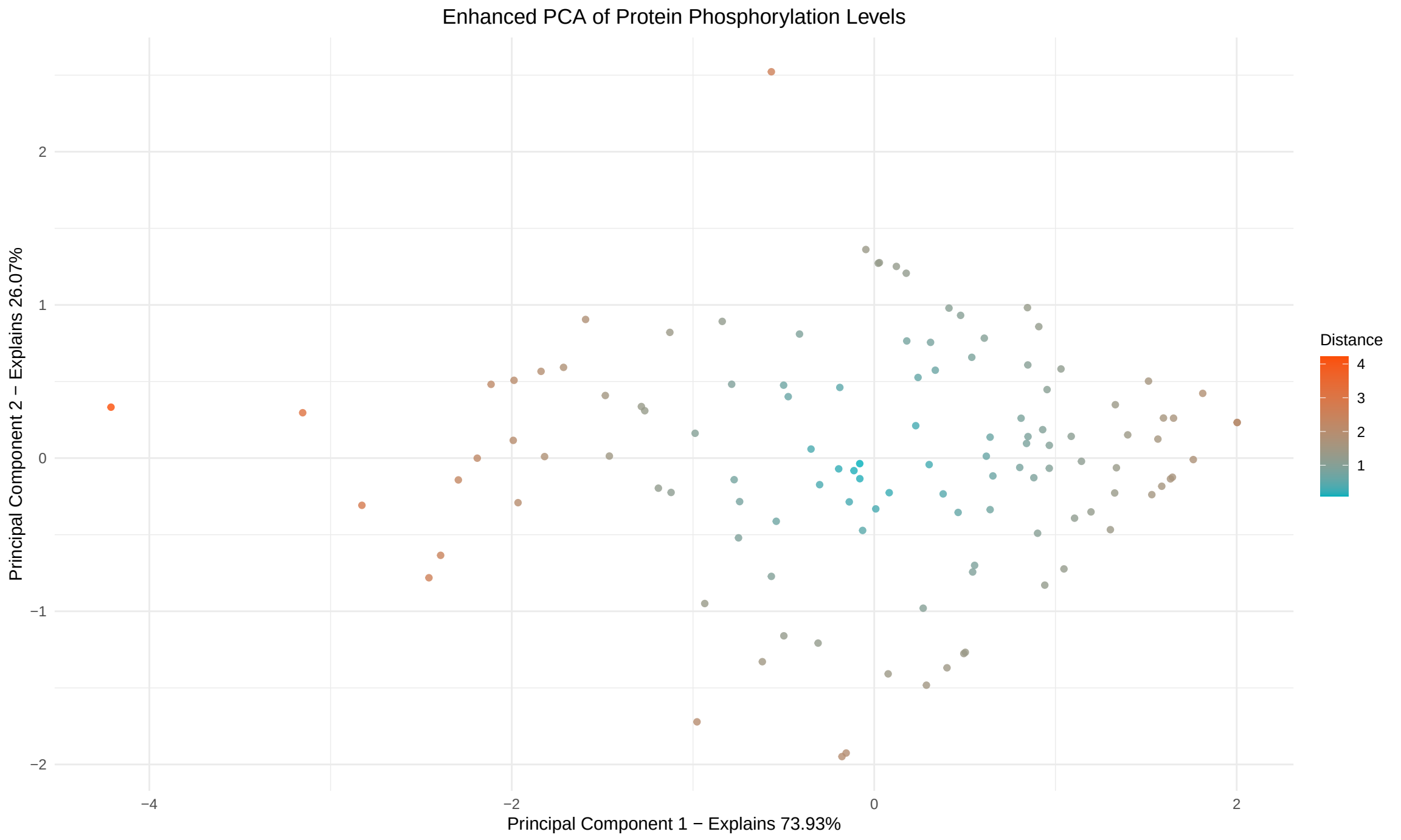

This scatter plot illustrates the distribution of protein phosphorylation levels analyzed through principal component analysis (PCA). The first principal component (horizontal axis) explains 73.93% of the variance, highlighting the major patterns of variation in phosphorylation across the dataset, while the second principal component (vertical axis) accounts for the remaining 26.07% of the variance. Each point represents a unique protein, color−coded based on their 'Distance' value, which quantifies the protein's contribution to the total variance.Points with higher 'Distance' values, shown in darker shades, contribute more significantly to the data's structure, identifying them as key drivers in the phosphorylation profile. This analysis helps in identifying proteins with significant roles in cellular signaling pathways, potentially pinpointing targets for further biochemical investigation or therapeutic intervention.