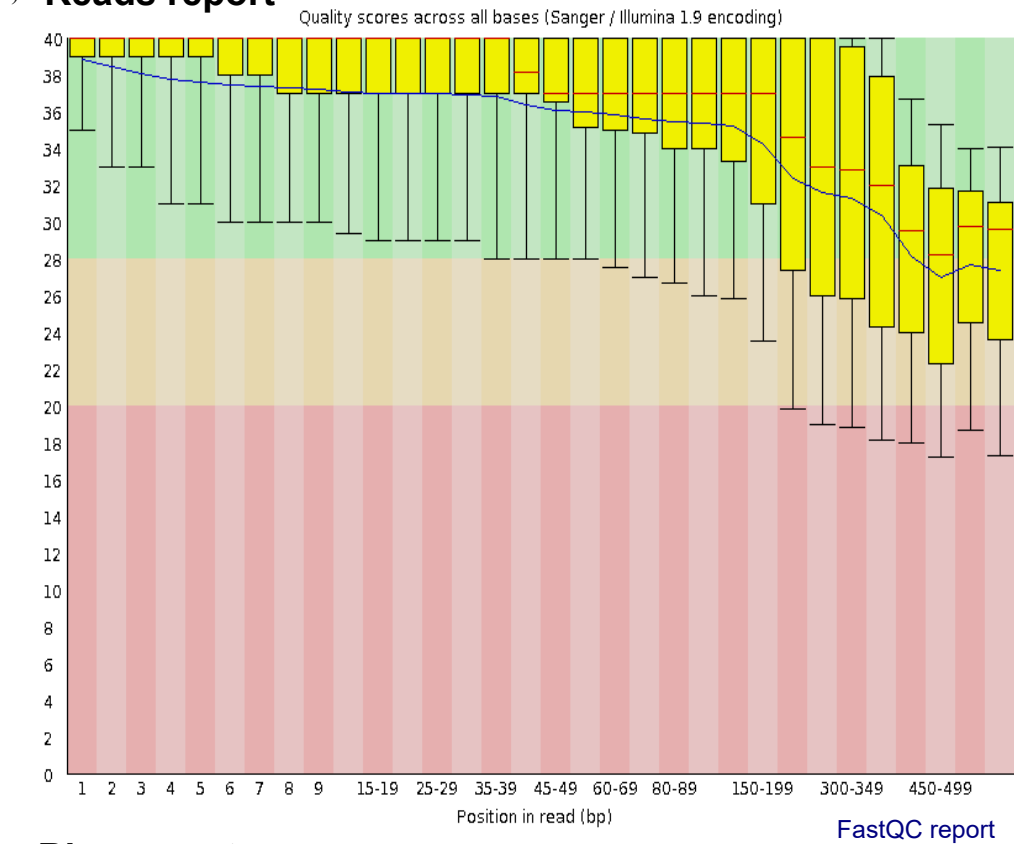


Supplementary figures

a) Reads report



b) Bins report

Bin	Size(reads)	bp	Contigs	Genome	ORFS	bp	Link
all 16S	9957	3576767	NA	NA	NA	NA	NA
Bin0	266869	81569006	131	3243019	3124	943731	fullLink
Bin1	335701	135467115	151	4198482	3985	1259949	fullLink
Bin2	1271	531435	2	4217	7	1240	fullLink
Bin3	1252	496908	1	14521	15	4380	fullLink

c) Assembly report

Bin Id	Marker lineage	UID	genomes	markers	marker sets	0	1	2	3	4	5+	Complete ness	Contami nation	Strain heteroge neity
Bin1	Mycobacterium	UID1816	100	690	300	15	674	1	0	0	0	97.54	0.33	0.00
Bin0	Brucella	UID3486	87	1402	225	25	1372	5	0	0	0	97.24	0.28	20.00
Bin4	root	UID1	5656	56	24	56	0	0	0	0	0	0.00	0.00	0.00
Bin3	root	UID1	5656	56	24	56	0	0	0	0	0	0.00	0.00	0.00
Bin2	root	UID1	5656	56	24	56	0	0	0	0	0	0.00	0.00	0.00

