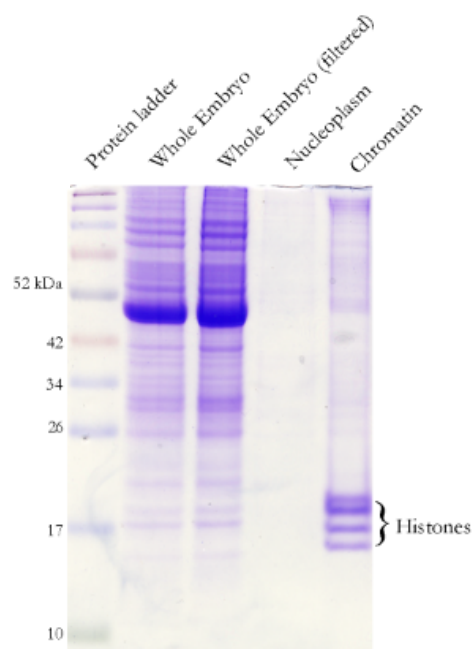
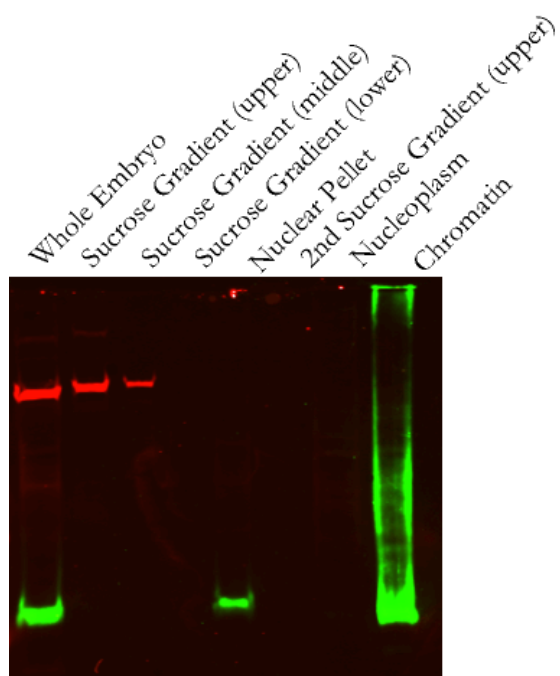


A

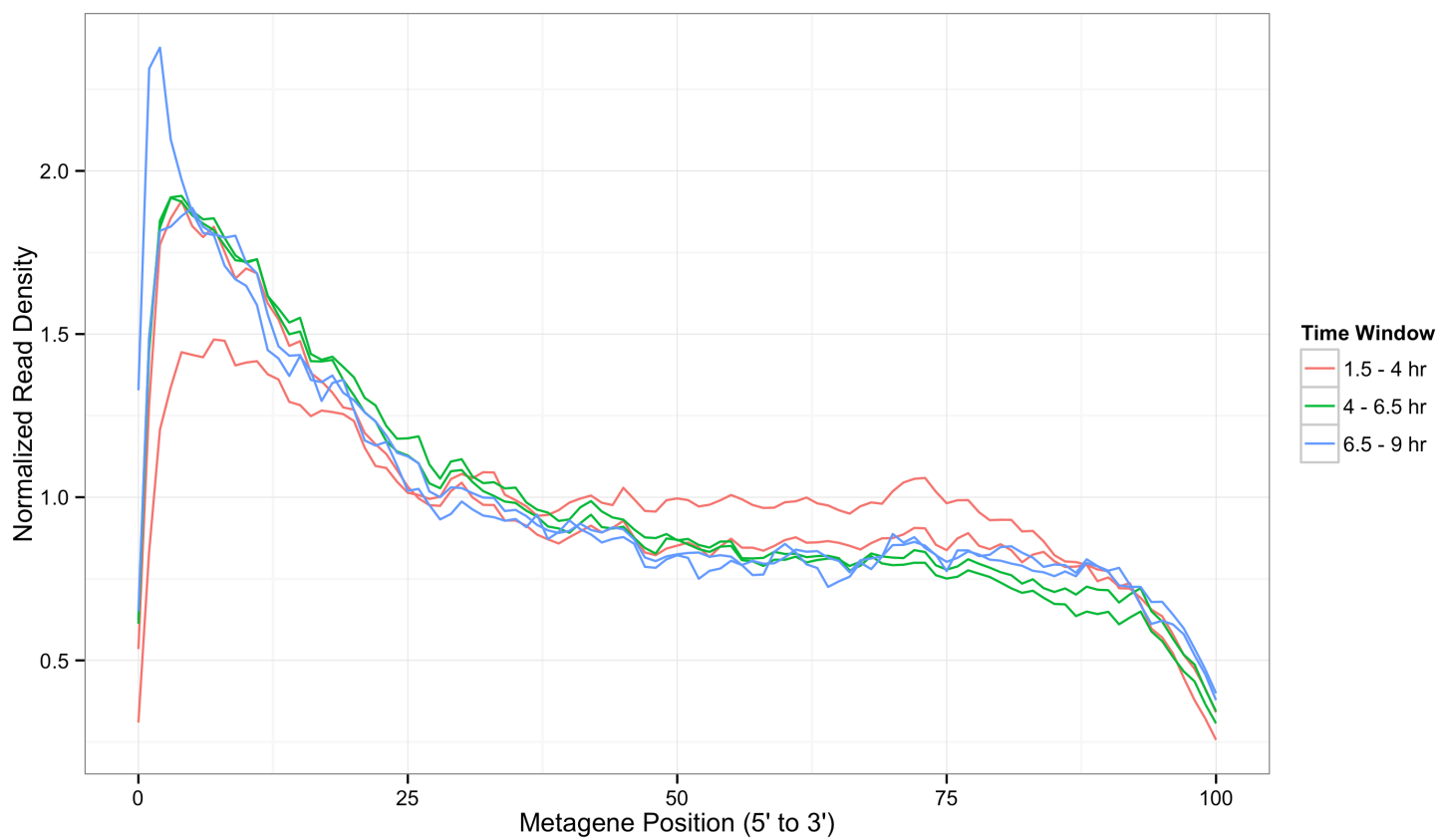


B

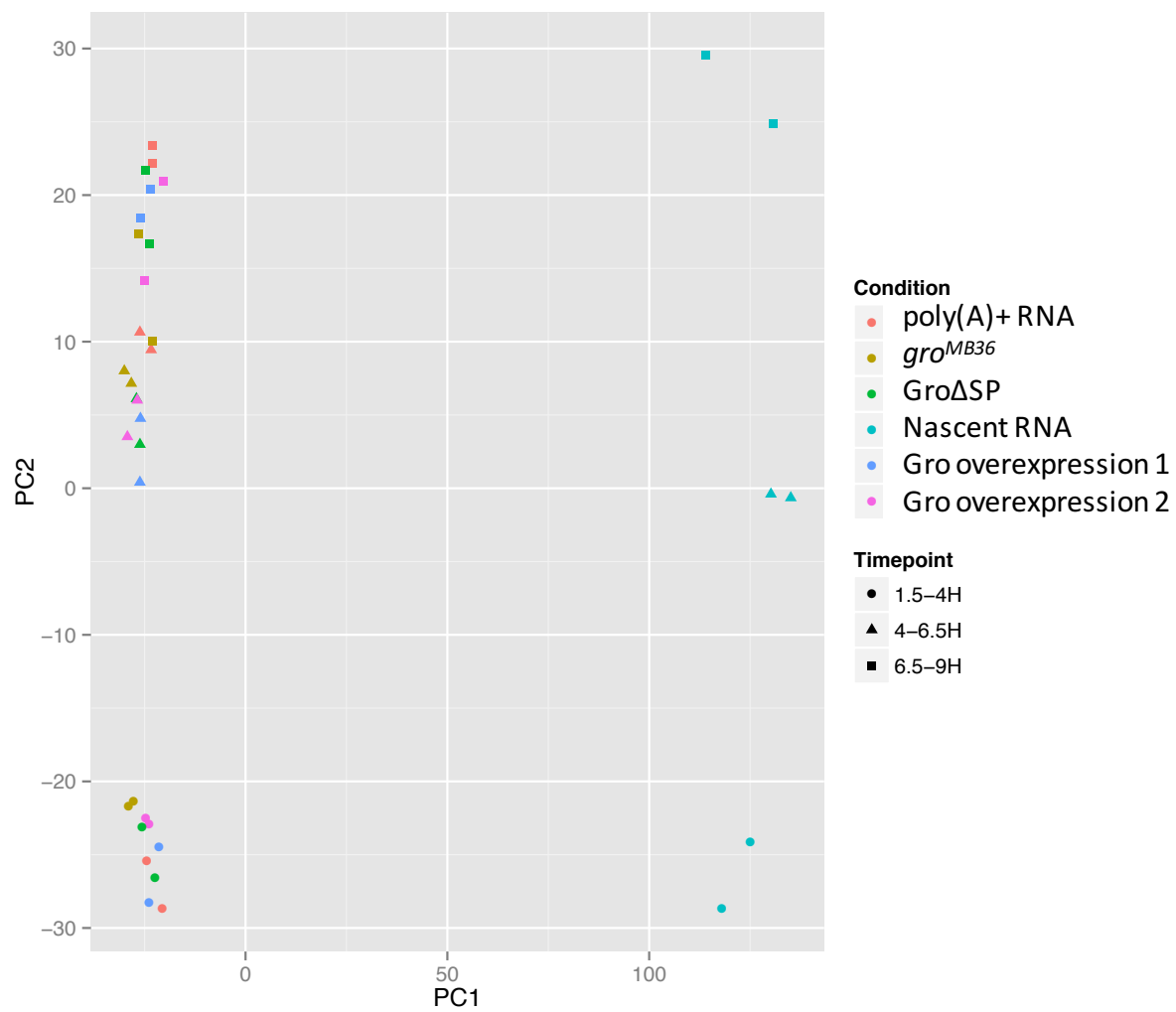


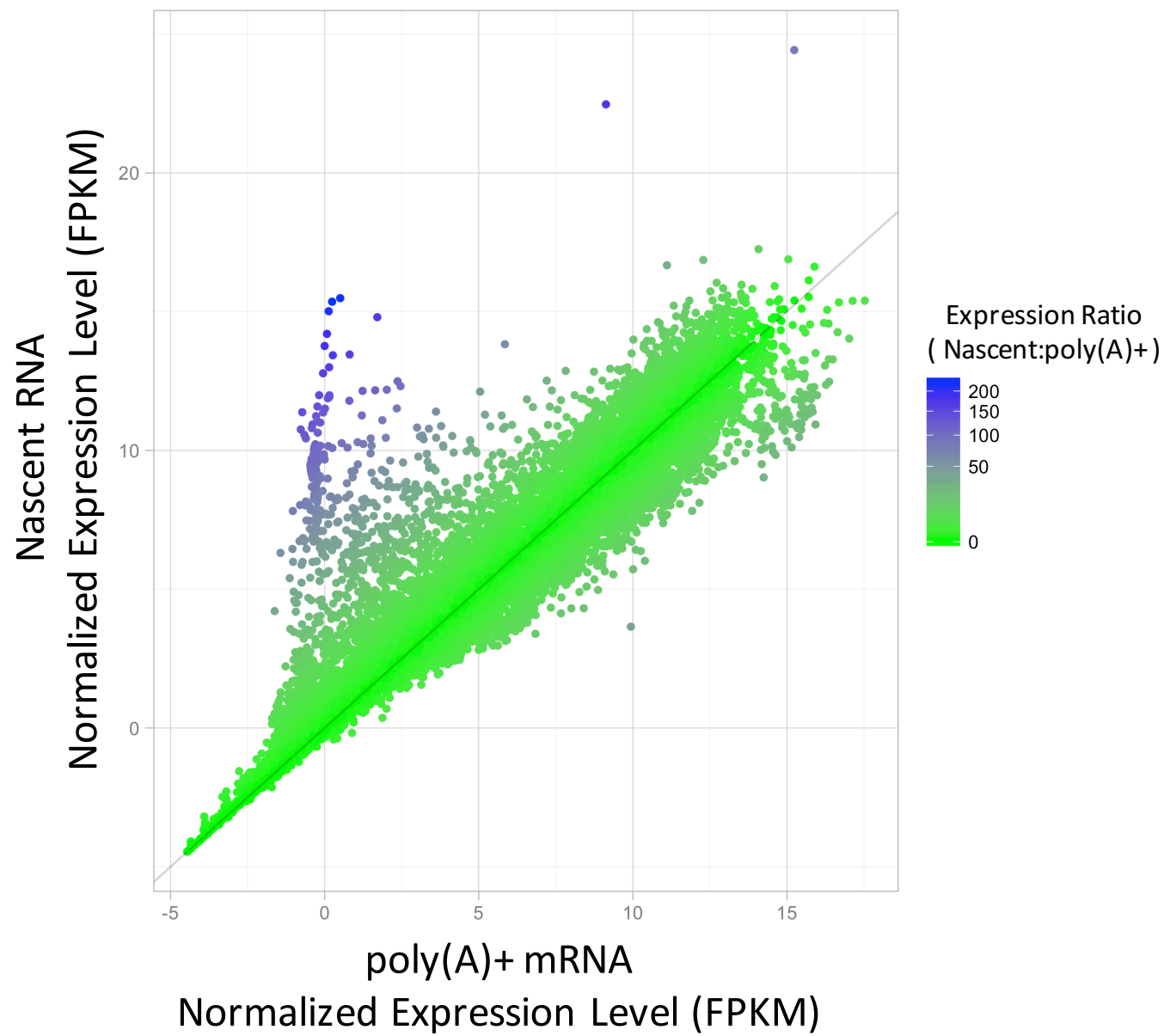
$\alpha$ -tubulin

$\alpha$ -H3



Condition	Time window	Total Reads	Transcript