

Appendix A Secondary classification histogram of GO enrichment analysis.

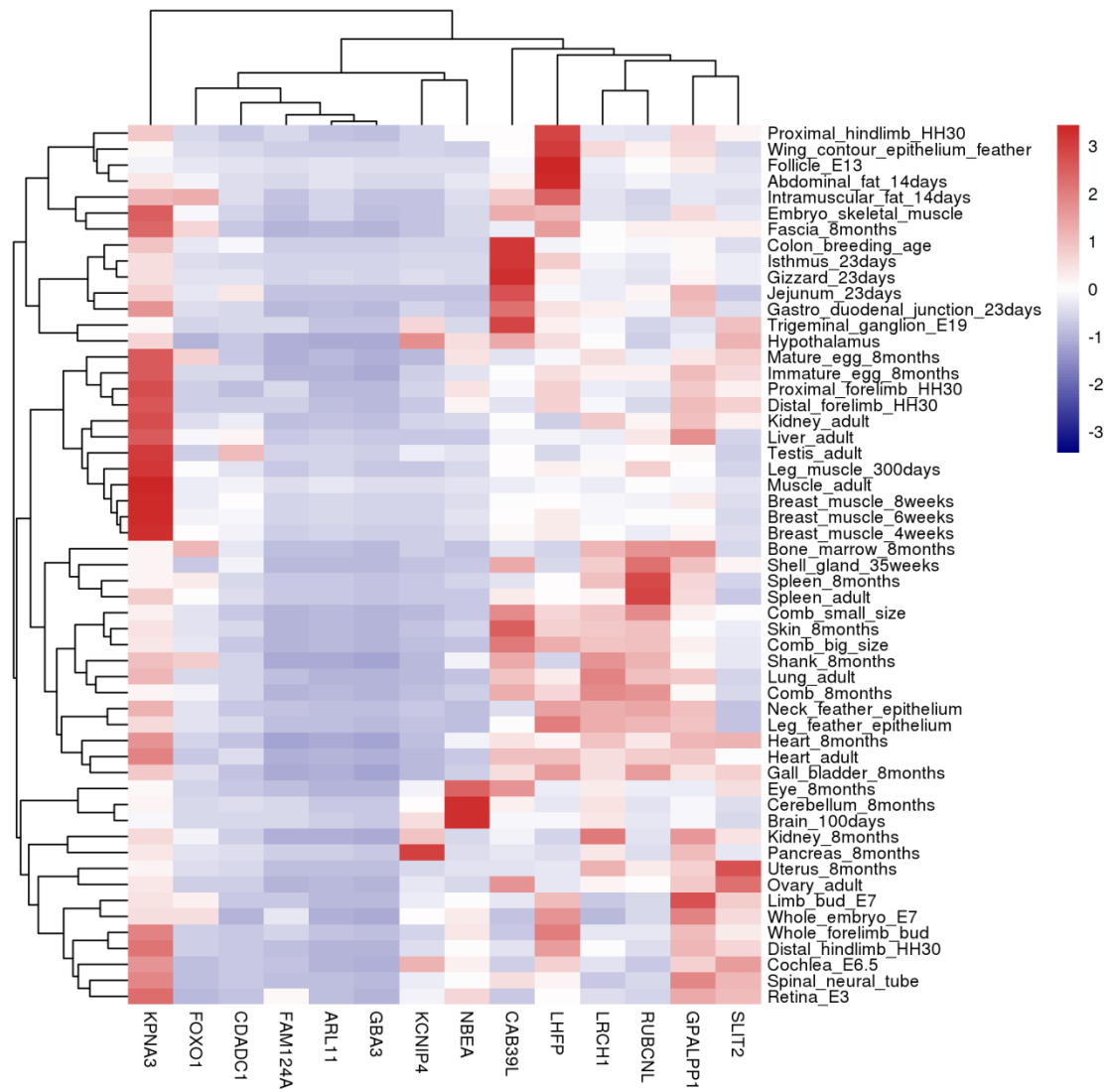
Appendix B Overlaps between the detected quantitative trait locus (QTL) herein, and published QTL for meat production traits in chickens based on GG 5.0 reference genome

G	Gene	Genomic position(bp) ¹⁾	Associate d trait	Known QTL (associated trait) ²⁾
GA				
1	<i>FAM</i>	170,018,259-170,05	PMW	QTL#16821
	<i>124A</i>	7,249	TMW ³⁾	
1	<i>FOX</i>	170,581,723-170,64	PMW	QTL#16826;16827
	<i>O1</i>	4,999	TMW	
1	<i>KPN</i>	169,278,602-169,33	PMW	QTL#16810
	<i>A3</i>	1,685		
4	<i>KCN</i>	75,415,551-75,452,3	TMW	QTL# 126583
	<i>IP4</i>	71		
4	<i>SLIT</i>	75,487,239-75,767,4	TMW	QTL# 126583
	<i>2</i>	55		

¹⁾ Genomic positions based on Gallus_gallus-5.0 assembly (NCBI)

²⁾ Chicken QTL db ID numbers database–release 44

³⁾ PMW: pectoral muscle weight; TMW: thigh muscle weight



Appendix C Gene expression of chicken tissues (from 259 samples) at different developmental stages in Animal Omics.