

SUPPLEMENTARY MATERIALS

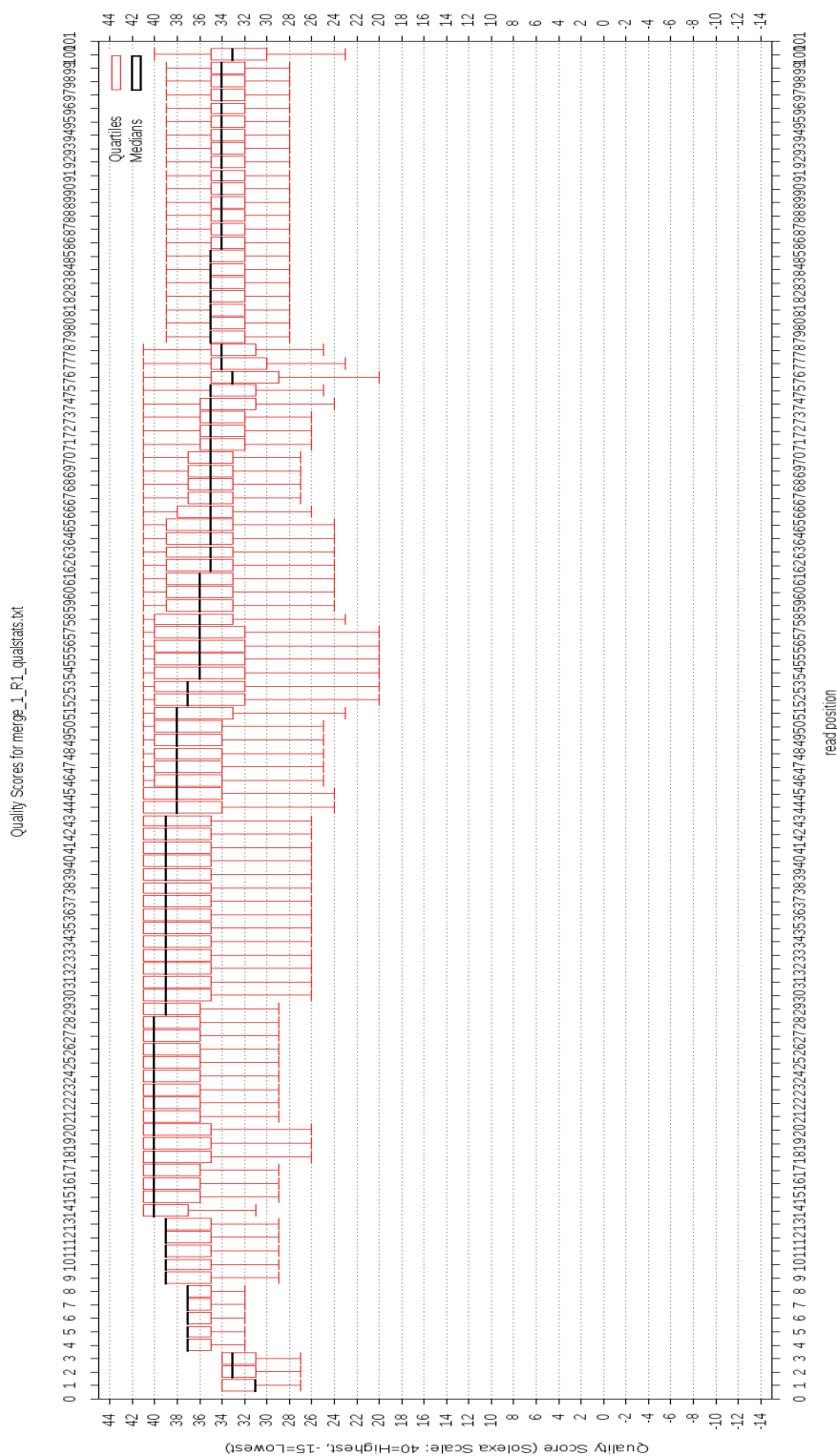


Fig. S1. Box plots after quality filtering to remove the noise. Reads quality threshold (Q = 30 – 40) was utilized in the subsequent down stream data analysis.

