**Virologica Sinica**

**Supplementary Data**

**GCRV NS38 counteracts SVCV proliferation by intracellular antagonization during co-infection**

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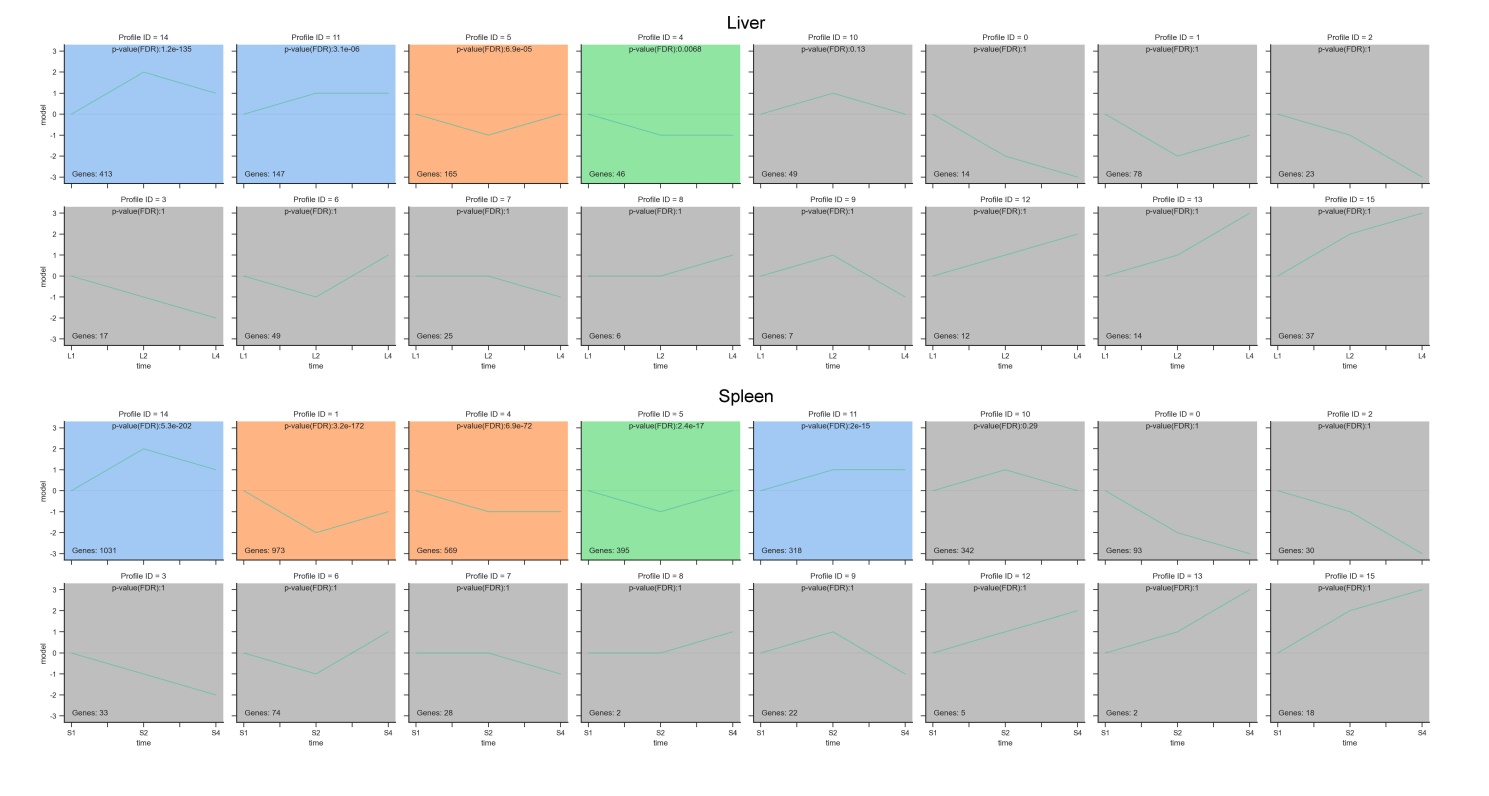
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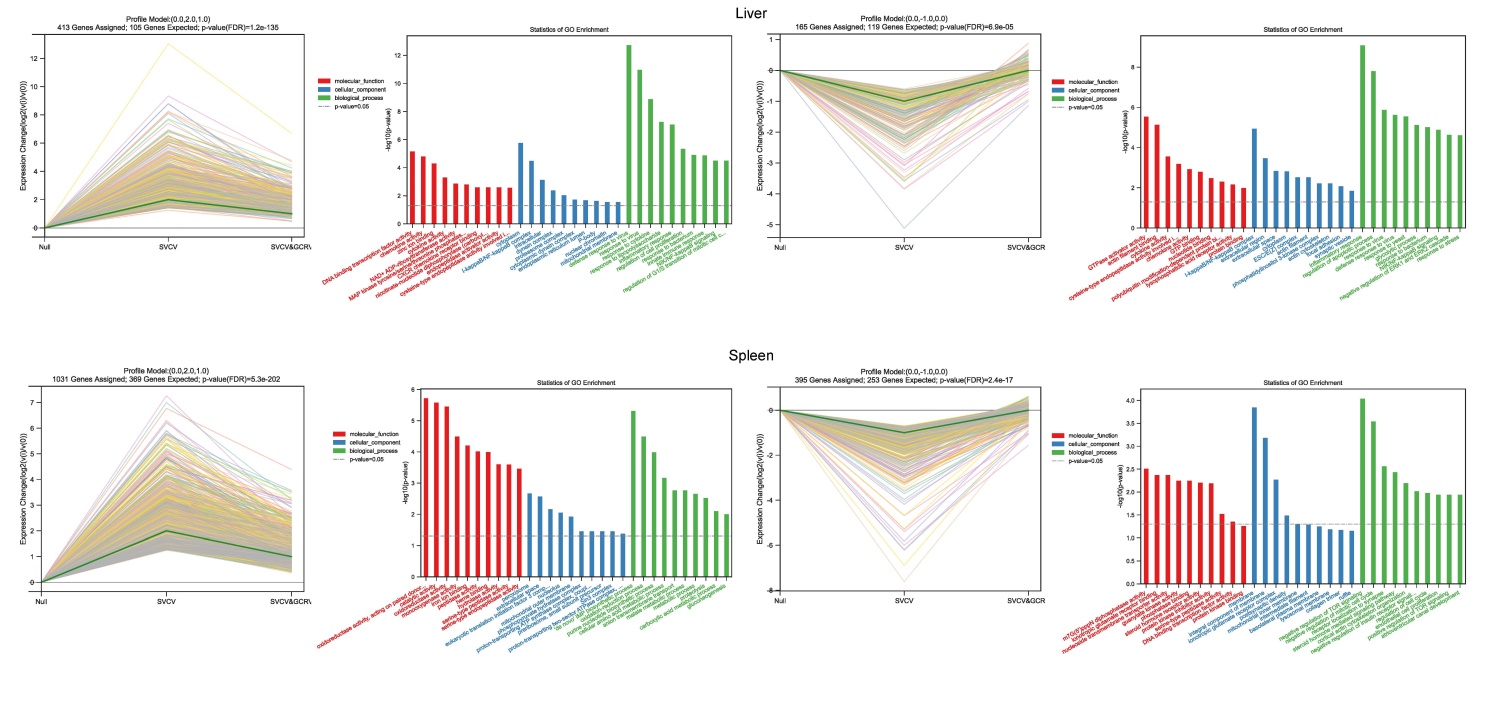
1 Zhuo-Cong Li and Long-Feng Lu contributed equally to this work.

