

**FIGS1 Related analysis of multiple DExH-box helicases.** (A) Analysis was performed using Metascape (<http://metascape.org>). To further capture the relationships between the terms, a subset of enriched terms were selected and rendered as a network plot. (B) Protein-protein interaction network and MCODE components were identified.

```

1      10      20      30      40      50      60
DDX5-HU.pro MSYSSDRDRGRDRGFGAPRFGGSRAGPLSGKKRFGNPGKLVKKRWNLDLPPKFEKNFYQ
DDX5-MO.pro MSYSSDRDRGRDRGFGAPRFGGSRAGPLSGKKRFGNPGKLVKKRWNLDLPPKFEKNFYQ

70      80      90      100     110     120
DDX5-HU.pro EHPDLARRTAQEVETIYRSKEITVRGHNCPKPVLNFEYANPPANVMDVIARQNFTEPTAI
DDX5-MO.pro EHPDLARRTAQEVETIYRSKEITVRGHNCPKPVLNFEYANPPANVMDVIARQNFTEPTAI

130     140     150     160     170     180
DDX5-HU.pro QAQGWVVALSGLDVMVGAQTGSGKTLISYLLPAIVHINHQPFLERGDGPICLVLAFTRELA
DDX5-MO.pro QAQGWVVALSGLDVMVGAQTGSGKTLISYLLPAIVHINHQPFLERGDGPICLVLAFTRELA

190     200     210     220     230     240
DDX5-HU.pro QOVQVAAEYCRACRLKSTCIYGGAPKGPQIRDLEKRVGVEICITATPGLRIDFLECGKTNLR
DDX5-MO.pro QOVQVAAEYCRACRLKSTCIYGGAPKGPQIRDLEKRVGVEICITATPGLRIDFLECGKTNLR

250     260     270     280     290     300
DDX5-HU.pro RTTYLVLDEADRMLDMGFEPQIRKIVDQIRPDRQTLMWSATWPKQVRLAEDFLKDYIHI
DDX5-MO.pro RTTYLVLDEADRMLDMGFEPQIRKIVDQIRPDRQTLMWSATWPKQVRLAEDFLKDYIHI

310     320     330     340     350     360
DDX5-HU.pro NIGALELSANHNILQIVDVCHDVEKDEKLIRLMEEMSEKENKTIIVFVETKRRCDLTKR
DDX5-MO.pro NIGALELSANHNILQIVDVCHDVEKDEKLIRLMEEMSEKENKTIIVFVETKRRCDLTKR

370     380     390     400     410     420
DDX5-HU.pro MRRDGPWAMGIHGDKSQQERDVLNFKHGKAPILITADVASRGLDVEDVKFVINYDYPN
DDX5-MO.pro MRRDGPWAMGIHGDKSQQERDVLNFKHGKAPILITADVASRGLDVEDVKFVINYDYPN

430     440     450     460     470     480
DDX5-HU.pro SSEDYIHRIGRTARSTKTGTAYTFFTPNNIKQVSDLISVLRANQAINPKLLQLVDRGCS
DDX5-MO.pro SSEDYIHRIGRTARSTKTGTAYTFFTPNNIKQVSDLISVLRANQAINPKLLQLVDRGCS

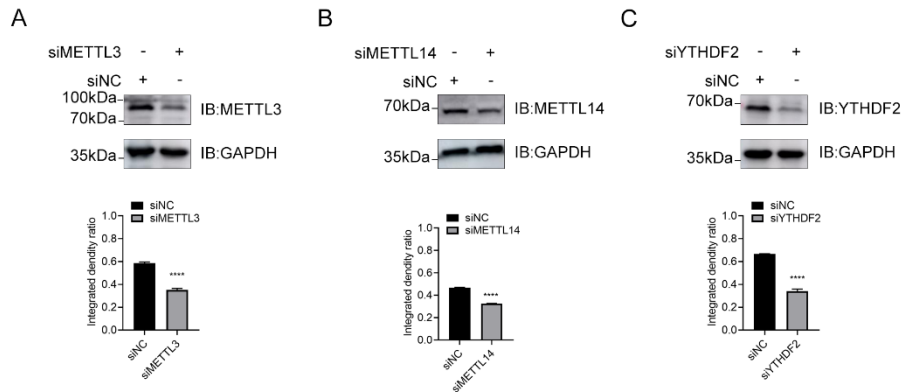
490     500     510     520     530     540
DDX5-HU.pro GRSRGRGGMKDDRRDRYSAGKRGGFNFRDRENYDRGYSLLKRDGAKTQNGVYSAANY
DDX5-MO.pro GRSRGRGGMKDDRRDRYSAGKRGGFNFRDRENYDRGYSLLKRDGAKTQNGVYSAANY

550     560     570     580     590     600
DDX5-HU.pro TNGSFGSNFVSAGIQTSFRTGNPTCTYQNGYDSTQQYGSNVANMHNMGMNQAYAYPATAA
DDX5-MO.pro TNGSFGSNFVSAGIQTSFRTGNPTCTYQNGYDSTQQYGSNVANMHNMGMNQAYAYPATAA

610
DDX5-HU.pro AFMIGYPMPTGYSQ
DDX5-MO.pro AFMIGYPMPTGYSQ

```

**FIGS2 Alignment of amino acids of DDX5 proteins.** All sequences were aligned with ClustalW and mapped online program, ESPript server.



**FIGS3 The relevant knockdown effect of target protein in figure 6.** (A, B and C) A549 cells were transfected with siRNA targeting METTL3 (A), METTL14 (B), YTHDF2 (C) or with scrambled siRNA for 48h. Cells were harvested and protein expression levels were detected by Western-blot. The expression level of viral protein was normalized to GAPDH using ImageJ respectively. \*\*\*\*\*,  $P < 0.0001$ .

**TableS1 Function and pathway enrichment analysis.**

**TableS2 Interaction of DEAD/H-box RNA helicases with influenza virus proteins**

**TableS3 Sequence analysis of related antiviral transcripts.**