Figure S.1: DATMA output. a)Reads Quality, b) CLAME report and c)Assembly metrics for every bin

BLASTn individual report



Figure S.2: DATMA output. Taxonomic annotation for each bin

BLASTn merge report

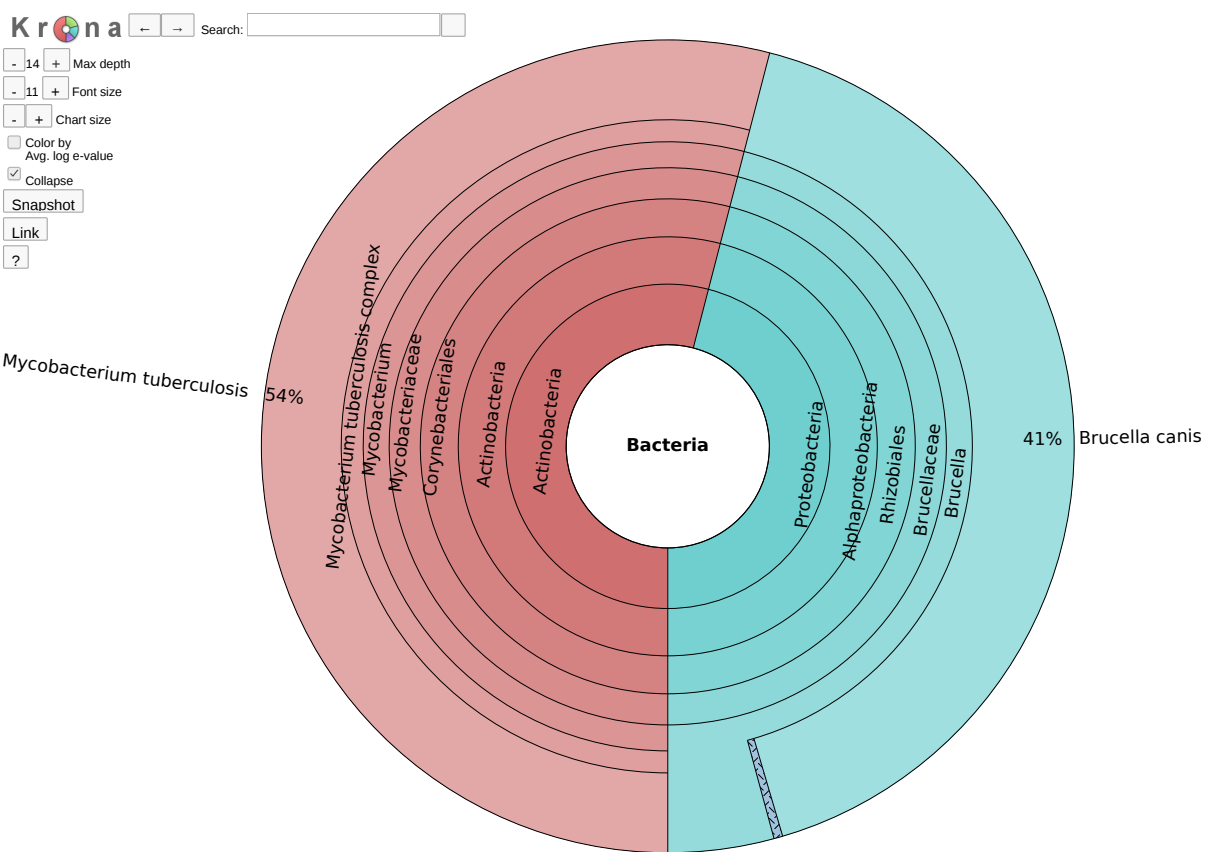


