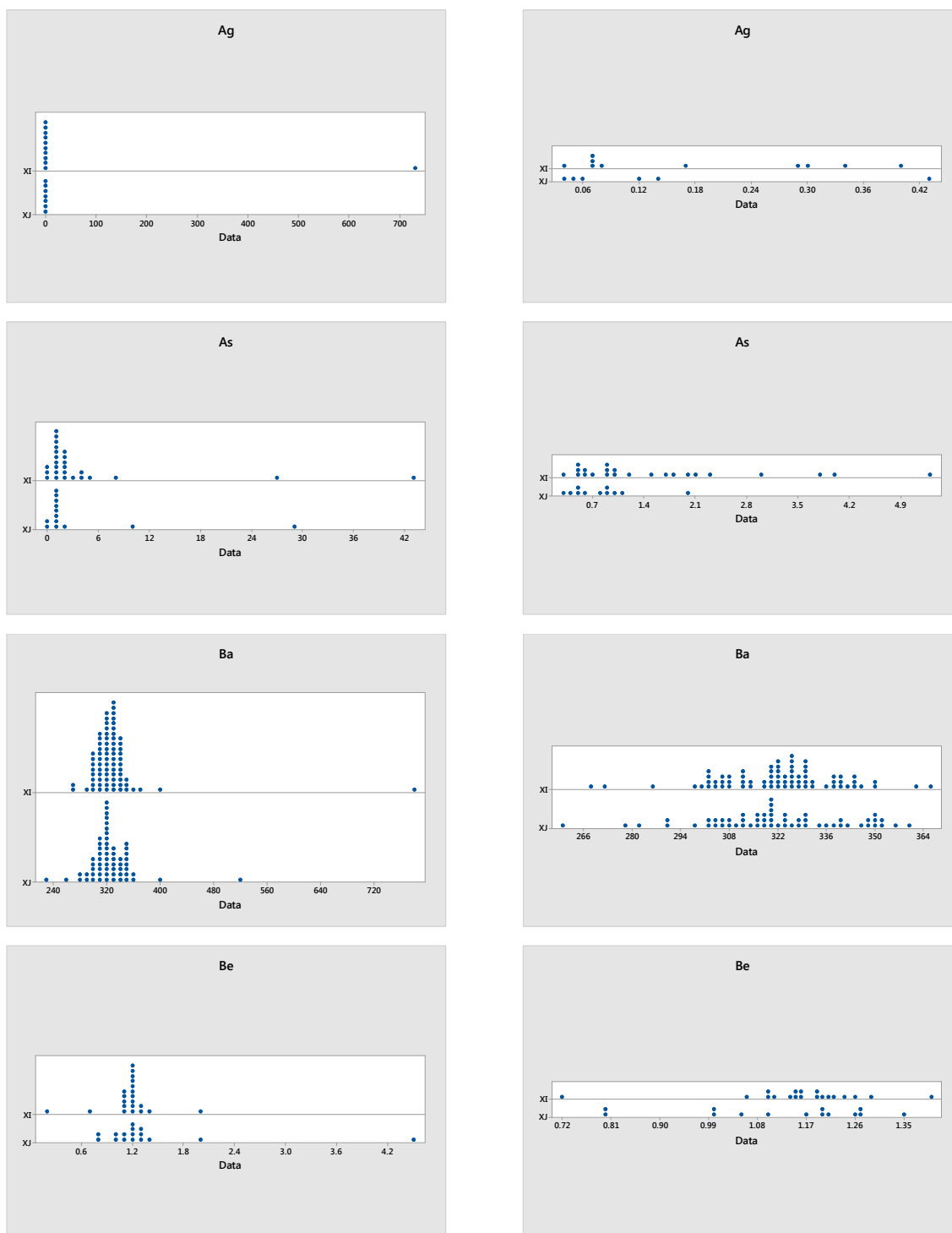
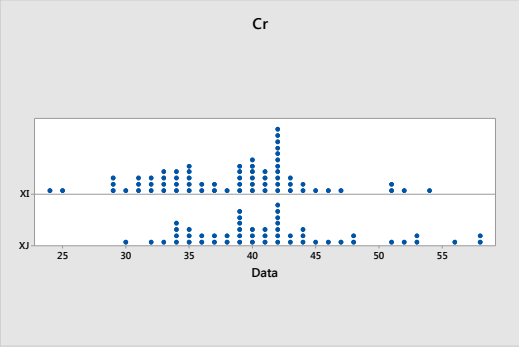
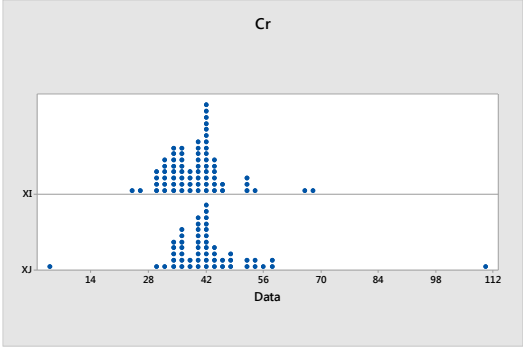
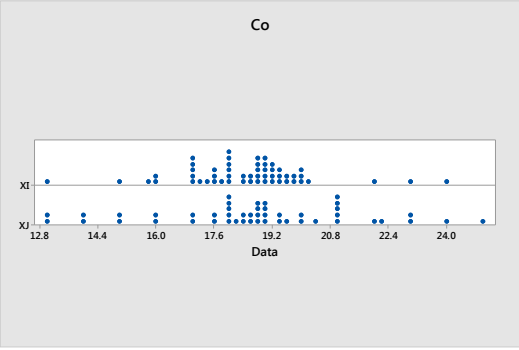
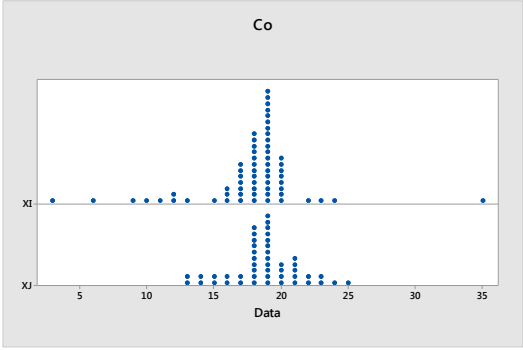
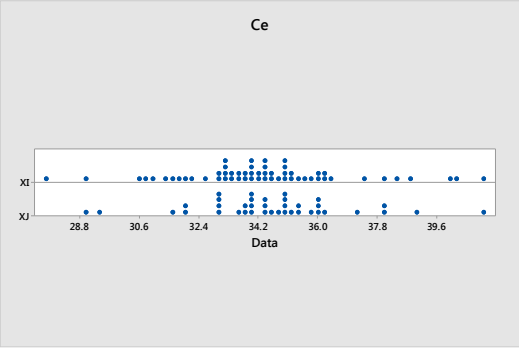
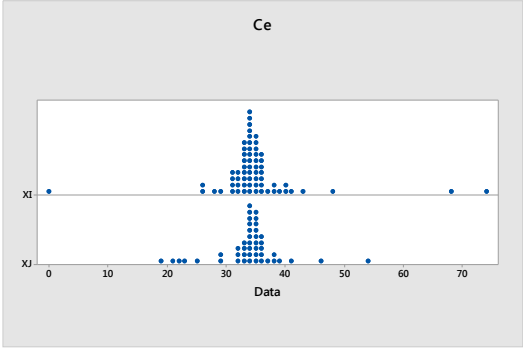
