier331 Outlier332 Outlier333 Outlier334 Outlier335 Outlier336 Outlier337 Outlier338 Outlier339 Outlier340 Outlier341 Outlier342 Outlier343 Outlier344 Outlier345 Outlier346 Outlier347 Outlier348 Outlier349 Outlier350 Outlier351 Outlier352 Outlier353 Outlier354 Outlier355 Outlier356 Outlier357 Outlier358 Outlier359 Outlier360 Outlier361 Outlier362 Outlier363 Outlier364 Outlier365 Outlier366 Outlier367 Outlier368 Outlier369 Outlier370 Outlier371 Outlier372 Outlier373 Outlier374 Outlier375 Outlier376 Outlier377 Outlier378 Outlier379 Outlier380 Outlier381 Outlier382 Outlier383 Outlier384 Outlier385 Outlier386 Outlier387 Outlier388 Outlier389 Outlier390 Outlier391 Outlier392 Outlier393 Outlier394 Outlier395 Outlier396 Outlier397 Outlier398 Outlier399 Outlier400 Outlier401 Outlier402 Outlier403 Outlier404 Outlier405 Outlier406 Outlier407 Outlier408 Outlier409 Outlier410 Outlier411 Outlier412 Outlier413 Outlier414 Outlier415 Outlier416 Outlier417 Outlier418 Outlier419 Outlier420 Outlier421 Outlier422 Outlier423 Outlier424 Outlier425 Outlier426 Outlier427 Outlier428 Outlier429 Outlier430 Outlier431 Outlier432 Outlier433 Outlier434 Outlier435 Outlier436 Outlier437 Outlier438 Outlier439 Outlier440 Outlier441 Outlier442 Outlier443 Outlier444	

ClusterID	Distribution	Marker	Percent of strains	Weighted Average Copy
Cluster22	11(10)	*	100.0%[10/10]	11
Cluster164	11(10)	*	100.0%[10/10]	11
Cluster141	11(10)	*	100.0%[10/10]	11
Cluster9	10(2) 11(8)	*	100.0%[10/10]	10.8
Cluster472	10(2) 11(8)	*	100.0%[10/10]	10.8
Cluster468	10(2) 11(8)	*	100.0%[10/10]	10.8
Cluster188	10(2) 11(8)	*	100.0%[10/10]	10.8
Cluster187	10(2) 11(8)	*	100.0%[10/10]	10.8
