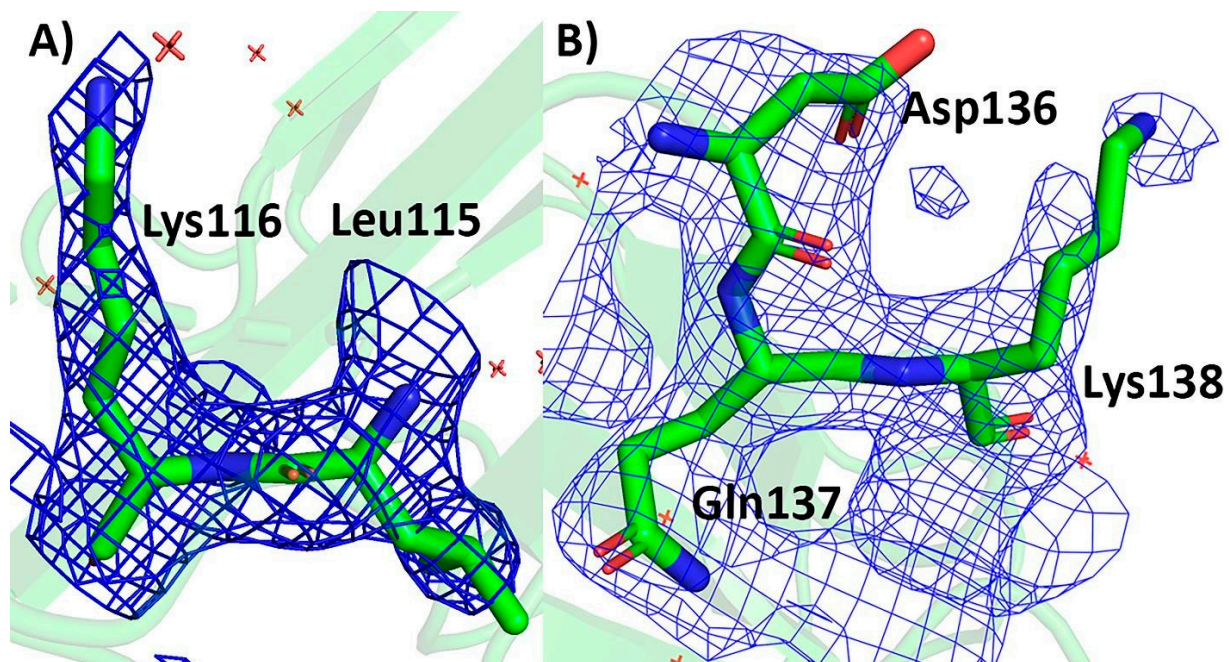
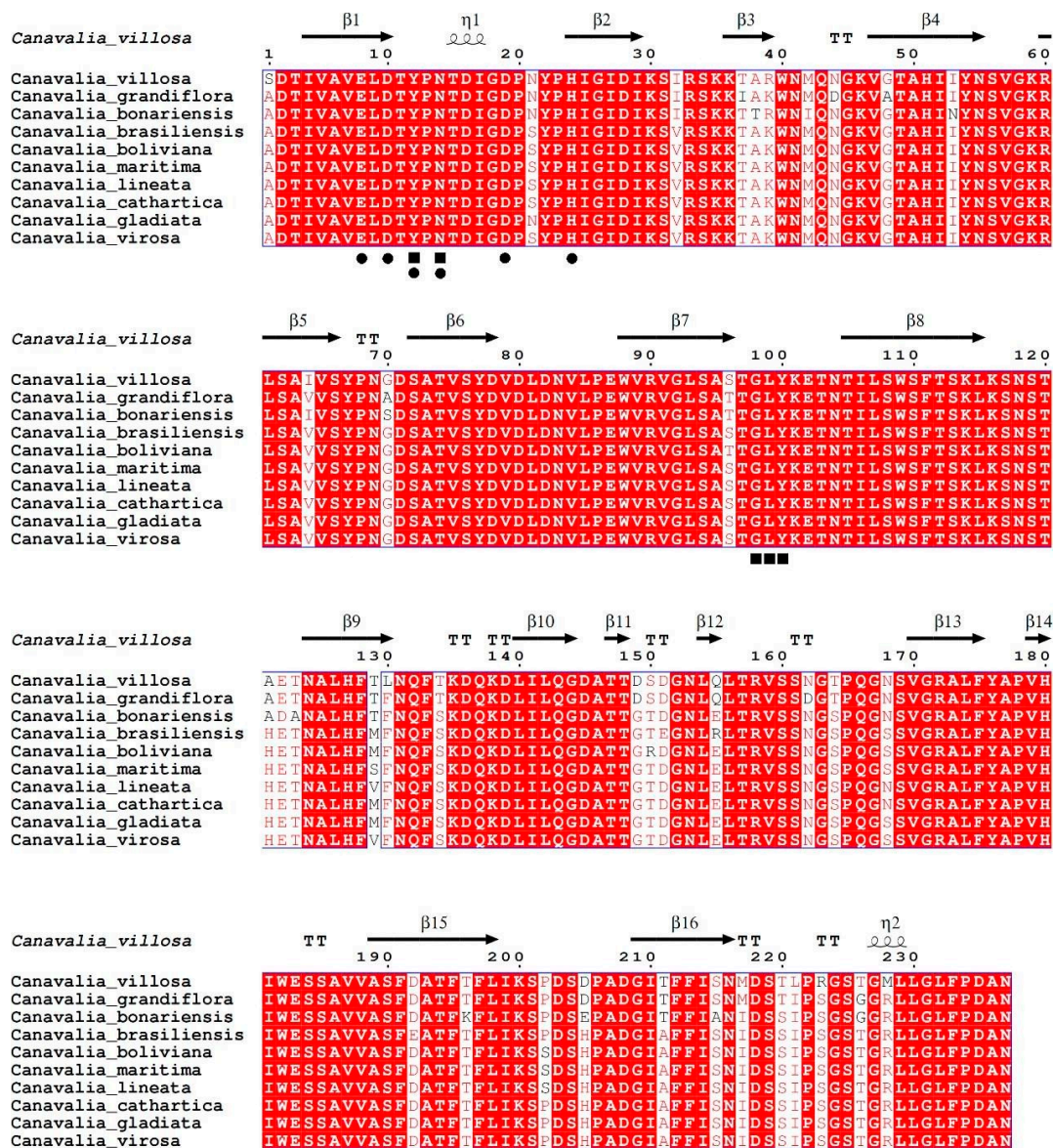


| | | |
|----------|--|-----|
| Contig1 | ttgatccttcaaggtgacgccacaactgattcagatggtaacttacaactcacaagggtg | 60 |
| Contig2 | ttgttccttcaaggtgacgccacagctgattcagatggtaacttacaactcacaagggtg | 60 |
| proCvill | L I L Q G D A T T D S D G N L Q L T R V | 20 |
| Contig1 | tcaagtaatgggactccacagggaacagtgatgggcccgggctttgttctacgccccagtc | 120 |
| Contig2 | tcaagtaatgggactccacagggaacagtgatgggcccgggctttgttctacgccccagtc | 120 |
| proCvill | S S N G T P Q G N S V G R A L F Y A P V | 40 |
| Contig1 | catatttgggaaagtctctgctgtggtggcaagctttgacgccacctttacattttctcata | 180 |
| Contig2 | catatttgggaaagtctctgctgtggtggcaagctttgacgccacctttacattttctcata | 180 |
| proCvill | H I W E S S A V V A S F D A T F T F L I | 60 |
| Contig1 | aagtcacccgacagggatccagctgatggaattaccttcttcatttcaaataatggacagt | 240 |
| Contig2 | aagtcacccgacagggatccagctgatggaattaccttcttcatttcaaataatggacagt | 240 |
| proCvill | K S P D S D P A D G I T F F I S N M D S | 80 |
| Contig1 | accctccctatgggttccactggaatgcttcttgactcttccctgatgctaattgttatc | 300 |