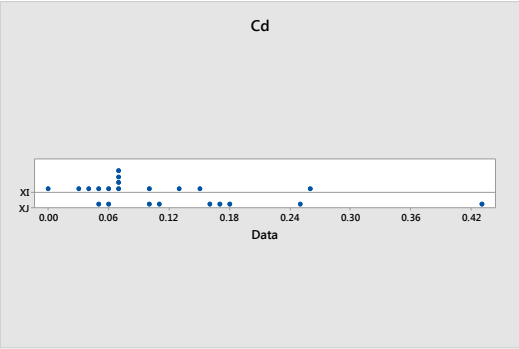
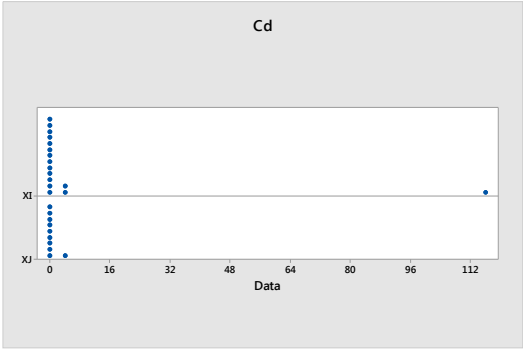
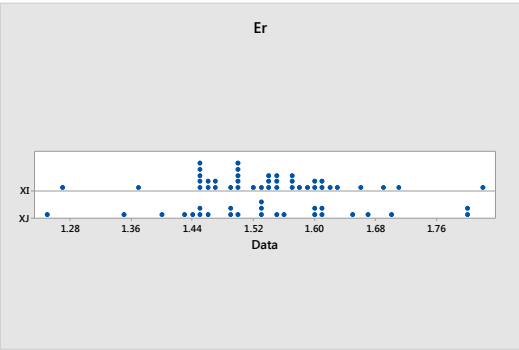
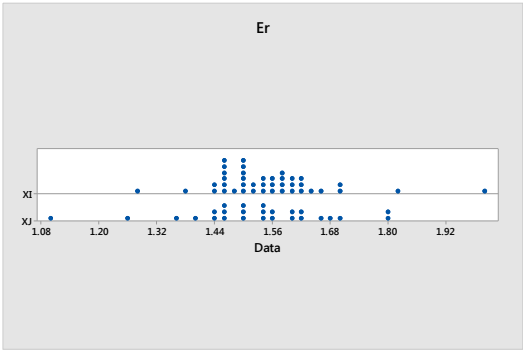
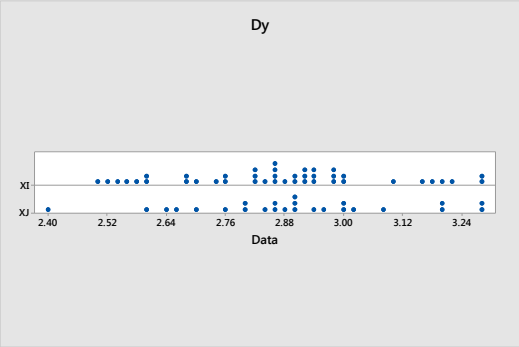
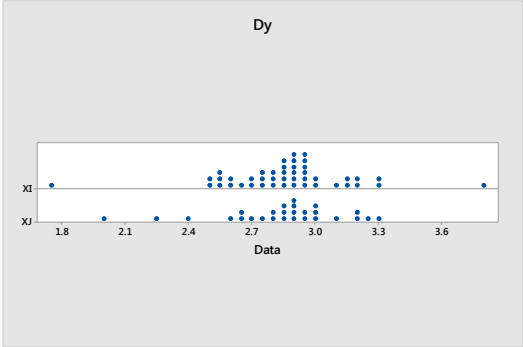
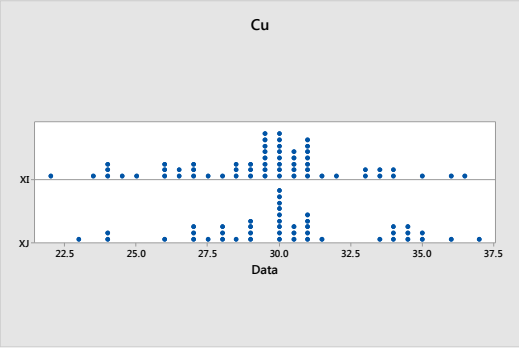
