Supplementary figure 1

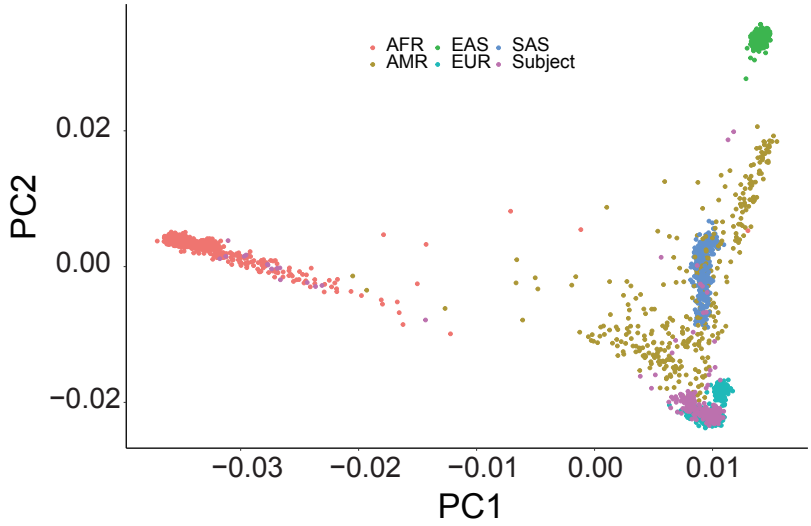

Figure S1. Genotype data distribution. Principal component analysis of genotype data from 348 HGSOC subjects compared with reference genome data from the 1,000 Genomes Project Phase 3.

Supplementary figure 2

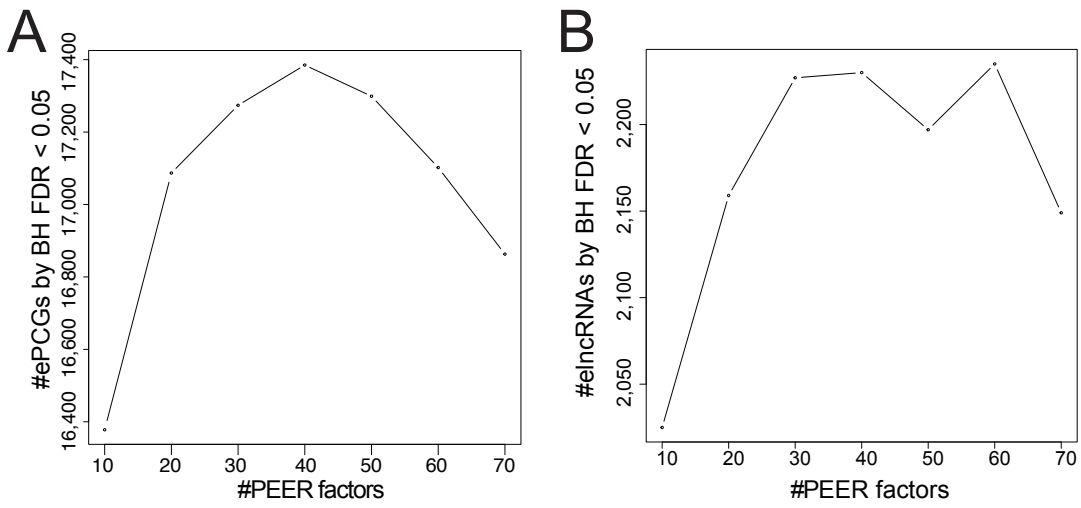

Figure S2. Optimization of PEER factors. The number of significant PCG-eQTLs (ePCGs, A) and lncRNA-eQTLs (eIncRNAs, B) varies with the number of included PEER factors. The ePCGs and eIncRNAs were identified using a Benjamin-Hochberg FDR threshold of < 0.05 for PEER factor optimization.