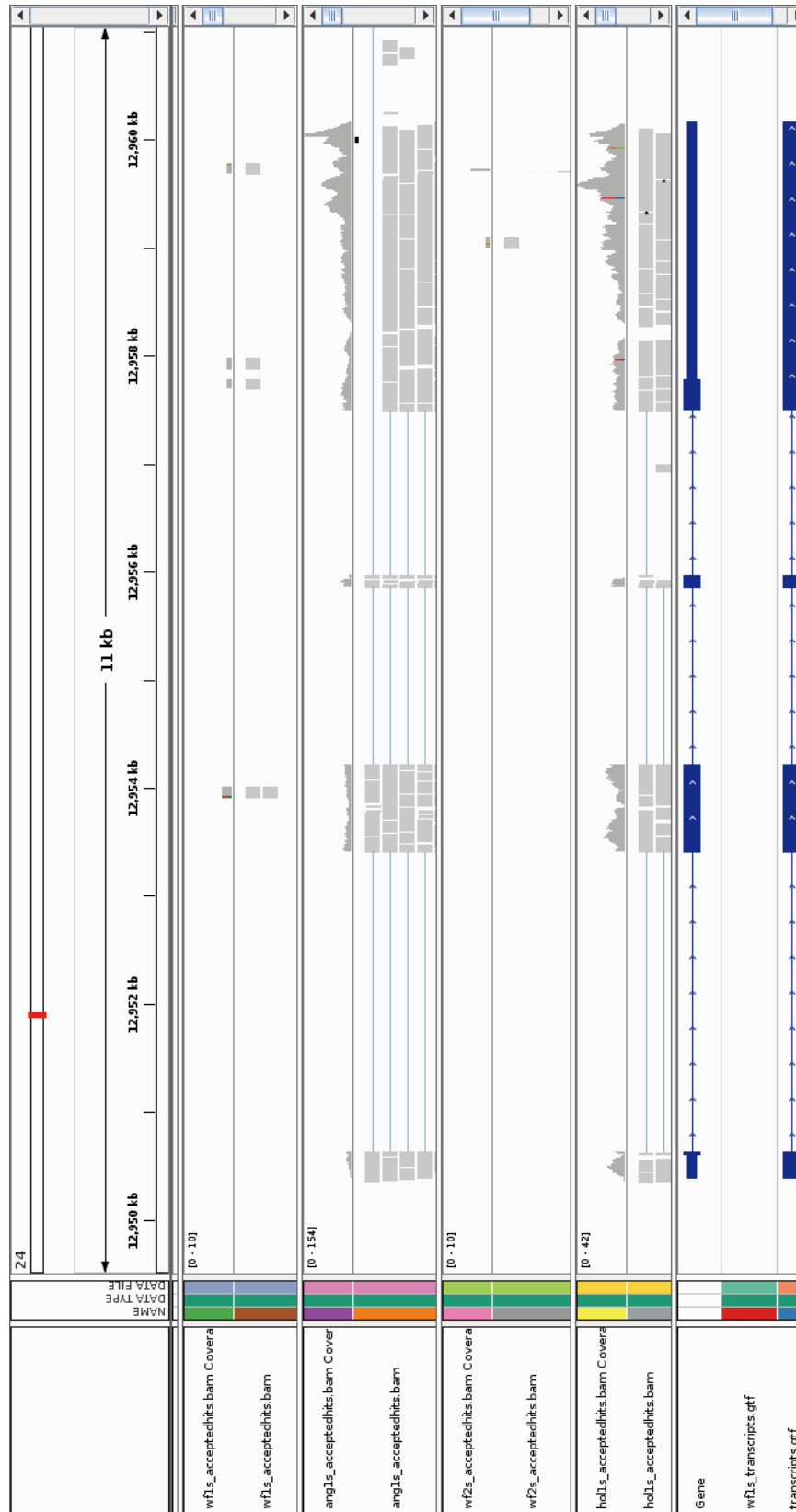


Fig. S2. Binary alignment map (BAM) files visualized using the Integrated genome browser (IGV) showing the majority of the sequence reads aligned to the coding regions of most genes in the bovine genome. White Fulani.

