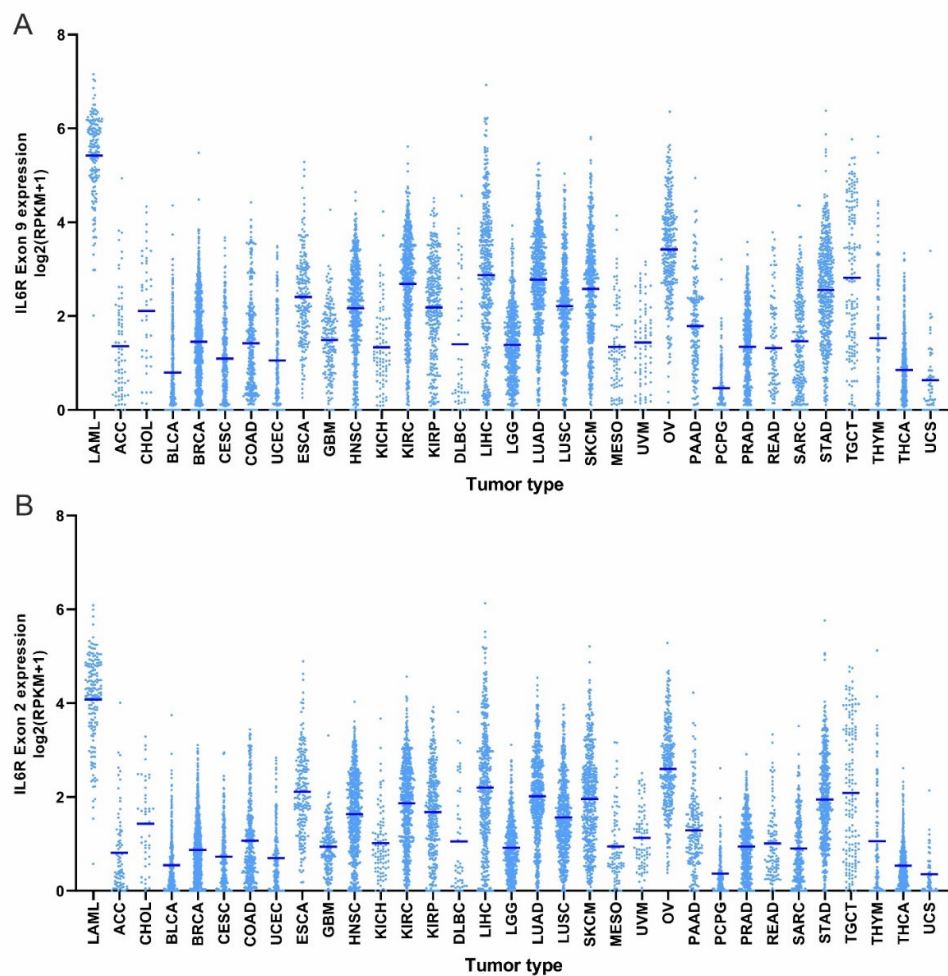
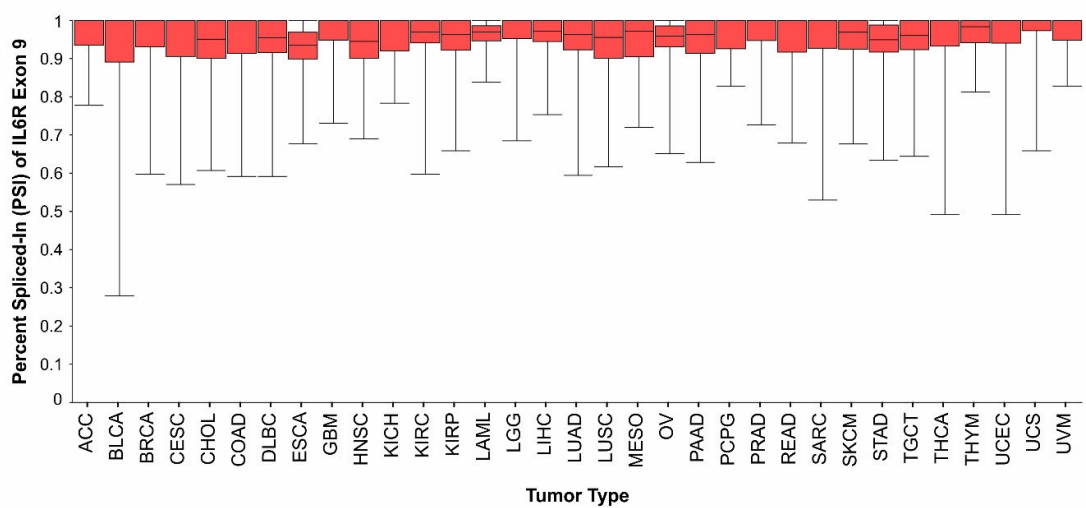


