**Supplementary Table 6**. P values for fitted multiple linear regression model for genera in HCV subjects associated with viral load, after correction for multiple comparisons.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Taxa** | **RNA.p** | **RNA.p.fdr** | **(Intercept).c** | **RNA.c** |
| f\_Lachnospiraceae | 0.094 | 0.74894 | 3.635 | -0.543 |
| Leptotrichia | 0.137 | 0.74894 | 15.729 | -2.29 |
| Fusobacterium | 0.251 | 0.74894 | -8.764 | 1.875 |
| Bacteroides | 0.262 | 0.74894 | -6.704 | 1.282 |
| Kingella | 0.281 | 0.74894 | -7.643 | 1.663 |
| f\_Erysipelotrichaceae | 0.284 | 0.74894 | -1.235 | 0.221 |
| Gemella | 0.3 | 0.74894 | -10.459 | 2.972 |
| Porphyromonas | 0.351 | 0.74894 | -12.482 | 2.638 |
| Neisseria | 0.371 | 0.74894 | -29.701 | 6.474 |
| Veillonella | 0.389 | 0.74894 | 0.798 | 6.22 |
| Atopobium | 0.41 | 0.74894 | -6.47 | 1.417 |
| Moryella | 0.442 | 0.74894 | -4.219 | 0.959 |
| Actinobacillus | 0.467 | 0.74894 | -6.458 | 1.35 |
| Parabacteroides | 0.494 | 0.74894 | 1.187 | -0.157 |
| Megasphaera | 0.519 | 0.74894 | 11.167 | -1.09 |
| Haemophilus | 0.521 | 0.74894 | -15.305 | 4.552 |
| Granulicatella | 0.712 | 0.94179 | 9.83 | -0.584 |
| Ruminococcus | 0.778 | 0.94179 | -0.596 | 0.132 |
| Collinsella | 0.778 | 0.94179 | -0.387 | 0.086 |
| Prevotella | 0.821 | 0.94415 | 31.578 | 2.881 |
| Actinomyces | 0.92 | 0.97123 | 31.132 | -0.562 |
| Streptococcus | 0.929 | 0.97123 | 142.636 | 0.864 |
| Rothia | 0.983 | 0.983 | 6.765 | -0.03 |

Significance defined as p < 0.05 and fdr < 0.1.

Abbreviations: RNA, ribonucleic acid; fdr, false discovery rate; f, family