

Alternative splicing and polyadenylation facilitate transcriptome diversity underlying high-altitude adaptation in pigs

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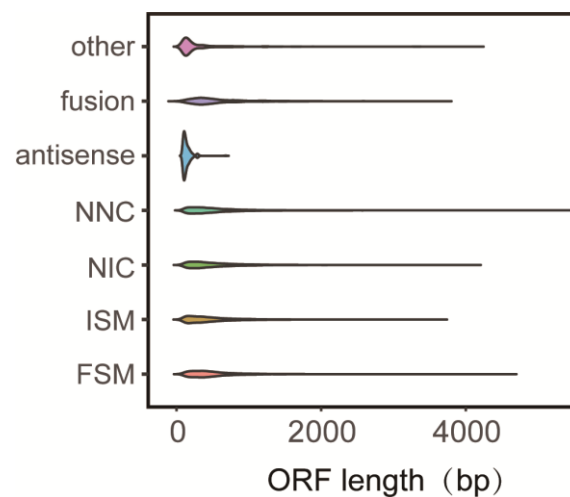
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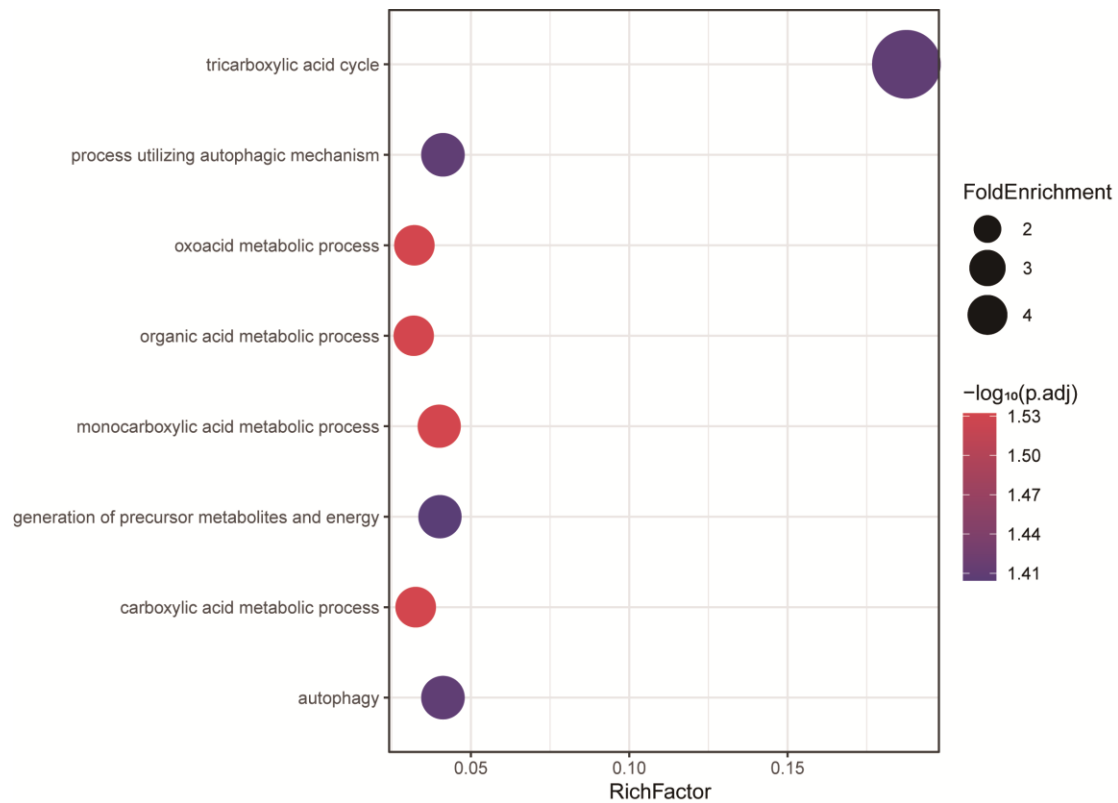
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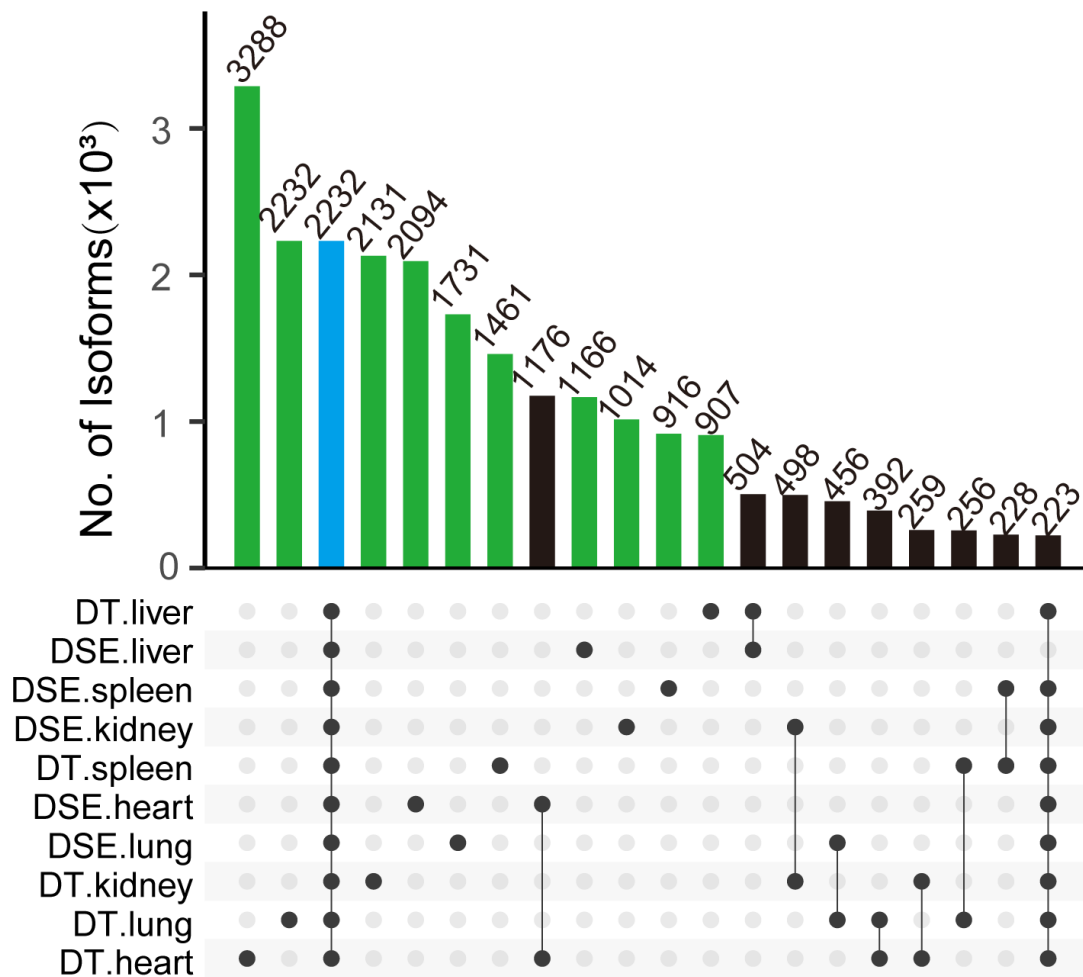
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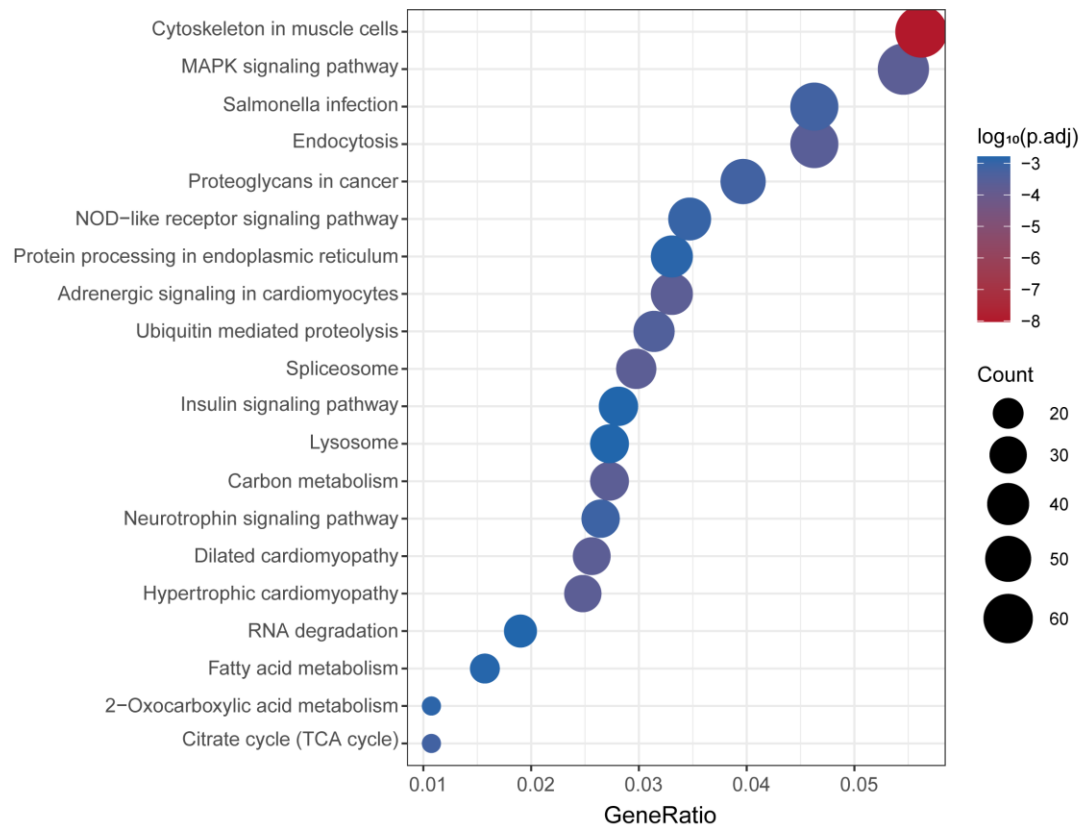
Supplementary Fig. 1 | Length distribution of open reading frames (ORF) of each category. FSM, full-splice match. ISM, incomplete splice match. NIC, novel in catalog. NNC, novel not in catalog.



