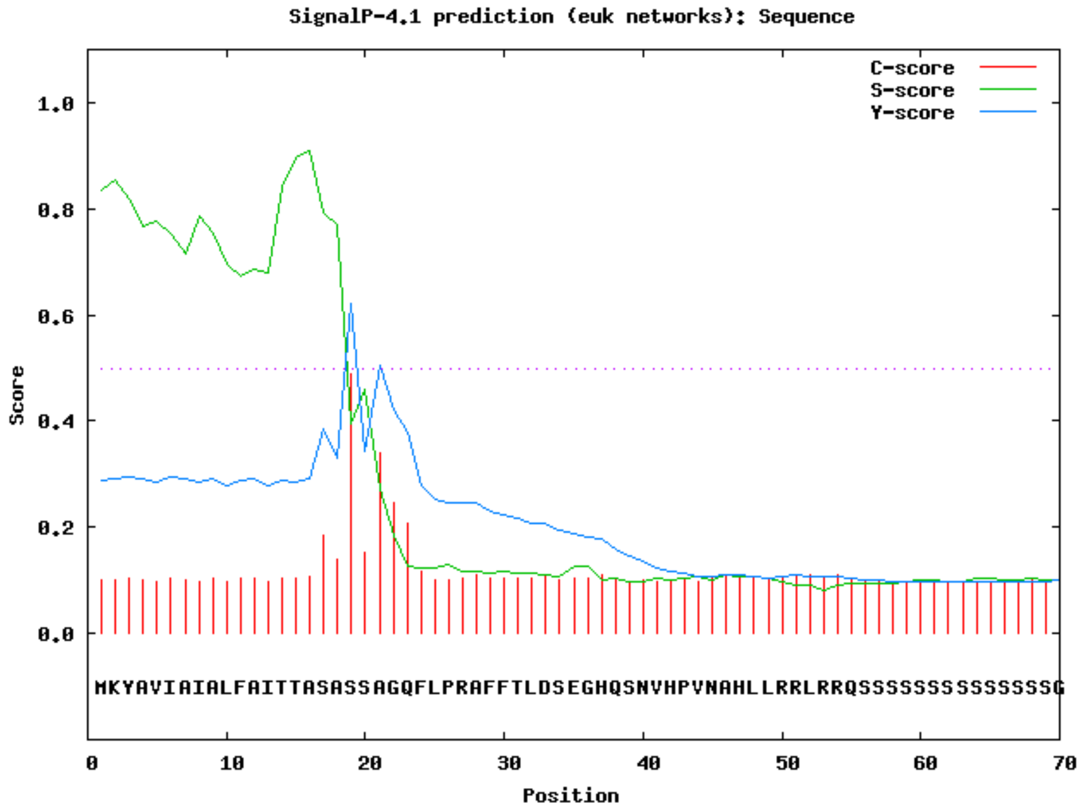
Table S2 Protein sequences and prediction of signal peptides. The predictions for signal peptides were generated with the SignalP 4.1 software (http://www.cbs.dtu.dk/services/SignalP/) from the Center for Biological Sequence Analysis of the Technical University of Denmark Lyngby.

SignalP 4.0: discriminating signal peptides from transmembrane regions
Petersen TN., Brunak S., von Heijne G. & Nielsen H.
Nature Methods, 8:785-786, 2011

CG10200 (*hui*) predicted Protein 1

```
MKYAVIAIALFAITTASASSAGQFLPRAFFTLDSEGHQSNVHPVNAHLLR
RLRRQSSSSSSSSSSSSSSGGNVFTYASHSVQNADGSGHSGSSYTQQAAA
PVLGGVSFDERFGESSLTGGDNYYPTYNGYTSAASISSNSGVGSTGSYQH
ISGVGPIPATQIQQTVAVVDASGNQKVTNIQGATDSNGVLNIKKTESTYS
SK
```

```
# SignalP-4.1 euk predictions
>Sequence
```



```
# Measure  Position  Value    Cutoff   signal peptide?

  max. C     19        0.490

  max. Y     19        0.621
```

