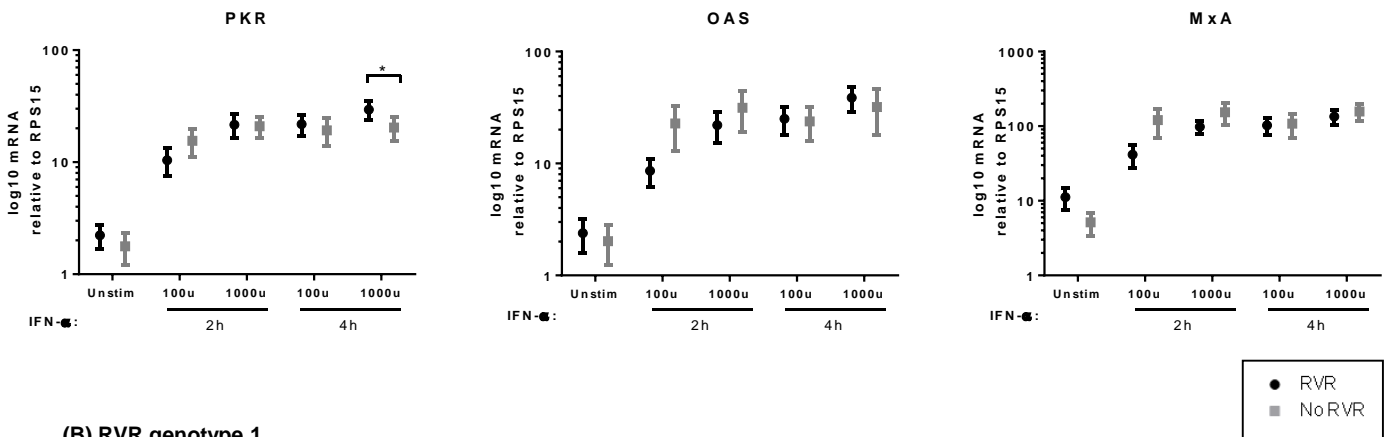
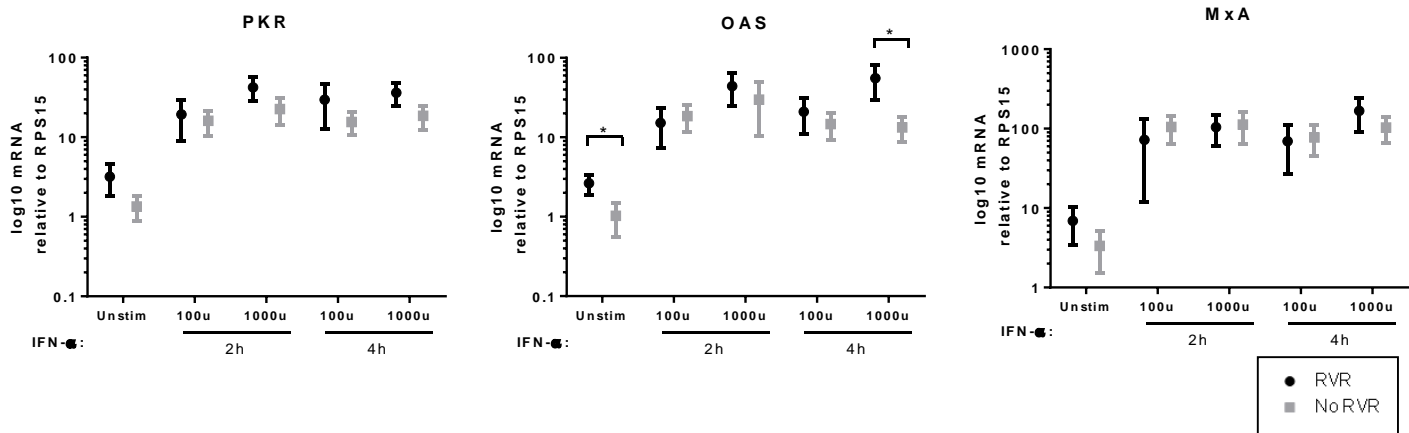


