**A:**

**AGG38744.1 VS A0A182YTN9** Score:1143 bits(2957), Expect:0.0, Method:Compositional matrix adjust.,Identities:538/572(**94%**), Positives:555/572(97%), Gaps:0/572(0%)

AGG38744.1 MFLQIFVAVTLVQYVSSQCTYSSWWYSFDTPGQSKCNEINSYINALDRNDVNWADDALSN 60

 M +Q A TL+QYVSSQCTYSSWWYSFDTPGQSKCNEINSYINALDRNDVNWADDALSN

A0A182YTN9 MLVQFLFAATLLQYVSSQCTYSSWWYSFDTPGQSKCNEINSYINALDRNDVNWADDALSN 60

AGG38744.1 LEGVQCCRPPAPWNNVEQQVVYEDWTATLDSDYTWAFCRVGYFLQGLYRSDTGWPRFKGY 120

 LEGVQCCRPPAPWNNVEQQVVYEDWTATLDSDYTWAFCRVGYFLQGLYRSDTGWPRFKGY

A0A182YTN9 LEGVQCCRPPAPWNNVEQQVVYEDWTATLDSDYTWAFCRVGYFLQGLYRSDTGWPRFKGY 120

AGG38744.1 LFNLESARCTKPANHPLNYGTCQDIDVSSCMGRKGQCSCPGGYFLTGLYRADGDDLYFLK 180

 LFNLESARCTKPANHPLNYG CQDIDVSSCMGRKGQCSCPGGYFLTGLYRADGDDLYFLK

A0A182YTN9 LFNLESARCTKPANHPLNYGNCQDIDVSSCMGRKGQCSCPGGYFLTGLYRADGDDLYFLK 180

AGG38744.1 KIRCCTPAAKPLEMDEKSKIQTRIMDTTLWNMATLAHYMGYGWCYGCHGLAVGEDFTRNG 240

 KIRCCTPAAKPLEMDEKSKIQTRIMDTTLWNMATLAHY+GYGWCYGC G+AVGEDFTRNG

A0A182YTN9 KIRCCTPAAKPLEMDEKSKIQTRIMDTTLWNMATLAHYLGYGWCYGCRGVAVGEDFTRNG 240

AGG38744.1 FTWAADTRTFWGKWCEGDKNGERLNLVFGDWGFAVKEIIYGKSVIEDLQAESVDSGVLYN 300

 FTWAADTR+FWGKWCEGDKNGERLNLVFGDWGFAVKEIIYGKSVIEDLQAESVDSGVLYN

A0A182YTN9 FTWAADTRSFWGKWCEGDKNGERLNLVFGDWGFAVKEIIYGKSVIEDLQAESVDSGVLYN 300

AGG38744.1 RASSPVTESIERSKTIQETITHSTTSTFTNSHGLGVELEFEIASVKGKASYKTRFEYSTS 360

 RASSPVTESI+R+KTI+ET+THSTTSTFTNSH LG+EL FEIASV GKASY T+FEYS +

A0A182YTN9 RASSPVTESIDRTKTIEETVTHSTTSTFTNSHELGIELNFEIASVSGKASYTTKFEYSKA 360

AGG38744.1 TTNSKSISETQGFTKQSSITLGPMEGAKYEVIMSKSRTTVPYTAIITTKFSTEMKGFLRW 420

 TTN KSIS+T GFTK+SSITLGPMEGAKYE+IMSKSRTTVPYTAIITTKFSTEMKGFLRW

A0A182YTN9 TTNEKSISQTAGFTKKSSITLGPMEGAKYEIIMSKSRTTVPYTAIITTKFSTEMKGFLRW 420

AGG38744.1 EDGNGNFHQDYRTNSGRPTFNYRFGDSSVPFYKALKKQSDNNEGVWMWGMLFQKFPDARR 480

 EDGNGNFHQDYRTNSGRPT+NYRFGDSSVPFYKALKKQSDNNEGVWMWGMLFQKFPDARR

A0A182YTN9 EDGNGNFHQDYRTNSGRPTYNYRFGDSSVPFYKALKKQSDNNEGVWMWGMLFQKFPDARR 480

AGG38744.1 VTNRLTDETQYQFTLAGKLEKVEGTSVNVKWEKMKLNRRDVSGNDEPGSNITTYIAASGP 540

 V NRLTDETQYQFTL GKLEKVEGTSVNVKWEK+KLNRRDVSGND PGSNITTYIAASGP

A0A182YTN9 VINRLTDETQYQFTLTGKLEKVEGTSVNVKWEKIKLNRRDVSGNDAPGSNITTYIAASGP 540

AGG38744.1 ADKPAVVEYPKVNLNNKEPFKPIEIPVTEVKV 572

 ADKPAVVEYPKVNLNNKEPFKPIEIPVTEVKV

A0A182YTN9 ADKPAVVEYPKVNLNNKEPFKPIEIPVTEVKV 572

**B:**

**AGG38744.1 VS A0A182YTZ4** Score:1184 bits(3064), Expect:0.0, Method:Compositional matrix adjust.,Identities:565/572(**99%**), Positives:567/572(99%), Gaps:0/572(0%)

