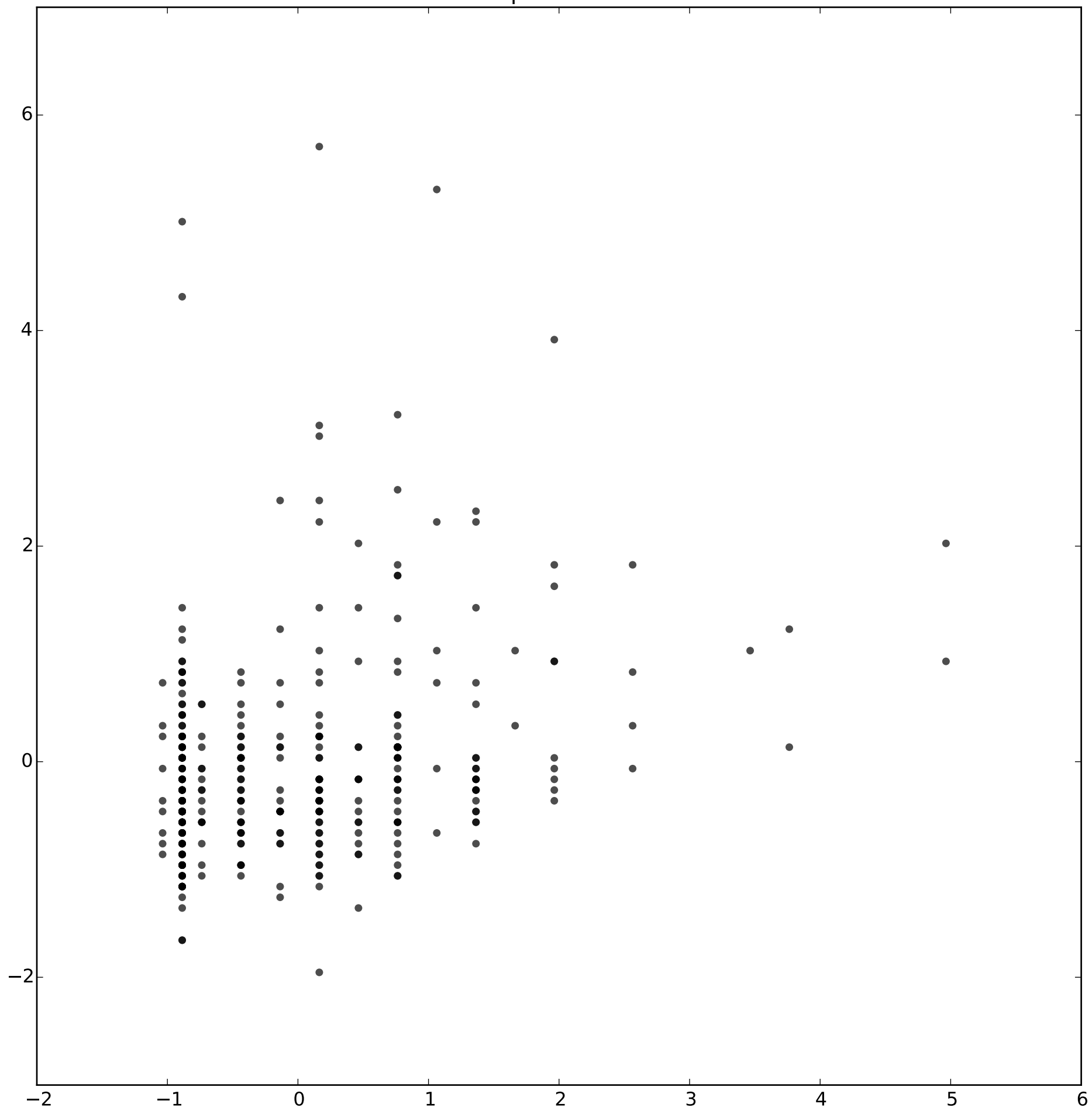
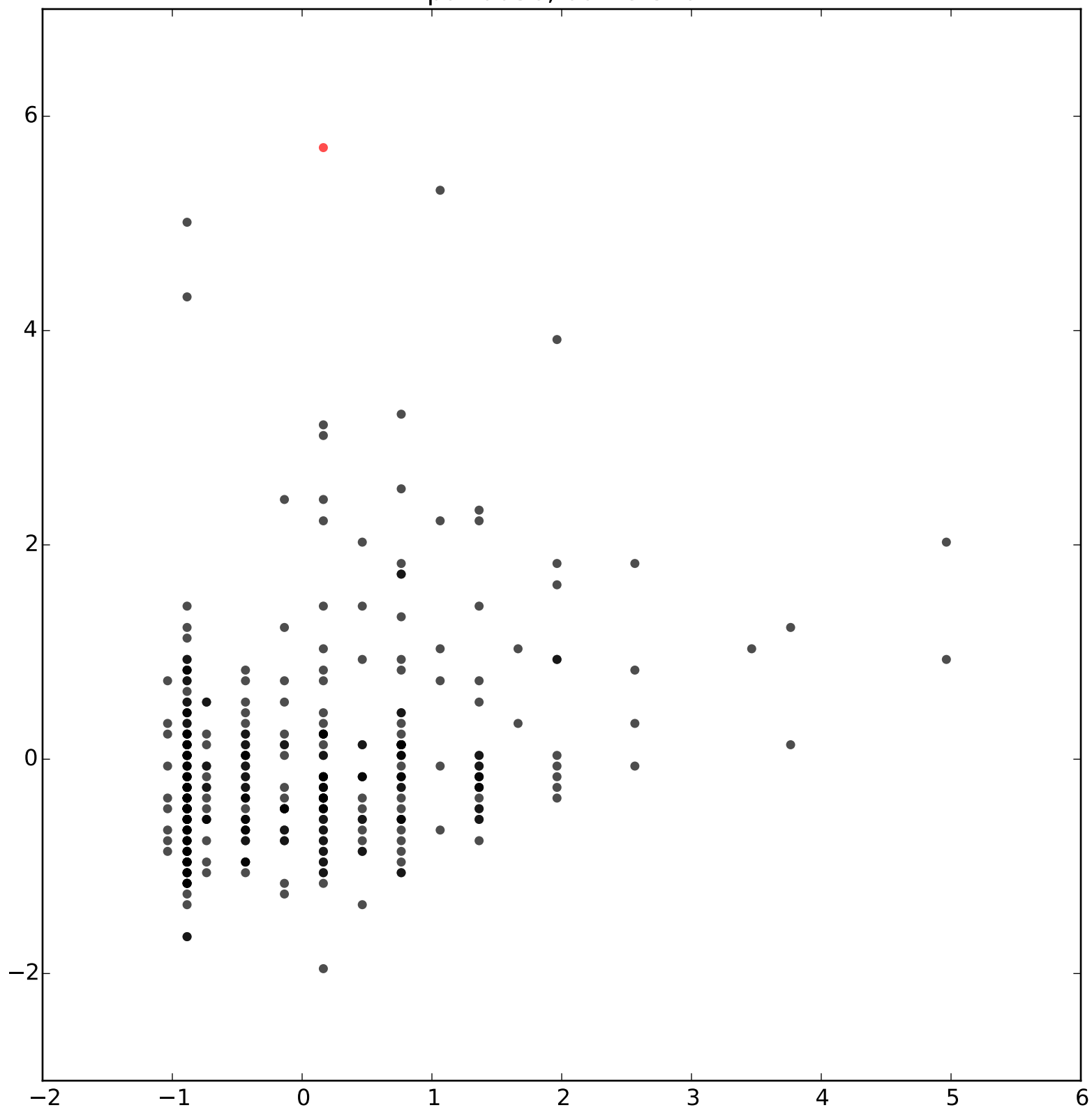


