Overexpressed AMPs

## Heatmap
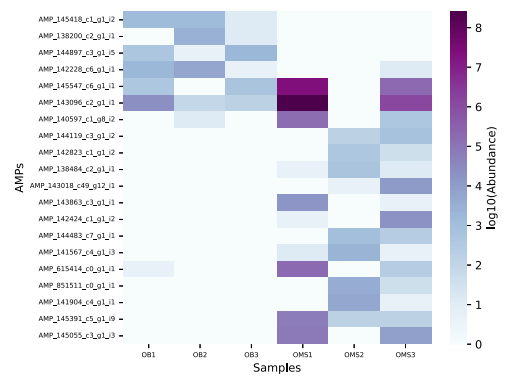
Classification and secuences overexpressed AMPs O group

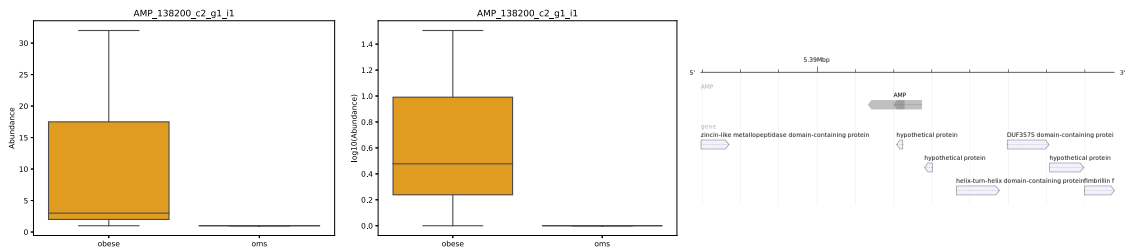| Transcript	Best-hit	AMP	Secuence
TRINITY_DN145418_c1_g1_i2	Bacteriophage sp.	AMP_145418_c1_g1_i2.p5	EGIGA
TRINITY_DN138200_c2_g1_i1	Bacteroides faecis	AMP_138200_c2_g1_i1.p2	MRIITSYCWKIIYKSGMRVRVLTNNSARFIGGCQTSTGTCTTRGYKFGPEVWMVFRTPDQRTLADSPEPGKP
TRINITY_DN144897_c3_g1_i5	Faecalibacterium prausnitzii	AMP_144897_c3_g1_i5.p10	MKRPVQTEK
TRINITY_DN142228_c6_g1_i1	Parabacteroides sp.	AMP_142228_c6_g1_i1.p9	MLTNHFNP

Individual boxplots and genomic context

AMP_145418_c1_g1_i2.p5

Transcript	Best-hit	AMP	Secuence
TRINITY_DN145418_c1_g1_i2	Bacteriophage sp.	AMP_145418_c1_g1_i2.p5	EGIGA
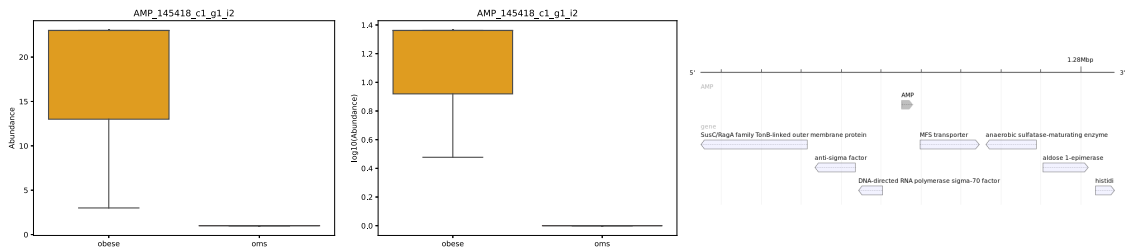
AMP_138200_c2_g1_i1.p2