| Contig2 | accctccctatgggttccactggaatgcttcttgactcttccctgatgctaattgttatc | 300 |
| ProCvill | T L P R G S T G M L L G L F P D A N V I | 100 |
| Contig1 | aaaaattccaccaatcttgatttcaacgctgcttataat-----tccgatactattgtt | 354 |
| Contig2 | aaaaattccaccaatcttgatttcaacgctgcttataatccaaattccgatactattgtt | 360 |
| proCvill | K N S T N L D F N A A Y N S N S D T I V | 120 |
| Contig1 | gctgttggaattggatacctatcccaatactgatattggagatccaaattatccacacatt | 414 |
| Contig2 | gctgttggaattggatacctatcccaatcctgatattggagatccaaattatccacacatt | 420 |
| ProCvill | A V E L D T Y P N T D I G D P N Y P H I | 140 |
| Contig1 | ggtatcgatatcaaattctattcgctccaagaaaaccgctaggtggaacatgcaaaatgga | 474 |
| Contig2 | ggtatcgatatcaaattctattcgctccaagaaaaccgctaggtggaacatgcaaaatgga | 480 |
| proCvill | G I D I K S I R S K K T A R W N M Q N G | 160 |
| Contig1 | aaggtaggcacggcacatatcacctataactctgtttgtaagagactaagtgccattggt | 534 |
| Contig2 | aaggtaggcactgcacacatcatctataactctgtttgtaagagactaagtgccattggt | 540 |
| proCvill | K V G T A H I I Y N S V G K R L S A I V | 180 |