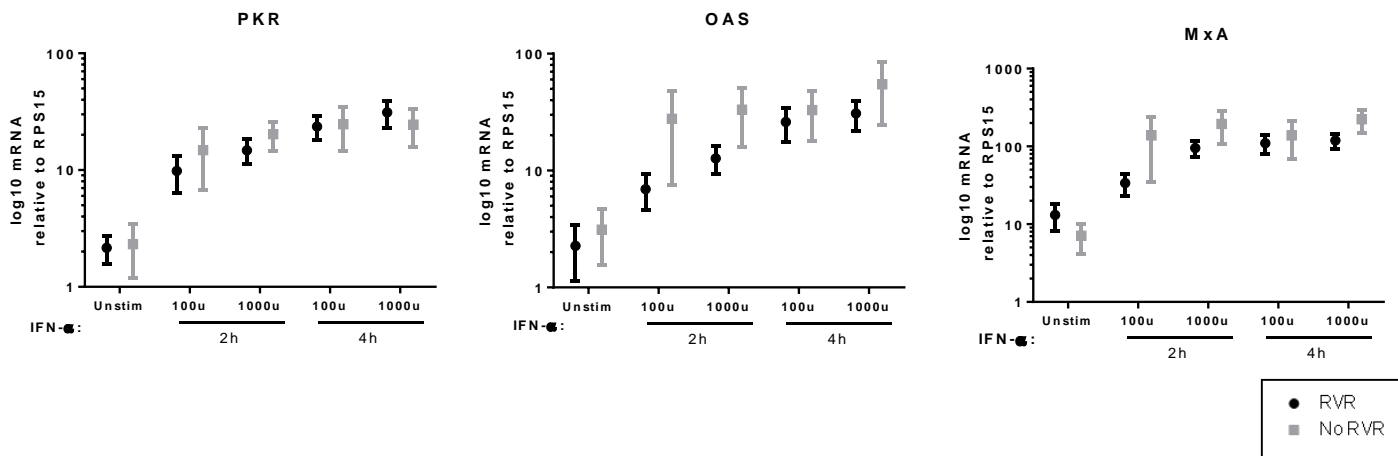
(A) RVR all genotypes



(B) RVR genotype 1

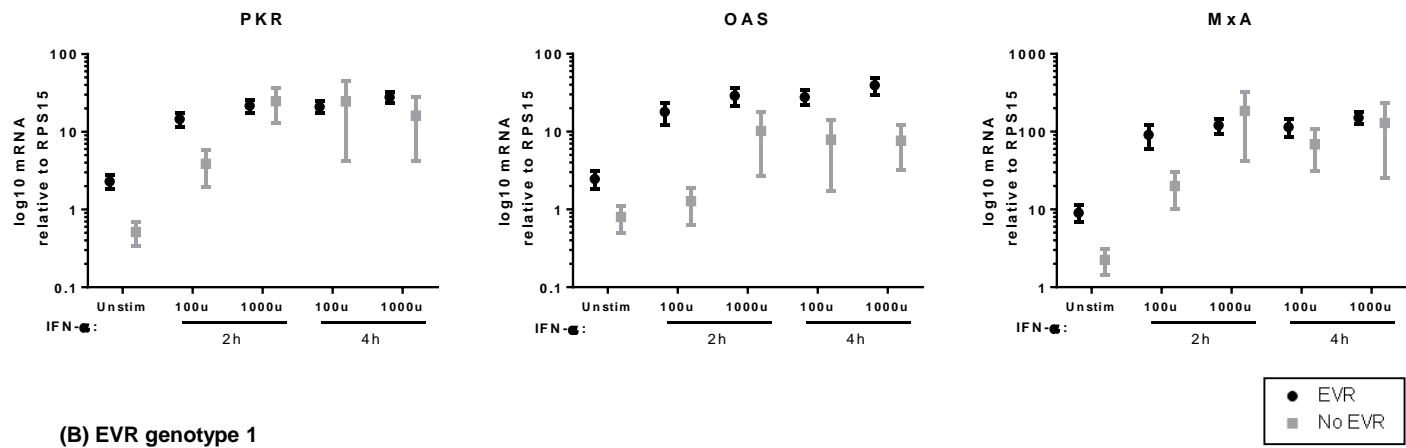


(C) RVR genotype 3

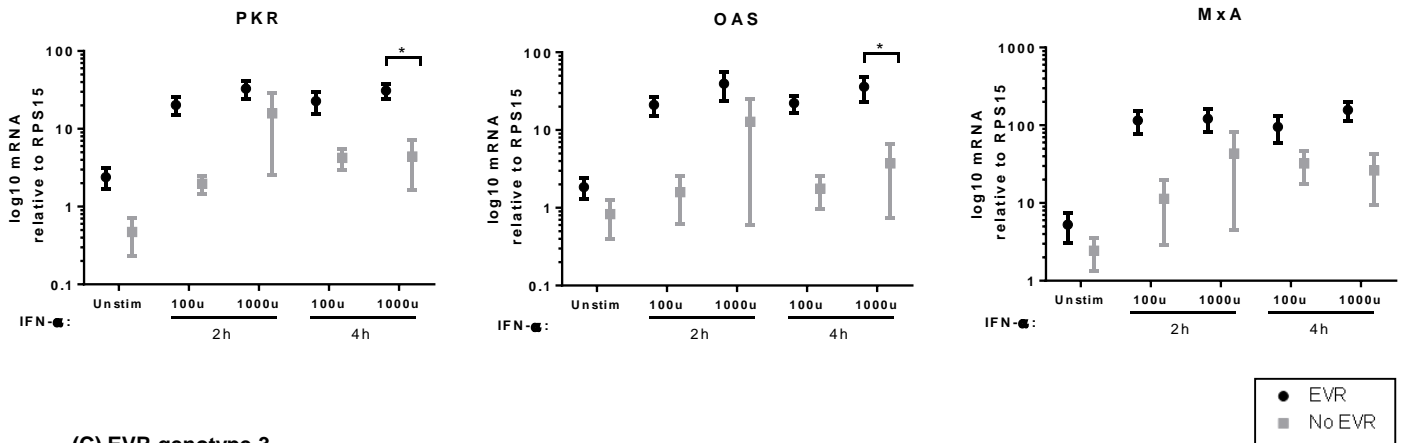


Supplemental Figure 1. Correlation between RVR and ISG expression. PBMCs were isolated from HCV infected patients prior to them commencing IFN- α therapy and were stimulated *in vitro* with 100IU or 1000IU of IFN- α for 2 or 4h. qRT-PCR was used to quantify ISG expression. Analysis stratified into those who achieved RVR and those who did not. (A) all viral genotypes, (B) genotype 1 infected patients and (C) genotype 3 infected patients. All gene expression was normalised to expression of the internal control gene RPS15 and expressed on a log scale. Mean and standard error of the mean (SEM) shown. Mann-Whitney statistical analysis, * $p < 0.05$.

