

Screening of the HBx transactivation domain interacting proteins and the function of interactor Pin1 in HBV replication

Authors and affiliations

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Running title: HBx transactivation domain interacting proteins

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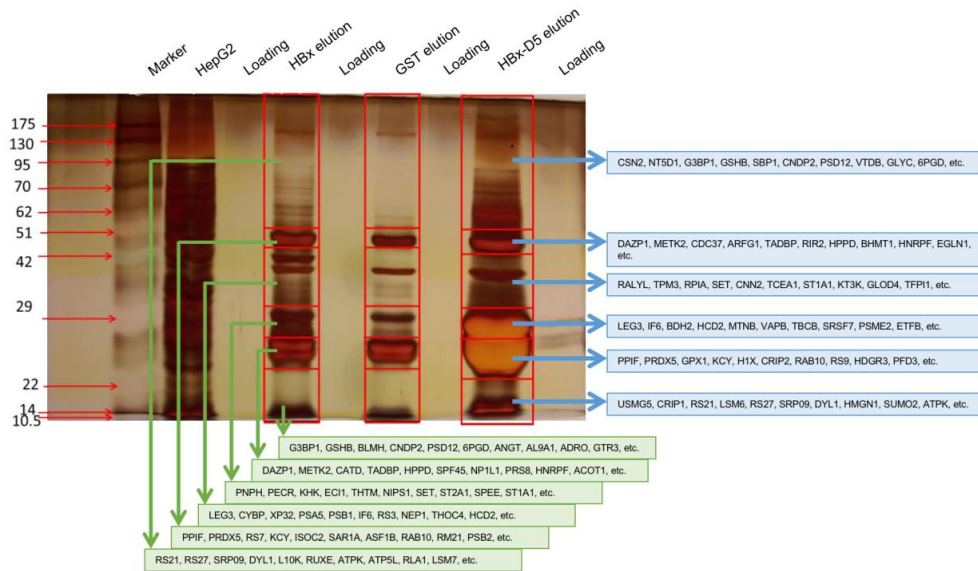
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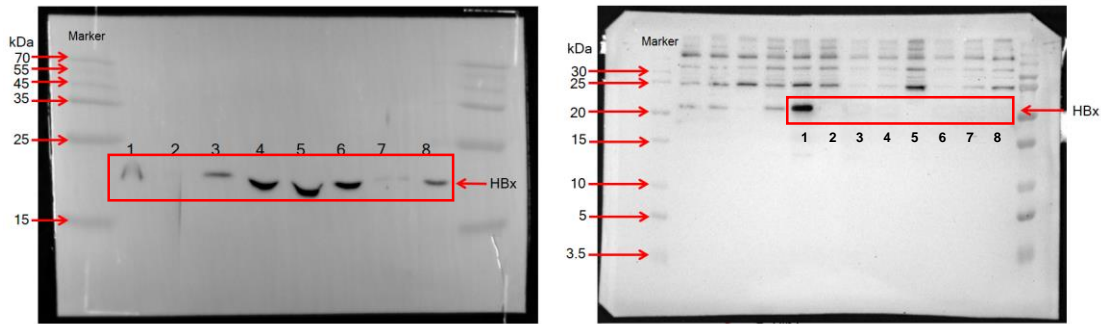
Supplementary Figure 1

SDS-PAGE blots of purified GST-fusion proteins (GST-HBx, GST-HBx-D5, GST). The purified proteins were loaded with 2 μ g of equal weight, separated with 10% gel and stained with Coomassie brilliant blue.



