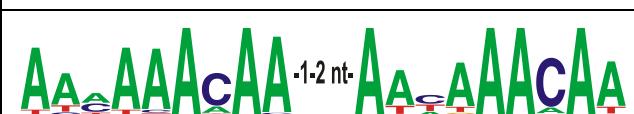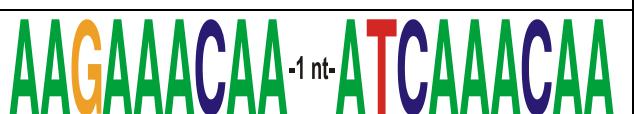Additional file 9. **Comparison of predicted binding site motifs in *Streptococcaceae* and *Lactobacillaceae*.**

TFs	Predicted site motif in *Streptococcaceae*		Predicted site motif in *Lactobacillaceae*		Category [3]	Genomes [4]	Target operons [5]
	Motif sequence Logo [1]	NS [2]	Motif sequence Logo [1]	NS [2]			
AdcR	(sequence logo)	69	(sequence logo)	2	I	16	4.3
AgaR2	(sequence logo)	5	(sequence logo)	6	I	9	1.1
ArgR	(sequence logo)	91	(sequence logo)	21	I	25	4.1
BirA	(sequence logo, -15-16 nt-)	28	(sequence logo, -15-16 nt-)	10	I	22	1.6
BusR	(sequence logo)	3	(sequence logo)	2	I	4	1.3
CcpA	(sequence logo)	814	(sequence logo)	486	I	30	43.5
CcpB	(sequence logo)	5	(sequence logo)	4	II	9	1.0
CcpN	(sequence logo)	7	(sequence logo)	6	II	9	1.3
CelR	(sequence logo)	13	(sequence logo)	1	II	9	1.6

TFs	Predicted site motif in *Streptococcaceae*		Predicted site motif in *Lactobacillaceae*		Category [3]	Genomes [4]	Target operons [5]
	Motif sequence Logo [1]	NS [2]	Motif sequence Logo [1]	NS [2]			
CopR		38		33	I	30	1.5
CtsR		63		39	I	25	4.5
FabT		47		12	I	24	2.2
FlpA		4		31	II	15	2.3
FlrR		3		6	II	5	1.8
FruR		33		18	I	25	1.0
FucR		2		1	III	2	1.5
GalR		20		28	I	20	2.3
GlnR		57		33	I	26	3.6
GntR1		6		26	I	10	2.1

TFs	Predicted site motif in *Streptococcaceae*		NS[2]	Predicted site motif in *Lactobacillaceae*		NS[2]	Category[3]	Genomes[4]	Target operons[5]
	Motif sequence Logo[1]			Motif sequence Logo[1]					
GutR	AAAAAAG -5 nt- CTTAATT		3	TTTTC -8-9 nt- GGAAAT		5	III	7	1.1
HrcA	TTAGCACTC...AGAGTGCTAA		47	TTAGCACT...gAGTGCTAA		66	I	29	3.3
LacR	AAAAAACAA -1-2 nt- AACAAACAA		37	AAGAAACAA -1 nt- ATCAAACAA		2	II	15	2.1
MalR	GcAAaCG TTGC GTAA		77	TTGcGcAA CGc TTGCAcAA		8	I	22	3.7
MdxR	TAAAGAAAACGTTTGCACAA		1	TTTTGATACGGTAACAT		11	II	7	1.7
MleR	ATAAATAATATTTAT		8	TATAAAATTATTTTATA		20	I	17	1.7
MntR	ATAATTAATATAACTTAATTAT		35	AAGTTAGGTCCTAAAA		14	III	22	2.1
MtaR	TATAGTTTAAACTATA		69	AATAGGCAATACCTATA		2	II	14	4.5
MtlR	ATTTTGTGACAAATTT		7	CAACTGTGCCAAAGTC		4	III	8	1.0
MurR	AATGAAATAATATTCTAA		4	ATGAAATTTTGTTACTT		4	II	6	1.0

TFs	Predicted site motif in *Streptococcaceae*		NS [2]	Predicted site motif in *Lactobacillaceae*		NS [2]	Category [3]	Genomes [4]	Target operons [5]
	Motif sequence Logo [1]			Motif sequence Logo [1]					
NagR	AAATGGTcTATACCAaTTA		62	AAATGGTcTAtACCAaT		48	I	30	2.6
NiaR	TACAaTGTcTTGACAccTGTA		22	TTaaGGTGTCaaGACAccTaTA		7	I	18	1.6
NrdR	ACaCAaTATaTTGTgT		59	cACaATaTTGTaT		80	I	28	3.0
NrtR	ATATTTATaaTAAAAaaATA		7	TaaAaGTAAaTaATACTTTtA		8	III	13	1.0
OglR	AATATGGAACGTTCCATGTA		1	AACTTaAAACGTTTaAAGTT		2	II	3	1.0
PadR	AAACATTTAAAAccTTaGAaGATT		2	AAaCaTGTAATTaaTTACATGaTT		6	II	6	1.3
PerR	TTAgAATaTTcTaA		71	TTAtAATaTTcTAA		47	I	22	4.4
PflR	AcGtAATaAaTTaaTTaCGt		28	TaaTTtCgTAaGAAAgTa		3	III	11	2.8
PurR	AaAaCGAACaTT		95	AAAaCGAACaTT		71	I	30	5.2
Rex	TTGTgAAAaaaTTaACAA		160	TTGTgAAaAaaTTcACaA		70	I	30	6.0

TFs	Predicted site motif in *Streptococcaceae*		NS [2]	Predicted site motif in *Lactobacillaceae*		NS [2]	Category [3]	Genomes [4]	Target operons [5]
	Motif sequence Logo [1]			Motif sequence Logo [1]					
ScrR	*(sequence logo)*		26	*(sequence logo)*		32	I	22	2.1
SusR	*(sequence logo)*		6	*(sequence logo)*		1	II	5	1.0
TagR	*(sequence logo)*		2	*(sequence logo)*		8	II	5	2.0
TreR	*(sequence logo)*		15	*(sequence logo)*		20	II	17	1.7
UxuR	*(sequence logo)*		4	*(sequence logo)*		3	II	3	2.3
YwzG	*(sequence logo)*		15	*(sequence logo)*		6	II	18	1.1
YxeR	*(sequence logo)*		2	*(sequence logo)*		17	II	3	1.0

[1] Sequences Logos were constructed using WebLogo package (http://weblogo.berkeley.edu/logo.cgi)

[2] NS. number of binding site sequences used to construct Logo.

[3] Category reflects a conservancy between TFBS motifs in *Streptococcaceae* and *Lactobacillaceae*: I. highly conserved motifs; II. moderately different motifs; III. substantially different motifs.

[4] Number of genomes where current TF regulon was found.

[5] Average number of target operon in regulon per genome.