**Supplementary Table S1A** Characteristics of the patients' study group

| Parameter | Variable | HCV-ACR (n = 10) | HCV-recurrence (n = 22) | p-value |
|---|---|---|---|---|
| | | | | |
| Age in years (range) | | 50 (43-54) | 54 (46-60) | 0.061 |
| | | | | |
| Race | White | 8 | 13 | 0.254 |
| | Black | 2 | 4 | |
| | Other | 0 | 5 | |
| | | | | |
| Gender | Female | 5 | 7 | 0.554 |
| | Male | 5 | 15 | |
| | | | | |
| Time post-LT in month (range) | | 3 (1-11) | 20 (1-67) | 0.045 |
| | | | | |
| HCV (IU/ml) | | 5.14E06 ± 4.81E06 | 6.02E06 ± 3.56E06 | 0.665 |

**Supplementary Table S1B** Characteristics of the patients' validation group

| Parameter | Variable | HCV-ACR (n = 10) | HCV-recurrence (n = 9) | p-value |
|---|---|---|---|---|
| | | | | |
| Age in years (range) | | 50 (37-65) | 58 (49-66) | 0.023 |
| | | | | |
| Race | White | 6 | 9 | 0.116 |
| | Black | 4 | 0 | |
| | | | | |
| Gender | Female | 5 | 3 | 0.791 |
| | Male | 5 | 6 | |
| | | | | |
| Time post-LT in month (range) | | 4 (1-10) | 5 (1-14) | 0.606 |
| | | | | |
| HCV (IU/ml) | | 1.89E06 ± 3.42E06 | 9.14E07 ± 1.93E08 | 0.184 |

Significance of race and gender variables was calculated using contingency tables (Chi-square statistic). Unpaired t test was performed for significance analysis of remaining variables. A p-value   0.05 was considered significant.

**Supplementary Table S2** Associated network functions identified for specific genes differentially expressed between HCV-ACR and HCV recurrence disease

| Network ID | Genes in Network | Score | Focus Genes | Top Functions |
|---|---|---|---|---|
| 1 | **BOLA1, BPHL, BRP44, CBARA1, COX11**, COX7A2, COX7A2L, COX7C (includes EG:1350), **COX8A**, D-glucose, ERO1L, G6PC, HNF1A, HNF4A, **JTB, KDELC1, L2HGDH, MRPL33**, MUT, NSF, ONECUT1, PDCD4, **PDIA5**, RB1, RPA2, RPLP1, **SLC17A2, SLC37A4**, SSSCA1, **TMEM176A, TMEM176B,** TRAPPC3, TRAPPC4, **TRAPPC6A** | 33 | 16 | Carbohydrate Metabolism, Molecular Transport, Small Molecule Biochemistry |
| 2 | **ATF6B**, **BAD, BAG1, CAMK2N1**, Caspase, **DHPS**, DUSP4, EF-1 alpha, **EPOR**, ERK, ERRFI1, Estrogen Receptor, Histone h3, **ING4**, INSL3, Mapk, Mapk kinase, Mek, **MGMT**, MOS, MST1, NFkB (complex), **NFKBIE**, **NRG1**, PDE3A, **PEMT, PHB2**, Pi3-kinase, Pkc(s), **PKP1**, **PSMA2**, Ras, **SERPINF1**, TNNI3, Vegf | 29 | 15 | Cellular Development, Reproductive System Development and Function, Renal and Urological Disease |
| 3 | **ARG2**, Arginase, Ca2+, **COX8A**, **ENTPD4**, HAS1, **HEXA**, HEXB, IFNB1, IFNG, IGHMBP2, IL8, **KCNS3**, MIR122 (includes EG:406906), | 25 | 13 | Cell Signaling, Small |

| | | | | |
|---|---|---|---|---|
| | MRPS18B, **NDUFA2, NDUFC1, OASL, PMS2L3**, POLR2F, POLR2I, **POLR2J**, POLR2K, <span style="color:green">**PRG2**</span>, PTEN, SETD7, TAF2, **TAF7**, TAF8, TAF15, TAF6L, TBP, TNF, **VPS28**, VPS37A | | | Molecule Biochemistry, Lipid Metabolism |
| 4 | **AHNAK**, CASP2, CCDC85B, **CLIC4**, Creatine Kinase, DBP, **ETHE1**, <span style="color:green">**GOLGA3**</span>, **HNMT**, **HSD17B8**, JUN, KDM5B, KRT17, LSM2, LSM4, LSM6, **LSM7**, MST1, MYOF, **N4BP1, NGFRAP1**, PERP, POP7, PPID, SMN1, SNRPD3, SUPT3H (includes EG:8464), **SUPT7L**, TADA1, TADA2B, TGFB1, **TMEM97, TOMM7**, TP53, TP53I3 | 22 | 12 | Cellular Function and Maintenance, Cell Death, Cell Morphology |
| 5 | **ADH1C (includes EG:126)**, ANXA2, AP1G1, AP2B1, **AP2S1**, AREG, AXL, beta-estradiol, **CD99 (includes EG:4267), CUTA**, EFS, ERBB, **FAM162A**, G-protein gamma, GAB2, GNG2, **GNG5**, GNG7, Gpcr, GRB2, MBTPS1, **MPDU1**, PHKA2, PPIA (includes EG:5478), **PPP1R3C**, PSMC5, RARA, RPL13, RPS3A, RPS6KA2, SHBG, SRC, SYP, TNK2, TRIM24 | 14 | 8 | Tissue Development, Gene Expression, Molecular Transport |

Differentially expressed genes in HCV recurrence disease and HCV-ACR are represented in red and green bold letter, respectively.