**Supplementary Table S1** Primers used in this study.

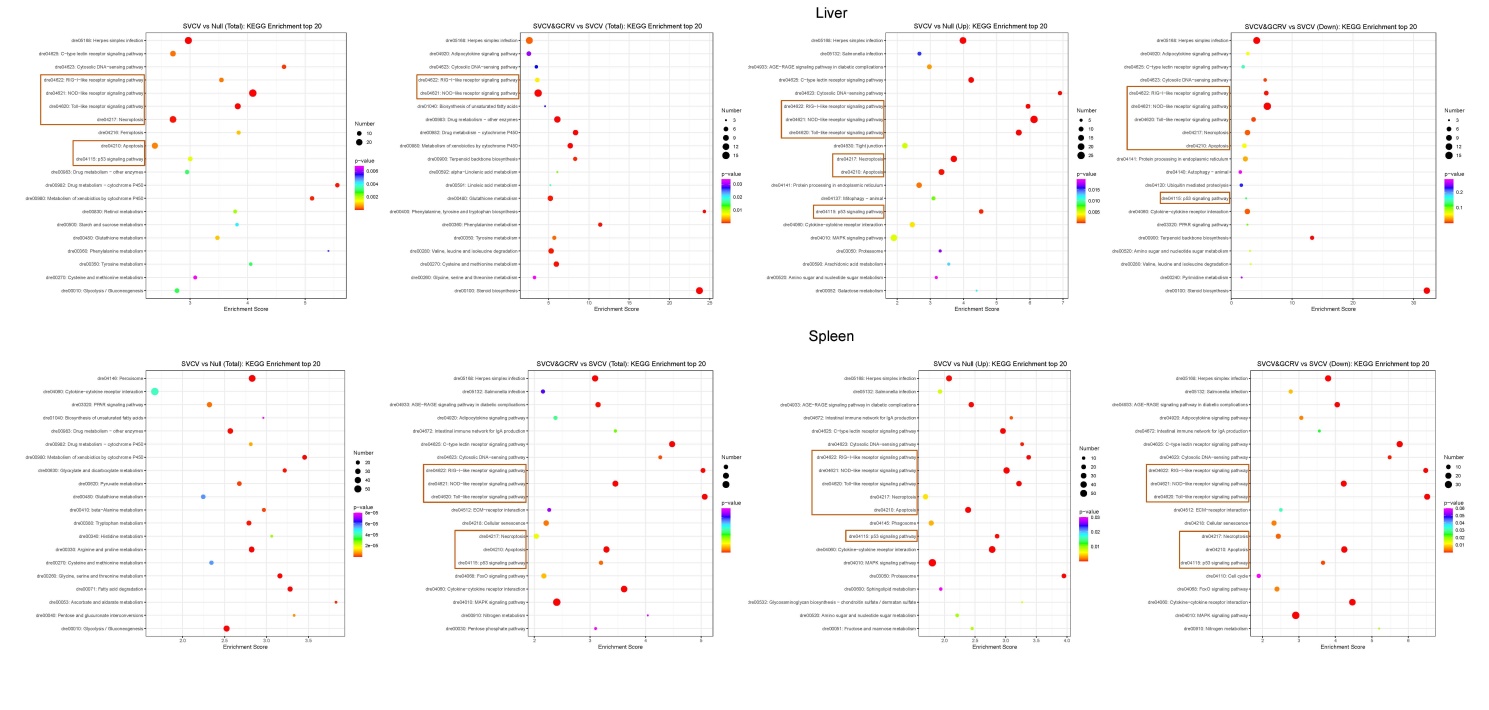
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| --- | --- | --- |
| **Name** | **Sequence (5**′**→3**′**)** | **Purpose** |
| pCMV-HA/Myc/Tag2C-NS38-F | CCGGAATTCGGATGGCACACACAGGCACC | Eukaryotic expression |
| pCMV-HA/Myc/Tag2C-NS38-R | CCGCTCGAGTTACATACCCCCGATCGGC |
| mCherry-N1-NS38-F | CCCATCGATGCCACCATGGCACACACAGGCACC |
| mCherry-N1-NS38-F | CCGGAATTCCGCATACCCCCGATCGGCAG |
| pCMV-Myc/Tag2C-N-F | CCGGAATTCCGATGAGTGTCATTCGGATCAA |
| pCMV-Myc/Tag2C-N-R | CCGCTCGAGTTATCCATAGGTTTGTTTTATCC |
| pCMV-Myc/Tag2C-P-F | CCGGAATTCCGATGTCTCTACATTCGAAATTG |
| pCMV-Myc/Tag2C-P-R | CCGCTCGAGTTACAACCTATATTTTTGATAC |
| pcDNA3.1-Flag-G-F | CGGGGTACCATGGGATCTATCATCAGCTACATC |
| pcDNA3.1-Flag-G-R | CCGCTCGAGTCATTTATCGTCATCATCTTTGTAGTCCTTGTCATCATCGTCCTTATAGTCCTTATCGTCGTCATCCTTGTAATCAACTAAAGACCGCATTTCG |
| pCMV-HA/Myc/Tag2C-S7-F | CCGGAATTCGGGCCACCATGCCTTGCCAGGATACTGTC |