Supplementary figure 3

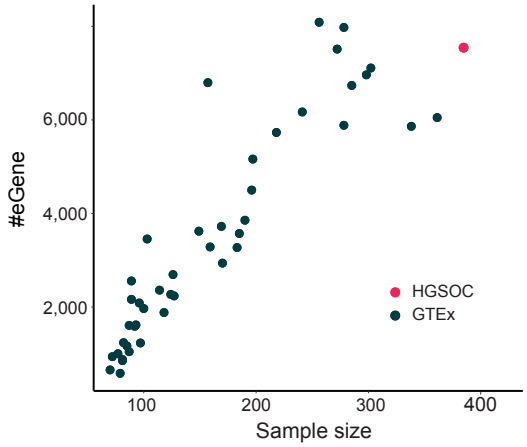

Figure S3. The number of identified eGenes in HGSOC samples. Relationship between sample size (x-axis) and the number of identified eGenes (y-axis). Red dot represents the number of identified eGenes in HGSOC samples; Black dots show the number of identified eGenes in 44 human tissues from GTEx (v7).

Supplementary figure 4

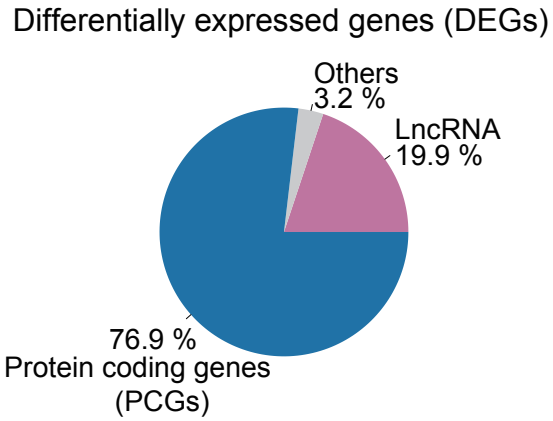

Figure S4. Composition of differentially expressed genes (DEGs). Of the DEGs, 76.9% were protein-coding genes (PCGs), and 19.9% were lncRNAs.

Supplementary figure 5

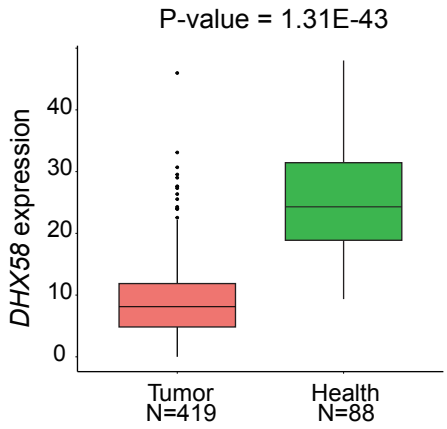

Figure S5. An example of differentially expressed gene, *DHX58*, between HGSOC tumor samples (N=419) and healthy samples (N=88). Two-sided P-value = 1.31E-43. Center lines show the medians; box limits indicate the 25th and 75th percentiles; whiskers extend to the 5th and 95th percentiles; outliers are represented by dots.

Supplementary figure 6

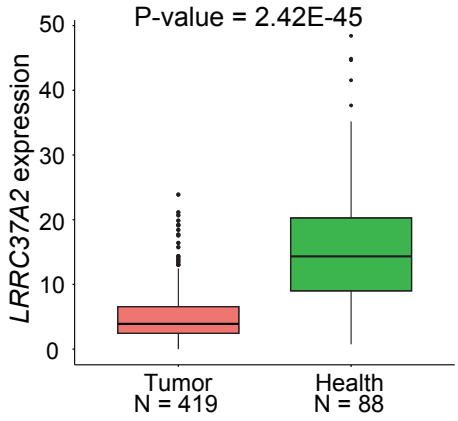

Figure S6. An example of differentially expressed gene (DEG), *LRRC37A2*, between HGSOC tumor samples (N=419) and healthy samples (N=88). Two-sided P-value = 2.42E-45. Center lines show the medians; box limits indicate the 25th and 75th percentiles; whiskers extend to the 5th and 95th percentiles; outliers are represented by dots.

