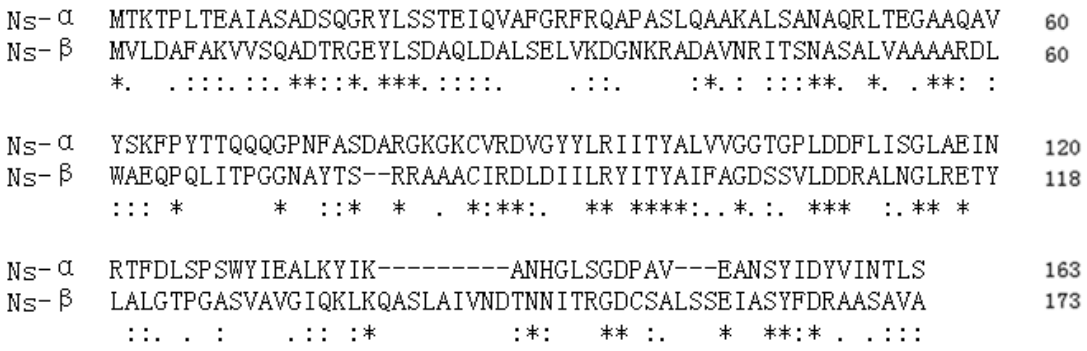
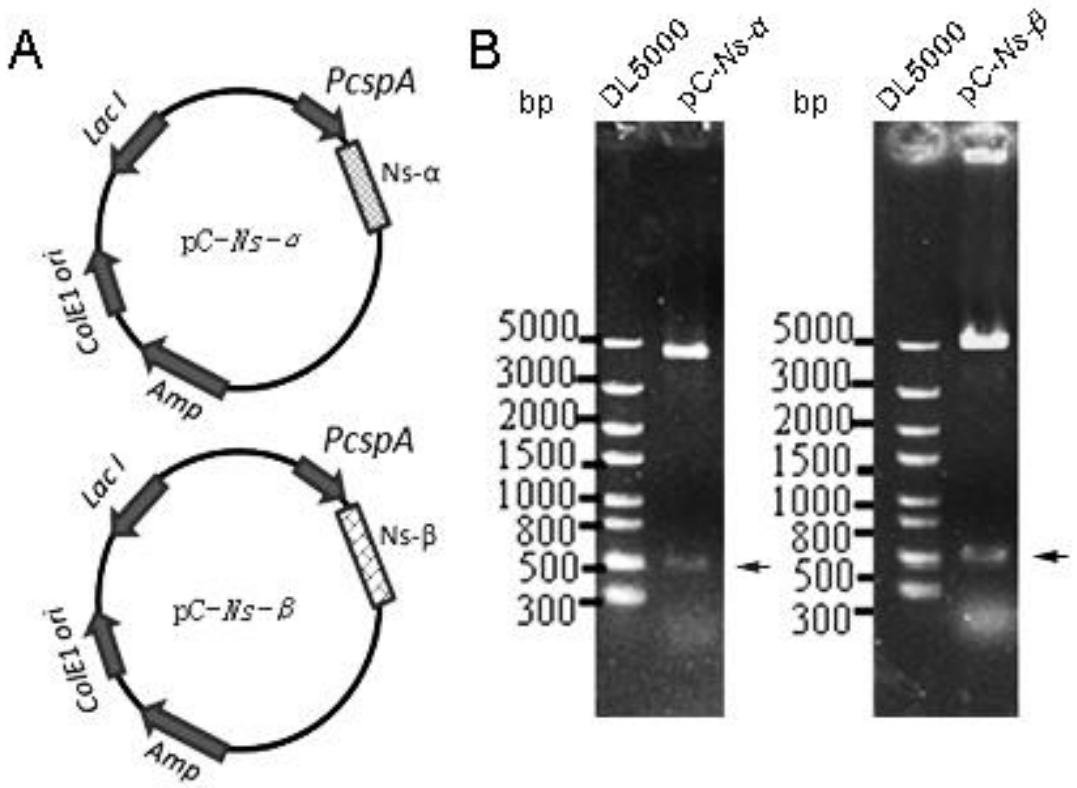


Supp.Figure 1 Sequence alignment for the Ns-α and Ns-β.