| pCMV-HA/Myc/Tag2C-S7-R | CCGCTCGAGCTACTGAAACGCCTCAGGC |
| mCherry-N1-N-F | CGCGGATCCGCCACCATGAGTGTCATTCGGATC |
| mCherry-N1-N-R | CCGGAATTCCGTCCATAGGTTTGTTTTATCC |
| pEGFP-N3-N-F | CTAGCTAGCATGTACCCATACGATGTTCCAGATTACGCTAGTGTCATTCGGATCAA |
| pEGFP-N3-N-R | CGCGGATCC TCCATAGGTTTGTTTTATCC |
| pEGFP-N3-P-F | CTAGCTAGCATGTACCCATACGATGTTCCAGATTACGCTTCTCTACATTCGAAATTG |
| pEGFP-N3-P-R | CGCGGATCCCAACCTATATTTTTGATAC |
| DsRed-N1-G-F | CTAGCTAGCATGTCTATCATCAGCTAC |
| DsRed-N1-G-R | CCGCTCGAGTCAAACTAAAGACCGCATTTC |
| pCMV-HA/Myc-p62-F | CCGCTCGAGGTATGTCGATGACAGTGAGAG |
| pCMV-HA/Myc-p62-R | ATTTGCGGCCGCCTACTTCTGTTGTCCTGGTGTTTTGGAG |
| pCMV-Tag2C-p62-F | CCCAAGCTTGGATGTCGATGACAGTGAGAGCTT |
| pCMV-Tag2C-p62-R | CCGCTCGAGCTACTTCTGTTGTCCTGGTGTTTTGG |
| pCMV-Tag2C-Tollip-F | CCGGAATTCGGATGGCGACAACAATAAG |
| pCMV-Tag2C-Tollip-R | CCGCTCGAGTTAAAGCTCCTCCGCCAT |
| pCMV-Tag2C-NDP52-F | CCGGATATCAAATGAGCGACAGAACGGAG |
| pCMV-Tag2C-NDP52-R | CCGCTCGAGCTAATCCGCATGACTGTAGAC |
| pCMV-Tag2C-OPTN-F | CCGGAATTCGGATGAATGGGGACATTAGTCAC |
