PCNA Role in Cell Cycle and Imaging

BRAD

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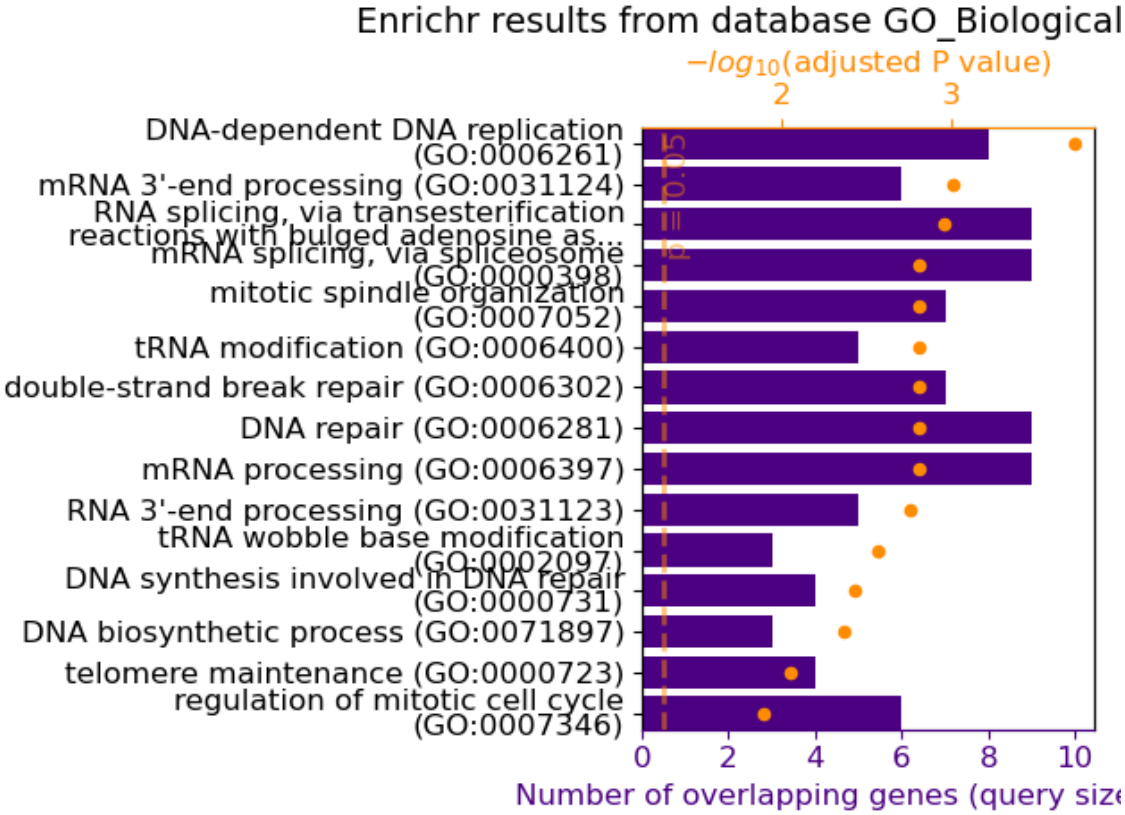
Summary of Process

GO_Biological_Process_2021

Summary of Steps

Based on the provided text database, the role of PCNA (Proliferating Cell Nuclear Antigen) in the cell cycle and cell cycle imaging is highlighted in the context of marking the boundaries of the S phase. PCNA is mentioned as a processivity factor for DNA polymerase epsilon and delta, indicating its involvement in DNA replication during the S phase. Additionally, PCNA is used as a marker to annotate the beginning and end of the S phase in living cells, suggesting its importance in accurately delineating cell cycle phase transitions. The text also mentions that the PCNA reporter precisely marks the boundaries of the S phase, emphasizing its role in cell cycle imaging.

