

## Supplementary information for the article

Kosanović, D.; Dyas, M.; Grogan, H.; Kavanagh, K. Differential Proteomic Response of *Agaricus Bisporus* and *Trichoderma Aggressivum* f. *Europaeum* to *Bacillus Velezensis* Supernatant. *European Journal of Plant Pathology* 2021, 160 (2). <https://doi.org/10.1007/s10658-021-02252-5>.



**Table S1.** Bacterial species used in this study with amplicon deposition number obtained from NCBI GeneBank.

<b>Bacterial species</b>	<i>Algoriphagus marisflavis</i> KEM-10	<i>Sphingopyxis italica</i> SCI3E-571	<i>Nocardioides humi</i> DCY24	<i>Bacillus velezensis</i>	<i>Bacillus subtilis</i> MU Prep Lab	<i>Bacillus velezensis</i> QST 713
<b>NCBI GeneBank number</b>	MT156333	MT156334	MT156335	MT156336	N/a	Serenade® - Bayer

Customer:	Maynooth University	Account:	604581 (MAY1)
Address:	Medical Mycology Lab Biology Department North Campus, Kildare, Maynooth, W23 F2H6, Ireland	ID Request Form#:	442048
Accugenix® C# / Run Date:	C4293357-20200930205 / 2020-09-30 16:11:28	Due Date:	2020-10-01
Customer Sample ID:	MD-19, revised to 189 DK Unknown D		

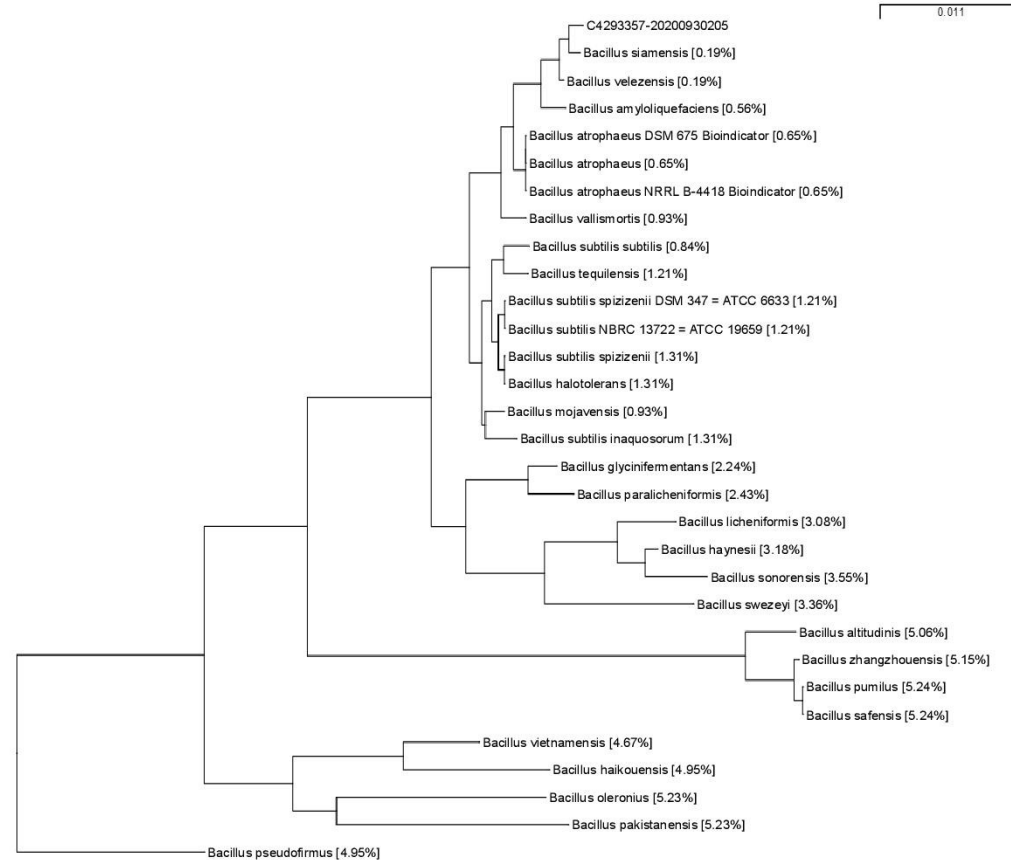
AccuGENX-ID® Database Search Result - Bacterial Library

Identification: *Bacillus amyloliquefaciens* / *siamensis* / *velezensis*

Confidence Level: Species\*

\*The Unknown matches two or more closely related species that cannot be differentiated by 16S rDNA. We may be able to distinguish between the above species using ProSeq. Contact technical support to request this service.