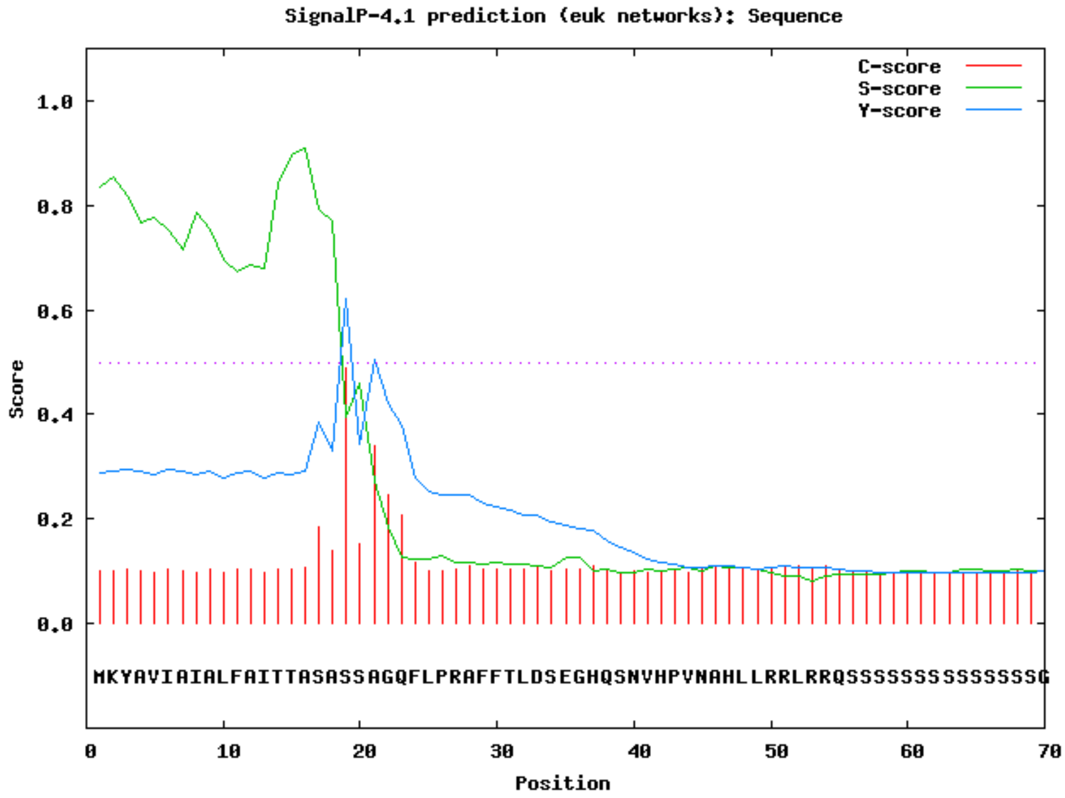
```
  max. S    16       0.910

  mean S     1-18    0.778

       D     1-18    0.706   0.340   YES

Name=Sequence  SP='YES' Cleavage site between pos. 18 and 19: ASA-SS D=0.706
D-cutoff=0.340 Networks=SignalP-noTM

# data

# gnuplot script
```

```
Signal peptides: 1
# processed fasta entries
# gff file of processed entries
```

CG10200 (*hui*) predicted Protein 2

```
MKYAVIAIALFAITTASASSAGQFLPRAFFTLDSEGHQSNVHPVNAHLLR
RLRRQSSSSSSSSSSSSSSGGNVFTYASHSVQNADGSGHSGSSYTQQAAA
PVLGGVSFDERFGESSLTGGDNYYPTYNGYTSAASISSNSGVGSTGSYQH
ISGVGPIPATQIQQTVAVVDASGNQKVTNIQGATDSNGVLNIKKTESTYS
SK
```

```
# SignalP-4.1 euk predictions
>Sequence
```



```
# Measure  Position  Value    Cutoff   signal peptide?

  max. C     19        0.490

  max. Y     19        0.621

  max. S     16        0.910

  mean S      1-18     0.778

       D      1-18     0.706   0.340    YES

Name=Sequence  SP='YES' Cleavage site between pos. 18 and 19: ASA-SS D=0.706
D-cutoff=0.340 Networks=SignalP-noTM

# data

# gnuplot script
```