Supplementary figure 7

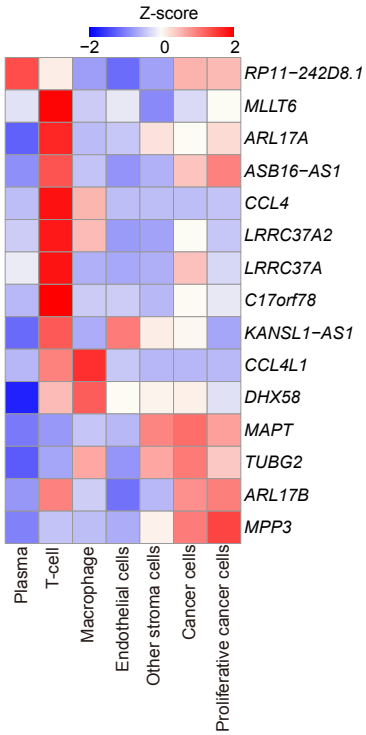

Figure S7. The single-cell expression patterns of candidate susceptibility genes on chromosome 17 identified by overlapping HGSOC GWAS with tumor eQTLs. Mean expression values for each gene were calculated in each cluster. The color scheme represents Z-score, derived from normalized gene expression levels, indicating relative expression levels compared to other cell types.

Supplementary figure 8

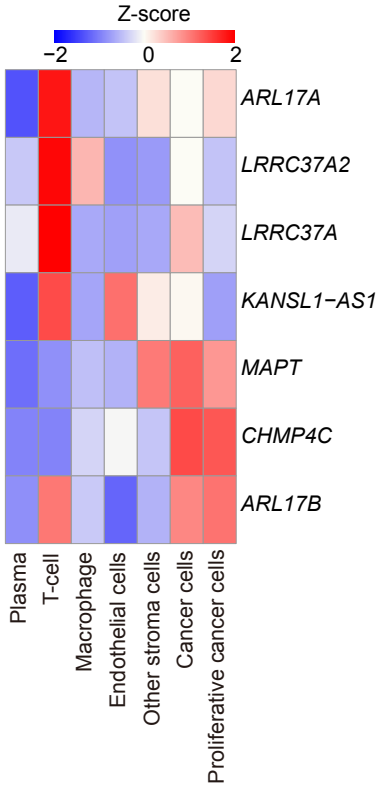

Figure S8. Expression of 7 colocalized genes in human HGSOC tumors. Mean expression value for each gene was calculated within each cluster. The color scheme represents Z-score, derived from normalized gene expression levels, indicating relative expression levels compared to other cell types.

