

The figure displays 25 box plots arranged in a 5x5 grid, comparing the expression values of various DNA repair genes between two groups: 0.Low\_expression (blue) and 1.High\_expression (orange). Each plot includes a p-value from a Wilcoxon test, indicating significant differences for all genes.

**Row 1:**

- Repair1\_DNA\_glycosylases:** Wilcoxon,  $p < 2.2e-16$
- Repair2\_Other\_BER\_and\_strand\_break\_joining\_factors:** Wilcoxon,  $p < 2.2e-16$
- Repair3\_PARP\_enzymes:** Wilcoxon,  $p < 2.2e-16$
- Repair4\_Direct\_reversal\_of\_damage:** Wilcoxon,  $p < 2.2e-16$
- Repair5\_Repair\_of\_DNA\_topoisomerase\_crosslinks:** Wilcoxon,  $p < 2.2e-16$

**Row 2:**

- Repair6\_Mismatch\_excision\_repair:** Wilcoxon,  $p < 2.2e-16$
- Repair7\_xeroderma\_pigmentosum:** Wilcoxon,  $p < 2.2e-16$
- Repair8\_TFIIH:** Wilcoxon,  $p < 2.2e-16$
- Repair9\_NER\_related:** Wilcoxon,  $p = 0.0018$
- Repair10\_Homologous\_recombination:** Wilcoxon,  $p < 2.2e-16$

**Row 3:**

- Repair11\_Fanconi\_anemia:** Wilcoxon,  $p < 2.2e-16$
- Repair12\_Non\_homologous\_end\_joining:** Wilcoxon,  $p < 2.2e-16$
- Repair13\_Modulation\_of\_nucleotide\_pools:** Wilcoxon,  $p < 2.2e-16$
- Repair14\_DNA\_polymerases:** Wilcoxon,  $p < 2.2e-16$
- Repair15\_Editing\_and\_processing\_nucleases:** Wilcoxon,  $p < 2.2e-16$

**Row 4:**

- Repair16\_Ubiquitination\_and\_modification:** Wilcoxon,  $p < 2.2e-16$
- Repair17\_Chromatin\_Structure:** Wilcoxon,  $p < 2.2e-16$
- Repair18\_Genes\_defective\_in\_diseases\_associated\_with:** Wilcoxon,  $p < 2.2e-16$
- Repair19\_Other\_identified\_genes\_with\_known\_or\_suspe:** Wilcoxon,  $p < 2.2e-16$
- Repair20\_Other\_conserved\_DNA\_damage\_response\_ge:** Wilcoxon,  $p < 2.2e-16$

**Row 5:**

- Repair21\_AllGenes:** Wilcoxon,  $p < 2.2e-16$