

Figure S1

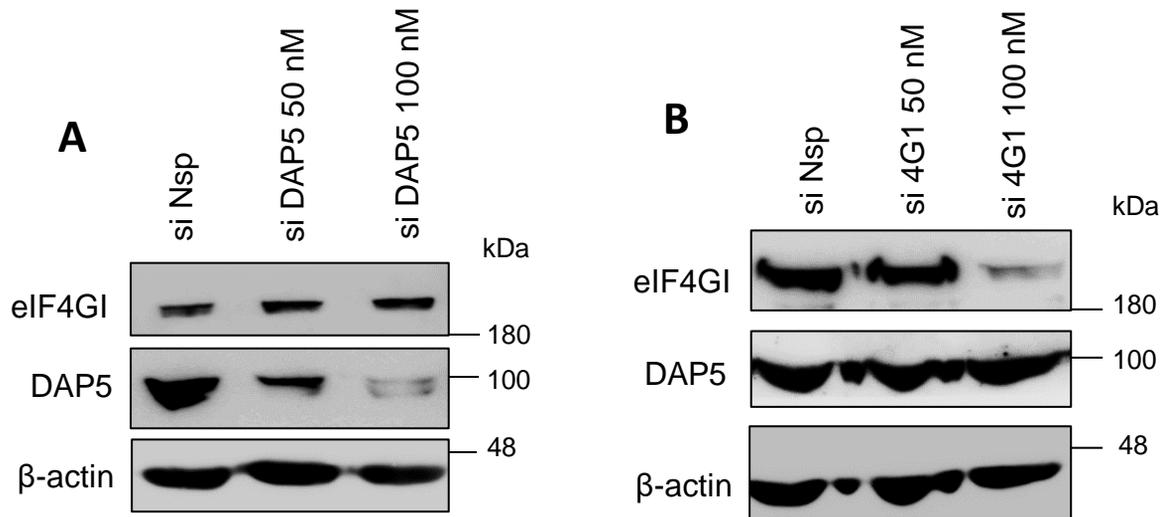


Figure S1: Specificity of the siRNAs used in the study. **A.** Western blots showing the DAP5 and eIF4GI protein levels upon si DAP5 treatment. **B.** Western blots showing the DAP5 and eIF4GI protein levels upon silencing using si eIF4GI. β-Actin protein levels are indicated as loading control.

Figure S2

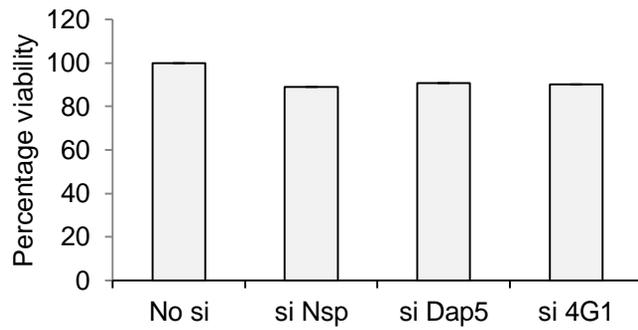


Figure S2: MTT assay performed on cells transfected with either siDAP5, si4GI or siNsp. At 30 hours post transfection, cells were treated with 0.5 mg/ml of MTT reagent and absorbance was measured at 550 nm after 3 hours.

