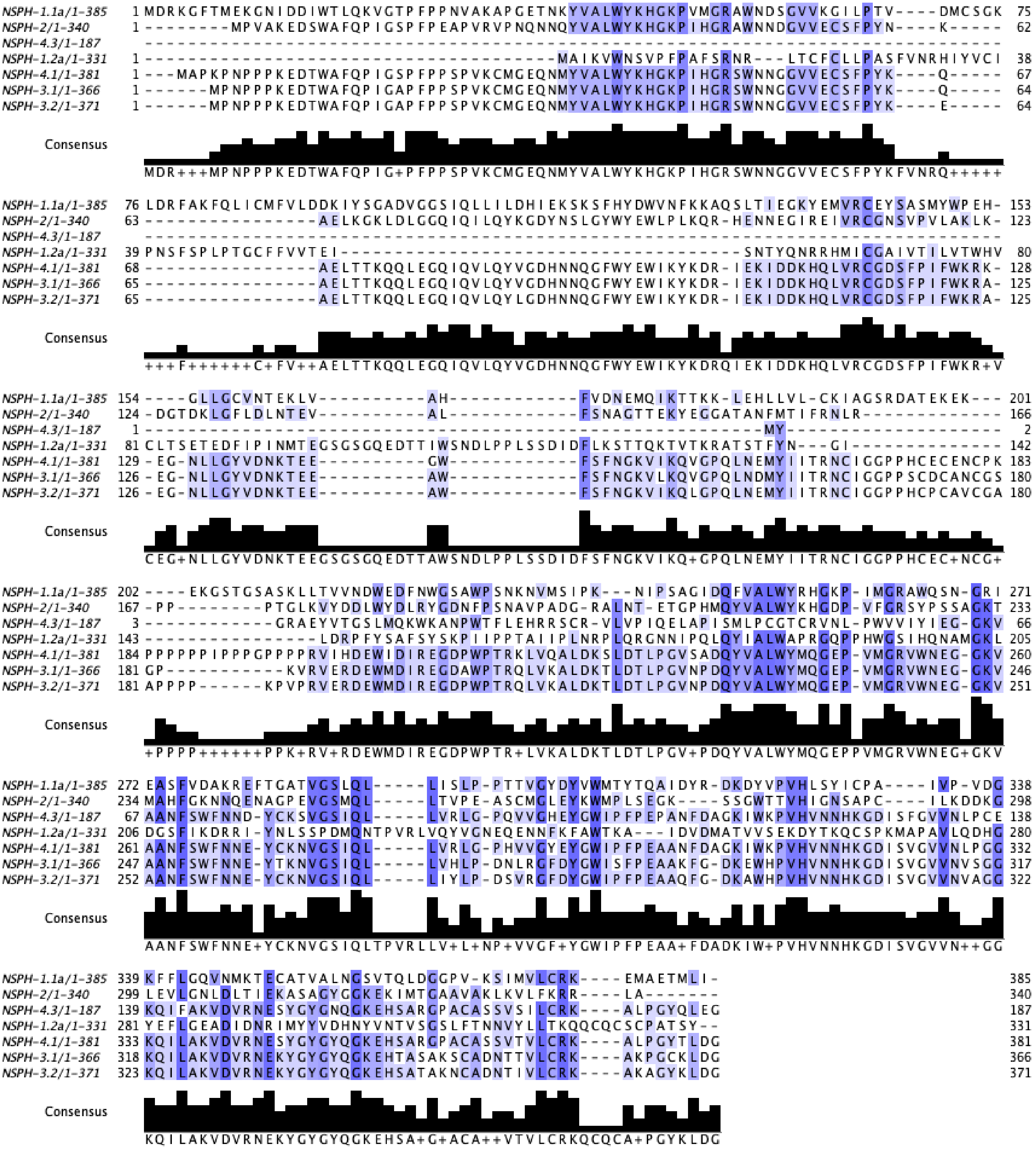

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NSPH-1.1a/1-385   1 MDRKGFTMEKGNIDDIWTLQKVGTPFPPNVAKAPGETNKYVALWYKHGKPVMGRAWNDSGVVKGILPTV----DMCSGK  75
NSPH-2/1-340      1 --------MPVAKEDSWAFQPIGSPFPEAPVRVPNQNNQYVALWYKHGKPIHGRAWNNDGVVECSFPYN----K-----  62
NSPH-4.3/1-187      -------------------------------------------------------------------------------
NSPH-1.2a/1-331   1 --------------------------------------MAIKVWNSVPFPAFSRNR---LTCFCLLPASFVNRHIYVCI  38
NSPH-4.1/1-381    1 ---MAPKPNPPPKEDTWAFQPIGSPFPPSPVKCMGEQNMYVALWYKHGKPIHGRSWNNGGVVECSFPYK----Q-----  67
NSPH-3.1/1-366    1 ------MPNPPPKEDTWAFQPIGAPFPPSPVKCMGEQNMYVALWYKHGKPIHGRSWNNGGVVECSFPYK----Q-----  64
NSPH-3.2/1-371    1 ------MPNPPPKEDTWAFQPIGAPFPPSPVKCMGEQNMYVALWYKHGKPIHGRSWNNGGVVECSFPYK----E-----  64