Cluster182	10(2) 11(8)	*	100.0%[10/10]	10.8
Cluster0	10(2) 11(8)	*	100.0%[10/10]	10.8
Cluster66	10(10)	*	100.0%[10/10]	10
Cluster16	10(10)	*	100.0%[10/10]	10
Cluster92	9(2) 10(8)	*	100.0%[10/10]	9.8
Cluster512	9(2) 10(8)	*	100.0%[10/10]	9.8
Cluster43	8(1) 10(9)	*	100.0%[10/10]	9.8
Cluster446	8(2) 10(8)	*	100.0%[10/10]	9.6
Cluster421	9(10)	*	100.0%[10/10]	9
Cluster34	9(10)	*	100.0%[10/10]	9
Cluster6	8(10)	*	100.0%[10/10]	8
Cluster51	8(10)	*	100.0%[10/10]	8
Cluster457	8(10)	*	100.0%[10/10]	8
Cluster413	8(10)	*	100.0%[10/10]	8
Cluster35	8(10)	*	100.0%[10/10]	8
Cluster299	8(10)	*	100.0%[10/10]	8
Cluster198	8(10)	*	100.0%[10/10]	8
Cluster19	8(10)	*	100.0%[10/10]	8
Cluster18	8(10)	*	100.0%[10/10]	8
Cluster13	8(10)	*	100.0%[10/10]	8
Cluster241	7(1) 8(9)	*	100.0%[10/10]	7.9
Cluster156	7(1) 8(9)	*	100.0%[10/10]	7.9
Cluster420	7(2) 8(8)	*	100.0%[10/10]	7.8
Cluster189	7(2) 8(8)	*	100.0%[10/10]	7.8
Cluster149	7(2) 8(8)	*	100.0%[10/10]	7.8
Cluster134	7(2) 8(8)	*	100.0%[10/10]	7.8
Cluster21	6(1) 7(1) 8(8)	*	100.0%[10/10]	7.7
Cluster27	7(8) 8(2)	*	100.0%[10/10]	7.2
Cluster82	7(10)	*	100.0%[10/10]	7
Cluster67	7(10)	*	100.0%[10/10]	7
Cluster54	7(10)	*	100.0%[10/10]	7
Cluster532	7(10)	*	100.0%[10/10]	7
Cluster509	7(10)	*	100.0%[10/10]	7
Cluster388	7(10)	*	100.0%[10/10]	7
Cluster257	7(10)	*	100.0%[10/10]	7
Cluster247	7(10)	*	100.0%[10/10]	7
Cluster239	7(10)	*	100.0%[10/10]	7
Cluster232	7(10)	*	100.0%[10/10]	7
Cluster230	7(10)	*	100.0%[10/10]	7
Cluster204	7(10)	*	100.0%[10/10]	7
Cluster173	7(10)	*	100.0%[10/10]	7
Cluster125	7(10)	*	100.0%[10/10]	7
Cluster102	7(10)	*	100.0%[10/10]	7
Cluster366	6(1) 7(9)	*	100.0%[10/10]	6.9