Reads	%	Exon Reads	%	Intron Reads	%	5'UTR Reads	%	3'UTR Reads	%
Nascent	1.5 - 4 hr	13,396,998	12,869,419	96%	9,630,349	72%	3,991,330	30%	827,902	6%	717,773	5%
Nascent	1.5 - 4 hr	14,402,702	14,074,143	98%	13,143,526	91%	1,256,036	9%	384,863	3%	405,031	3%
Nascent	4 - 6.5 hr	19,102,357	18,102,323	95%	10,249,092	54%	9,274,889	49%	1,495,488	8%	1,038,051	5%
Nascent	4 - 6.5 hr	15,913,811	15,082,718	95%	8,935,177	56%	7,285,111	46%	1,198,370	8%	883,736	6%
Nascent	6.5 - 9 hr	15,747,237	15,201,712	97%	10,200,282	65%	5,976,815	38%	1,035,707	7%	853,559	5%
Nascent	6.5 - 9 hr	13,952,494	13,493,631	97%	8,784,412	63%	5,694,037	41%	1,117,133	8%	897,345	6%
poly(A) RNA	1.5 - 4 hr	23,796,734	20,604,743	87%	19,752,186	83%	2,168,260	9%	975,884	4%	3,986,880	17%
poly(A) RNA	1.5 - 4 hr	38,083,224	30,341,487	80%	27,976,746	73%	4,214,078	11%	1,392,513	4%	5,761,724	15%