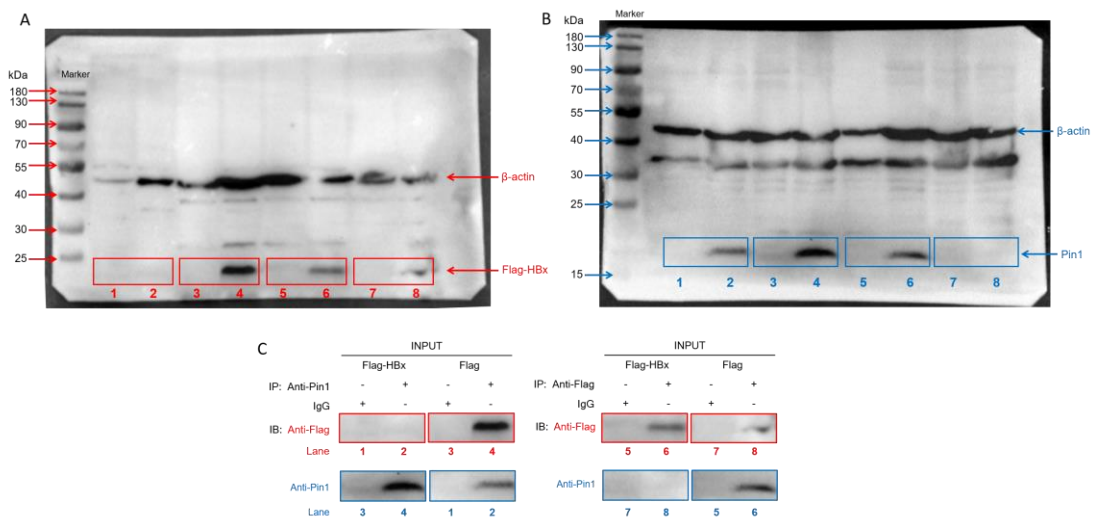
Supplementary Figure 2

Silver-stained SDS-PAGE of GST-fusion proteins (GST-HBx or GST-HBx-D5) incubated with HepG2 cell lysate. The arrows indicate the HBx-interacting proteins identified by mass spectrometry as listed in the bottom (HBx) or right (HBx-D5).



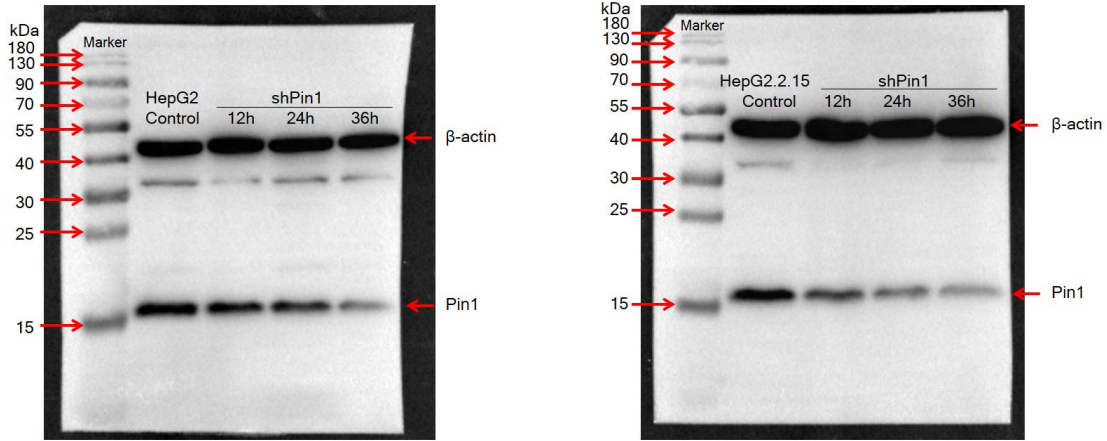
Supplementary Figure 3

Full-length blot for Figure 3A. Cell lysate of BL21 transfected with Flag-tagged HBx expression plasmids was incubated with Ni²⁺-NTA beads adding (left) or not adding (right) purified His6-tagged Pin1. HBx was detected in both the whole cell lysate isolated from Ni²⁺-NTA beads and imidazole eluent. Lane 1 to lane 8 were: (1) cell lysate after incubating with purified Pin1 and Ni²⁺-NTA; (2) low concentration of imidazole elution for removing non-specific binding bacteria proteins; (3-8) high concentration of imidazole elution for removing His6-tagged Pin1 and its binding proteins including HBx.



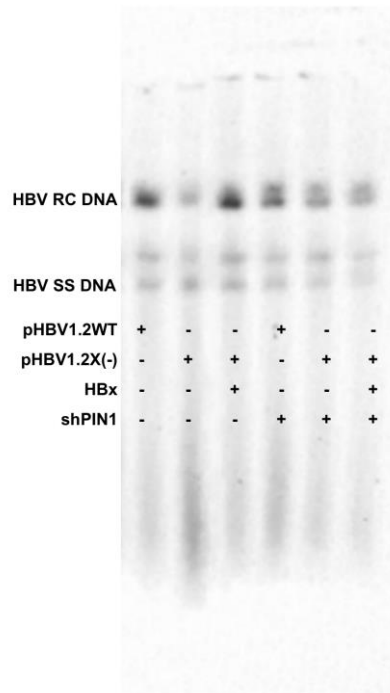
Supplementary Figure 4

Full-length blot for Figure 3B. HepG2 cells were transfected with Flag-HBx or Flag-control plasmids and harvested 24 hours after transfection. Immunoprecipitation was carried out using protein A/G sepharose dealt with anti-Pin1, anti-FLAG or nonimmune serum antibodies previously, and incubated with protein samples for immunoprecipitation. Flag-HBx or Pin1 pulled down as protein complex was detected using western blot. Co-immunoprecipitation assay results showed that with the transfection of Flag-tagged HBx, HBx was detected in eluent after incubated with anti-Pin1 beads (Fig. S4A and blots with red border in Fig. S4C), while endogenous Pin1 protein pulled down by HBx was detected in eluent after incubated with anti-Flag beads (Fig. S4B and blots with blue border in Fig. S4C). Fig. S4C summarized the cropped blots and marked with lane numbers.