Supplementary figure 9

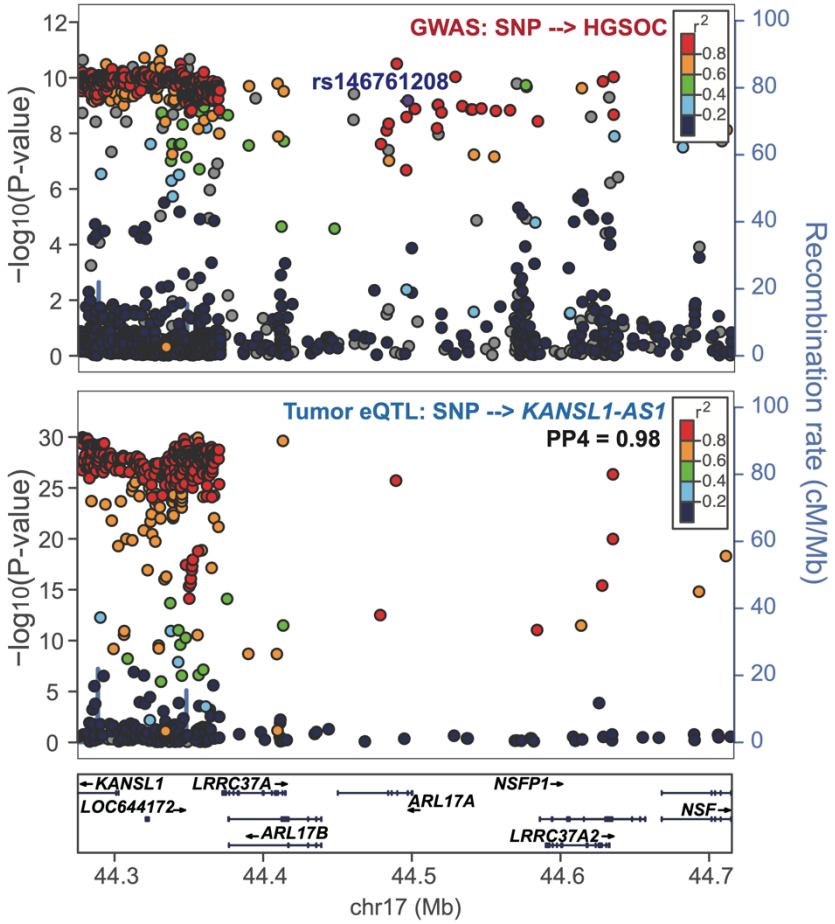

Figure S9. LocusZoom plots for HGSOC GWAS variants and HGSOC tumor lncRNA-eQTLs on *KANSL1-AS1*. The x-axis displays the ± 200 kb genomic region around rs146761208. The y-axis represents GWAS significance -$\log_{10}$(two-sided P-value). Each data point represents a variant, with color indicating the r^2 (degree of linkage disequilibrium). N = 53,978 individuals for HGSOC GWAS; N= 348 individuals for HGSOC tumor lncRNA-eQTLs.