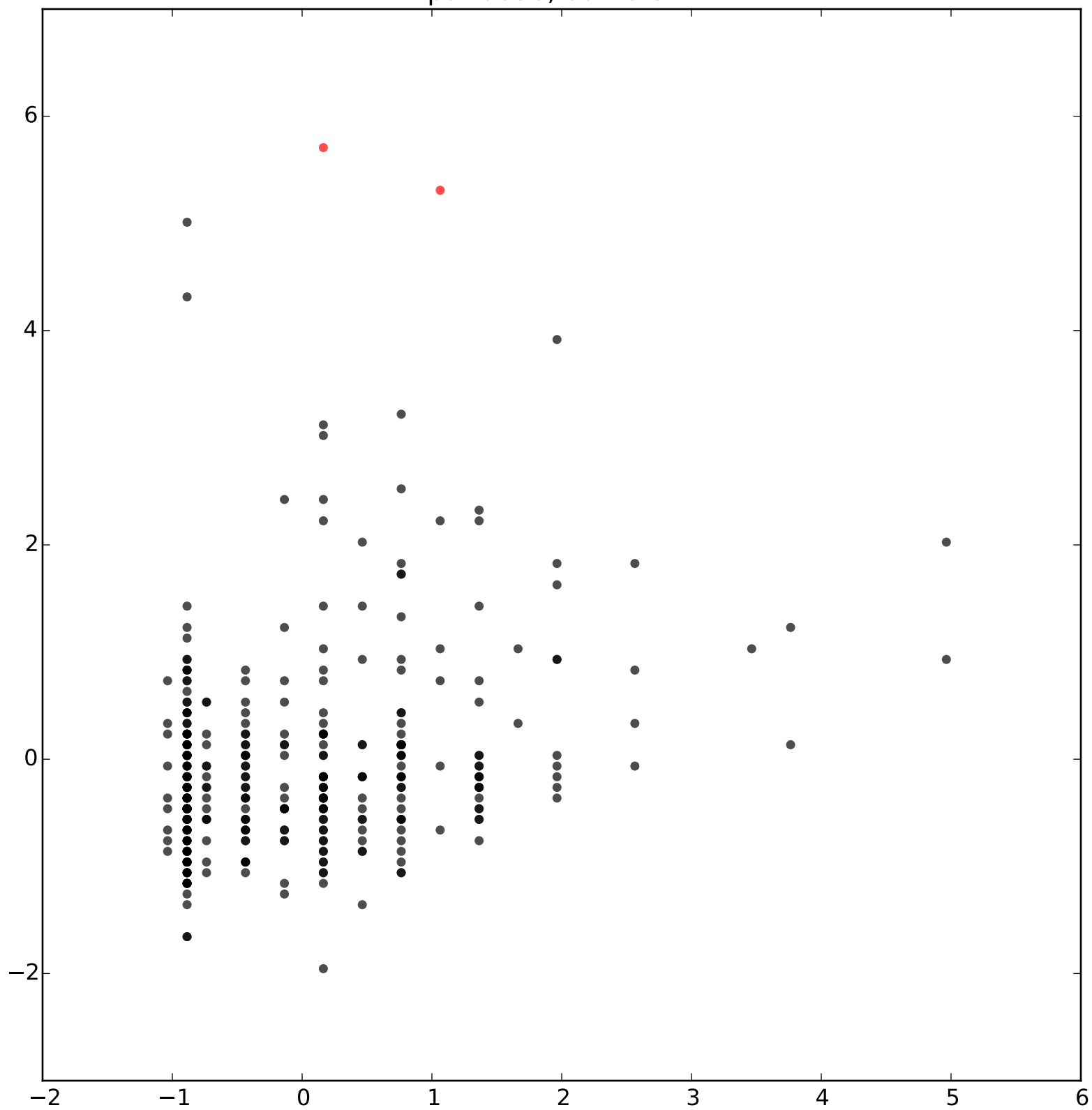
pair0036



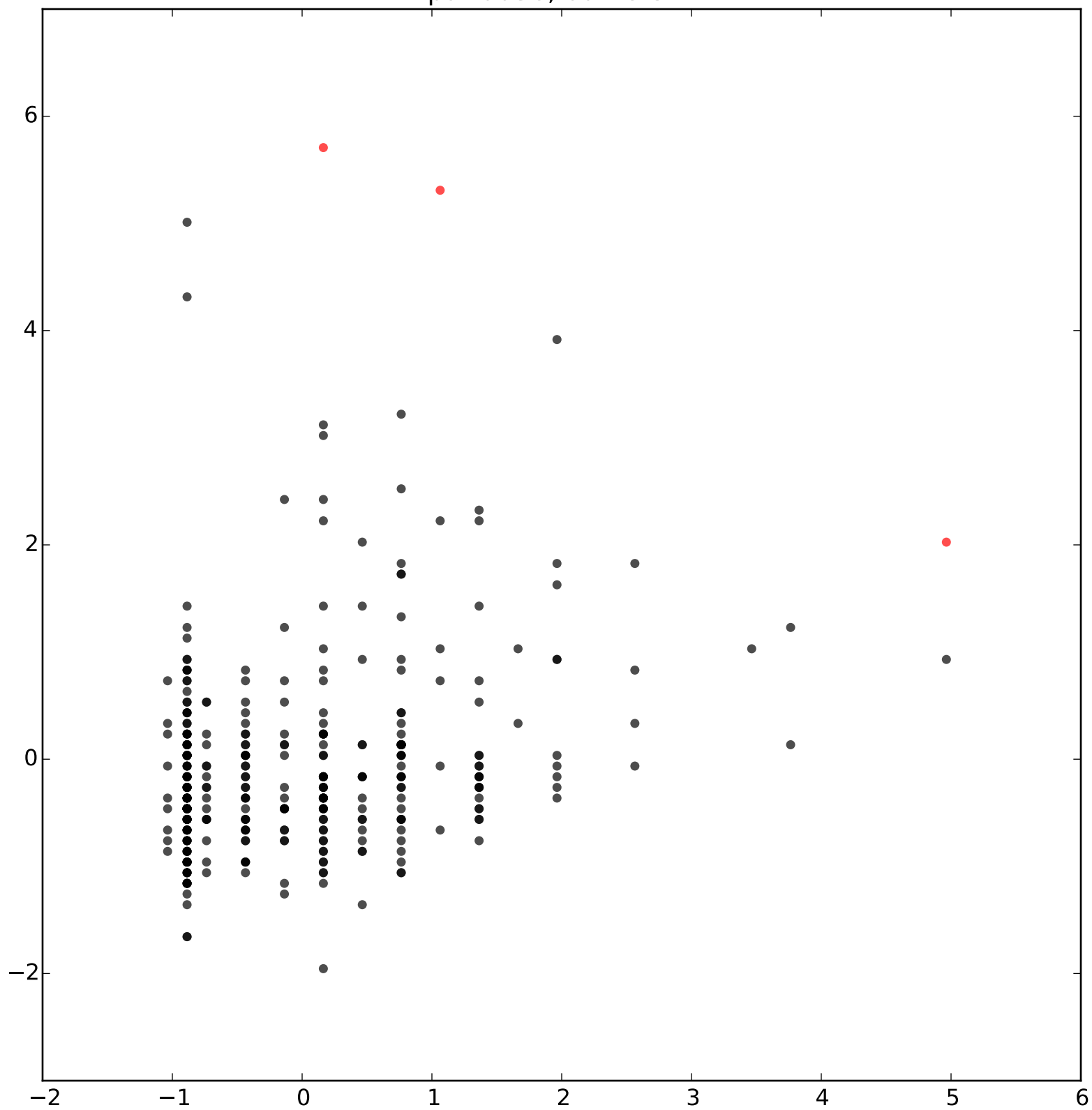
pair0036, outliers: 0



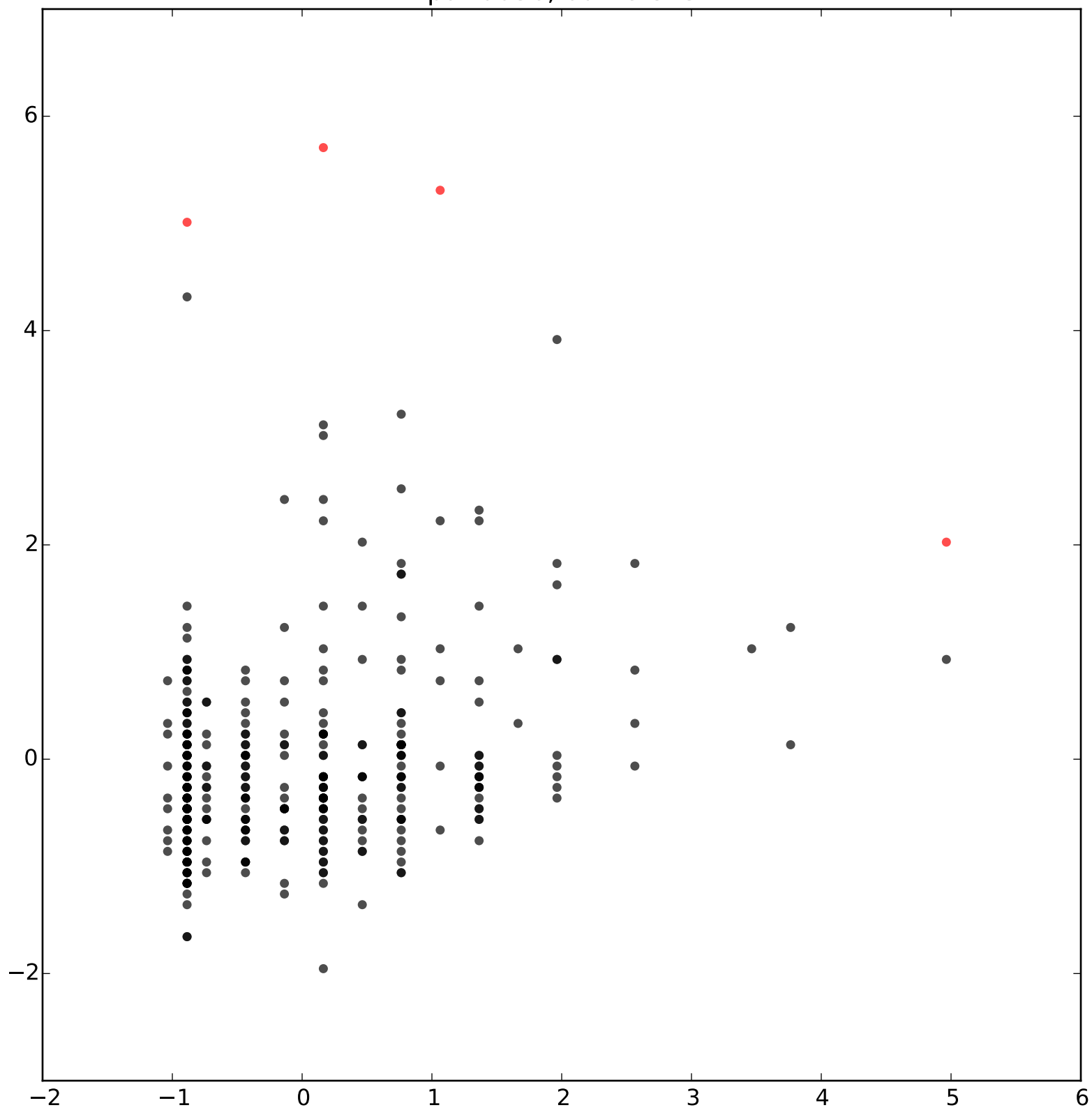
pair0036, outliers: 1



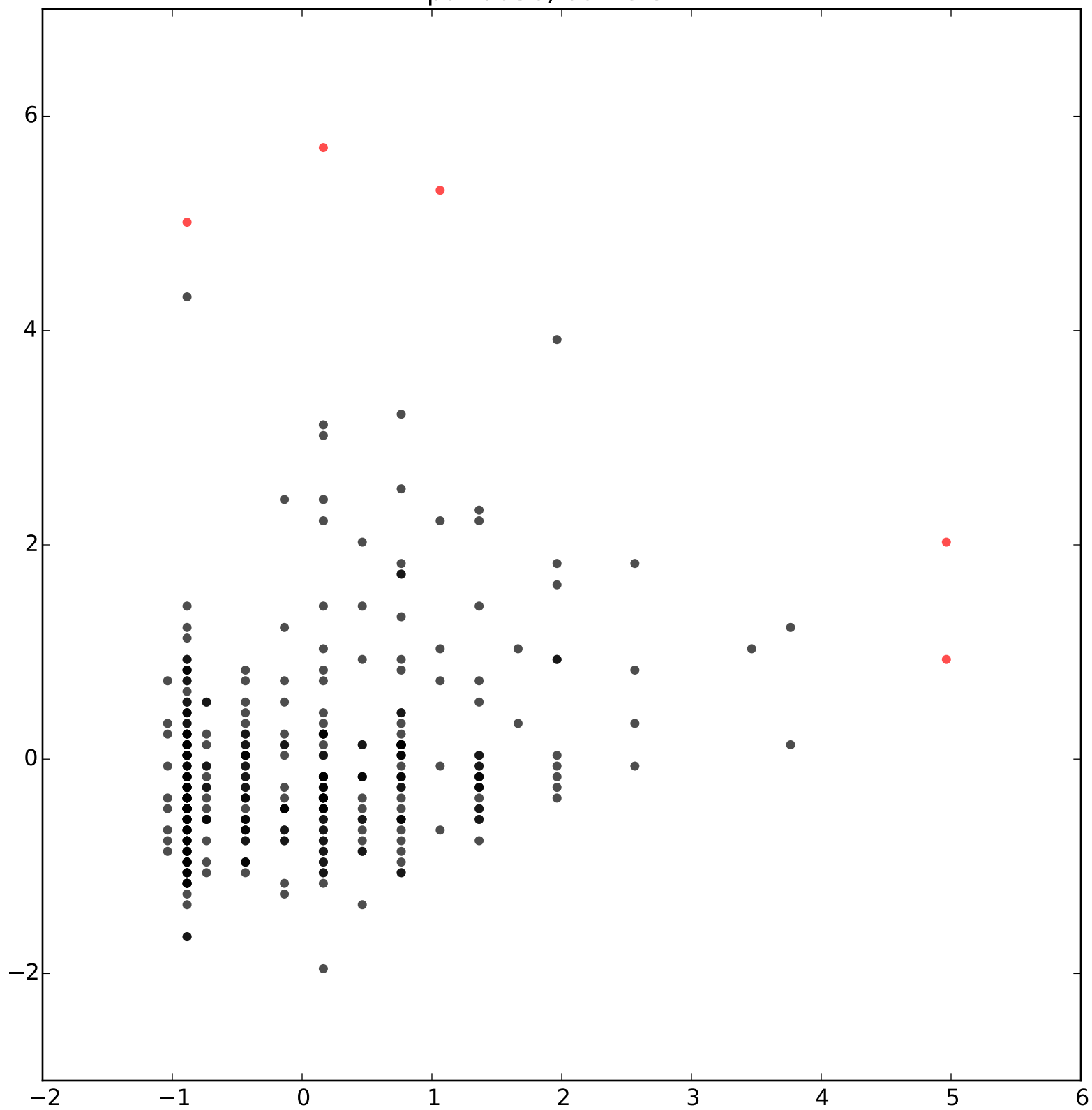
pair0036, outliers: 2



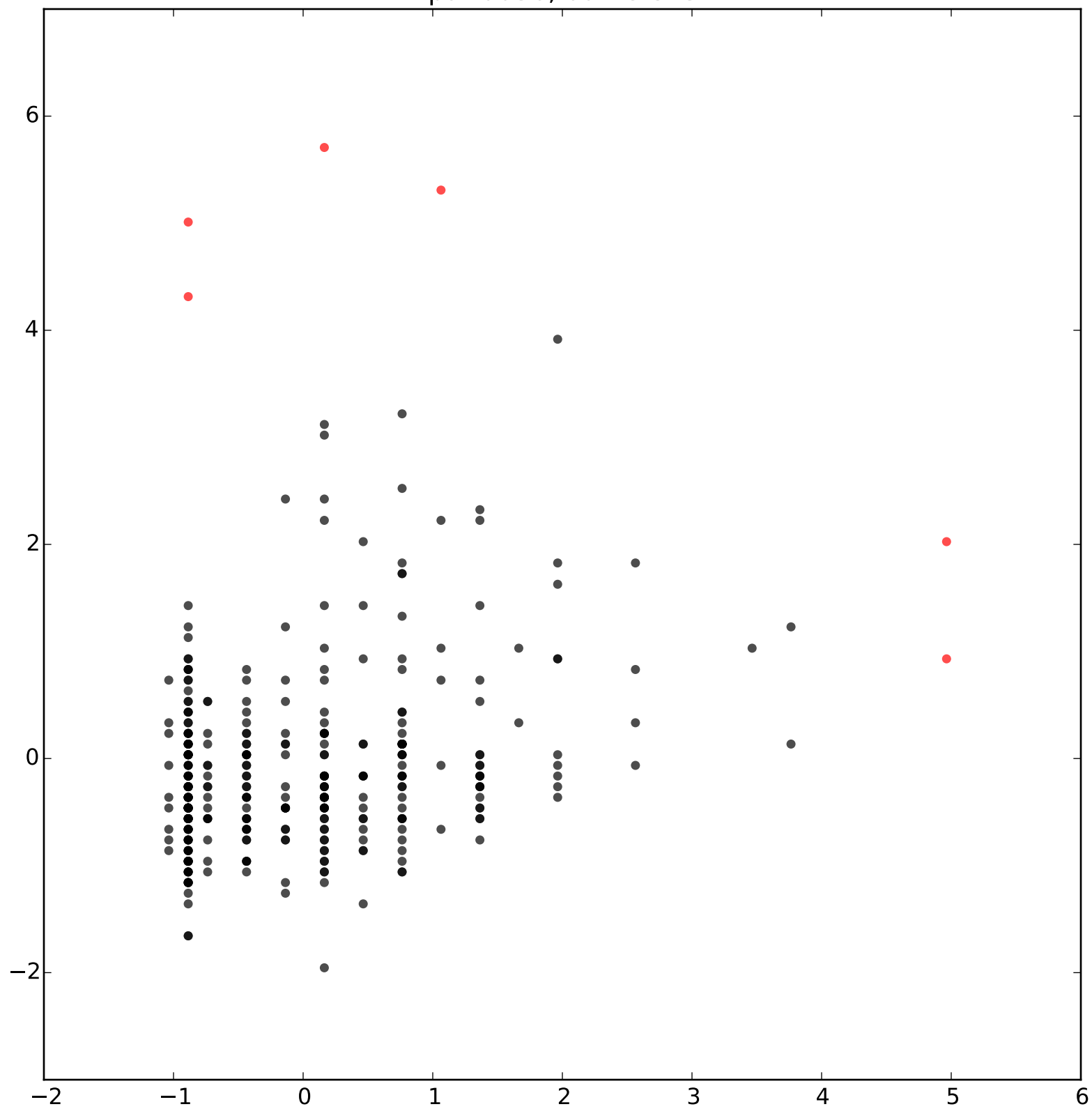
pair0036, outliers: 3



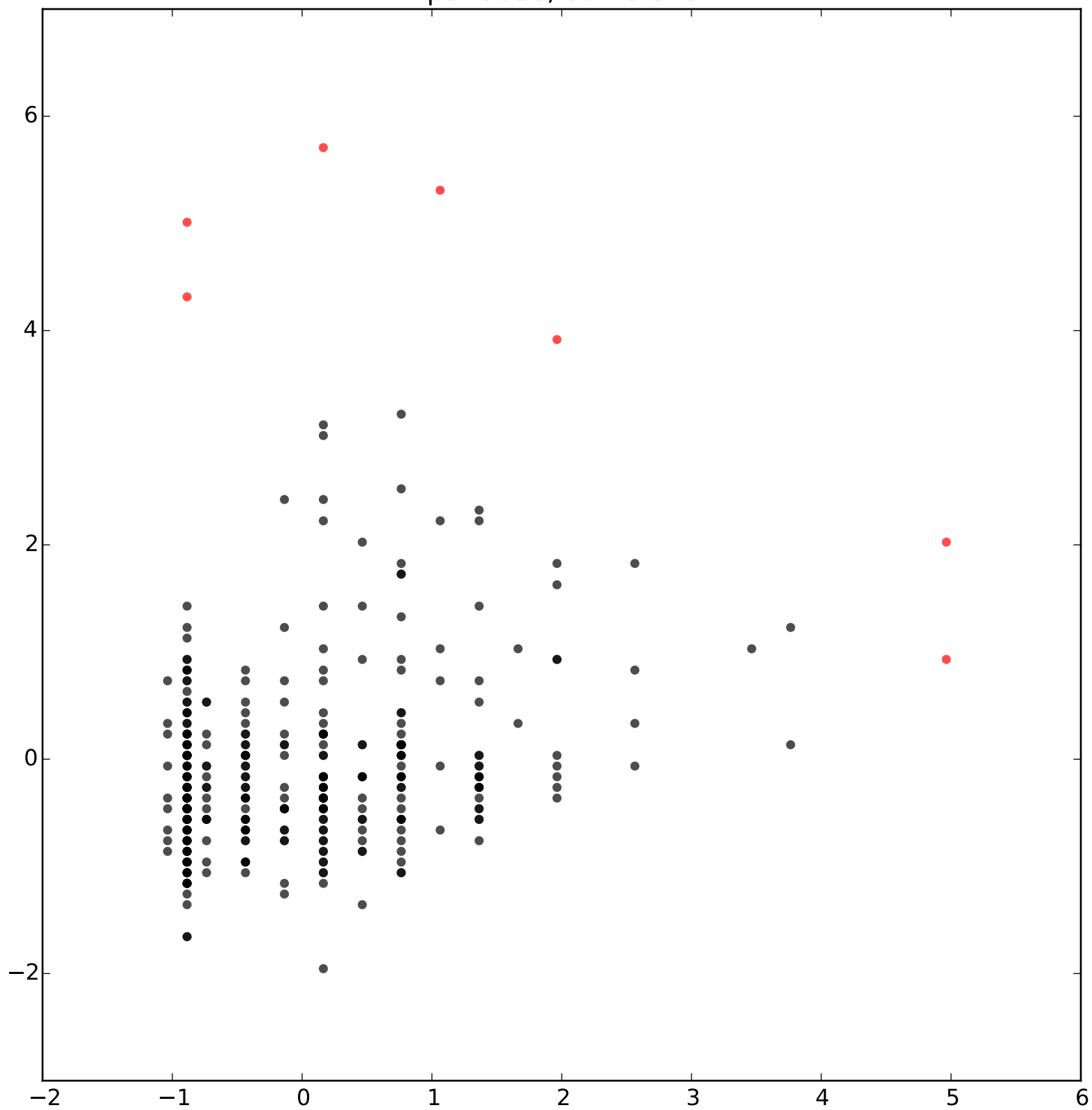
pair0036, outliers: 4



pair0036, outliers: 5

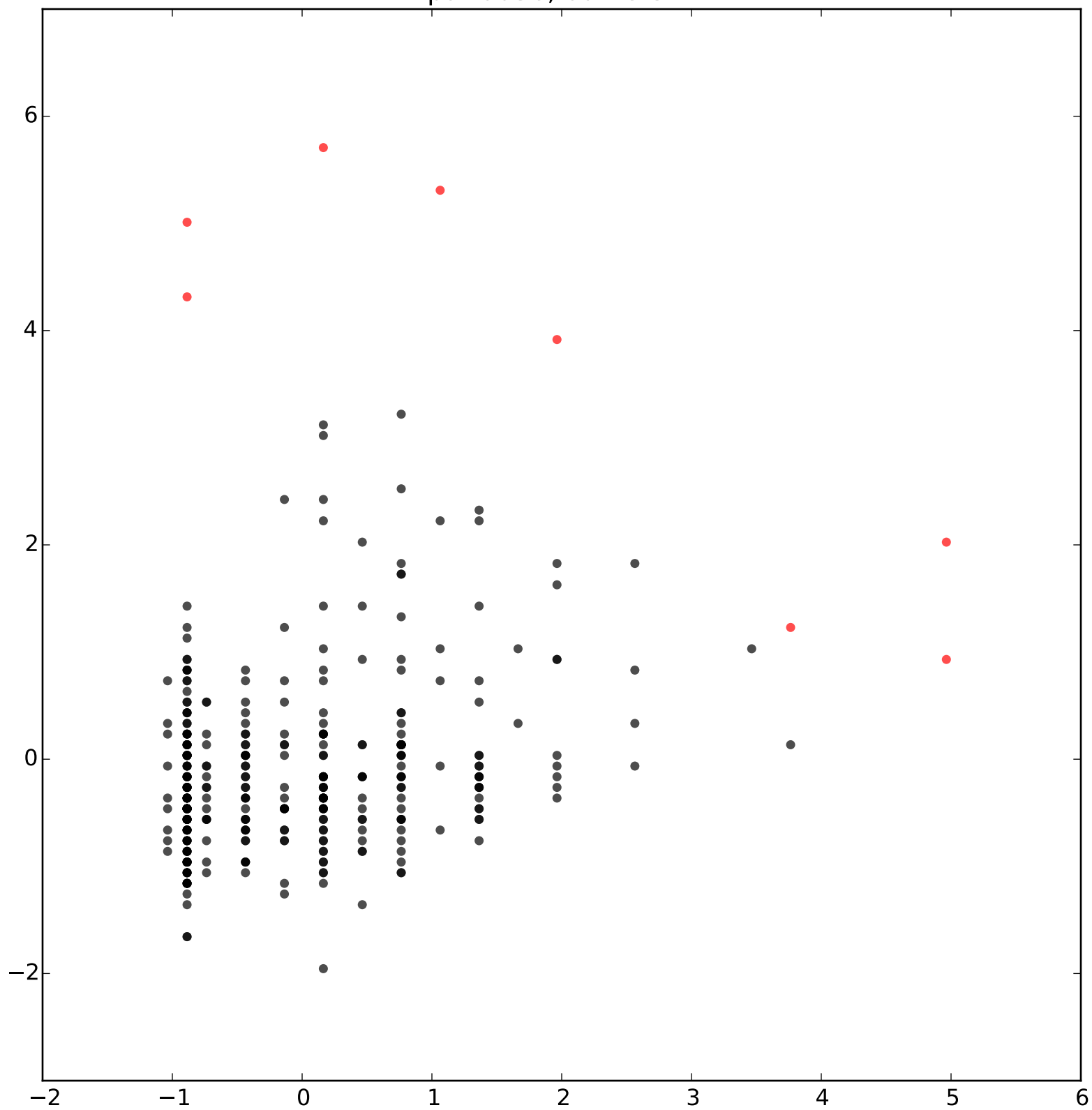


pair0036, outliers: 6