| Contig1 | tcttatcctaacgggtgactctgccaccgtctcttatgacgttgacctcgacaatgtcctt | 594 |
| Contig2 | tcttatcctaacgggtgactcttccaccgtctcttatgacgttgacctcgacaatgtcctt | 600 |
| proCvill | S Y P N G D S A T V S Y D V D L D N V L | 200 |
| Contig1 | cctgaatggggttagagttgggctttctgcttcaaccggactcaacaaagaaaccaataacc | 654 |
| Contig2 | cctgaatggggttagagttgggctttctgcttcaaccggactcaacaaagaaaccaataacc | 660 |
| proCvill | P E W V R V G L S A S T G L Y K E T N T | 220 |
| Contig1 | attctc | 660 |
| Contig2 | attctc | 666 |
| proCvill | I L | 222 |

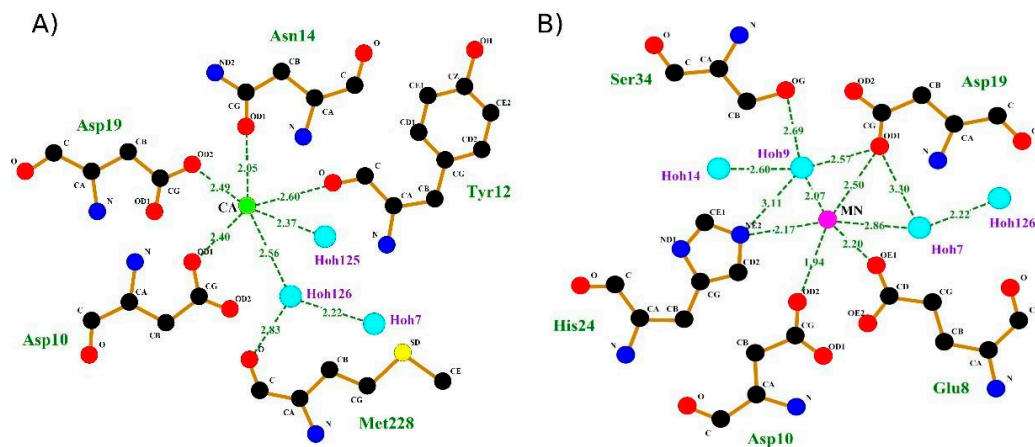
Supplementary Figure S1. Nucleotide sequence of two contigs of Cvill gene and the translated amino acid sequence of the lectin precursor. If more than one amino acid could be coded in the same position due to isoform variations, the most commonly found residue in MS/MSdata was used to depict the translated sequence. The region highlighted in gray is lost during posttranslational processing and the remaining regions are thereafter reconnected in reverse order to assemble the mature Cvill.



