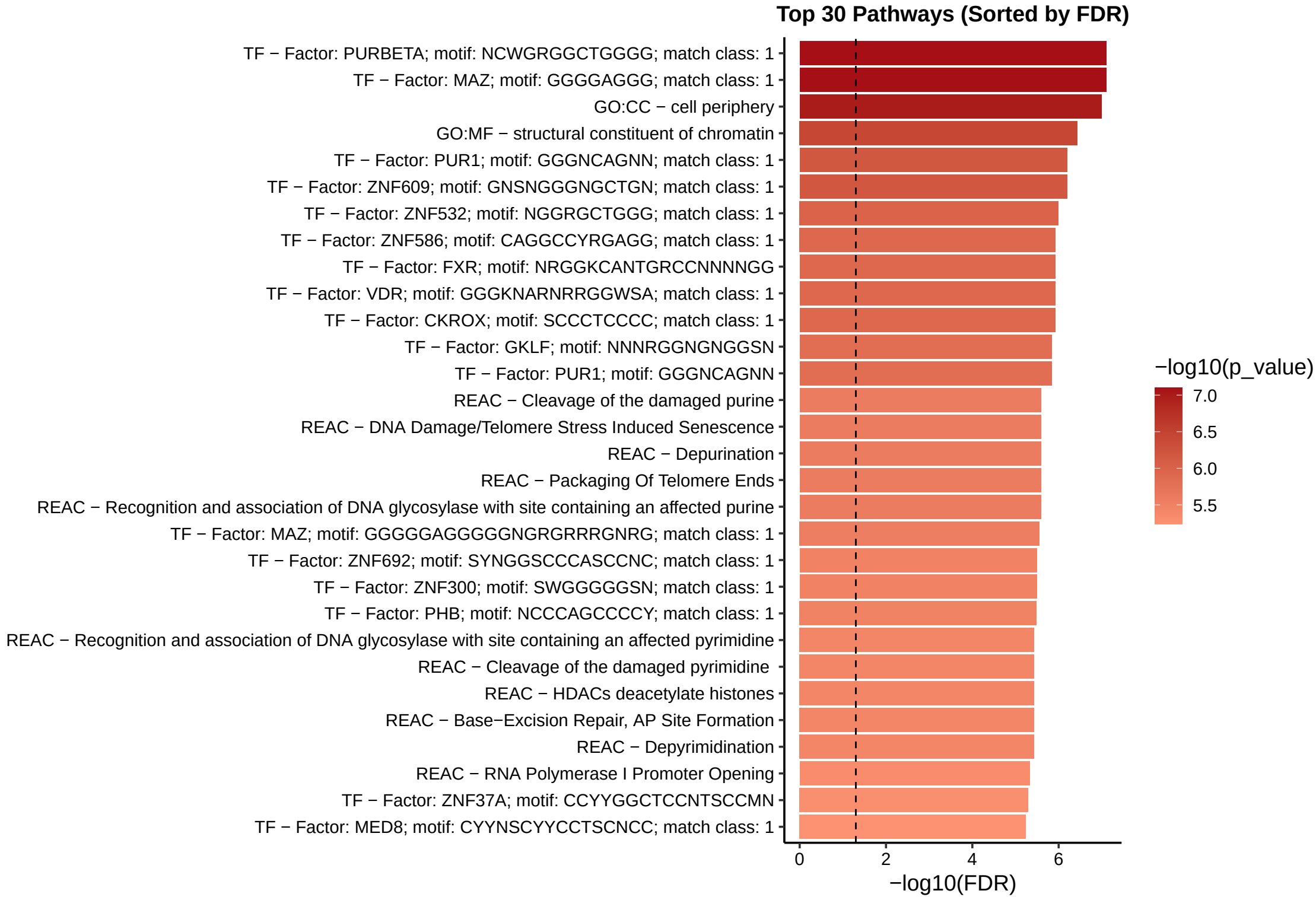
Top 30 Pathways (Sorted by FDR)
TF − Factor: PURBETA; motif: NCWGRGGCTGGGG; match class: 1
TF − Factor: MAZ; motif: GGGGAGGG; match class: 1
GO:CC − cell periphery
GO:MF − structural constituent of chromatin
TF − Factor: PUR1; motif: GGGNCAGNN; match class: 1
TF − Factor: ZNF609; motif: GNSNGGGNGCTGN; match class: 1
TF − Factor: ZNF532; motif: NGGRGCTGGG; match class: 1
TF − Factor: ZNF586; motif: CAGGCCYRGAGG; match class: 1
TF − Factor: FXR; motif: NRGGKCANTGRCCNNNNGG
TF − Factor: VDR; motif: GGGKNARNRRGGWSA; match class: 1
TF − Factor: CKROX; motif: SCCCTCCCC; match class: 1
TF − Factor: GKLF; motif: NNNRGGNGNGGSN
TF − Factor: PUR1; motif: GGGNCAGNN
REAC − Cleavage of the damaged purine
REAC − DNA Damage/Telomere Stress Induced Senescence
REAC − Depurination
REAC − Packaging Of Telomere Ends
REAC − Recognition and association of DNA glycosylase with site containing an affected purine
TF − Factor: MAZ; motif: GGGGGAGGGGGNGRGRRRGNRG; match class: 1
TF − Factor: ZNF692; motif: SYNGGSCCCASCCNC; match class: 1
TF − Factor: ZNF300; motif: SWGGGGGSN; match class: 1
TF − Factor: PHB; motif: NCCCAGCCCCY; match class: 1
REAC − Recognition and association of DNA glycosylase with site containing an affected pyrimidine
REAC − Cleavage of the damaged pyrimidine
REAC − HDACs deacetylate histones
REAC − Base−Excision Repair, AP Site Formation
REAC − Depyrimidination
REAC − RNA Polymerase I Promoter Opening
TF − Factor: ZNF37A; motif: CCYYGGCTCCNTSCCMN
TF − Factor: MED8; motif: CYYNSCYYCCTSCNCC; match class: 1
0
2
4
6
−log10(FDR)
−log10(p_value)
7.0
6.5
6.0
5.5