

Figure S1: Expression profile ($\log_2(\text{Fold-change})$) in high-ADG steers of the five differentially expressed (DE) genes common across all three breeds.

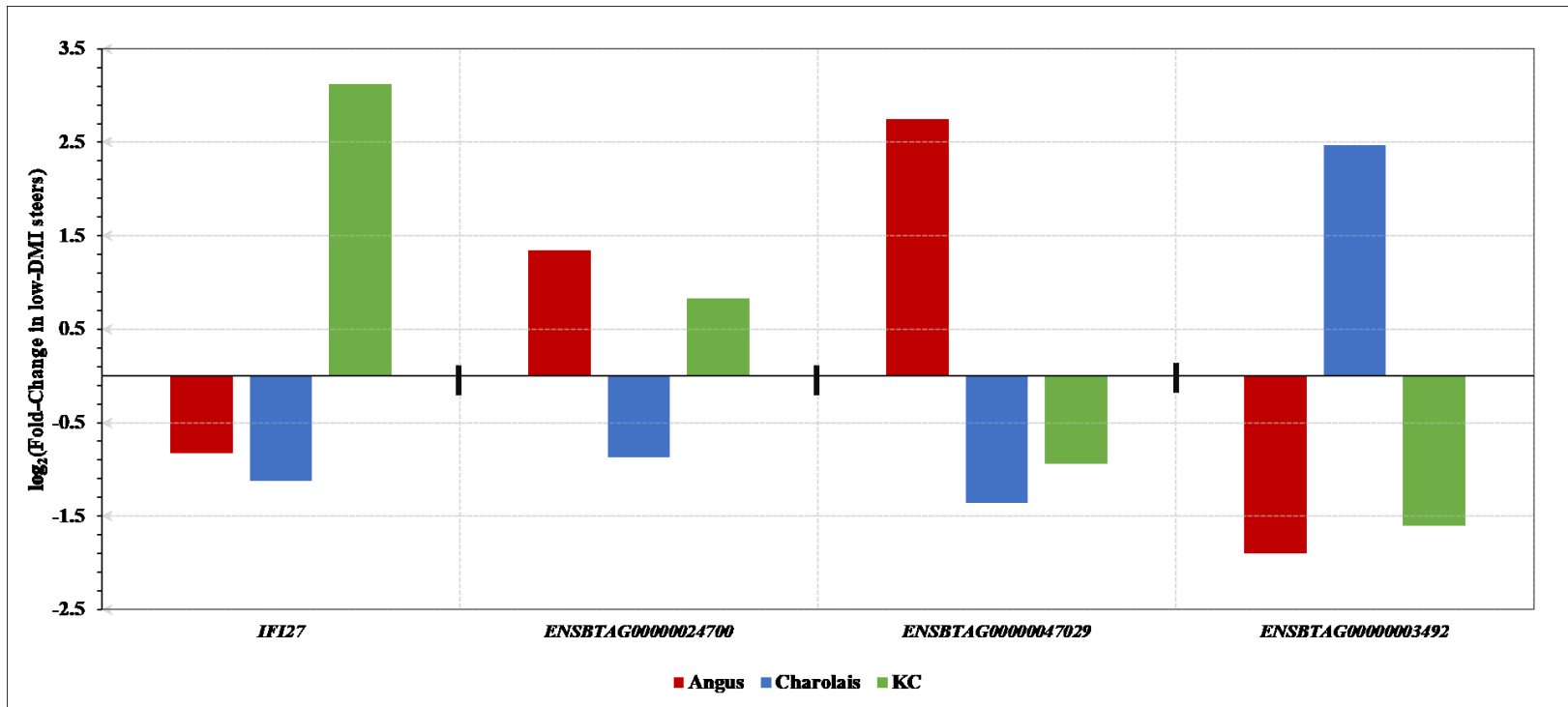


Figure S2: Expression profile ($\log_2(\text{Fold-change})$) in low-DMI steers of the four differentially expressed (DE) genes common across all three breeds.

