

Figure S1. Mass spectrometric coverage of immunopurified bands.

Regions identified as peptides hits are colored orange and boxed. For band 1, turquoise marks the site of the first amino acid of each exon. Yellow marks amino acids that differ from the genome strain ME49. Pink marks a mass spec peptide annotated in ToxoDB Genome Browser that was not identified in our peptide sequences, but was identified by the Einstein high throughput proteomics project. The RH amino acid sequence is shown in Band 1 and the ME49 sequence in the others.

Band 1

```
MAPDSCRDPD VGAPNGRGS L KEVSSSFCTT SSLFSRSL SLL FLLFSLFASP RQLSLTSAIS
LEPSPGSPAA AOVSSGVAPK PVEKESGNGG QVKVHLKRDE AGRPLPVSA S SLFAAEKPHE
EEEREVL R VG VDAGDSRREK RAVEPTRMLA SIDPQHPSVS AOVVSPAPSS SLTAPPTARP
RDEGNNTCVR NNETCQRRE R YA EKSIQRHR HDSTSSRESV AFASFGSSKN SFATAYAPFD
DEDEEGALAH LKNKVKTA VS CPAAK ILLGI SGVVALGTLG IKYTR NVLRR RRR EQLQRPP
TPFTDLLGHV LLKR ERGKHA AETR ELATGD VLGKPGSVTA LYFSGRGVEE MLQTRGYQPF
TPRLER IVEG CR ERGQELNV VYLSADADSS DAEKHFSDMS WYALPFDDAP GQAR IHR LFR
KFRVSTLPHV VLLDSNARV L NSHAYASMIV RPTAFPWKQ TPAELLGDAF VSGEGQKVGK
DALDNNVVG I YFSASWCPPC QAFTP KLV EA LKGWKEQ GKD VSVV FVS NDR DEKAFEEYFK
KMEGFVAIPF ADTTRALLQ EALNVR SLPT LVWLSK EGEV LTR RGVPHV L EDPEGRNFPW
KDKDVNDVSD SVEGIADEPA LILFMEHLDE KAKEEQEKAL EEAMQALQS Q KNDGGVPPLV
RLFTAKSLSP RSIALRRICR QDPPDADKEK KGPILTIVDL LDQSYFTALQ EPGRIFSADE
IVAFINKFR R EELERN SLAV PE
```

Band 2

```
MAPDSCRDPD VGAPNGRGS L KEVSSSFCTT SSLFSRSL SLL FLLFSLFASP RQLSLTSAIS
LEPSPGSPAA AOVSSGVAPT PVEKESGNGG QVKVHLKRDE AGRPLPVSA S SLFAAEKPHE
EEEREVL R VG VDAGDSRREK RAVEPTRMLA SIDPQHPSVS AOVVSPAPSS SLTAPPTARP
RDEGNNTCVR NNETCQRRE R YA EKSIQRHR HDSTSSRESV AFASF GSSKN SFATAYAPFD
DEDEEGALAH LKNKVKTA VS CPAAK ILLGI SGVVALGTLG IKYTR NVLRR RRR EQLQRPP
TPFTDLLGHV LLKR ERGKHA AETR ELATGD VLGKPGSVTA LYFSGRGVEE MLQTRGYQPF
TPRLER IVEG CR ERGQELNV VYLSADADSS DAEKHFSDMS WYALPFDDAP GQAR IHR LFR
KFRVSTLPHV VLLDSNARV L NSHAYASMIV RPTAFPWKQ TPAELLGDAF VAGEGQK VGK
DALDNNVVG I YFSASWCPPC QAFTP KLV EA LKGWKEQ GKD VSVV FVS NDR DEKAFEEYFK
KMEGFVAIPF ADTTRALLQ EALNVR SLPT LVWLSK EGEI LTR RGVPHV L EDPEGRNFPW
KDKDVNDVSD SVEGIADEPA LILFMEHLDE KAKEEQEKAL EEAMQALQS Q KNDGGVPPLP
RLFTAKSLSP RSIALRRICR QDPPDADKEK KGPILTIVDL LDQSYFTALQ EPGRIFSADE
IVAFINKFR R EELERN SLAV PE
```