Supplementary figure 10

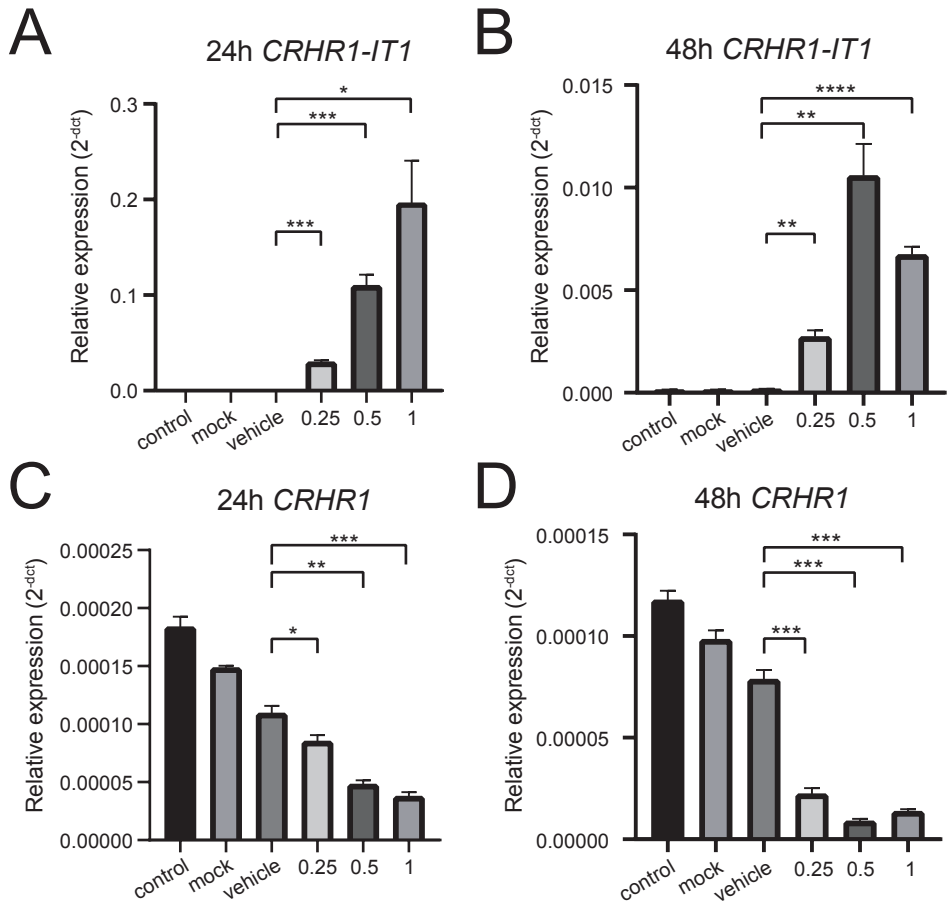

Figure S10. Expression of *CRHR1-IT1* and *CRHR1* in OVCAR-3 cells at 24 and 48 hours after transfection. (A) *CRHR1-IT1* (24 hours), (B) *CRHR1-IT1* (48 hours), (C) *CRHR1* (24 hours), and (D) *CRHR1* (48 hours). Transfection conditions include: control (0 µg/well vector, null condition), mock (0 µg/well vector, baseline transfection reagents), vehicle (1 µg/well pcDNA3.1 (+) vector), and increasing concentrations of pcDNA3.1(+)-*CRHR1-IT1* vector: 0.25 µg/well, 0.5 µg/well, and 1 µg/well. Results are presented as mean ± SE of three technical replicates per group. Significance levels are indicated as *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$ and ****$p < 0.0001$, determined by unpaired t-test.

Supplementary figure 11

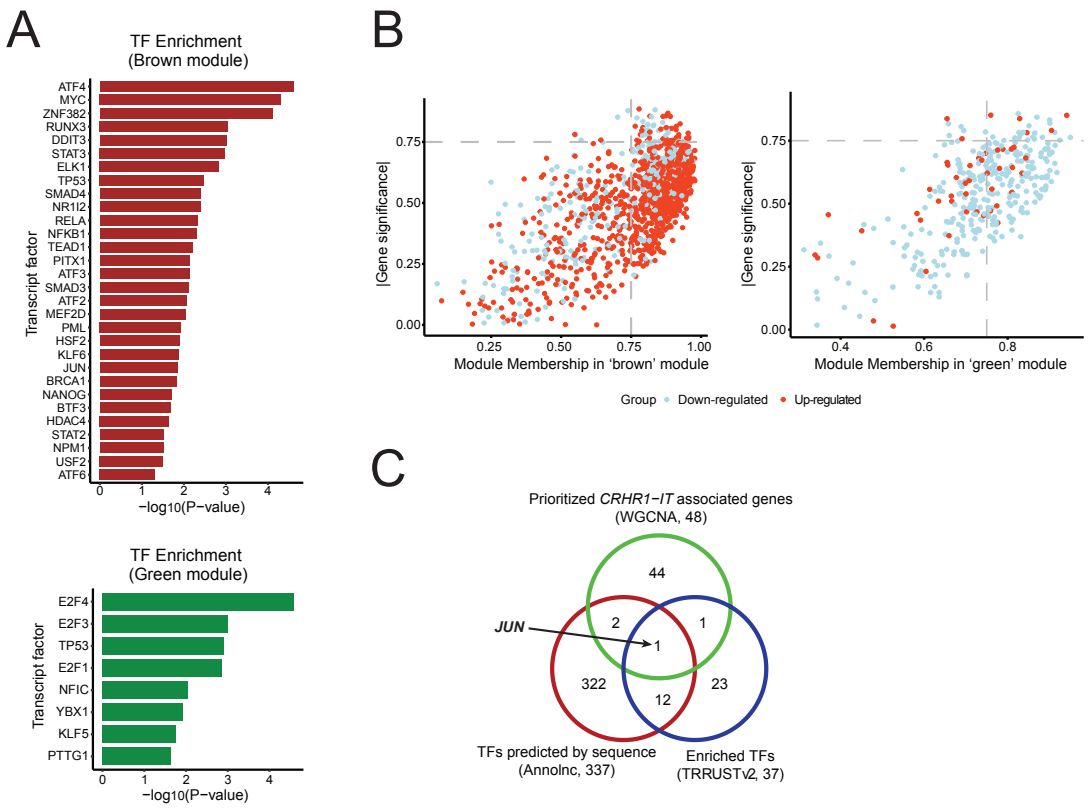

Figure S11. Co-expression network analysis highlights the role of *JUN* following *CRHR1-IT1* transfection. (A) Transcription factor enrichment analysis of genes in the 'green' and 'brown' modules. (B) Scatter plot showing Module Membership (MM, x-axis) and the absolute value of Gene Significance (GS, y-axis) for genes in the 'green' and 'brown' modules. Key genes are those with |GS| in the top 25% and MM > 0.9. (C) Venn diagram comparing sequence-based predictions (by AnnoLnc), enriched TFs (TRRUST v2), and prioritized *CRHR1-IT* expression correlated hub genes in the 'green' and 'brown' modules. *JUN* is the only gene that satisfies all three criteria.

