

The figure displays 21 box plots arranged in a grid, showing the expression values of various genes across two groups: 0.Low\_expression (blue boxes) and 1.High\_expression (orange boxes). Each plot includes a Wilcoxon test result and a p-value, indicating a significant difference in expression between the two groups for all genes shown.

**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,  $p < 2.2e-16$

**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,  $p < 2.2e-16$

**Repair10\_Homologous\_recombination**: Wilcoxon,  $p < 2.2e-16$

**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,  $p < 2.2e-16$

**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,  $p < 2.2e-16$

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