Supplementary material: Treatment of saline high strength bilgewater using lab scale Moving Bed Biofilm Reactors (MBBRs), tested with two different biocarrier types: microbial adaptation to organic, hydraulic and salinity load shocks.

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Table S1: Relative abundance, illustrated in Figure 4.

System A	R1aS-31d	R1aA-31d	R1bS-31d	R1bA-31d	R1aS-41d	R1aA-41d	R1bS-41d	R1bA-41d
Betaproteobacteria, Thauera (g)	15.7	0.4	12.7	0.0	1.7	3.8	0.8	0.0
Flavobacteriia, Flavobacterium (g)	13.1	3.8	11.9	0.0	7.5	11.2	3.4	0.0
Alphaproteobacteria, Roseovarius (g)	12.9	19.6	10.9	0.0	5.1	10.7	2.7	0.0
Alphaproteobacteria, Celeribacter (g)	4.5	4.0	0.2	0.0	29.6	6.5	37.2	0.0
Alphaproteobacteria, Rhodobacteraceae (f)	3.1	6.8	0.6	0.0	2.8	2.9	0.4	0.0
Alphaproteobacteria, Pseudodonghicola (g)	3.0	3.4	2.1	0.0	2.2	2.2	2.5	0.0
Gammaproteobacteria, Thiogranum (g)	2.7	8.0	0.3	0.0	3.1	3.4	0.2	0.0
Alphaproteobacteria, Stappia (g)	2.6	5.5	2.1	0.0	1.5	2.8	3.5	0.0
Alphaproteobacteria, DB1-14	2.6	1.1	0.6	0.0	0.8	1.1	0.3	0.0
Alphaproteobacteria, T9d (f)	2.3	1.6	1.9	0.0	0.9	3.7	0.2	0.0
Alphaproteobacteria, Hyphomicrobiaceae (f)	2.2	5.2	1.6	0.0	1.2	2.9	0.8	0.0
Sphingobacteriia, Saprospiraceae (f)	2.1	1.9	24.8	0.0	2.7	5.1	17.7	0.0
Alphaproteobacteria, Rhodobacter (g)	1.6	4.3	1.5	0.0	1.7	1.8	0.0	0.0
Alphaproteobacteria, Actibacterium (g)	1.9	3.1	0.6	0.0	1.0	1.7	0.2	0.0
Alphaproteobacteria, Rhizobium (g)	0.8	2.8	0.3	0.0	0.0	0.9	0.0	0.0
Betaproteobacteria, Methyloversatilis (g)	1.9	2.6	0.0	0.0	1.6	2.2	0.0	0.0
Deltaproteobacteria, GR-WP33-58 (f)	1.0	2.6	1.6	0.0	0.8	1.5	4.6	0.0
Alphaproteobacteria, Sphingosinicella (g)	0.9	2.4	0.4	0.0	0.9	0.9	0.0	0.0
Flavobacteriia, Flavobacterium (g)	1.1	0.8	2.6	0.0	1.1	1.8	1.1	0.0
Gammaproteobacteria, Marinobacterium (g)	0.2	0.0	0.0	0.0	3.6	0.0	5.6	0.0
Epsilonproteobacteria, Sulfurospirillum (g)	0.0	0.0	0.0	0.0	5.2	0.7	1.2	0.0
Clostridia, Acetobacterium (g)	0.4	0.0	0.0	0.0	2.4	4.8	0.8	0.0
Betaproteobacteria, Parapusillimonas (g)	0.9	0.4	0.3	0.0	1.3	0.3	2.7	0.0
Other < 2%	22.5	19.6	23.1	100.0	21.4	27.2	14.2	100.0