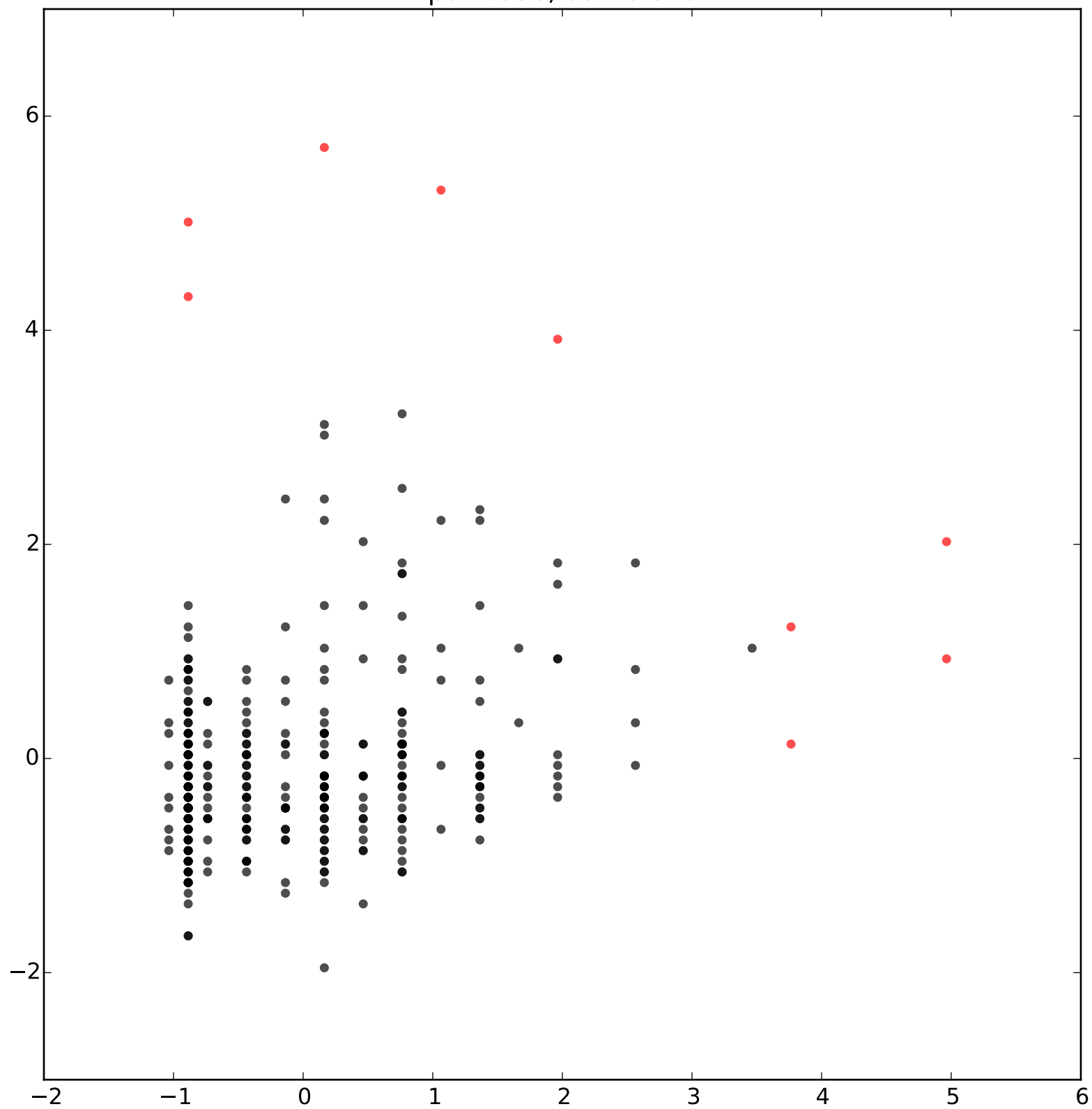




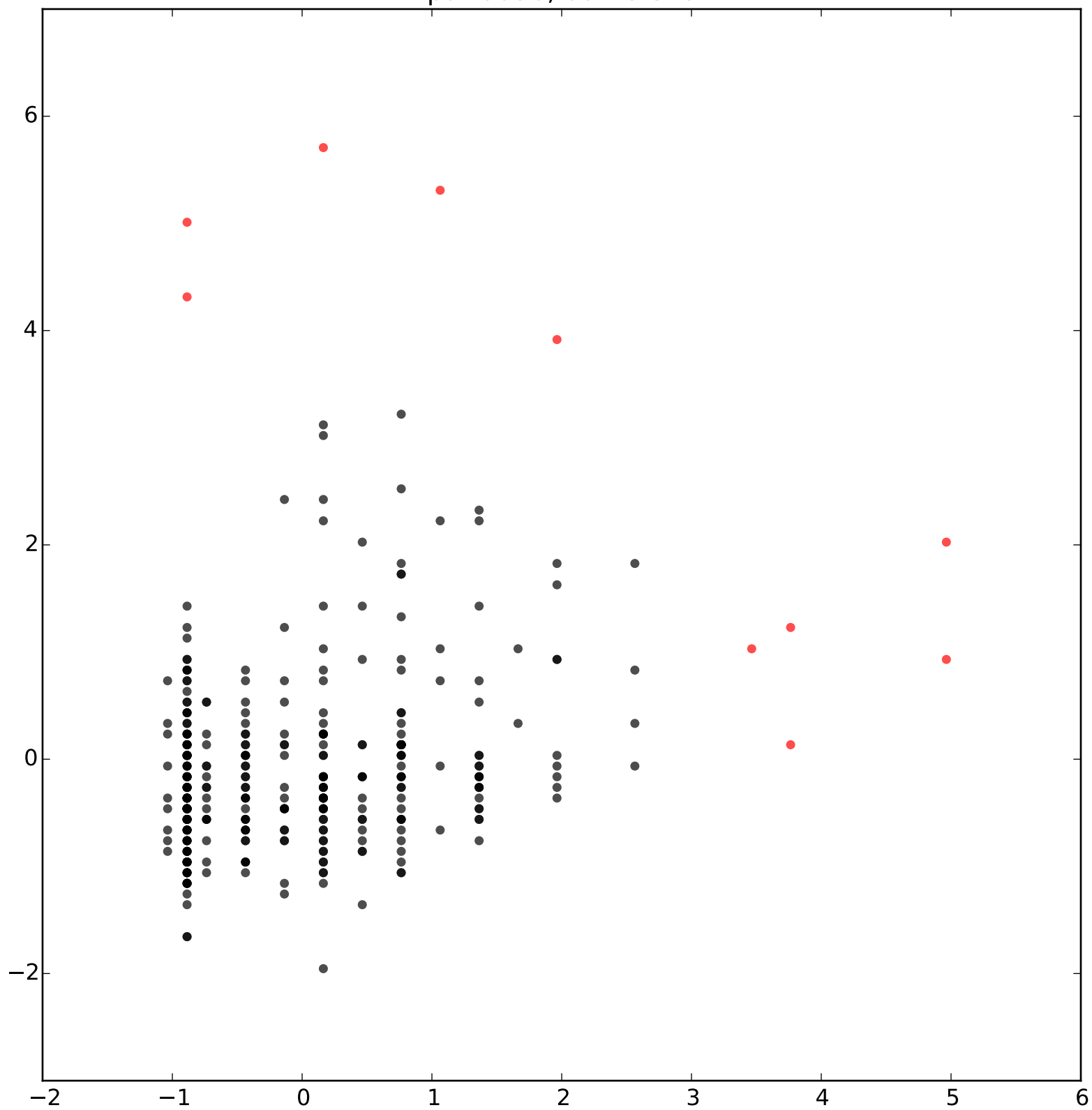
pair0036, outliers: 7



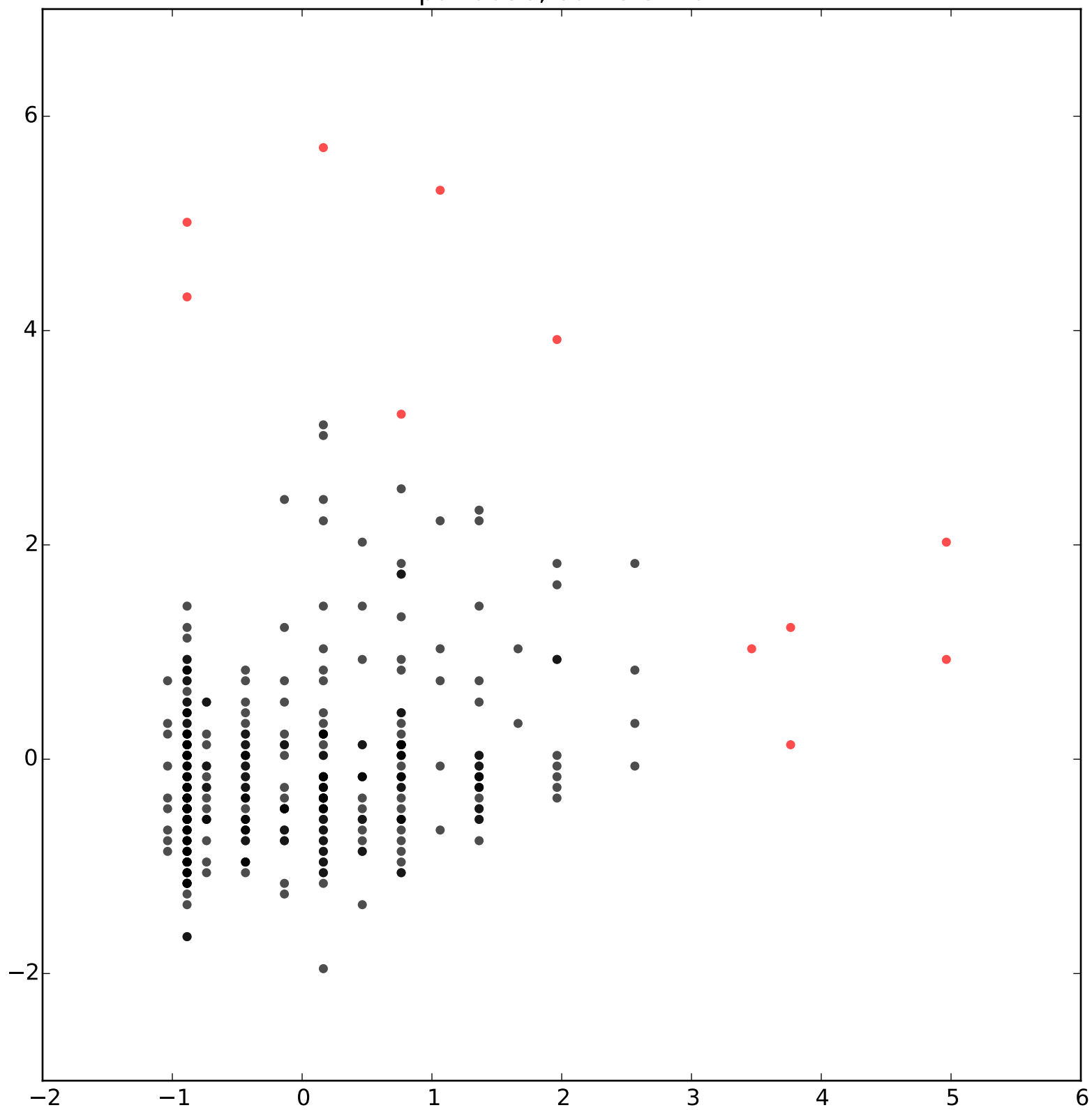
pair0036, outliers: 8



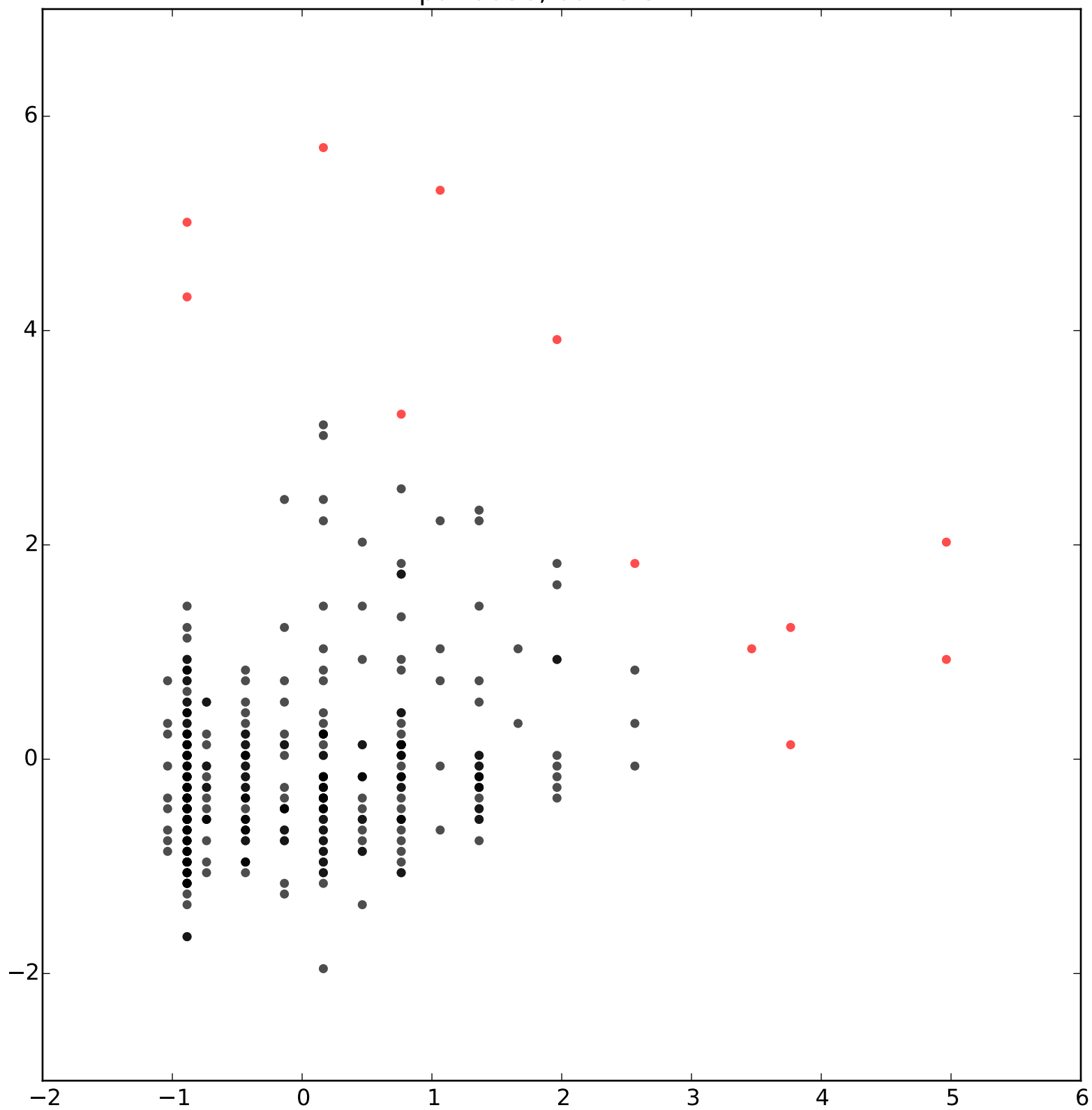
pair0036, outliers: 9



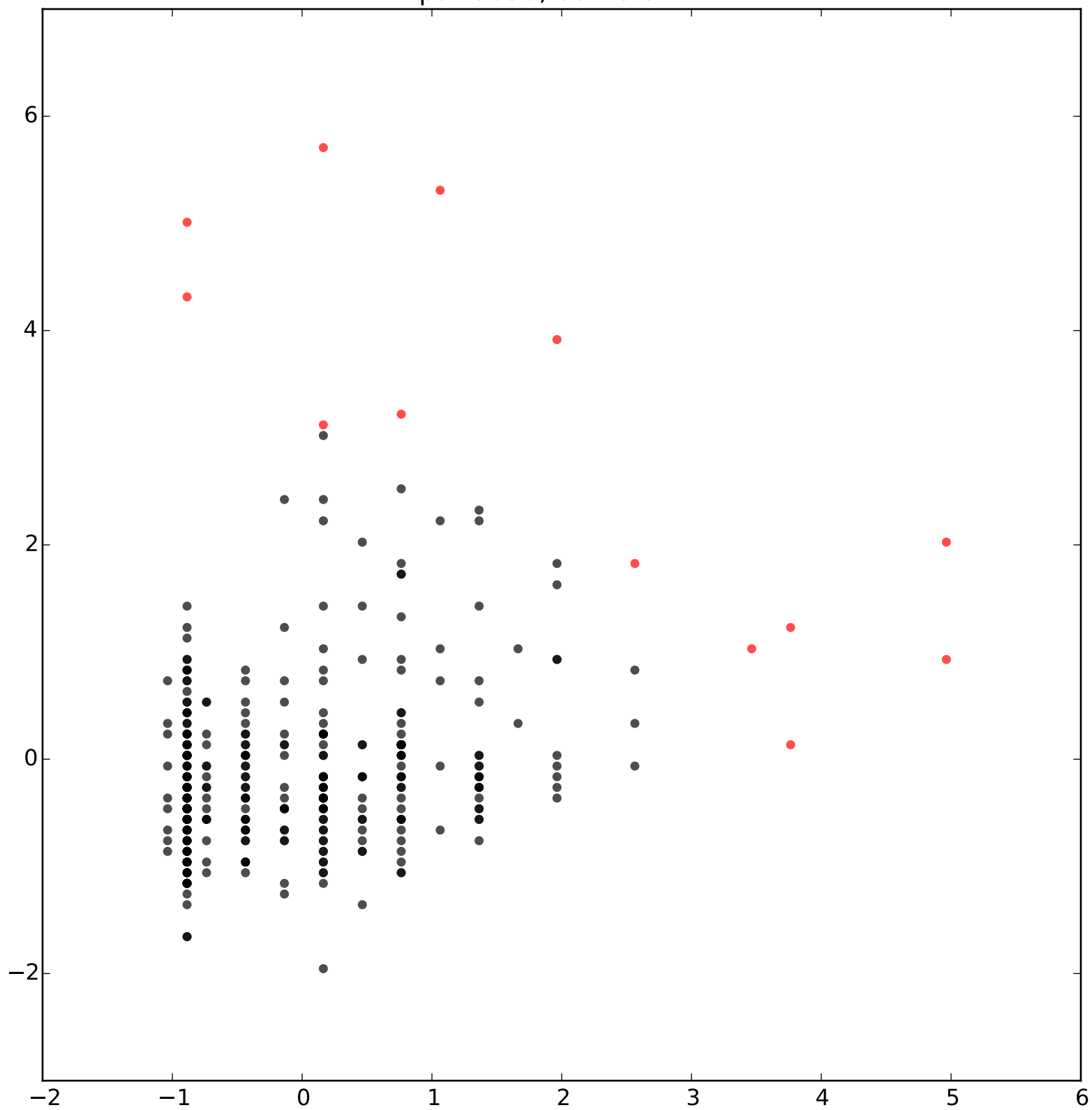
pair0036, outliers: 10



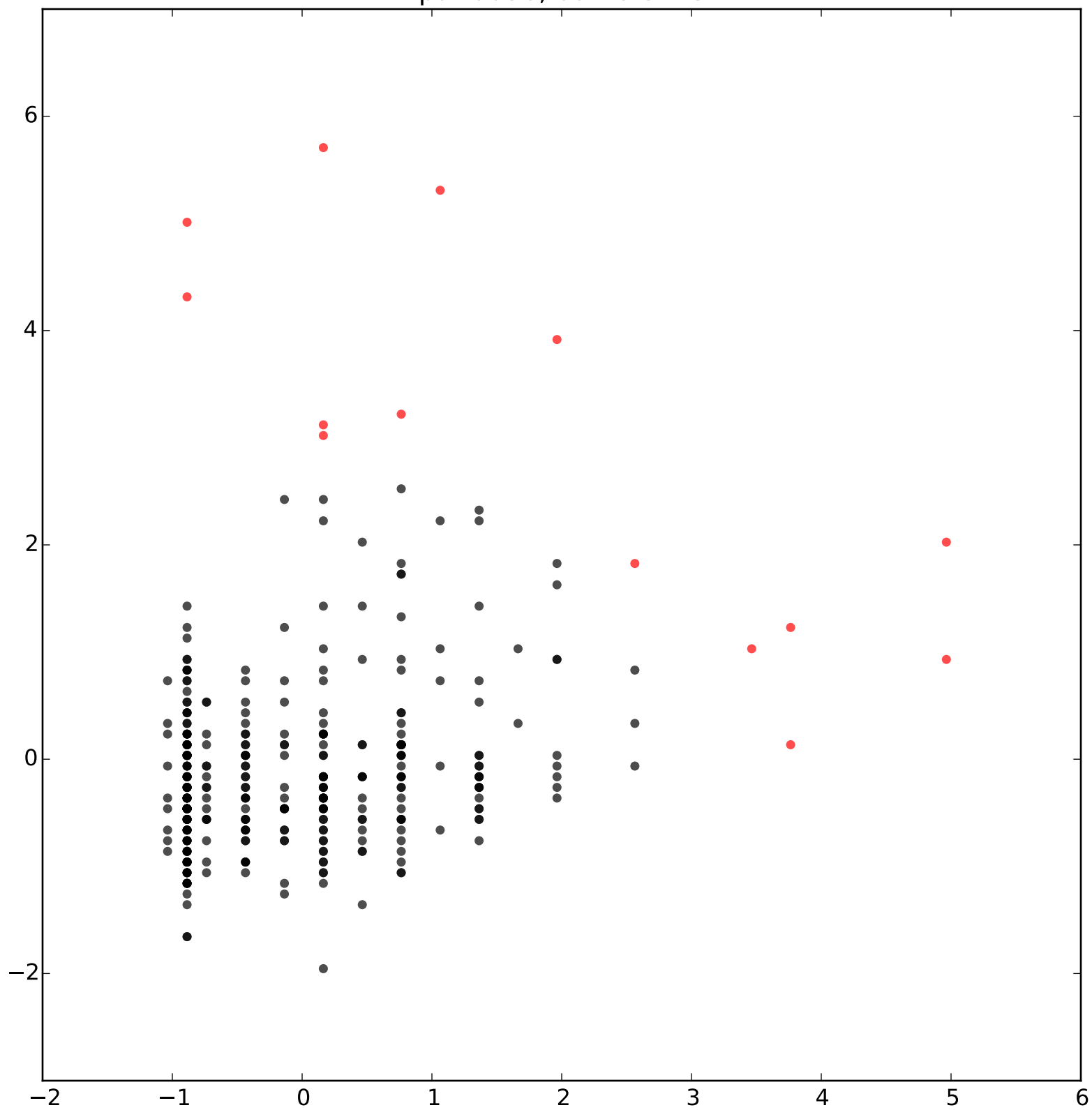
pair0036, outliers: 11



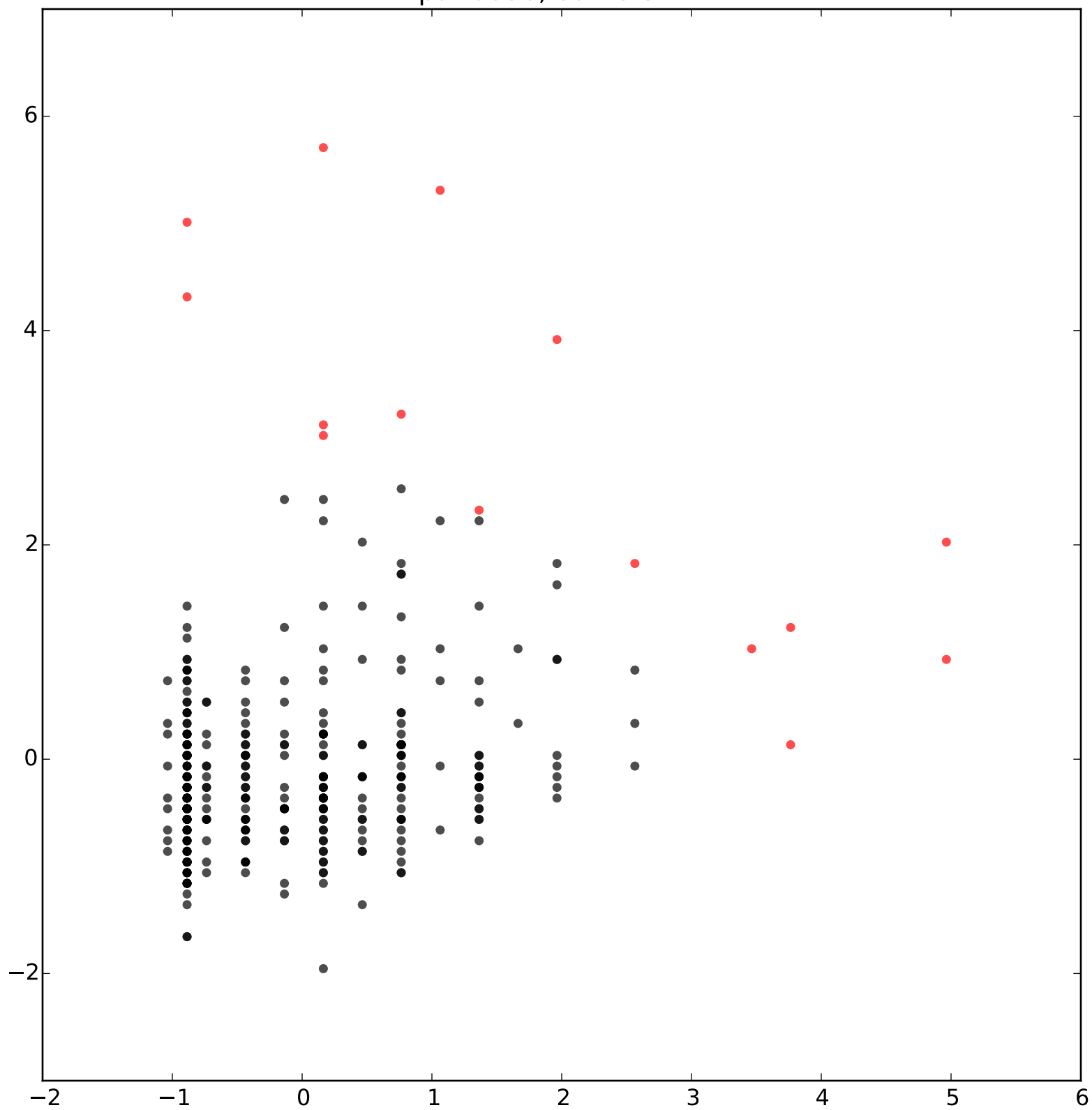
pair0036, outliers: 12



pair0036, outliers: 13

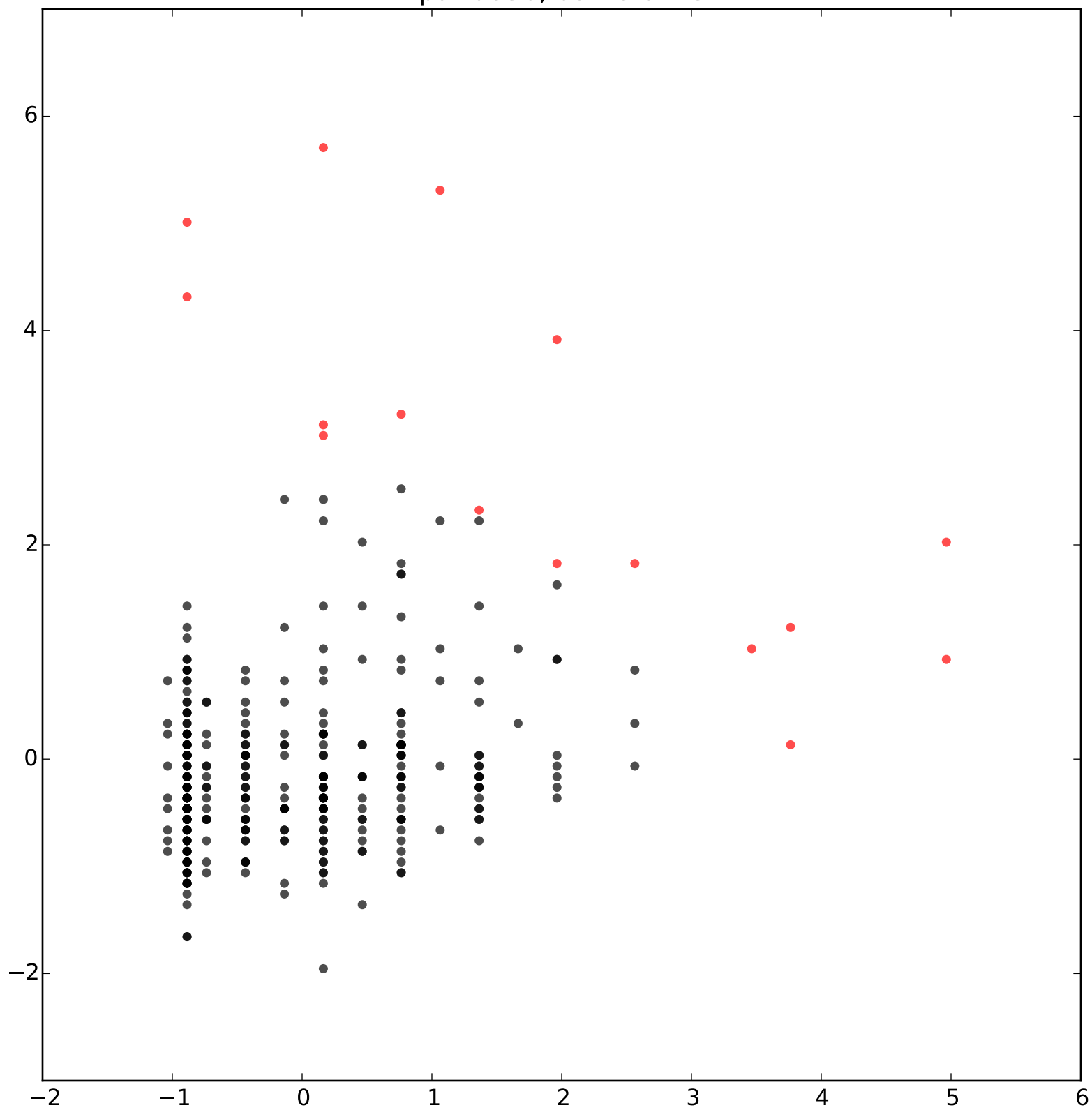