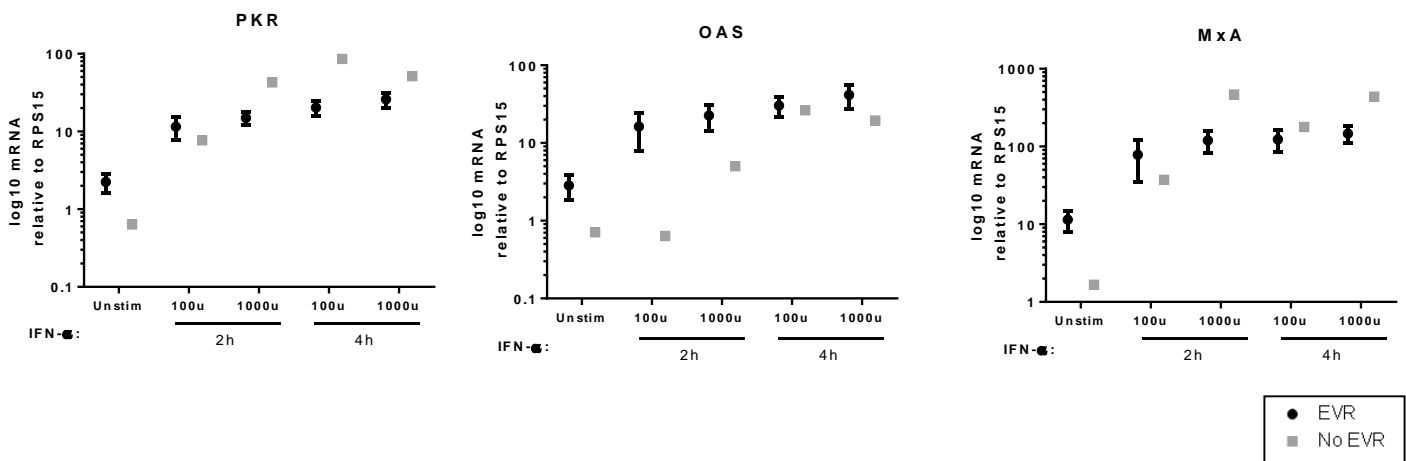
(A) EVR all genotypes



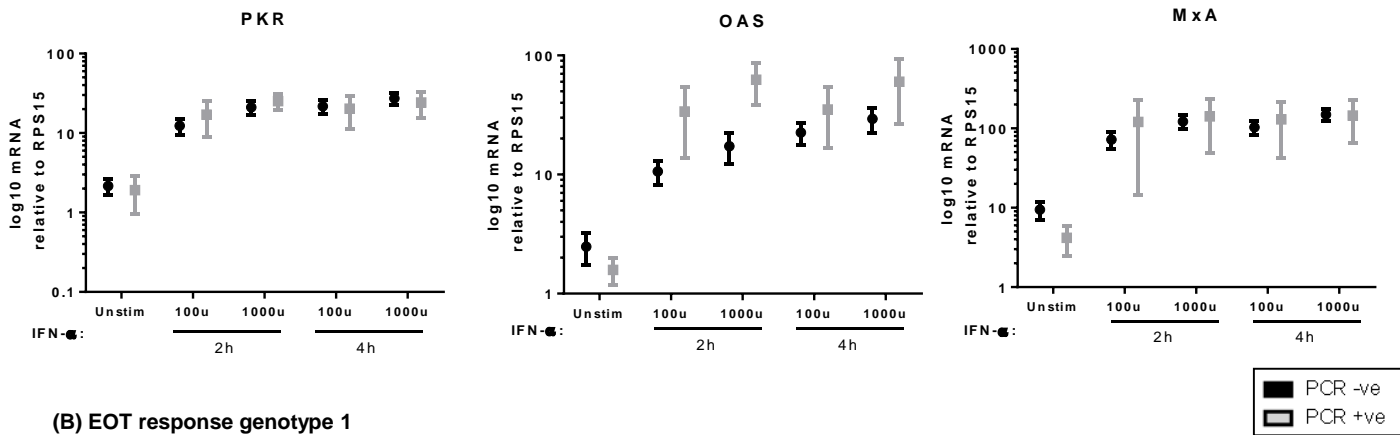