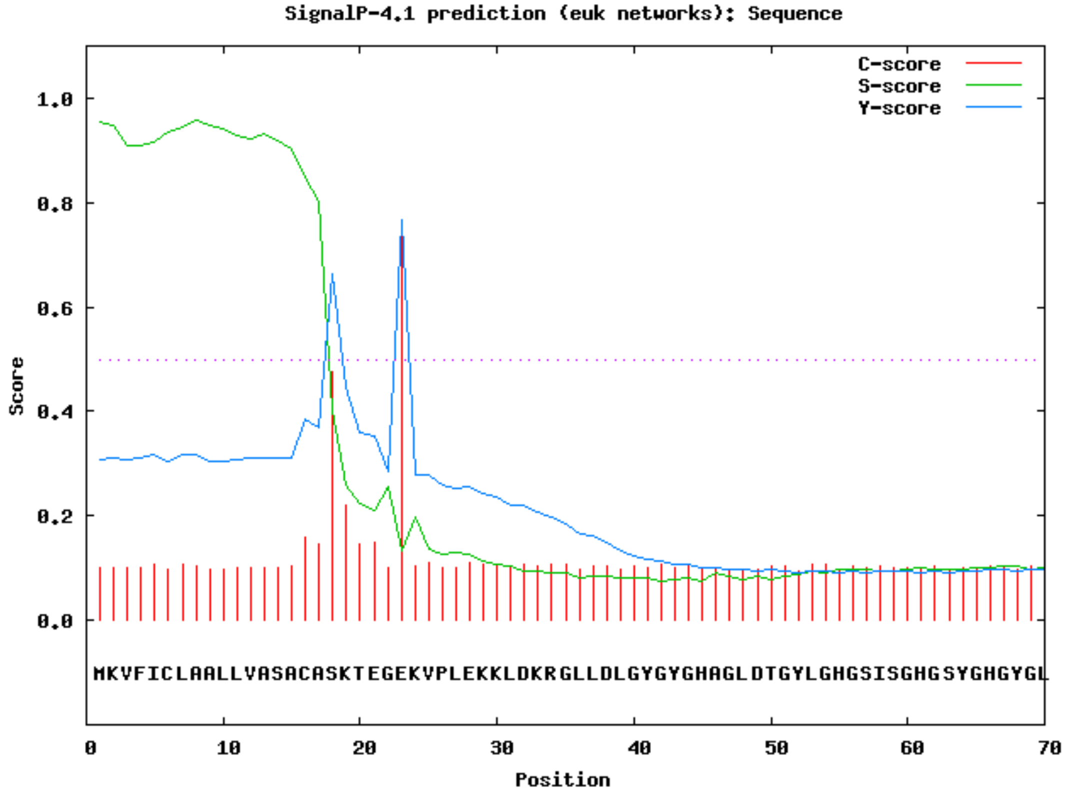
```
Signal peptides: 1
# processed fasta entries
# gff file of processed entries
```

CG16884 predicted Protein

```
MKVFICLAALLVASACASKTEGEKVPLEKKLDKRGLLDLGYGYGHAGLDT
GYLGHGSISGHGSYGHGYGLTGYSAPAAVAVGHSGPAIAVGHTAPAVAVH
HAPAPYVISKQADVHKTITITKGIPVPVHVDRPYPVVHEKRVPVEVKVPV
PQPYEVIRKVPVTVKEYVKVPVPVPQPYEVIRHEKVPVHVPVDRPVPVEV
PRPYPVPVAKPYPVYVEKAVNVQVPVHVDRPYPVYVKVPVVSHSVVKHAP
TVAVSSYPVSAIGHDATVYSDHHGYHK
```

```
# SignalP-4.1 euk predictions
```

>Sequence



```
# Measure  Position  Value    Cutoff   signal peptide?

  max. C    23       0.762

  max. Y    23       0.767

  max. S     8       0.958

  mean S     1-22    0.772
```

```
          D     1-22    0.770   0.340   YES

Name=Sequence   SP='YES' Cleavage site between pos. 22 and 23: TEG-EK D=0.770
D-cutoff=0.340 Networks=SignalP-noTM

# data

# gnuplot script
```