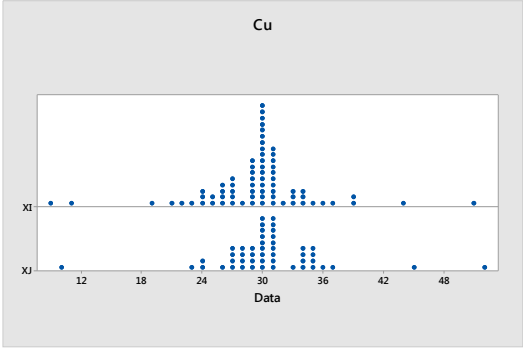
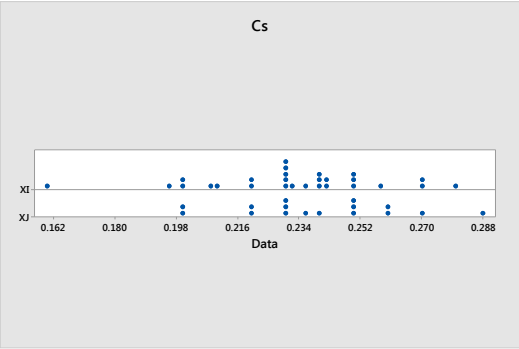
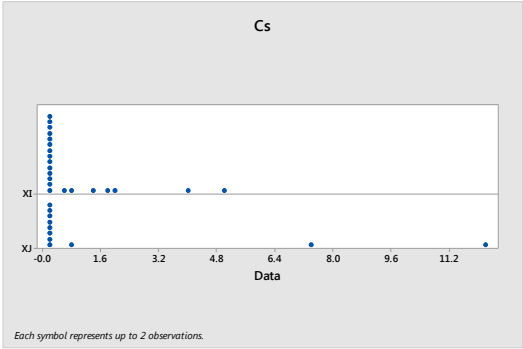
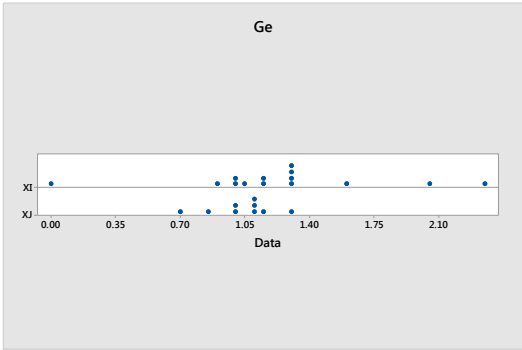
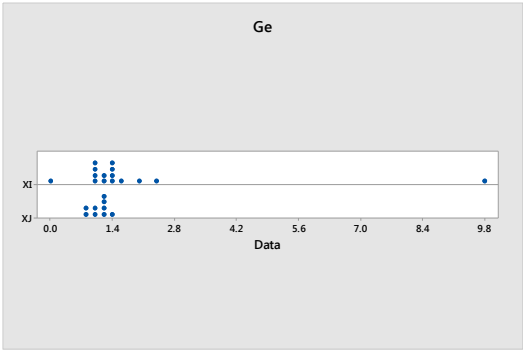
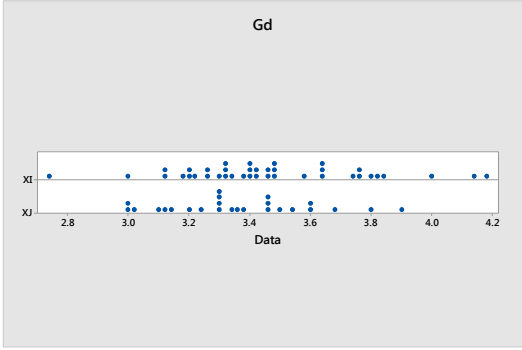
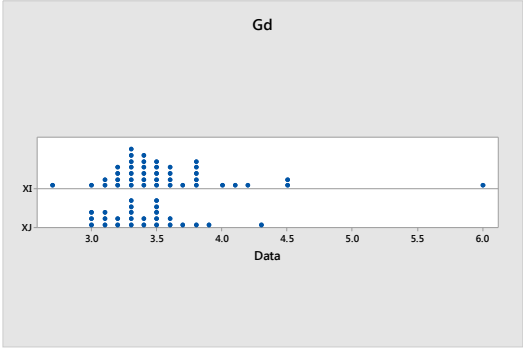