Supplementary Figure 5

Full-length blot for Figure 4A. Levels of Pin1 expression detected by Western Blot after transfected with Pin1 shRNA for 12h, 24h, and 36h in HepG2 (left) and HepG2.2.15 cells (right).



Supplementary Figure 6

Full-length blot for Figure 5A. Levels of HBV DNA replication intermediates detected by Southern Blot in HepG2 cells which were transfected with wild-type HBV, or HBx-deficient HBV, with or without exogenous expression of HBx plasmid.

Supplementary Table 1.

Supplementary Table 1. Biological process by GO analysis of the proteins specifically interacting with the transactivation domain of HBx

| Category | Count | % | PValue | Top 10 Genes | Fold Enrichment |
|--|-------|------------|------------|---|-----------------|
| regulation of cellular amino acid metabolic process | 15 | 7.89473684 | 1.79E-16 | P43686, P25789, P25786, P25787, Q99460, P62195, P20618, P28072, P28070, O14818, I | 26.8414322 |
| regulation of mRNA stability | 18 | 9.47368421 | 9.85E-16 | P43686, P25789, P25786, Q5RKY6, P25787, P39687, Q99460, P62195, P20618, P28072, I | 15.9485015 |
| antigen processing and presentation of exogenous peptide antigen via MHC class I | 15 | 7.89473684 | 4.69E-15 | P43686, P25789, P25786, P25787, Q99460, P62195, P20618, P28072, P28070, O14818, I | 21.7287785 |
| NIK/NF- κ B signaling | 15 | 7.89473684 | 9.53E-15 | P43686, P25789, P25786, P25787, Q99460, P62195, P20618, P28072, P28070, O14818, I | 20.7411067 |
| positive regulation of canonical Wnt signaling pathway | 18 | 9.47368421 | 1.46E-14 | P43686, P25789, P25786, P25787, Q66K66, Q99460, P14923, P62195, P20618, P28072, I | 13.6891304 |
| negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle | 15 | 7.89473684 | 2.83E-14 | P43686, P25789, P25786, P25787, Q99460, P62195, P20618, P28072, P28070, O14818, I | 19.2804654 |
| Wnt signaling pathway, planar cell polarity pathway | 16 | 8.42105263 | 6.42E-14 | P43686, P25789, P25786, P25787, Q99460, P62195, P20618, P28072, P28070, O14818, I | 15.8714556 |
| positive regulation of ubiquitin-protein ligase activity involved in regulation of mitosis | 15 | 7.89473684 | 7.70E-14 | P43686, P25789, P25786, P25787, Q99460, P62195, P20618, P28072, P28070, O14818, I | 18.0120137 |
| anaphase-promoting complex-dependent catabolic process | 15 | 7.89473684 | 1.36E-13 | P43686, P25789, P25786, P25787, Q99460, P62195, P20618, P28072, P28070, O14818, I | 17.3280137 |
| stimulatory C-type lectin receptor signaling pathway | 15 | 7.89473684 | 7.81E-12 | P43686, P25789, P25786, P25787, Q99460, P62195, P20618, P28072, P28070, O14818, I | 13.0327671 |
| tumor necrosis factor-mediated signaling pathway | 15 | 7.89473684 | 3.93E-11 | P43686, P25789, P25786, P25787, Q99460, P62195, P20618, P28072, P28070, O14818, I | 11.6009598 |
| protein polyubiquitination | 17 | 8.94736842 | 1.75E-10 | P43686, P25789, P25786, P25787, Q13867, Q99460, P62195, P20618, P28072, P28070, C | 8.43171078 |
| negative regulation of canonical Wnt signaling pathway | 16 | 8.42105263 | 3.00E-10 | P43686, P25789, P25786, P25787, Q99460, P62195, P20618, P28072, P20649, P28070, C | 8.95812217 |
| T cell receptor signaling pathway | 15 | 7.89473684 | 8.34E-10 | P43686, P25789, P25786, P25787, Q99460, P62195, P20618, P28072, P28070, O14818, I | 9.24941246 |
| Fc-epsilon receptor signaling pathway | 16 | 8.42105263 | 1.03E-09 | P43686, P25789, P25786, P25787, Q99460, P62195, P20618, P28072, P62993, P28070, C | 8.20322423 |
| proteolysis involved in cellular protein catabolic process | 10 | 5.26315789 | 2.07E-09 | P20618, P28072, P25789, P25786, P28070, P25787, O14818, P60900, P49721, P49720 | 19.0126812 |