Neighbor Joining Tree



\*\*\*The value shown in the bracket represents the percent difference in the sequence alignment between the unknown and each individual library entry.\*\*\*

Figure S1. 16S rRNA gene analysis.

Customer: Maynooth University Account: 604581 ( MAY1 )  
Address: Medical Mycology Lab Biology Department North Campus, Kildare, Maynooth, W23 F2H6,  
Accugenix C#: C4293357-20201012193 ID Request Form #: 442048  
Customer Sample ID: MD-19, revised to 18/9 DK Unknown D Due Date: 2020-10-12

**Accugenix Database Search Result - ProSeq-BacilAmylo-gyrB**

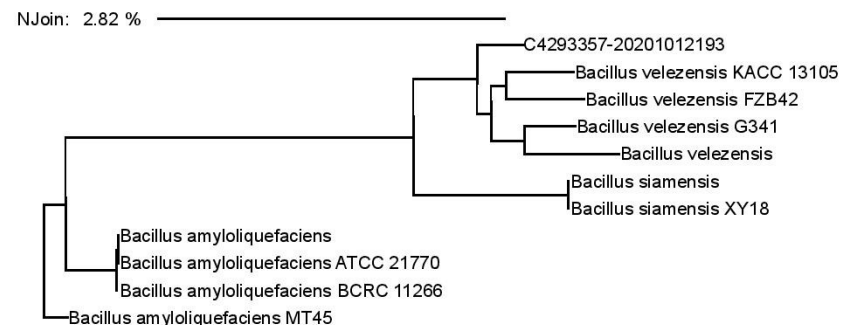
Identification: **Bacillus velezensis**

Confidence Level: **Species**

**Sequence Alignment**

Alignment: 514 C4293357-20201012193  
0.97 % 514 Bacillus velezensis KACC 13105  
1.17 % 514 Bacillus velezensis G341  
1.36 % 514 Bacillus velezensis FZB42  
1.56 % 514 Bacillus velezensis  
1.95 % 514 Bacillus siamensis  
1.95 % 514 Bacillus siamensis XY18  
4.09 % 514 Bacillus amyloliquefaciens MT45  
4.47 % 514 Bacillus amyloliquefaciens  
4.47 % 514 Bacillus amyloliquefaciens ATCC 21770  
4.47 % 514 Bacillus amyloliquefaciens BCRC 11266