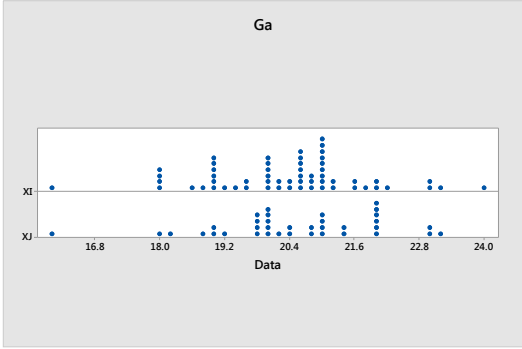
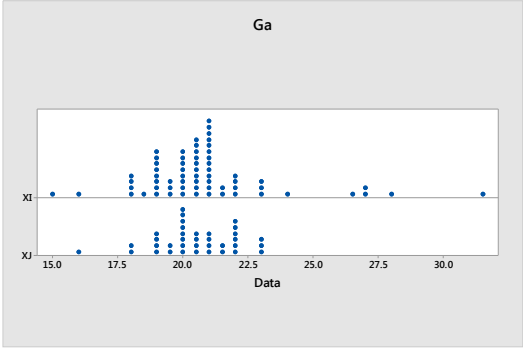
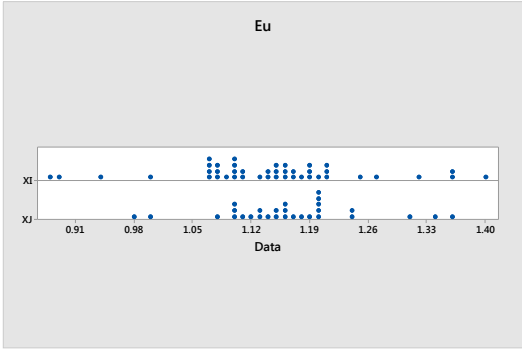
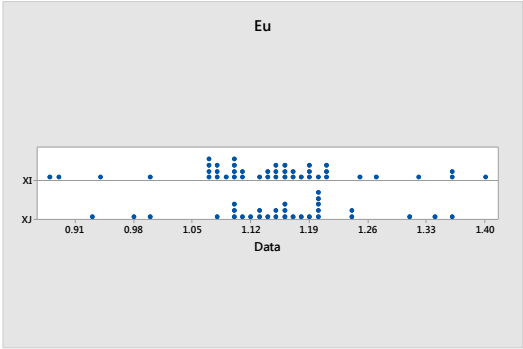


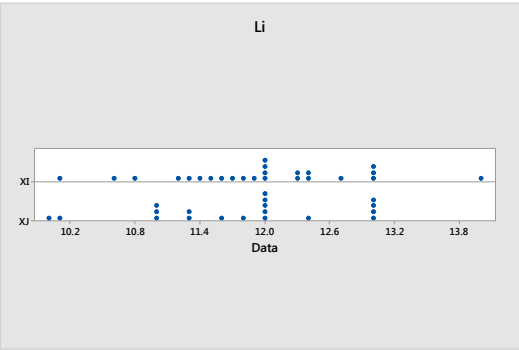
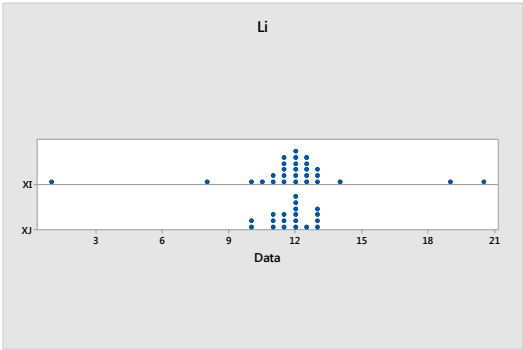