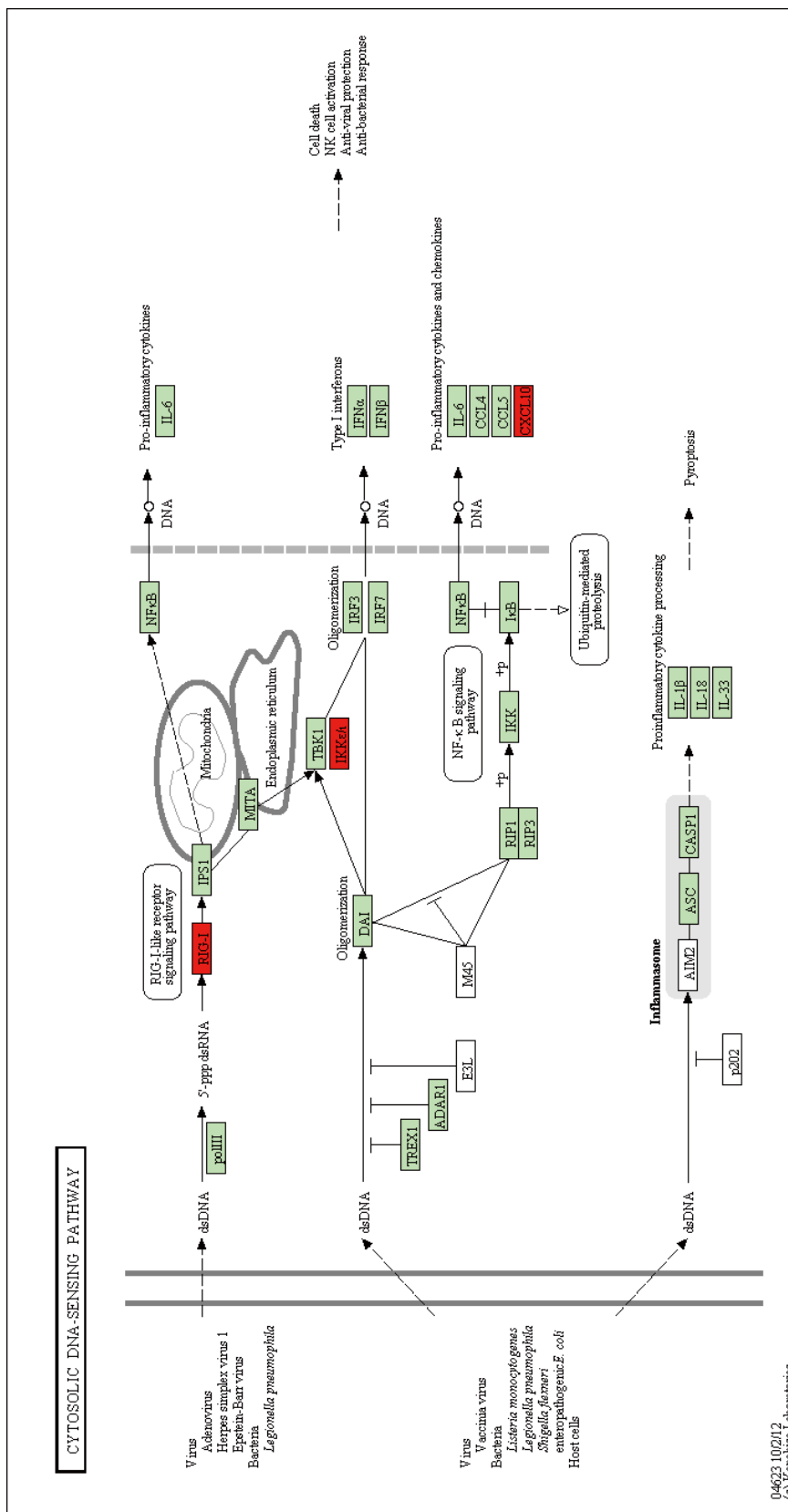


Fig. S3. Cytosolic DNA-sensing pathway. Three genes RIG-I and IKK ϵ were differentially expressed (Fold change between 1.5 and 2) while CXCL10 was significantly differentially expressed (fold change > 2) in White Fulani compared to Angus.