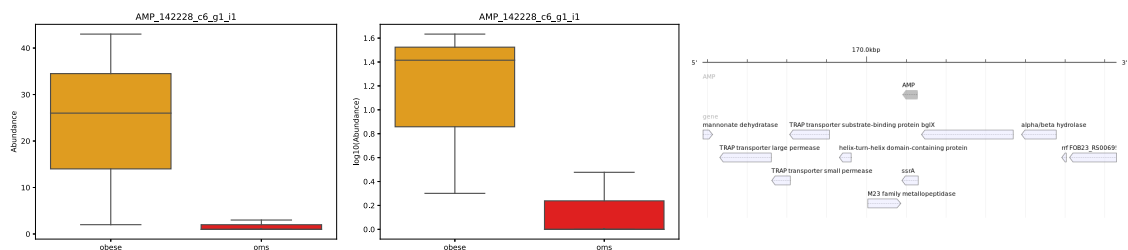| Transcript	Best-hit	AMP	Secuence
TRINITY_DN138200_c2_g1_i1	Bacteroides faecis	AMP_138200_c2_g1_i1.p2	MRIITSYCWKIIYKSGMRVRVLTNNSARFIGGCQTSTGTCTTRGYKFGPEVWMVFRTPDQRTLADSPEPGKP

AMP_144897_c3_g1_i5.p10

Transcript	Best-hit	AMP	Secuence
TRINITY_DN144897_c3_g1_i5	Faecalibacterium prausnitzii	AMP_144897_c3_g1_i5.p10	MKRPVQTEK
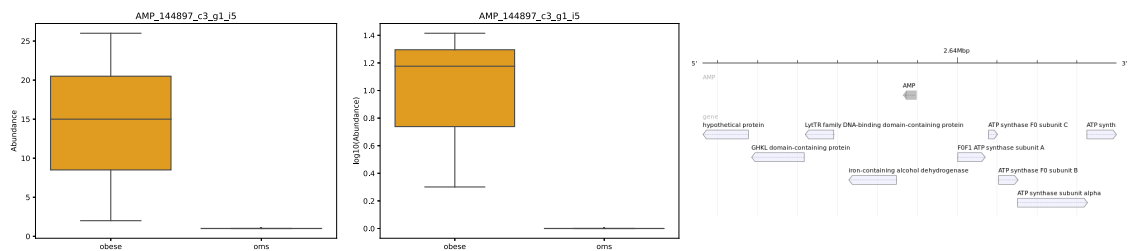
AMP_142228_c6_g1_i1.p9

Transcript	Best-hit	AMP	Secuence
TRINITY_DN142228_c6_g1_i1	Parabacteroides sp.	AMP_142228_c6_g1_i1.p9	MLTNHFNP