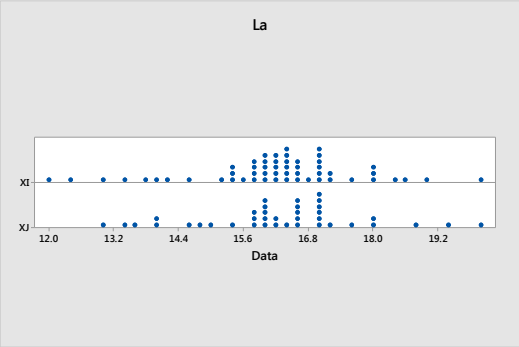
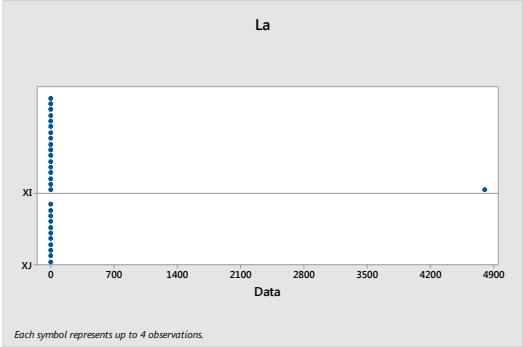
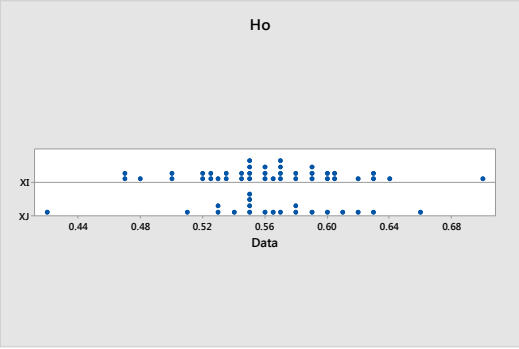
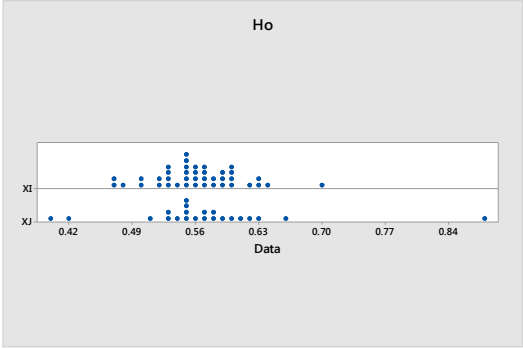
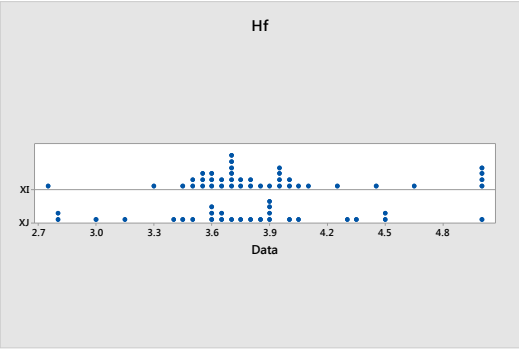
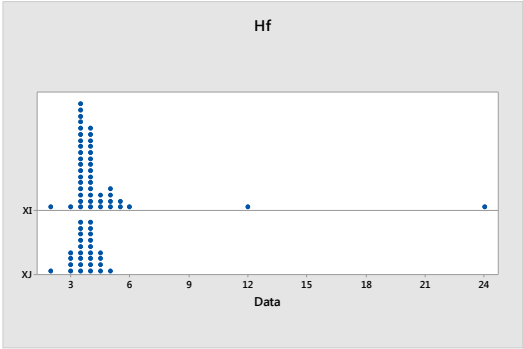
Fig 2. Raw and trimmed datasets: 'trace' analytes. In