AGG38744.1 MFLQIFVAVTLVQYVSSQCTYSSWWYSFDTPGQSKCNEINSYINALDRNDVNWADDALSN 60

 MFLQIF+AVTLVQYVSSQCTYSSWWYSFDTPGQSKCN+INSYINALDRNDVNWADDALSN

A0A182YTZ4 MFLQIFLAVTLVQYVSSQCTYSSWWYSFDTPGQSKCNDINSYINALDRNDVNWADDALSN 60

AGG38744.1 LEGVQCCRPPAPWNNVEQQVVYEDWTATLDSDYTWAFCRVGYFLQGLYRSDTGWPRFKGY 120

 LEGVQCCRPPAPWNNVEQQVVYEDWTATLDSDYTWAFCRVGYFLQGLYRSDTGWPRFKGY

A0A182YTZ4 LEGVQCCRPPAPWNNVEQQVVYEDWTATLDSDYTWAFCRVGYFLQGLYRSDTGWPRFKGY 120

AGG38744.1 LFNLESARCTKPANHPLNYGTCQDIDVSSCMGRKGQCSCPGGYFLTGLYRADGDDLYFLK 180

 LFNLESARCTKPANHPLNYGTCQDIDVSSCMGRKGQCSCPGGYFLTGLYRADGDDLYFLK

A0A182YTZ4 LFNLESARCTKPANHPLNYGTCQDIDVSSCMGRKGQCSCPGGYFLTGLYRADGDDLYFLK 180

AGG38744.1 KIRCCTPAAKPLEMDEKSKIQTRIMDTTLWNMATLAHYMGYGWCYGCHGLAVGEDFTRNG 240

 KIRCCTPAAKPLEMDEKSKIQTRIMDTTLWNMATLAHYMGYGWCYGCHGLAVGEDFTRNG

A0A182YTZ4 KIRCCTPAAKPLEMDEKSKIQTRIMDTTLWNMATLAHYMGYGWCYGCHGLAVGEDFTRNG 240

AGG38744.1 FTWAADTRTFWGKWCEGDKNGERLNLVFGDWGFAVKEIIYGKSVIEDLQAESVDSGVLYN 300

 FTWAADTRTFWGKWCEGDKNGERLNLVFGDWGFAVKEIIYGKSVIEDLQAESVDSGVLYN

A0A182YTZ4 FTWAADTRTFWGKWCEGDKNGERLNLVFGDWGFAVKEIIYGKSVIEDLQAESVDSGVLYN 300

AGG38744.1 RASSPVTESIERSKTIQETITHSTTSTFTNSHGLGVELEFEIASVKGKASYKTRFEYSTS 360

 RASSPVTESIERSKTIQETITHSTTSTFTNSH LGVELEFEIASVKGKASYKTRFEYSTS

A0A182YTZ4 RASSPVTESIERSKTIQETITHSTTSTFTNSHELGVELEFEIASVKGKASYKTRFEYSTS 360

AGG38744.1 TTNSKSISETQGFTKQSSITLGPMEGAKYEVIMSKSRTTVPYTAIITTKFSTEMKGFLRW 420

 TTNSKSISETQGFTKQSSITLGPMEGAKYEVIMSKSRTTVPYTAIITTKFSTEMKGFLRW

A0A182YTZ4 TTNSKSISETQGFTKQSSITLGPMEGAKYEVIMSKSRTTVPYTAIITTKFSTEMKGFLRW 420

AGG38744.1 EDGNGNFHQDYRTNSGRPTFNYRFGDSSVPFYKALKKQSDNNEGVWMWGMLFQKFPDARR 480

 EDGNGNFHQDYRTNSGRPTFNYRFGDSSVPFYKALKKQSDNNEGVWMWGMLFQKFPDARR

A0A182YTZ4 EDGNGNFHQDYRTNSGRPTFNYRFGDSSVPFYKALKKQSDNNEGVWMWGMLFQKFPDARR 480

