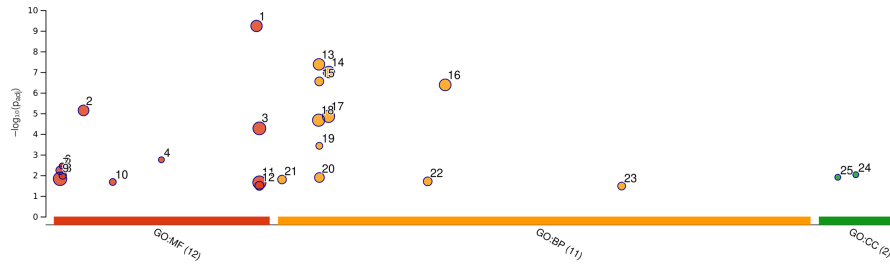


**a**

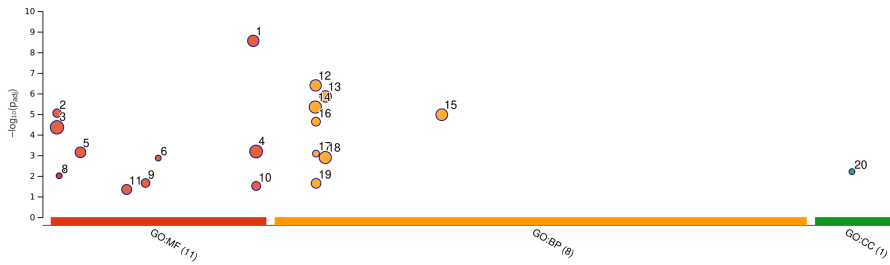


ID	Source	Term ID	Term Name	Padj (query_1)
1	GO:MF	GO:0140097	catalytic activity, acting on DNA	5.827×10 <sup>-10</sup>
2	GO:MF	GO:0008094	ATP-dependent activity, acting on DNA	7.179×10 <sup>-9</sup>
3	GO:MF	GO:0140640	catalytic activity, acting on a nucleic acid	5.338×10 <sup>-9</sup>
4	GO:MF	GO:0042162	telomeric DNA binding	1.768×10 <sup>-8</sup>
5	GO:MF	GO:0003909	DNA ligase activity	3.542×10 <sup>-8</sup>
6	GO:MF	GO:0003910	DNA ligase (ATP) activity	3.542×10 <sup>-8</sup>
7	GO:MF	GO:0003684	damaged DNA binding	5.753×10 <sup>-8</sup>
8	GO:MF	GO:0003950	NAD+ ADP-ribosyltransferase activity	1.023×10 <sup>-7</sup>
9	GO:MF	GO:0003677	DNA binding	1.487×10 <sup>-7</sup>
10	GO:MF	GO:0016886	ligase activity, forming phosphoric ester bonds	2.113×10 <sup>-7</sup>
11	GO:MF	GO:0140657	ATP-dependent activity	2.237×10 <sup>-7</sup>
12	GO:MF	GO:0140658	ATP-dependent chromatin remodeler activity	3.221×10 <sup>-7</sup>
13	GO:BP	GO:0006281	DNA repair	4.234×10 <sup>-8</sup>
14	GO:BP	GO:0006974	DNA damage response	9.943×10 <sup>-8</sup>
15	GO:BP	GO:0006302	double-strand break repair	2.828×10 <sup>-7</sup>
16	GO:BP	GO:0033554	cellular response to stress	4.177×10 <sup>-7</sup>
17	GO:BP	GO:0006950	response to stress	1.399×10 <sup>-6</sup>
18	GO:BP	GO:0006259	DNA metabolic process	2.138×10 <sup>-6</sup>
19	GO:BP	GO:0006303	double-strand break repair via nonhomologous ...	3.738×10 <sup>-6</sup>
20	GO:BP	GO:0006310	DNA recombination	1.280×10 <sup>-5</sup>
21	GO:BP	GO:0000723	telomere maintenance	1.604×10 <sup>-5</sup>
22	GO:BP	GO:0032200	telomere organization	1.967×10 <sup>-5</sup>
23	GO:BP	GO:0071897	DNA biosynthetic process	3.324×10 <sup>-5</sup>
24	GO:CC	GO:0043564	Ku70:Ku80 complex	9.374×10 <sup>-3</sup>
25	GO:CC	GO:0030870	Mre11 complex	1.242×10 <sup>-3</sup>

version e109\_eg56\_p17\_1d3191d  
 date 6/27/2023, 9:55:36 AM  
 organism hegca002082055v1