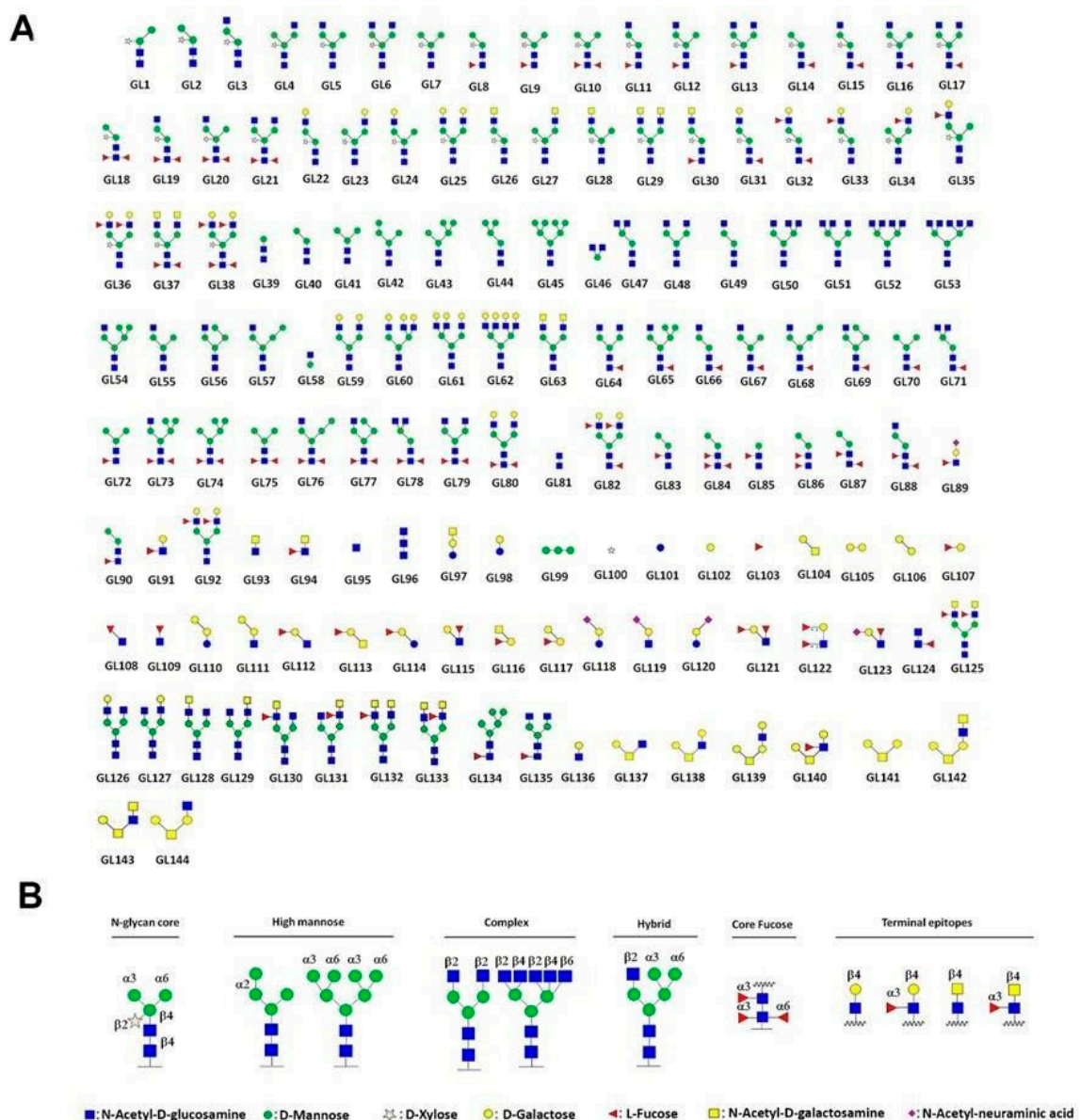
Supplementary Figure S2. Fit of residues Leu115-Lys116 (A) and Asp136-Gln137-Lys138 (B) in the electron density map of Cvill. The electron density map, along with mass spectrometry digestion pattern, and sequence identity with other Diocleinae lectins were used to solve the sequencing information of these two small fragments.