[illegible]

Streptococcus agalactiae

ClusterID	Distribution	Marker	Percent_of_strains	Weighted_Average_Copy
Cluster99	0(1)(1(2)(3(2)(4(1)(7(1))	*	85.7%(6/7)	2.714285714
Cluster89	0(1)(1(2)(3(2)(4(1)(7(1))	*	85.7%(6/7)	2.714285714
Cluster87	0(1)(1(2)(3(2)(4(1)(7(1))	*	85.7%(6/7)	2.714285714
Cluster86	0(1)(1(2)(3(2)(4(1)(7(1))	*	85.7%(6/7)	2.714285714
Cluster81	0(1)(1(2)(3(2)(4(1)(7(1))	*	85.7%(6/7)	2.714285714
Cluster80	0(1)(1(2)(3(2)(4(1)(7(1))	*	85.7%(6/7)	2.714285714
Cluster74	0(1)(1(2)(3(2)(4(1)(7(1))	*	85.7%(6/7)	2.714285714
Cluster7	0(1)(1(2)(3(2)(4(1)(7(1))	*	85.7%(6/7)	2.714285714
Cluster68	0(1)(1(2)(3(2)(4(1)(7(1))	*	85.7%(6/7)	2.714285714
Cluster19	0(1)(1(2)(3(2)(4(1)(7(1))	*	85.7%(6/7)	2.714285714
Cluster67	0(1)(1(2)(3(3)(4(1))	*	85.7%(6/7)	2.142857143
Cluster53	0(1)(1(2)(3(3)(4(1))	*	85.7%(6/7)	2.142857143
Cluster91	2(7)	*	100.0%(7/7)	2
Cluster77	2(7)	*	100.0%(7/7)	2
Cluster75	2(7)	*	100.0%(7/7)	2
Cluster63	2(7)	*	100.0%(7/7)	2
Cluster56	2(7)	*	100.0%(7/7)	2
Cluster51	2(7)	*	100.0%(7/7)	2
Cluster30	2(7)	*	100.0%(7/7)	2
Cluster27	2(7)	*	100.0%(7/7)	2
Cluster25	2(7)	*	100.0%(7/7)	2
Cluster45	0(1)(1(1)(2(4)(3(1))	*	85.7%(6/7)	1.714285714
Cluster32	0(1)(1(1)(2(4)(3(1))	*	85.7%(6/7)	1.714285714
Cluster64	0(1)(1(2)(2(4))	*	85.7%(6/7)	1.428571429
Cluster31	0(1)(1(2)(2(4))	*	85.7%(6/7)	1.428571429
Cluster15	1(4)(2(3))	*	100.0%(7/7)	1.428571429
Cluster6	0(1)(1(3)(2(3))	*	85.7%(6/7)	1.285714286
Cluster2	0(1)(1(3)(2(3))	*	85.7%(6/7)	1.285714286
Cluster26	0(1)(1(5)(2(1))	*	85.7%(6/7)	1
Cluster98	0(5)(6(1)(8(1))	*	28.6%(2/7)	2
Cluster97	0(6)(2(1))	*	14.3%(1/7)	0.285714286
Cluster96	0(6)(26(1))	*	14.3%(1/7)	3.714285714
Cluster95	0(6)(26(1))	*	14.3%(1/7)	3.714285714
Cluster94	0(6)(26(1))	*	14.3%(1/7)	3.714285714
Cluster93	0(6)(2(1))	*	14.3%(1/7)	0.285714286
Cluster92	0(4)(2(1)(8(1)(10(1))	*	42.0%(3/7)	2.857142857
Cluster9	0(5)(8(1)(10(1))	*	28.6%(2/7)	2.571428571
Cluster90	0(6)(2(1))	*	14.3%(1/7)	0.285714286
Cluster88	0(6)(2(1))	*	14.3%(1/7)	0.285714286
Cluster85	0(6)(2(1))	*	14.3%(1/7)	0.285714286
Cluster84	0(6)(2(1))	*	14.3%(1/7)	0.285714286
Cluster83	0(6)(2(1))	*	14.3%(1/7)	0.285714286
Cluster82	0(6)(2(1))	*	14.3%(1/7)	0.285714286
Cluster8	0(2)(1(1)(2(1)(5(1)(10(1)(11(1))	*	71.4%(5/7)	4.142857143
Cluster79	0(5)(4(1)(16(1))	*	28.6%(2/7)	2.857142857
Cluster78	0(6)(9(1))	*	14.3%(1/7)	1.285714286
Cluster76	0(5)(1(1)(2(1))	*	28.6%(2/7)	0.428571429
Cluster73	0(6)(26(1))	*	14.3%(1/7)	3.714285714
Cluster72	0(5)(3(1)(16(1))	*	28.6%(2/7)	2.714285714
Cluster71	0(5)(3(1)(20(1))	*	28.6%(2/7)	3.285714286
Cluster70	0(6)(16(1))	*	14.3%(1/7)	2.285714286
Cluster69	0(6)(3(1))	*	14.3%(1/7)	0.428571429

