**Interpretation of Correlation Plots**

We pitted our regions of interest (protein-bindings and histone marks; ChIP-Seq data) against the band of long-range interactions in GREG. *regioneR* 1 was employed to test this overlap, and whether it was statistically significant. We considered 100 permutations and concluded a consistent p-value of 0.0099, except for the following cases.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Index | Cell | Mark | P-Value | Z-Score | Significant |
| 1. | A549 | H3K4me1 | 0.0297 | -2.505 | Yes |
| 2. | A549 | H3K9ac | 0.0891 | -1.394 | No |
| 3. | IMR90 | H3K4me3 | 0.0198 | -2.348 | Yes |

[[1]](#footnote-1) Premise

**References**

1. Gel, B. *et al.* RegioneR: An R/Bioconductor package for the association analysis of genomic regions based on permutation tests. *Bioinformatics* **32**, 289–291 (2016).

1. The threshold for statistical significance is deemed 0.05. Also, a negative z-score indicates a value that is below the mean for the group of values. [↑](#footnote-ref-1)