**Supplementary Figure S1.**

SNP chip analysis of three tumors from cohort 1. Total (blue) and allele-specific (red and green) copy numbers are shown along with the locations of the SNP probes (green). The locations of the genes are indicated by red arrows.

**Supplementary Figure S2.**

Copy number alterations in SCLC tumor samples based on SNP 6.0 Array data. **A**. SNP 6.0 array data for cohort 1 and cohort 2 samples was analysed with GISTIC 2.0. The *Q*-values for significant copy number amplifications are plotted. The green dashed line marks the significance threshold at *Q*-value 0.25. The significantly amplified region on the 9p24 locus is highlighted, and the genes identified within this locus are indicated. **B.** Amplification events with copy numbers of more than 4 were quantified for 88 out of 142 SCLC tumor samples. The number of amplificant events was plotted for each sample and grouped as *CD274* amplified (*CD274*amp) and non-amplified cases (no *CD274*amp). Significant enrichment of genomic copy number events were determined by Mann-Whitney-U-test.

**Supplementary Figure S3.**

Genomic rearrangements described as circos plots for case 9-P from cohort 1. **A.** and case S02404 from cohort 2. **B**. Genomic rearrangements involving chromosome 9 are indicated by purple lines, while other rearrangements are indicated by grey lines. The inner ring displays the integral copy number (iCN) state determined by whole genome sequencing (gains in red and losses in blue).

**Supplementary Figure S4.**

Chromosome 9p24, clinical and pathological features of SCLC. **A.** Expression of genes located in the 9p24.1 amplicon, expressed as FPKM values. Case 9-P and S00213 were compared to the expression data of 75 non-amplified cases (mean+SD). The range of the amplification found in all four tumor cases with 9p24 amplification is described below the bar graph. Dashed blue lines indicate the minimally amplified region on 9p24. **B**. Immunohistochemistry for SCLC markers. Scale bar as indicated. **C.** Immunhistochemistry for PD-L1 protein expression in case 6-P (cohort 1). Scale bar as indicated.

**Supplementary Figure S5.**

Analysis of immune cell signatures. **A**. Analysis of the transcriptome sequencing data for B-cells (CD19) and T-cells (CD3E), which were further distinguished for CD4-T-cells, CD8-T-cells (CD8A, CD8B) and regulatory T-cells (FOXP3, CD25). *CD274* amplified cases are highlighted in purple (9-P) and red (case S00213). Spearman correlation coefficients were dertermined to correlate the expression of PD-L1 with the respective immune cell marker. **B.** Immunhistochemistry for T-cell markers (CD3, CD4 and CD8) and B-cell markers (CD19). Black wedges point to regions with positive staining. Scale bar as indicated.