Table S2: Relative abundance, illustrated in Figure 5

R1a	R1aS.I	R1aA.I	R1aS.II	R1aA.II	R1aS.III	R1aA.III
Bacteroidia, Lentimicrobiaceae (f)	2.3	4.1	4.0	6.0	1.3	1.6
Alphaproteobacteria, Rhodospirillaceae (f)	5.2	2.6	0.3	1.0	0.3	0.2
Deltaproteobacteria, Desulfoplanes (g)	0.0	0.0	0.3	0.2	0.0	0.7
Alphaproteobacteria, Tistrella (g)	1.2	2.4	4.5	6.0	2.6	2.2
Alphaproteobacteria, Tropicibacter (g)	2.5	1.6	3.7	5.9	1.1	2.0
Gammaproteobacteria, Azoarcus (g)	0.5	0.7	6.8	4.0	2.3	2.0
Thermotogae, Oceanotoga (g)	0.1	0.0	0.0	0.0	0.1	0.1
Bacteroidia, Cytophagales (g)	2.5	0.8	7.8	7.3	4.8	5.2
Deinococci, Truepera (g)	1.3	3.7	1.2	1.6	4.7	1.8
Alphaproteobacteria, Rhodobacteraceae (f)	5.5	3.7	2.0	2.3	1.3	1.6
Gammaproteobacteria, Halomonas (g)	0.7	1.1	1.8	0.5	1.1	0.8
Alphaproteobacteria, Hyphomicrobiaceae (f)	3.4	5.7	1.6	1.2	2.1	1.1
Bacteroidia, Membranicola (g)	0.3	0.5	0.2	0.5	0.1	0.2
Clostridia, FamilyXI (f)	1.9	0.3	2.3	1.5	1.4	1.1
Sericytochromatia, Hyaloperonospora arabidopsidis (g)	0.1	0.1	1.0	1.7	0.2	0.3
Bacteroidia, Prolixibacteraceae (f)	1.8	1.7	4.2	3.5	3.8	6.2
Deltaproteobacteria, Desulfovibrio (g)	0.1	0.0	0.1	0.1	0.2	0.7
Alphaproteobacteria, Paracoccus (g)	0.2	0.3	0.1	0.0	0.1	0.1
Gracilibacteria	0.1	0.0	0.1	0.0	6.8	4.7
Bacteroidia, Xanthomarina (g)	0.1	0.1	0.5	0.2	0.4	0.3
Deltaproteobacteria, Nannocystaceae (f)	0.1	0.0	0.0	0.0	0.1	0.0
Bacteroidia, Bacteroides (g)	0.0	0.0	0.0	0.0	0.1	0.1
Negativicutes, Acidaminococcaceae (f)	0.0	0.0	0.0	0.0	0.0	0.1
Other < 5%	70.3	70.4	57.7	56.4	65.2	66.9

R1b	R1bS.I	R1bA.I	R1bS.II	R1bA.II	R1bS.III	R1bA.III
Bacteroidia, Lentimicrobiaceae (f)	2.6	7.1	10.1	10.8	13.7	12.0
Alphaproteobacteria, Rhodospirillaceae (f)	16.0	13.2	0.7	1.0	0.4	1.4

Deltaproteobacteria, Desulfoplanes (g)	0.0	0.0	0.7	0.3	0.1	0.1
Alphaproteobacteria, Tistrella (g)	3.4	3.4	4.7	3.1	2.5	10.8
Alphaproteobacteria, Tropicibacter (g)	2.2	2.5	5.4	3.9	1.6	2.7
Gammaproteobacteria, Azoarcus (g)	0.5	0.6	3.4	7.8	7.1	9.5
Thermotogae, Oceanotoga (g)	0.1	0.0	0.0	0.0	0.1	0.1
Bacteroidia, Cytophagales (g)	1.3	0.5	1.7	0.4	1.1	0.3
Deinococci, Truepera (g)	0.4	0.4	0.5	1.0	0.5	0.2
Alphaproteobacteria, Rhodobacteraceae (f)	2.1	1.1	0.8	1.4	1.3	0.5
Gammaproteobacteria, Halomonas (g)	1.2	1.2	0.7	0.6	0.5	0.2
Alphaproteobacteria, Hyphomicrobiaceae (f)	1.4	1.4	0.4	0.6	0.8	0.5
Bacteroidia, Membranicola (g)	5.9	9.4	0.8	4.2	1.5	1.6
Clostridia, FamilyXI (f)	0.6	0.2	0.6	0.2	0.3	0.1
Sericytochromatia, Hyaloperonospora arabidopsidis (g)	0.1	0.2	1.1	0.9	4.4	6.0
Bacteroidia, Prolixibacteraceae (f)	3.2	2.5	1.7	1.5	2.0	0.6
Deltaproteobacteria, Desulfovibrio (g)	0.1	0.0	0.2	0.1	0.3	0.6
Alphaproteobacteria, Paracoccus (g)	0.1	0.1	0.1	0.4	0.1	0.1
Gracilibacteria	0.1	0.0	0.0	0.0	2.3	1.8
Bacteroidia, Xanthomarina (g)	0.1	0.0	0.2	0.2	0.1	0.0
Deltaproteobacteria, Nannocystaceae (f)	0.1	0.0	0.9	0.3	8.2	4.7
Bacteroidia, Bacteroides (g)	0.0	0.0	0.0	0.0	0.1	0.1
Negativicutes, Acidaminococcaceae (f)	0.0	0.0	0.1	0.0	0.0	0.0
Other < 5%	58.4	56.1	65.2	61.0	51.2	46.2