pair0036, outliers: 14

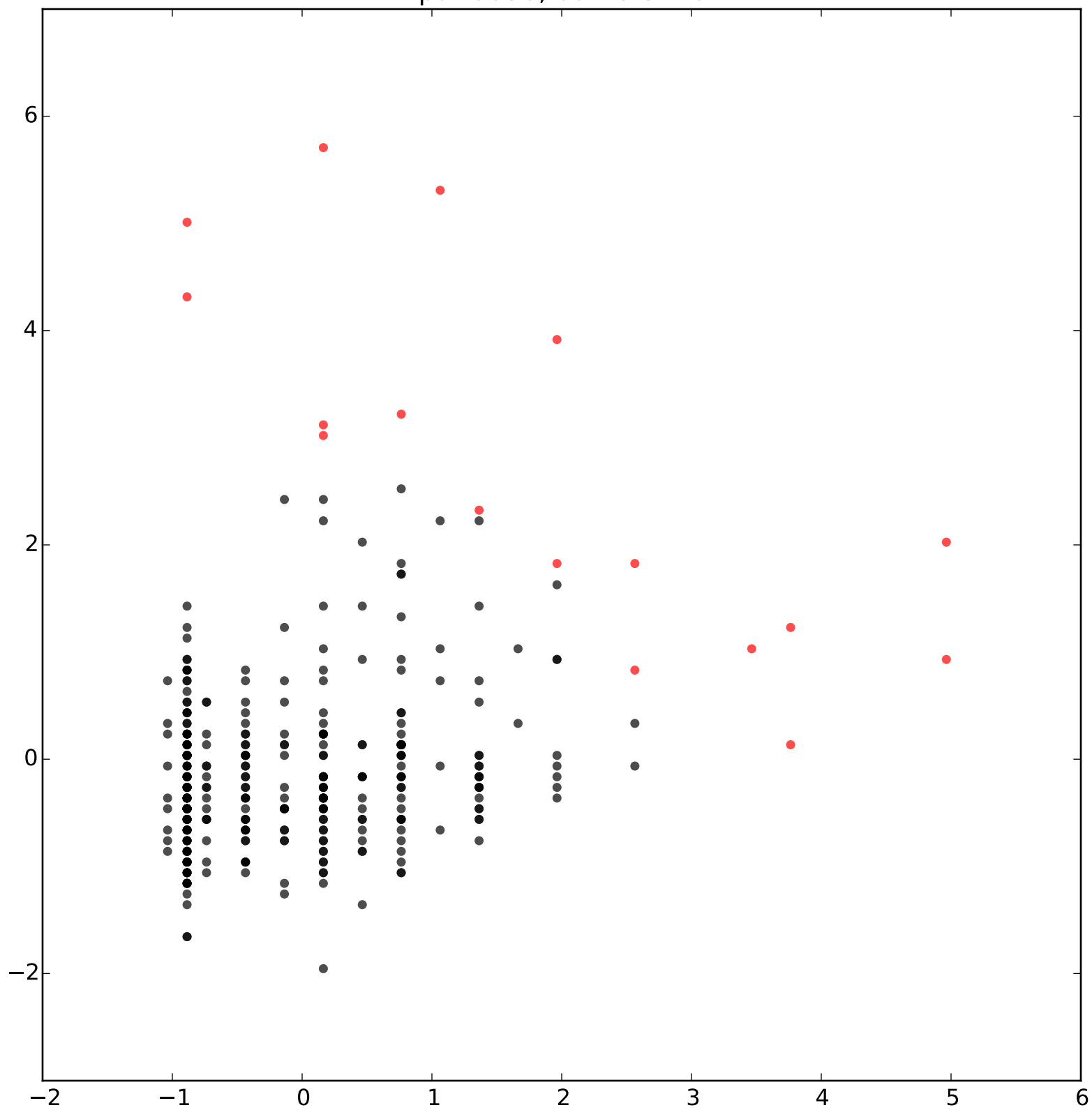




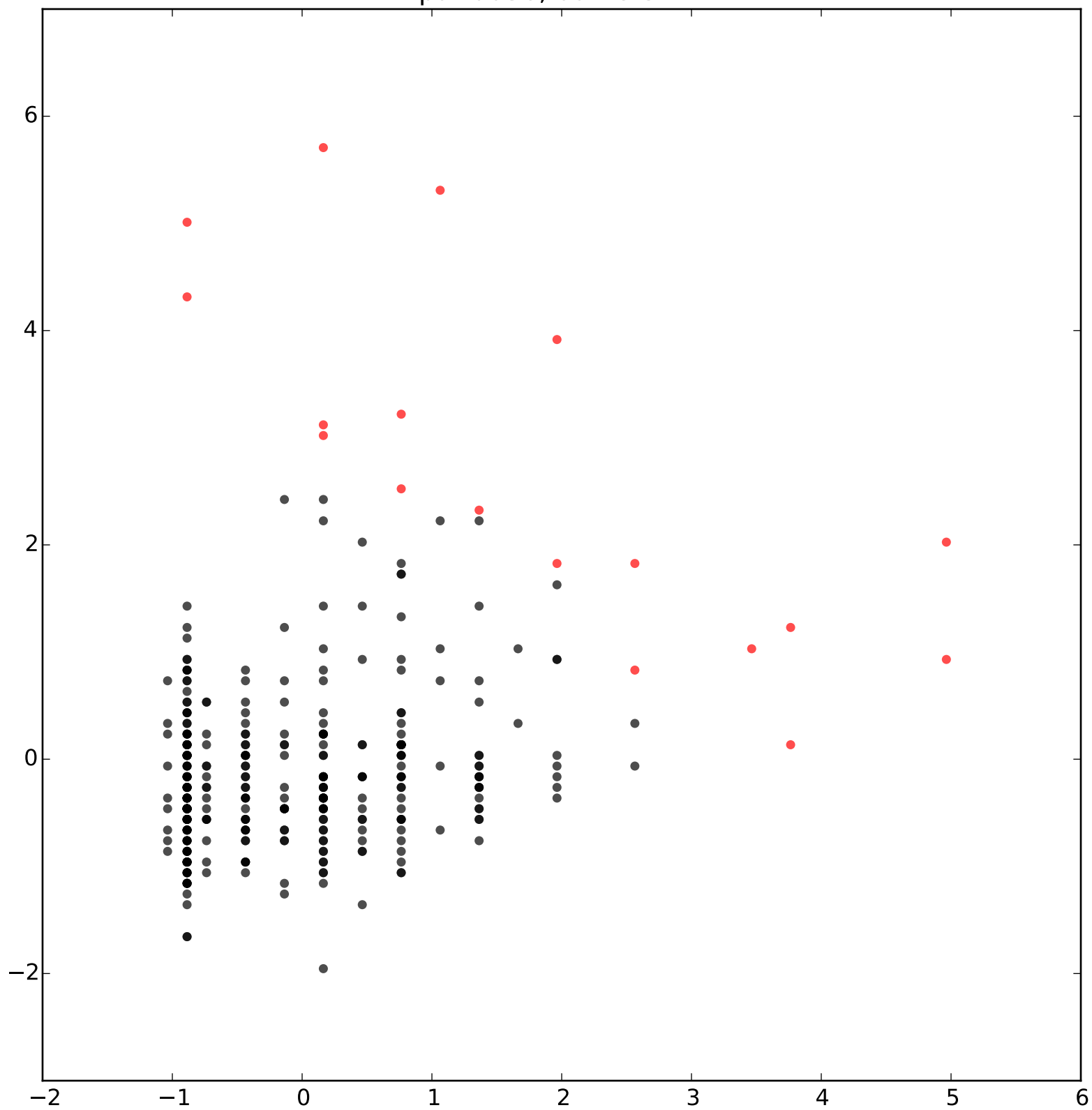
pair0036, outliers: 15



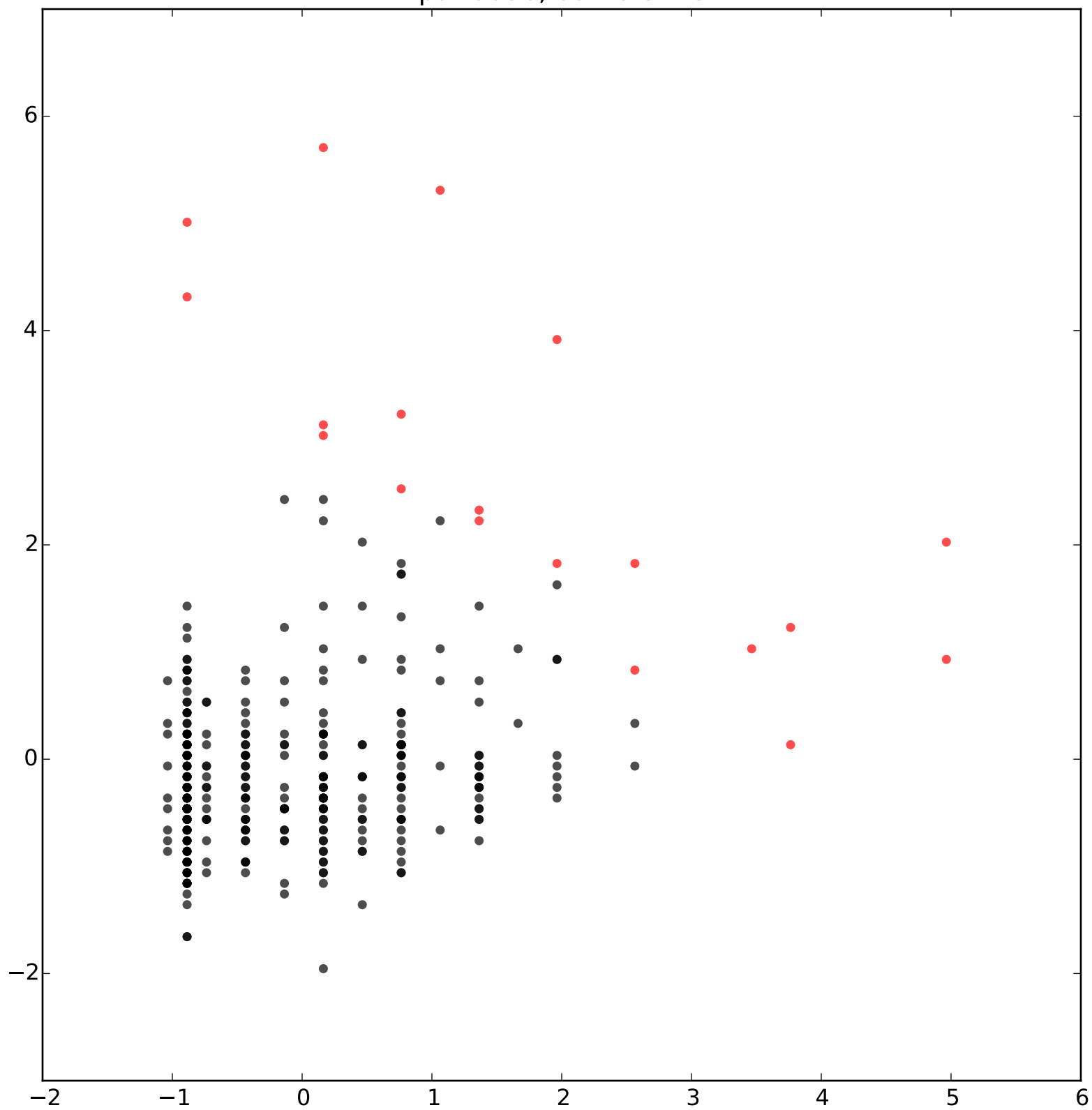
pair0036, outliers: 16



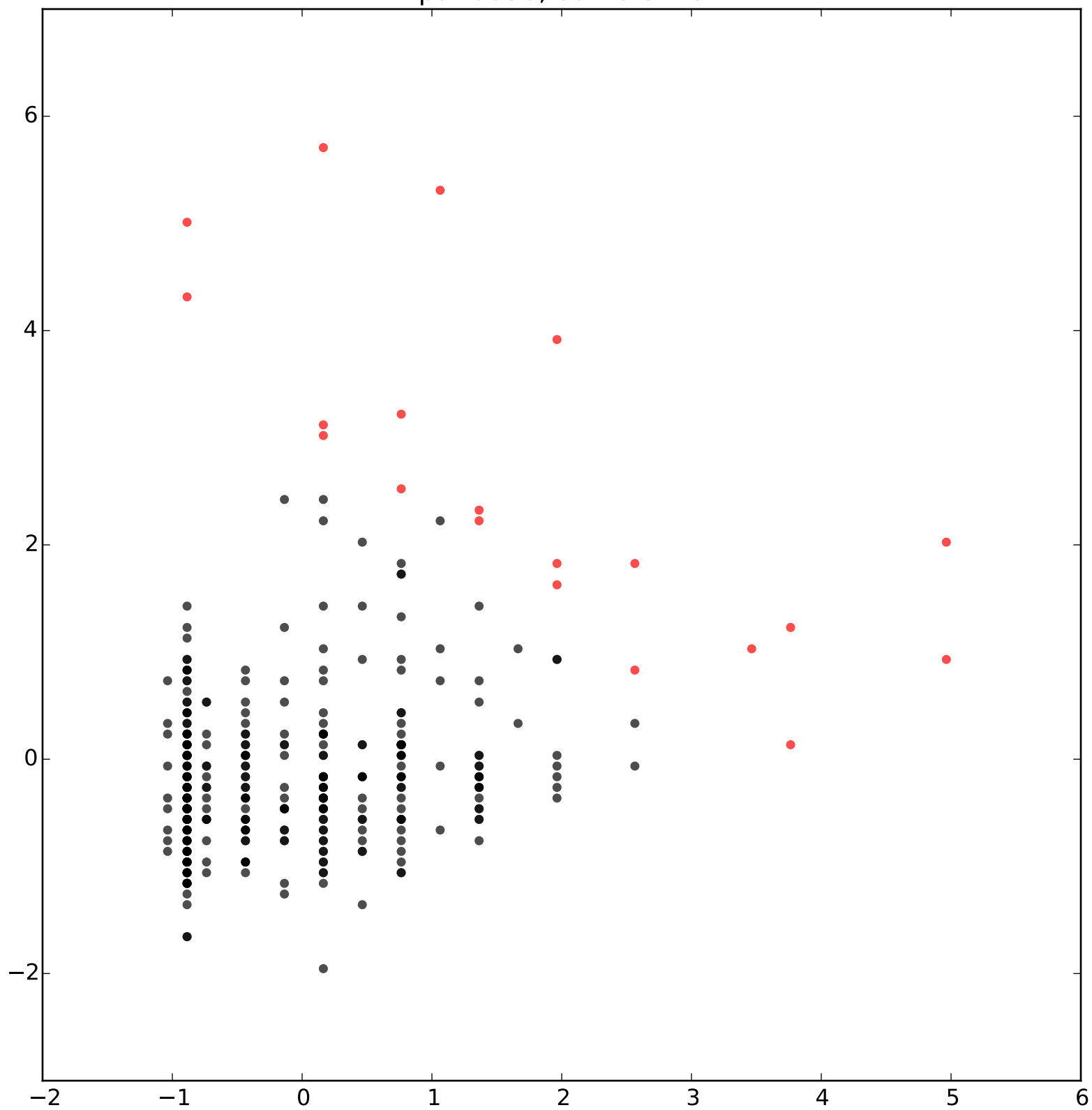
pair0036, outliers: 17



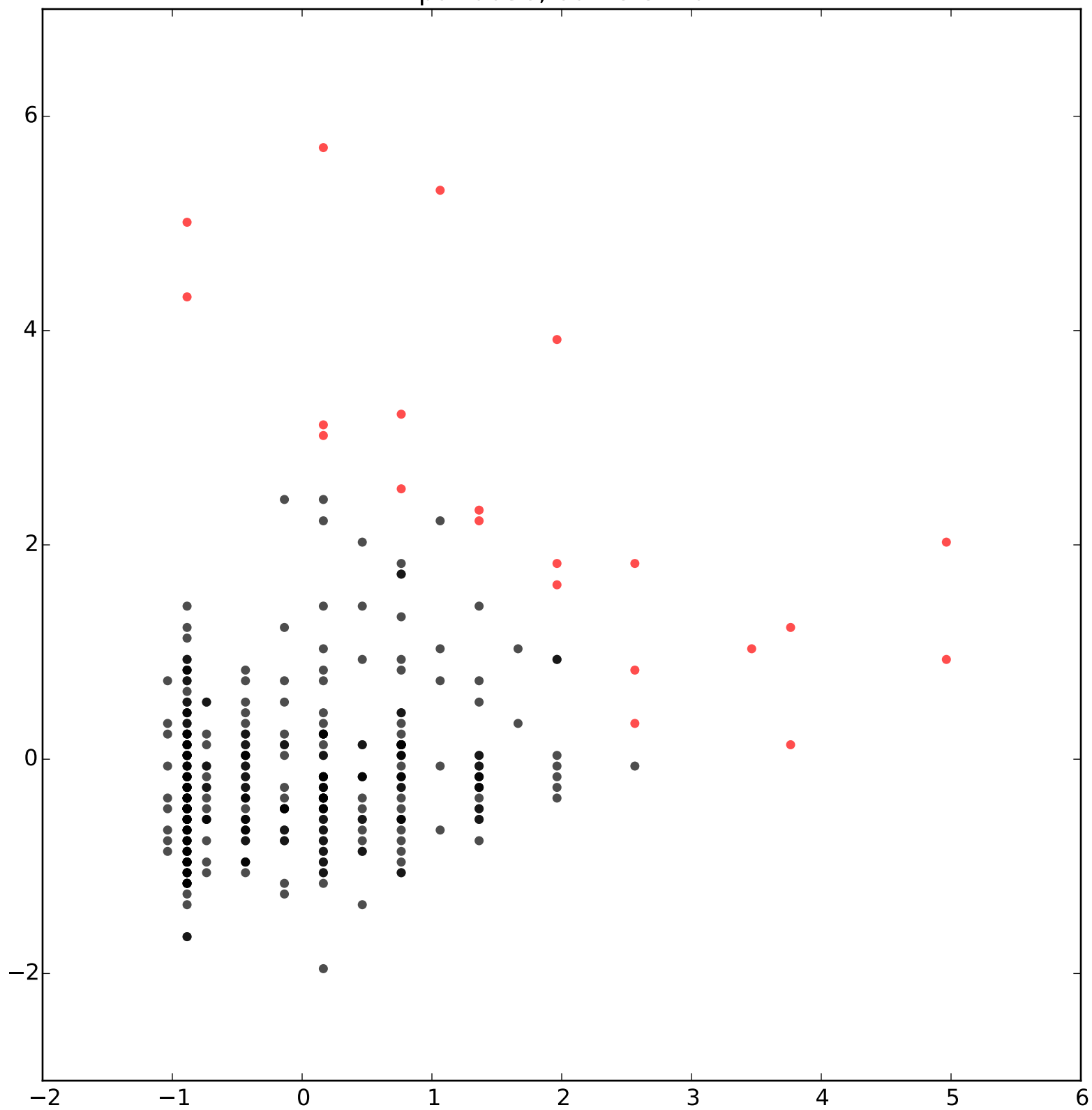
pair0036, outliers: 18



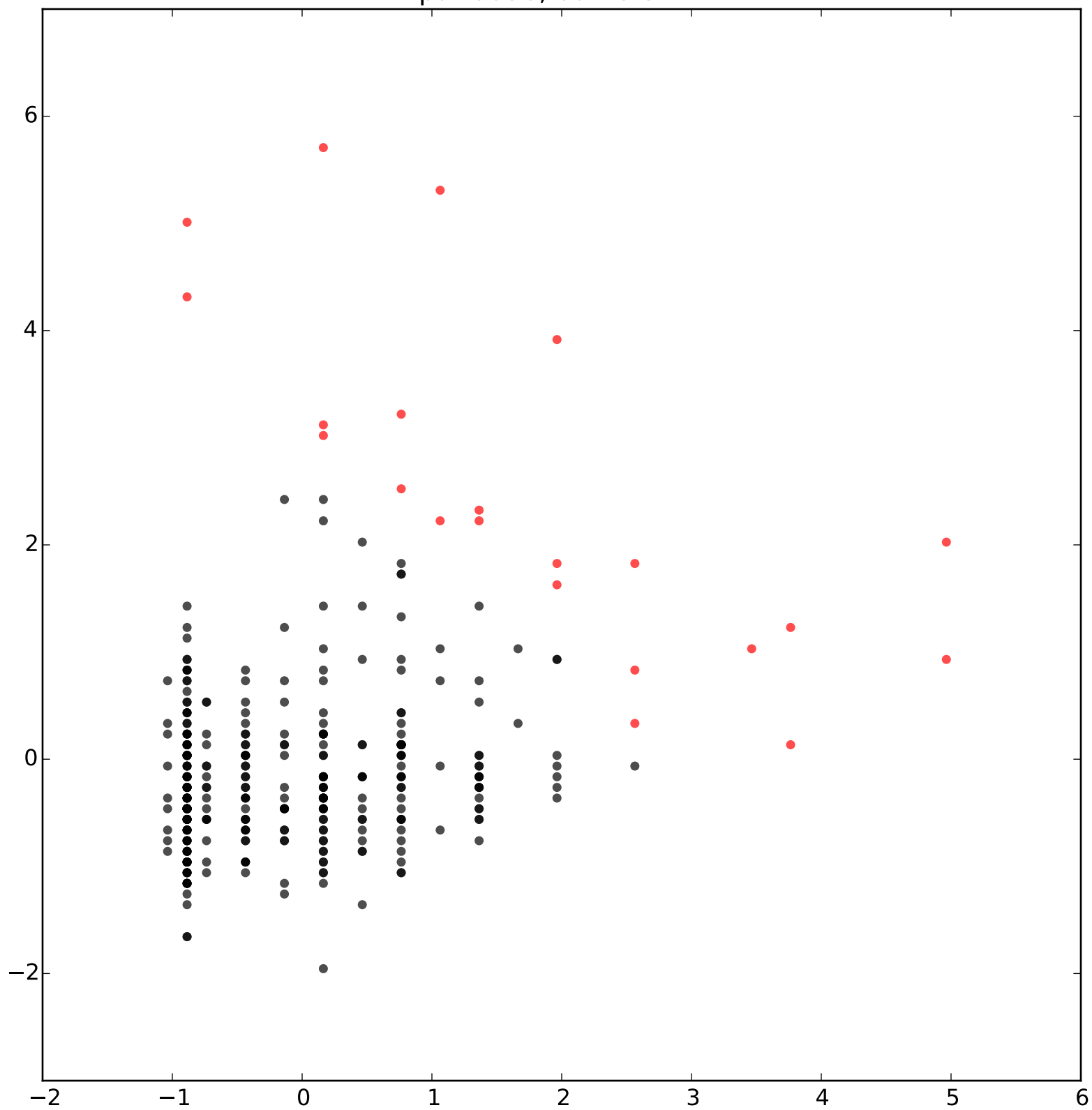
pair0036, outliers: 19



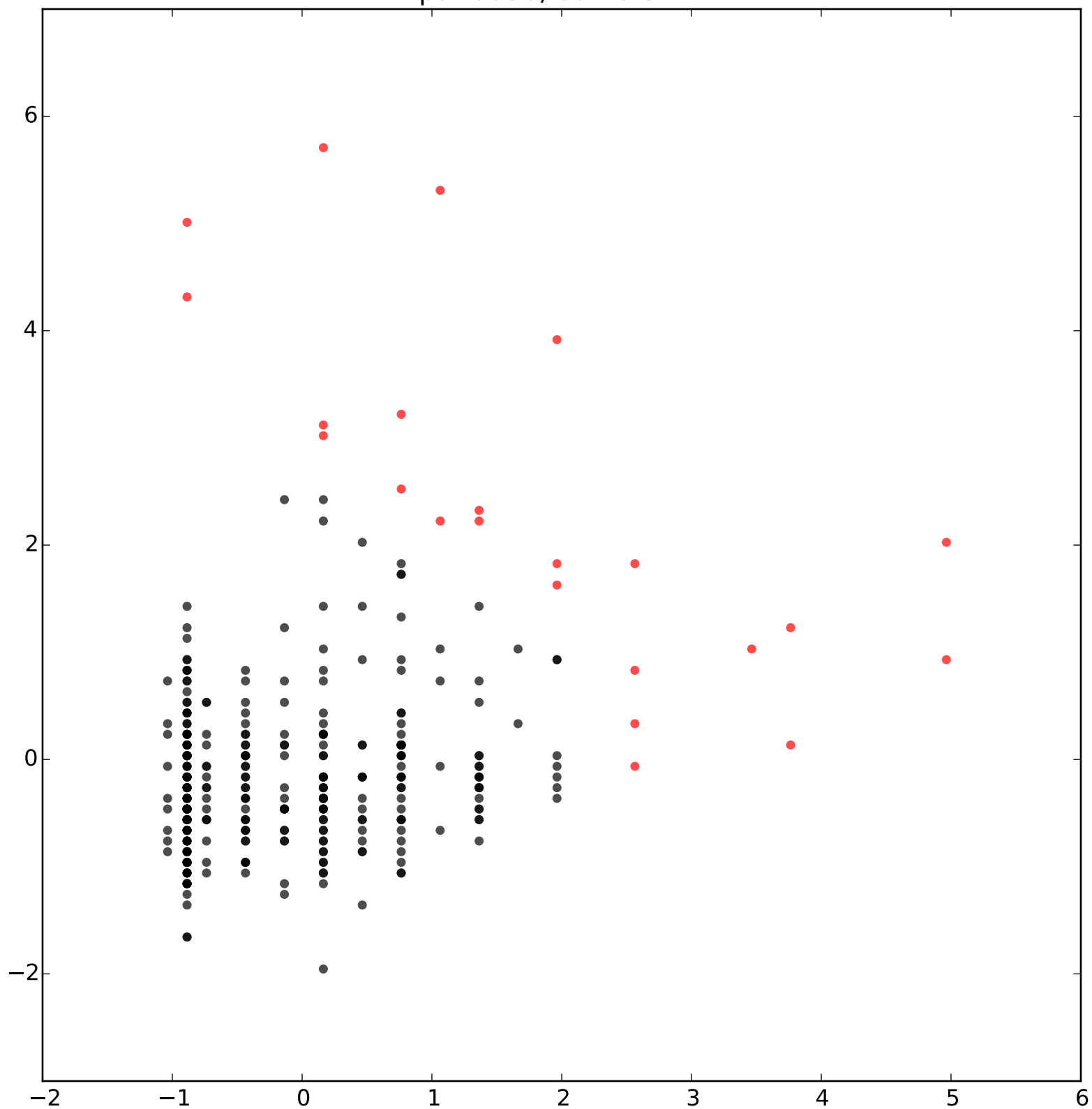
pair0036, outliers: 20