g:Profiler

**b**

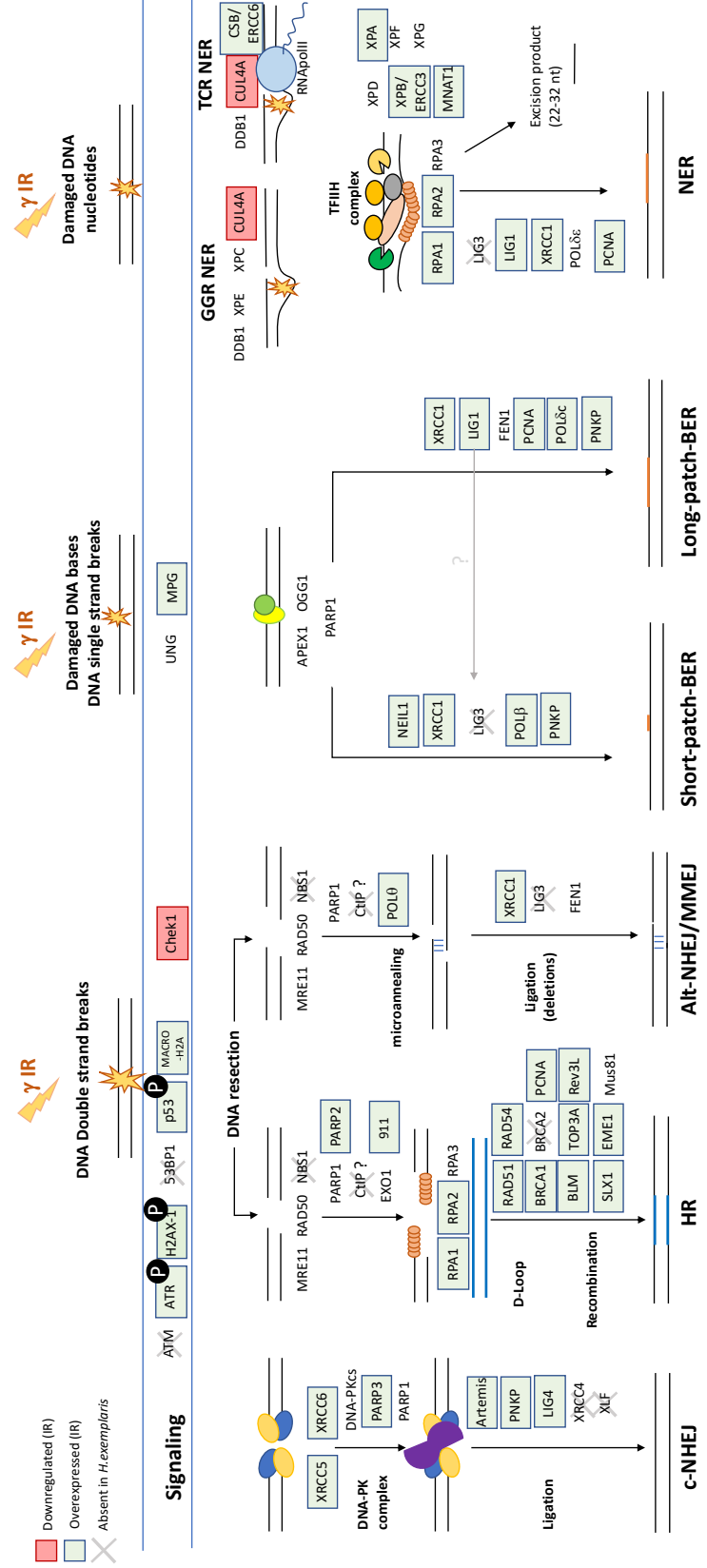


ID	Source	Term ID	Term Name	Padj (query_1)
1	GO:MF	GO:0140097	catalytic activity, acting on DNA	2.786×10 <sup>-9</sup>
2	GO:MF	GO:0003684	damaged DNA binding	8.895×10 <sup>-9</sup>
3	GO:MF	GO:0003677	DNA binding	4.371×10 <sup>-8</sup>
4	GO:MF	GO:0140640	catalytic activity, acting on a nucleic acid	6.492×10 <sup>-8</sup>
5	GO:MF	GO:0008094	ATP-dependent activity, acting on DNA	7.142×10 <sup>-8</sup>
6	GO:MF	GO:0042162	telomeric DNA binding	1.360×10 <sup>-7</sup>
7	GO:MF	GO:0003910	DNA ligase (ATP) activity	9.840×10 <sup>-8</sup>
8	GO:MF	GO:0003909	DNA ligase activity	9.840×10 <sup>-8</sup>
9	GO:MF	GO:0034061	DNA polymerase activity	2.203×10 <sup>-7</sup>
10	GO:MF	GO:0140658	ATP-dependent chromatin remodeler activity	3.083×10 <sup>-7</sup>
11	GO:MF	GO:0030527	structural constituent of chromatin	4.549×10 <sup>-7</sup>
12	GO:BP	GO:0006281	DNA repair	4.044×10 <sup>-7</sup>
13	GO:BP	GO:0006974	DNA damage response	1.389×10 <sup>-6</sup>
14	GO:BP	GO:0006259	DNA metabolic process	4.551×10 <sup>-6</sup>
15	GO:BP	GO:0033554	cellular response to stress	1.069×10 <sup>-5</sup>
16	GO:BP	GO:0006302	double-strand break repair	2.318×10 <sup>-5</sup>
17	GO:BP	GO:0006303	double-strand break repair via nonhomologous ...	8.244×10 <sup>-5</sup>
18	GO:BP	GO:0006950	response to stress	1.281×10 <sup>-3</sup>
19	GO:BP	GO:0006310	DNA recombination	2.291×10 <sup>-2</sup>
20	GO:CC	GO:0043564	Ku70:Ku80 complex	6.174×10 <sup>-3</sup>