R2	R2S.I	R2A.I	R2S.II	R2A.II	R2S.III	R2A.III
Bacteroidia, Lentimicrobiaceae (f)	1.9	9.8	2.2	10.5	1.0	3.0
Alphaproteobacteria, Rhodospirillaceae (f)	5.5	4.4	3.9	5.8	0.7	19.6
Deltaproteobacteria, Desulfoplanes (g)	0.0	0.0	0.3	0.3	0.0	0.0
Alphaproteobacteria, Tistrella (g)	0.8	1.5	1.1	2.3	0.5	1.2
Alphaproteobacteria, Tropicibacter (g)	0.5	0.9	1.2	2.4	0.5	1.2
Gammaproteobacteria, Azoarcus (g)	1.4	1.5	0.8	1.9	0.4	0.9

Thermotogae, Oceanotoga (g)	0.1	0.0	0.0	0.1	0.1	0.2
Bacteroidia, Cytophagales (g)	0.3	0.2	2.5	0.9	1.8	0.6
Deinococci, Truepera (g)	0.3	0.4	2.1	1.1	6.8	0.4
Alphaproteobacteria, Rhodobacteraceae (f)	9.7	4.8	1.5	2.5	0.8	2.5
Gammaproteobacteria, Halomonas (g)	2.1	3.1	0.6	2.2	0.5	0.8
Alphaproteobacteria, Hyphomicrobiaceae (f)	2.8	2.6	1.2	2.0	1.8	0.8
Bacteroidia, Membranicola (g)	0.3	0.5	0.1	0.2	0.2	0.3
Clostridia, FamilyXI (f)	0.8	0.1	6.1	1.2	4.5	0.6
Sericytochromatia, Hyaloperonospora arabidopsidis (g)	0.2	0.3	0.2	0.2	0.1	0.4
Bacteroidia, Prolixibacteraceae (f)	1.1	0.9	3.2	3.1	3.2	1.5
Deltaproteobacteria, Desulfovibrio (g)	0.2	0.0	0.2	0.5	0.3	2.8
Alphaproteobacteria, Paracoccus (g)	8.7	7.4	0.6	0.5	0.2	0.3
Gracilibacteria	0.0	0.0	0.0	0.0	0.5	0.5
Bacteroidia, Xanthomarina (g)	0.1	0.0	7.3	2.3	3.7	0.7
Deltaproteobacteria, Nannocystaceae (f)	0.1	0.0	0.1	0.5	0.1	0.4
Bacteroidia, Bacteroides (g)	0.0	0.0	0.0	0.1	0.1	0.9
Negativicutes, Acidaminococcaceae (f)	0.0	0.0	0.1	0.0	0.0	0.0
Other < 5%	63.3	61.4	64.6	59.4	72.3	60.1