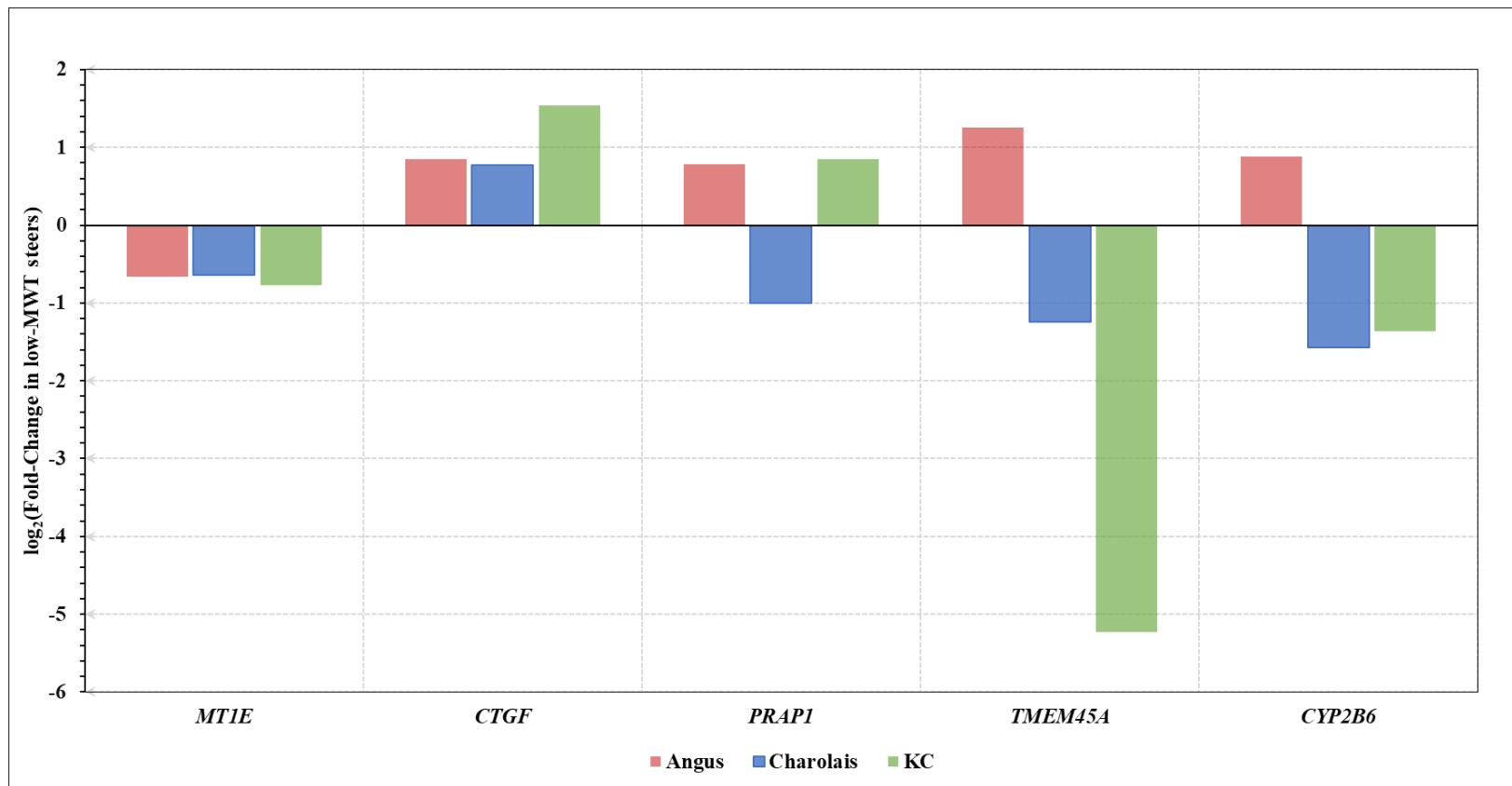


Figure S3: Expression profile ($\log_2(\text{Fold-change})$) in low-MWT steers of the four differentially expressed (DE) genes common across all three breeds.

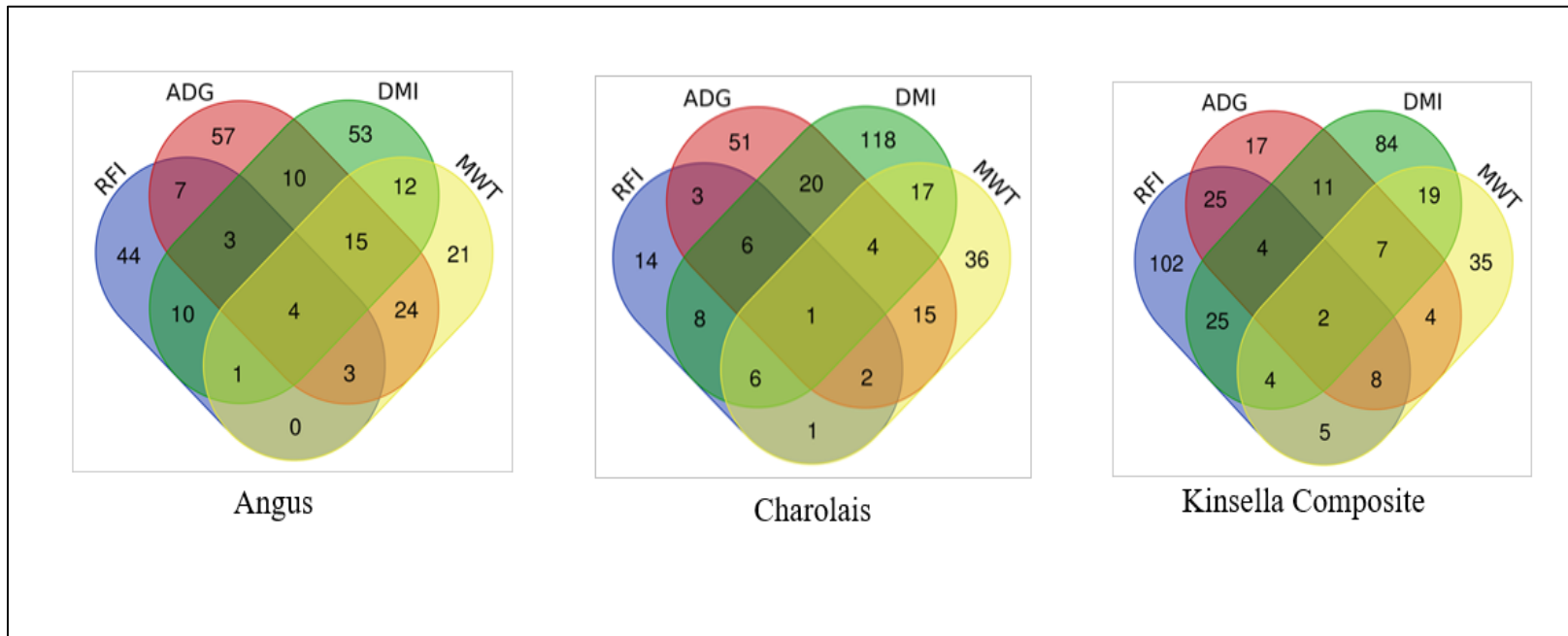


Figure S4: Venn diagram showing overlap between DE gene of ADG, DMI, MWT and RFI from (Mukiibi *et al.* 2018), within Angus, Charolais and Kinsella Composite populations.

