

Step 1

❖ Get the list of KEGG pathways regarding the dataset GSE6978

Tools: a R Bioconductor package called GAGE

Pathway number	Pathway name
1	"hsa00010 Glycolysis / Gluconeogenesis"
2	"hsa00020 Citrate cycle (TCA cycle)"
3	"hsa00030 Pentose phosphate pathway"
4	"hsa00040 Pentose and glucuronate interconversions"
...	...
177	"hsa04977 Vitamin digestion and absorption"

Step 2

❖ Evaluate the differential activation level of each pathway

Metrics: t Statistic and p-value

Step 3

❖ Rank the pathways

Pathway number	Absolute t-Statistic
109	3.855921051770997
98	3.633893585839424
107	3.4438627392035968
122	3.412159403042847
120	3.392530729363069
97	3.3339468341115266
146	3.328991073861387
92	3.3198215987266497
99	3.236418889836765
172	3.2160227759322635

Step 3

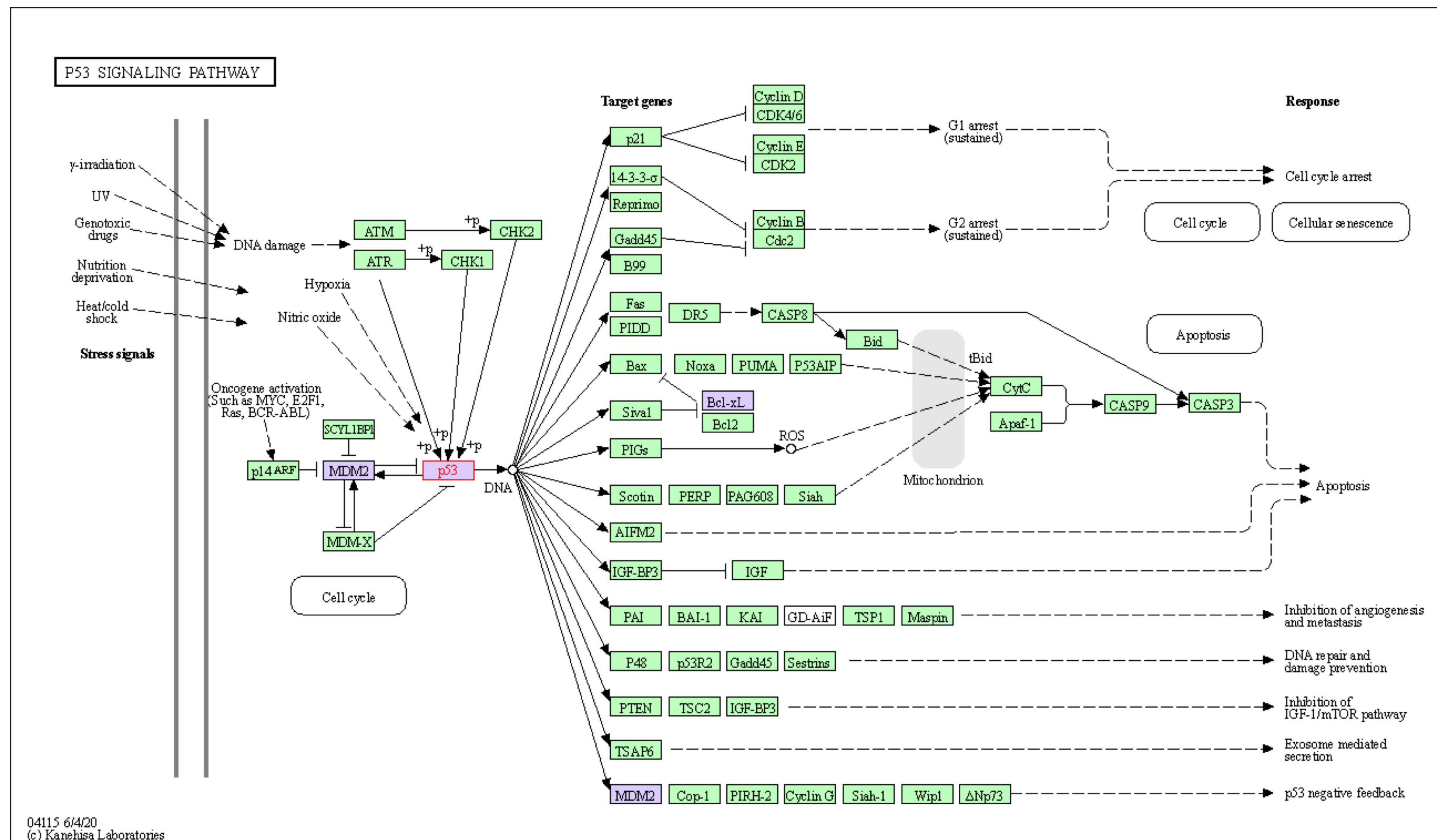
❖ Rank the pathways

Pathway number	Pathway name
109	"hsa04115 p53 signaling pathway"
98	"hsa03420 Nucleotide excision repair"
107	"hsa04110 Cell cycle"
122	"hsa04270 Vascular smooth muscle contraction"
120	"hsa04210 Apoptosis"
97	"hsa03410 Base excision repair"
146	"hsa04650 Natural killer cell mediated cytotoxicity"
92	"hsa03030 DNA replication"
99	"hsa03430 Mismatch repair"
172	"hsa04972 Pancreatic secretion"