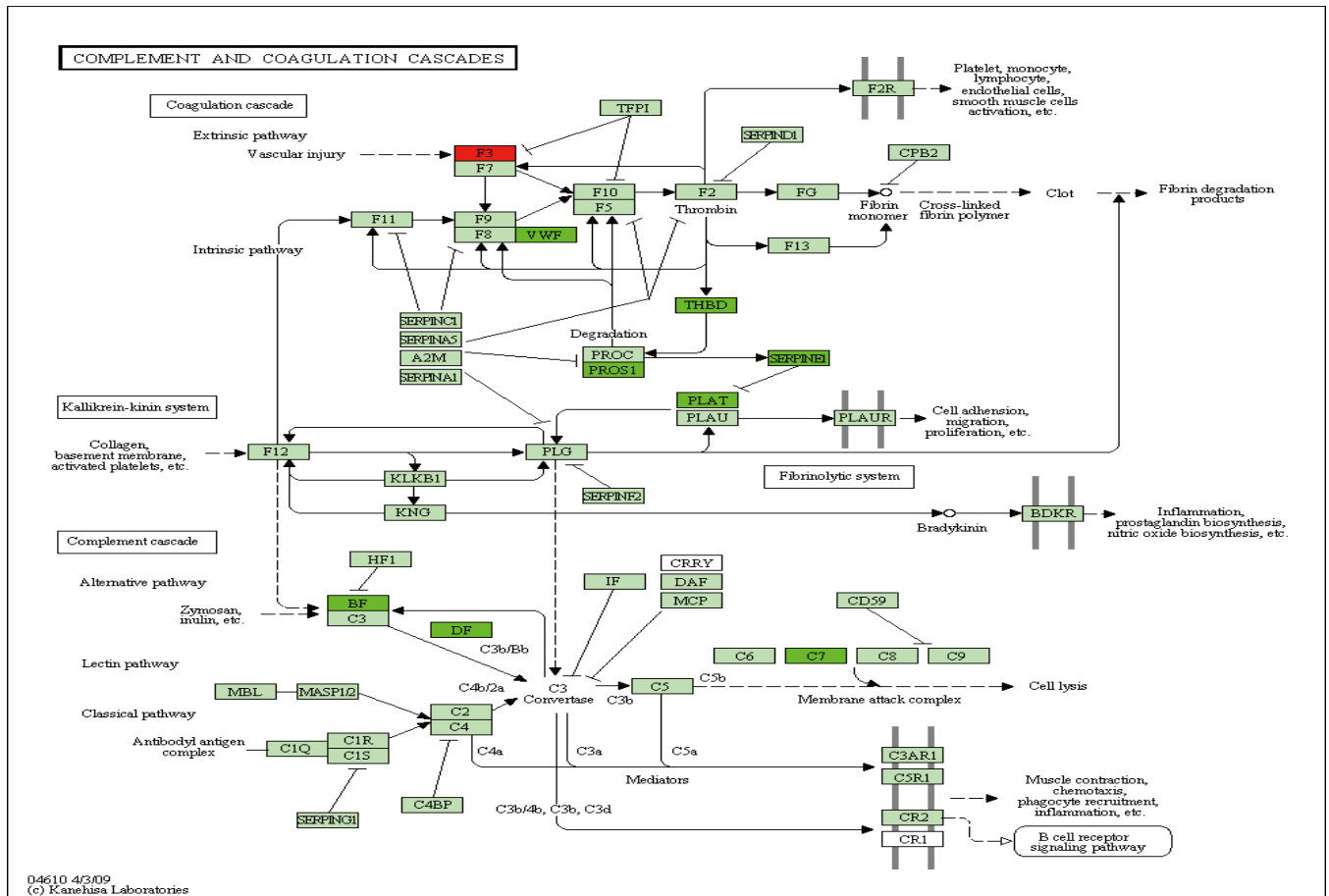


Fig. S4. Complement and coagulation pathway. Genes shaded green depicts those that were significantly down regulated while red color depicts those that were significantly upregulated in White Fulani.