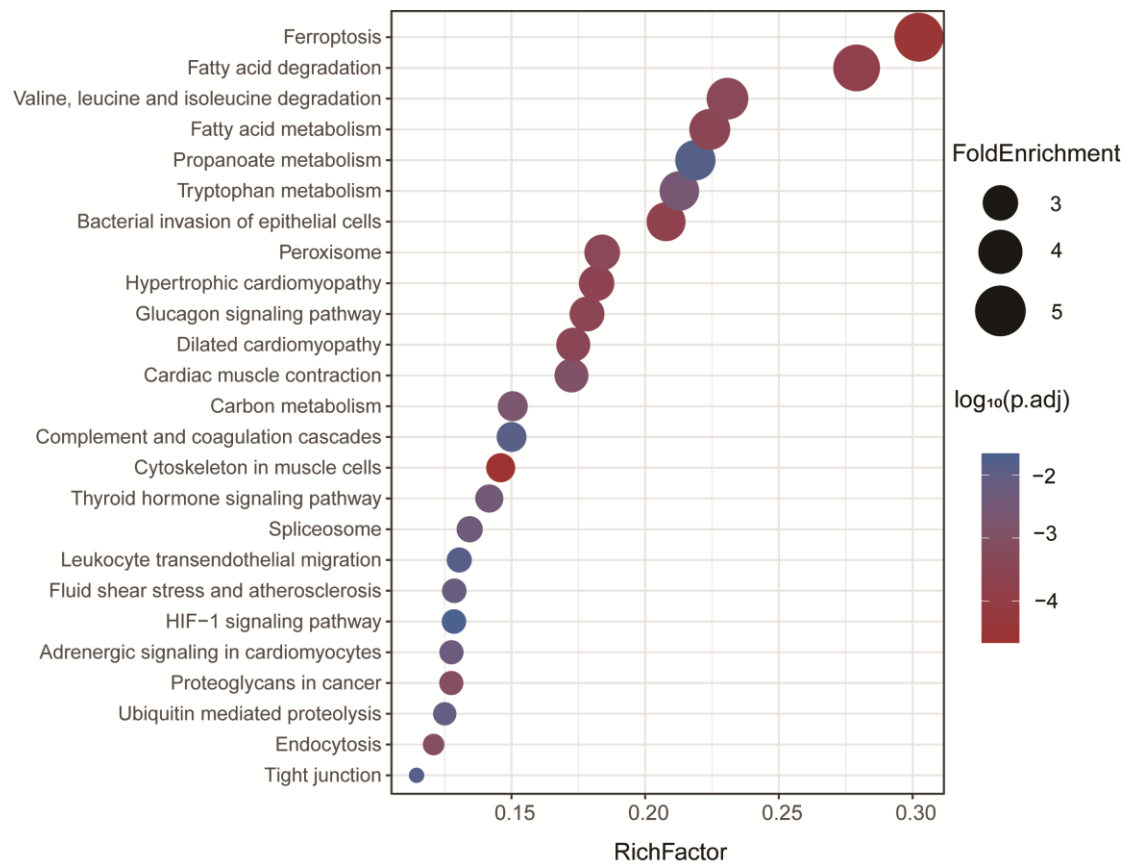
Supplementary Fig. 2| GO enrichment analysis of isoform-difference genes with expressed transcripts (TPM > 1) that exhibited inter-breed differences greater than three in transcript number between Diannan small-ear pigs (DSE) and Diqing Tibetan pigs (DT) in kidney ($p.adj < 0.01$).