[illegible]

Helicobacter pylori

ClusterID	Distribution	Marker	Percent of strains	Weighted Average Copy
Cluster8	1(3) 2(8) 3(6) 4(3) 5(1)	*	100.0%[21/21]	2.571428571
Cluster107	1(6) 2(9) 3(6)	*	100.0%[21/21]	2
Cluster66	1(5) 2(15) 3(1)	*	100.0%[21/21]	1.80952381
Cluster24	1(6) 2(13) 3(2)	*	100.0%[21/21]	1.80952381
Cluster42	0(3) 1(2) 2(13) 3(3)	*	85.7%[18/21]	1.761904762
Cluster299	0(2) 1(4) 2(12) 3(3)	*	90.5%[19/21]	1.761904762
Cluster133	0(4) 3(3) 2(11) 3(3)	*	81.0%[17/21]	1.619047619
Cluster55	1(13) 2(5) 3(3)	*	100.0%[21/21]	1.523809524
Cluster40	0(4) 1(5) 2(9) 3(3)	*	81.0%[17/21]	1.523809524
Cluster262	1(10) 2(11)	*	100.0%[21/21]	1.523809524
Cluster236	0(4) 1(7) 2(6) 3(4)	*	81.0%[17/21]	1.476190476
Cluster109	0(4) 1(5) 2(11) 3(1)	*	81.0%[17/21]	1.428571429
Cluster333	0(1) 1(13) 2(7)	*	95.2%[20/21]	1.285714286
Cluster3	0(3) 1(11) 2(5) 3(2)	*	85.7%[18/21]	1.285714286
Cluster211	0(4) 1(10) 2(4) 3(3)	*	81.0%[17/21]	1.285714286
Cluster158	0(3) 1(12) 2(3) 3(3)	*	85.7%[18/21]	1.285714286
Cluster354	0(1) 1(14) 2(6)	*	95.2%[20/21]	1.238095238
Cluster25	0(4) 1(9) 2(7) 3(1)	*	81.0%[17/21]	1.238095238
Cluster214	1(17) 2(4)	*	100.0%[21/21]	1.19047619
Cluster2	0(4) 1(10) 2(6) 3(1)	*	81.0%[17/21]	1.19047619
Cluster20	0(4) 1(10) 2(6) 3(1)	*	81.0%[17/21]	1.19047619
Cluster150	0(3) 1(11) 2(7)	*	85.7%[18/21]	1.19047619
Cluster41	0(1) 1(16) 2(4)	*	95.2%[20/21]	1.142857143
Cluster355	0(4) 1(11) 2(5) 3(1)	*	81.0%[17/21]	1.142857143
Cluster32	0(3) 1(13) 2(4) 3(1)	*	85.7%[18/21]	1.142857143
Cluster250	1(18) 2(3)	*	100.0%[21/21]	1.142857143
Cluster227	1(18) 2(3)	*	100.0%[21/21]	1.142857143
Cluster201	1(19) 2(1) 3(1)	*	100.0%[21/21]	1.142857143
Cluster141	0(3) 1(12) 2(6)	*	85.7%[18/21]	1.142857143
Cluster62	1(19) 2(2)	*	100.0%[21/21]	1.095238095
Cluster53	0(4) 1(12) 2(4) 3(1)	*	81.0%[17/21]	1.095238095
Cluster373	0(3) 1(13) 2(5)	*	85.7%[18/21]	1.095238095
Cluster350	0(4) 1(12) 2(4) 3(1)	*	91.0%[17/21]	1.095238095
Cluster287	0(4) 1(13) 2(5)	*	85.7%[18/21]	1.095238095
Cluster216	1(19) 2(2)	*	100.0%[21/21]	1.095238095
Cluster205	0(4) 1(12) 2(4) 3(1)	*	81.0%[17/21]	1.095238095
Cluster200	0(4) 1(12) 2(4) 3(1)	*	81.0%[17/21]	1.095238095
Cluster19	0(4) 1(12) 2(4) 3(1)	*	81.0%[17/21]	1.095238095
Cluster155	1(19) 2(2)	*	100.0%[21/21]	1.095238095
Cluster135	0(1) 1(17) 2(3)	*	95.2%[20/21]	1.095238095
Cluster134	0(3) 1(13) 2(5)	*	85.7%[18/21]	1.095238095
Cluster117	0(1) 1(18) 2(1) 3(1)	*	95.2%[20/21]	1.095238095
Cluster95	1(20) 2(1)	*	100.0%[21/21]	1.047619048
Cluster85	1(20) 2(1)	*	100.0%[21/21]	1.047619048
Cluster84	1(20) 2(1)	*	100.0%[21/21]	1.047619048
Cluster83	1(20) 2(1)	*	100.0%[21/21]	1.047619048
Cluster81	1(20) 2(1)	*	100.0%[21/21]	1.047619048
Cluster77	1(20) 2(1)	*	100.0%[21/21]	1.047619048
Cluster72	1(20) 2(1)	*	100.0%[21/21]	1.047619048
Cluster68	0(4) 1(12) 2(5)	*	81.0%[17/21]	1.047619048
Cluster6	1(20) 2(1)	*	100.0%[21/21]	1.047619048
Cluster5	1(20) 2(1)	*	100.0%[21/21]	1.047619048

[illegible]