pair0036, outliers: 21

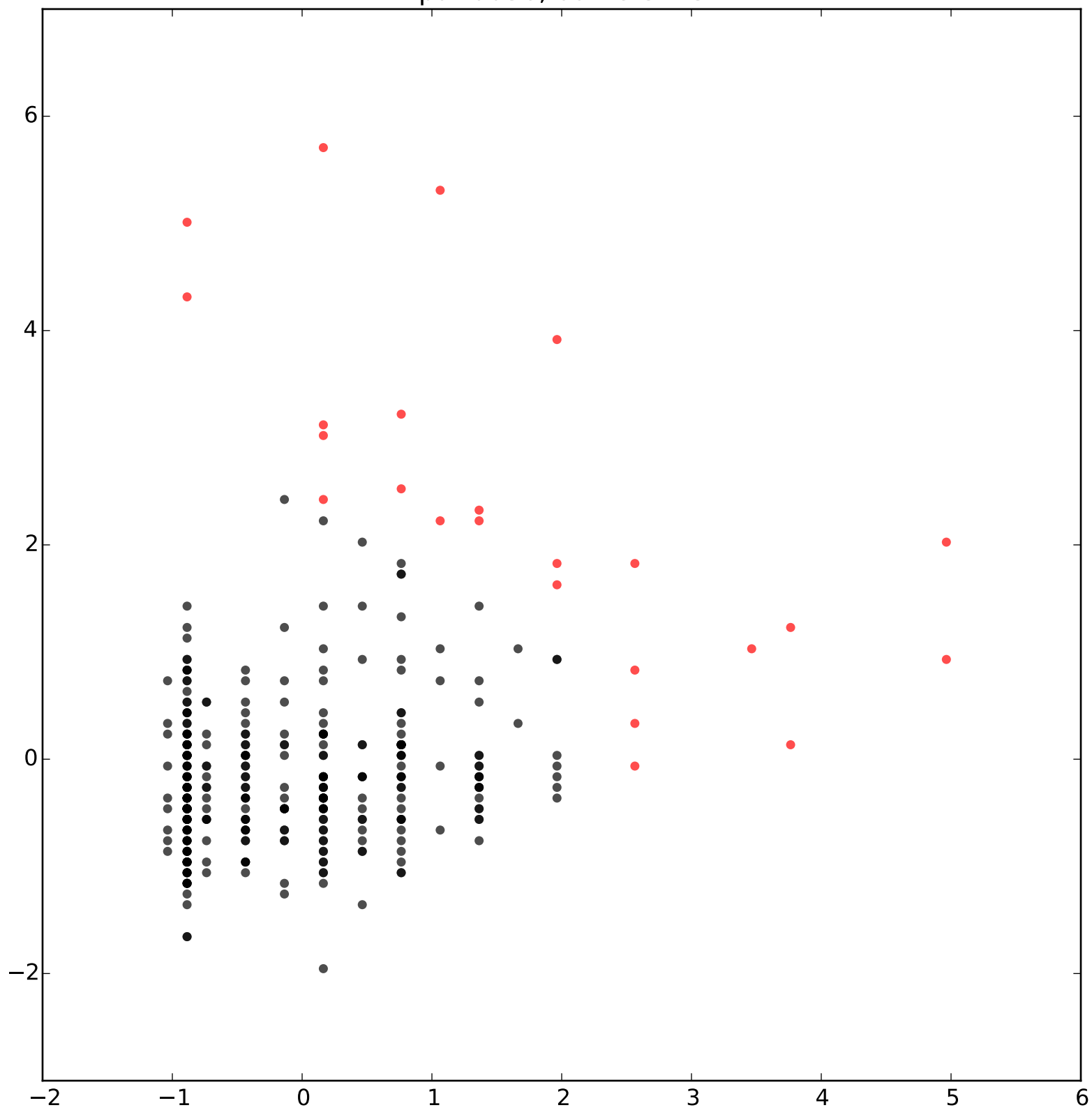


pair0036, outliers: 22

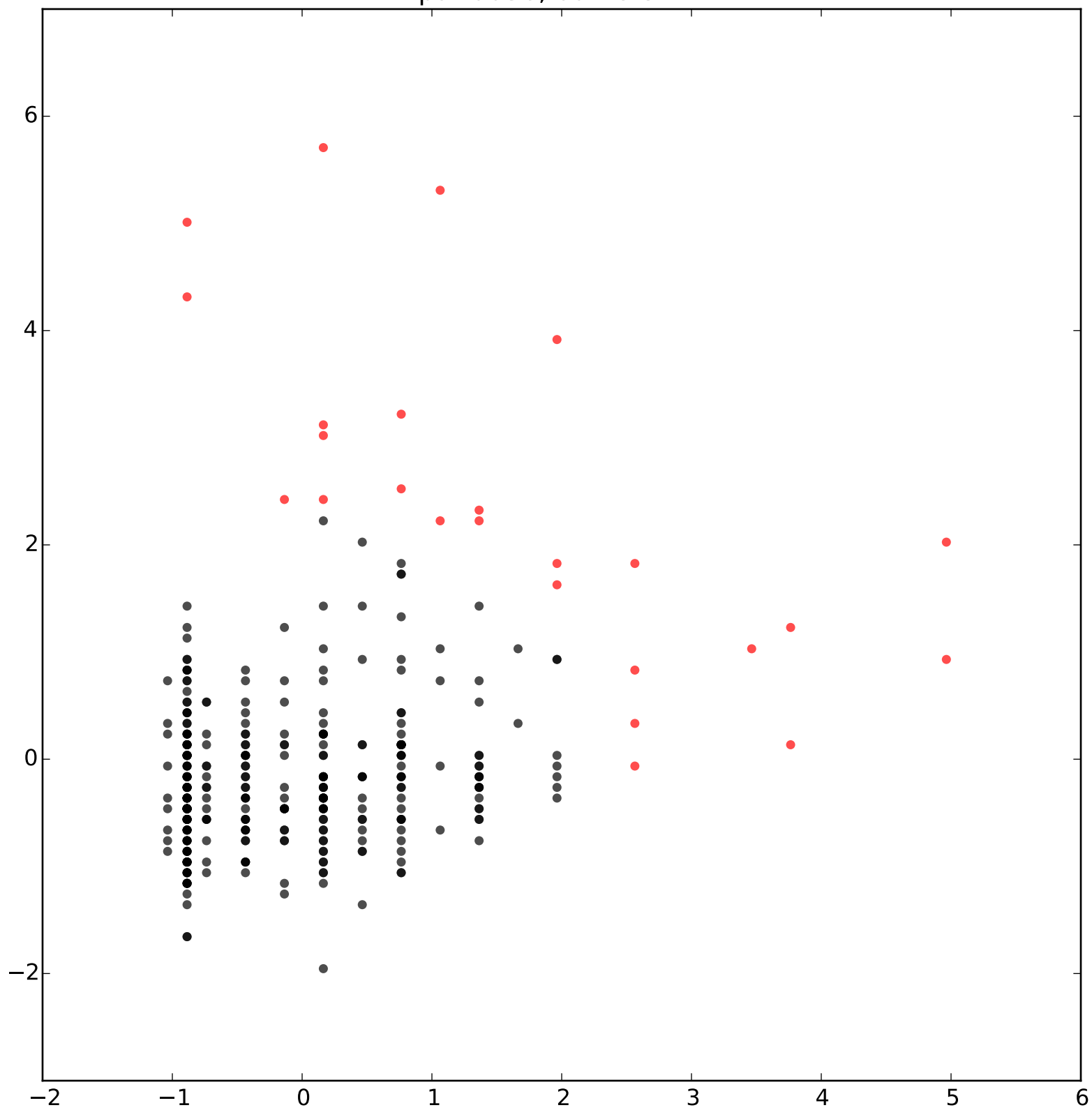




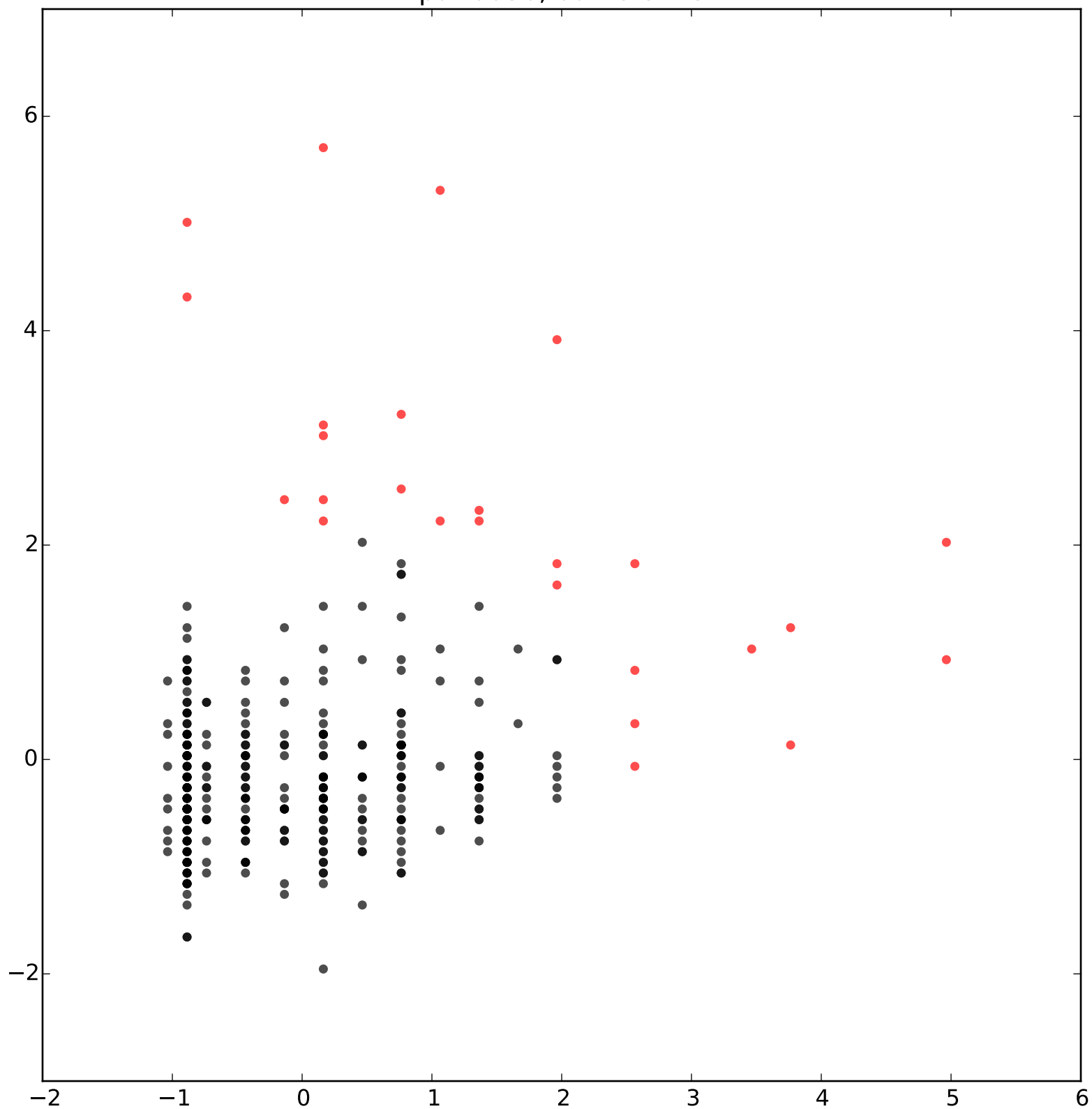
pair0036, outliers: 23



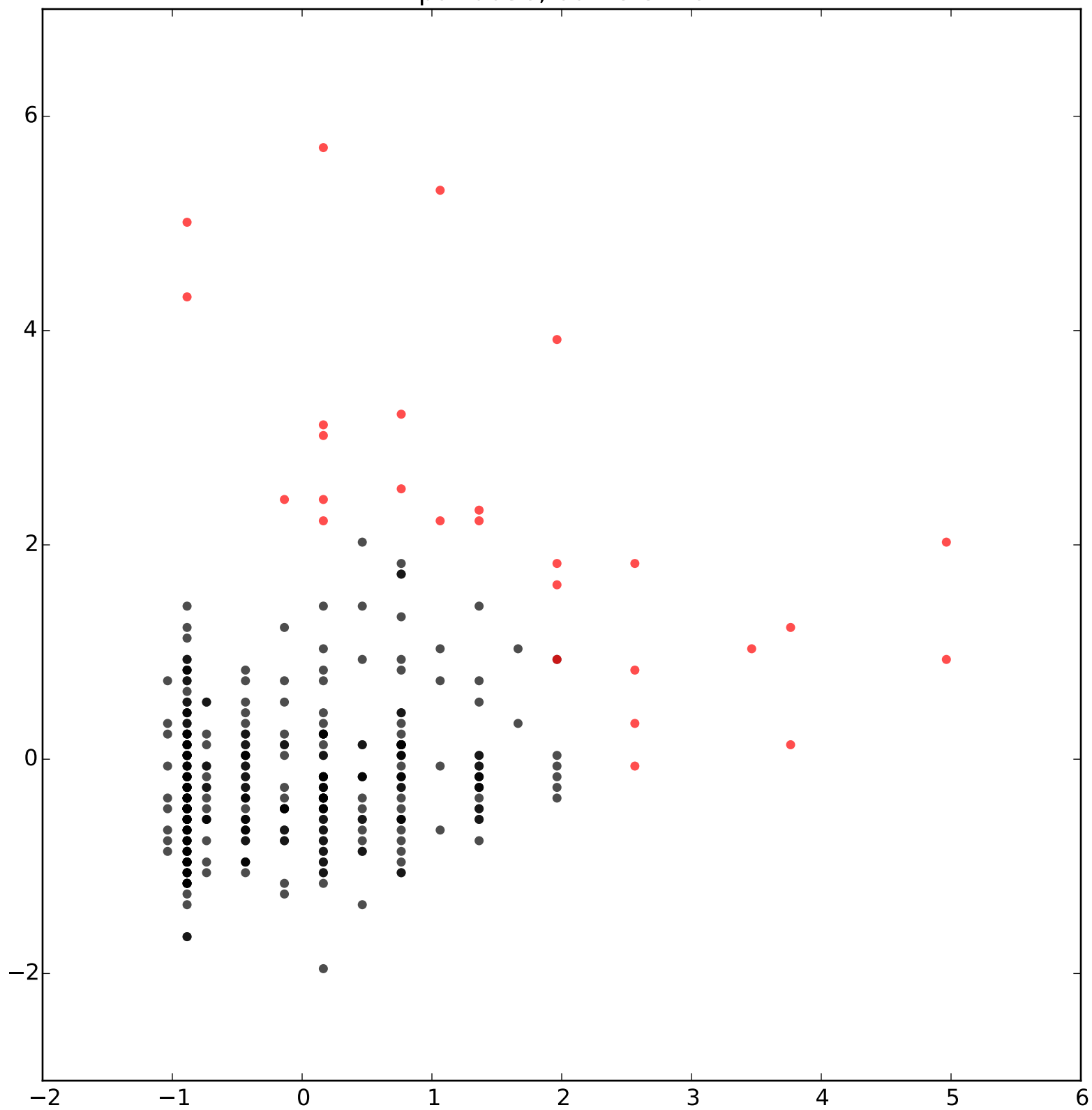
pair0036, outliers: 24



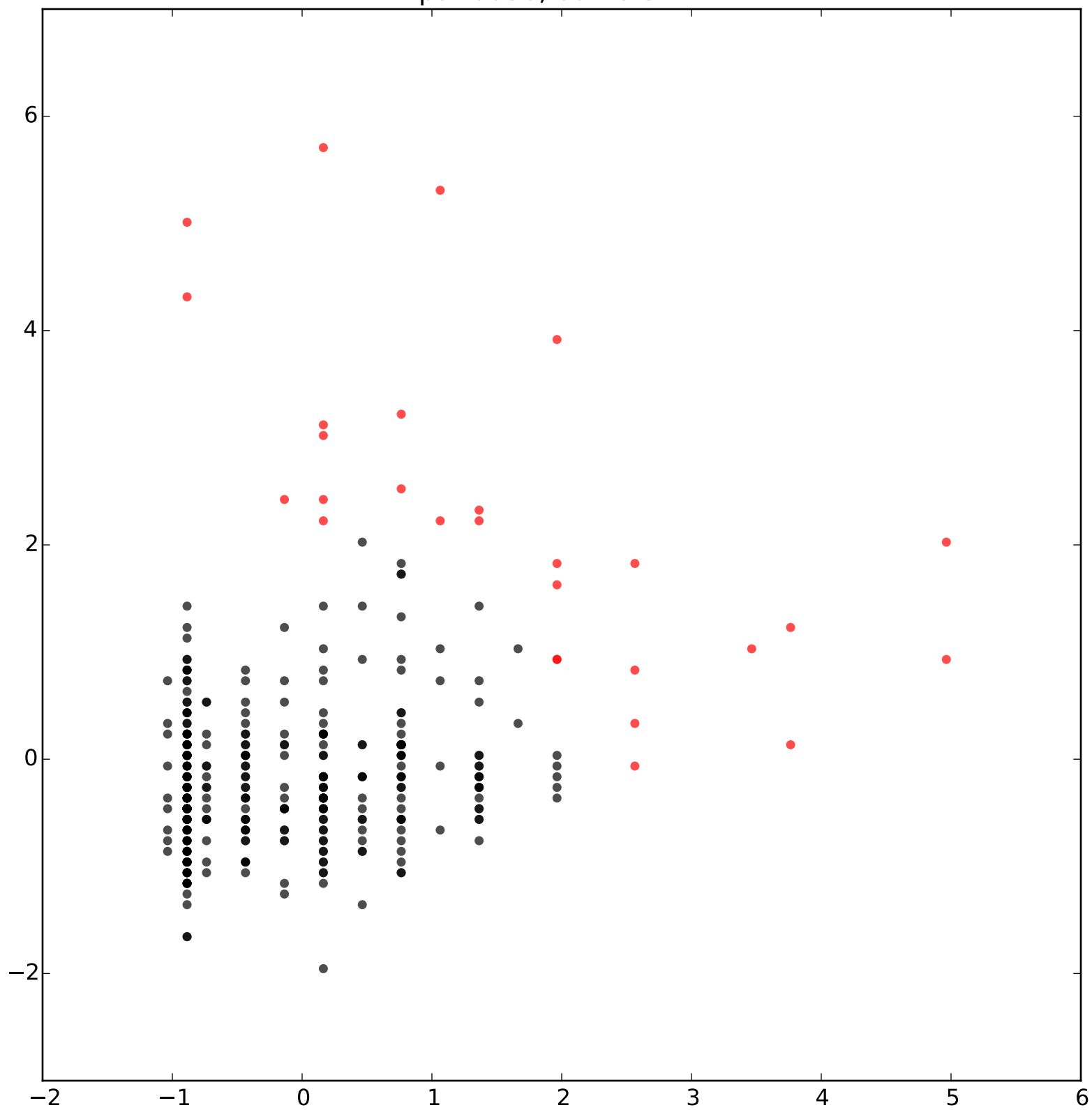
pair0036, outliers: 25



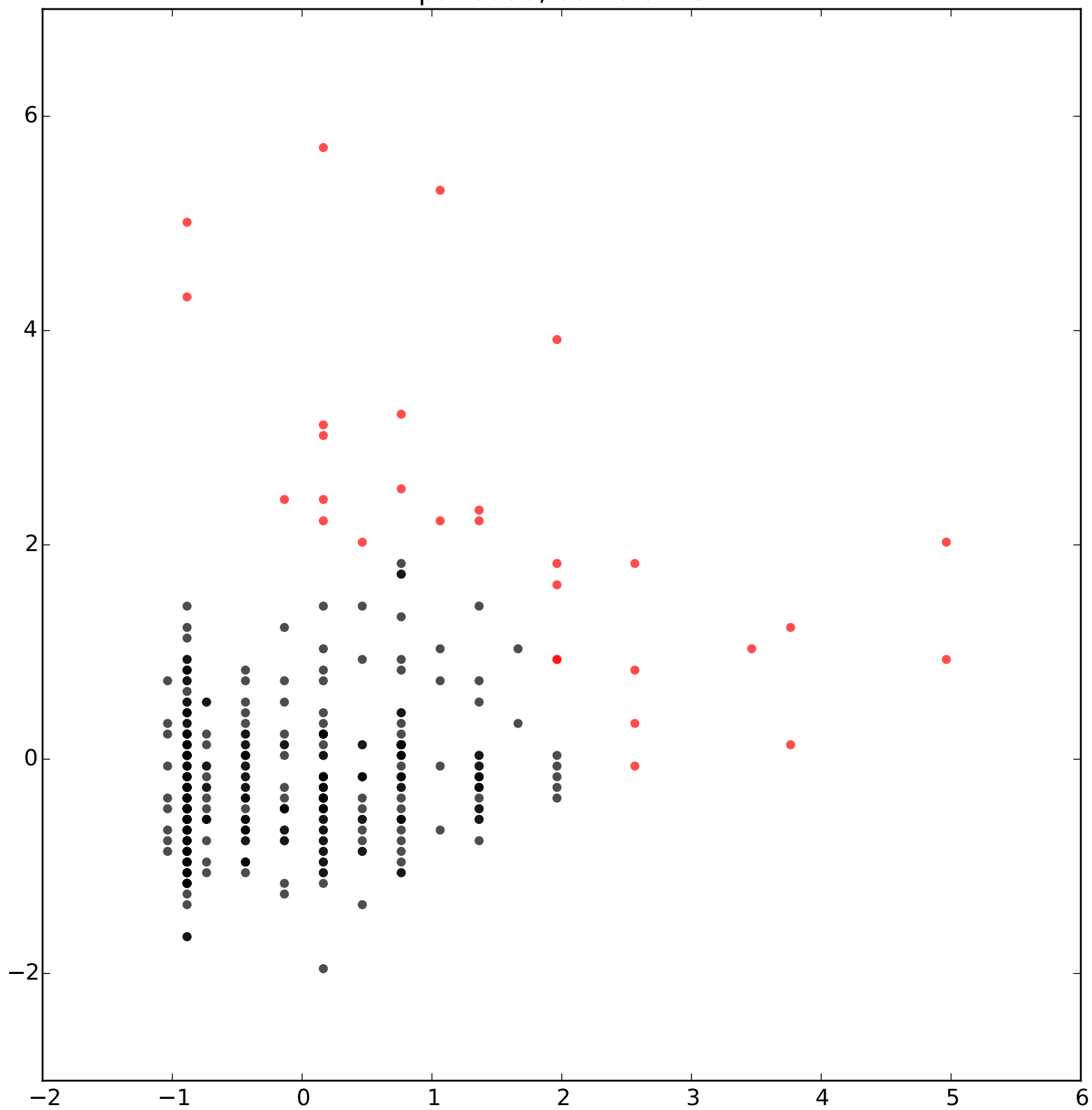
pair0036, outliers: 26



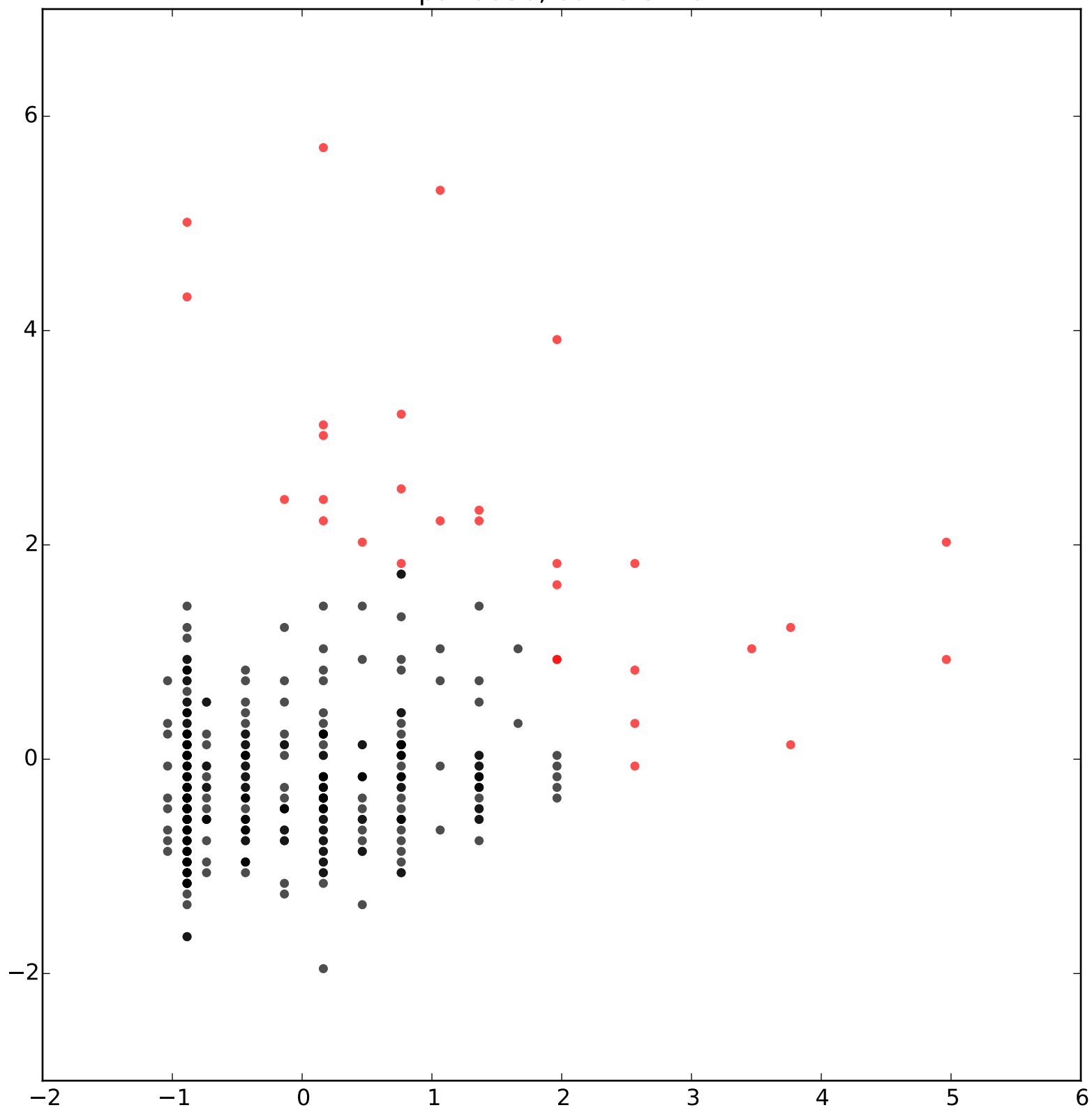
pair0036, outliers: 27