| MAPK cascade | 17 | 8.94736842 | 2.94E-08 | P43686, P25789, P25786, P25787, Q99460, P62195, Q9UH4A, P20618, P28072, P62993, I | 5.9215068 |
| proteasome-mediated ubiquitin-dependent protein catabolic process | 15 | 7.89473684 | 4.93E-08 | P43686, P25789, P25786, P25787, Q99460, P62195, P20618, P28072, P28070, O14818, I | 6.74431401 |
| nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | 11 | 5.78947368 | 7.04E-07 | P62280, P83881, P05386, P67775, P62906, P62266, P62081, P61353, P15170, P23396, P | 8.4358787 |
| viral process | 16 | 8.42105263 | 1.01E-06 | Q15LNI, P25789, Q9Y490, P14324, P20618, Q95373, Q15046, Q7KZF4, P28072, P62993, I | 4.88352479 |
| translational initiation | 11 | 5.78947368 | 2.56E-06 | P62280, P83881, P05386, P62906, P62266, P62081, Q14152, P61353, P23396, P46782, F | 7.32751507 |
| viral transcription | 10 | 5.26315789 | 3.37E-06 | P62280, P83881, P05386, P62906, P62266, P62081, P61353, Q9NRG9, P23396, P46782, I | 8.14829193 |
| rRNA processing | 13 | 6.84210526 | 4.07E-06 | P62280, P83881, Q5RKY6, P05386, Q14137, Q15024, P62906, P62266, P62081, P61353, I | 5.5438846 |
| SRP-dependent cotranslational protein targeting to membrane | 9 | 4.73684211 | 8.55E-06 | P62280, P83881, P05386, P62906, P62266, P62081, P61353, P23396, P46782, I | 8.73774283 |
| translation | 12 | 6.31578947 | 1.05E-06 | P62280, P83881, P05386, P62906, P62266, P62081, Q722W9, Q9Y3D3, P61353, I | 4.32857879 |
| nucleosome assembly | 8 | 4.21052632 | 3.27E-04 | Q15020, Q9BTT0, Q9Y294, P55209, P39687, Q9NV2P, Q5SSJ5, Q92688 | 6.13518451 |
| cell-cell adhesion | 11 | 5.78947368 | 7.95E-04 | Q8WWM7, Q7KZF4, P28072, Q9UH1X, Q96AG4, Q15691, P31947, O00571, P25685, O1 | 3.70431547 |
| osteoblast differentiation | 7 | 3.68421053 | 9.68E-04 | P62280, P84090, Q7KZF4, P35232, Q9Y294, Q86V81, Q00610 | 6.14255853 |
| cell redox homeostasis | 6 | 3.15789474 | 0.00152553 | P02788, Q95881, Q8NBF2, P09622, Q6DKJ4, Q13162 | 7.11123659 |
| mRNA splicing, via spliceosome | 9 | 4.73684211 | 0.00304773 | Q07955, Q15020, P52434, Q86V81, O43390, Q9UK45, Q9Y3B4, P31943, P62304 | 3.69976498 |
| negative regulation of protein catabolic process | 4 | 2.10526316 | 0.00500599 | P35232, Q13526, P21333, Q99497 | 11.4076087 |
| platelet degranulation | 6 | 3.15789474 | 0.00539019 | P02763, Q9Y490, P01009, P21333, P04217, P01011 | 5.31616716 |
| histone exchange | 3 | 1.57894737 | 0.00608992 | Q9BTT0, P39687, Q92688 | 24.8893281 |
| mitotic spindle assembly | 4 | 2.10526316 | 0.00698072 | Q15018, P21333, Q00610, P62491 | 10.14400966 |
| acute-phase response | 4 | 2.10526316 | 0.00872490 | Q07263, P01009, P00734, P01011 | 9.36608919 |
| proteolysis | 13 | 6.84210526 | 0.00803133 | O43464, P43686, P01861, P00751, P02788, Q13867, P55786, P12273, P07339, P09622, I | 2.37278261 |
| ceramide metabolic process | 3 | 1.57894737 | 0.01442718 | Q9Y5P4, O43464, P67775 | 16.1048593 |
| nitinamide riboside catabolic process | 2 | 1.05263158 | 0.02167797 | P00491, Q13126 | 9.12608696 |
| oxidation-reduction process | 13 | 6.84210526 | 0.0289895 | O04699, P12268, Q8N4T8, O14618, Q13162, P11586, Q8I283, Q9BY49, Q95881, P1512 | 2.00403937 |
| nucleocytoplasmic transport | 3 | 1.57894737 | 0.03006841 | Q9BTT0, P39687, Q9NRG9 | 10.9513043 |
| positive regulation of B cell activation | 3 | 1.57894737 | 0.03234473 | P01861, P01871, P01877 | 10.5301003 |
| phagocytosis, recognition | 3 | 1.57894737 | 0.03709217 | P01861, P01871, P01877 | 9.77795031 |
| exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation | 3 | 1.57894737 | 0.03955995 | Q5RKY6, Q15024, Q9UK45 | 9.44077961 |
