

The figure displays 25 box plots arranged in a 5x5 grid, comparing the expression levels of various DNA repair genes between two groups: 'High_expression' (blue boxes) and 'Low_expression' (orange boxes). The y-axis for all plots is 'expression value'. Each plot includes a p-value indicating the statistical significance of the difference between the two groups.

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, $p = 0.061$
- 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, $p < 2.2e-16$
- 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, $p < 2.2e-16$