Supplementary Material S5

- Transcriptomic analyses of RNA-seq data.
- **a)** Heatmap of Euclidean sample-to-sample distances based on variance-stabilized counts of expressed genes. The lighter the color, the greater the distance. The two *ALK*-positive cases are shown clustering together.
- **b)** Unsupervised hierarchical clustering based on variance-stabilized counts of the 1000 highest expressed genes. Blue color indicates low count numbers, white color indicates medium count numbers, and red color indicates high count numbers. Again, the two cases with *ALK* rearrangement cluster together.