| cellular oxidant detoxification | 4 | 2.10526316 | 0.04096168 | O02649, Q6DKJ4, Q13162, Q99497 | 5.21490683 |
| positive regulation of protein insertion into mitochondrial membrane involved in apc | 3 | 1.57894737 | 0.04208828 | P27348, P31947, Q04917 | 9.12608696 |
| positive regulation of reactive oxygen species metabolic process | 3 | 1.57894737 | 0.04208828 | P62993, P01019, P00734 | 9.12608696 |
| intracellular protein transport | 7 | 3.68421053 | 0.04465578 | Q9NR31, Q95373, Q04917, Q00610, Q10567, P30040, Q4G0F5 | 2.7068902 |
| membrane organization | 3 | 1.57894737 | 0.04732018 | P27348, P31947, Q04917 | 8.55570652 |
| protein folding | 6 | 3.15789474 | 0.04735204 | O75347, Q14697, Q95816, P67870, P25685, P30040 | 3.04202899 |
| ubiquitin-dependent protein catabolic process | 6 | 3.15789474 | 0.04919666 | P25789, P25786, P25787, O14818, P60900, O00233 | 3.0086001 |
| regulation of immune system process | 2 | 1.05263158 | 0.0532164 | P02763, P12273 | 36.5043478 |
| transsulfuration | 2 | 1.05263158 | 0.0532164 | P25325, P11586 | 36.5043478 |
| phagocytosis, engulfment | 3 | 1.57894737 | 0.05558303 | P01861, P01871, P01877 | 7.82236025 |
| positive regulation of host of viral process | 2 | 1.05263158 | 0.06364166 | P11498, P02649 | 30.4020899 |
| positive regulation of gene expression | 7 | 3.68421053 | 0.06744683 | P35232, P12273, O00571, P30040, P23396, Q99497, P34913 | 2.43826751 |
| retina homeostasis | 3 | 1.57894737 | 0.070363 | Q02788, P01877, P12273 | 6.84456522 |
| negative regulation of neuron death | 3 | 1.57894737 | 0.070363 | O43464, P02649, Q99497 | 6.84456522 |
| protein catabolic process | 3 | 1.57894737 | 0.07345766 | P43686, P07339, P62195 | 6.6776246 |
| negative regulation of protein ubiquitination | 3 | 1.57894737 | 0.07345766 | P23396, Q6DKJ4, Q99497 | 6.6776246 |
| modulation by virus of host process | 2 | 1.05263158 | 0.07384979 | O15131, O00505 | 26.0745342 |
| negative regulation of inflammatory response to antigenic stimulus | 2 | 1.05263158 | 0.07384979 | P25786, P28070 | 26.0745342 |
| antibacterial humoral response | 3 | 1.57894737 | 0.08299504 | P02788, P01871, P01877 | 6.22232022 |
| doxorubicin metabolic process | 2 | 1.05263158 | 0.08394722 | Q8N4T8, P15121 | 22.8152174 |
| negative regulation of platelet activation | 2 | 1.05263158 | 0.08394722 | P02649, P00734 | 22.8152174 |
| U4 snRNA 3'-end processing | 2 | 1.05263158 | 0.08394722 | Q5RKY6, Q15024 | 22.8152174 |
| positive regulation of actin filament depolymerization | 2 | 1.05263158 | 0.08394722 | Q9Y281, Q96G00 | 22.8152174 |
| daunorubicin metabolic process | 2 | 1.05263158 | 0.08394722 | Q8N4T8, P15121 | 22.8152174 |
| nuclear mRNA surveillance | 2 | 1.05263158 | 0.09393517 | Q5RKY6, Q15024 | 20.2801932 |
| catecholamine metabolic process | 2 | 1.05263158 | 0.09393517 | P0DMM9, P21964 | 20.2801932 |
| nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5' | 2 | 1.05263158 | 0.09393517 | Q5RKY6, Q15024 | 20.2801932 |
| positive regulation of cholesterol esterification | 2 | 1.05263158 | 0.09393517 | P02649, P01019 | 20.2801932 |
| positive regulation of RNA polymerase II transcriptional preinitiation complex assembl | 2 | 1.05263158 | 0.09393517 | P43686, P62195 | 20.2801932 |
| gene expression | 3 | 1.57894737 | 0.09625594 | P52434, O43390, P31943 | 5.70380435 |
| substantia nigra development | 3 | 1.57894737 | 0.09966034 | P24539, P27348, Q04917 | 5.58740018 |
| nucleobase-containing compound metabolic process | 3 | 1.57894737 | 0.09966034 | P84090, P00491, Q13126 | 5.58740018 |