**Neighbor Joining Tree**

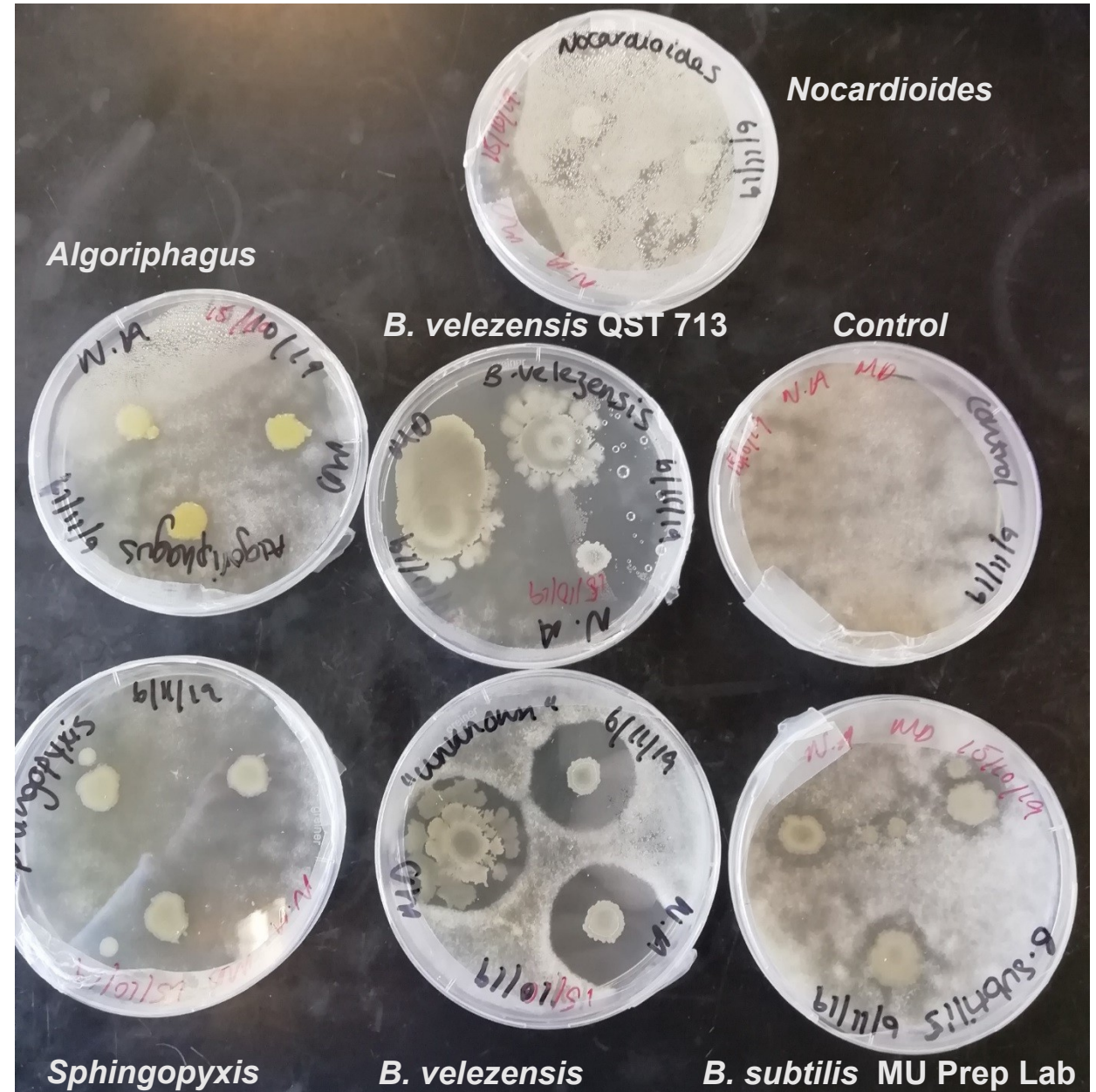


Not intended for in vitro diagnostic use

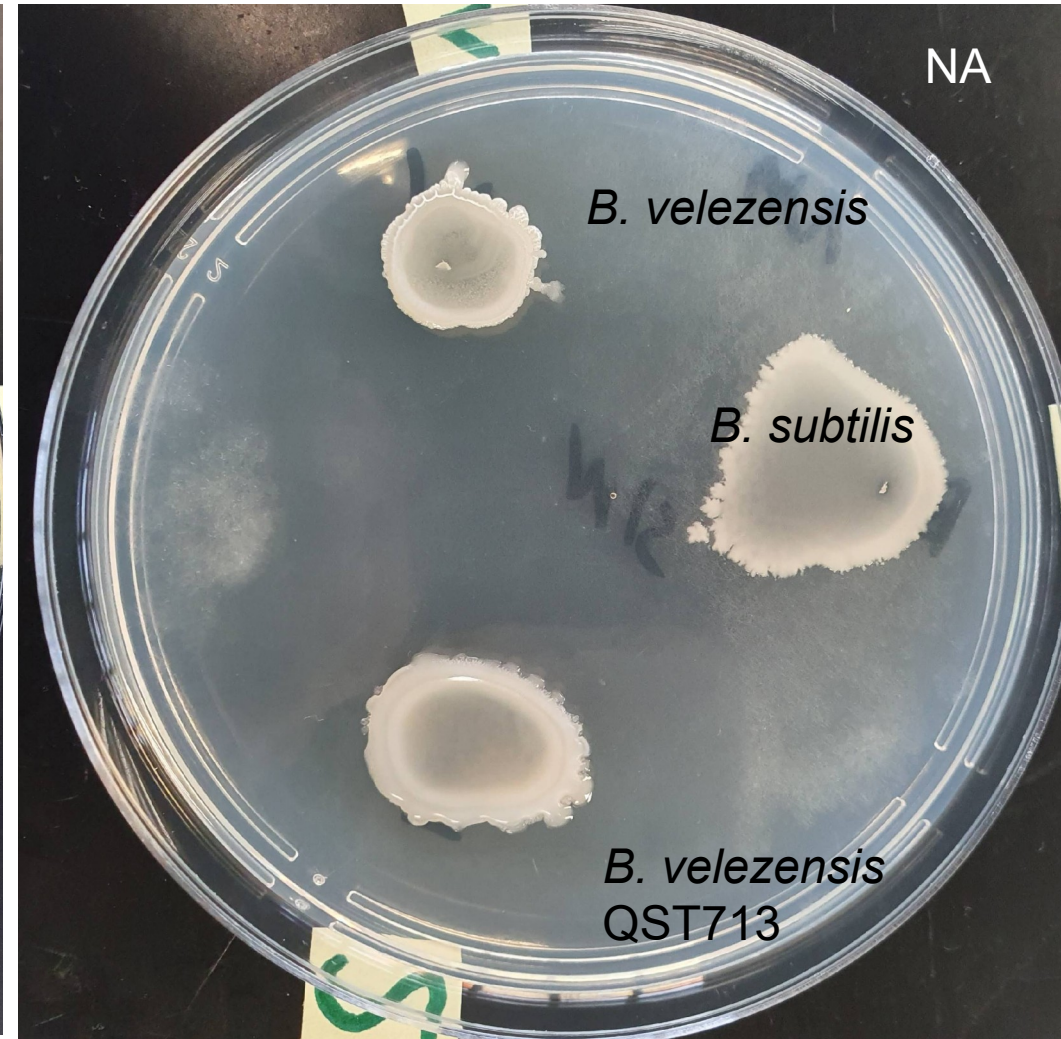
**Figure S2.** Specific protein analysis- gyrB gene analysis.