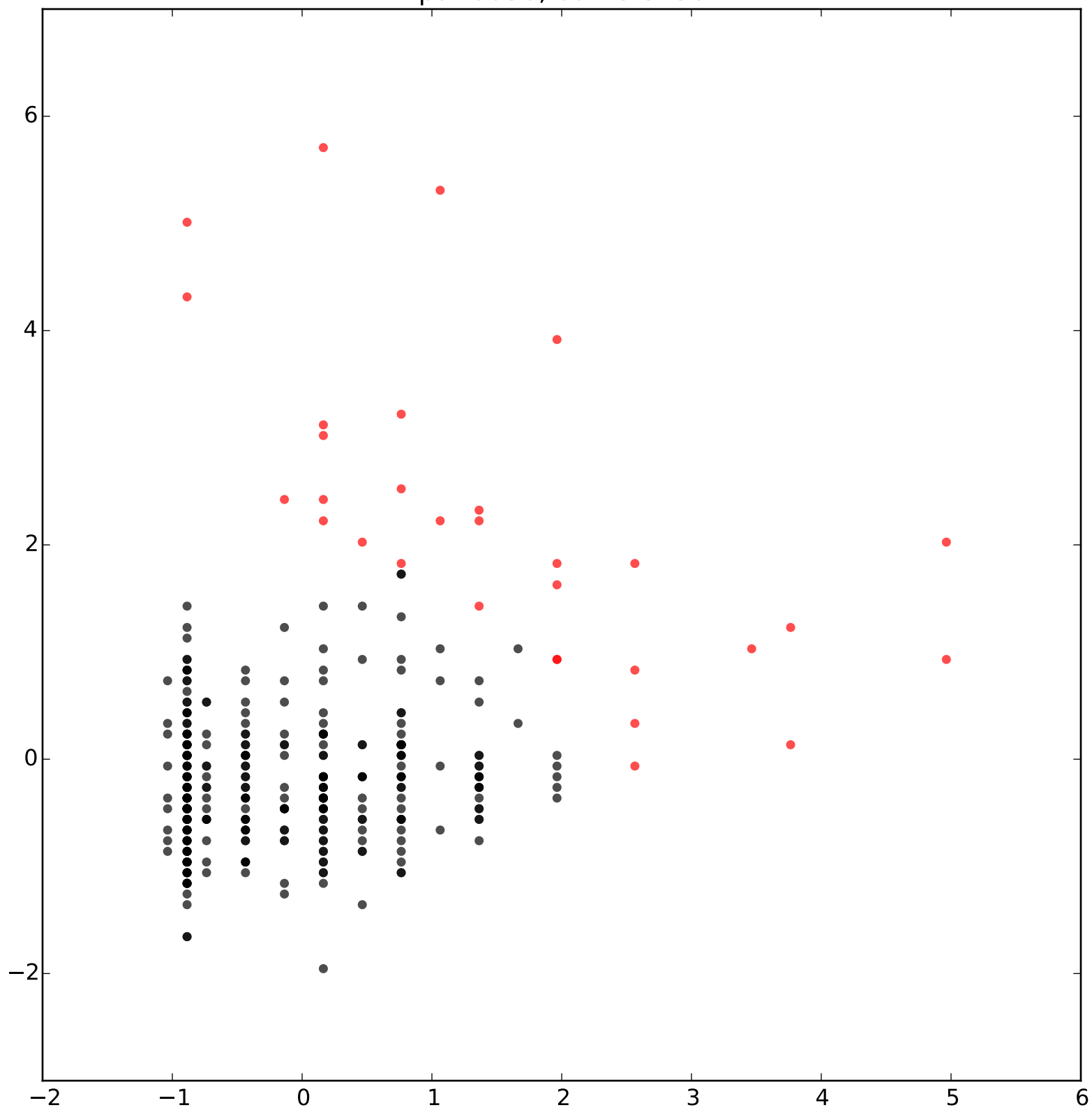
pair0036, outliers: 28



pair0036, outliers: 29

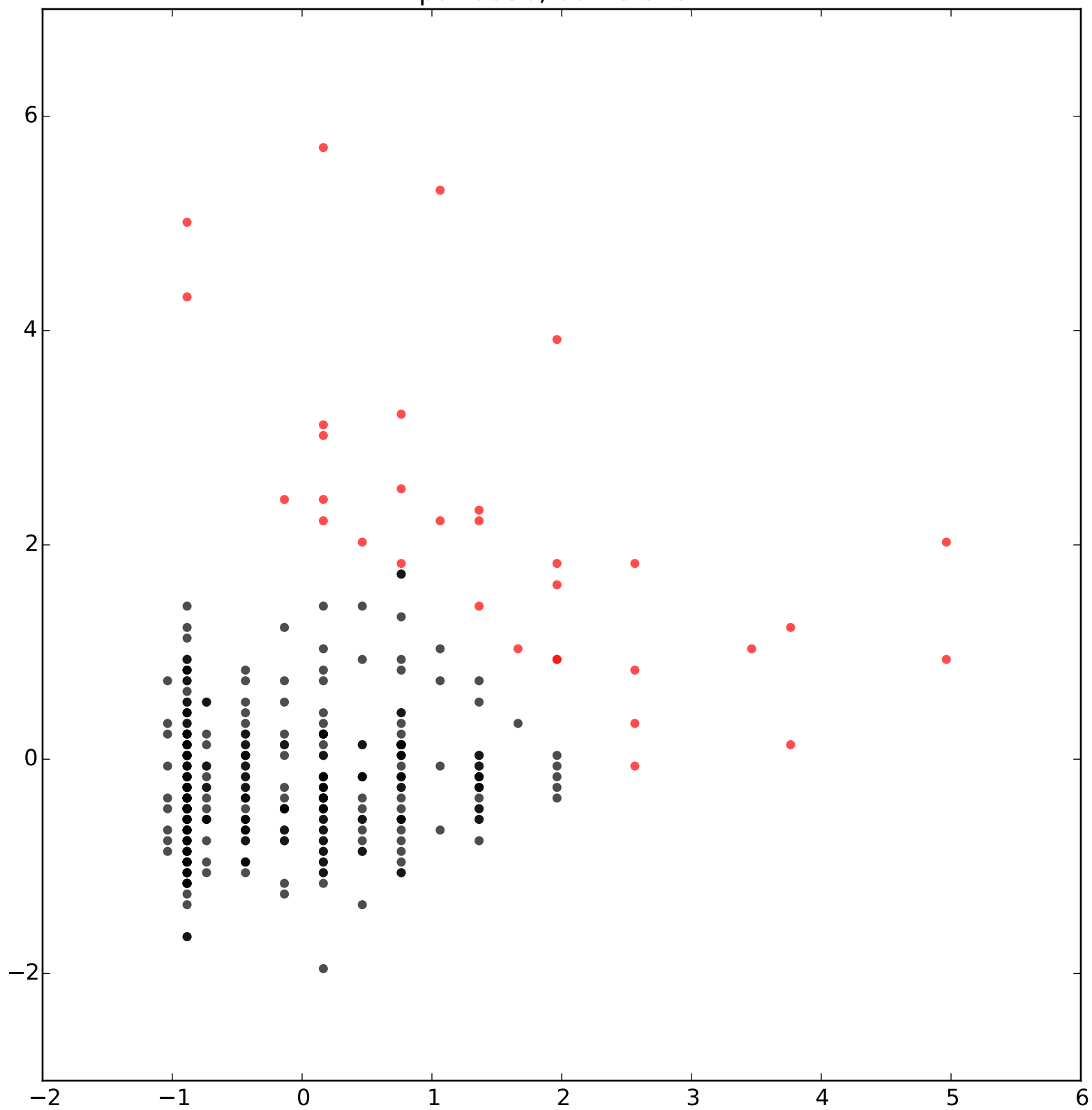


pair0036, outliers: 30

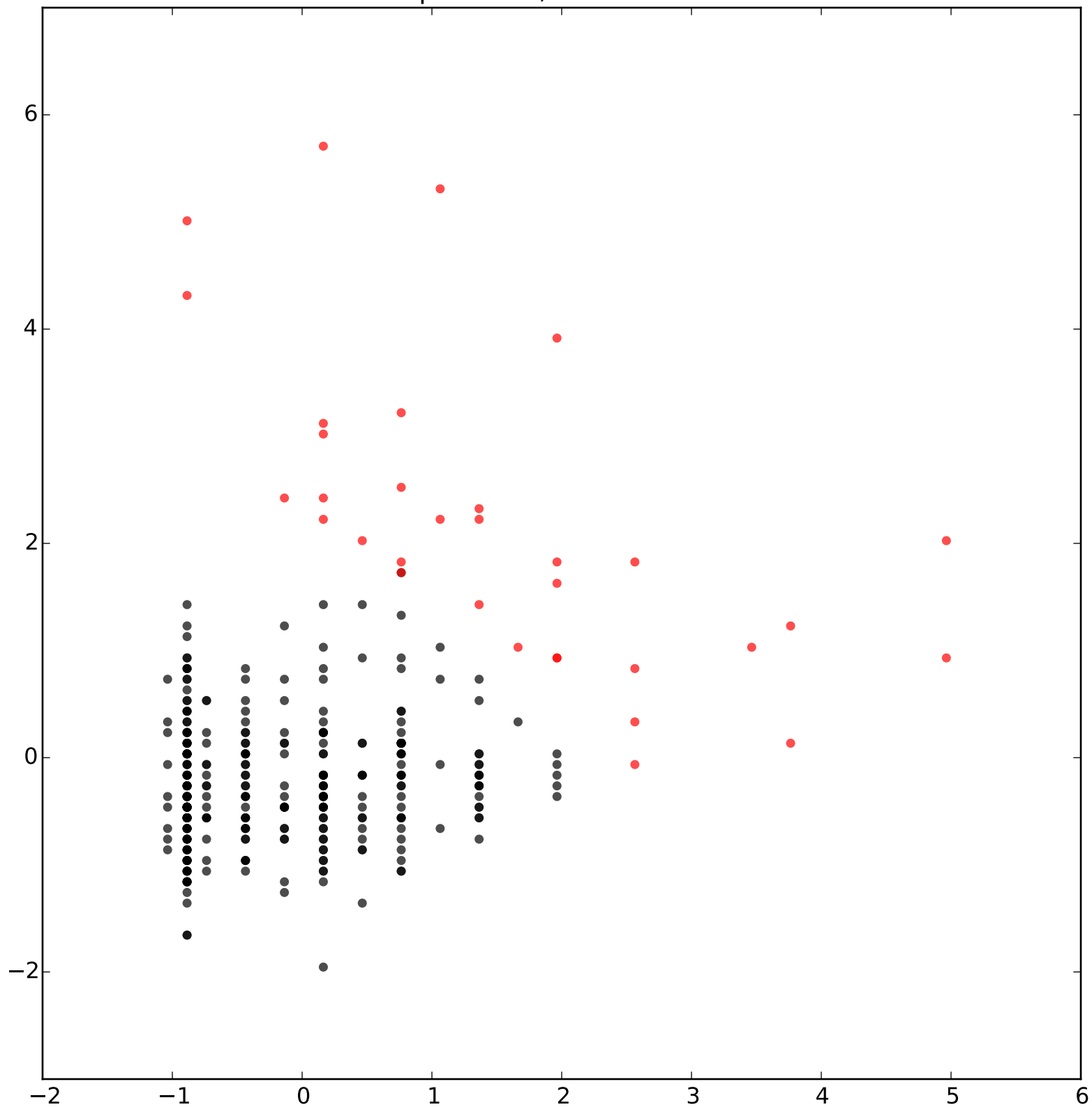




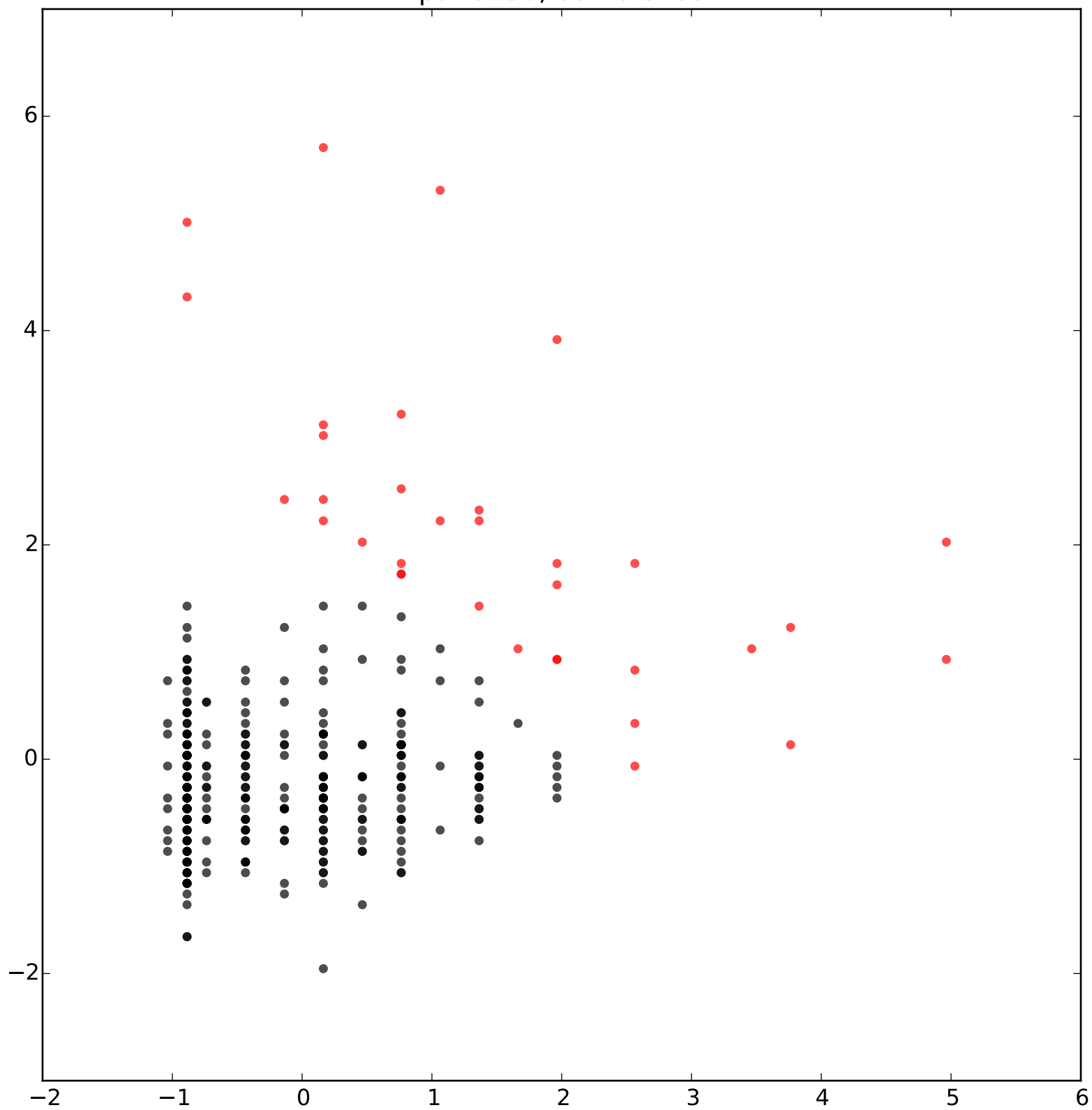
pair0036, outliers: 31



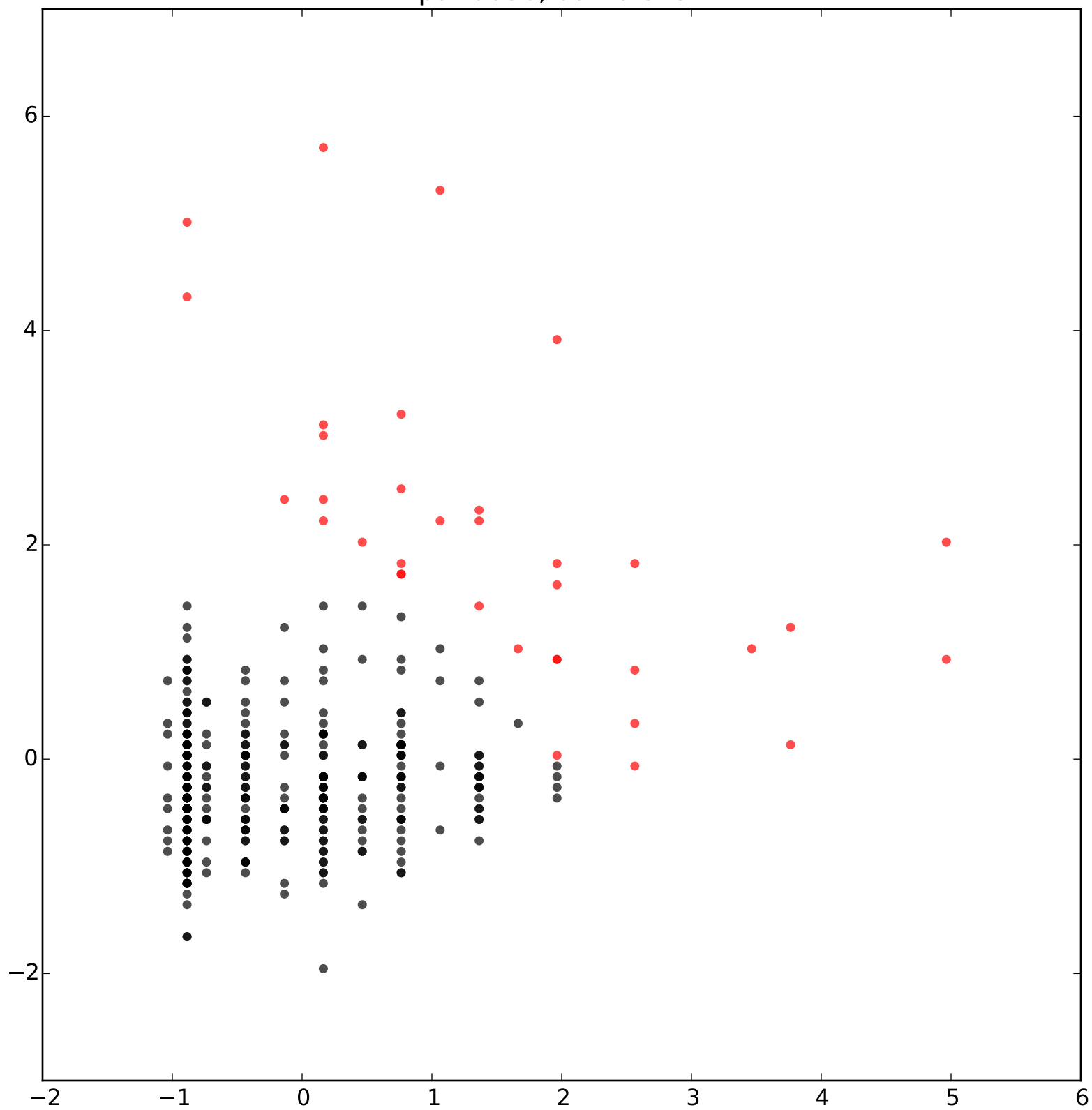
A scatter plot showing the relationship between the negative logarithm of the p-value ( $-\log_{10}(p\text{-value})$ ) on the y-axis and the base-2 logarithm of the fold change ( $\log_2(\text{FC})$ ) on the x-axis. The plot displays 1000 genes, with red dots indicating genes that are significantly differentially expressed (FDR < 0.05) and grey dots indicating non-significant genes. The significant genes are clustered at higher  $-\log_{10}(p\text{-value})$  values, particularly for those with higher  $\log_2(\text{FC})$  values, suggesting a strong correlation between the magnitude of the fold change and the statistical significance of the differential expression.