AGG38744.1 VTNRLTDETQYQFTLAGKLEKVEGTSVNVKWEKMKLNRRDVSGNDEPGSNITTYIAASGP 540

 V NRLTDETQYQFTL GKLEKVEGTSVNVKWEKMKLNRRDVSGND PGSNITTYIAASGP

A0A182YTZ4 VINRLTDETQYQFTLTGKLEKVEGTSVNVKWEKMKLNRRDVSGNDAPGSNITTYIAASGP 540

AGG38744.1 ADKPAVVEYPKVNLNNKEPFKPIEIPVTEVKV 572

 ADKPAVVEYPKVNLNNKEPFKPIEI VTEVKV

A0A182YTZ4 ADKPAVVEYPKVNLNNKEPFKPIEISVTEVKV 572

**C:**

CLUSTAL O (1.2.4) multiple sequence alignment

A0A182YTN9 MLVQFLFAATLLQYVSSQCTYSSWWYSFDTPGQSKCNEINSYINALDRNDVNWADDALSN 60

AGG38744.1 MFLQIFVAVTLVQYVSSQCTYSSWWYSFDTPGQSKCNEINSYINALDRNDVNWADDALSN 60

A0A182YTZ4 MFLQIFLAVTLVQYVSSQCTYSSWWYSFDTPGQSKCNDINSYINALDRNDVNWADDALSN 60

 \*::\*::.\*.\*\*:\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*:\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

A0A182YTN9 LEGVQCCRPPAPWNNVEQQVVYEDWTATLDSDYTWAFCRVGYFLQGLYRSDTGWPRFKGY 120

AGG38744.1 LEGVQCCRPPAPWNNVEQQVVYEDWTATLDSDYTWAFCRVGYFLQGLYRSDTGWPRFKGY 120

A0A182YTZ4 LEGVQCCRPPAPWNNVEQQVVYEDWTATLDSDYTWAFCRVGYFLQGLYRSDTGWPRFKGY 120

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

A0A182YTN9 LFNLESARCTKPANHPLNYGNCQDIDVSSCMGRKGQCSCPGGYFLTGLYRADGDDLYFLK 180

AGG38744.1 LFNLESARCTKPANHPLNYGTCQDIDVSSCMGRKGQCSCPGGYFLTGLYRADGDDLYFLK 180

A0A182YTZ4 LFNLESARCTKPANHPLNYGTCQDIDVSSCMGRKGQCSCPGGYFLTGLYRADGDDLYFLK 180

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*.\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

A0A182YTN9 KIRCCTPAAKPLEMDEKSKIQTRIMDTTLWNMATLAHYLGYGWCYGCRGVAVGEDFTRNG 240

AGG38744.1 KIRCCTPAAKPLEMDEKSKIQTRIMDTTLWNMATLAHYMGYGWCYGCHGLAVGEDFTRNG 240

A0A182YTZ4 KIRCCTPAAKPLEMDEKSKIQTRIMDTTLWNMATLAHYMGYGWCYGCHGLAVGEDFTRNG 240

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*:\*\*\*\*\*\*\*\*:\*:\*\*\*\*\*\*\*\*\*\*