**Figure S3a.** Zone of inhibition test on NA plates  $10^4$  *T. aggressivum* conidia per plate vs 10  $\mu$ l of bacterial overnight culture incubated on 30°C.

Zone of inhibition [mm <sup>2</sup> ]						
Control	Algoriphagus Nocardioides		<i>B. velezensis</i> QST 713	<i>B. subtilis</i> MU Prep Lab	Unknown = <i>B. velezensis</i>	
0	0	0	36.18±2.2	67.86±5.1	32.8±2.9	81.0±6.2

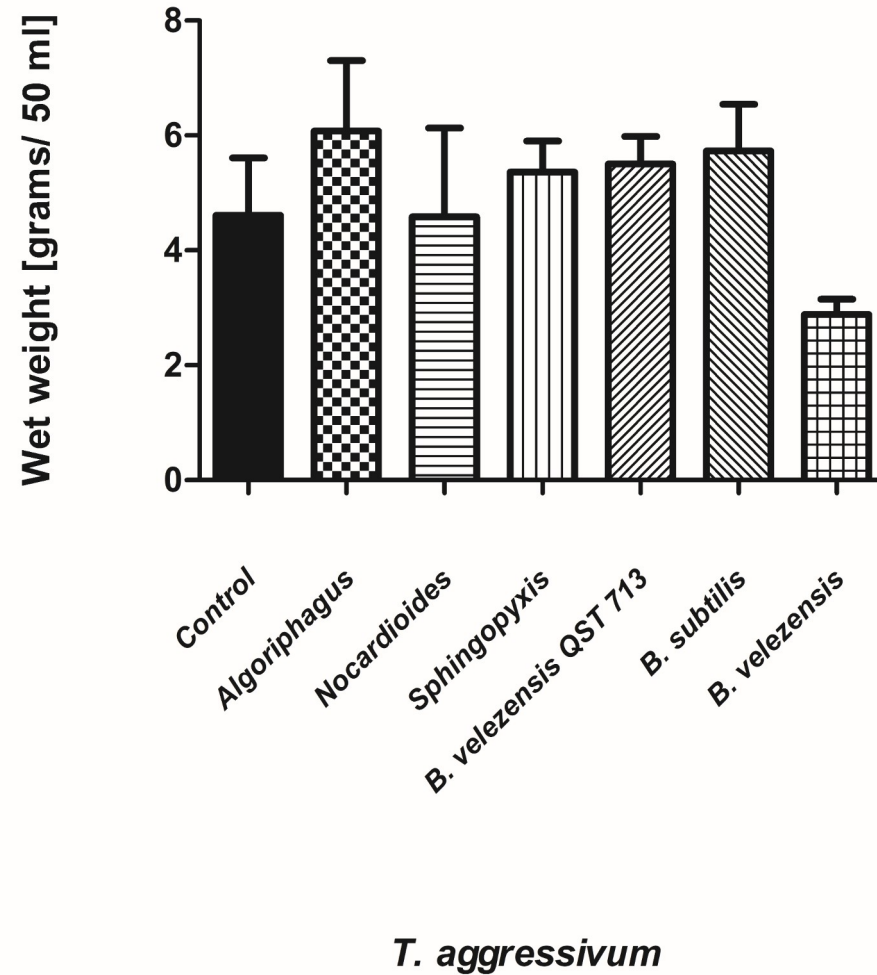


**Figure S3b.** Zone of inhibition test on YMEA and NA plates  $10^4$  *T. aggressivum* conidia per plate vs  $10^6$   $\mu$ l of bacterial overnight culture incubated on 25°C.

