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APPENDIX 1

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SUPPORTING INFORMATION

Additional Supporting Information may be found in the online version of this article:

Fig. S1 Quartiles of LDL_C by HCV RNA level during treatment at week 2, week 4 and week 12 timepoints.

Fig. S2 LDL_C (</>130 mg/dL) by HCV RNA level during treatment at week 2, week 4 and week 12 timepoints.

Table S1: Measures of linkage disequilibrium between genome wide significant SNPs and rs12980275 by race.

Table S2: Multiple regression model for baseline LDL in Caucasians.

Table S3: Top GWAS association polymorphisms in association with total cholesterol in Caucasians.

Table S4: Top GWAS association polymorphisms in association with serum HDL-cholesterol in Caucasians.

Table S5: Top GWAS association polymorphisms in association with serum triglycerides in Caucasisans.

Table S6: Multiple regression model for LDL at 24 weeks post treatment for non-SVR patients.

Table S7: Multiple regression model for LDL at 24 weeks post treatment for patients who attained SVR.

Table S8: Comparison between treatment response at the timepoint LDL was measured.

Table S9: Comparison between genotypes within treatment response levels at the timepoint LDL was measured.

Table S10: Multiple logistic regression model for SVR.

Table S11: Multiple logistic regression model results testing interaction between LDL and IL28B genotype (rs12980275) for SVR.

Table S12: Univariate comparison of SVR rates by each *IL28B* genotype (rs12980275).

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