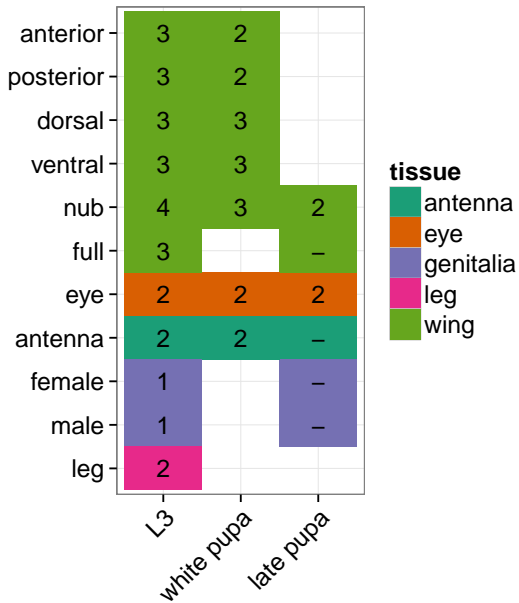
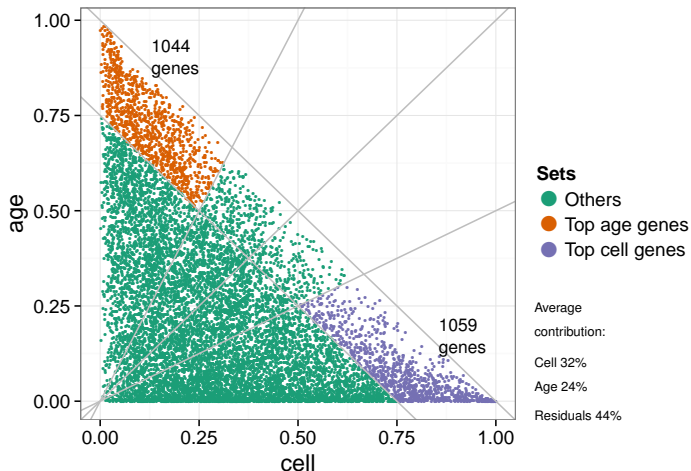


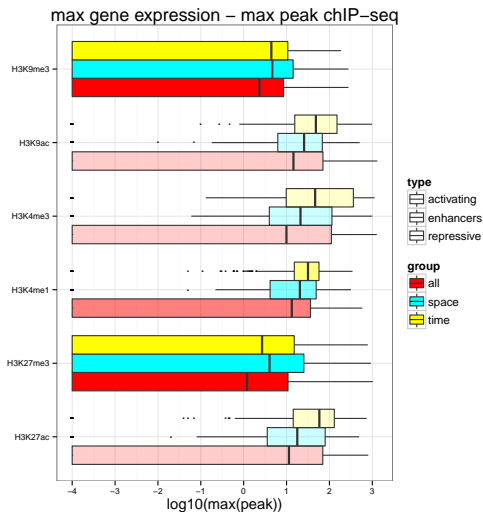
Overview of processed RNA-seq samples



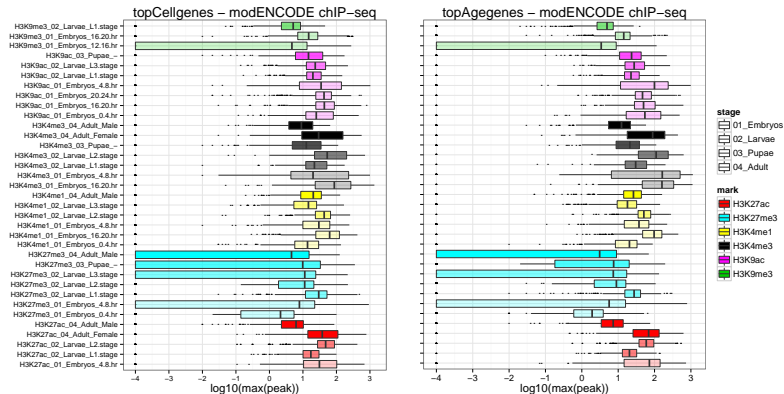
Decomposing the variation of gene expression across time and space



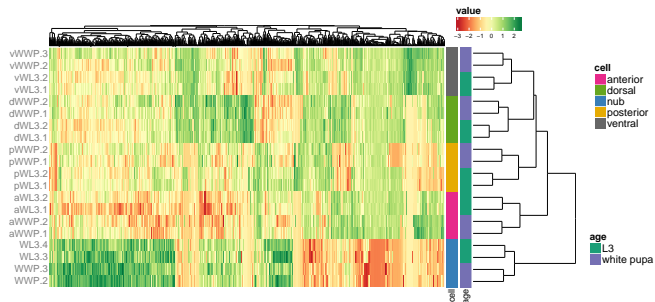
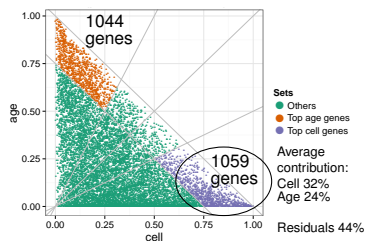
The highest peak (measured as the log10 of the signal profiles reported by modENCODE) within the gene body at the time point which the expression is maximum



The highest peak (measured as the log₁₀ of the signal profiles reported by modENCODE) within the gene body

