

Terme	Libellé	nombre de gènes	p.value ajustée
KEGG_pathway_2021	Cell cycle	20/124	0.0003
	One carbon pool by folate	7/20	0.0033
	Histidine metabolism	6/22	0.04086
GO_Molecular_Function_2021	non significatif	NA	NA
GO_Cellular_Component_2021	intracellular membrane-bounded organelle (GO:0043231)	310/5192	0.0001
	nucleus (GO:0005634)	266/4484	0.0011
	nuclear chromosome (GO:0000228)	14/83	0.0023
	trans-Golgi network transport vesicle (GO:0030140)	5/15	0.0270
	spindle microtubule (GO:0005876)	10/60	0.0270
	spindle (GO:0005819)	20/192	0.0338
	integral component of Golgi membrane (GO:0030173)	9/55	0.0387
GO_Biological_Process-2021	DNA metabolic process (GO:0006259)	35/277	1.0954E-07
	DNA replication (GO:0006260)	20/108	1.3547E-07
	double-strand break repair via break-induced replication (GO:0000727)	7/12	3.2359E-07
	mitotic spindle organization (GO:0007052)	24/157	3.4284E-07
	melanosome localization (GO:0032400)	8/21	2.764E-06
	DNA replication initiation (GO:0006270)	10/38	7.2578E-06
	DNA-dependent DNA replication (GO:0006261)	19/129	9.7521E-06
	melanosome transport (GO:0032402)	7/18	1.0131E-05
	pigment granule transport (GO:0051904)	7/18	1.0131E-05
	establishment of melanosome localization (GO:0032401)	7/19	1.5390E-05
	mitotic sister chromatid segregation (GO:0000070)	16/102	2.1758E-05
	tetrahydrofolate interconversion (GO:0035999)	5/9	2.4658E-05
	DNA repair (GO:0006281)	31/298	3.2187E-05
	mitotic DNA replication (GO:1902969)	5/10	4.7400E-05
	tetrahydrofolate metabolic process (GO:0046653)	5/11	8.3527E-05
	regulation of transferase activity (GO:0051338)	6/17	8.4973E-05
	DNA strand elongation (GO:0022616)	6/18	0.0001
	sister chromatid segregation (GO:0000819)	8/34	0.0001
	double-strand break repair via homologous recombination (GO:0000724)	14/97	0.0001
	water-soluble vitamin metabolic process (GO:0006767)	12/76	0.0002
	folic acid-containing compound metabolic process (GO:0006760)	6/20	0.0002