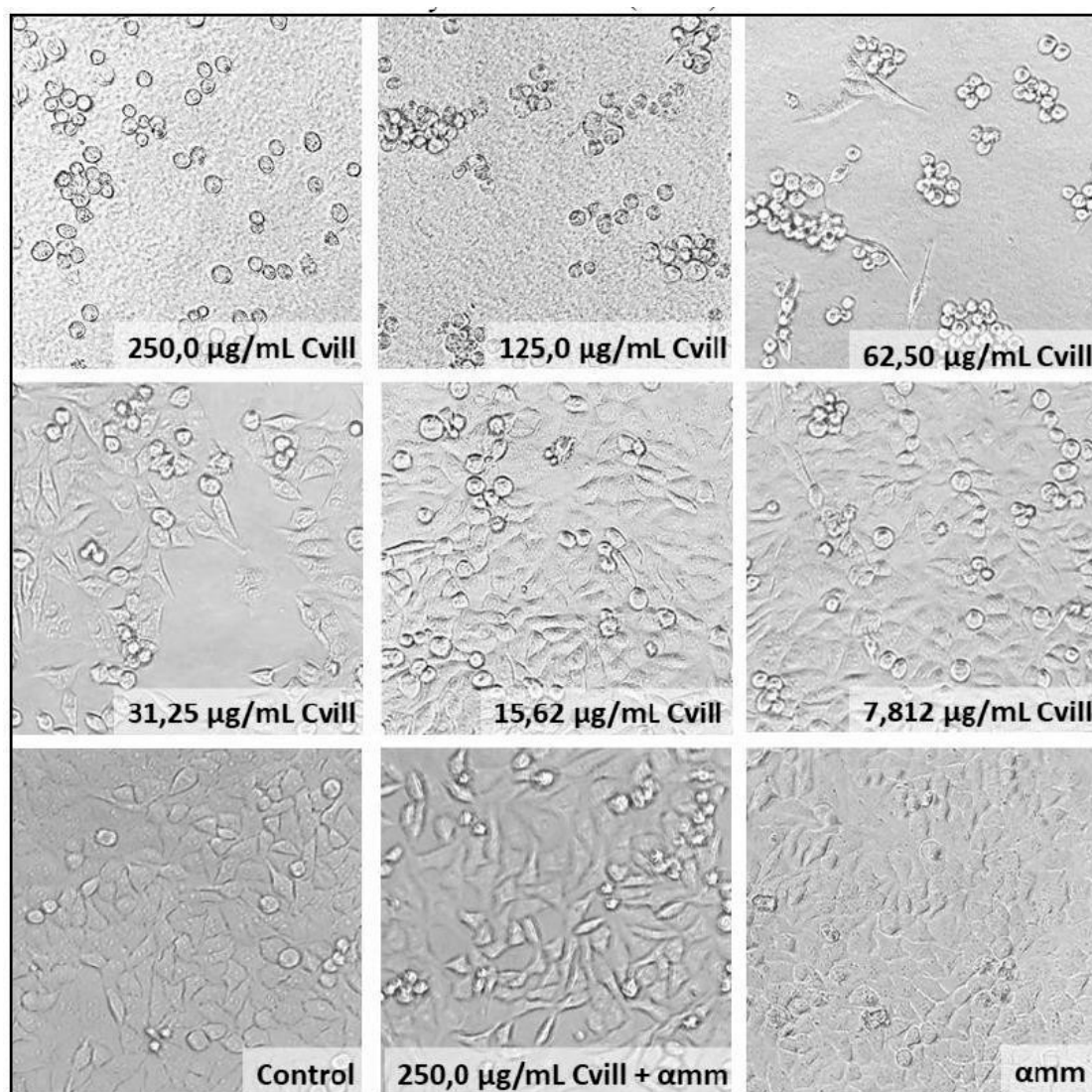
Supplementary Figure S3. Alignment of Cvill with *Canavalia* lectins. Residues involved in the Carbohydrate Recognition Domain (CRD) are represented by a square, while residues involved in the Metal Binding Site are marked with a circle. Sequence alignment was performed using the online tool ClustalW. Sequence similarities and secondary structure prediction were obtained using ESPript 3.0.



