| Gene<br>Name | Hg19 location              | TSS_K4Me3<br>log2 fold<br>change | TSS_K4Me3<br>adjusted<br>P. value | mRNA<br>log2<br>fold<br>change | mRNA<br>adjusted P.<br>value | Gene Ontology*   |
|--------------|----------------------------|----------------------------------|-----------------------------------|--------------------------------|------------------------------|--|
| DDX60        | 4:169239000-<br>169240000  | 0.52                             | 0.0458728                         | 5.54                           | 3.60E-92                     | Induce interferon and gene expression in response to viral infection.  |
| CEBPD        | 8:48649000-<br>48650000    | 0.41                             | 0.0209813                         | 3.32                           | 2.70E-91                     | Cell differentiation, motility, growth<br>arrest, proliferation, cell death,<br>metabolism and immune responses  |
| WNT10A       | 2:219762000-<br>219763000  | 1.56                             | 0.0002341                         | 3.05                           | 0.0038363                    | Activation of Wnt/ $\beta$ -catenin signaling  |
| KLF4         | 9:110250000-<br>110251000  | 1.68                             | 4.56E-15                          | 2.45                           | 9.65E-107                    | High expression level is associated with vascular invasion and poor survival   |
| JUNB         | 19:12902000-<br>12903000   | 0.44                             | 0.0027387                         | 2.23                           | 2.87E-272                    | Cell Growth/Signal Transduction Related.   |
| EDN1         | 6:12291000-<br>12292000    | 2.17                             | 0.0068791                         | 2.20                           | 2.97E-159                    | Maintenance of vascular tone. Co-<br>mitogenic activity, potentiating the effects<br>of other growth factors such as PDGF.   |
| PDGFB        | 22:39639000-<br>39640000   | 0.57                             | 1.67E-05                          | 2.17                           | 3.51E-72                     | Growth factor, regulation of embryonic<br>development, cell proliferation, cell<br>migration, survival and chemotaxis.   |
| FOSL1        | 11:65666000-<br>65667000   | 0.8                              | 0.0120007                         | 1.7                            | 4.06E-13                     | Regulator of cell proliferation,<br>differentiation, transformation, adhesion<br>and migration.  |
| DUSP1        | 5:172195000-<br>172196000  | 1.28                             | 0.00959                           | 1.46                           | 3.68E-224                    | Induced in oxidative/heat stress, negative regulation of cellular proliferation.   |
| APOA1-<br>AS | 11:116707000-<br>116708000 | -0.6                             | 0.0143811                         | -0.75                          | 2.53E-20                     | The major protein component of high<br>density lipoprotein (HDL) in plasma. The<br>protein promotes cholesterol efflux from<br>tissues to the liver for excretion. |
| DLK1         | 14:101194000-<br>101195000 | -1                               | 0.0481319                         | -1.01                          | 7.36E-65                     | Notch signaling pathway, regulation of gene expression, cell differentiation and development.  |
| PCSK9        | 1:55506000-<br>55507000    | -0.6                             | 1.21E-08                          | -1.21                          | 8.23E-150                    | Liver development, regulation of receptor<br>recycling and internalization, regulation of<br>lipid metabolism, regulation of apoptosis.                            |

**Supplementary Table 1.** Integration of changes in histone mark H3K4Me3 (ChIP-Seq) and mRNA expression (RNA-Seq) in HCV infected compared to non-infected cells

\*Gene Ontology-adjusted from GeneCards (https://www.genecards.org/)