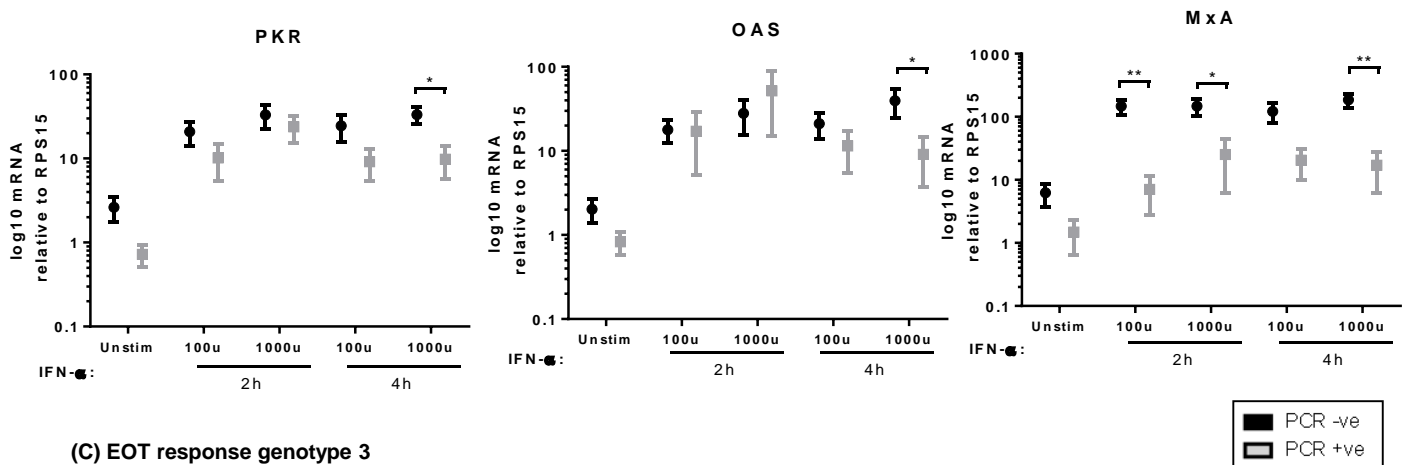
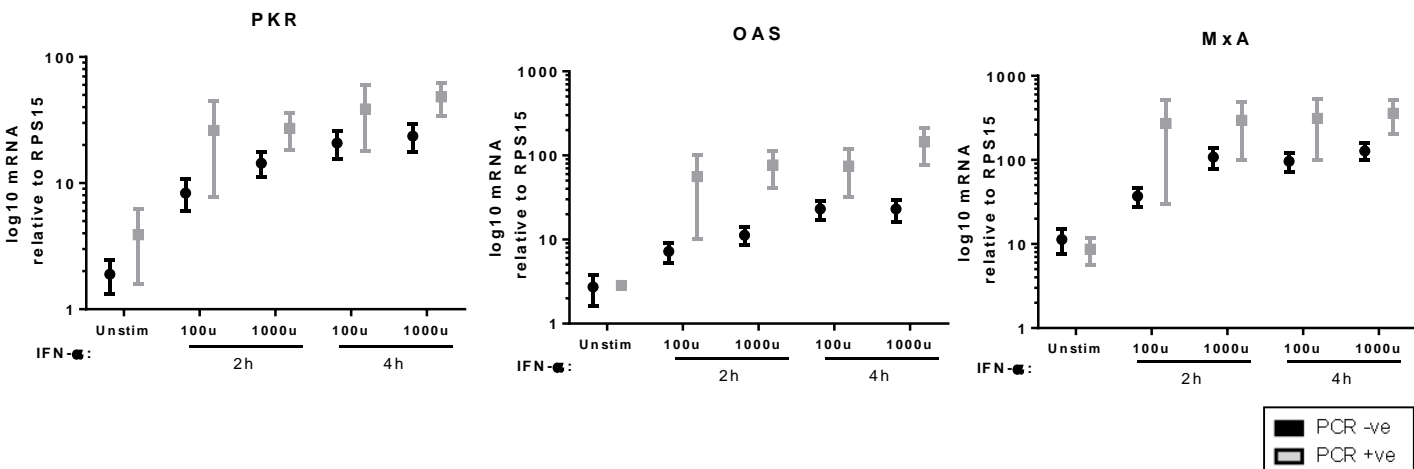
(B) EVR genotype 1