Classification and secuences overexpressed AMPs OMS group

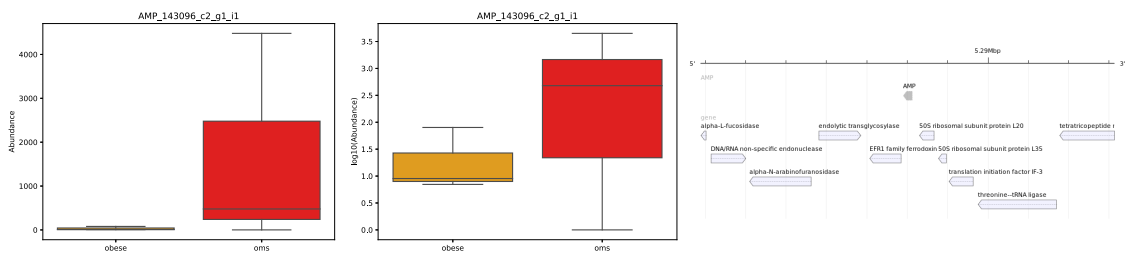| Transcript	Best-hit	AMP	Secuence
TRINITY_DN145547_c6_g1_i1	Escherichia coli	AMP_145547_c6_g1_i1.p3	MPRGGWPRKKPQKIVANDENYALAA
TRINITY_DN143096_c2_g1_i1	Phocaeicola dorei	AMP_143096_c2_g1_i1.p6	KKKKGVYLSYGKR
TRINITY_DN140597_c1_g8_i2	Bifidobacterium pseudocatenulatum	AMP_140597_c1_g8_i2.p5	MASLIGSKAKQKAFEGCSPEAFG
TRINITY_DN144119_c3_g1_i2	Blautia obeum	AMP_144119_c3_g1_i2.p6	ALTHQESGVDYVRNLAG
TRINITY_DN142823_c1_g1_i2	Romboutsia ilealis	AMP_142823_c1_g1_i2.p2	MGGRQWHGGVRPIFRGGMTALRHENLHGGTKAACSVACLERSWVDHGTTHGDQRLTEAAAIAV
TRINITY_DN138484_c2_g1_i1	Faecalibacterium prausnitzii	AMP_138484_c2_g1_i1.p2	RMPNIKSHKDRVVQAAAEQAHNKAIKPNLKTVVKKADAAIDANAADKDATVLAAVSAIDKARAKGVIKKNTASRKISRMAKRANKNA
TRINITY_DN143018_c49_g12_i1	Parabacteroides merdae	AMP_143018_c49_g12_i1.p9	MKIGTNSEK
TRINITY_DN143863_c3_g1_i1	Clostridium sp.	AMP_143863_c3_g1_i1.p5	TIQRHNPAYRLAHKMI
TRINITY_DN142424_c1_g1_i2	Lachnospiraceae bacterium	AMP_142424_c1_g1_i2.p4	GFMPVLLPFISGDEVWVLRNGCL
TRINITY_DN144483_c7_g1_i1	Uncultured organism	AMP_144483_c7_g1_i1.p5	MIIISQMLAGHNPAYSAAHIY
TRINITY_DN141567_c4_g1_i3	Parabacteroides merdae	AMP_141567_c4_g1_i3.p5	MLTNHFYPLSKPVIP
TRINITY_DN615414_c0_g1_i1	Myoviridae sp.	AMP_615414_c0_g1_i1.p9	MIKIGR
TRINITY_DN851511_c0_g1_i1	Faecalibacterium prausnitzii	AMP_851511_c0_g1_i1.p12	MLLAMGQ
TRINITY_DN141904_c4_g1_i1	Lachnospiraceae bacterium	AMP_141904_c4_g1_i1.p1	GVVQVSTGSLKMEKLSVVGHHVKSSKLKLNAEDNLALAA
TRINITY_DN145391_c5_g1_i9	Faecalibacterium prausnitzii	AMP_145391_c5_g1_i9.p5	MKRPEQTEK
TRINITY_DN145055_c3_g1_i3	Uncultured human fecal virus clone	AMP_145055_c3_g1_i3.p7	MDLKA

Individual boxplots

AMP_145547_c6_g1_i1.p3

Transcript	Best-hit	AMP	Secuence
TRINITY_DN145547_c6_g1_i1	Escherichia coli	AMP_145547_c6_g1_i1.p3	MPRGGWPRKKPQKIVANDENYALAA
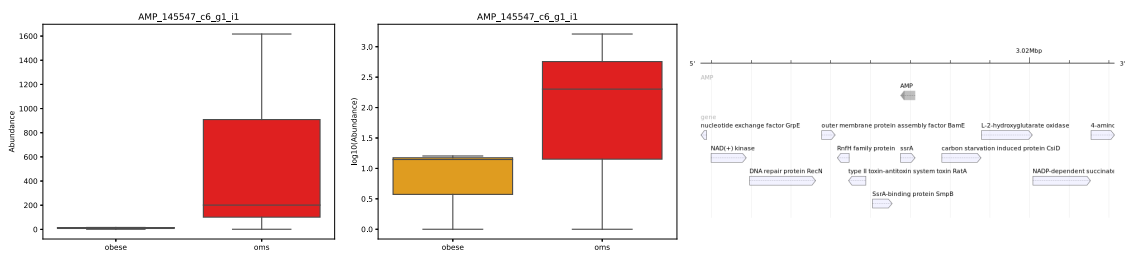
AMP_143096_c2_g1_i1.p6