Consensus           MDR+++MPNPPPKEDTWAFQPIG+PFPPSPVKCMGEQNMYVALWYKHGKPIHGRSWNNGGVVECSFPYKFVNRQ+++++

NSPH-1.1a/1-385  76 LDRFAKFQLICMFVLDDKIYSGADVGGSIQLLILDHIEKSKSFHYDWVNFKKAQSLTIEGKYEMVRCEYSASMYWPEH- 153
NSPH-2/1-340     63 ----------------AELKGKLDLGGQIQILQYKGDYNSLGYWYEWLPLKQR-HENNEGIREIVRCGNSVPVLAKLK- 123
NSPH-4.3/1-187      -------------------------------------------------------------------------------
NSPH-1.2a/1-331  39 PNSFSPLPTGCFFVVTEI-------------------------------------SNTYQNRRHMICGAIVTILVTWHV  80
NSPH-4.1/1-381   68 ----------------AELTTKQQLEGQIQVLQYVGDHNNQGFWYEWIKYKDR-IEKIDDKHQLVRCGDSFPIFWKRK- 128
NSPH-3.1/1-366   65 ----------------AELTTKQQLEGQIQVLQYVGDHNNQGFWYEWIKYKDR-IEKIDDKHQLVRCGDSFPIFWKRA- 125
NSPH-3.2/1-371   65 ----------------AELTTKQQLEGQIQVLQYLGDHNNQGFWYEWIKYKDR-IEKIDDKHQLVRCGDSFPIFWKRA- 125

Consensus           +++F++++++C+FV++AELTTKQQLEGQIQVLQYVGDHNNQGFWYEWIKYKDRQIEKIDDKHQLVRCGDSFPIFWKR+V

NSPH-1.1a/1-385 154 ----GLLGCVNTEKLV----------AH------------FVDNEMQIKTTKK-LEHLLVL-CKIAGSRDATEKEK--- 201
NSPH-2/1-340    124 -DGTDKLGFLDLNTEV----------AL------------FSNAGTTEKYEGGATANFMTIFRNLR------------- 166
NSPH-4.3/1-187    1 ---------------------------------------------------------MY--------------------   2
NSPH-1.2a/1-331  81 CLTSETEDFIPINMTEGSGSGQEDTTIWSNDLPPLSSDIDFLKSTTQKTVTKRATSTFYN---GI-------------- 142
NSPH-4.1/1-381  129 -EG-NLLGYVDNKTEE----------GW------------FSFNGKVIKQVGPQLNEMYIITRNCIGGPPHCECENCPK 183
NSPH-3.1/1-366  126 -EG-NLLGYVDNKTEE----------AW------------FSFNGKVLKQVGPQLNDMYIITRNCIGGPPSCDCANCGS 180
NSPH-3.2/1-371  126 -EG-NLLGYVDNKTEE----------AW------------FSFNGKVIKQLGPQLNEMYIITRNCIGGPPHCPCAVCGA 180