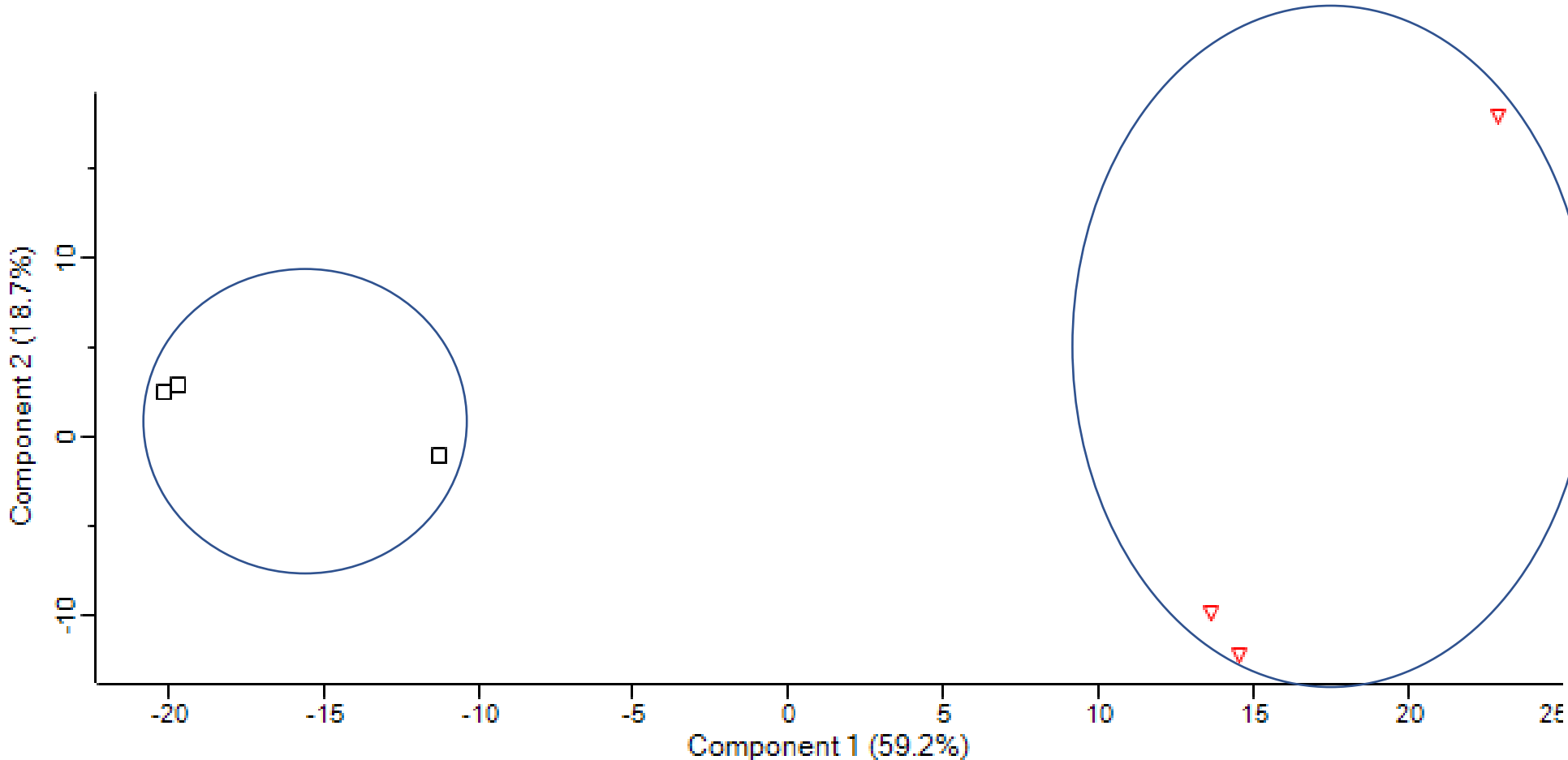


Species	YMEA media zone (area) of inhibition
<i>B. velezensis</i> QST713	$309 \pm 46 \text{ mm}^2$
<i>B. velezensis</i>	$196.6 \pm 19.5 \text{ mm}^2$
<i>B. subtilis</i>	$0 \pm 0 \text{ mm}^2$

**Figure S4.** The effect of 25%v/v bacterial supernatants on *T. aggressivum* growth was assessed. *B. subtilis* R8.3 supernatant was found to inhibit growth of *T. aggressivum* by 37% and that was the maximum effect compared to other bacterial supernatants.