Supplementary Table 2.

Supplementary Table 2. Molecular function by GO analysis of the proteins specifically interacting with the transactivation domain of HBx

| Category | Count | % | PValue | Genes | Fold Enrichme |
|---|-------|------------|------------|---|---------------|
| threonine -type endopeptidase activity | 11 | 5.78947368 | 4.93E-15 | P20618, P28072, P25789, P25786, P28070, P25787, O14818, P60900, P49721, P49720, F | 48.5847724 |
| poly(A) RNA binding | 43 | 22.6315789 | 6.97E-13 | P39687, O00571, P61353, P31943, P14324, P62280, Q7KZF4, P62993, Q9UHX1, Q14137 | 3.53265556 |
| protein binding | 131 | 68.9473684 | 3.75E-08 | O15131, Q969U7, P19623, Q13867, Q5H9R7, P12268, O00571, P21964, Q14137, P1227 | 1.3831087 |
| RNA binding | 22 | 11.5789474 | 4.36E-07 | Q9H361, P25786, P26639, O00571, P12268, Q96125, Q14152, P62081, Q92667, P31943, | 3.73045784 |
| cadherin binding involved in cell-cell adhesion | 14 | 7.36842105 | 1.53E-05 | Q9Y490, P31947, O00571, P21333, P25685, P14923, O14618, Q8WWM7, Q7KZF4, P280 | 4.47771883 |
| structural constituent of ribosome | 11 | 5.78947368 | 1.44E-04 | P62280, P83881, P05386, P62906, P62266, P62081, Q7ZZW9, Q9Y3D3, P61353, P23396, | 4.59585685 |
| histone binding | 7 | 3.68421053 | 0.00202482 | O95373, Q15020, Q98TT0, Q9Y294, P39687, Q9NVP2, Q92688 | 5.32187894 |
| protein transporter activity | 5 | 2.63157895 | 0.00746388 | O15131, Q95373, Q10567, O00505, Q4G0F5 | 6.441163 |
| phosphoprotein phosphatase activity | 4 | 2.10526316 | 0.01236817 | O00743, P62140, P67775, Q96GDD | 8.24468864 |
| nucleotide binding | 10 | 5.26315789 | 0.01281505 | Q9H361, Q07955, Q15020, Q9UHX1, Q86V81, O43390, Q96125, P12268, Q9Y3B4, P319 | 2.66530883 |
| catalytic activity | 7 | 3.68421053 | 0.01594549 | P00491, P46020, P42126, Q96AB3, P12268, P34913, Q13126 | 3.45355974 |
| protein homodimerization activity | 15 | 7.89473684 | 0.02568084 | P19623, Q8WUM4, P26639, P21333, P14923, P68402, P30040, Q13162, P34913, P02648 | 1.90587837 |
| immunoglobulin receptor binding | 3 | 1.57894737 | 0.0313937 | P01861, P01871, P01877 | 10.7022401 |
| superoxide dismutase copper chaperone activity | 2 | 1.05263158 | 0.03182455 | O14618, Q99497 | 61.8351648 |
| proteinase activated receptor binding | 2 | 1.05263158 | 0.03182455 | P35232, Q8WUM4 | 61.8351648 |
| ubiquitin-like protein conjugating enzyme binding | 2 | 1.05263158 | 0.04220728 | P23396, Q99497 | 46.3763736 |
| phosphoserine phosphatase activity | 2 | 1.05263158 | 0.04220728 | Q96GDD, P78330 | 46.3763736 |
| mRNA binding | 5 | 2.63157895 | 0.0456348 | Q07955, Q14152, P23396, Q99497, P46782 | 3.71010989 |
| hydrolase activity | 6 | 3.15789474 | 0.05505521 | P43686, P62140, P68402, Q9UKK9, P11586, P34913 | 2.91369887 |
| chaperone binding | 4 | 2.10526316 | 0.05636982 | O75347, Q95816, P25685, P30040 | 4.58038258 |
| peroxiredoxin activity | 2 | 1.05263158 | 0.06264171 | Q13162, Q99497 | 30.9175824 |
| proteasome-activating ATPase activity | 2 | 1.05263158 | 0.06264171 | P43686, P62195 | 30.9175824 |
| oxidoreductase activity | 6 | 3.15789474 | 0.06468813 | P13804, Q8N4T8, P15121, P12268, Q13162, P37268 | 2.78258242 |
| phosphatase activity | 3 | 1.57894737 | 0.06840055 | P62140, Q96GDD, P34913 | 6.95645604 |
| rRNA binding | 3 | 1.57894737 | 0.06840055 | P62280, P46782, Q92979 | 6.95645604 |
| magnesium ion binding | 6 | 3.15789474 | 0.06884977 | P36871, Q96GDD, P21964, Q9UKK9, P78330, P34913 | 2.72802198 |
| serine -type endopeptidase inhibitor activity | 4 | 2.10526316 | 0.08628548 | O10119, P01009, P19827, P01011 | 3.82485556 |
| transmembrane transporter activity | 3 | 1.57894737 | 0.09697556 | P24539, P11169, P48047 | 5.67873963 |