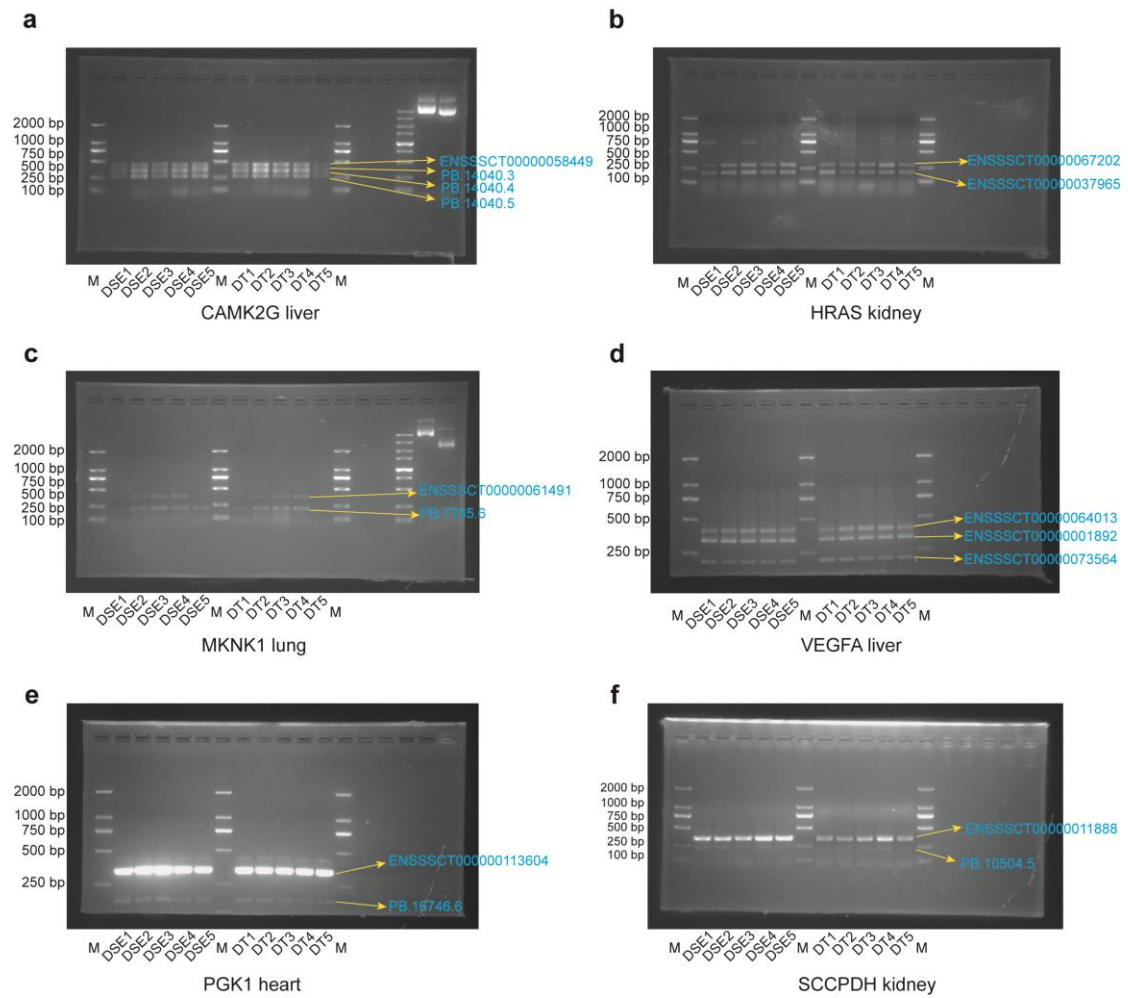
Supplementary Fig. 3 | Distribution of breed-/tissue-specific and shared transcripts of alternative splicing (AS) genes between Diannan small-ear pigs (DSE) and Diqing Tibetan pigs (DT) among five visceral tissues.