Transcript	Best-hit	AMP	Secuence
TRINITY_DN143096_c2_g1_i1	Phocaeicola dorei	AMP_143096_c2_g1_i1.p6	KKKKGVYLSYGKR

AMP_140597_c1_g8_i2.p5

Transcript	Best-hit	AMP	Secuence
TRINITY_DN140597_c1_g8_i2	Bifidobacterium pseudocatenulatum	AMP_140597_c1_g8_i2.p5	MASLIGSKAKQKAFEGCSPEAFG
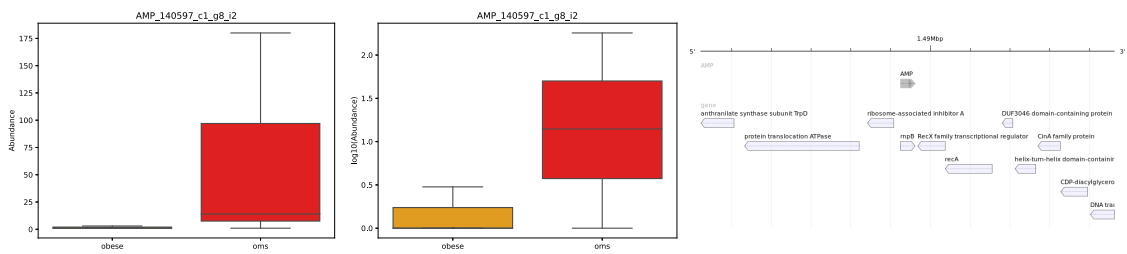
AMP_144119_c3_g1_i2.p6

Transcript	Best-hit	AMP	Secuence
TRINITY_DN144119_c3_g1_i2	Blautia obeum	AMP_144119_c3_g1_i2.p6	ALTHQESGVDYVRNLAG
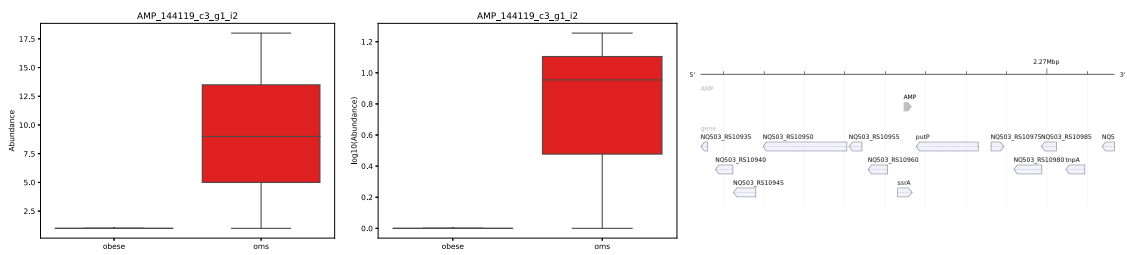
AMP_142823_c1_g1_i2.p2

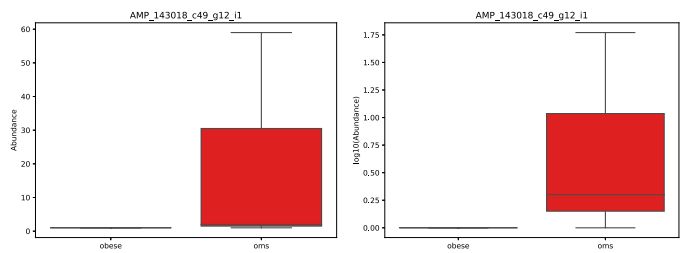| Transcript	Best-hit	AMP	Secuence
TRINITY_DN142823_c1_g1_i2	Romboutsia ilealis	AMP_142823_c1_g1_i2.p2	MGGRQWHGGVRPIFRGGMTALRHENLHGGTKAACSVACLERSWVDHGTTHGDQRLTEAAAIAV
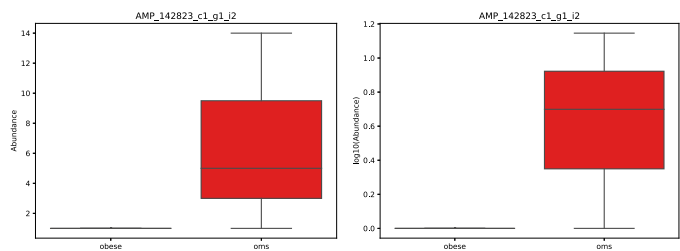
AMP_138484_c2_g1_i1.p2