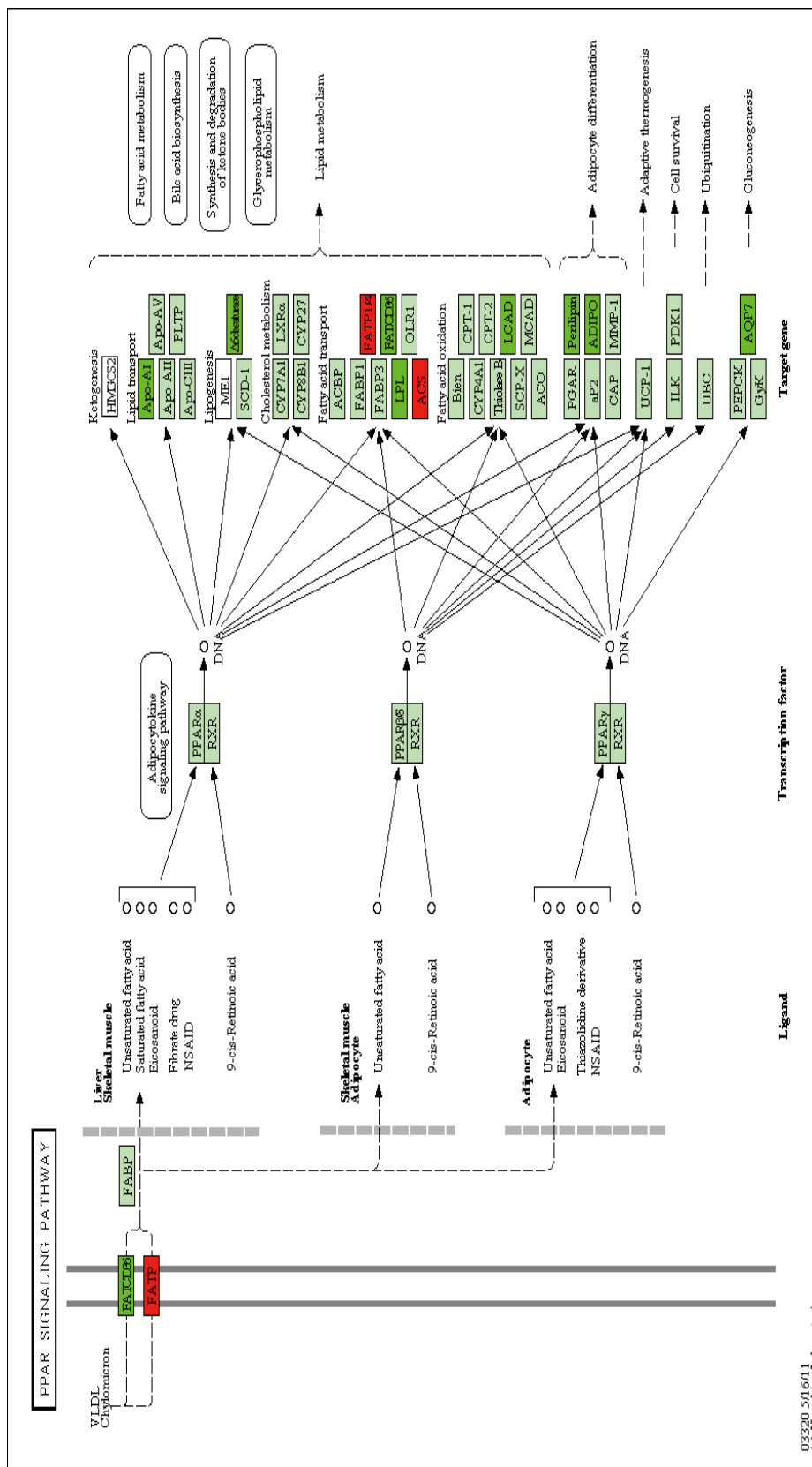


Fig. S5. PPAR signaling pathway. Genes shaded green depicts those that were significantly down regulated while red color depict those that were significantly upregulated in White Fulani. PPAR, peroxisome proliferator-activated receptors.