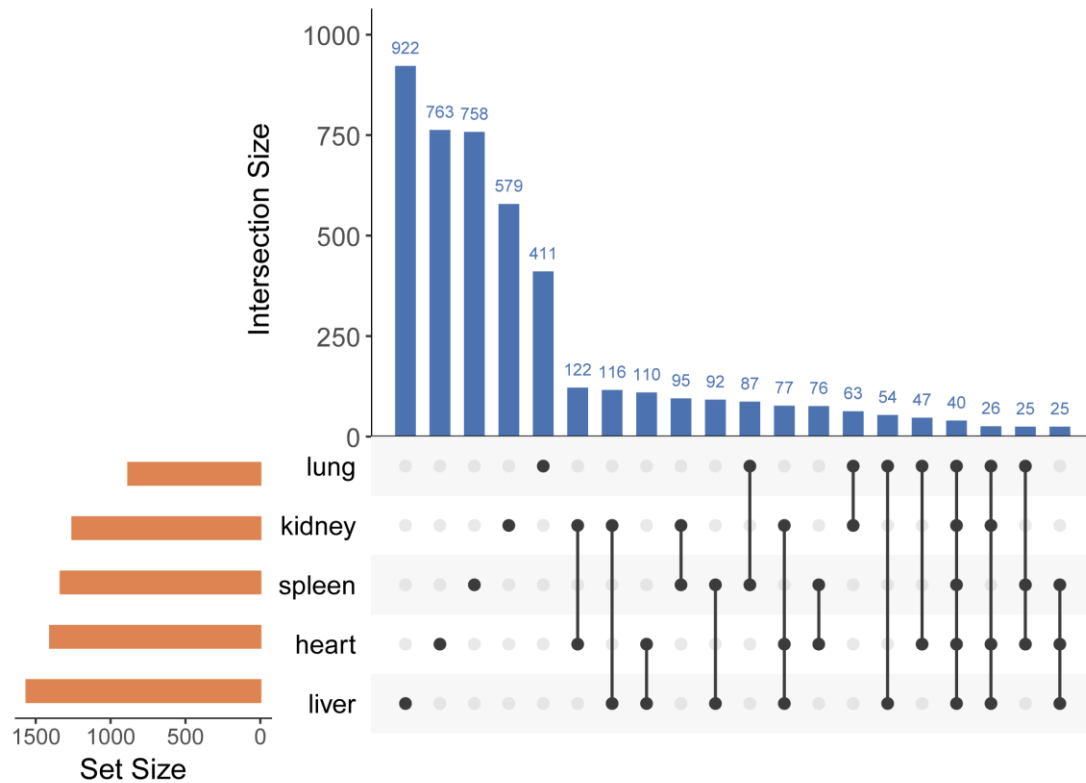
Supplementary Fig. 4|KEGG pathways enriched from the heart- and lung-specific alternative splicing (AS) transcript genes in Diqing Tibetan pigs (DT) (p.adj < 0.01).



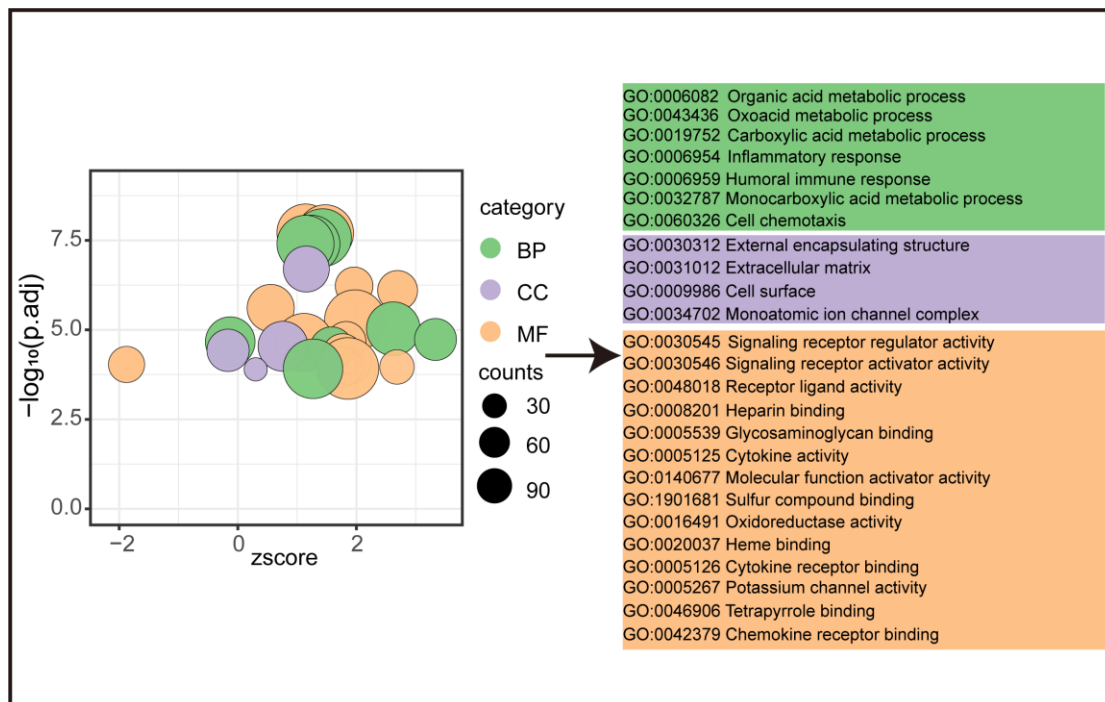
Supplementary Fig. 5|KEGG pathways enriched from the top 1000 most isoformic genes ($p.adj < 0.01$) between Diannan small-ear pigs (DSE) and Diqing Tibetan pigs (DT) among five visceral tissues.



Supplementary Fig. 6 | Uncropped and unedited gel images of **Fig. 3**.

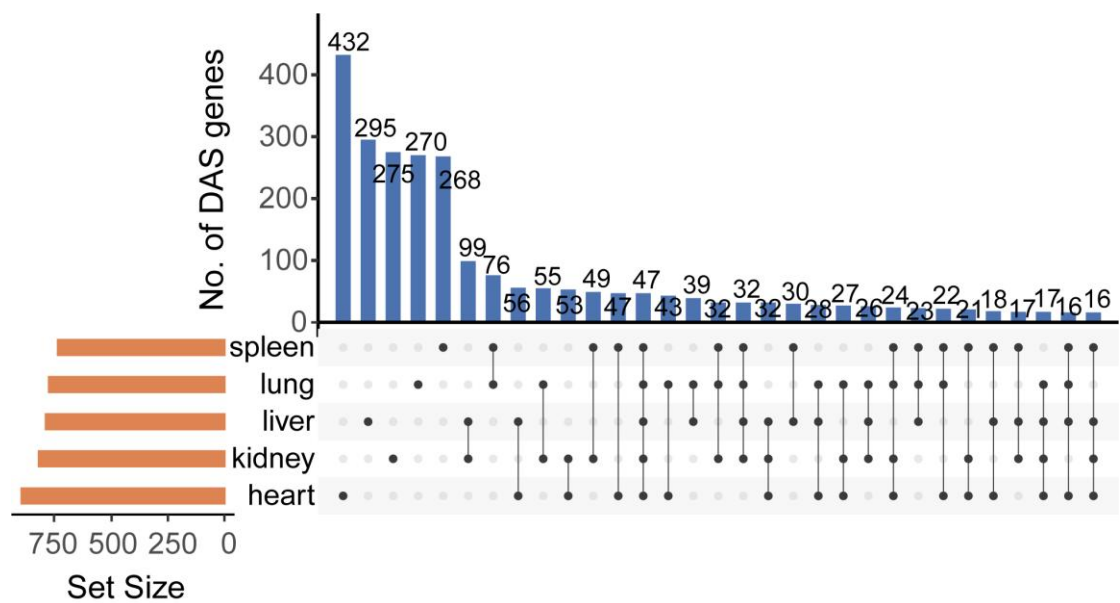


Supplementary Fig. 7 | Distribution of differentially expressed genes (DEGs) between Diannan small-ear pigs (DSE) and Diqing Tibetan pigs (DT) among five visceral tissues.