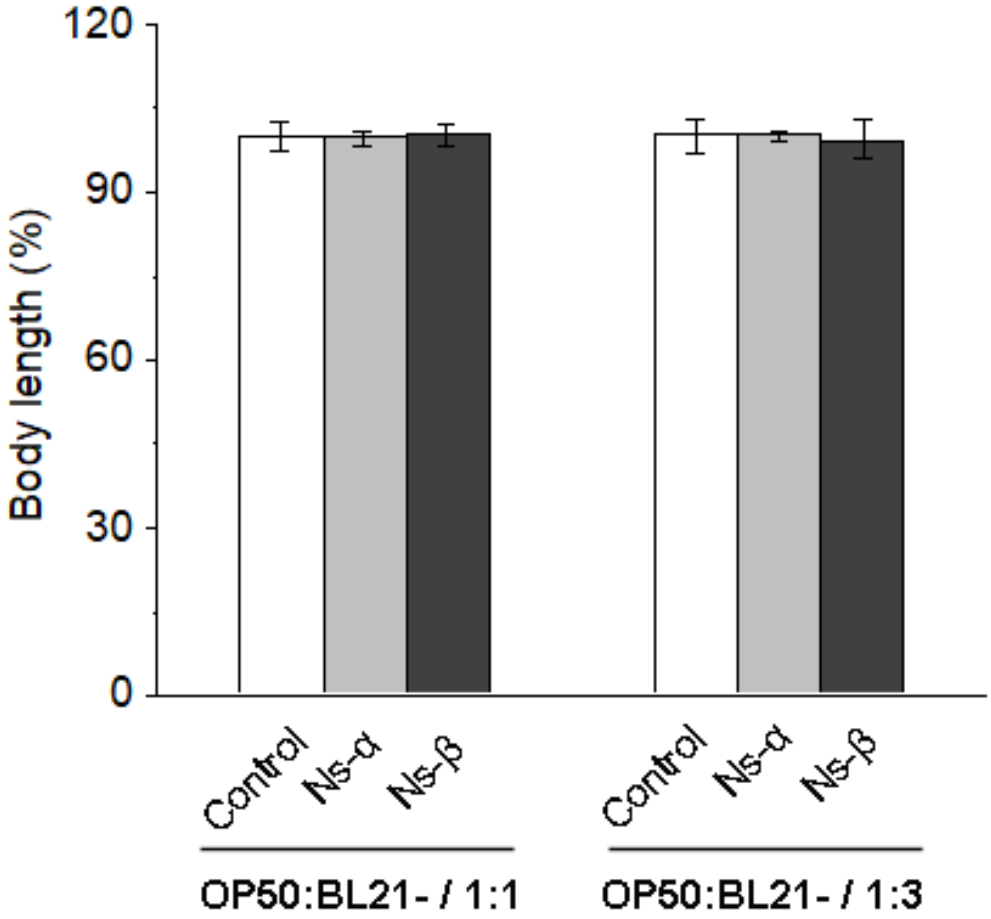
Overall, the two proteins have a low similarity in amino acid residues base on the MAFFT server (L-INS-i strategy; BLOSUM30 scoring matrix; GAP open and extension penalty: 1.53 and 0.123, respectively, and the output format: ClustalW) (https://www.ebi.ac.uk/Tools/msa/mafft/). High conservation, less conserved sites of the amino acid residues were separately indicated by “*” , “:“ or “.” under the sequences, and the cysteine residues are highlighted by inverted triangle in black.



Supp.Figure 2 Plasmid map of the constructed expression vectors and identification of the vectors by restriction endonuclease digestion.

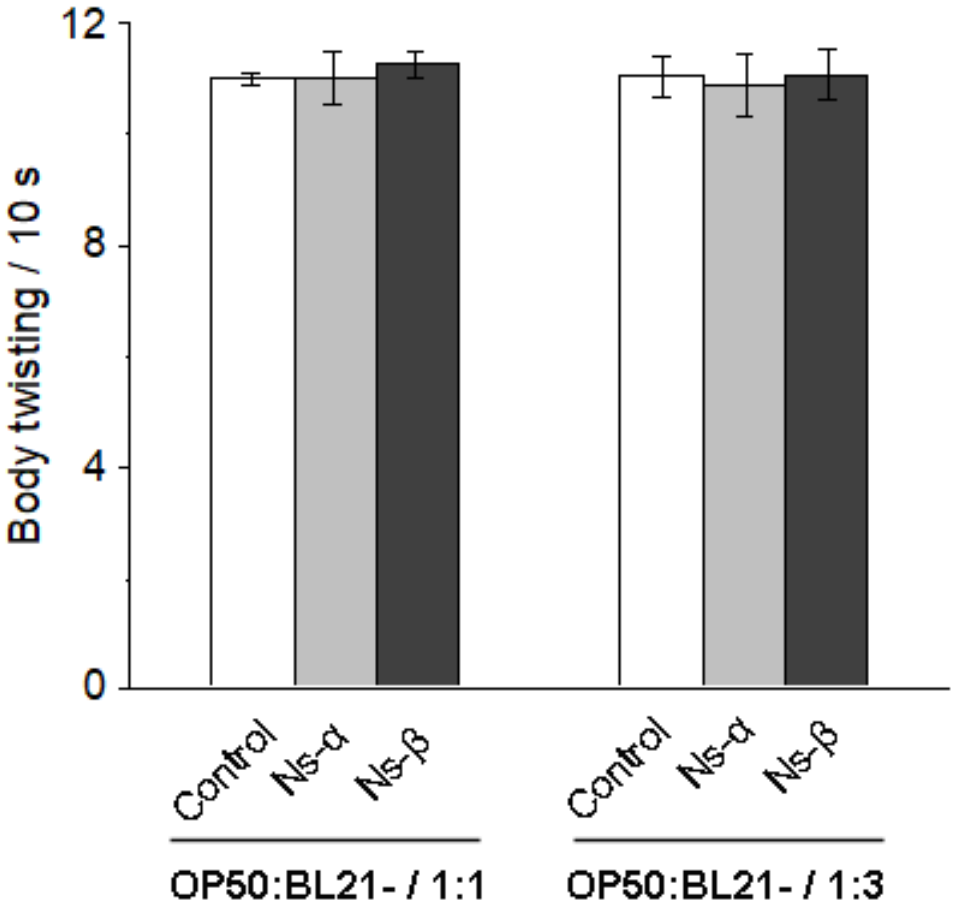
A, Maps for the expression vector based on the original vector pCold I (here referred to as pC, simplly). Ns-α and Ns-β CDS were recombined into the Nde I and EcoR I sites, making the genes under the control of the *PcspA* promoter.