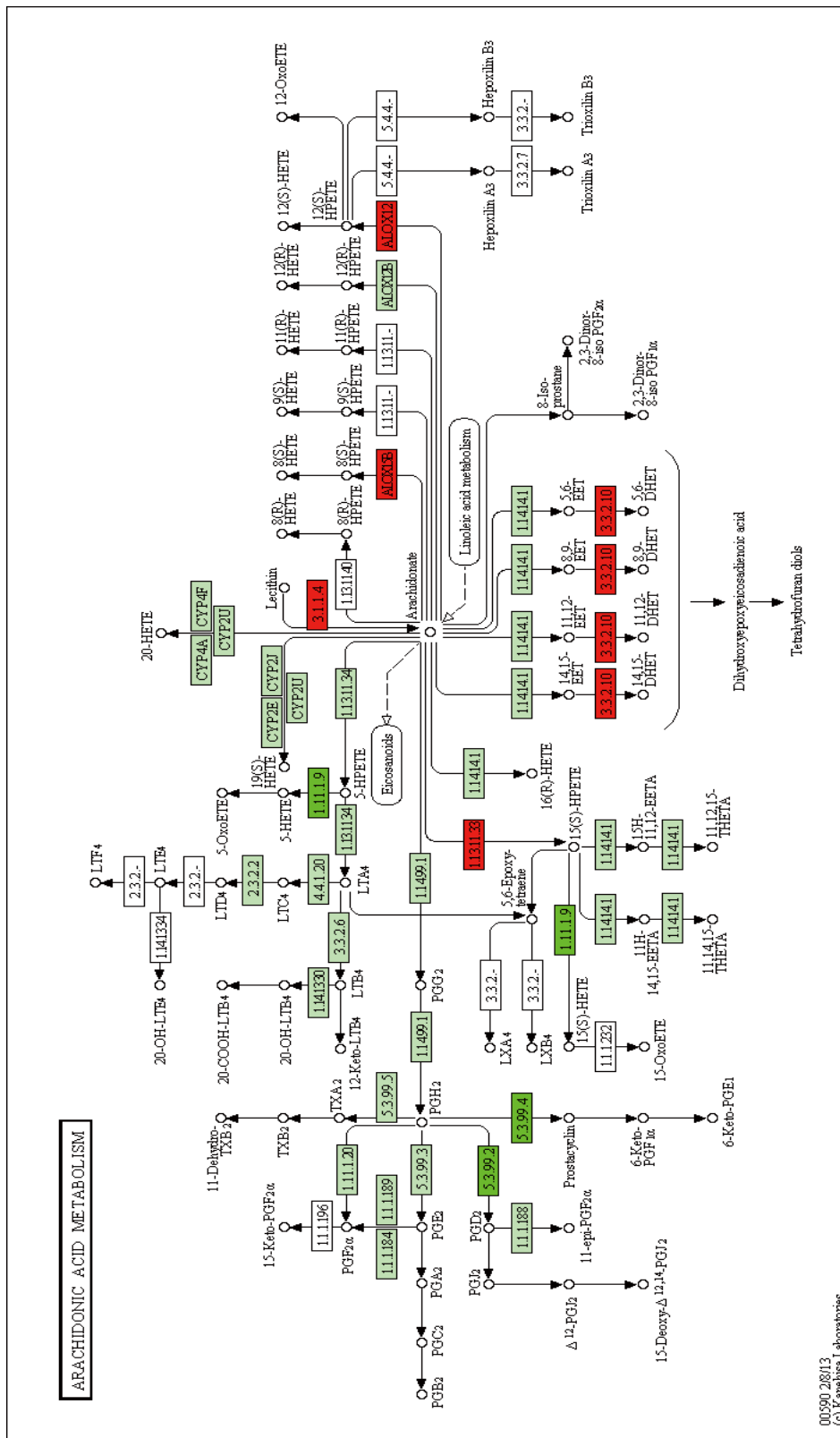


Fig. S6. Arachidonic acid metabolism pathway. Genes shaded green depicts those that were significantly down regulated while red color depict those that were significantly upregulated in White Fulani. 3.1.1.4 represents *PLA2G4E*; 1.11.19, *GPX7*; 5.3.99.2, *PTGDS*; 5.3.99.4, *PTGIS*; 1.13.11.33, *ALOX15B*; 3.3.2.10, *EPHX2* genes.