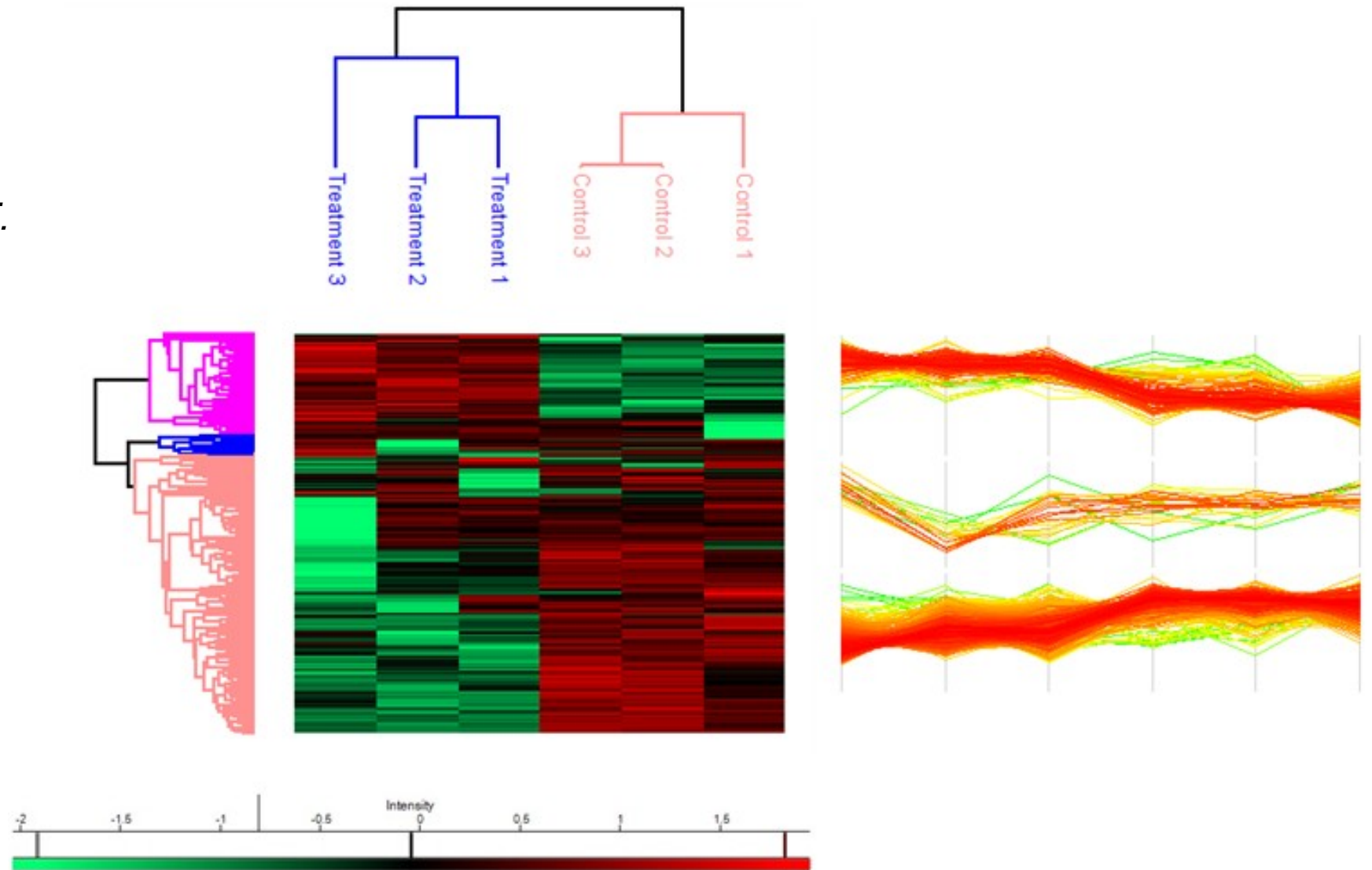


**Figure S5.** PCA analysis.  $\square$  - Control group and  $\triangle$  - *T. aggresivum* + *B. velezensis* SN group.



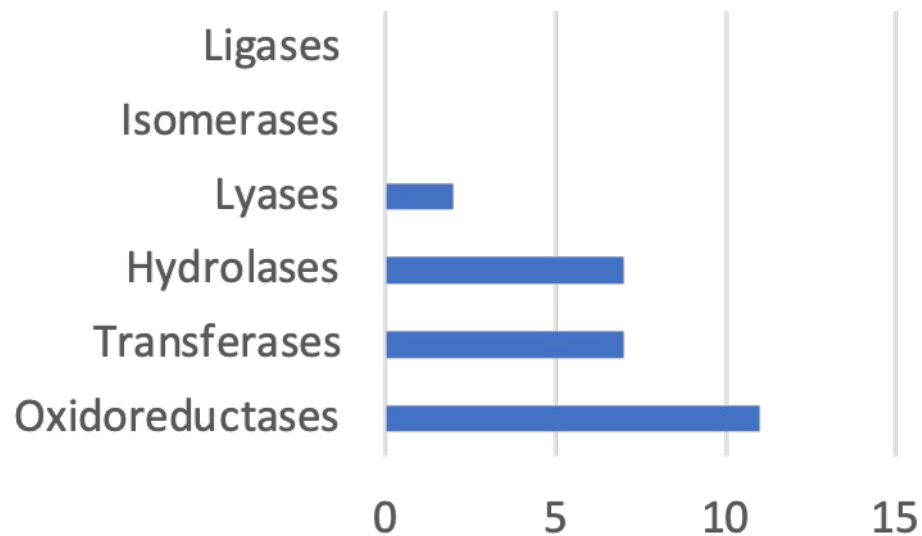


**Figure S6.** Protein abundance similarities of two sample group (*T. aggressivum* control and *T. aggressivum* treated with *B. velezensis* SN) based on hierarchical clustering.