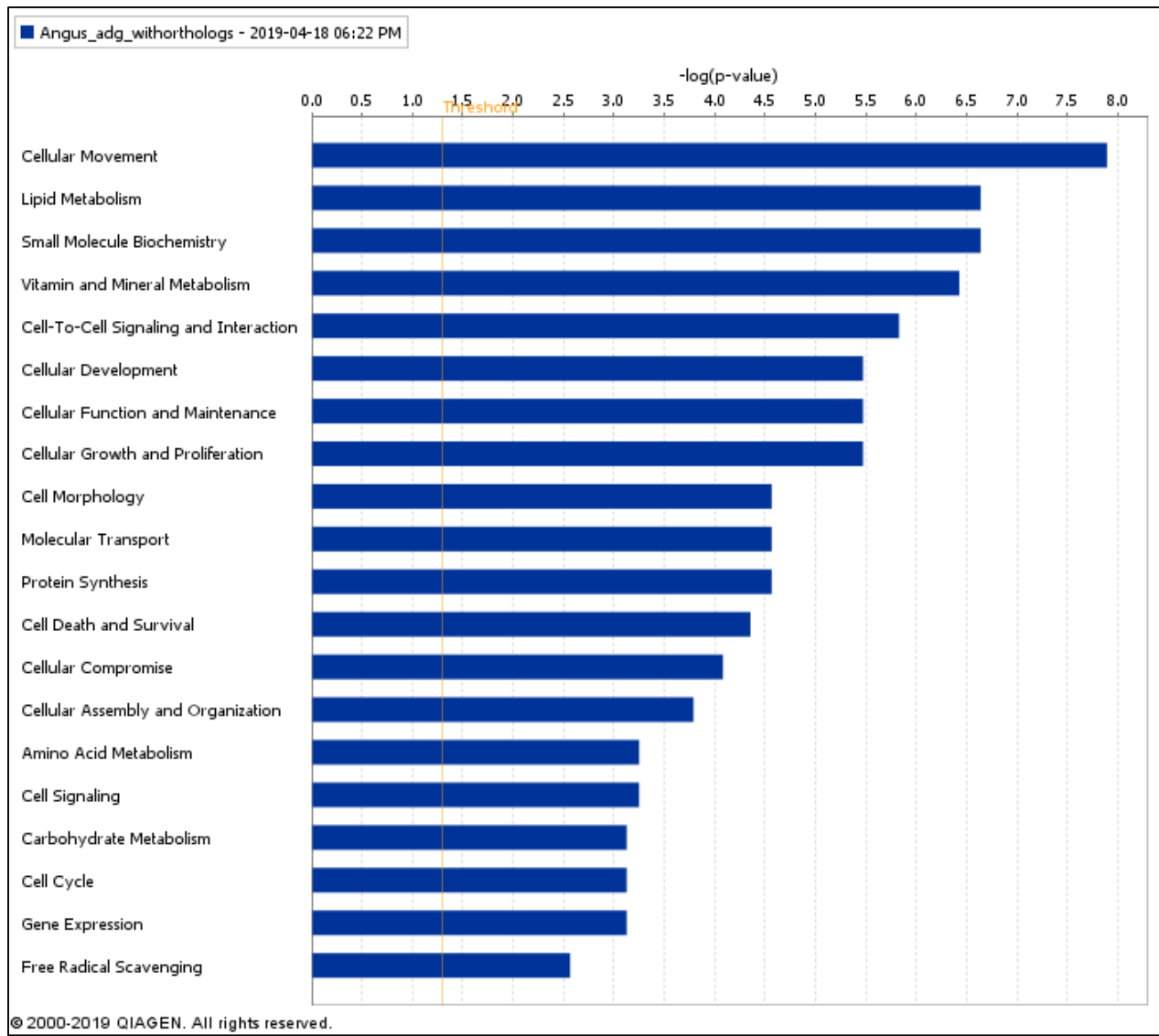


Figure S5: Enriched molecular and cellular functions associated with ADG in Angus steers.

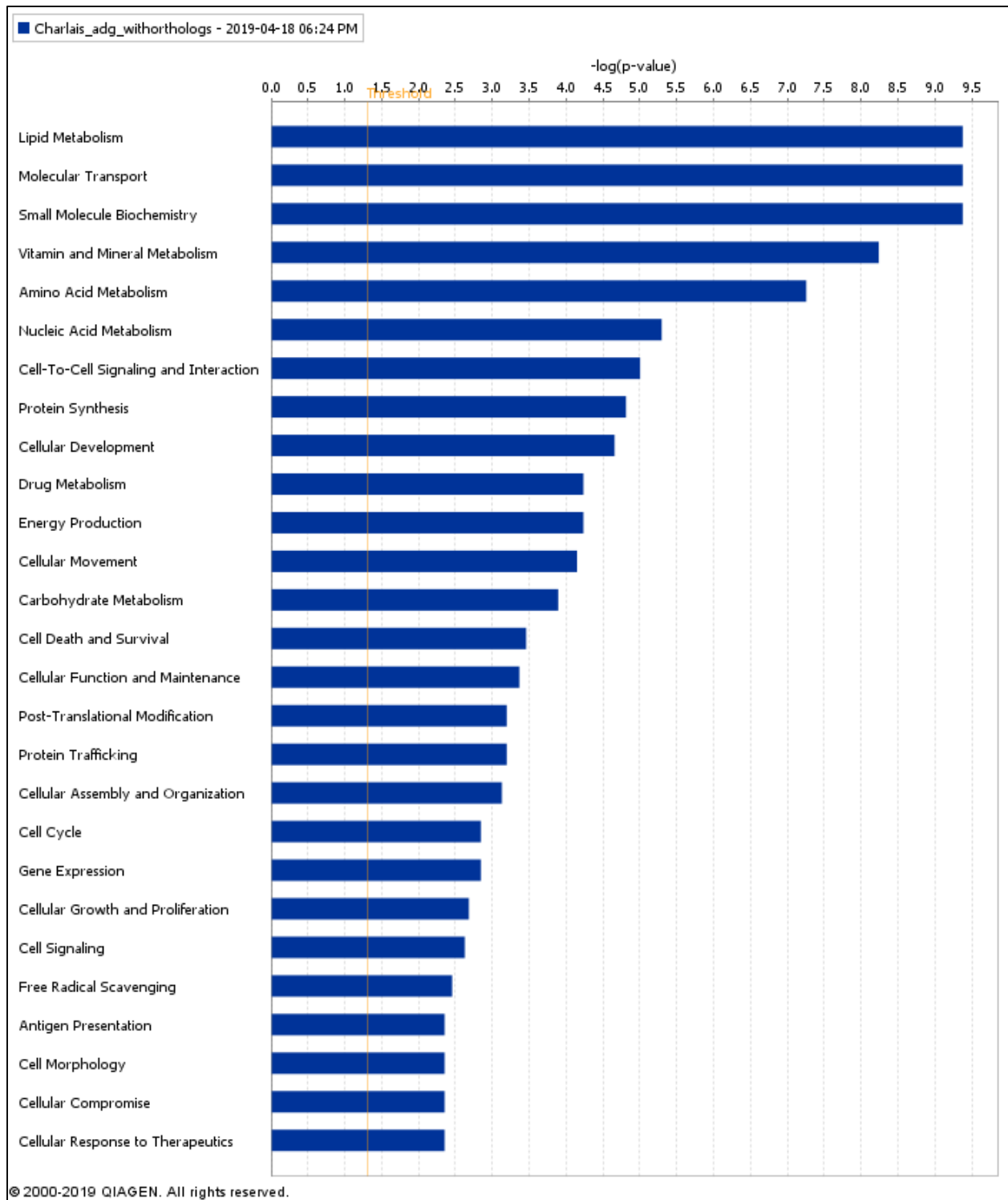


Figure S6: Enriched molecular and cellular functions associated with ADG in Charolais steers.