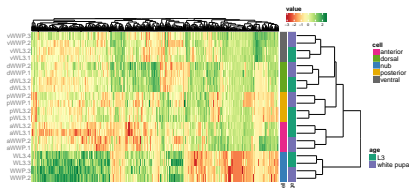


Gene sets with high variation across space



Decomposing the variation of gene expression across space

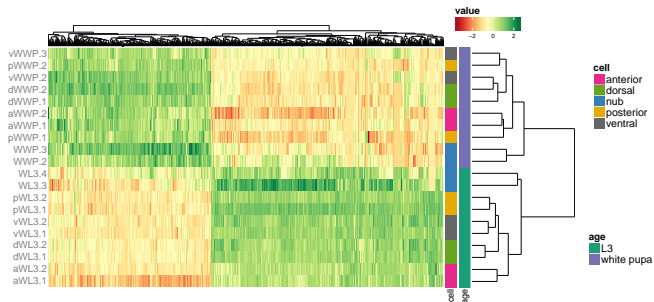
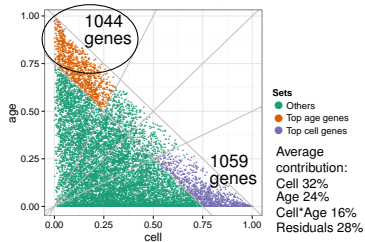
topCellGenes = 608 genes



Pvalue	Term
2.32846460522083e-06	Oxidative phosphorylation
2.51047792269406e-05	Proteasome

Pvalue	Term
1e-11	morphogenesis of an epithelium
7e-10	digestive system development
2e-09	appendage morphogenesis
5e-09	imaginal disc-derived appendage development
8e-09	post-embryonic organ development
2e-08	antennal development
2e-08	instar larval or pupal development
4e-08	renal system development
4e-08	tube morphogenesis
Pvalue	Term
5e-07	respiratory chain
8e-07	proteasome complex
2e-06	mitochondrial respiratory chain complex I
2e-06	NADH dehydrogenase complex
7e-06	mitochondrial inner membrane
3e-05	proteasome core complex, alpha-subunit complex
Pvalue	Term
2e-11	sequence-specific DNA binding transcription factor activity
1e-07	oxidoreductase activity
4e-06	threonine-type endopeptidase activity
6e-06	sequence-specific DNA binding
7e-06	glutathione transferase activity
1e-05	RNA polymerase II distal enhancer sequence-specific DNA binding transcription factor activity
1e-05	NADH dehydrogenase activity

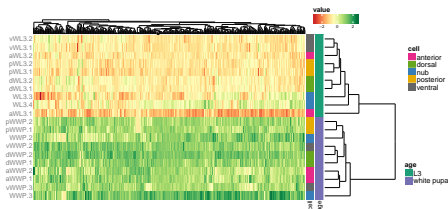
Gene sets with high variation across time



Variance decomposition

topAgeGenes = 395 genes, cluster 1 = 435

genes

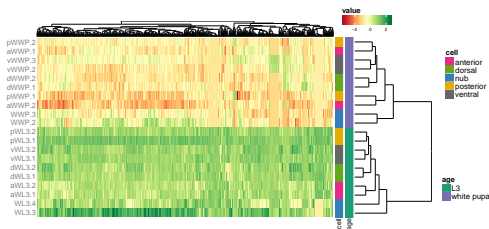


Pvalue	Term - Cluster1
1.00401087099388e-09	Protein export
2.43046134848088e-09	Protein processing in endoplasmic reticulum

Pvalue	Term - Cluster1
1e-11	morphogenesis of an epithelium
7e-10	digestive system development
2e-09	appendage morphogenesis
5e-09	imaginal disc-derived appendage development
8e-09	post-embryonic organ development
2e-08	antennal development
2e-08	instar larval or pupal development
4e-08	renal system development
4e-08	tube morphogenesis
Pvalue	Term - Cluster1
5e-07	respiratory chain
8e-07	proteasome complex
2e-06	mitochondrial respiratory chain complex I
2e-06	NADH dehydrogenase complex
7e-06	mitochondrial inner membrane
3e-05	proteasome core complex, alpha-subunit complex
Pvalue	Term - Cluster1
2e-11	sequence-specific DNA binding transcription factor activity
1e-07	oxidoreductase activity
4e-06	threonine-type endopeptidase activity
6e-06	sequence-specific DNA binding
7e-06	glutathione transferase activity
1e-05	RNA polymerase II distal enhancer sequence-specific DNA binding transcription factor activity
1e-05	NADH dehydrogenase activity

Variance decomposition

topAgeGenes = 395 genes, cluster 2 = 624 genes



Pvalue	Term - Cluster2
4.12201666158476e-21	DNA replication
7.50087633662912e-12	Mismatch repair
8.1618297773066e-08	Nucleotide excision repair
1.66795771880413e-06	Ribosome biogenesis in eukaryotes
7.98022928115518e-05	Pyrimidine metabolism

Pvalue	Term - Cluster2
1e-11	morphogenesis of an epithelium
7e-10	digestive system development
2e-09	appendage morphogenesis
5e-09	imaginal disc-derived appendage development
8e-09	post-embryonic organ development
2e-08	antennal development
2e-08	instar larval or pupal development
4e-08	renal system development
4e-08	tube morphogenesis
Pvalue	Term - Cluster2
5e-07	respiratory chain
8e-07	proteasome complex
2e-06	mitochondrial respiratory chain complex I
2e-06	NADH dehydrogenase complex
7e-06	mitochondrial inner membrane
3e-05	proteasome core complex, alpha-subunit complex
Pvalue	Term - Cluster2
2e-11	sequence-specific DNA binding transcription factor activity
1e-07	oxidoreductase activity
4e-06	threonine-type endopeptidase activity
6e-06	sequence-specific DNA binding
7e-06	glutathione transferase activity
1e-05	RNA polymerase II distal enhancer sequence-specific DNA binding transcription factor activity
1e-05	NADH dehydrogenase activity