version e109\_eg56\_p17\_1d3191d  
 date 6/27/2023, 10:03:30 AM  
 organism hegca002082055v1

g:Profiler

C



d

term_name term_id Species	Base excision repair KEGG:03410			Nucleotide excision repair KEGG:03420			Mismatch repair KEGG:03430			Homologous recombination KEGG:03440			Non-homologous end-joining KEGG:03450			Fanconi anemia pathway KEGG:03460		
	H.exemplaris	A.antarcticus	P.fairbanksi	H.exemplaris	A.antarcticus	P.fairbanksi	H.exemplaris	A.antarcticus	P.fairbanksi	H.exemplaris	A.antarcticus	P.fairbanksi	H.exemplaris	A.antarcticus	P.fairbanksi	H.exemplaris	A.antarcticus	P.fairbanksi
APEX1	APEX1																	
APEX2	APEX2																	
ATR																ATR		ATR
BLM										BLM		BLM				BLM		BLM
BRIP1										BRIP1		BRIP1				BRIP1		BRIP1
CCNH				CCNH														
CDK7				CDK7	CDK7	CDK7												
CUL4A				CUL4A	CUL4A	CUL4A												
DCLRE1C													DCLRE1C					
DDB1				DDB1		DDB1												
ERCC1				ERCC1														ERCC1
ERCC2					ERCC2													
ERCC3				ERCC3	ERCC3	ERCC3												
ERCC4				ERCC4		ERCC4												ERCC4
ERCC5					ERCC5													
ERCC6				ERCC6	ERCC6	ERCC6												
FAN1																		FAN1
FANCM																		FANCM
FEN1		FEN1												FEN1				FANCM
FTF2H1				FTF2H1														
FTF2H2				FTF2H2		FTF2H2												
FTF2H3					FTF2H3													
FTF2H4				FTF2H4		FTF2H4												
FTF2H5				FTF2H5														
HES1																		HES1
HMGB1	HMGB1	HMGB1	HMGB1															
LIG1	LIG1	LIG1	LIG1	LIG1	LIG1	LIG1	LIG1	LIG1	LIG1				LIG4	LIG4	LIG4			
LIG4																		
MLH1																		MLH1
MLH3																		
MNAT1				MNAT1		MNAT1												
MPG	MPG																	
MRE11A										MRE11A	MRE11A		MRE11A	MRE11A				
MSH2								MSH2	MSH2									
MUS81										MUS81	MUS81							MUS81
NEIL1	NEIL1	NEIL1	NEIL1															MUS81
OGG1	OGG1																	
PARP1																		
PARP2	PARP2	PARP2	PARP2															
PARP3	PARP3	PARP3	PARP3															
PARP4	PARP4																	
PCNA	PCNA			PCNA	PCNA		PCNA	PCNA										
POLB																		
POLD1	POLD1	POLD1	POLD1	POLD1	POLD1	POLD1	POLD1	POLD1	POLD1	POLD1	POLD1	POLD1	POLD1	POLD1	POLD1			
POLD2	POLD2	POLD2	POLD2	POLD2	POLD2	POLD2	POLD2	POLD2	POLD2	POLD2	POLD2	POLD2	POLD2	POLD2	POLD2			
POLD3																		
POLD4	POLD4	POLD4		POLD4	POLD4		POLD4	POLD4		POLD4	POLD4							
POLE																		
POLE2																		
POLE4	POLE4			POLE4														
POLH																		
POLK																		POLK
POLL	POLL	POLL	POLL										POLL	POLL	POLL			POLL
PRKDC																		
RAD23A																		
RAD23B				RAD23B		RAD23B												
RAD50																		
RAD51										RAD51	RAD51	RAD51						RAD51
RAD54B										RAD54B	RAD54B	RAD54B						
RAD54L										RAD54L	RAD54L	RAD54L						
REV1																		REV1
REV3L																		REV3L
RFC1				RFC1	RFC1	RFC1	RFC1	RFC1	RFC1									
RFC4																		
RFC5				RFC5		RFC5	RFC5	RFC5	RFC5									
RM11																		RM11
RPA1	RPA1			RPA1			RPA1	RPA1	RPA1	RPA1								RM11
RPA2	RPA2			RPA2		RPA2	RPA2	RPA2	RPA2	RPA2								RPA2
RPA3																		RPA3
SHFM1																		
SLX4																		SLX4
SSBP1																		
TOP3A																		
TOP3B																		
TOPBP1																		
UNG																		
XPA				XPA	XPA	XPA												
XPC				XPC		XPC												
XRCC1	XRCC1	XRCC1	XRCC1															
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XRCC6													XRCC6	XRCC6	XRCC6			

Differentially expressed genes