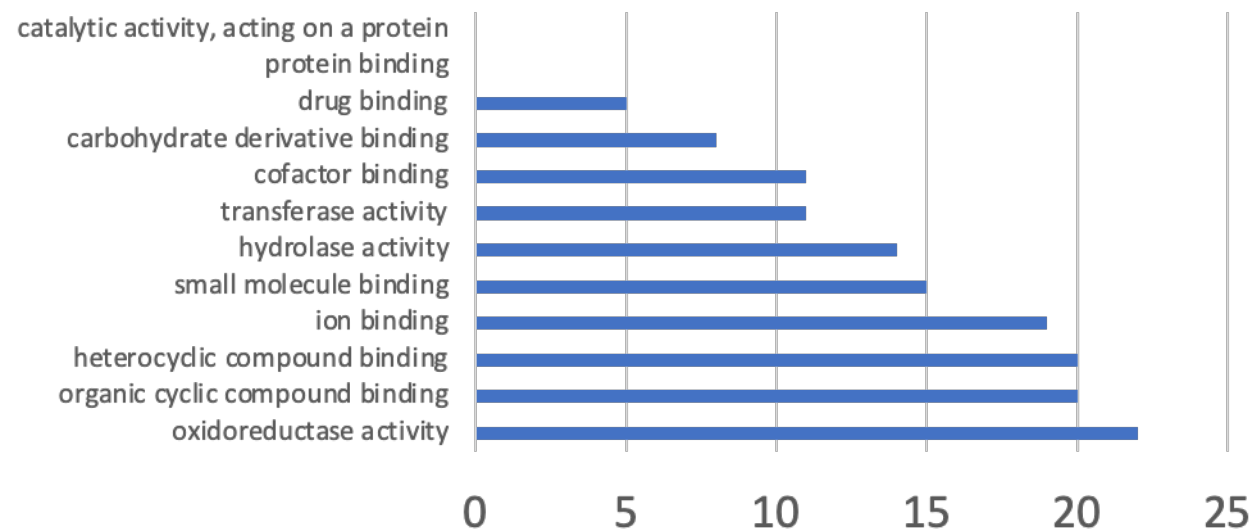


**Figure S7.**

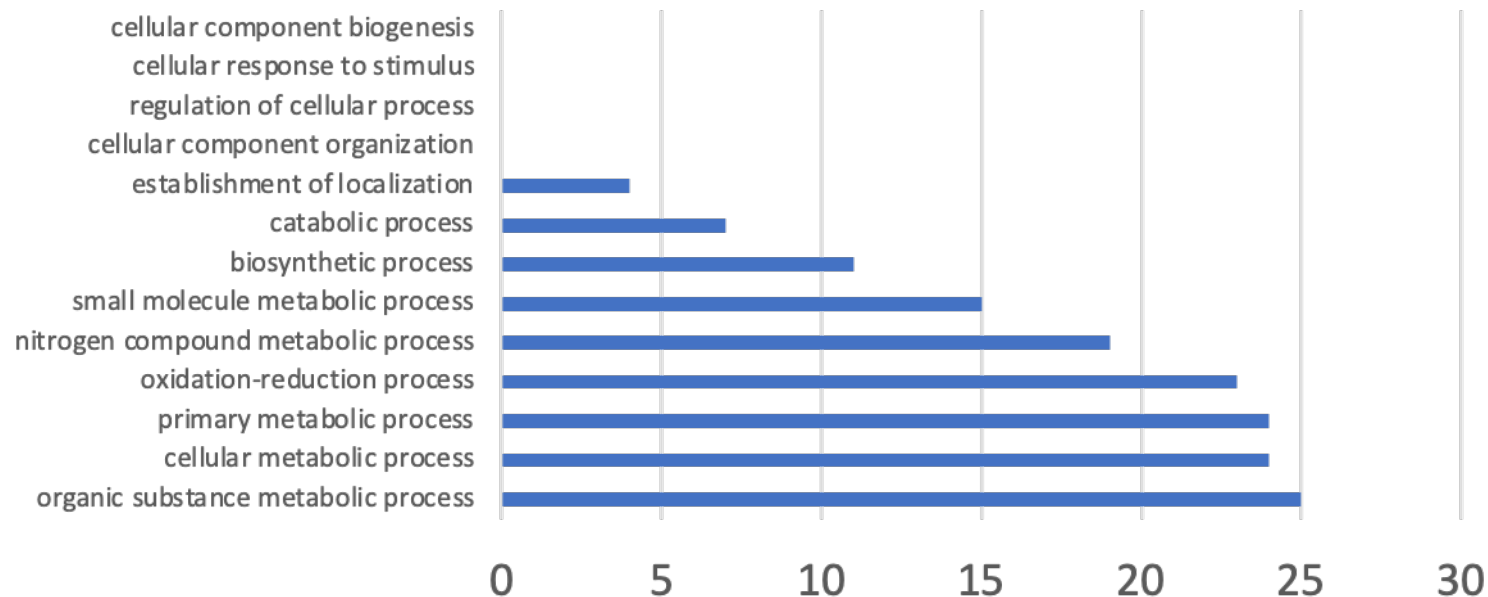
**a) Enzymes**



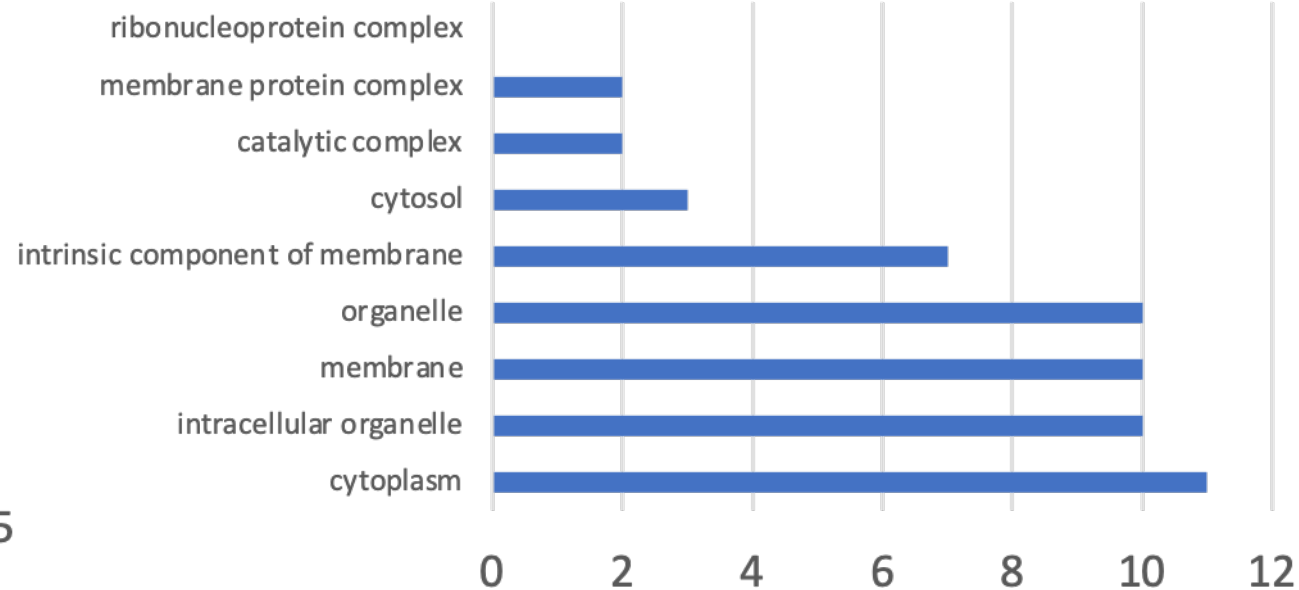
**c) Molecular Function**



**b) Biological Processes**



**d) Cellular Component**



**Figure S8.** PCA analysis.  $\square$  - Control group and  $\triangle$  - *A. bisporus* + *B. velezensis* SN group.