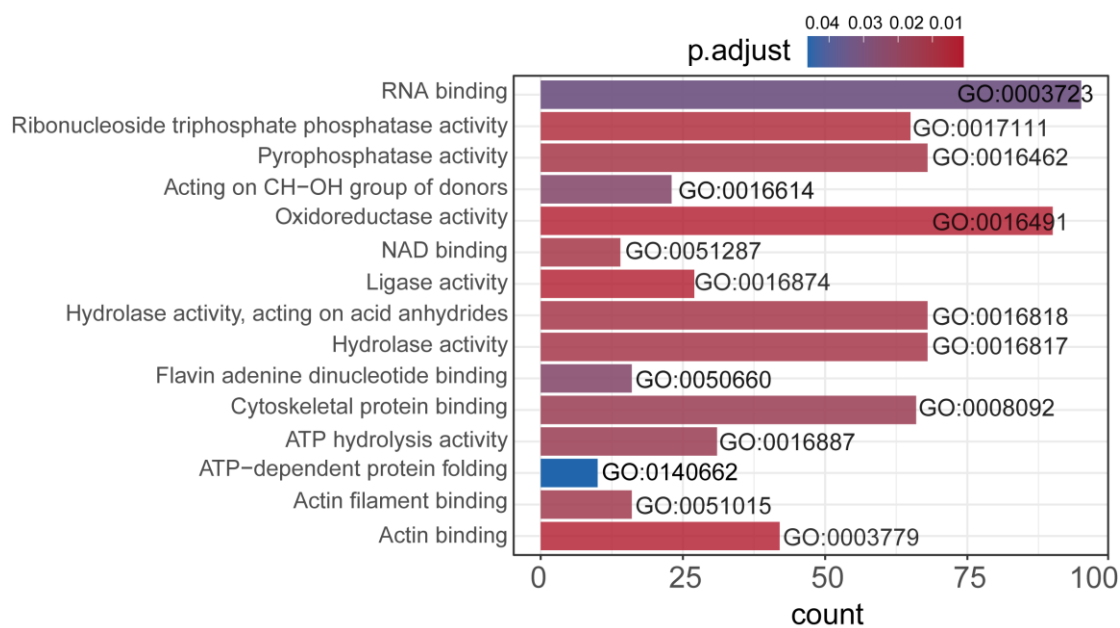


Supplementary Fig. 8 | Significantly enriched top 25 GO terms of differentially expressed genes (DEGs) ($p_{\text{adj}} < 0.01$) between Diannan small-ear pigs (DSE) and Diqing Tibetan pigs

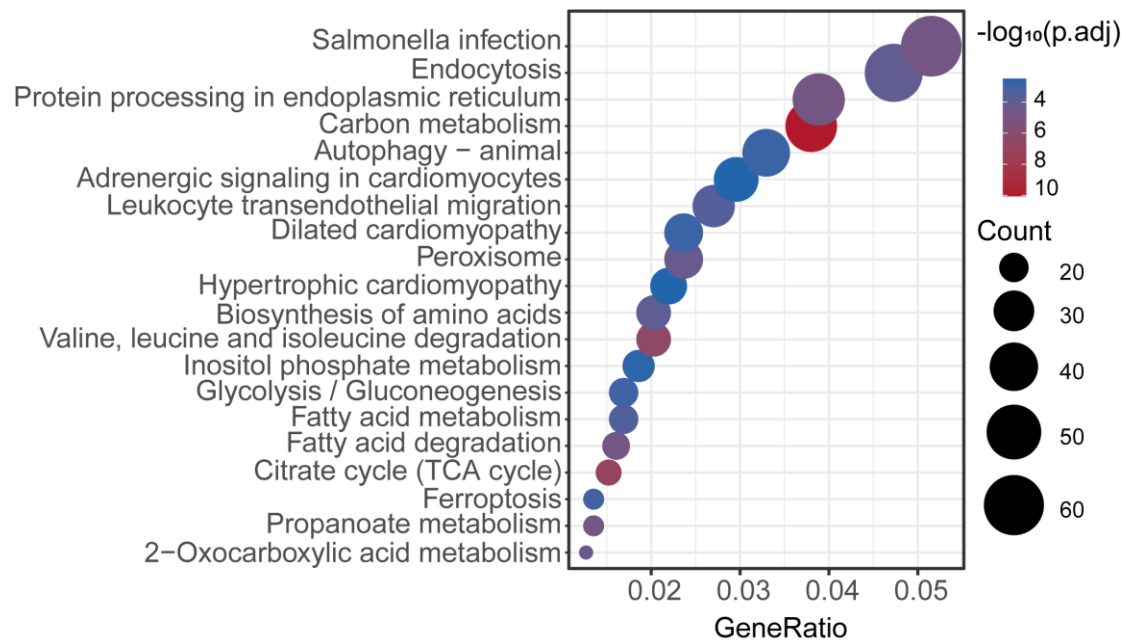
(DT) among five visceral tissues.