B, Identification the plasmids by restriction endonuclease digestion. The pC-Ns-α and -Ns-β were separately double digested with NdeI and EcoRI. And the reliant signals of Ns-α and Ns-β were indicated by the target bands, which were highlighted two black arrows on the right of the gel, and corresponding molecular weight were referred to DNA marker DL5000.



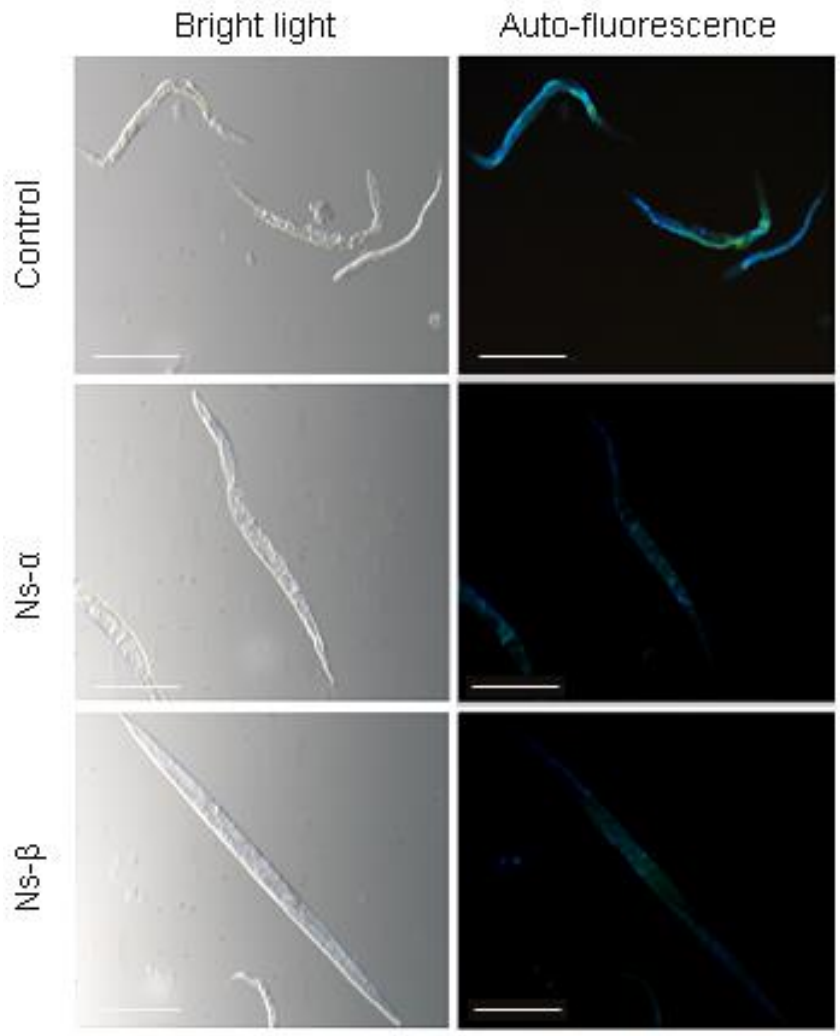
Supp.Figure 3 Characterization of the nematode body lengths.