Band 3

```
MAPDSCRDPD VGAPNGRGS L KEVSSSFCTT SSLFSRSL SLL FLLFSLFASP RQLSLTSAIS
LEPSPGSPAA AOVSSGVAPT PVEKESGNGG QVKVHLKRDE AGRPLPVSA S SLFAAEKPHE
EEEREVL R VG VDAGDSRREK RAVEPTRMLA SIDPQHPSVS AOVVSPAPSS SLTAPPTARP
RDEGNNTCVR NNETCQRRE R YA EKSIQRHR HDSTSSRESV AFASFGSSKN SFATAYAPFD
DEDEEGALAH LKNKVKTA VS CPAAK ILLGI SGVVALGTLG IKYTR NVLRR RRR EQLQRPP
TPFTDLLGHV LLKR ERGKHA AETR ELATGD VLGKPGSVTA LYFSGRGVEE MLQTRGYQPF
TPRLER IVEG CR ERGQELNV VYLSADADSS DAEKHFSDMS WYALPFDDAP GQAR IHR LFR
KFRVSTLPHV VLLDSNARV L NSHAYASMIV RPTAFPWKQ TPAELLGDAF VAGEGQK VGK
DALDNNVVG I YFSASWCPPC QAFTP KLV EA LKGWKEQ GKD VSVV FVS NDR DEKAFEEYFK
KMEGFVAIPF ADTTRALLQ EALNVR SLPT LVWLSK EGEI LTR RGVPHV L EDPEGRNFPW
KDKDVNDVSD SVEGIADEPA LILFMEHLDE KAKEEQEKAL EEAMQALQS Q KNDGGVPPLP
```

RLFTAKSLSP RSIALRRICR QDPPDADKEK **KGPILTIVDL LDQSYFTALQ EPGRIFSADE**
IVAFINKFRR EELERNSLAV PE

Bands 4/5

MAPDSCRDPD VGAPNGRGS L KEVSSSFCTT SSLFSRLSLL FLLFSLFASP RQLSLTSAIS
LEPSPGSPAA AQVSSGVAPT PVEKESGNGG QVKVHLKRDE AGRPLPVSA SLFAAEKPHE
EEEREVLRVG VDAGDSRREK RAVEPTRMLA SIDPQHPSVS AQVVSPAPSS SLTAPPTARP
RDEGNNTCVR NNETCQRER YAEKSIQRHR HDSTSSR **ESV AFASFGSSKN SFATAYAPFD**
DEDEEGALAH LKNKVKTAVS CPAAKILLGI SGVVALGTLG IKYTRNVLRR RRR **EGLQRPP**
TPFTDLLGHV LLKRERKHA AETR **ELATGD VLGKPGSVTA LYFSGR**GVEE MLQTRGYQPF
TPRLERIVEG CRER **GOELNV VYLSADADSS DAEK**HFS DMS WYALPFDDAP GQARIHRLFR
KFR **VSTLPHV VLLDSNARVL NSHAYASMIV RPTAFPWK**KQ TPAELLGDAF VAGEGQKVGK
DALDNNVGI YFSASWCPPC QAFTPKLVEA LKGWKEQGK **D VSVVVSNDR DEK**AFE EYFK
KMEGFVAIPF ADTTR **RALLQ EALNVR**SLPT LVWLSKEGEI LTR **RGVPHVL EDPEGRNFPW**
KDKDVNDVSD SVEGIADEPA LILFMEHLDE KAKEEQEKAL EEAMQALQSQ KNDGGVPLP
RLFTAKSLSP RSIALRRICR QDPPDADKEK **KGPILTIVDL LDQSYFTALQ EPGRIFSADE**
IVAFINKFRR EELERNSLAV PE