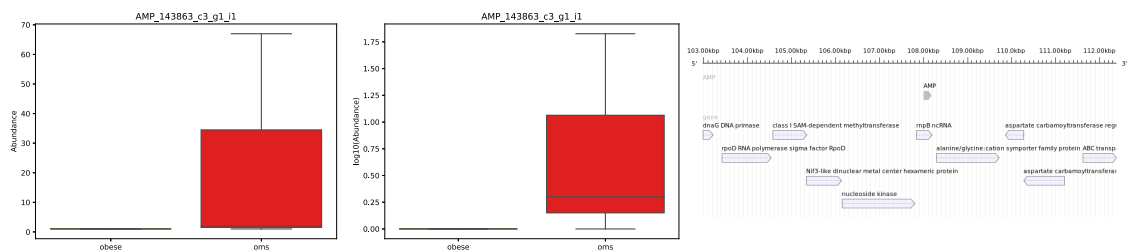| Transcript	Best-hit	AMP	Secuence
TRINITY_DN138484_c2_g1_i1	Faecalibacterium prausnitzii	AMP_138484_c2_g1_i1.p2	RMPNIKSHKDRVVQAAAEQAHNKAIKPNLKTVVKKADAAIDANAADKDATVLAAVSAIDKARAKGVIKKNTASRKISRMAKRANKNA
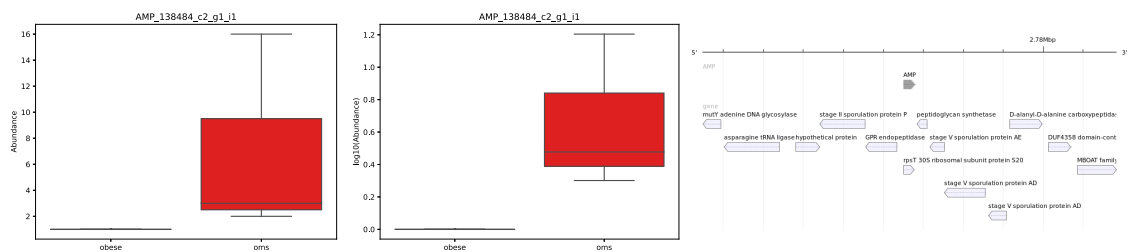
AMP_143018_c49_g12_i1.p9

Transcript	Best-hit	AMP	Secuence
TRINITY_DN143018_c49_g12_i1	Parabacteroides merdae	AMP_143018_c49_g12_i1.p9	MKIGTNSEK

AMP_143863_c3_g1_i1.p5

Transcript	Best-hit	AMP	Secuence
TRINITY_DN143863_c3_g1_i1	Clostridium sp.	AMP_143863_c3_g1_i1.p5	TIQRHNPAYRLAHKMI