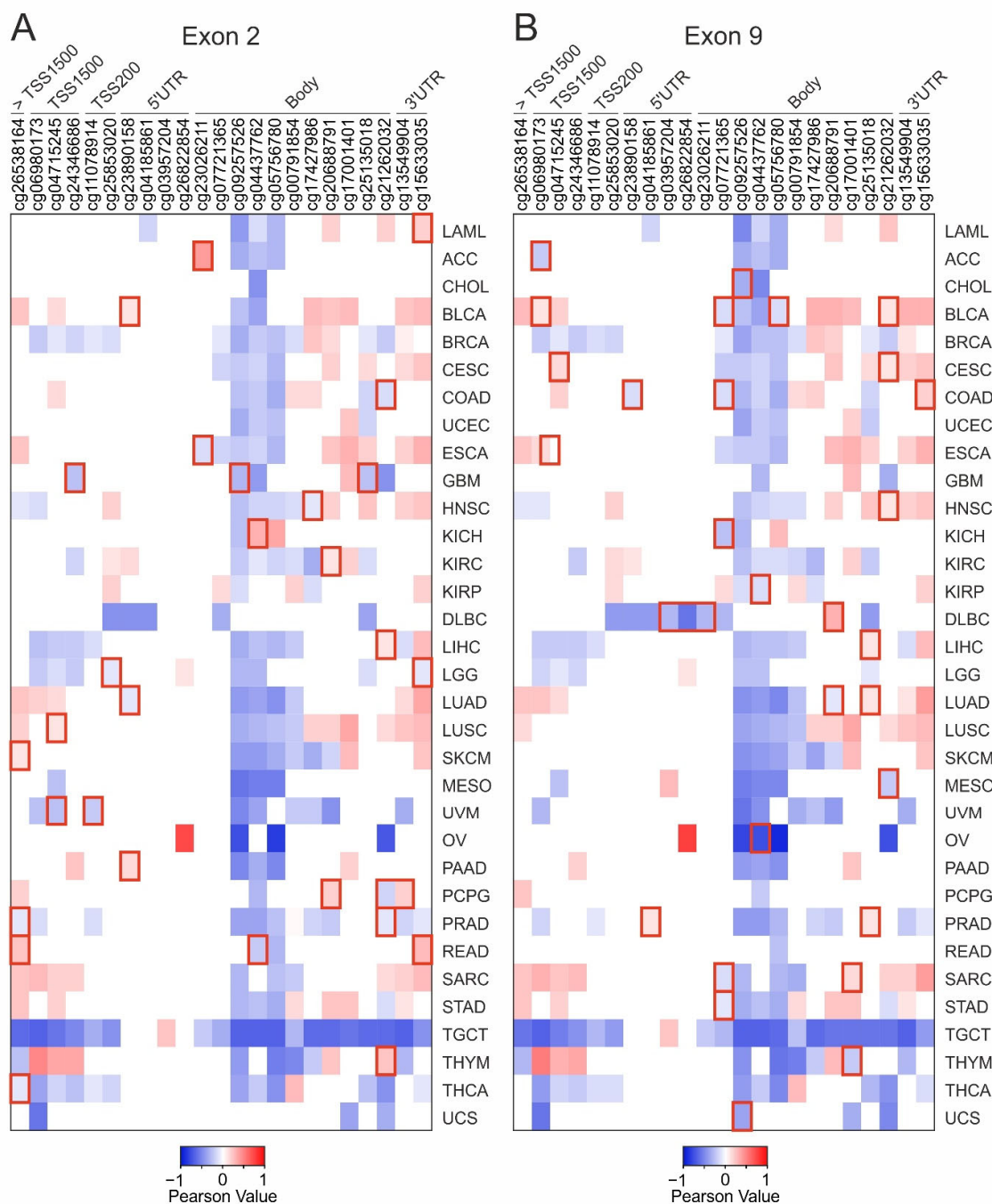
**Figure S1.** Expression levels of IL6 (A), IL6R (B) and IL6ST (C) for each TCGA cohort. The expression data were retrieved from UCSC Xena tool.