A0A182YTN9 FTWAADTRSFWGKWCEGDKNGERLNLVFGDWGFAVKEIIYGKSVIEDLQAESVDSGVLYN 300

AGG38744.1 FTWAADTRTFWGKWCEGDKNGERLNLVFGDWGFAVKEIIYGKSVIEDLQAESVDSGVLYN 300

A0A182YTZ4 FTWAADTRTFWGKWCEGDKNGERLNLVFGDWGFAVKEIIYGKSVIEDLQAESVDSGVLYN 300

 \*\*\*\*\*\*\*\*:\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

A0A182YTN9 RASSPVTESIDRTKTIEETVTHSTTSTFTNSHELGIELNFEIASVSGKASYTTKFEYSKA 360

AGG38744.1 RASSPVTESIERSKTIQETITHSTTSTFTNSHGLGVELEFEIASVKGKASYKTRFEYSTS 360

A0A182YTZ4 RASSPVTESIERSKTIQETITHSTTSTFTNSHELGVELEFEIASVKGKASYKTRFEYSTS 360

 \*\*\*\*\*\*\*\*\*\*:\*:\*\*\*:\*\*:\*\*\*\*\*\*\*\*\*\*\*\* \*\*:\*\*:\*\*\*\*\*\*.\*\*\*\*\*.\*:\*\*\*\*.:

A0A182YTN9 TTNEKSISQTAGFTKKSSITLGPMEGAKYEIIMSKSRTTVPYTAIITTKFSTEMKGFLRW 420

AGG38744.1 TTNSKSISETQGFTKQSSITLGPMEGAKYEVIMSKSRTTVPYTAIITTKFSTEMKGFLRW 420

A0A182YTZ4 TTNSKSISETQGFTKQSSITLGPMEGAKYEVIMSKSRTTVPYTAIITTKFSTEMKGFLRW 420

 \*\*\*.\*\*\*\*:\* \*\*\*\*:\*\*\*\*\*\*\*\*\*\*\*\*\*\*:\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

A0A182YTN9 EDGNGNFHQDYRTNSGRPTYNYRFGDSSVPFYKALKKQSDNNEGVWMWGMLFQKFPDARR 480

AGG38744.1 EDGNGNFHQDYRTNSGRPTFNYRFGDSSVPFYKALKKQSDNNEGVWMWGMLFQKFPDARR 480

A0A182YTZ4 EDGNGNFHQDYRTNSGRPTFNYRFGDSSVPFYKALKKQSDNNEGVWMWGMLFQKFPDARR 480

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*:\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

A0A182YTN9 VINRLTDETQYQFTLTGKLEKVEGTSVNVKWEKIKLNRRDVSGNDAPGSNITTYIAASGP 540

AGG38744.1 VTNRLTDETQYQFTLAGKLEKVEGTSVNVKWEKMKLNRRDVSGNDEPGSNITTYIAASGP 540

A0A182YTZ4 VINRLTDETQYQFTLTGKLEKVEGTSVNVKWEKMKLNRRDVSGNDAPGSNITTYIAASGP 540

 \* \*\*\*\*\*\*\*\*\*\*\*\*\*:\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*:\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*

A0A182YTN9 ADKPAVVEYPKVNLNNKEPFKPIEIPVTEVKV 572

AGG38744.1 ADKPAVVEYPKVNLNNKEPFKPIEIPVTEVKV 572

A0A182YTZ4 ADKPAVVEYPKVNLNNKEPFKPIEISVTEVKV 572

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*

**Figure 1—figure supplement 4. The two Biomphalysin variants (UniProtKB/TrEMBL: A0A182YTN9 and A0A182YTZ4) identified by LC-MS/MS were different from the previously published Biomphalysin (GenBank: AGG38744.1).**