Synchronised L1 larvae were incubated in S-medium containing the bacterial mixtures as up described. The length of the nematodes in the tree groups was respectively analysed during flowing three days via ImageJ. For each sample, three repeats were conducted to comparing with the body size as mean values ±SD, n≥20.



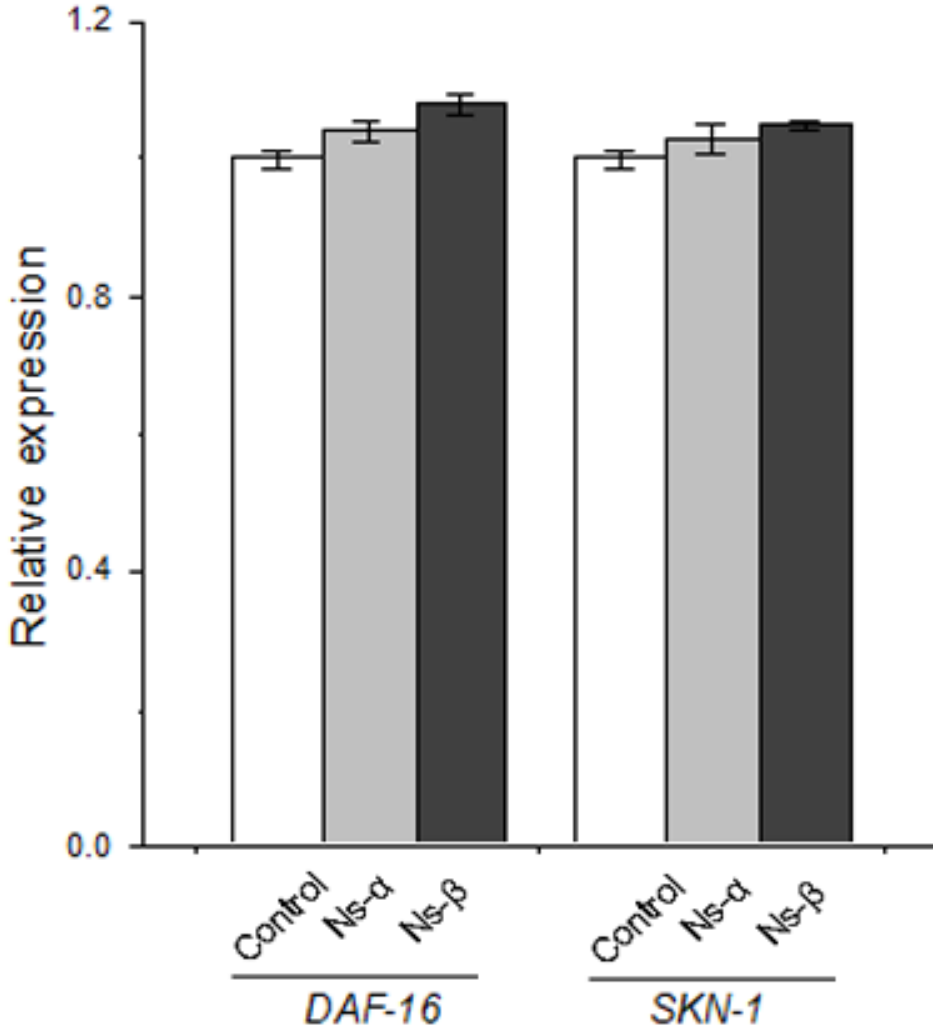
Supp.Figure 4 Without the protein Ns-α and Ns-β nematode motility displays similarly.

The mobility of nematodes was unchanged if without the engineered proteins Ns-α and Ns-β treatment. L4 stage C. elegans were cultured in S liquid medium for 3 days for each treatment, after which the nematodes were collected and their body bends were observed at 10 s intervals. For each sample n≥20, and three replicates were conducted.



Supp.Figure 5 Lipofuscin accumulation of the nematode.

Intestinal lipofuscin was assayed in synchronized (day 8 of adulthood) nematodes from the three treated groups. At depicted time points the nematodes were transferred in 10 μl medium to a microscope slide and mixed with 10 μl of levamisole (20mM). Images were then taken using a fluorescence microscope (wavelength for excitation/ emission was selected as 350 nm/470 nm). The relative fluorescence intensity was quantified using the ImageJ software. For each sample, three repeats were conducted to comparing the body size as mean values ±SD, n≥10.



Supp.Figure 6 Relative expression of the redox regulation-related genes in nematodes.

The transcript levels of *DAF-16* and *SKN-1* in the two groups of nematodes treated with the two proteins showed little changes when compared to the control group. Quantitative reverse transcription polymerase chain reaction (RT-PCR) was conducted with specific primer pairs corresponding to the genes listed in the supplementary table. *Actin* was used an endogenous reference.