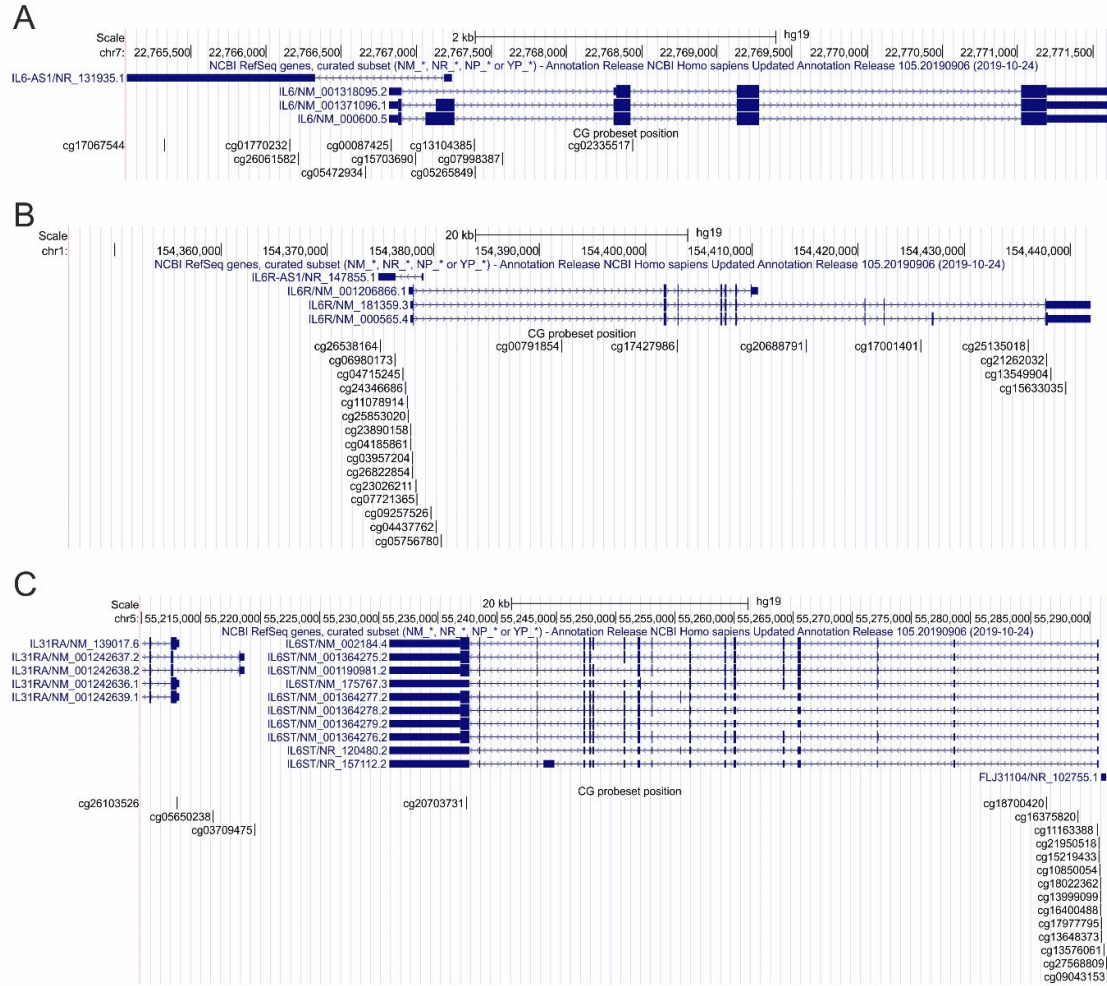
**Figure S2.** Exon expression levels IL6R Exon 9 (A) and IL6R Exon 2 (B) for each TCGA cohort. The Exon expression data were retrieved from UCSC Xena tool.



**Figure S3.** SpliceSeq analysis of IL6R gene. The percent-spliced-in (PSI) value for splicing events of IL6R Exon 9 were evaluated in all TCGA tumors.



**Figure S4.** Correlation analysis between IL6R Exon 2 and 9 expression and DNA methylation for each tumor type. The heatmap shows the correlation (Pearson's  $r \leq -0.3$  or  $\geq 0.3$ ,  $p \leq 0.05$ ) between and methylation levels of CG probesets relative to IL6R gene and Exon 9 (A) and Exon 2 (B) expression, separately. The red outlines highlight the CG probesets correlation values that are discordant or mutually exclusive among Exon 2 (A) and Exon 9 (B) correlation analysis.



**Figure S5.** Genome position of CG probesets of IL6, IL6R and IL6ST. UCSC portal (Assembly: GRCh37/hg19) was used to retrieve the genomic position of CG probeset within IL6 (A) IL6R (B) and IL6ST (C) loci. RefSeq gene annotation (NCBI: Annotation Release 105.20190906) was used to display the isoforms of each gene.