IN	IN.I	IN.II	IN.III
Bacteroidia, Lentimicrobiaceae (f)	n.a.	0.3	0.6
Alphaproteobacteria, Rhodospirillaceae (f)	n.a.	0.5	0.5
Deltaproteobacteria, Desulfoplanes (g)	n.a.	56.6	0.4
Alphaproteobacteria, Tistrella (g)	n.a.	0.3	0.3
Alphaproteobacteria, Tropicibacter (g)	n.a.	0.3	0.3
Gammaproteobacteria, Azoarcus (g)	n.a.	0.3	0.3
Thermotogae, Oceanotoga (g)	n.a.	0.0	16.8
Bacteroidia, Cytophagales (g)	n.a.	0.3	0.3
Deinococci, Truepera (g)	n.a.	0.0	0.4
Alphaproteobacteria, Rhodobacteraceae (f)	n.a.	0.0	0.4
Gammaproteobacteria, Halomonas (g)	n.a.	0.0	0.2
Alphaproteobacteria, Hyphomicrobiaceae (f)	n.a.	0.0	0.4
Bacteroidia, Membranicola (g)	n.a.	0.0	0.0
Clostridia, FamilyXI (f)	n.a.	0.2	0.4
Sericytochromatia, Hyaloperonospora arabidopsidis (g)	n.a.	0.0	0.0
Bacteroidia, Prolixibacteraceae (f)	n.a.	0.3	0.5
Deltaproteobacteria, Desulfovibrio (g)	n.a.	13.0	22.4
Alphaproteobacteria, Paracoccus (g)	n.a.	0.0	0.0

Gracilibacteria	n.a.	0.0	0.0
Bacteroidia, Xanthomarina (g)	n.a.	0.0	0.0
Deltaproteobacteria, Nannocystaceae (f)	n.a.	0.0	0.0
Bacteroidia, Bacteroides (g)	n.a.	0.2	7.6
Negativicutes, Acidaminococcaceae (f)	n.a.	6.1	0.0
Other < 5%	n.a.	21.6	48.1

Shannon Index			
	I	**II**	**III**
IN	n.a.	1.688	2.932
R1a S	3.862	3.74	3.850
R1a A	3.760	3.717	3.940
R1b S	3.473	3.598	3.473
R1b A	3.294	3.532	3.334
R2 S	3.480	3.719	3.801
R2 A	3.395	3.719	3.579

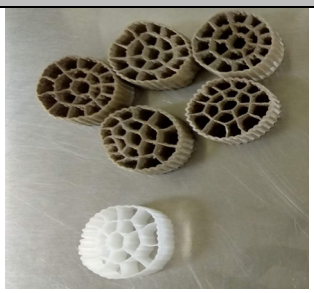
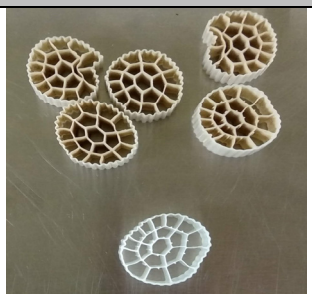
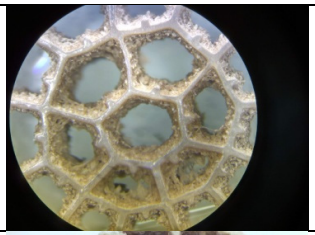
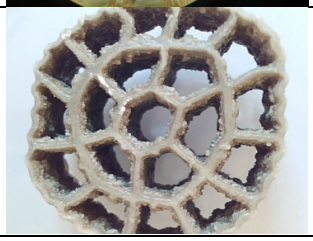
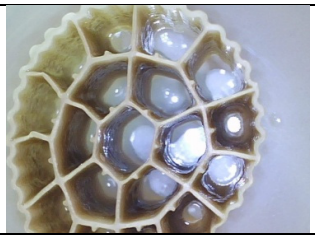
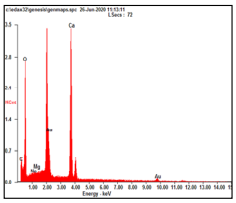
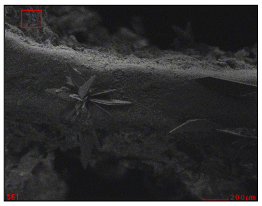
	R1a – K3	**R1b –K3**	**Mutag Biochip**
Period II			
Period II			
Period III			

Figure S1: visual observation of dried biofilm

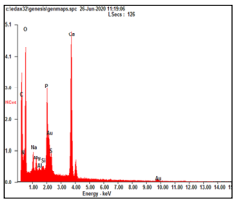
Biocarrier Type	EDX report
R1a	

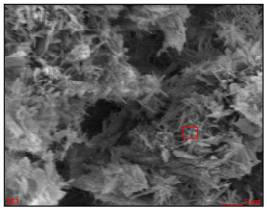
Element	Wt%	At%
CK	10.08	18.59
OK	46.32	64.12
NaK	00.29	00.28
MgK	00.12	00.11
CaK	27.36	15.12
AuL	15.82	01.78