Figure S3

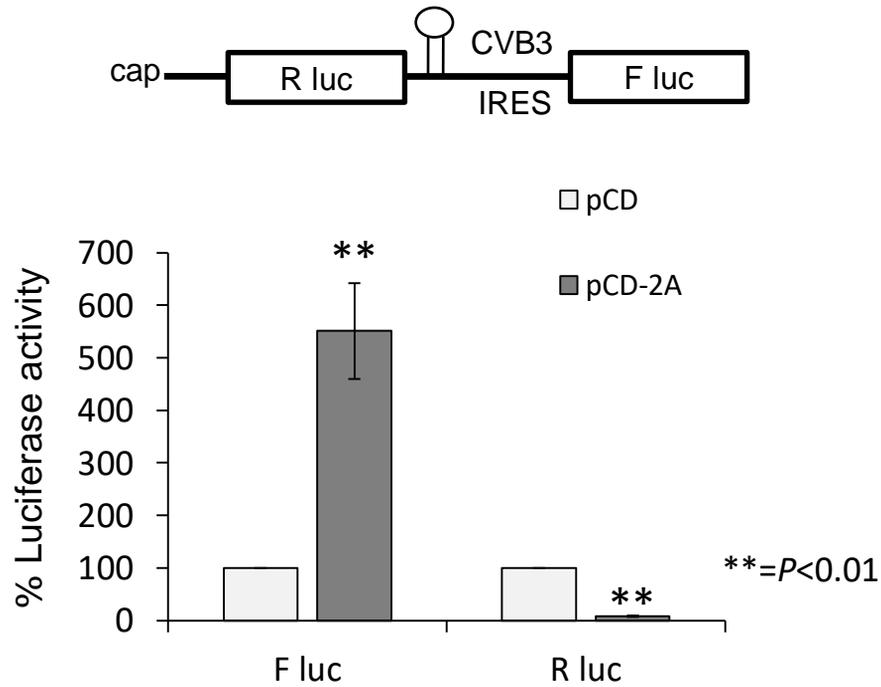


Figure S3: Effect of 2A protease on CVB3 IRES activity using bicistronic construct. *In vitro* transcribed capped CVB3 bicistronic RNA was transfected in cells previously transfected with plasmid expressing 2A protease or vector control. 8 hours post transfection of bicistronic RNA, cells were processed for luciferase assay. F luc activity represents CVB3 IRES mediated translation and R luc activity represents cap-dependent translation.

Figure S4

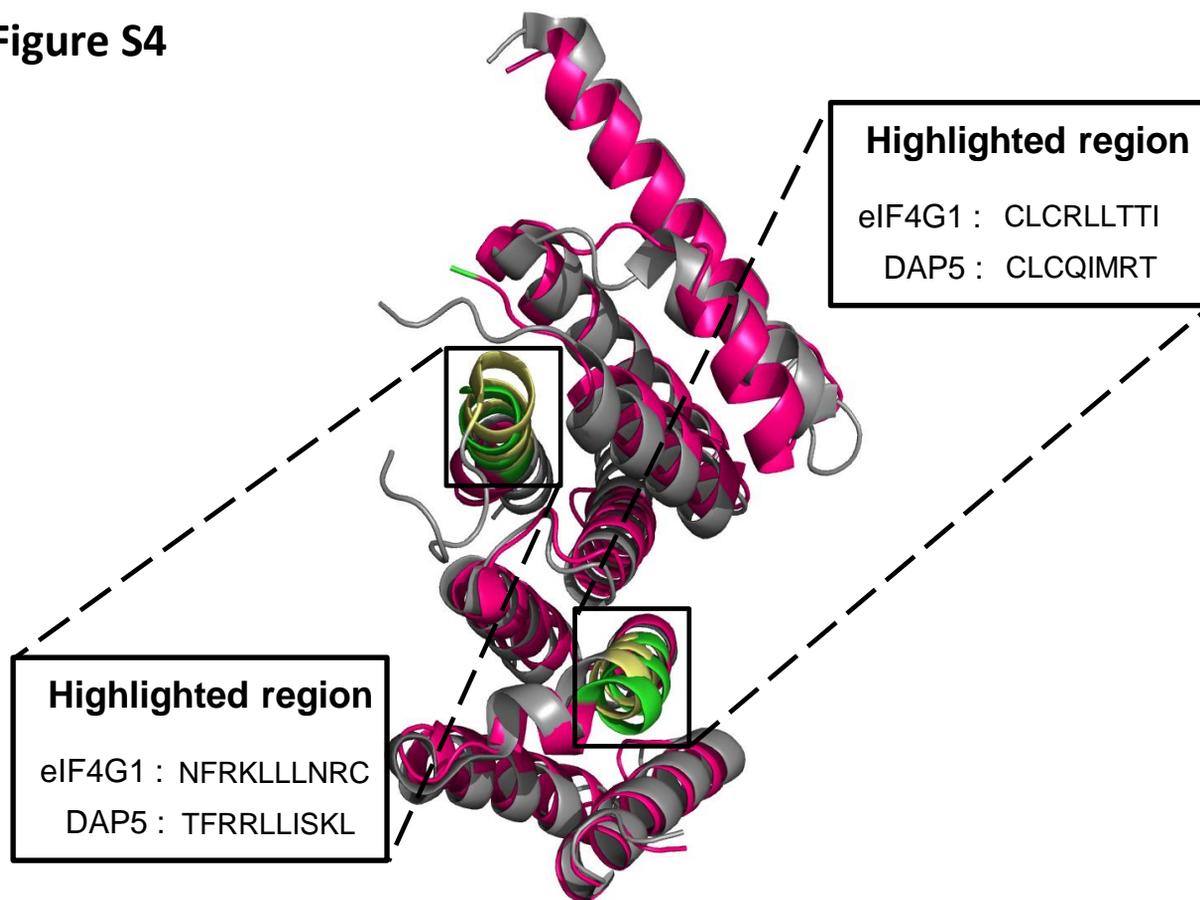


Figure S4: Structural alignment of MIF4G domains of DAP5 (grey) and eIF4GI (magenta). The CVB3 IRES interacting regions (adapted from de Breyne et al., 2009, [5](#)) in DAP5 and eIF4GI are indicated by yellow and green color respectively. The amino acid composition in the interacting region is indicated in the box.