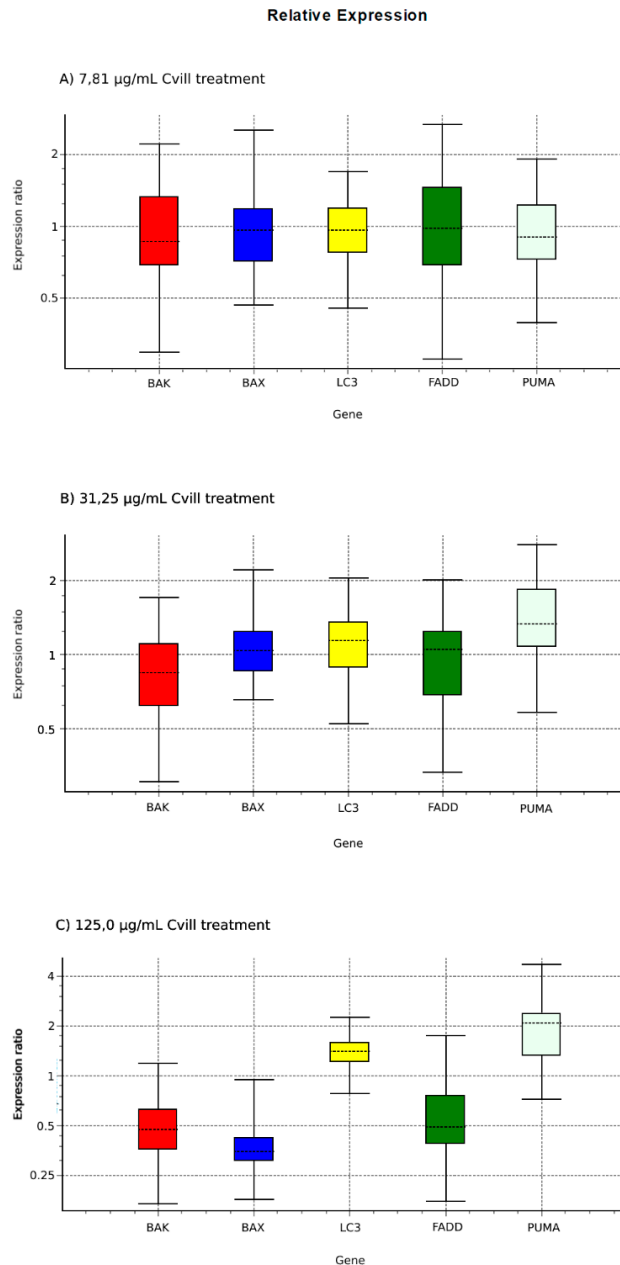
Supplementary Figure S4. Graphical representation of the octahedral coordination of calcium (A) and manganese (B) ions in the metal binding site of Cvilla.



Supplementary Figure S5. Glycan library used in the array experiments. (A) Glycan structures included on the microarrays, (B) Nature of the glycosidic linkages of the N-glycan structures on the microarrays.



Supplementary Figure S6. Morphology of HeLa cells in presence and absence of lectin and α -methyl-D-mannopyranoside. Images were taken at 20x magnification.



Supplementary Figure S7. Relative expression level of genes related to cell death in HeLa cells treated with Cvill at 7.81 $\mu\text{g/mL}$ (A), 31.25 $\mu\text{g/mL}$ (B), and 125.0 $\mu\text{g/mL}$ (C), concentrations for the incubation period of 48 h. The box diagram provides the visualization of data asymmetry and dispersion, in which 50% are distributed within the boxes and 50% are within the range delimited by the lines. The dashed line within the boxes represents the median of the expression ratio values. Boxes that move upwards from the ratio value equal to 1 indicate increased expression in relation to the control, while those which move downwards indicate decreased expression. The two reference genes HPRT1 and GADPH were used to normalize the expression data. The statistics were calculated based on a 95% confidence interval considering 2000 randomizations. The graphics were generated using the REST 2009 program.

| Gene | Primers |
|------------------------|---|
| <i>Apoptosis</i> | |
| <i>PUMA</i> | Fw: 5' ATGCCTGCCTCACCTTCATC 3' Rv: 5' TCAGCCAAAATCTCCCACCC 3' |
| <i>BAX</i> | Fw: 5' AGTAACATGGAGCTGCAGAGG 3' Rv: 5' ATGGTTCTGATCAGTTCCGG 3' |
| <i>BAK</i> | Fw: 5' ACTCTACCCCTGCTCCCATT 3' Rv: 5' CTTGGAGGCTTCTGACACGT 3' |
| <i>FADD</i> | Fw: 5' GTGCGGGAGTCACTGAGAAT 3' Rv: 5' CTCCTGTTCTGGAGGTCACG 3' |
| <i>Autophagy</i> | |
| <i>LC3</i> | Fw: 5' AGAAGGCGCTTACAGCTCAA 3' Rv: 5' AGATTGGTGTGGAGACGCTG 3' |
| <i>Reference genes</i> | |
| <i>GAPDH</i> | Fw: 5' GAAGGTGAAGGTCGGAGTC 3' Rv: 5' GAAGATGGTGATGGGATTTC 3' |
| <i>HPRT1</i> | Fw: 5' TGAGGATTTGGAAAGGGTGTT 3' |

Supplementary Figure S8. Primers applied in the qPCR experiments.