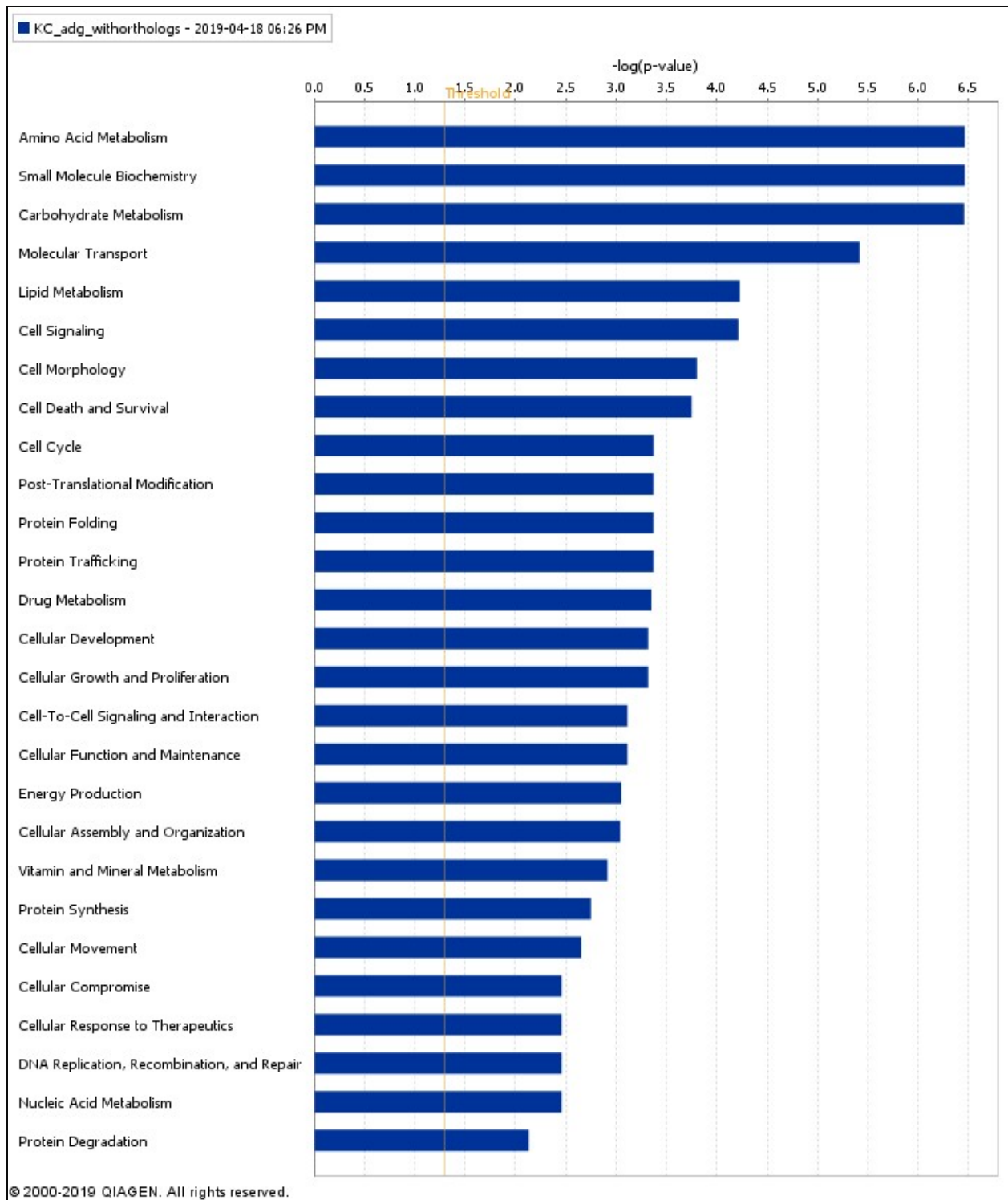


Figure S7: Enriched molecular and cellular functions associated with ADG in KC steers.

