

The figure displays 21 box plots arranged in a grid, showing the expression values of various DNA repair genes and pathways. Each plot compares two groups: '0.Low\_expression' (blue box) and '1.High\_expression' (orange box). The y-axis represents the 'expression value'. A horizontal line within each box indicates the median, and the box itself represents the interquartile range. Whiskers extend to the minimum and maximum values, with individual data points plotted as black dots. Each plot includes a p-value from a Wilcoxon test, indicating the statistical significance of the difference between the two groups.

Repair Pathway	Wilcoxon p-value
Repair1_DNA_glycosylases	$p < 2.22e-16$
Repair2_Other_BER_and_strand_break_joining_factors	$p < 2.22e-16$
Repair3_PARP_enzymes	$p < 2.22e-16$
Repair4_Direct_reversal_of_damage	$p = 8.6e-09$
Repair5_Repair_of_DNA_topoisomerase_crosslinks	$p < 2.22e-16$
Repair6_Mismatch_excision_repair	$p < 2.22e-16$
Repair7_xeroderma_pigmentosum	$p < 2.22e-16$
Repair8_TFIIH	$p < 2.22e-16$
Repair9_NER_related	$p < 2.22e-16$
Repair10_Homologous_recombination	$p < 2.22e-16$
Repair11_Fanconi_anemia	$p < 2.22e-16$
Repair12_Non_homologous_end_joining	$p < 2.22e-16$
Repair13_Modulation_of_nucleotide_pools	$p < 2.22e-16$
Repair14_DNA_polymerases	$p < 2.22e-16$
Repair15_Editing_and_processing_nucleases	$p < 2.22e-16$
Repair16_Ubiquitination_and_modification	$p < 2.22e-16$
Repair17_Chromatin_Structure	$p < 2.22e-16$
Repair18_Genes_defective_in_diseases_associated_with	$p < 2.22e-16$
Repair19_Other_identified_genes_with_known_or_suspe	$p < 2.22e-16$
Repair20_Other_conserved_DNA_damage_response_ge	$p < 2.22e-16$
Repair21_AllGenes	$p < 2.22e-16$