In summary, PCNA plays a crucial role in DNA replication during the S phase of the cell cycle and is utilized as a marker for accurately delineating cell cycle phase transitions in living cells during cell cycle imaging.**Summary:** The code was successfully executed to find the first order interactions of the gene PCNA in the Hardwired Genome. The output indicates that the script is currently in the process of finding these interactions. The next step would be to wait for the script to complete its execution and generate the output file 'S¡Step `number>-HWG-1stOrder-PCNA.csv`'.The 'Genes' column from the output file generated in step 2 was loaded and searched in Enrichr. The gene list was queried against the GO_Biological_Process_2021 database, resulting in a table with 649 entries.


Enrichr results from database GO_Biological
−log10(adjusted P value)
2
3
DNA-dependent DNA replication (GO:0006261)
mRNA 3'-end processing (GO:0031124)
RNA splicing, via transesterification reactions with bulged adenosine as...
mRNA splicing, via spliceosome (GO:0000398)
mitotic spindle organization (GO:0007052)
tRNA modification (GO:0006400)
double-strand break repair (GO:0006302)
DNA repair (GO:0006281)
mRNA processing (GO:0006397)
RNA 3'-end processing (GO:0031123)
tRNA wobble base modification (GO:0002097)
DNA synthesis involved in DNA repair (GO:0000731)
DNA biosynthetic process (GO:0071897)
telomere maintenance (GO:0000723)
regulation of mitotic cell cycle (GO:0007346)
p = 0.05
0
2
4
6
8
10
Number of overlapping genes (query size

rank	path_name	p_val	z_score	combined_score	overlapping_genes
1	DNA-dependent DNA replication (GO:0...	2.72468e-07	14.2142	214.858	['POLD3', 'MGME1', '
2	mRNA 3'-end processing (GO:0031124)...	2.7791e-06	17.3363	221.79	['DDX39A', 'CPSF3', '
3	RNA splicing, via transesterificati...	4.71279e-06	8.03388	98.5373	['DDX39A', 'NONO', '
4	mRNA splicing, via spliceosome (GO:...	9.55686e-06	7.32801	84.699	['DDX39A', 'NONO', '
5	mitotic spindle organization (GO:00...	1.39542e-05	9.91039	110.796	['INTS13', 'INCENP',
6	tRNA modification (GO:0006400)...	1.83979e-05	17.4035	189.755	['MOCS3', 'WDR4', 'F
7	double-strand break repair (GO:0006...	1.85146e-05	9.46517	103.142	['POLA1', 'XRCC6', 'V
8	DNA repair (GO:0006281)...	1.86389e-05	6.71124	73.0872	['POLD3', 'MGME1', '
9	mRNA processing (GO:0006397)...	1.96497e-05	6.66444	72.2255	['DDX39A', 'NONO', '
10	RNA 3'-end processing (GO:0031123)...	2.46401e-05	16.3125	173.094	['DDX39A', 'CPSF3', '
11	tRNA wobble base modification (GO:0...	4.24153e-05	55.9203	563.006	['MOCS3', 'ELP3', 'AI
12	DNA synthesis involved in DNA repai...	6.25094e-05	21.219	205.404	['POLD3', 'POLA1', 'V
13	DNA biosynthetic process (GO:007189...	7.83783e-05	43.9308	415.32	['POLD3', 'POLA1', 'V
14	telomere maintenance (GO:0000723)...	0.000177012	15.9038	137.398	['POLD3', 'WRN', 'XR
15	regulation of mitotic cell cycle (G...	0.000272588	7.32113	60.0885	['INTS13', 'BORA', 'P
16	microtubule cytoskeleton organizati...	0.000459779	8.46256	65.0328	['INTS13', 'INCENP',
17	recombinational repair (GO:0000725)...	0.000663247	11.0139	80.6036	['WRN', 'POLN', 'REV
18	isoprenoid metabolic process (GO:00...	0.000679555	67.6667	493.566	['PDSS2', 'PDSS1']
19	isoprenoid biosynthetic process (GO...	0.000870867	57.9971	408.649	['PDSS2', 'PDSS1']
20	translesion synthesis (GO:0019985)...	0.00120859	15.7502	105.815	['POLD3', 'POLN', 'R