AMP_142424_c1_g1_i2.p4

Transcript	Best-hit	AMP	Secuence
TRINITY_DN142424_c1_g1_i2	Lachnospiraceae bacterium	AMP_142424_c1_g1_i2.p4	GFMPVLLPFISGDEVWVLRNGCL
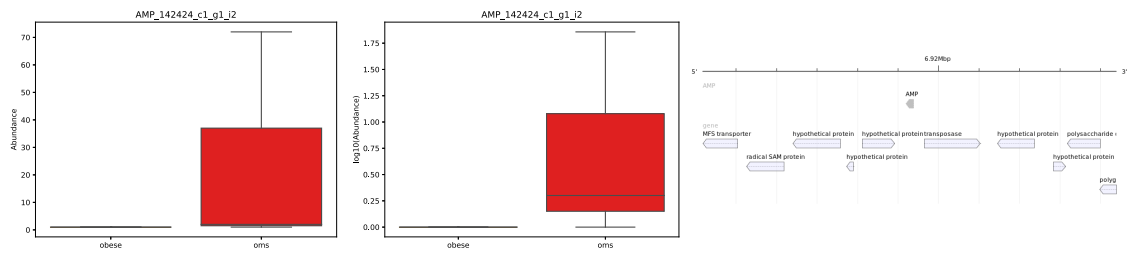
AMP_144483_c7_g1_i1.p5

Transcript	Best-hit	AMP	Secuence
TRINITY_DN144483_c7_g1_i1	Uncultured organism	AMP_144483_c7_g1_i1.p5	MIIISQMLAGHNPAYSAAHIY
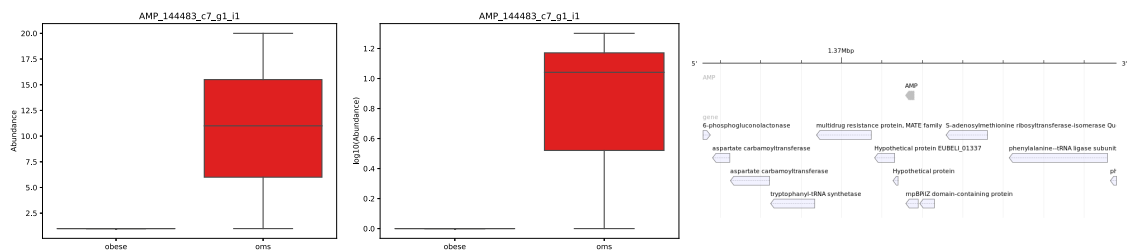
AMP_141567_c4_g1_i3.p5

Transcript	Best-hit	AMP	Secuence
TRINITY_DN141567_c4_g1_i3	Parabacteroides merdae	AMP_141567_c4_g1_i3.p5	MLTNHFYPLSKPVIP
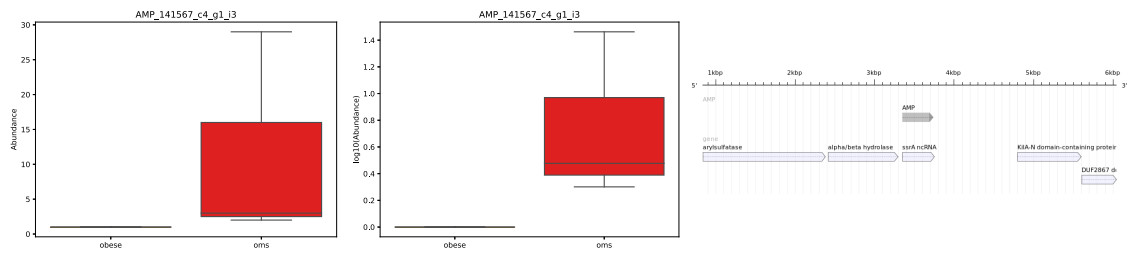
AMP_615414_c0_g1_i1.p9