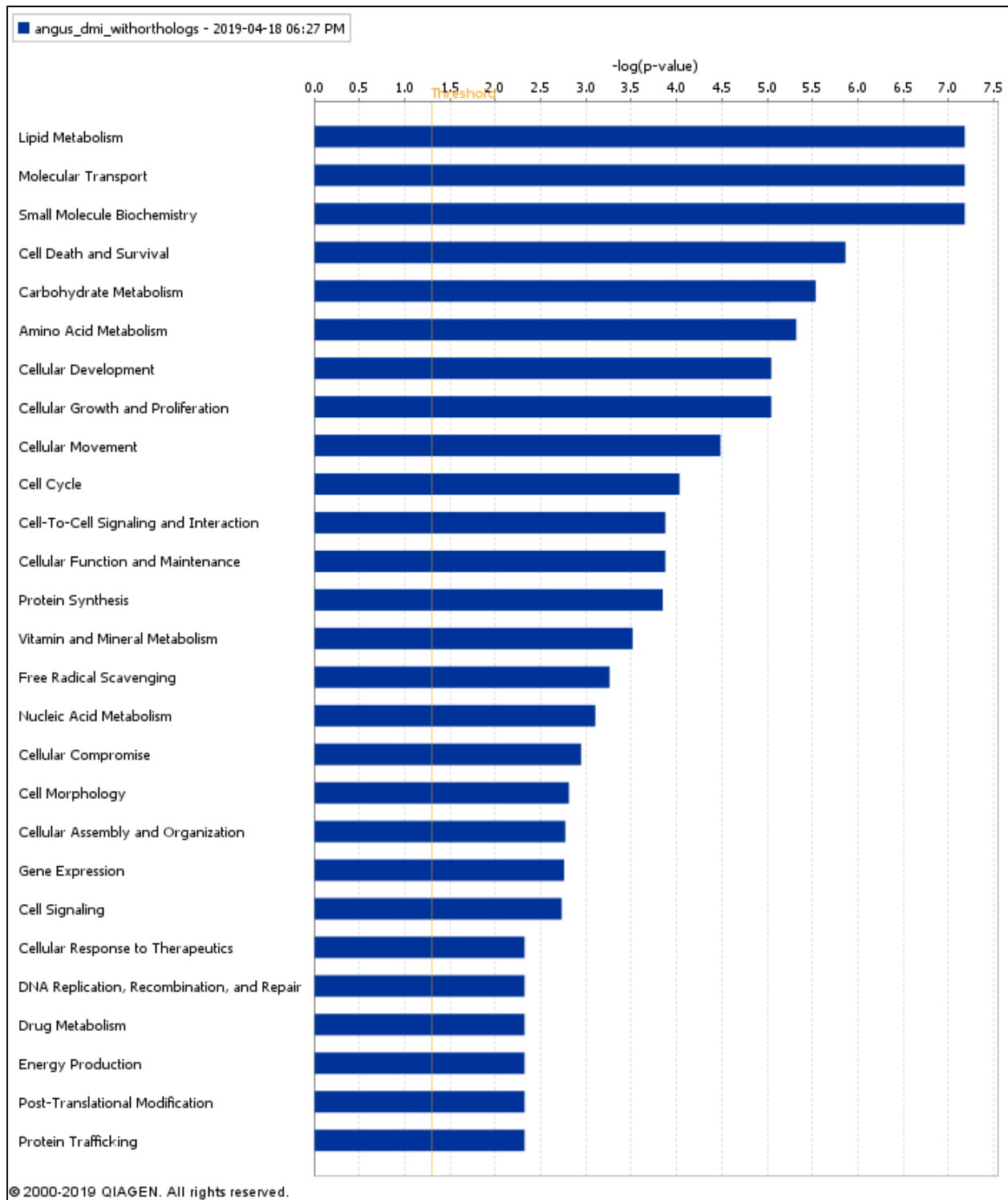


Figure S8: Enriched molecular and cellular functions associated with DMI in Angus steers.

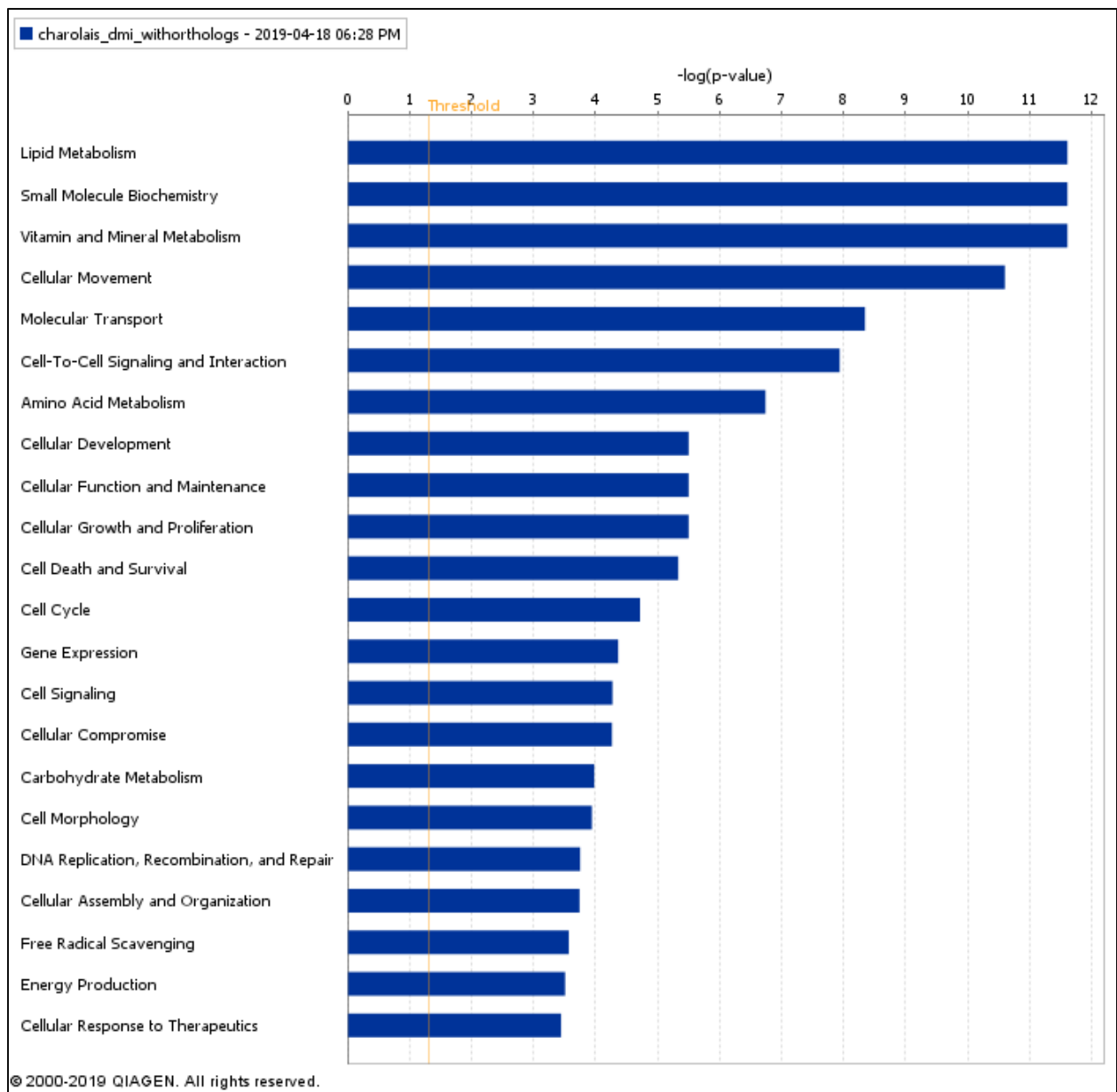


Figure S9: Enriched molecular and cellular functions associated with DMI in Charolais steers.