each figure the upper dotplot represents Round 41, the lower Round 5. Results are mass fractions as parts per million.

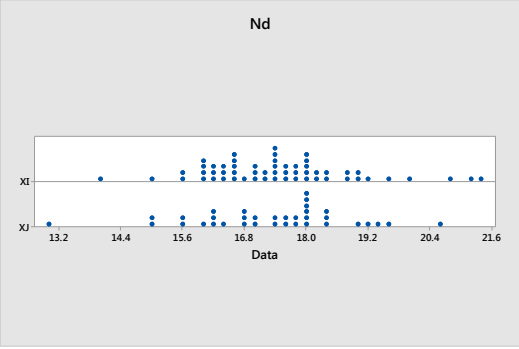
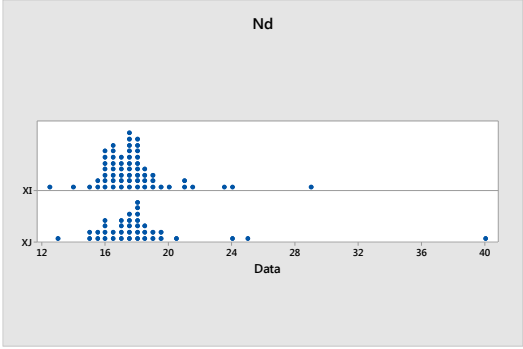
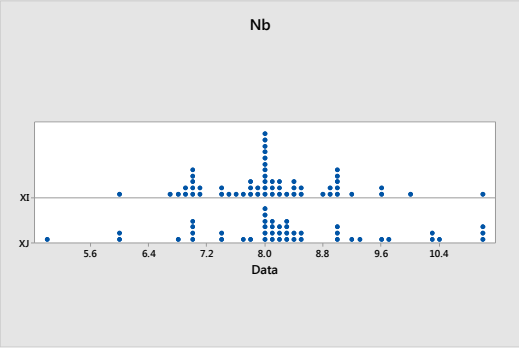
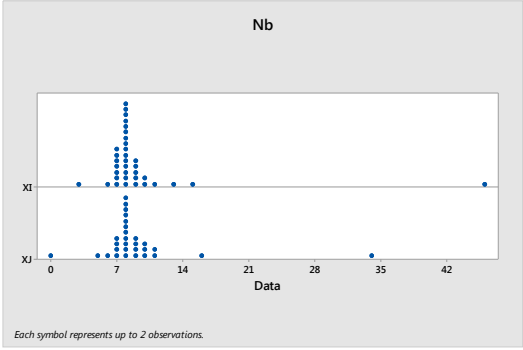