Transcript	Best-hit	AMP	Secuence
TRINITY_DN615414_c0_g1_i1	Myoviridae sp.	AMP_615414_c0_g1_i1.p9	MIKIGR
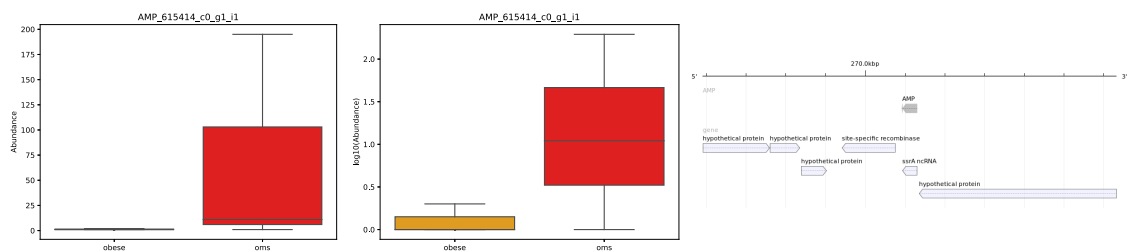
AMP_851511_c0_g1_i1.p12

Transcript	Best-hit	AMP	Secuence
TRINITY_DN851511_c0_g1_i1	Faecalibacterium prausnitzii	AMP_851511_c0_g1_i1.p12	MLLAMGQ
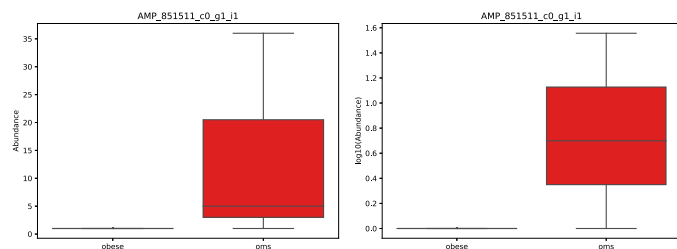
AMP_141904_c4_g1_i1.p1

Transcript	Best-hit	AMP	Secuence
TRINITY_DN141904_c4_g1_i1	Lachnospiraceae bacterium	AMP_141904_c4_g1_i1.p1	GVVQVSTGSLKMEKLSVVGHHVKSSKLKLNAEDNLALAA
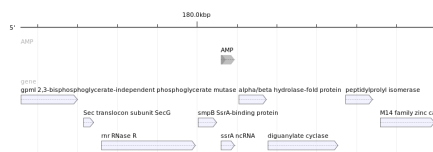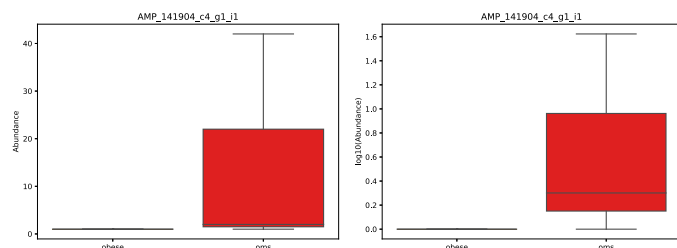
AMP_145391_c5_g1_i9.p5

Transcript	Best-hit	AMP	Secuence
TRINITY_DN145391_c5_g1_i9	Faecalibacterium prausnitzii	AMP_145391_c5_g1_i9.p5	MKRPEQTEK
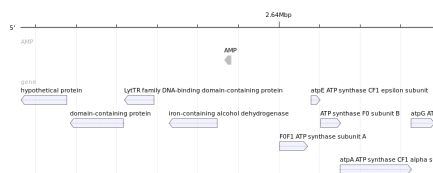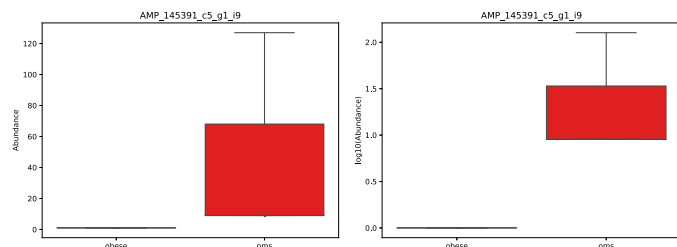
AMP_145055_c3_g1_i3.p7

Transcript	Best-hit	AMP	Secuence
TRINITY_DN145055_c3_g1_i3	Uncultured human fecal virus clone	AMP_145055_c3_g1_i3.p7	MDLKA

AMP_145055_c3_g1_i3