| pCMV-Tag2C-OPTN-R | CCGCTCGAGTCAGATGATGCAATCCATGATGTGGATCTGCAGGGAG |
| pCMV-Tag2C-NBR1-F | CCGGAATTCGGATGAACCTCCCCGTCACTG |
| pCMV-Tag2C-NBR1-R | CCGCTCGAGCTAATGTCTTGAGATGTGC |
| *Drifn*-F | GAATGGCTTGGCCGATACAGGATA | qPCR |
| *Drifn*-R | TCCTCCACCTTTGACTTGTCCATC |
| *Drirf3*-F | AAGGTGCTGTCGGTGGTTTG |
| *Drirf3*-R | ATGTGGTTGAGTGGCAGTCT |
| *S9-*F | GCCGCTCGTGATTTGTTA |
| *S9-*R | GGGTAGGTGTCGGGTAGTTC |
| *EPCβ-actin*-F | CACTGTGCCCATCTACGAG |
| *EPCβ-actin*-R | CCATCTCCTGCTCGAAGT |
| *Drβ-actin*-F | CACTGTGCCCATCTACGAG |
| *Drβ-actin*-R | CCATCTCCTGCTCGAAGTC |
| *n*-F | TGAGTGCTGAGGACGAT |
| *n*-R | TTTGTGAGTTGCCGTTA |
| *p*-F | TTGGACCTGGGATAGTGA |
| *p*-R | CTTGCTTGGTTTGTGGG |
| *m*-F | TACTCCTCCCACTTACGA |
| *m*-R | CAAGAGTCCGAGAAGGTC |
| *g*-F | CGACCTGGATTAGACTTG |
| *g*-R | AATGTTCCGTTTCTCACT |
| *l*-F | GCCCACTTTGCATCCAGTCC |
| *l*-R | GAGATGCCACAGACTCCTCC |
| sh-S9#1-FP | CCGGGCACCGCTACTCTGATCAATGCTCGAGCATTGATCAGAGTAGCGGTGCTTTTTG | RNAi |