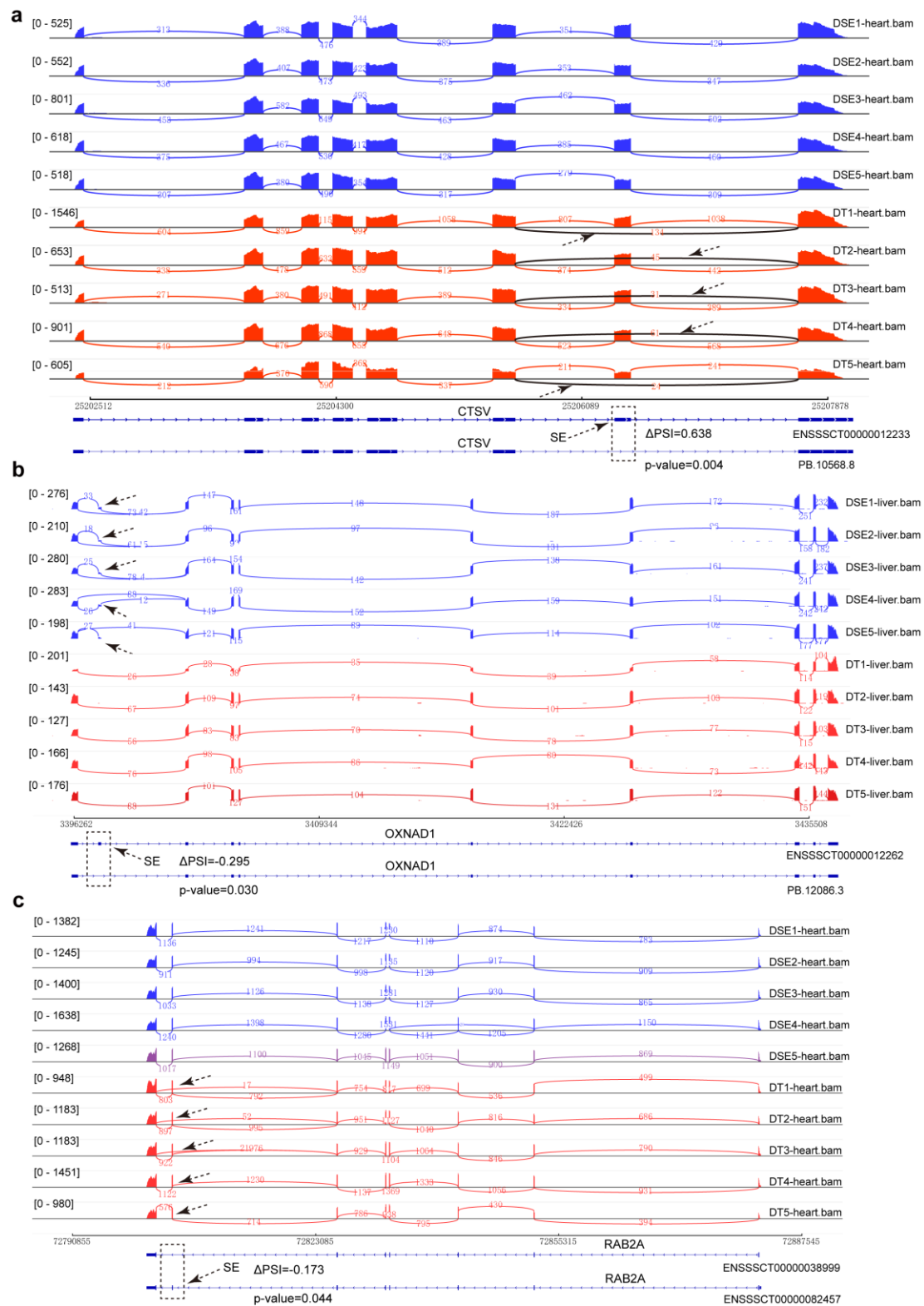
Supplementary Fig. 9|Distribution of differentially alternative splicing (DAS) events between Diannan small-ear pigs (DSE) and Diqing Tibetan pigs (DT) among five visceral tissues.