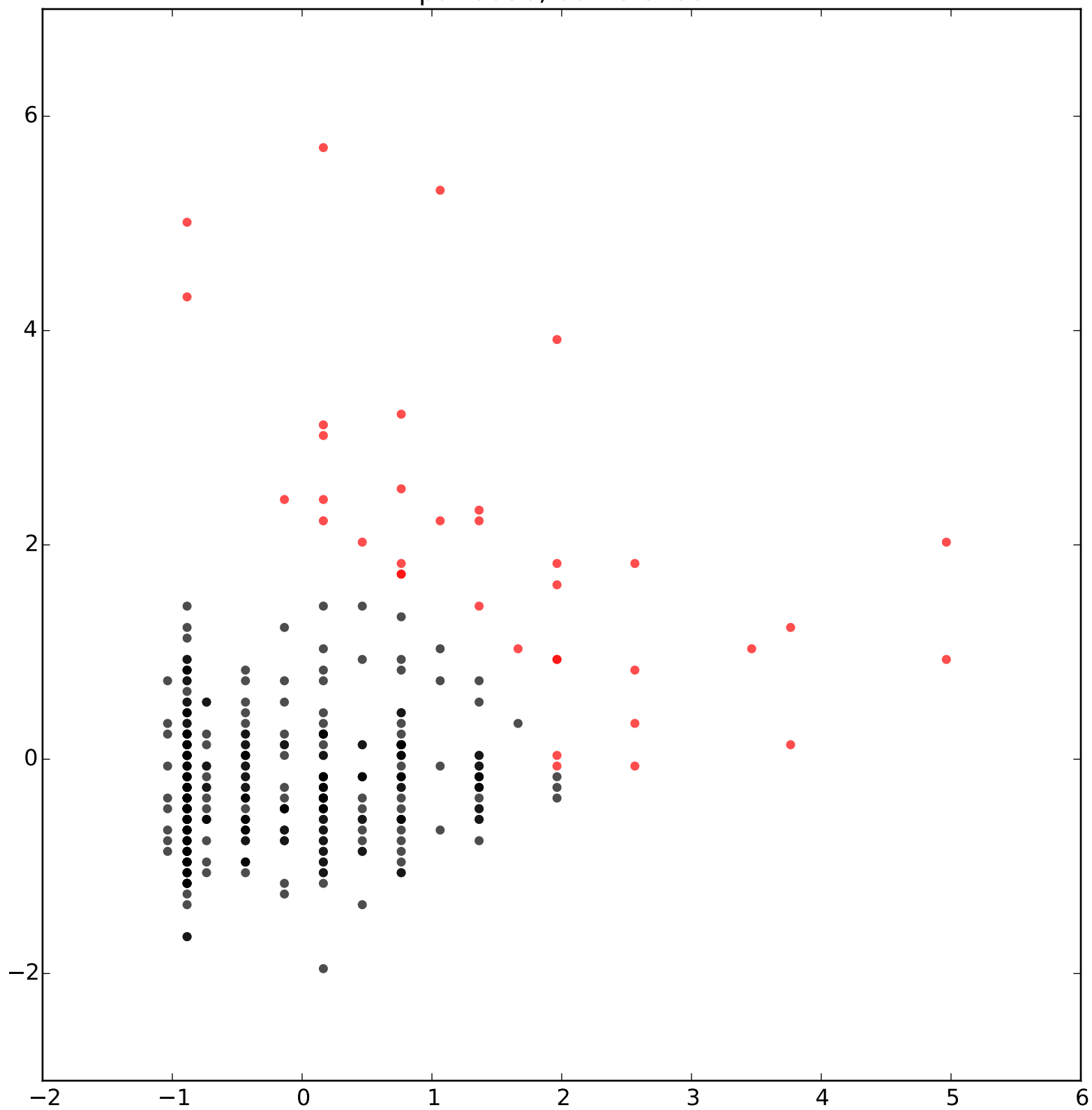
pair0036, outliers: 33



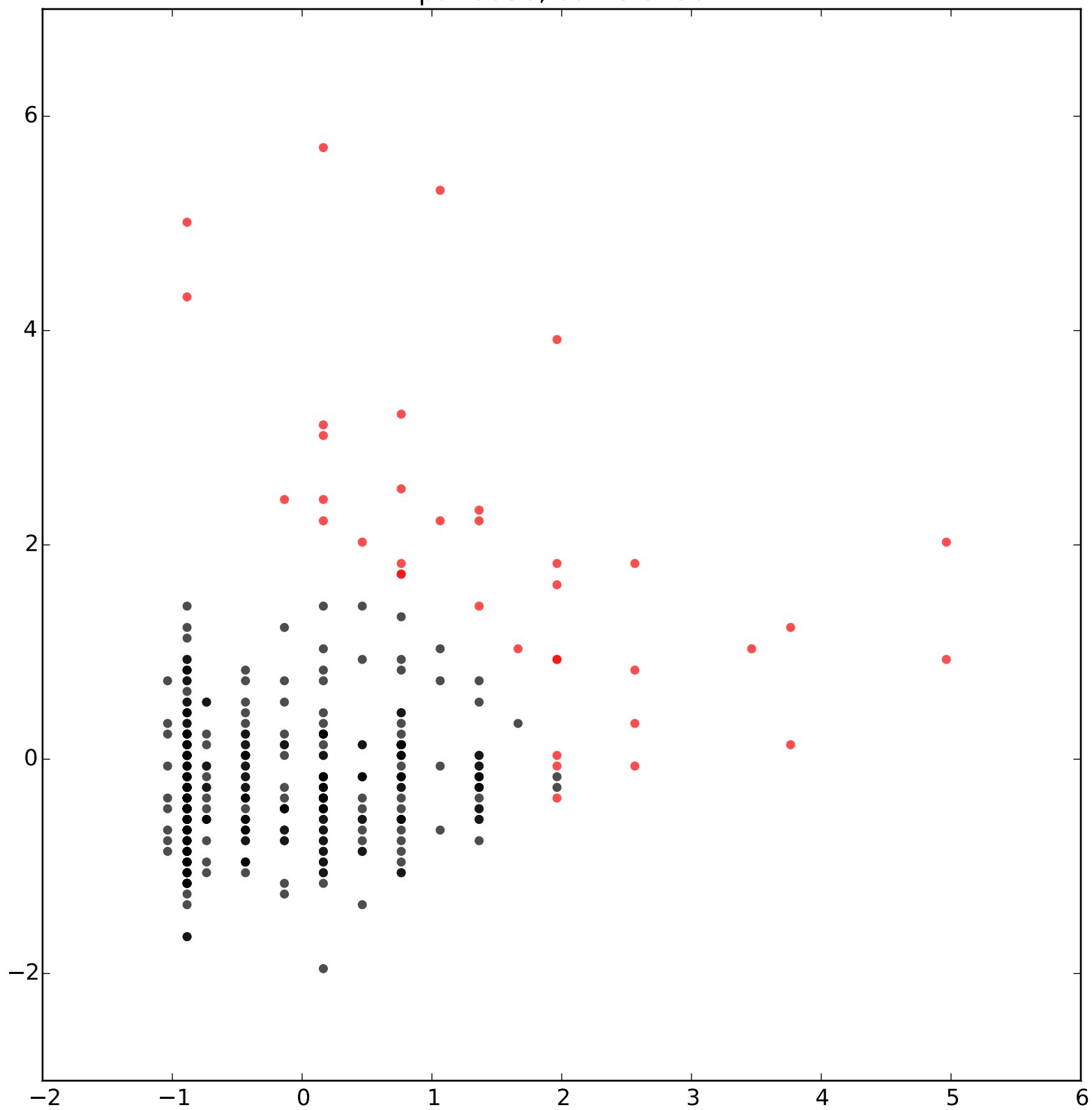
pair0036, outliers: 34



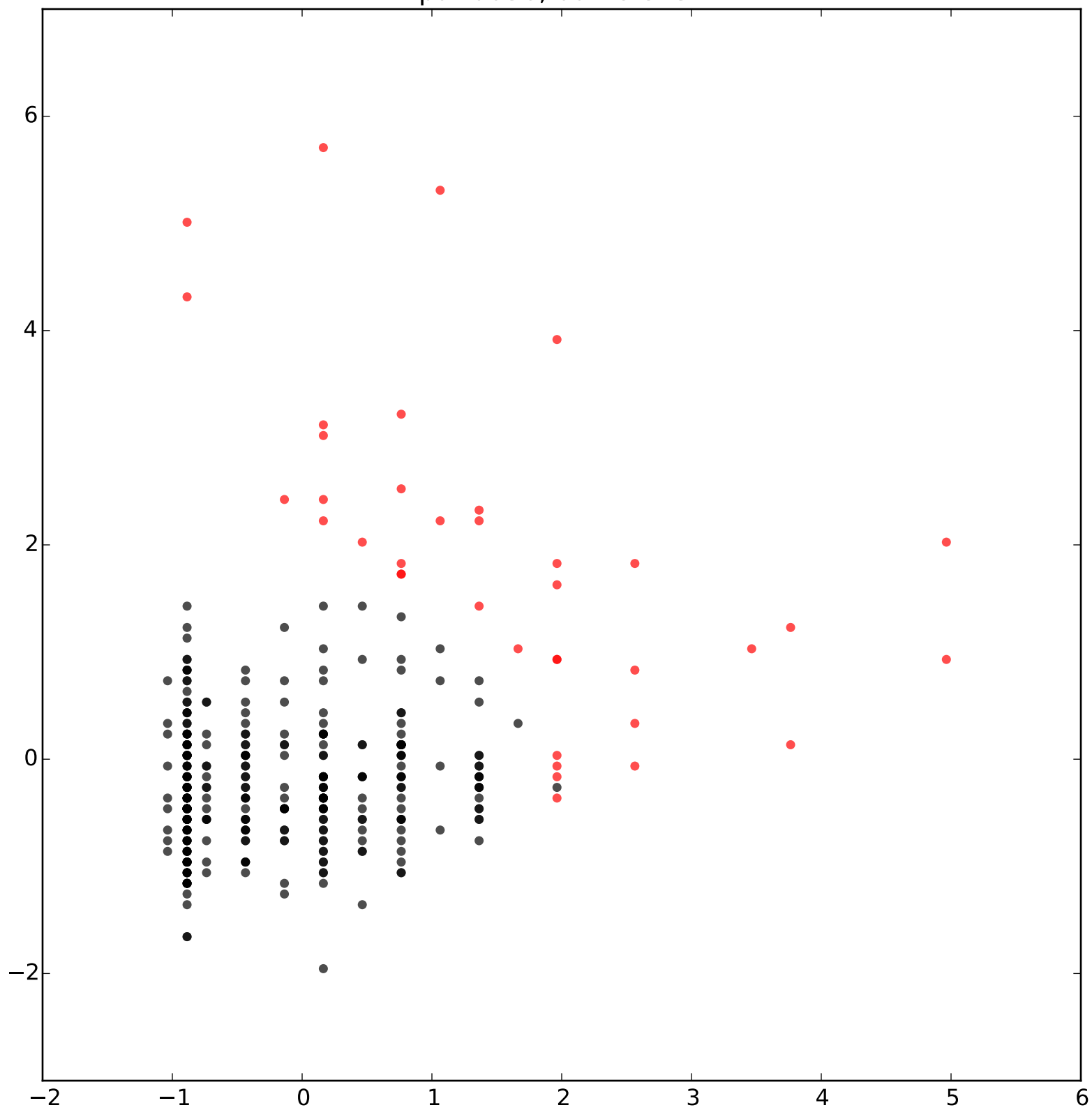
pair0036, outliers: 35



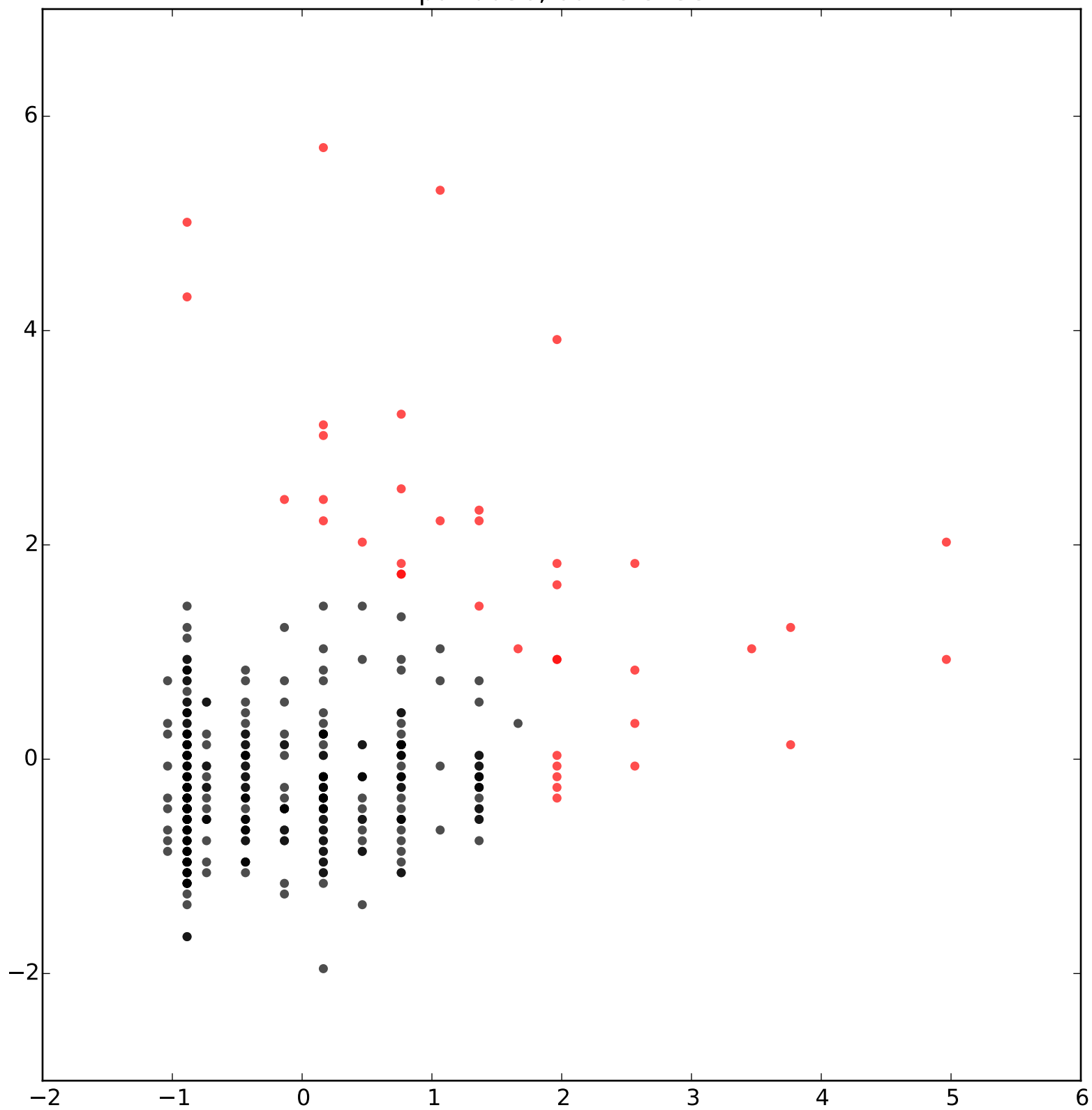
pair0036, outliers: 36



pair0036, outliers: 37

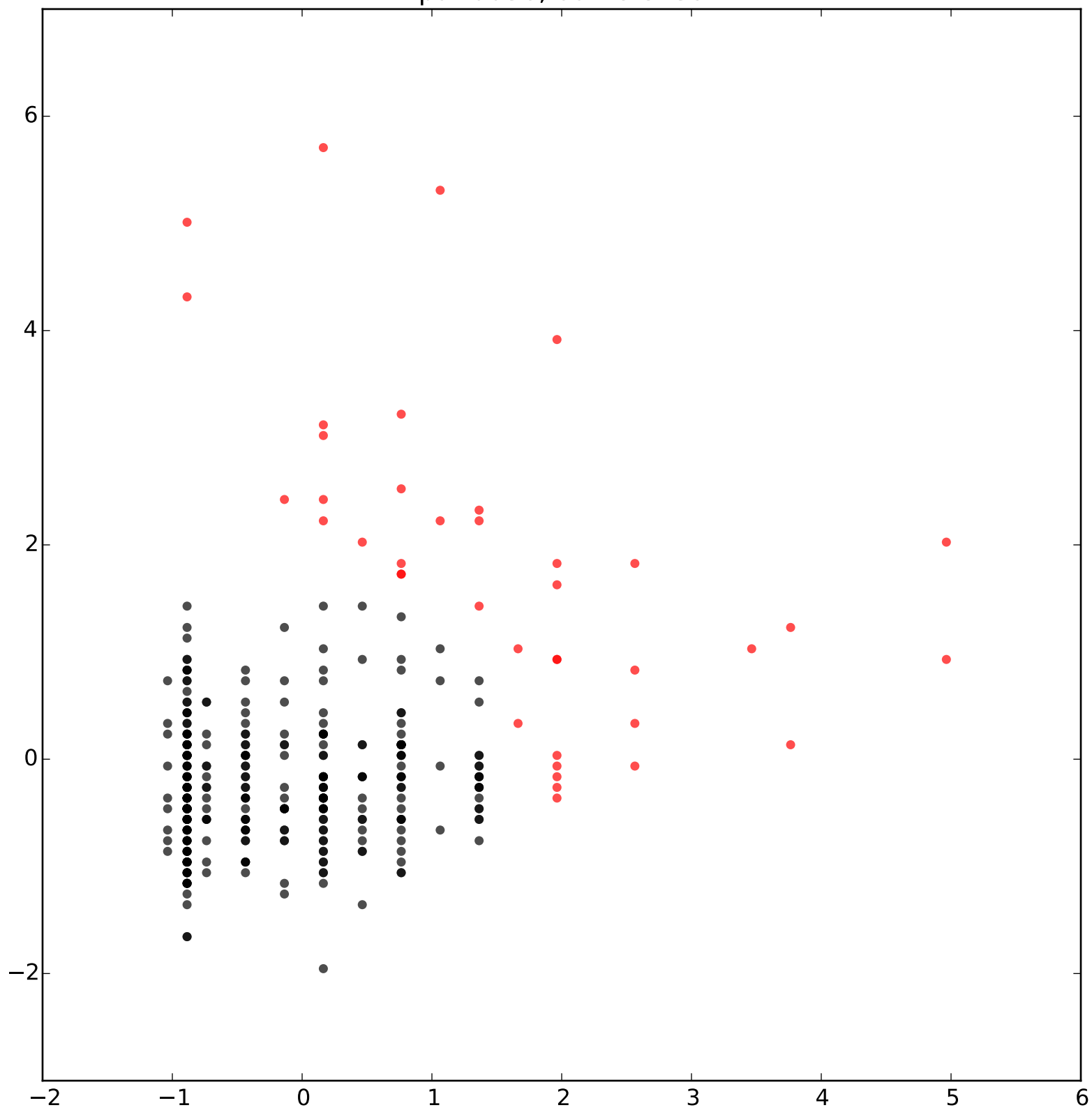


pair0036, outliers: 38

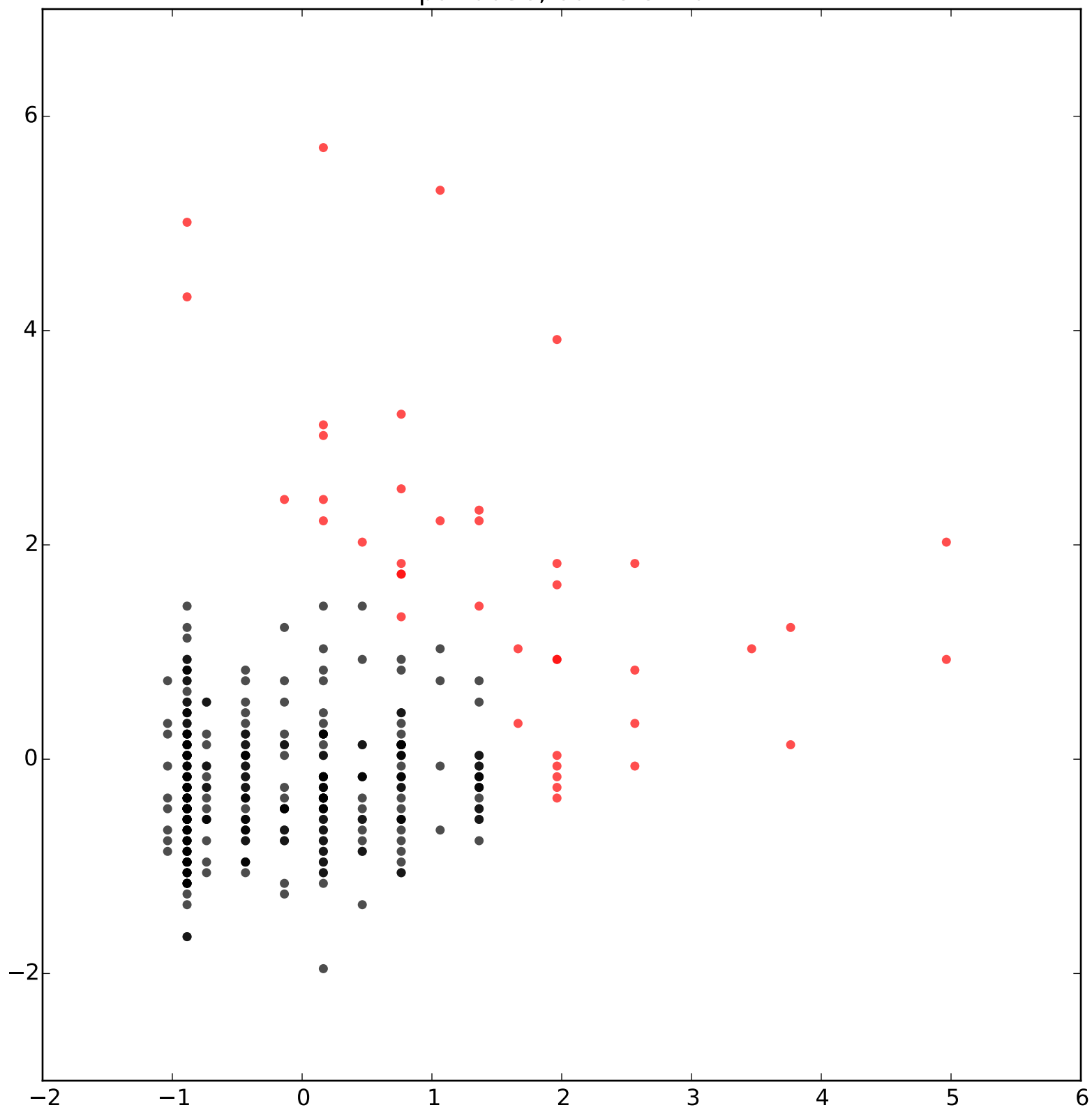




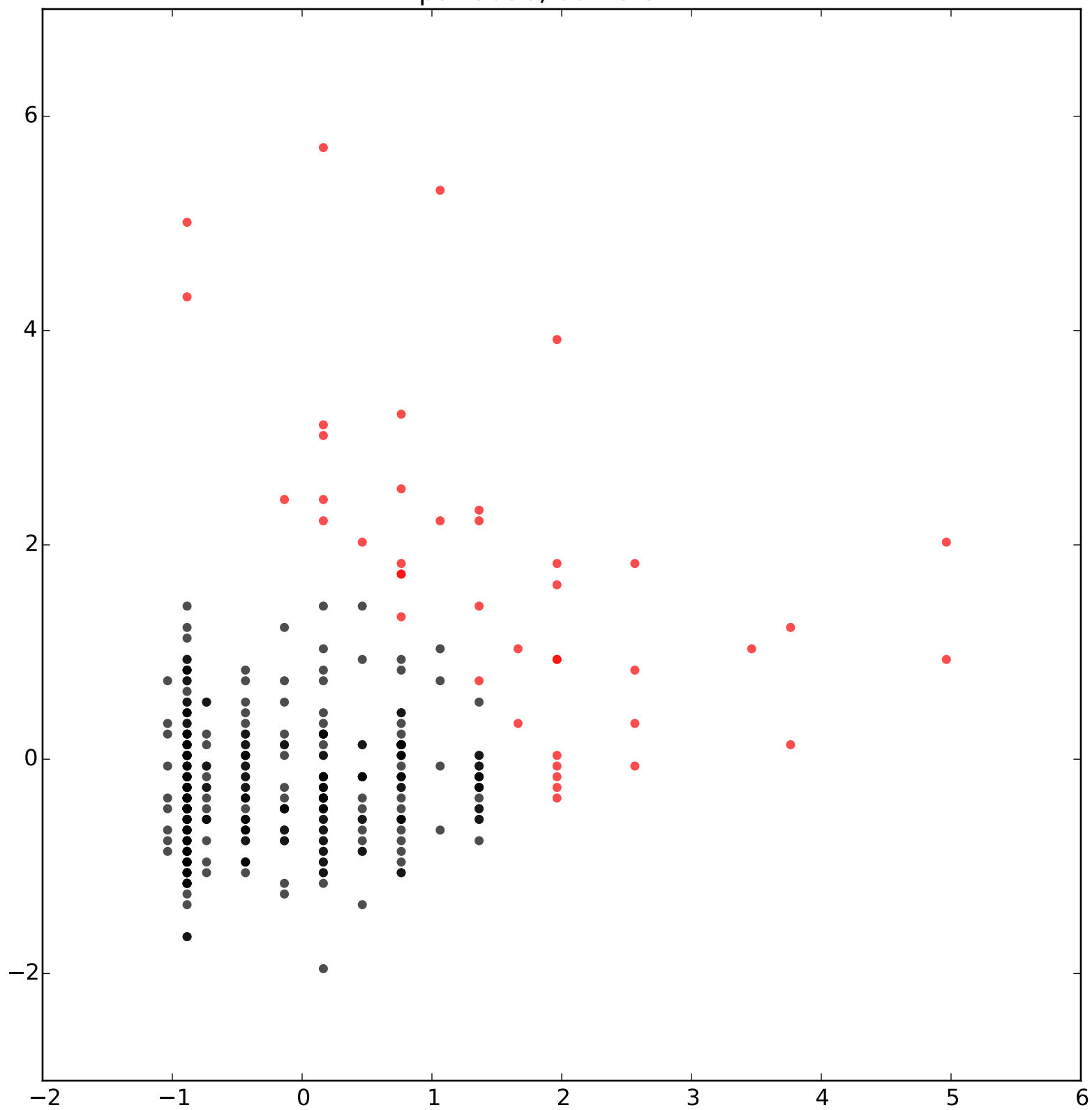
pair0036, outliers: 39

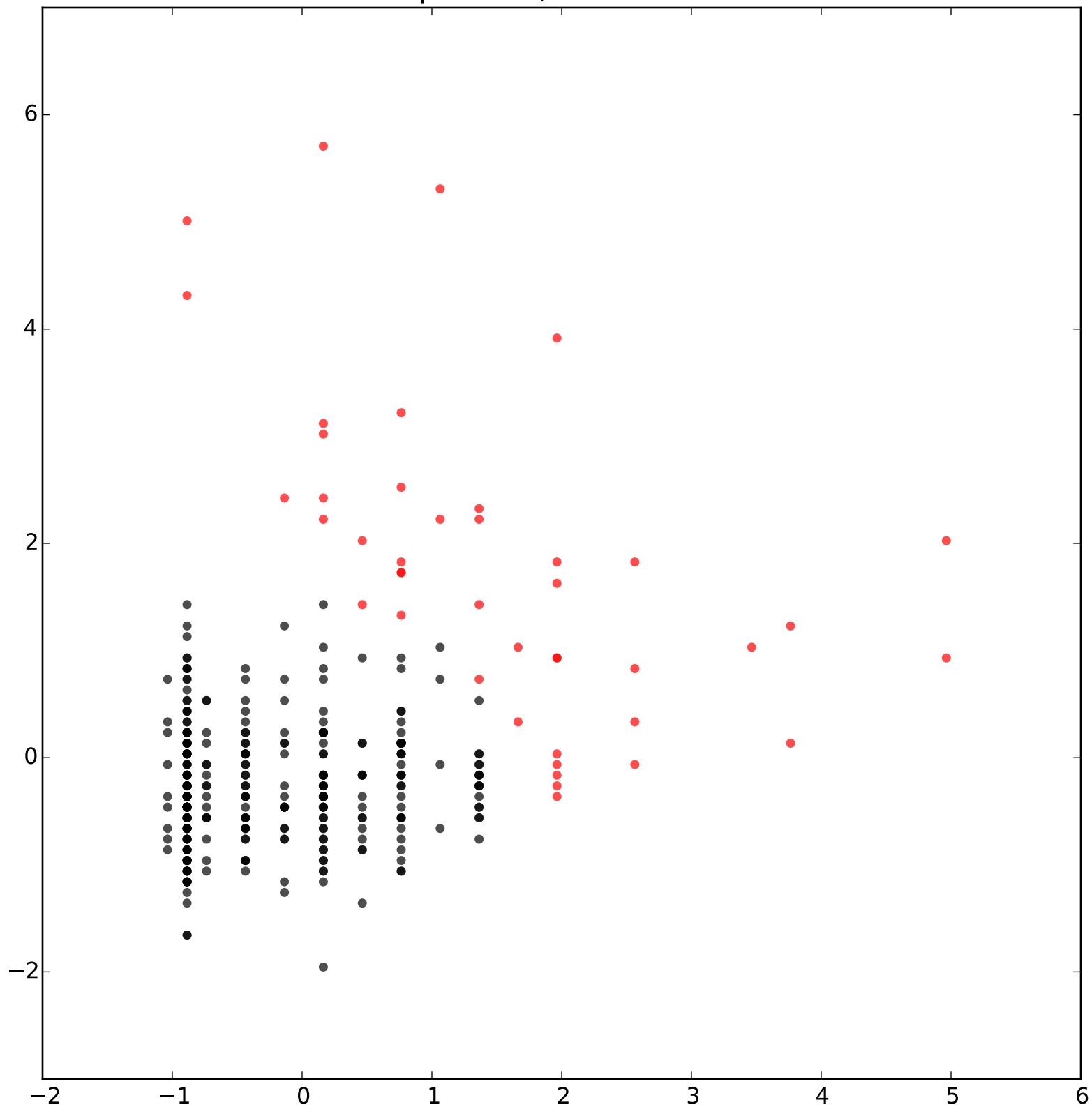


pair0036, outliers: 40

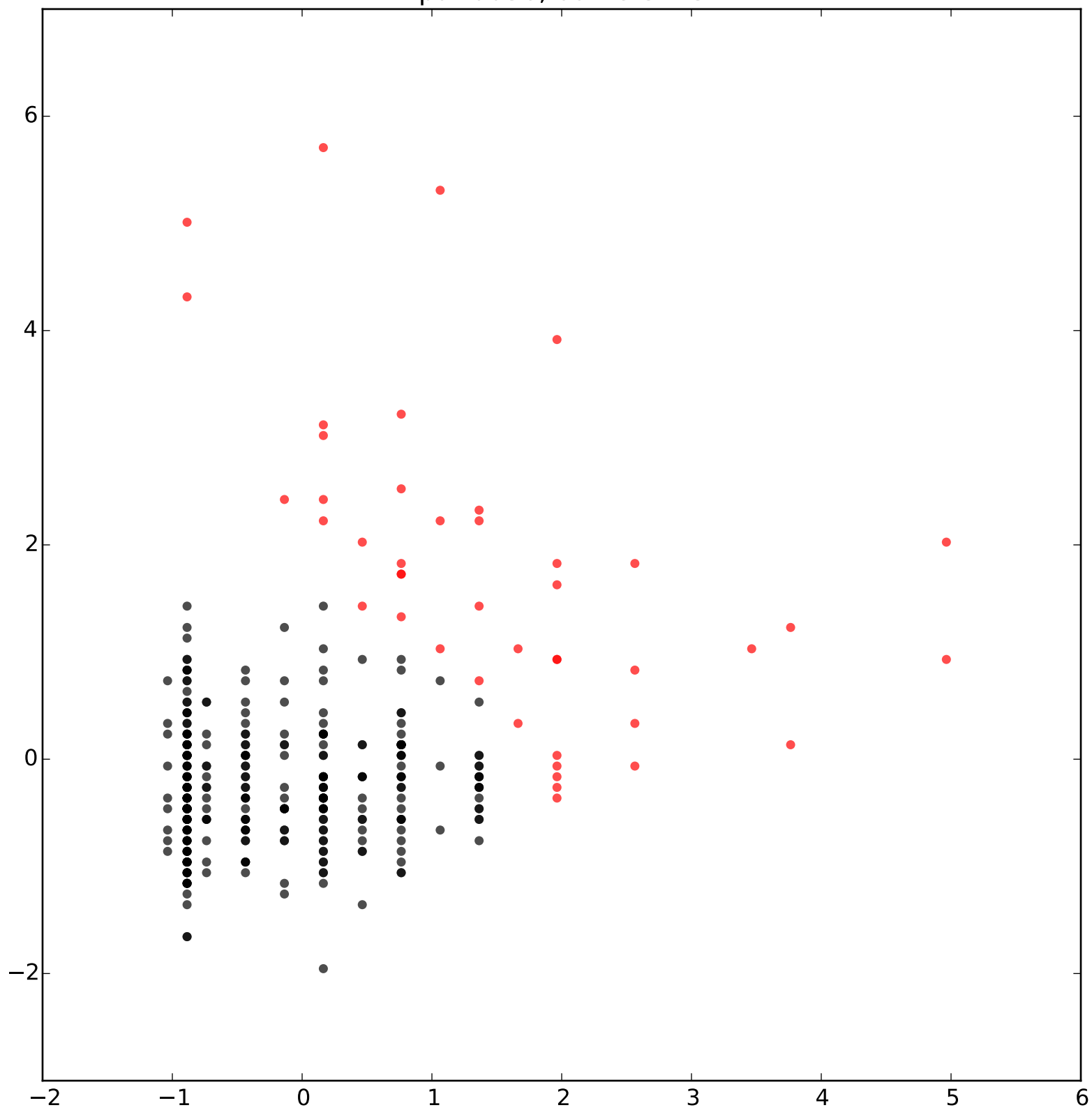


pair0036, outliers: 41





pair0036, outliers: 43



pair0036, outliers: 44