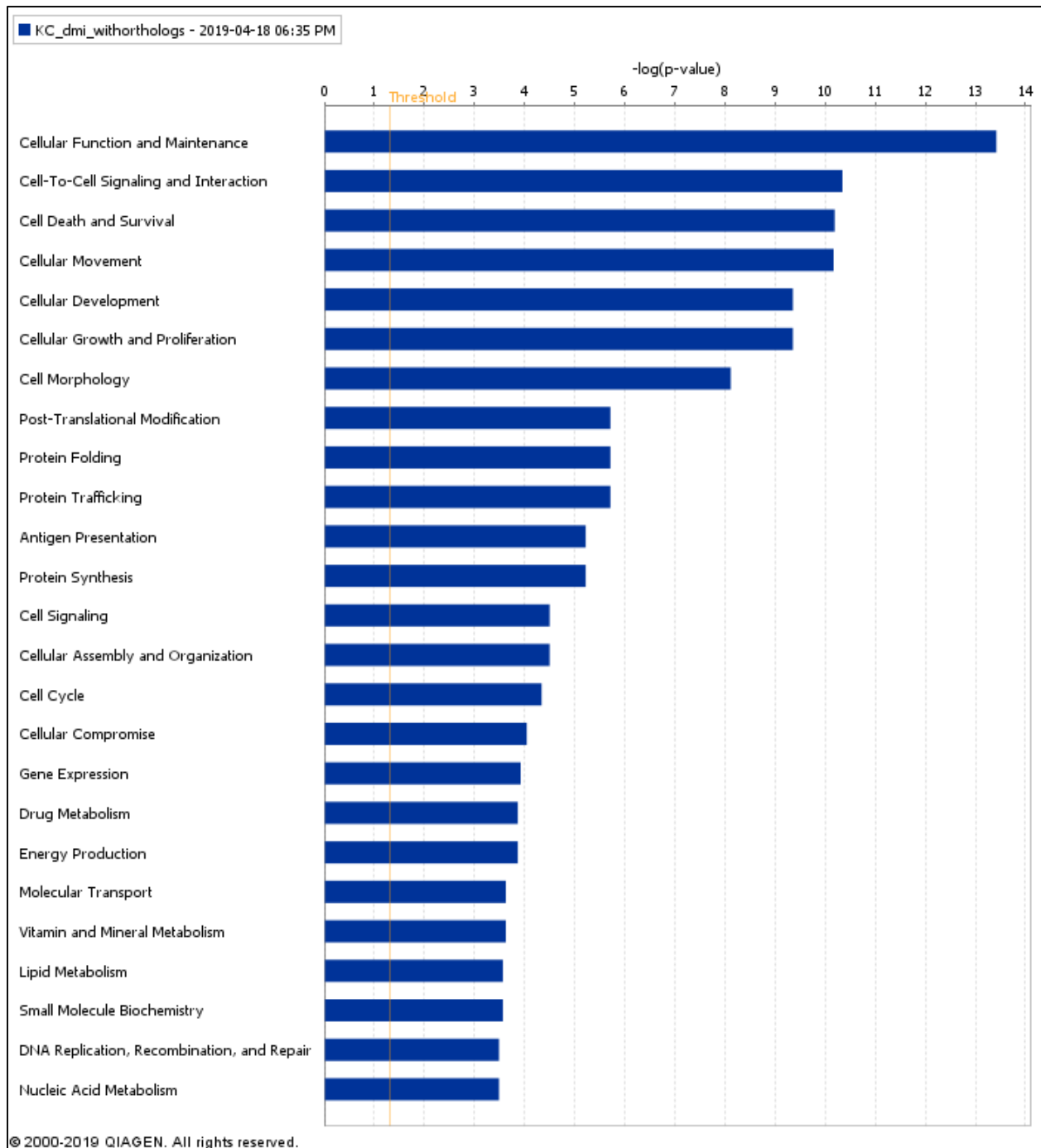


Figure S10: Enriched molecular and cellular functions associated with DMI in KC steers.

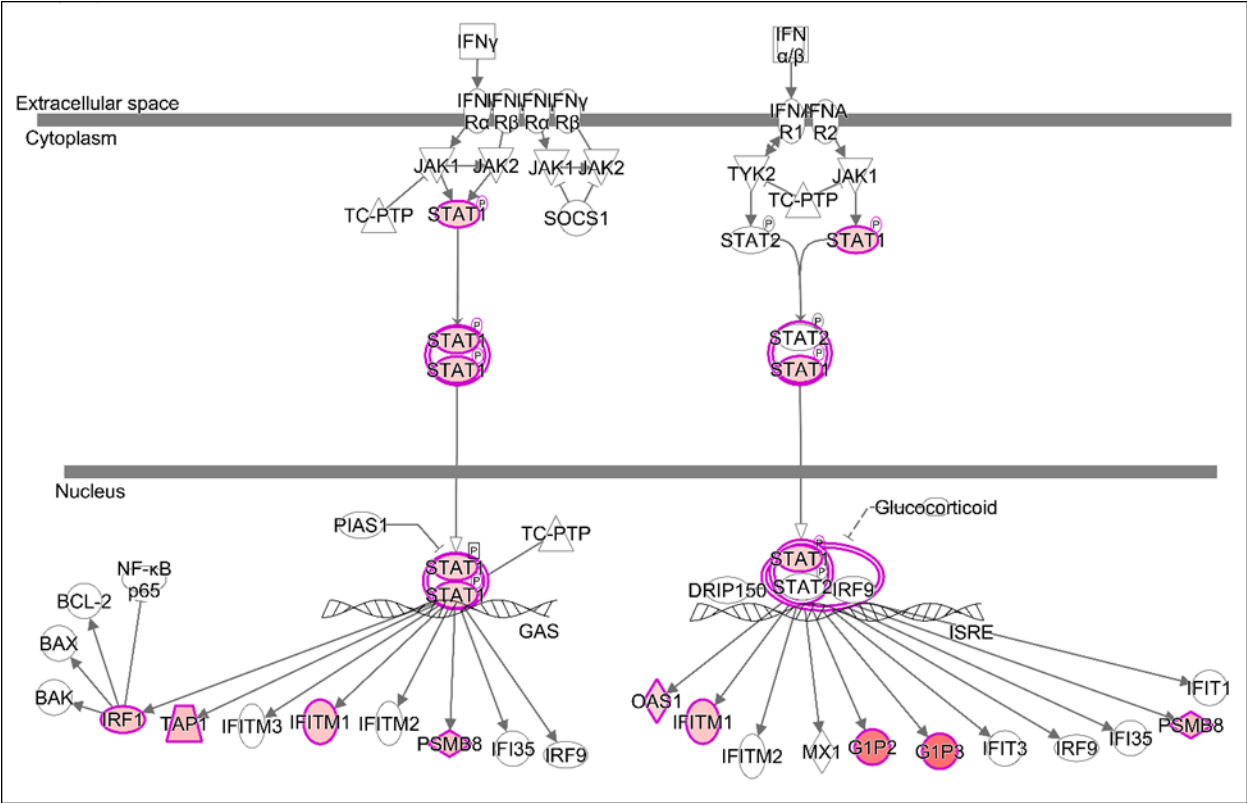


Figure S11: Interferon Signaling Canonical pathway associated with DMI in KC animals