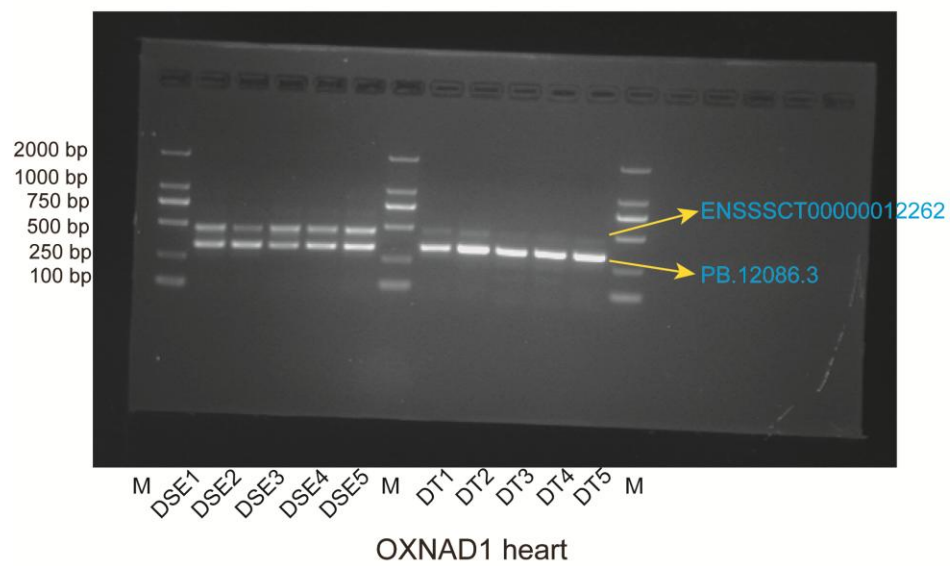
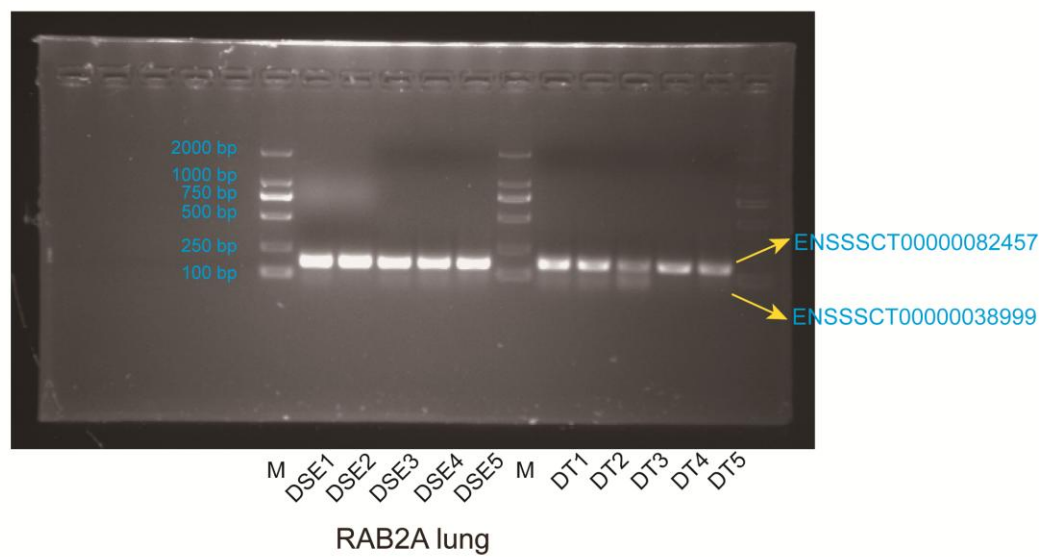
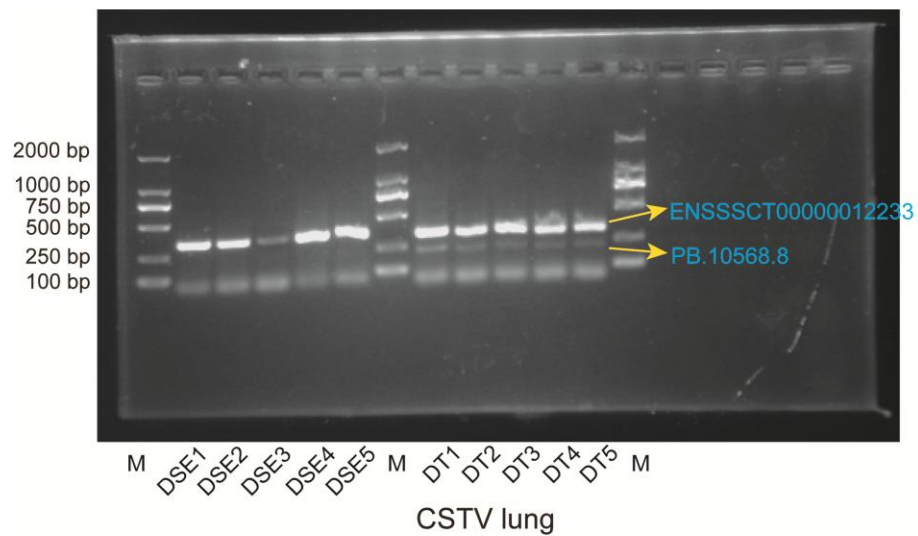
Supplementary Fig. 10|Significantly enriched top 15 GO terms of differentially alternative splicing (DAS) genes ($p_{\text{adj}} < 0.01$) between Diannan small-ear pigs (DSE) and Diqing Tibetan pigs (DT) among five visceral tissues.



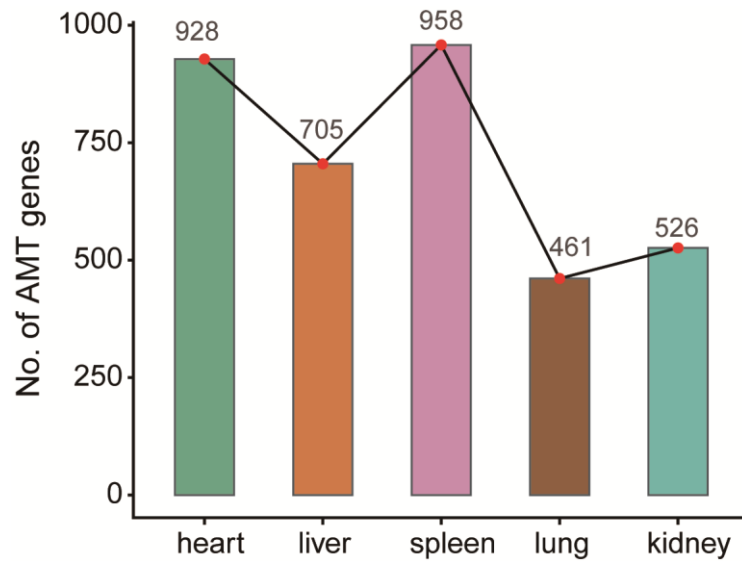
Supplementary Fig. 11 | Significantly enriched top 20 KEGG pathways of differentially alternative splicing (DAS) genes ($p.adj < 0.01$) between Diannan small-ear pigs (DSE) and Diqing Tibetan pigs (DT) among five visceral tissues.



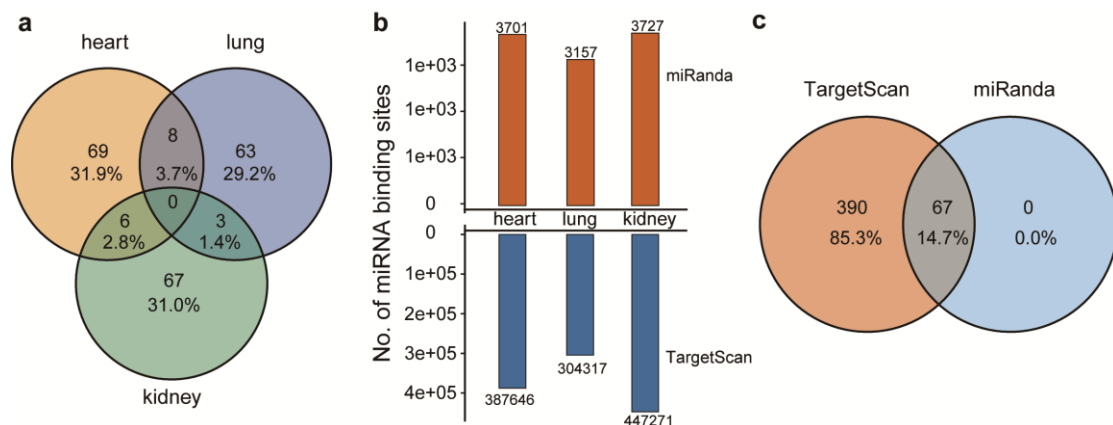
Supplementary Fig. 12 IGV sashimi plots show the transcript structure of three differentially alternative splicing (DAS) genes. **a** Exon usage difference of *CTSV*. **b** Exon usage difference of *OXNAD1*. **c** Exon usage difference of *RAB2A*.