Supplementary Table 3.

Supplementary Table 3. Cellular component by GO analysis of the proteins specifically interacting with the transactivation domain of HBx

| Category | Count | % | PValue | Genes | Fold Enrichment |
|---|-------|------------|------------|--|-----------------|
| extracellular exosome | 110 | 57.8947368 | 1.56E-41 | Q13867, P42126, O00571, P12268, P21964, P04217, P34913, Q7Z794, P38606, P15153, | 3.79330442 |
| cytosol | 99 | 52.1052632 | 2.19E-26 | O15131, Q969U7, Q13867, P19623, Q5H9R7, P12268, P21964, P34913, P14324, P38606 | 2.89492635 |
| proteasome complex | 15 | 7.89473684 | 9.79E-16 | P43686, P25789, Q969U7, P25786, P25787, Q99460, P62195, P20618, P28072, P28070, | 24.2340426 |
| proteasome core complex | 11 | 5.78947368 | 3.22E-15 | P20618, P28072, P25789, P25786, P28070, P25787, O14818, P60900, P49721, P49720, F | 50.7760892 |
| cytoplasm | 94 | 49.4736842 | 8.32E-10 | O15131, Q13867, Q5H9R7, P31947, P12268, O00571, O14618, P31943, P31944, P34911, | 1.74492532 |
| proteasome core complex, alpha-subunit complex | 6 | 3.15789474 | 5.89E-09 | P25789, P25786, P25787, O14818, P60900, P28066 | 72.7021277 |
| nucleoplasm | 60 | 31.5789474 | 1.56E-08 | O15131, Q5H9R7, Q99460, P31943, P14324, P62280, P62993, Q14137, Q13526, O4339 | 2.0891416 |
| blood microparticle | 13 | 6.84210526 | 5.57E-08 | P02763, P01861, P01871, P01877, P19827, P04217, P01011, P62195, P00751, P02649, P1 | 8.29059351 |
| mitochondrion | 36 | 18.9473684 | 2.16E-07 | Q9BPW8, P42126, P31947, P21964, P09622, Q13162, P11586, Q9BY49, O43464, P14324 | 2.62186486 |
| extracellular matrix | 14 | 7.36842105 | 1.21E-05 | P62081, P21333, P14923, P61353, P31944, P68371, P62280, P02649, Q14697, P48047, P | 4.58481886 |
| focal adhesion | 16 | 8.42105263 | 1.29E-05 | Q9Y490, P62140, P05386, Q8WUM4, P62081, P21333, P14923, P61353, Q9UHA4, P6226 | 3.9666975 |
| nucleus | 83 | 43.6842105 | 2.69E-05 | O15131, Q969U7, Q13867, P31947, P12268, O00571, Q99460, O14618, P61353, P3194 | 1.48581757 |
| cell-cell adherens junction | 14 | 7.36842105 | 3.03E-05 | Q9Y490, P31947, O00571, P21333, P25685, P14923, O14618, Q8WWM7, Q7KZF4, P280 | 4.20156775 |
| ribosome | 10 | 5.26315789 | 5.52E-05 | P62280, P83881, P05386, P62906, P62266, P62081, Q7Z2W9, Q9Y3D3, P61353, P23396 | 5.83952833 |
| melanosome | 8 | 4.21052632 | 8.17E-05 | Q7KZF4, Q14697, P55209, Q8WUM4, A6NMY6, P07339, Q00610, P30040 | 7.67811249 |
| membrane | 42 | 22.1052632 | 9.80E-05 | P43686, P12268, P21964, Q99460, P61353, P31943, P11586, P62195, O43464, P62280, (| 1.85059961 |
| cytosolic small ribosomal subunit | 6 | 3.15789474 | 1.29E-04 | P62280, P62266, O00571, P62081, P23396, P46782 | 12.1170213 |
| proteasome regulatory particle, base subcomplex | 4 | 2.10526316 | 2.18E-04 | P43686, Q99460, O00233, P62195 | 32.3120567 |