Figure S5

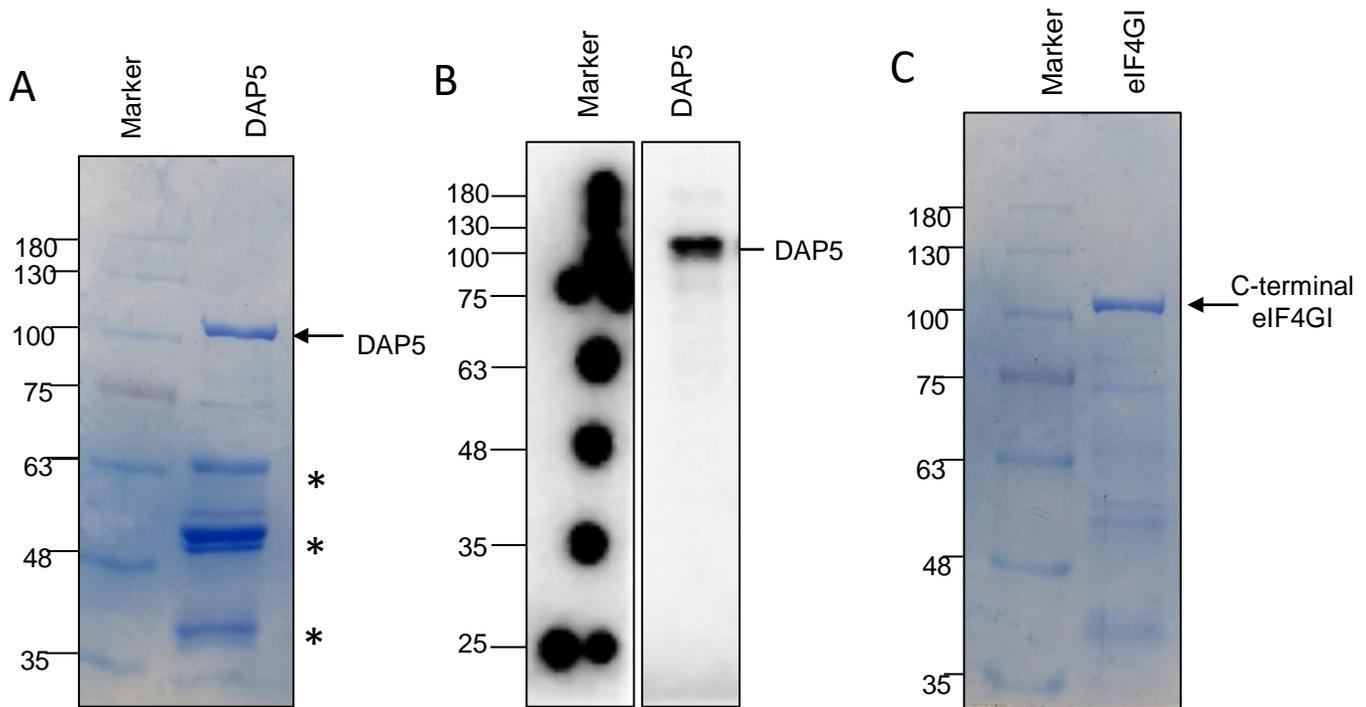


Figure S5.A. Purified recombinant DAP5 protein from bacteria. The * mark indicates the bacterial contaminants that co-purified along with DAP5 protein. **B.** UV crosslinking experiment carried out with recombinant protein obtained in panel A. As can be observed in the gel, the contaminant proteins were not found to be interacting with CVB3 5'UTR. **C.** Purified recombinant C-terminal eIF4GI protein.