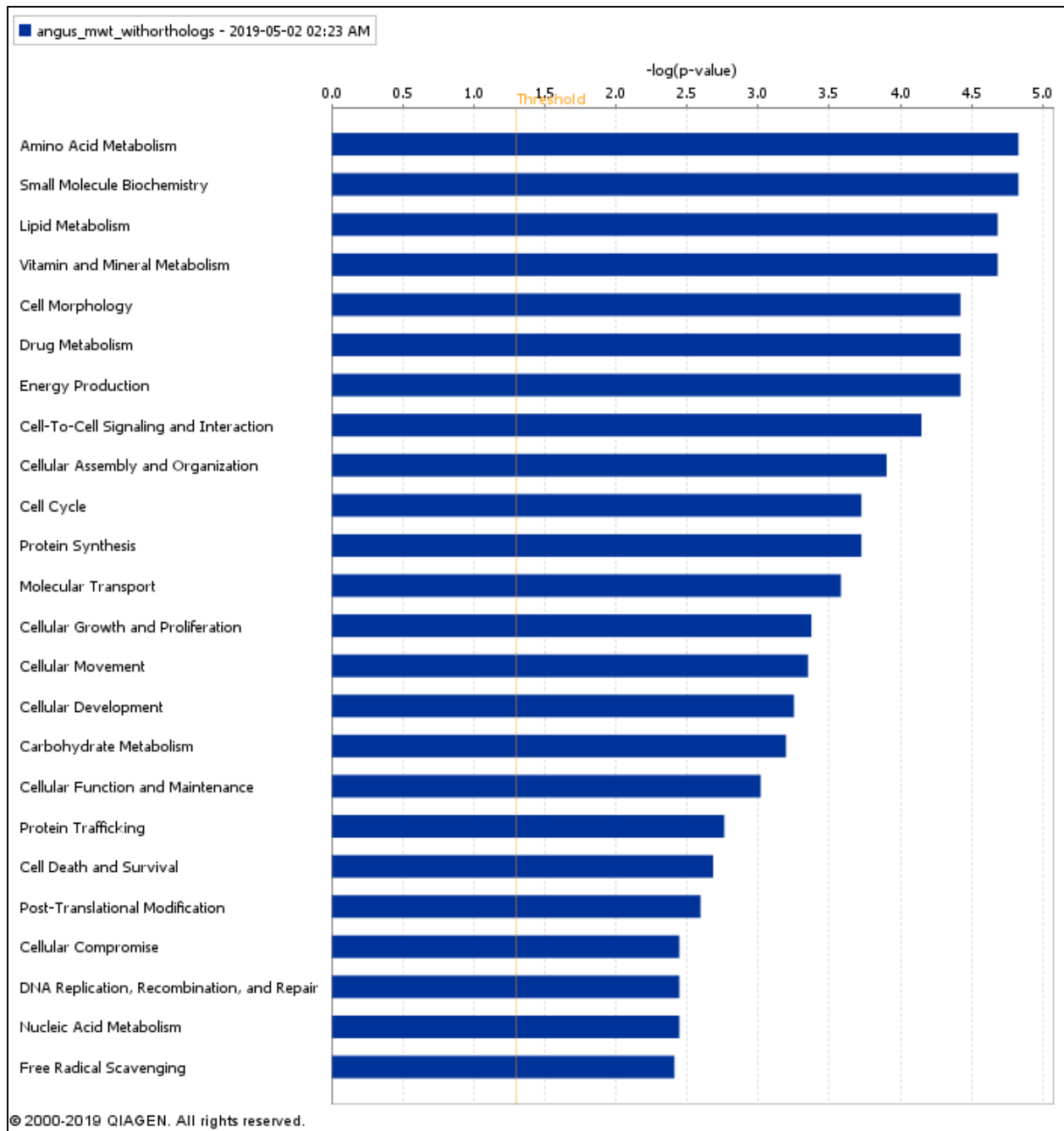


Figure S12: Enriched molecular and cellular functions associated with MWT in Angus steers.