| sh-S9#1-RP | AATTCAAAAAGCACCGCTACTCTGATCAATGCTCGAGCATTGATCAGAGTAGCGGTGC |
| sh-S9#2-FP | CCGGGCTCACACCGCTACCAATACTCTCGAGAGTATTGGTAGCGGTGTGAGCTTTTTG |
| sh-S9#2-RP | AATTCAAAAAGCTCACACCGCTACCAATACTCTCGAGAGTATTGGTAGCGGTGTGAGC |
| sh-p62#1-FP | CCGGGCCCTTTCAAATGCACTATAACTCGAGTTATAGTGCATTTGAAAGGGCTTTTTG |
| sh-p62#1-RP | AATTCAAAAAGCCCTTTCAAATGCACTATAACTCGAGTTATAGTGCATTTGAAAGGGC |
| sh-p62#2-FP | CCGGGGACTCACCTGAGCTCTAAAGCTCGAGCTTTAGAGCTCAGGTGAGTCCTTTTTG |
| sh-p62#2-RP | AATTCAAAAAGGACTCACCTGAGCTCTAAAGCTCGAGCTTTAGAGCTCAGGTGAGTCC |

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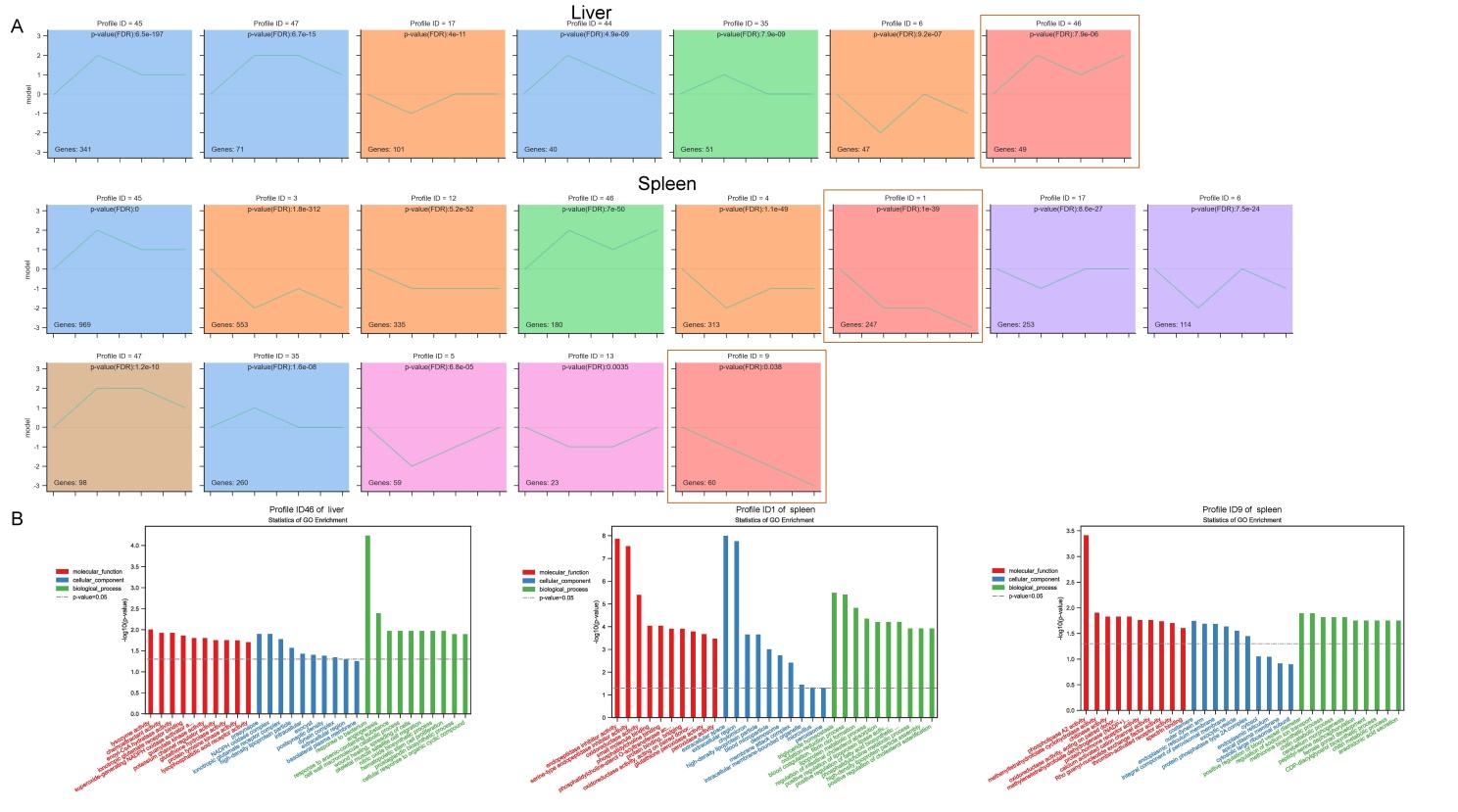
**Supplementary Fig. S1.** The gene modules enriched by STEM analysis in liver and spleen tissues of zebrafish. Three different treatment groups (Null, SVCV, and SVCV&GCRV) of genes were analyzed, with grey representing modules with no-significant changes and FDR less than 0.05 being distinguished by colour. The same colours represent similar patterns of gene variation.