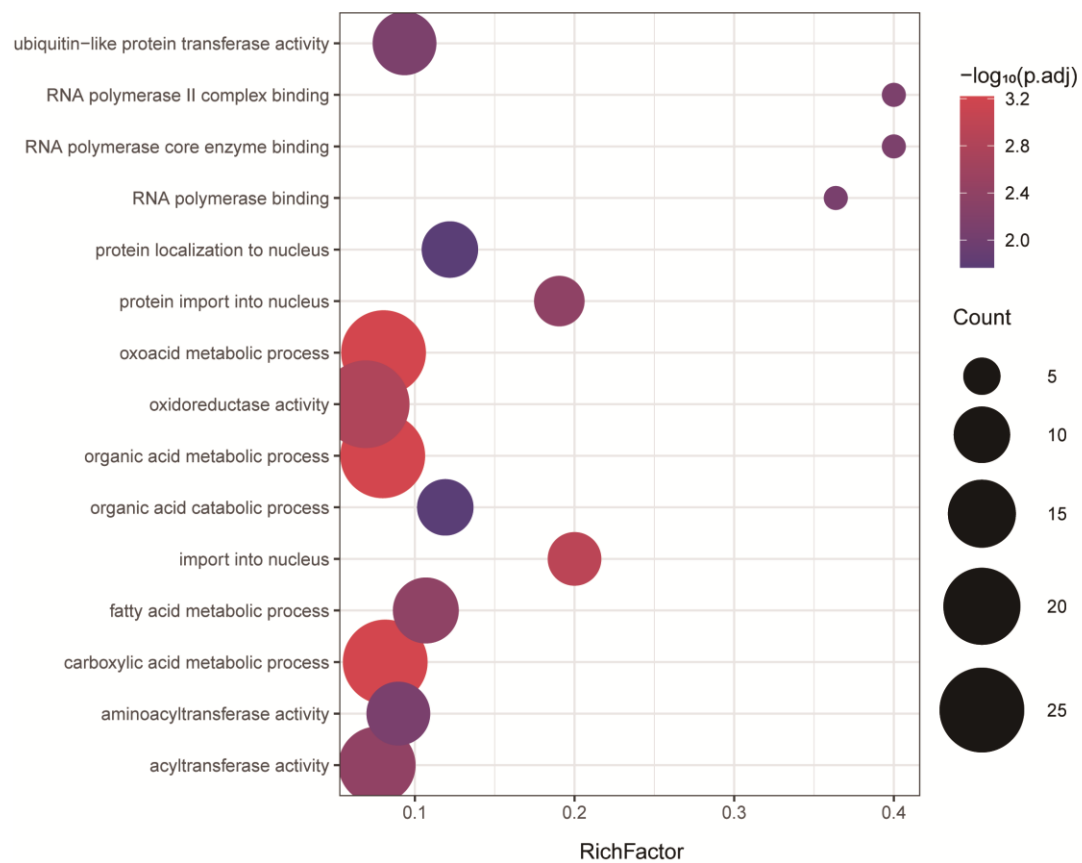
Supplementary Fig. 13 | Uncropped and unedited gel images of **Fig. 5f**.



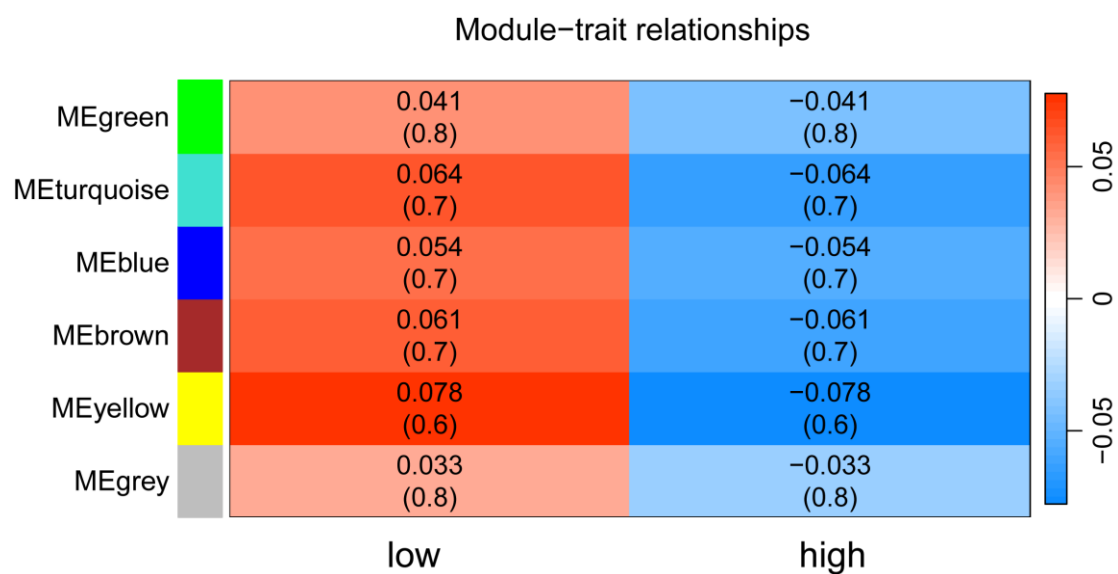
Supplementary Fig. 14 | Number of gene with alternative major transcript (AMT) between Diannan small-ear pigs (DSE) and Diqing Tibetan pigs (DT) among five visceral tissues.



Supplementary Fig. 15 | **a** Venn diagram of distal polyadenylation site usage genes (Dgene) in heart, lung, kidney of Diqing Tibetan pigs (DT), which correspond to genes exhibiting proximal polyadenylation site usage (Pgene) in Diannan small-ear pigs (DSE). **b** The number of miRNA binding sites enriched in the extended 3'UTR of the distal polyadenylation site usage genes (Dgene) in heart, lung, kidney of DT, as predicted by TargetScan and miRanda. **c** Venn diagram of unique miRNA predicted by TargetScan and miRanda.



Supplementary Fig. 16 Top 10 GO terms enriched by the proximal polyadenylation site usage genes (Pgene) in liver of Diqing Tibetan pigs (DT).



Supplementary Fig. 17 Module-trait relationship heatmap showing that the yellow module exhibited the strongest correlation with altitude.