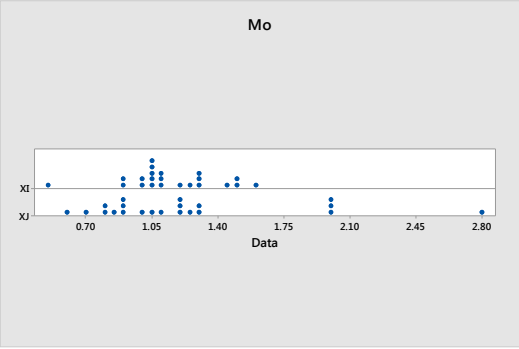
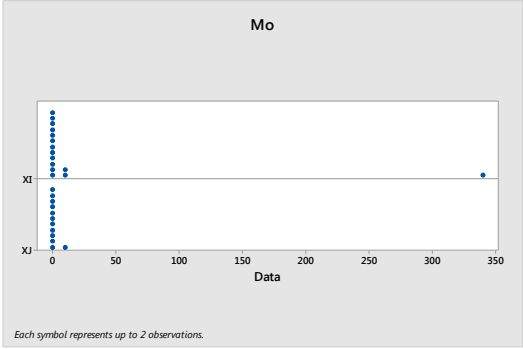
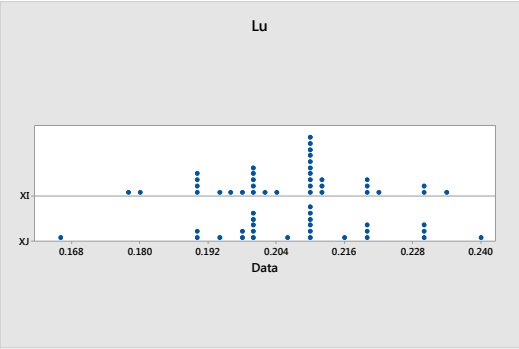
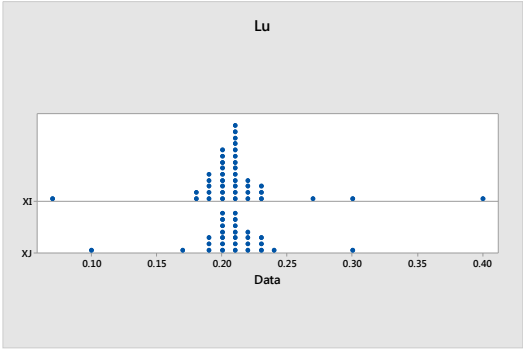


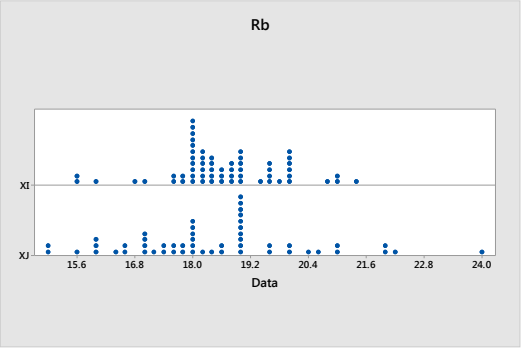
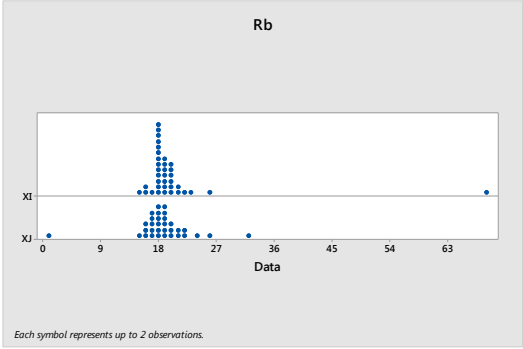
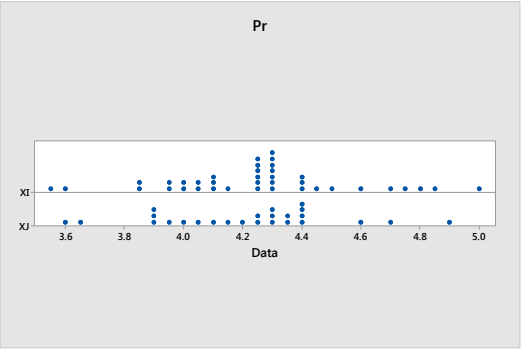