Step 4

❖ Check the pathway diagram for top pathways

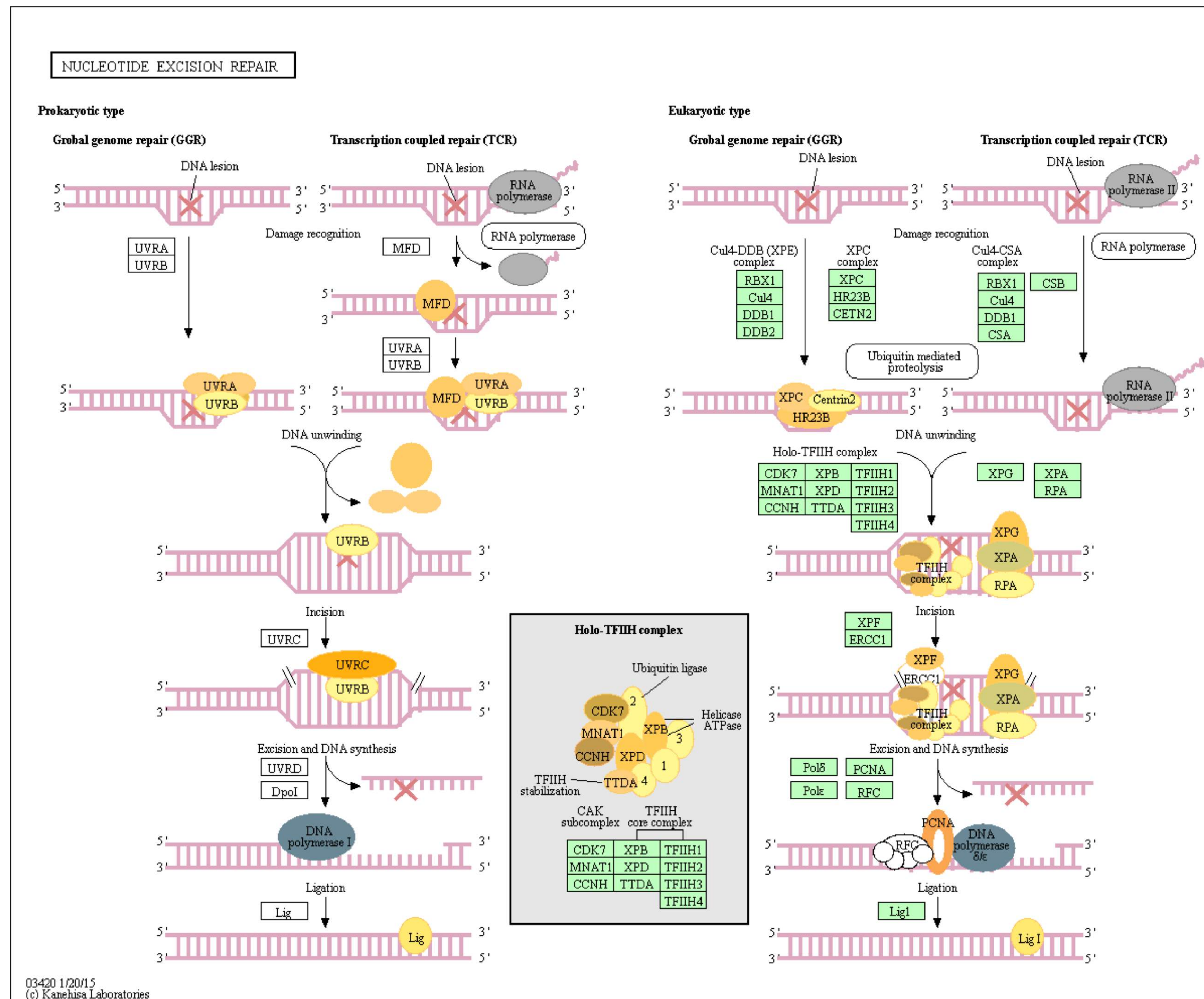
#109 pathway: "hsa04115 p53 signaling pathway"



Step 4

❖ Check the pathway diagram for top pathways

#98 pathway: "hsa03420 Nucleotide excision repair"



Step 4

❖ Check the pathway diagram for top pathways

#107 pathway: "hsa04110 Cell cycle"