Supplementary figure 12

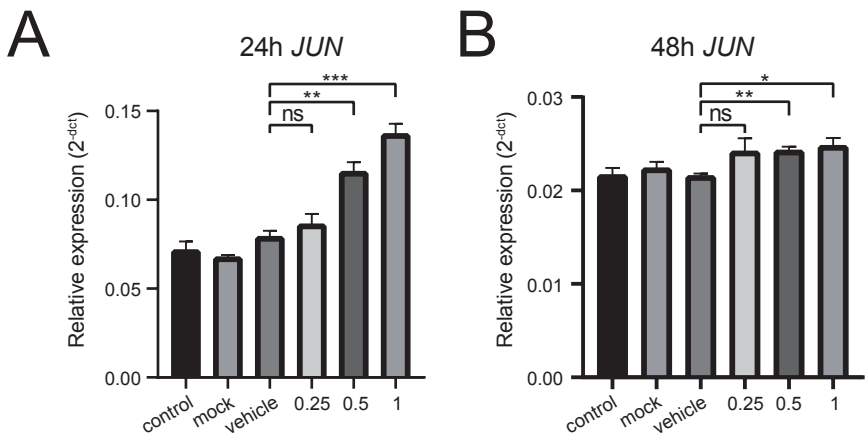

Figure S12. *JUN* expression in OVCAR-3 cells at 24 and 48 hours after transfection. (A) *JUN* (24 hours), (B) *JUN* (48 hours). Transfection conditions include: control (0 µg/well vector, null condition), mock (0 µg/well vector, with baseline transfection reagents), vehicle (1 µg/well pcDNA3.1 (+) vector), and increasing concentrations of pcDNA3.1(+)-*CRHR1-IT1* vector: 0.25 µg/well, 0.5 µg/well, and 1 µg/well. Results are shown as mean ± SE of three technical replicates per group. Significance levels are indicated as *p < 0.05, **p < 0.01, ***p < 0.001 and ****p < 0.0001, determined by unpaired t-test.

Supplementary figure 13

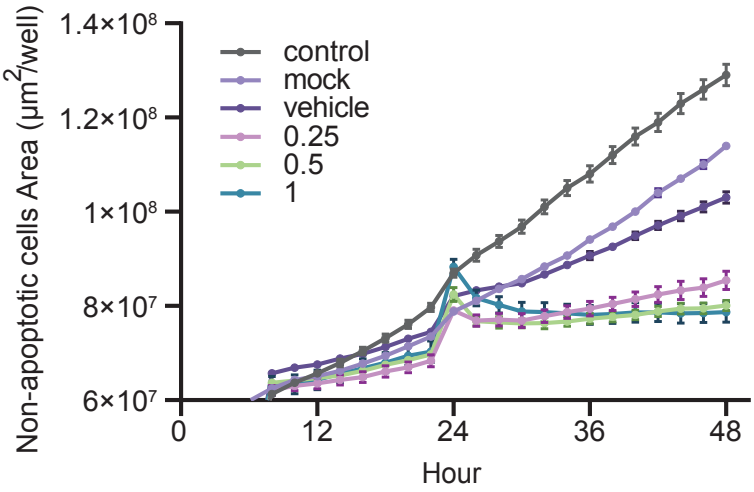

Figure S13. Real-time growth monitoring of non-apoptosis cells using the Incucyte live imaging and analysis system, starting at 6h after transfection. OVCAR-3 cells were transfected with: control (0 μg/well vector, null condition), mock (0 μg/well vector, baseline transfection reagents), vehicle (1 μg/well pcDNA3.1 (+) vector), and increasing concentrations of pcDNA3.1(+)-*CRHR1-IT1* vector: 0.25 μg/well, 0.5 μg/well, and 1 μg/well. The x-axis represents hours after transfection. The y-axis is the area of non-apoptotic cells (μm^2/well).