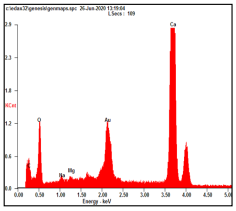


Element	Wt%	At%
CK	27.74	39.13
NK	13.69	16.57
OK	31.62	33.49
NaK	01.58	01.17
MgK	00.71	00.49
AlK	00.15	00.09
SiK	00.24	00.14
PK	04.46	02.44
SK	01.05	00.55
CaK	12.80	05.41
AuL	05.97	00.51

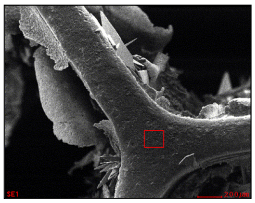




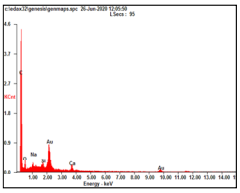
Element	Wt%	At%
CK	09.87	23.40
OK	23.30	41.46
NaK	00.79	00.98
MgK	00.60	00.70
CaK	42.43	30.13
AuL	23.01	03.33

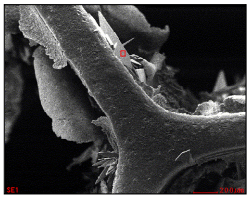


R1b	

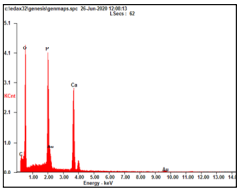


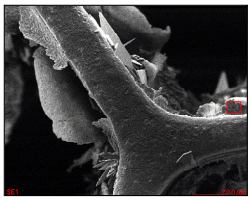
Element	Wt%	At%
CK	71.32	90.57
OK	06.72	06.41
NaK	00.85	00.57
SiK	00.72	00.39
CaK	01.59	00.60
AuL	18.79	01.46



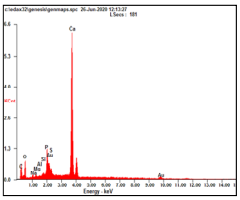


Element	Wt%	At%
CK	13.25	21.89
OK	48.26	59.82
PK	14.46	09.26
CaK	16.78	08.30
AuL	07.26	00.73

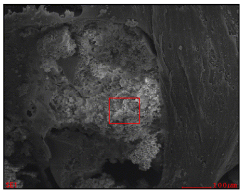




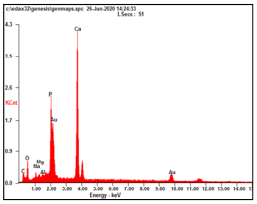
Element	Wt%	At%
CK	13.94	31.28
OK	17.70	29.83
NaK	00.83	00.98
MgK	00.62	00.69
AlK	00.19	00.19
SiK	00.68	00.65
PK	04.98	04.33
SK	01.45	01.22
CaK	42.32	28.46
AuL	17.28	02.37
Matrix	Correction	ZAF

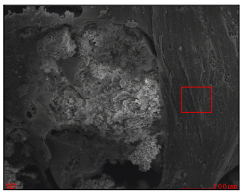


Mutag BioChip



Element	Wt%	At%
CK	07.41	23.62
OK	10.84	25.95
NaK	00.99	01.65
MgK	00.44	00.69
AlK	00.40	00.56
PK	09.16	11.33
CaK	29.47	28.17
AuL	41.31	08.03





Element	Wt%	At%
CK	29.67	79.31
OK	01.82	03.66
AlK	02.00	02.38
CaK	05.03	04.03
TiK	01.19	00.80
AuL	60.29	09.83

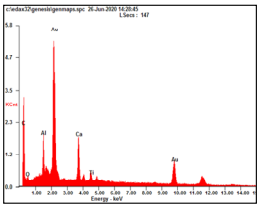


Figure S2: EDX report from biofilm and biocarriers