| catalytic step 2 spliceosome | 7 | 3.68421053 | 3.70E-04 | Q07955, Q86V81, O43390, Q9UK45, Q9Y3B4, P31943, P62304 | 7.37557817 |
| intracellular ribonucleoprotein complex | 8 | 4.21052632 | 5.13E-04 | P42704, Q9UHX1, Q14137, O43390, P62081, P61353, P23396, P46782 | 5.70212766 |
| mitochondrial matrix | 11 | 5.78947368 | 0.00208315 | P11498, P24539, Q15046, P43897, P30084, P42126, P13804, Q8N4T8, P09622, P23396, | 3.26084976 |
| nucleolus | 19 | 10 | 0.00318698 | O75347, Q5RKV6, P62140, Q14152, P62081, P21333, P25685, P68402, Q92688, P62280 | 2.14910996 |
| myelin sheath | 7 | 3.68421053 | 0.00485447 | P24539, P35232, P38606, Q8WUM4, Q00610, P09622, P68371 | 4.46416573 |
| proteasome regulatory particle | 3 | 1.57894737 | 0.00541995 | Q99460, O00233, P62195 | 26.43711373 |
| proteasome accessory complex | 3 | 1.57894737 | 0.01287187 | P43686, Q99460, P62195 | 17.106383 |
| extracellular vesicle | 4 | 2.10526316 | 0.01463725 | P02649, Q8WUM4, Q00610, P68371 | 7.75489362 |
| platelet alpha granule lumen | 4 | 2.10526316 | 0.01887872 | P02763, P01009, P04217, P01011 | 7.04990329 |
| actin cytoskeleton | 7 | 3.68421053 | 0.02519901 | P36871, Q9Y281, P26639, P21333, Q96GD0, P14923, P49720 | 3.11262932 |
| U12-type spliceosomal complex | 3 | 1.57894737 | 0.02896392 | Q9UK45, Q9Y3B4, P62304 | 11.1849427 |
| Myb complex | 2 | 1.05263158 | 0.03047044 | P21333, Q00610 | 64.6241135 |
| small ribosomal subunit | 3 | 1.57894737 | 0.03107351 | P62266, P23396, P46782 | 10.7706856 |
| cytosolic large ribosomal subunit | 4 | 2.10526316 | 0.03276248 | P83881, P05386, P62906, P61353 | 5.70212766 |
| nuclear pore | 4 | 2.10526316 | 0.03785899 | O15131, Q95373, Q9NRG9, O00505 | 5.38534279 |
| cytoplasmic vesicle membrane | 5 | 2.63157895 | 0.04093959 | P27348, P31947, Q04917, Q10567, P62491 | 3.84667342 |
| nuclear speck | 6 | 3.15789474 | 0.05656607 | Q07955, Q8WWM7, Q15020, Q86V81, Q13526, O00571 | 2.89361702 |
| polysome | 3 | 1.57894737 | 0.05786349 | P25786, P60900, P23396 | 7.65285554 |
| spliceosomal complex | 4 | 2.10526316 | 0.07247007 | Q98Z25, O43390, Q96I25, P62304 | 4.12494341 |
| nuclear proteasome complex | 2 | 1.05263158 | 0.07921578 | P43686, P62195 | 24.2340426 |
| cell | 4 | 2.10526316 | 0.08370648 | P02649, Q8NBF2, Q6DKJ4, Q13162 | 3.87744681 |
| cytoskeleton | 8 | 4.21052632 | 0.08863626 | O43464, Q7Z794, P00491, P42704, P52565, Q96GD0, P14923, P68371 | 2.09026782 |
| neuron projection | 6 | 3.15789474 | 0.09738294 | P25325, P16949, Q13526, Q9HB71, Q99497, P78330 | 2.45408026 |
| cytosolic proteasome complex | 2 | 1.05263158 | 0.09802425 | P43686, P62195 | 19.387234 |
| extracellular space | 20 | 10.5263158 | 0.09816487 | P02763, P01861, P02788, P01871, Q9Y281, P01877, P52565, P31947, P04217, Q13162, I | 1.43928983 |