Figure S.3: DATMA output. Taxonomic annotation for all bins

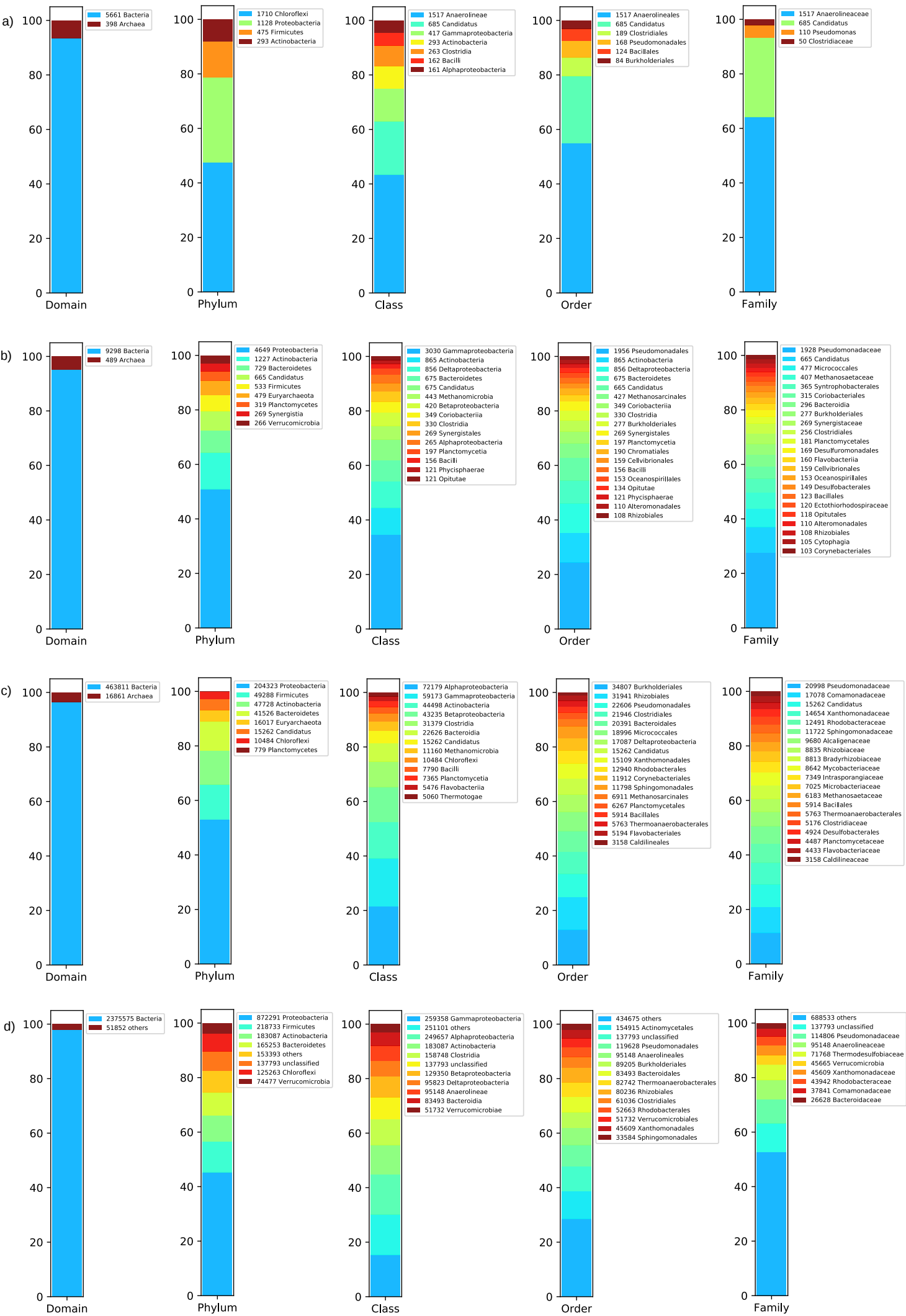


Figure S.4: Taxonomic report for the biosolid metagenome using: a)DATMA, b)MetaWRAP, c)SqueezeMeta, and d)MG-RAST