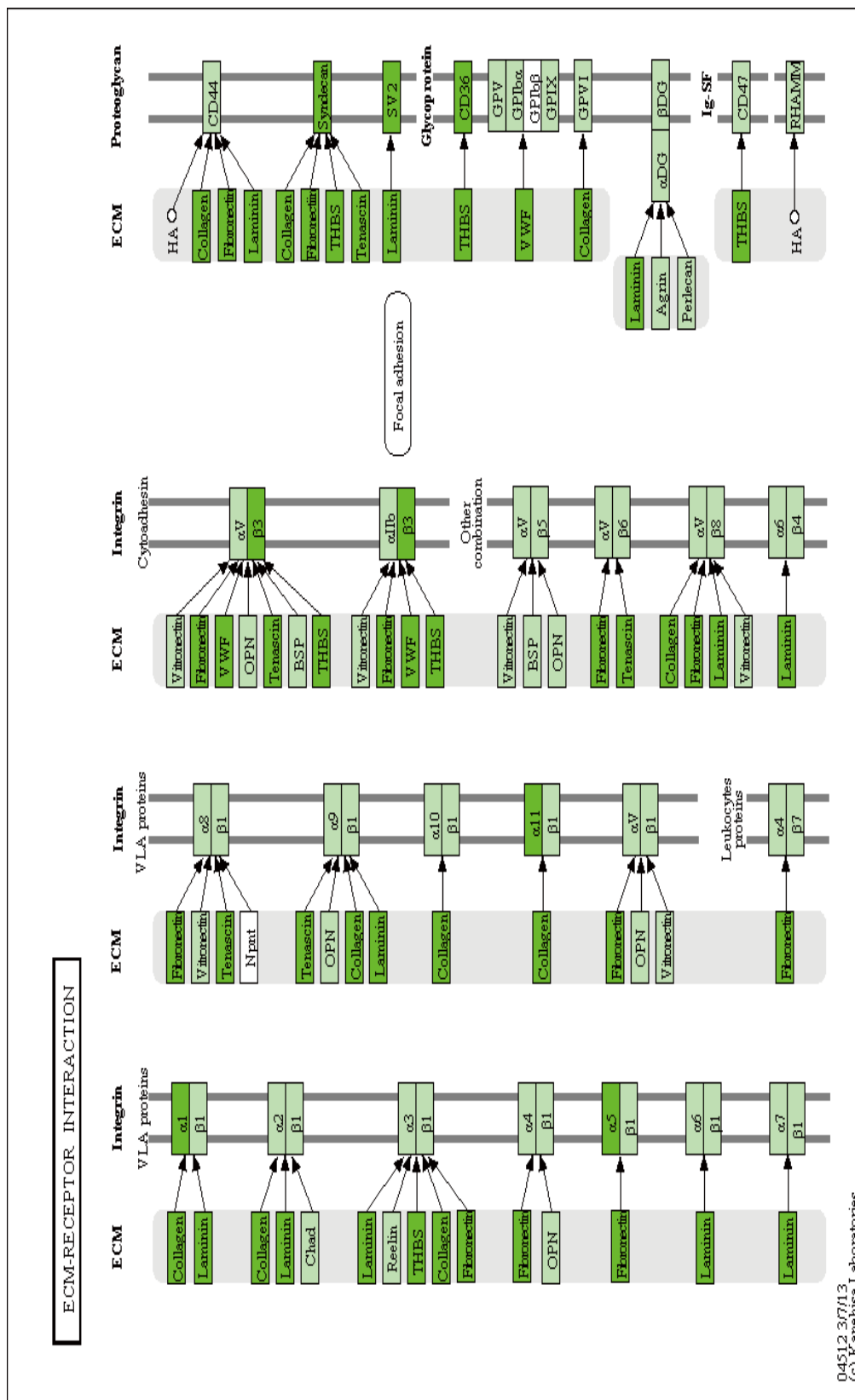


Fig. S7. Extracellular cell matrix-receptor interaction pathway. Genes shaded green depicts those that were significantly down regulated in White Fulani.

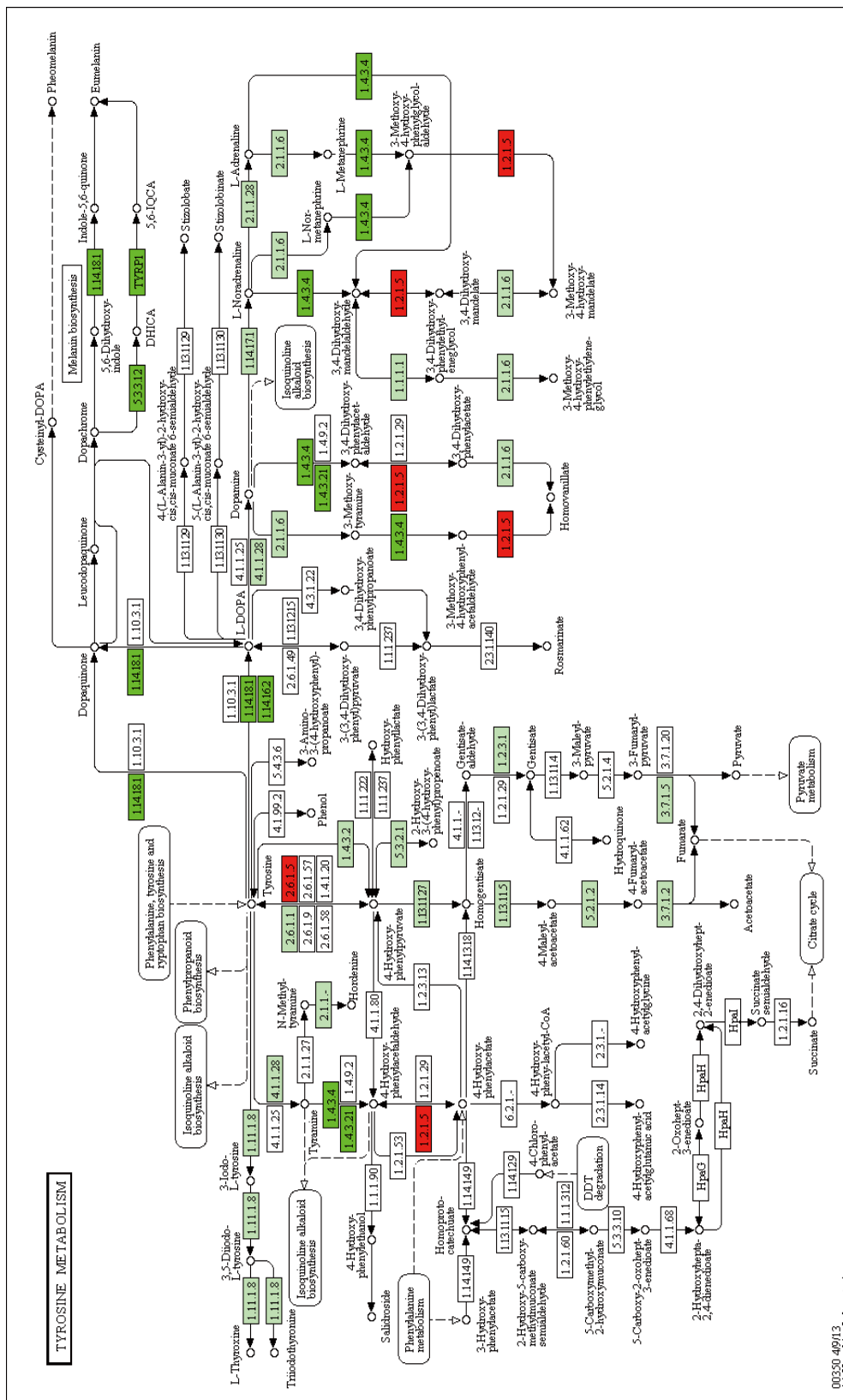


Fig. S8. Tyrosine metabolism pathway. Genes shaded green depicts those that were significantly down regulated while red color depict those that were significantly upregulated in White Fulani. 1.14.18.1, *TYR*; 5.33.12, *DCT* or *TYRP2*; 1.14.18.1, *TYR*; 1.14.16.2, *TH*; 1.43.4, *MAOB*; 1.2.15, *ALDH3A1*; 2.6.15, *TAT* genes.

