

The figure displays 21 box plots arranged in a 5x5 grid (with the last row containing only one plot), representing different DNA repair pathways. Each plot compares gene expression values between two groups: 0.Low_expression (blue box) and 1.High_expression (orange box). The y-axis represents the expression value, and the x-axis represents the group. Each plot includes a Wilcoxon test p-value and a significance bracket indicating the difference between the groups.

Repair Pathway	Wilcoxon p-value
Repair1_DNA_glycosylases	$p < 2.22 \times 10^{-16}$
Repair2_Other_BER_and_strand_break_joining_factors	$p < 2.22 \times 10^{-16}$
Repair3_PARP_enzymes	$p < 2.22 \times 10^{-16}$
Repair4_Direct_reversal_of_damage	$p = 0.45$
Repair5_Repair_of_DNA_topoisomerase_crosslinks	$p < 2.22 \times 10^{-16}$
Repair6_Mismatch_excision_repair	$p < 2.22 \times 10^{-16}$
Repair7_xeroderma_pigmentosum	$p < 2.22 \times 10^{-16}$
Repair8_TFIIH	$p < 2.22 \times 10^{-16}$
Repair9_NER_related	$p < 2.22 \times 10^{-16}$
Repair10_Homologous_recombination	$p < 2.22 \times 10^{-16}$
Repair11_Fanconi_anemia	$p < 2.22 \times 10^{-16}$
Repair12_Non_homologous_end_joining	$p < 2.22 \times 10^{-16}$
Repair13_Modulation_of_nucleotide_pools	$p < 2.22 \times 10^{-16}$
Repair14_DNA_polymerases	$p < 2.22 \times 10^{-16}$
Repair15_Editing_and_processing_nucleases	$p < 2.22 \times 10^{-16}$
Repair16_Ubiquitination_and_modification	$p < 2.22 \times 10^{-16}$
Repair17_Chromatin_Structure	$p < 2.22 \times 10^{-16}$
Repair18_Genes_defective_in_diseases_associated_with	$p < 2.22 \times 10^{-16}$
Repair19_Other_identified_genes_with_known_or_suspe	$p < 2.22 \times 10^{-16}$
Repair20_Other_conserved_DNA_damage_response_ge	$p < 2.22 \times 10^{-16}$
Repair21_AllGenes	$p < 2.22 \times 10^{-16}$