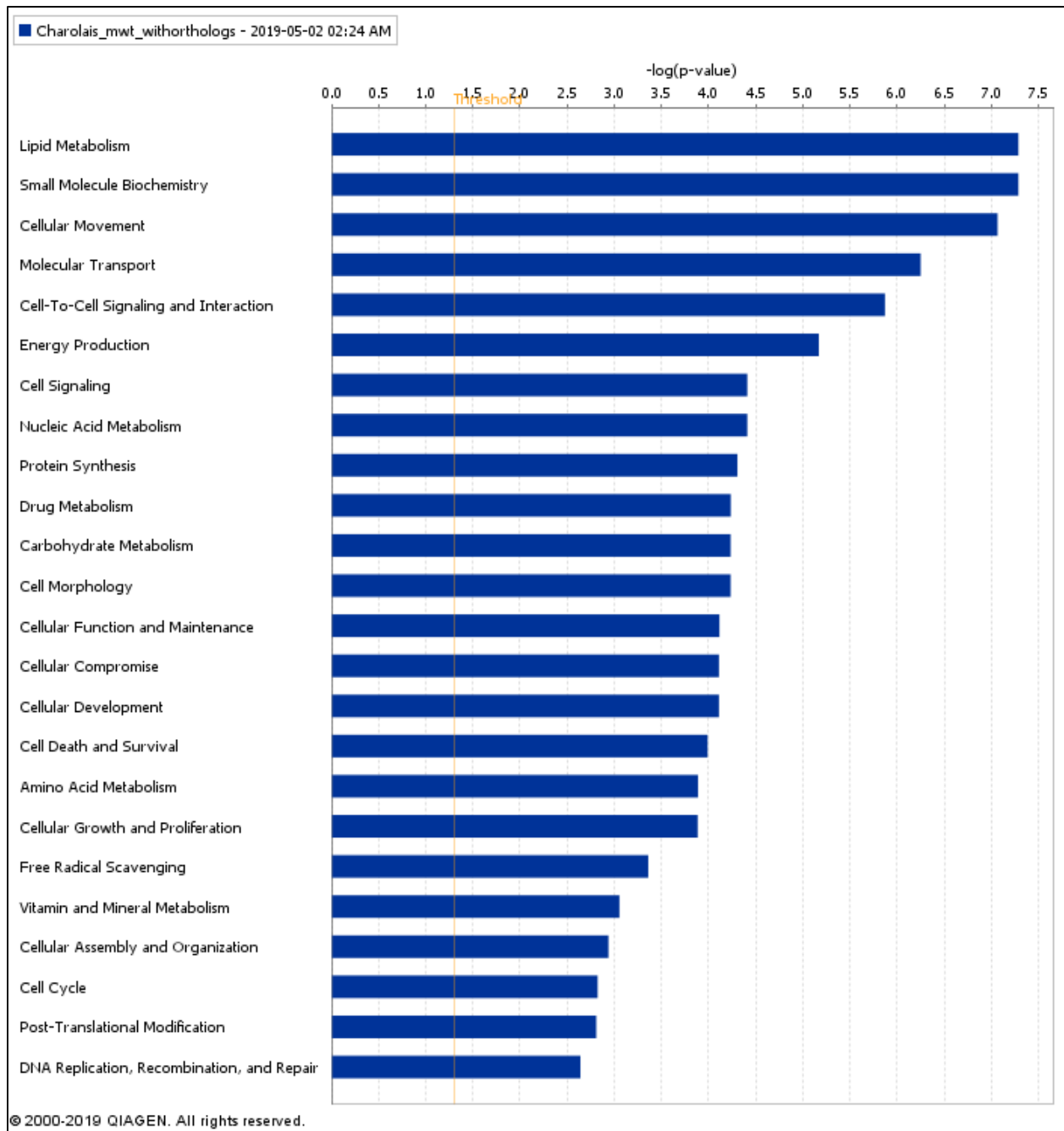


Figure S13: Enriched molecular and cellular functions associated with MWT in Charolais steers.

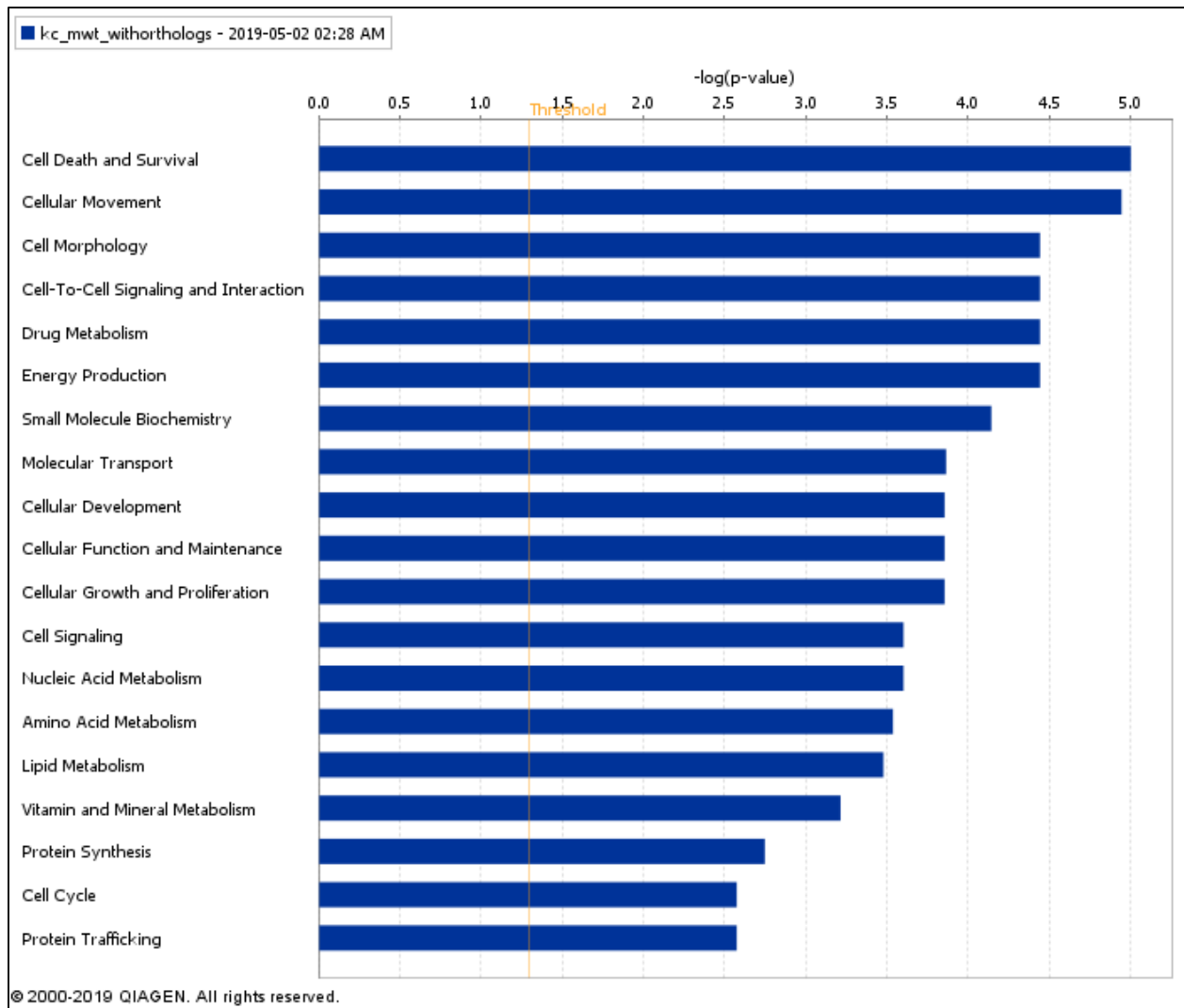


Figure S14: Enriched molecular and cellular functions associated with MWT in KC steers.