(C) EVR genotype 3



Supplemental Figure 2. Correlation between EVR and ISG expression. PBMCs were isolated from HCV infected patients prior to them commencing IFN-α therapy and were stimulated *in vitro* with 100IU or 1000IU of IFN-α for 2 or 4h. qRT-PCR was used to quantify ISG expression. Analysis stratified into those who achieved EVR and those who did not. (A) all viral genotypes (B) genotype 1 infected patients and (C) genotype 3 infected patients. All gene expression was normalised to expression of the internal control gene RPS15 and expressed on a log scale. Mean and standard error of the mean (SEM) shown. Mann-Whitney statistical analysis, *p<0.05.

(A) EOT response all genotypes**(B) EOT response genotype 1****(C) EOT response genotype 3**

Supplemental Figure 3. Correlation between EOT response and ISG expression. PBMCs were isolated from HCV infected patients prior to them commencing IFN- α therapy and were stimulated *in vitro* with 100IU or 1000IU of IFN- α for 2 or 4h. qRT-PCR was used to quantify ISG expression. Analysis stratified into those who were PCR -ve at EOT and those who were PCR +ve. (A) all viral genotypes, (B) genotype 1 infected patients and (C) genotype 3 infected patients. All gene expression was normalised to expression of the internal control gene RPS15 and expressed on a log scale. Mean and standard error of the mean (SEM) shown. Mann-Whitney statistical analysis, *p<0.05, **p<0.01.

Variables	AUC	95% CI	Cut-Off	Sensitivity (%)	Specificity (%)	PPV (%)	NPV (%)	Likelihood ratio
PKR	0.86	0.67-1.1	27.56	100	62.5	100	72.7	2.7
OAS	0.94	0.82-1.1	31.92	100	62.5	100	72.7	2.7
MxA	0.94	0.82-1.1	91.72	100	87.5	100	88.9	8

Supplemental Table 1. Predictability of SVR based on cut-off gene expression values

Gene cut off values quantified following 4h *in vitro* IFN- α stimulation, as determined by qRT-PCR, were analysed to predict response of g1 infected patients to respond to therapeutic IFN- α using receiver operating characteristic (ROC) analysis. AUC: area under curve in ROC analysis, CI: confidence intervals, PPV: positive predictive value, NPV: negative predictive value.