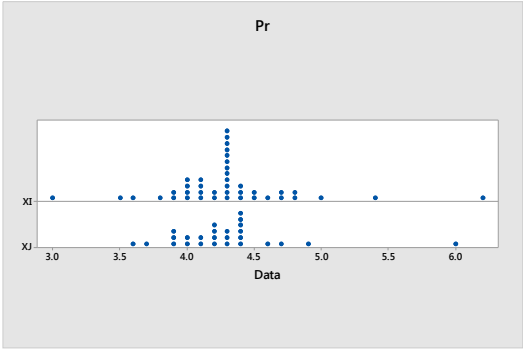
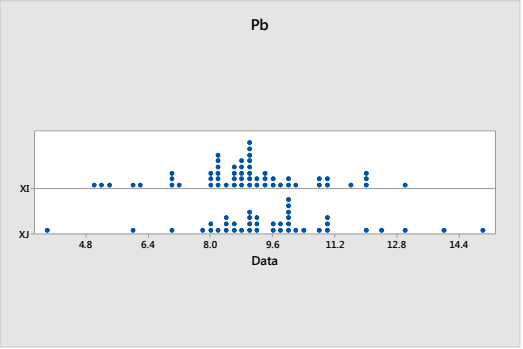
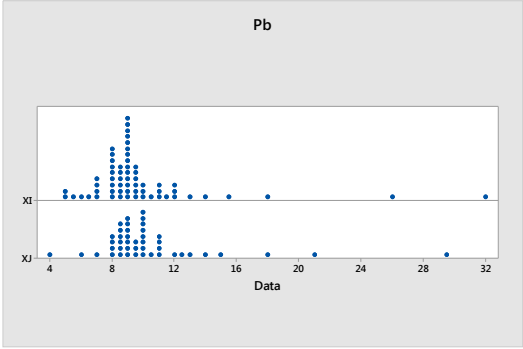
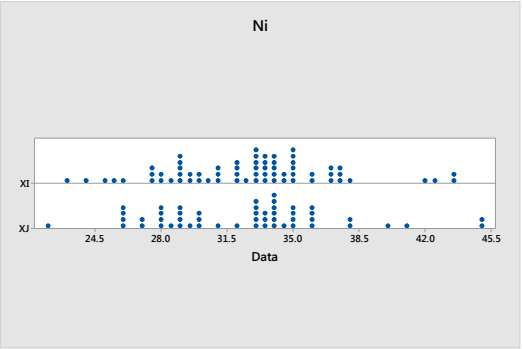
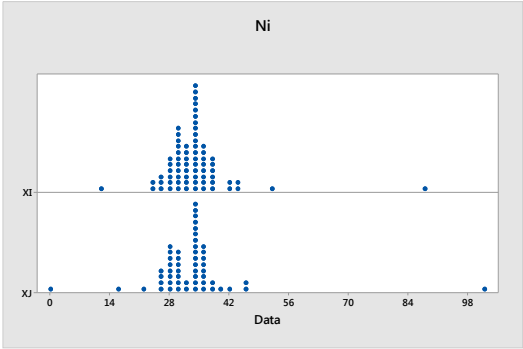












Each symbol represents up to 2 observations.