ClusterID	Distribution	Marker	Percent of strains	Weighted Average Copy
Cluster66	7(1)(12)(1)(23)(1)(28)(1)(30)(4)(31)(1)	*	100.0%/9/9	24.55555556
Cluster67	5(1)(12)(1)(21)(1)(27)(1)(28)(2)(29)(30)(1)	*	100.0%/9/9	23.22222222
Cluster491	4(1)(11)(20)(1)(26)(1)(27)(2)(29)(30)(1)	*	100.0%/9/9	22.55555556
Cluster65	6(1)(9)(1)(19)(1)(26)(2)(28)(4)	*	100.0%/9/9	22
Cluster351	5(1)(10)(1)(18)(1)(23)(2)(24)(1)(27)(2)(29)(1)	*	100.0%/9/9	20.66666667
Cluster180	0(1)(1)(2)(1)(13)(1)(15)(1)(19)(1)(20)(1)(21)(2)(22)(1)	*	88.9%/8/9	14.77777778
Cluster280	4(2)(6)(1)(8)(1)(9)(2)(11)(1)(12)(2)	*	100.0%/9/9	8.33333333
Cluster111	3(1)(4)(1)(8)(1)(7)(3)(9)(3)	*	100.0%/9/9	6.77777778
Cluster253	3(1)(4)(2)(5)(5)	*	100.0%/9/9	4.33333333
Cluster208	1(1)(2)(1)(3)(1)(4)(2)(5)(4)	*	100.0%/9/9	3.77777778
Cluster185	1(1)(2)(3)(1)(3)(1)(4)(3)(5)(2)(8)(1)	*	100.0%/9/9	3.33333333
Cluster250	1(2)(3)(4)(4)(2)(6)(1)	*	100.0%/9/9	3.11111111
Cluster364	0(1)(2)(2)(3)(3)(4)(3)(5)(2)	*	88.9%/8/9	3
Cluster100	1(3)(3)(5)(4)(1)	*	100.0%/9/9	2.44444444
Cluster186	1(2)(2)(3)(5)	*	100.0%/9/9	2.33333333
Cluster678	1(4)(3)(4)(4)(1)	*	100.0%/9/9	2.22222222
Cluster31	1(3)(2)(1)(3)(5)	*	100.0%/9/9	2.22222222
Cluster137	1(1)(2)(5)(3)(3)	*	100.0%/9/9	2.22222222
Cluster120	2(7)(3)(2)	*	100.0%/9/9	2.22222222
Cluster60	1(2)(2)(4)(3)(3)	*	100.0%/9/9	2.11111111
Cluster54	1(1)(2)(4)(3)(3)	*	100.0%/9/9	2
Cluster631	1(5)(3)(3)(4)(1)	*	100.0%/9/9	2
Cluster533	2(9)	*	100.0%/9/9	1.88888889
Cluster71	0(1)(1)(5)(4)(3)	*	88.9%/8/9	1.88888889
Cluster205	0(1)(1)(2)(2)(3)(3)(3)	*	88.9%/8/9	1.88888889
Cluster197	1(5)(3)(4)	*	100.0%/9/9	1.88888889
Cluster73	1(3)(2)(5)(3)(1)	*	100.0%/9/9	1.77777778
Cluster581	1(5)(2)(1)(3)(3)	*	100.0%/9/9	1.77777778
Cluster565	1(2)(2)(7)	*	100.0%/9/9	1.77777778
Cluster455	1(5)(2)(1)(3)(3)	*	100.0%/9/9	1.77777778
Cluster409	1(2)(2)(7)	*	100.0%/9/9	1.77777778
Cluster90	1(6)(3)(3)	*	100.0%/9/9	1.66666667
Cluster88	1(6)(3)(3)	*	100.0%/9/9	1.66666667
Cluster649	1(6)(3)(3)	*	100.0%/9/9	1.66666667
Cluster429	1(3)(2)(6)	*	100.0%/9/9	1.66666667
Cluster344	1(3)(2)(6)	*	100.0%/9/9	1.66666667
Cluster248	1(3)(2)(6)	*	100.0%/9/9	1.66666667
Cluster148	1(3)(2)(6)	*	100.0%/9/9	1.66666667
Cluster743	1(5)(2)(3)(3)(1)	*	100.0%/9/9	1.55555556
Cluster738	1(4)(2)(5)	*	100.0%/9/9	1.55555556
Cluster70	0(1)(1)(5)(3)(3)	*	88.9%/8/9	1.55555556
Cluster68	0(1)(1)(5)(3)(3)	*	88.9%/8/9	1.55555556
Cluster624	0(1)(1)(2)(2)(6)	*	88.9%/8/9	1.55555556
Cluster591	1(4)(2)(5)	*	100.0%/9/9	1.55555556
Cluster56	1(4)(2)(5)	*	100.0%/9/9	1.55555556
Cluster532	1(4)(2)(5)	*	100.0%/9/9	1.55555556
Cluster331	1(4)(2)(5)	*	100.0%/9/9	1.55555556
Cluster693	1(5)(2)(4)	*	100.0%/9/9	1.44444444
Cluster437	1(5)(2)(4)	*	100.0%/9/9	1.44444444
Cluster397	1(5)(2)(4)	*	100.0%/9/9	1.44444444
Cluster165	1(5)(2)(4)	*	100.0%/9/9	1.44444444