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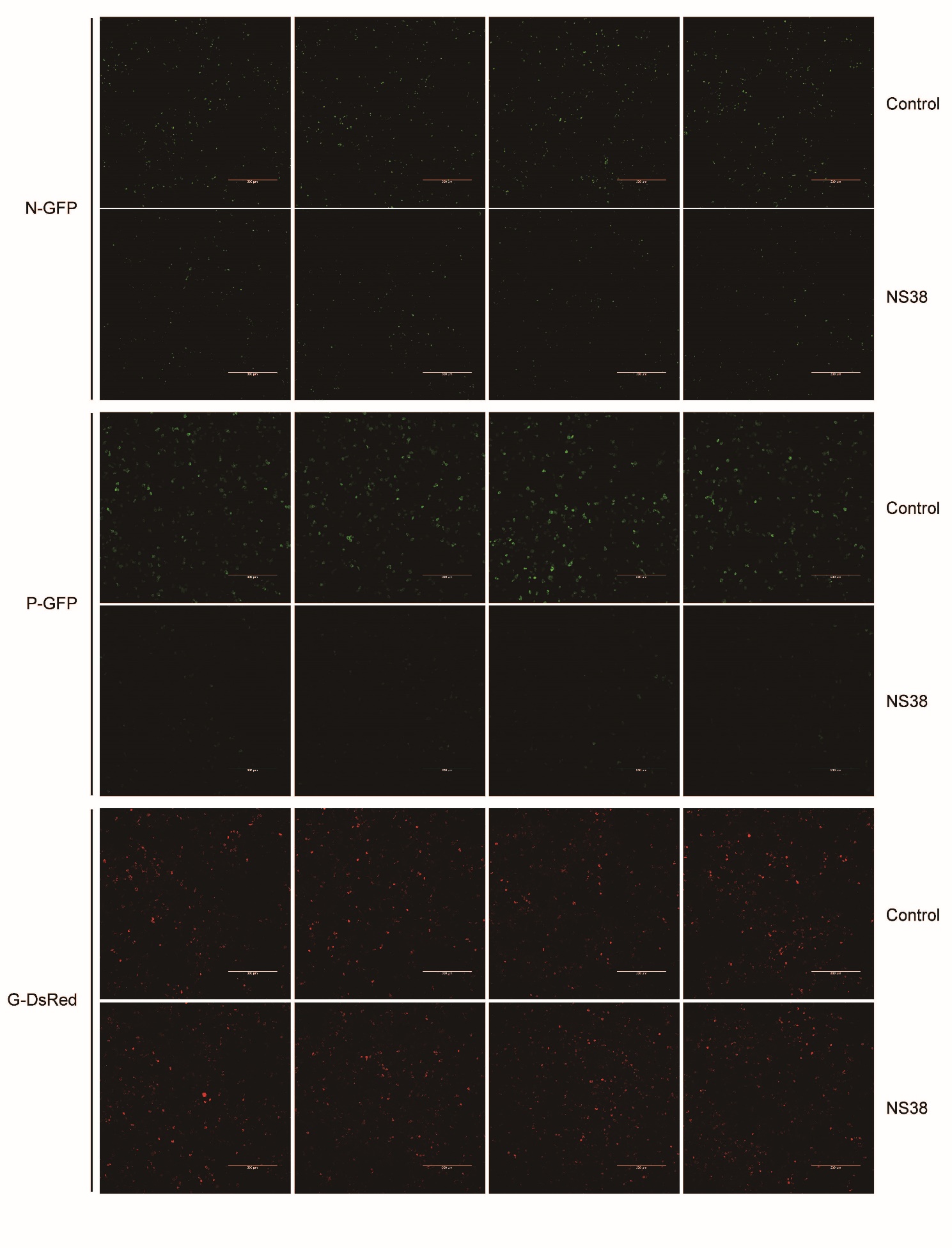
**Supplementary Fig. S2.** Gene profiles and GO analysis of representative gene modules in STEM analysis for different tissues.

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**Supplementary Fig. S3.** KEGG enrichment top 20 of two comparison groups (SVCV versus Null and SVCV&GCRV versus SVCV). Typical immune and cell-cycle related signaling pathways are framed in orange.

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**Supplementary Fig. S4.** STEM analysis in liver and spleen tissues of zebrafish. Four different treatment groups (Null, SVCV, SVCV&GCRV and GCRV) of genes were analyzed. Gene modules with the same gene expression trends in the groups GCRV and SVCV were framed and subjected to GO analysis.

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**Supplementary Fig. S5.** Reference images for fluorescence intensity analysis of NS38-induced fluorescently labelled N/P proteins degradation. EPC cells were plated onto coverslips in 6-well plates and transfected with indicated plasmids (1 μg each). After 24 h, the cells were fixed and subjected for confocal microscopy analysis. Green or red signals represent overexpressed N, P, and G proteins (original magnification 10×; Non-immersion objective). Scale bar, 300 μm.