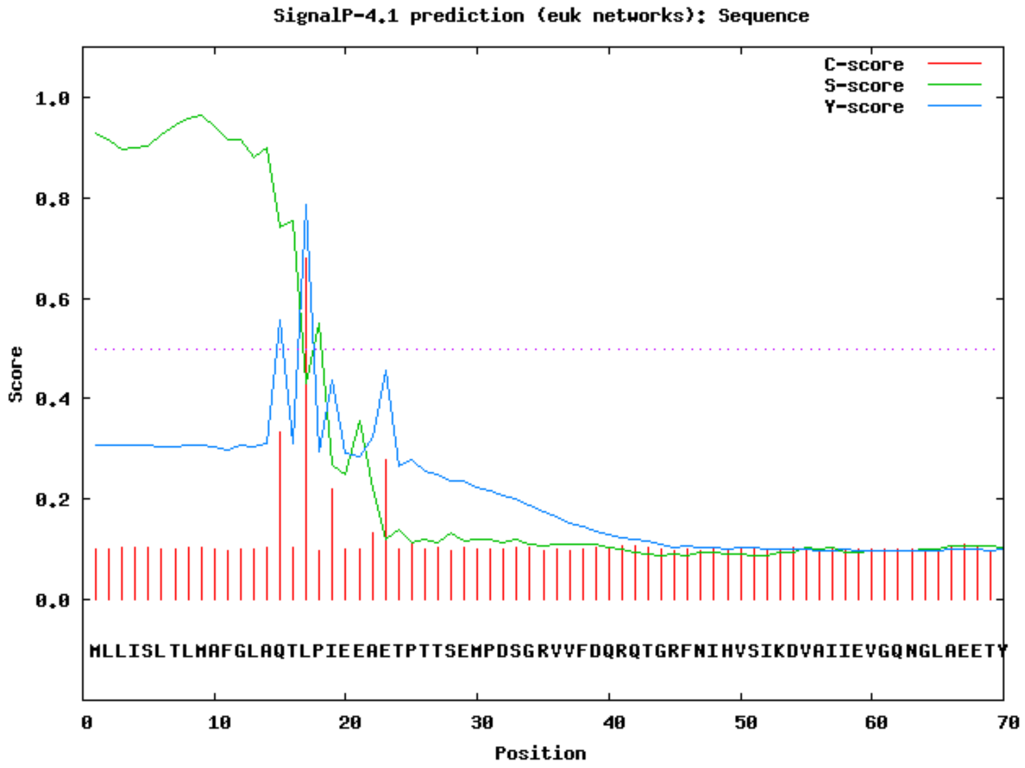
```
Signal peptides: 1
# processed fasta entries
# gff file of processed entries
```

CG15905 predicted Protein

```
MLLISLTLMAFGLAQTLPIEEAETPTTSEMPDSGRVVFDQRQTGRFNIHV
SIKDVAIIEVGQNGLAEETYNDEEDYYYDDSALTVKPIKLTTGTSSTTTT
STTSATLPESTVSTVAPTTEATQLNTSLNLLADIAASGITKPKSRLNNLM
IVETPIGGLTKPLHHPLHARSKDIPSMAAAAPTALITPPTLRENIEYTPP
KGHNSPIFKVKVQRSSVPATKKPARCRNHQVRDAQGKCTDSIYRKLYSML
MGMNFPFLAAANAAESA
```

```
# SignalP-4.1 euk predictions
```

>Sequence



```
# Measure  Position  Value    Cutoff   signal peptide?

  max. C    17       0.680

  max. Y    17       0.785

  max. S     9       0.963

  mean S     1-16    0.899

       D     1-16    0.846   0.340   YES

Name=Sequence  SP='YES' Cleavage site between pos. 16 and 17: AQT-LP D=0.846
D-cutoff=0.340 Networks=SignalP-noTM

# data

# gnuplot script
```

```
Signal peptides: 1
# processed fasta entries
# gff file of processed entries
```