Figure S6

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KF537633.1      CCCAACCCAGGAGCAAGTAGTTGCAAACCAGCAACCAGCTTGTTCGTAACGGCGTAAGTCTG 532
DQ890386.1      CCCAACCCAGGAGCAAGTGCTCACAAACCAGTGAGTGGCTTGTTCGTAACGGGGTAACTCTG 530
KJ849619.1      CCTAACTGCCGAGCAGATACCCACGCACCCAGTGGGCAGTCTGTTCGTAACGGGCAACTCTG 512
MG780414.1      CCTAACTGCCGAGCAGATACCCACACGCCAGTGGGCAGTCTGTTCGTAATGGGCAACTCTG 524
AJ493062.2      CCCAACTGCCGAGCAGGTACCCACACACCAGTGGGCAGCCTGTTCGTAACGGGCAACTCTG 532
JQ729993.1      CCTAACTGCCGAGCAGATACCCACATGCCAGTGGGCAGTCTGTTCGTAACGGGCAACTCTG 533
AB705308.1      CCTAACTGCCGAGCAGATACCTACATGCCAGTGGGCGGTCTGTTCGTAACGGGCAACTCTG 532
KC570453.1      CCCAACTGCCGAGCACACGCCACCAAGCCAGCGGGTAGTGTTCGTAACGGGTAACTCTG 530
M33854.1        CCTAACTGCCGAGCACACACCCTCAAGCCAGAGGGCAGTGTTCGTAACGGGCAACTCTG 531
M88483.1        CCTAACTGCCGAGCACACACCCTCAAGCCAGAGGGCAGTGTTCGTAACGGGCAACTCTG 532
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KF537633.1      TGGCGGAACCGACTACTTTGGGTGTCCGTGTTTCC-TTTATTTTACACTGGCTGCTTA 591
DQ890386.1      TGGCGGAACCGACTACTTTGGGTGTCCGTGTTTCC-TTTATTTTGTGTA-TGGCTGCTTA 589
KJ849619.1      CAGCGGAACCGACTACTTTGGGTGACCGTGTTCCTTTTATTTTGTGTA-TGGCTGCTTA 571
MG780414.1      CAGCGGAACCGACTACTTTGGGTGTCCGTGTTTCC-TTTATTTTATACTGGCTGCTTA 583
AJ493062.2      CAGCGGAACCGACTACTTTGGGTGTCCGTGTTTCC-TTTATTTCTATACTGGCTGCTTA 591
JQ729993.1      CAGCGGAACCGACTACTTTGGGTGTCCGTGTTTCC-TTTATTTCTATACTGGCTGCTTA 592
AB705308.1      CAGCGGAACCGACTACTTTGGGTGTCCGTGTTTCC-TTTATTTCTATACTGGCTGCTTA 591
KC570453.1      CAGCGGAACCGACTACTTTGGGTGTCCGTGTTTCC-TTTATTTTATATTGGCTGCTTA 589
M33854.1        CAGCGGAACCGACTACTTTGGGTGTCCGTGTTTCA-TTTATTTCTATACTGGCTGCTTA 590
M88483.1        CAGCGGAACCGACTACTTTGGGTGTCCGTGTTTCA-TTTATTTCTATACTGGCTGCTTA 591
                *****
KF537633.1      TGGTGACAATC-ATAGATTGTTATCATAAGGCCGAATTGGATTGGCCACCCGGTGTAAAGTC 650
DQ890386.1      TGGTGACAATC-AGAGATTGTTATCATAAAGCGTATTGGATTGGCCATCCGGTGAGTGTT 648
KJ849619.1      TGGTGACAATTGAAAGATTGTTACCATATAGC-TATTGGATTGGCCATCCGGTAACAAAC 630
MG780414.1      TGGTGACAATTGAGAGATTGTTACCATATAGC-TATTGGATTGGCCATCCAGTGACAAAC 642
AJ493062.2      TGGTGACAATTGAAAGATTGTTACCATATAGC-TATTGGATTGGCCATCCAGTGACAAAC 650
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M33854.1        TGGTGACAATTGAGAGATCGTTACCATATAGC-TATTGGATTGGCCATCCGGTGACTAAT 649
M88483.1        TGGTGACAATTGAGAGATTGTTACCATATAGC-TATTGGATTGGCCATCCGGTGACCAAT 650
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Figure S6: Multiple sequence alignment of 5' UTR from different picornaviruses. The box indicates conserved eIF4GI and DAP5 binding sites. KF537633.1- Human poliovirus 1, DQ890386.1- Human poliovirus 2, KJ849619.1-Human coxsackievirus B1, MG780414.1- Coxsackievirus B1, AJ493062.2- Human enterovirus 77, JQ729993.1- Human echovirus 6, AB705308.1- Echovirus E6, KC570453.1- Human enterovirus 71, M33854.1- Coxsackievirus B3 , M88483.1- Coxsackievirus B3