	ClusterID	Distribution	Marker	Percent of strains	Weighted Average Copy
	Cluster538	6(1)(7)(2)(10)(1)(13)(1)	*	100.0%(5)/5	8.6
	Cluster151	6(2)(7)(3)(8)(12)(4)	*	100.0%(5)/5	7.8
	Cluster206	2(1)(7)(2)(9)(12)(1)	*	100.0%(5)/5	7.4
	Cluster843	1(1)(2)(3)(1)(10)(1)(20)(1)	*	100.0%(5)/5	7.2
	Cluster236	0(1)(2)(1)(4)(1)(10)(1)(2)(1)	*	80.0%(4)/5	7.2
	Cluster298	4(1)(5)(3)(6)(9)(1)(11)(1)	*	100.0%(5)/5	7
	Cluster16	5(1)(6)(2)(7)(1)(11)(1)	*	100.0%(5)/5	7
	Cluster896	1(2)(4)(3)(1)(20)(1)	*	100.0%(5)/5	6.8
	Cluster706	1(2)(4)(3)(1)(20)(1)	*	100.0%(5)/5	6.8
	Cluster39	1(2)(4)(3)(1)(20)(1)	*	100.0%(5)/5	6.8
	Cluster959	1(2)(3)(8)(10)(2)(1)	*	100.0%(5)/5	6.6
	Cluster544	1(2)(2)(1)(9)(1)(19)(1)	*	100.0%(5)/5	6.4
	Cluster960	1(2)(2)(3)(1)(19)(1)	*	100.0%(5)/5	6.2
	Cluster895	1(2)(2)(3)(1)(19)(1)	*	100.0%(5)/5	6.2
	Cluster86	1(2)(2)(3)(8)(19)(1)	*	100.0%(5)/5	6.2
	Cluster802	1(2)(2)(3)(8)(19)(1)	*	100.0%(5)/5	6.2
	Cluster731	1(2)(2)(3)(8)(19)(1)	*	100.0%(5)/5	6.2
	Cluster36	1(2)(2)(3)(8)(19)(1)	*	100.0%(5)/5	6.2
	Cluster11	1(2)(2)(3)(8)(19)(1)	*	100.0%(5)/5	6.2
	Cluster649	1(2)(2)(1)(7)(1)(19)(1)	*	100.0%(5)/5	6
	Cluster569	1(2)(2)(1)(7)(1)(19)(1)	*	100.0%(5)/5	6
	Cluster349	1(3)(8)(1)(19)(1)	*	100.0%(5)/5	6
	Cluster962	0(1)(1)(2)(8)(1)(19)(1)	*	80.0%(4)/5	5.8
	Cluster065	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster893	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster735	1(2)(2)(3)(8)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster72	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster71	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster65	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster554	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster550	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster545	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster352	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster234	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster226	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster223	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster219	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster215	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster214	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster213	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.8
	Cluster91	0(1)(1)(2)(7)(1)(19)(1)	*	80.0%(4)/5	5.6
	Cluster902	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.6
	Cluster82	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.6
	Cluster803	0(1)(1)(2)(8)(1)(18)(1)	*	80.0%(4)/5	5.6
	Cluster738	1(3)(6)(1)(19)(1)	*	100.0%(5)/5	5.6
	Cluster454	1(2)(2)(1)(8)(1)(18)(1)	*	100.0%(5)/5	5.6
	Cluster377	0(1)(1)(2)(7)(1)(19)(1)	*	80.0%(4)/5	5.6
	Cluster360	0(1)(1)(2)(7)(1)(19)(1)	*	80.0%(4)/5	5.6
	Cluster356	1(3)(6)(1)(19)(1)	*	100.0%(5)/5	5.6
	Cluster354	1(2)(2)(1)(8)(1)(18)(1)	*	100.0%(5)/5	5.6
	Cluster350	1(3)(7)(1)(19)(1)	*	100.0%(5)/5	5.6
	Cluster211	0(1)(1)(2)(7)(1)(19)(1)	*	80.0%(4)/5	5.6

Candida auris

