

GO ID	GO Name	Gene Counts	Gene Amount in	Enrichment Score	p-value
GO:0006355	regulation of transcription, DNA-dependent	311	1852	4.8773469	8.82E-124
GO:0006351	transcription, DNA-dependent	290	1756	4.7966466	3.97E-113
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	157	745	6.1207919	7.55E-76
GO:0006810	transport	213	1712	3.6136	8.40E-60
GO:0007275	multicellular organismal development	150	954	4.5667488	8.08E-55
GO:0000122	negative regulation of transcription from RNA polymerase II promoter	108	561	5.5914588	3.50E-48
GO:0045893	positive regulation of transcription, DNA-dependent	104	523	5.7755838	8.46E-48
GO:0006468	protein phosphorylation	106	611	5.0388206	6.97E-43
GO:0007395	nervous system development	75	307	7.0955673	2.99E-41
GO:0016310	phosphorylation	109	684	4.62844	1.74E-40
GO:0030154	cell differentiation	101	636	4.6124163	1.97E-37
GO:0006915	apoptotic process	91	540	4.8945399	6.90E-36
GO:0008285	negative regulation of cell proliferation	66	315	6.0855189	4.32E-32
GO:0007155	cell adhesion	82	500	4.7633017	1.45E-31
GO:0006357	regulation of transcription from RNA polymerase II promoter	55	241	6.6284179	6.55E-29
GO:0015031	protein transport	81	538	4.3728742	1.46E-28
GO:0045892	negative regulation of transcription, DNA-dependent	70	429	4.7391994	5.90E-27
GO:0008284	positive regulation of cell proliferation	65	382	4.9421308	3.67E-26
GO:0043066	negative regulation of apoptotic process	72	480	4.3566783	2.12E-25
GO:0016568	chromatin modification	52	251	6.0171919	2.84E-25

FDR	Gene Symbol	Rank
3.49E-120	Ikzf4 Zzz3 L	1
7.86E-110	Esr2 Thrap3	2
9.96E-73	Cask Nr2f1	3
8.31E-57	Rab11a Bic	4
6.40E-52	Nr6a1 Diap3	5
2.31E-45	Ciita Sox6 F	6
4.78E-45	Ikzf1 Nr4a2	7
3.45E-40	Glyctk Ttbk3	8
1.31E-38	Hoxa1 Amic	9
6.89E-38	Tesk1 Etnk1	10
7.10E-35	Myt1 Fzd5 S	11
2.28E-33	Ntn1 Traf1 E	12
1.32E-29	Rbpj Tob1 F	13
4.11E-29	Arvcf Lamc2	14
1.73E-26	Sp4 Trak2 F	15
3.62E-26	Sec63 Rab2	16
1.37E-24	Foxp1 Kdm	17
8.07E-24	Ntn1 Id4 Ac	18
4.42E-23	Ivns1abp Br	19
5.61E-23	Prkcb Suv3	20