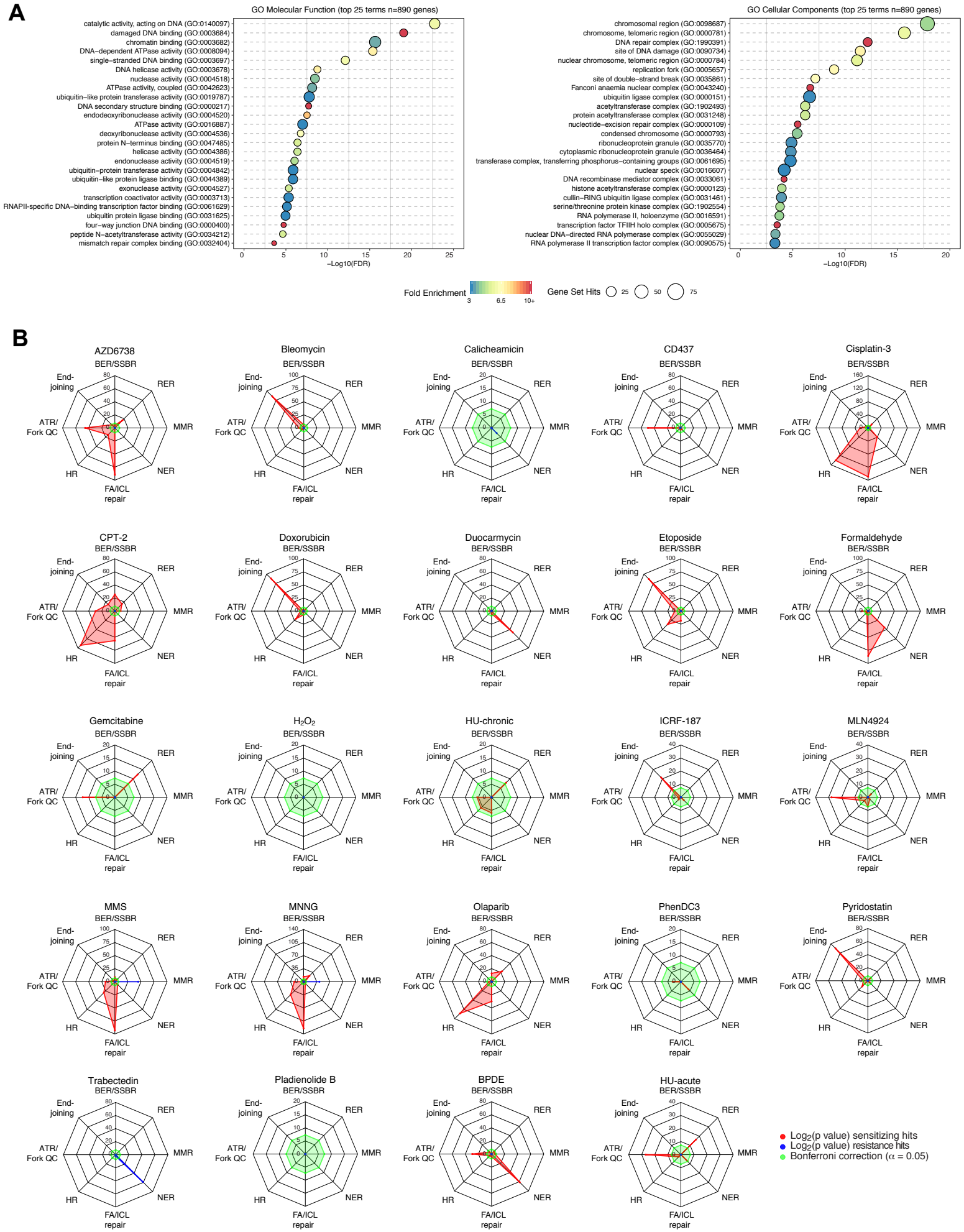
A
GO Molecular Function (top 25 terms n=890 genes)
catalytic activity, acting on DNA (GO:0140097)
damaged DNA binding (GO:0003684)
chromatin binding (GO:0003682)
DNA−dependent ATPase activity (GO:0008094)
single−stranded DNA binding (GO:0003697)
DNA helicase activity (GO:0003678)
nuclease activity (GO:0004518)
ATPase activity, coupled (GO:0042623)
ubiquitin−like protein transferase activity (GO:0019787)
DNA secondary structure binding (GO:0000217)
endodeoxyribonuclease activity (GO:0004520)
ATPase activity (GO:0016887)
deoxyribonuclease activity (GO:0004536)
protein N−terminus binding (GO:0047485)
helicase activity (GO:0004386)
endonuclease activity (GO:0004519)
ubiquitin−protein transferase activity (GO:0004842)
ubiquitin−like protein ligase binding (GO:0044389)
exonuclease activity (GO:0004527)
transcription coactivator activity (GO:0003713)
RNAPII-specific DNA−binding transcription factor binding (GO:0061629)
ubiquitin protein ligase binding (GO:0031625)
four−way junction DNA binding (GO:0000400)
peptide N−acetyltransferase activity (GO:0034212)
mismatch repair complex binding (GO:0032404)
0 5 10 15 20 25
−Log10(FDR)
GO Cellular Components (top 25 terms n=890 genes)
chromosomal region (GO:0098687)
chromosome, telomeric region (GO:0000781)
DNA repair complex (GO:1990391)
site of DNA damage (GO:0090734)
nuclear chromosome, telomeric region (GO:0000784)
replication fork (GO:0005657)
site of double−strand break (GO:0035861)
Fanconi anaemia nuclear complex (GO:0043240)
ubiquitin ligase complex (GO:0000151)
acetyltransferase complex (GO:1902493)
protein acetyltransferase complex (GO:0031248)
nucleotide−excision repair complex (GO:0000109)
condensed chromosome (GO:0000793)
ribonucleoprotein granule (GO:0035770)
cytoplasmic ribonucleoprotein granule (GO:0036464)
transferase complex, transferring phosphorus−containing groups (GO:0061695)
nuclear speck (GO:0016607)
DNA recombinase mediator complex (GO:0033061)
histone acetyltransferase complex (GO:0000123)
cullin−RING ubiquitin ligase complex (GO:0031461)
serine/threonine protein kinase complex (GO:1902554)
RNA polymerase II, holoenzyme (GO:0016591)
transcription factor TFIIH holo complex (GO:0005675)
nuclear DNA−directed RNA polymerase complex (GO:0055029)
RNA polymerase II transcription factor complex (GO:0090575)
0 5 10 15 20
−Log10(FDR)
Fold Enrichment
3 6.5 10+
Gene Set Hits
25 50 75
B
AZD6738
Bleomycin
Calicheamicin
CD437
Cisplatin-3
CPT-2
Doxorubicin
Duocarmycin
Etoposide
Formaldehyde
Gemcitabine
H2O2
HU-chronic
ICRF-187
MLN4924
MMS
MNNG
Olaparib
PhenDC3
Pyridostatin
Trabectedin
Pladienolide B
BPDE
HU-acute
BER/SSBR
RER
MMR
NER
FA/ICL repair
HR
ATR/ Fork QC
End-joining
Log2(p value) sensitizing hits
Log2(p value) resistance hits
Bonferroni correction (α = 0.05)

Figure S1