Consensus           CEG+NLLGYVDNKTEEGSGSGQEDTTAWSNDLPPLSSDIDFSFNGKVIKQ+GPQLNEMYIITRNCIGGPPHCEC+NCG+

NSPH-1.1a/1-385 202 ----EKGSTGSASKLLTVVNDWEDFNWGSAWPSNKNVMSIPK---NIPSAGIDQFVALWYRHGKP-IMGRAWQSN-GRI 271
NSPH-2/1-340    167 -PP--------PTGLKVYDDLWYDLRYGDNFPSNAVPADG-RALNT-ETGPHMQYVALWYKHGDP-VFGRSYPSSAGKT 233
NSPH-4.3/1-187    3 ------------GRAEYVTGSLMQKWKANPWTFLEHRRSCR-VLVPIQELAPISMLPCGTCRVNL-PWVVIYIEG-GKV  66
NSPH-1.2a/1-331 143 ----------------LDRPFYSAFSYSKPIIPPTAIIPLNRPLQRGNNIPQLQYIALWAPRGQPPHWGSIHQNAMGKL 205
NSPH-4.1/1-381  184 PPPPPPIPPPGPPPPRVIHDEWIDIREGDPWPTRKLVQALDKSLDTLPGVSADQYVALWYMQGEP-VMGRVWNEG-GKV 260
NSPH-3.1/1-366  181 GP-----------KVRVERDEWMDIREGDAWPTRQLVKALDKTLDTLPGVNPDQYVALWYMQGEP-VMGRVWNEG-GKV 246
NSPH-3.2/1-371  181 APPPP------KPVPRVERDEWMDIREGDPWPTRQLVKALDKTLDTLPGVNPDQYVALWYMQGEP-VMGRVWNEG-GKV 251

Consensus           +PPPP++++++PPK+RV+RDEWMDIREGDPWPTR+LVKALDKTLDTLPGV+PDQYVALWYMQGEPPVMGRVWNEG+GKV

NSPH-1.1a/1-385 272 EASFVDAKREFTGATVGSLQL-----LISLP-PTTVGYDYVWMTYTQAIDYR-DKDYVPVHLSYICPA----IVP-VDG 338
NSPH-2/1-340    234 MAHFGKNNQENAGPEVGSMQL-----LTVPE-ASCMGLEYKWMPLSEGK----SSGWTTVHIGNSAPC----ILKDDKG 298
NSPH-4.3/1-187   67 AANFSWFNND-YCKSVGSIQL-----LVRLG-PQVVGHEYGWIPFPEPANFDAGKIWKPVHVNNHKGDISFGVVNLPCE 138
NSPH-1.2a/1-331 206 DGSFIKDRRI-YNLSSPDMQNTPVRLVQYVGNEQENNFKFAWTKA---IDVDMATVVSEKDYTKQCSPKMAPAVLQDHG 280
NSPH-4.1/1-381  261 AANFSWFNNE-YCKNVGSIQL-----LVRLG-PHVVGYEYGWIPFPEAANFDAGKIWKPVHVNNHKGDISVGVVNLPGG 332
NSPH-3.1/1-366  247 AANFSWFNNE-YTKNVGSIQL-----LVHLP-DNLRGFDYGWISFPEAAKFG-DKEWHPVHVNNHKGDISVGVVNVSGG 317
NSPH-3.2/1-371  252 AANFSWFNNE-YCKNVGSIQL-----LIYLP-DSVRGFDYGWIPFPEAAQFG-DKAWHPVHVNNHKGDISVGVVNVAGG 322

Consensus           AANFSWFNNE+YCKNVGSIQLTPVRLLV+L+NP+VVGF+YGWIPFPEAA+FDADKIW+PVHVNNHKGDISVGVVN++GG

NSPH-1.1a/1-385 339 KFFLGQVNMKTECATVALNGSVTQLDGGPV-KSIMVLCRK----EMAETMLI-                           385
NSPH-2/1-340    299 LEVLGNLDLTIEKASAGYGGKEKIMTGAAVAKLKVLFKRR----LA-------                           340
NSPH-4.3/1-187  139 KQIFAKVDVRNESYGYGNQGKEHSARGPACASSVSILCRK----ALPGYQLEG                           187
NSPH-1.2a/1-331 281 YEFLGEADIDNRIMYYVDHNYVNTVSGSLFTNNVYLLTKQQCQCSCPATSY--                           331
NSPH-4.1/1-381  333 KQILAKVDVRNESYGYGYQGKEHSARGPACASSVTVLCRK----ALPGYTLDG                           381
NSPH-3.1/1-366  318 KQILAKVDVRNEKYGYGYQGKEHTASAKSCADNTTVLCRK----AKPGCKLDG                           366
NSPH-3.2/1-371  323 KQILAKVDVRNEKYGYGYQGKEHSATAKNCADNTIVLCRK----AKAGYKLDG                           371

Consensus           KQILAKVDVRNEKYGYGYQGKEHSA+G+ACA++VTVLCRKQCQCA+PGYKLDG
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Figure S3. NSPH paralog alignment. An alignment produced with Clustal Omega (Goujon et al., 2010; Sievers et al., 2011) and visualized with JalView2 (Waterhouse et al., 2009). Protein identity for each row and total length in amino acids is provided in the left column. To the left and right of the alignment are amino acid position references. The consensus sequence is shown beneath each row. Only the sequence for NSPH-4.1 is shown as NSPH-4.2 has identical sequence and its protein product is annotated as NSPH-4.1 in Wormbase.