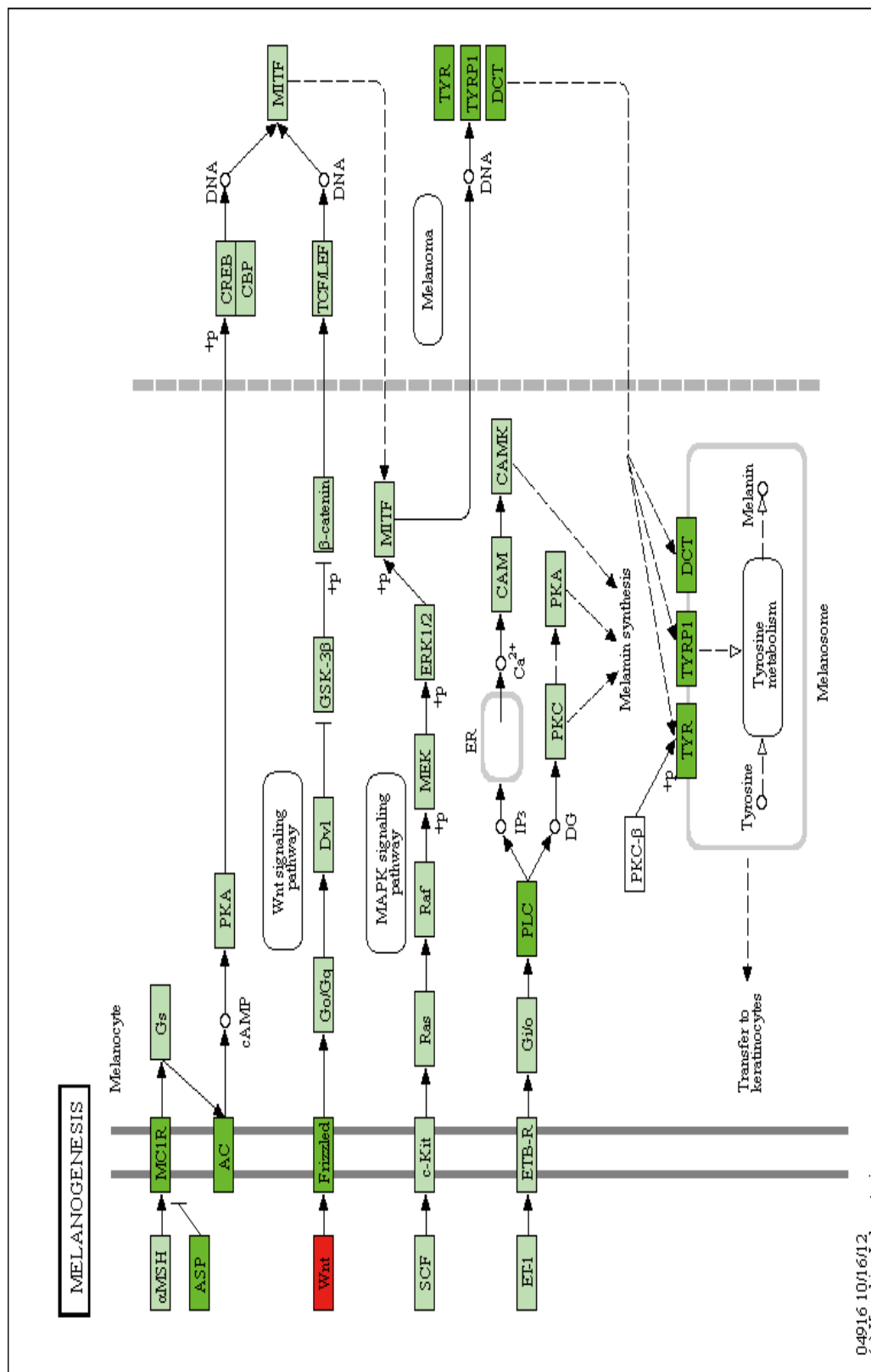


Fig. S9. Melanogenesis pathway. Genes shaded green depicts those that were significantly down regulated while red color depict those that were significantly upregulated in White Fulani. Note DCT gene is also called TYRP2 gene and ASP is agouti signaling protein. DCT, dopachrome tautomerase; TYRP, tyrosinase-related protein.