poly(A) RNA	4 - 6.5 hr	37,870,358	32,424,416	86%	28,651,441	76%	5,631,405	15%	1,385,828	4%	6,037,661	16%
poly(A) RNA	4 - 6.5 hr	36,076,928	29,887,172	83%	26,704,160	74%	4,787,606	13%	1,198,679	3%	5,352,807	15%
poly(A) RNA	6.5 - 9 hr	30,597,716	26,509,005	87%	24,452,990	80%	3,777,231	12%	1,258,219	4%	5,190,917	17%
poly(A) RNA	6.5 - 9 hr	26,551,585	23,282,466	88%	20,952,590	79%	3,886,388	15%	1,196,059	5%	4,597,938	17%





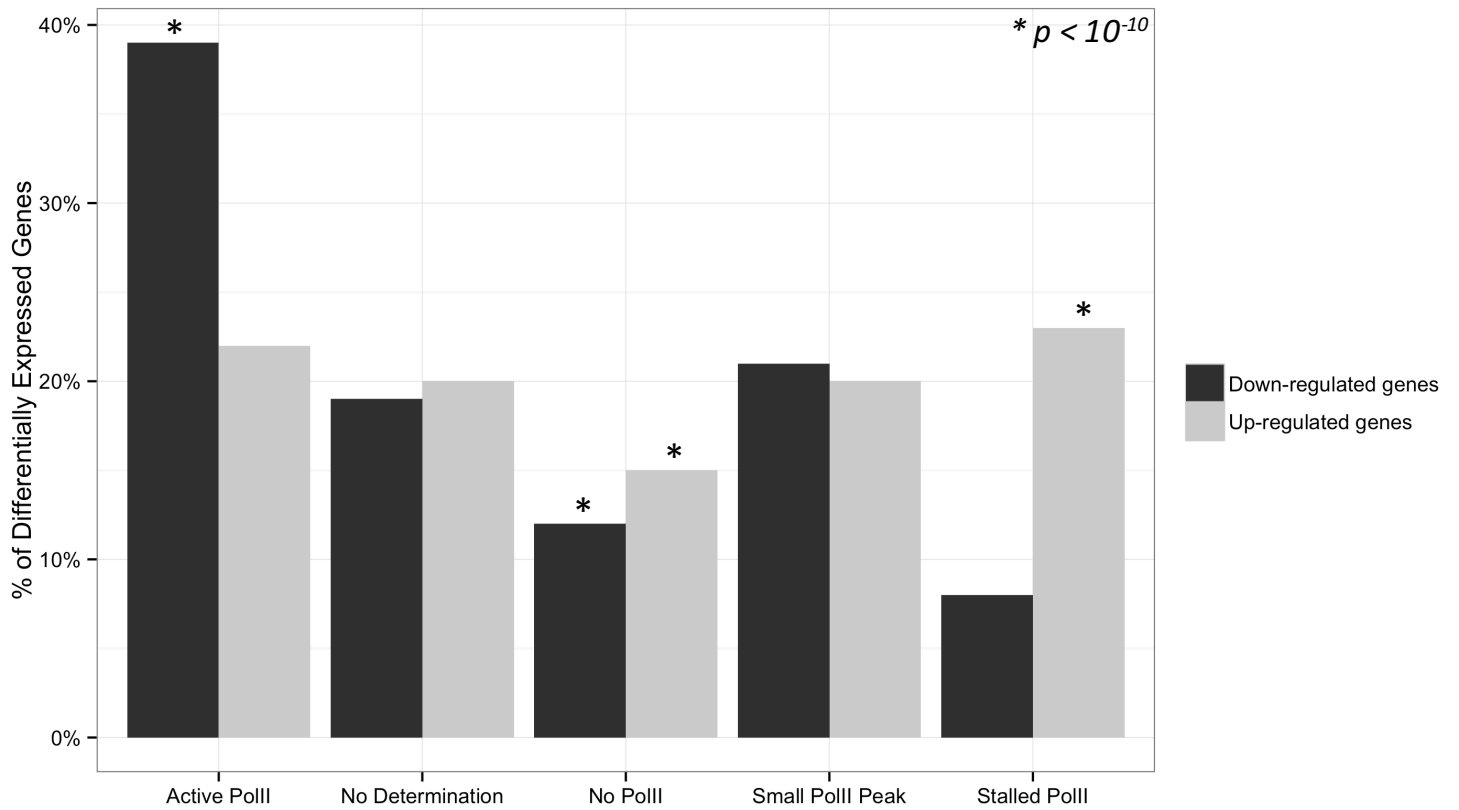
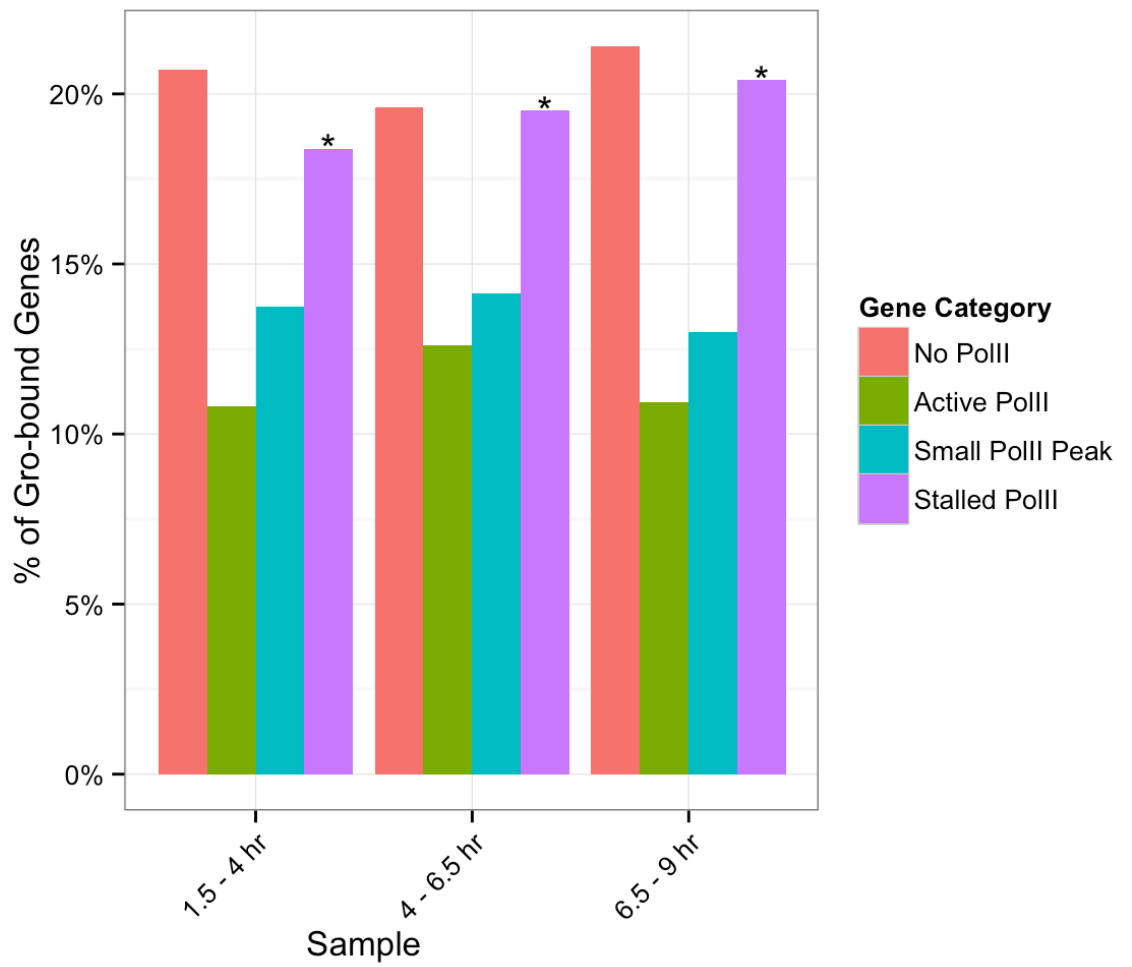
A

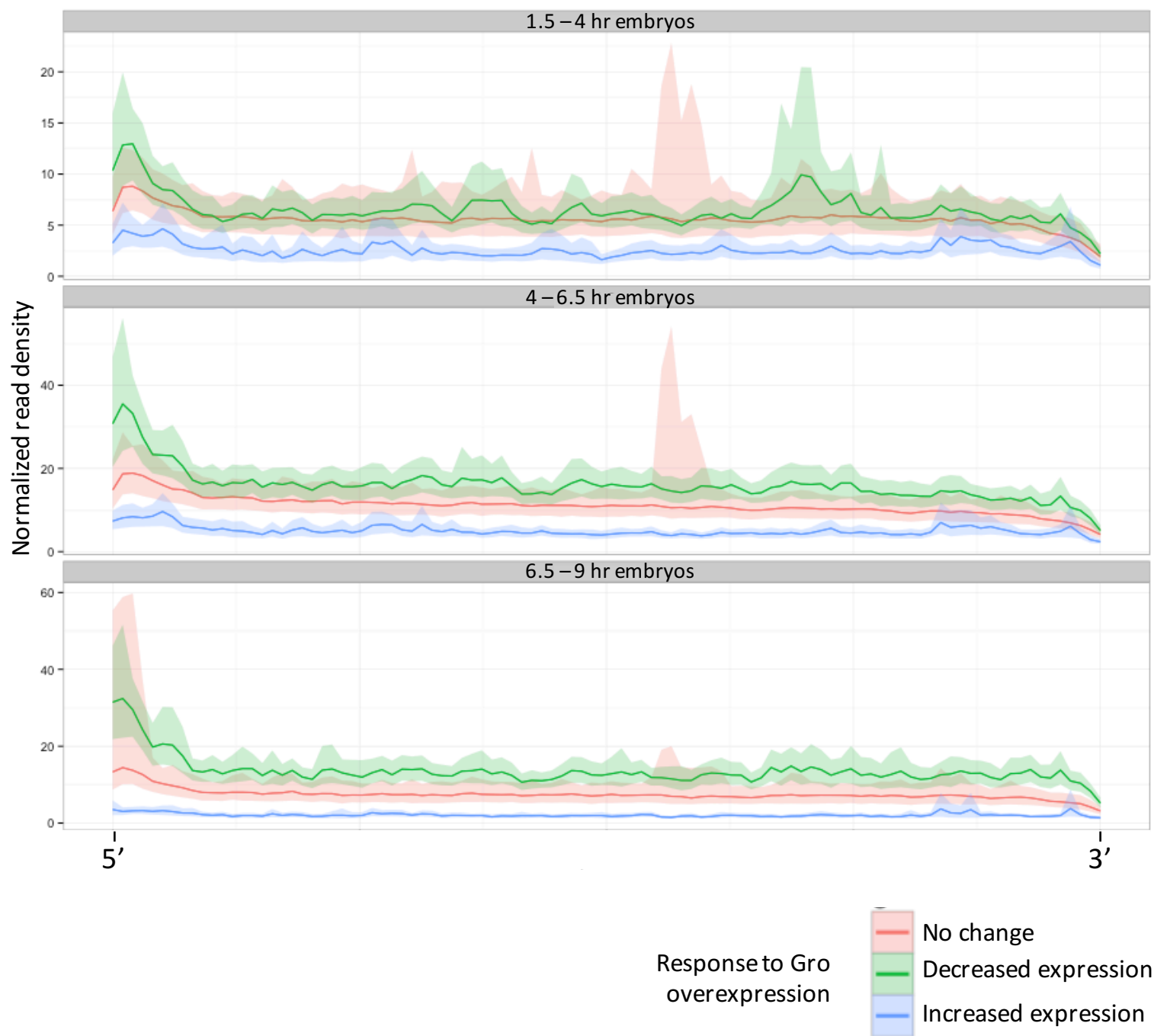
	Relative nascent transcript abundance	
	Lower	Higher
1.5 - 4 hr	2,831	3,097
4 - 6.5 hr	3,200	3,735
6.5 - 9 hr	2,910	3,187

B

BDGP Term Enrichment	p-value	# genes
maternal	3.09E-86	1541
ubiquitous	7.16E-45	847
anterior midgut primordium	6.21E-29	505
posterior midgut primordium	2.40E-26	514
trunk mesoderm primordium	1.80E-20	411
anterior endoderm primordium	3.51E-15	292
embryonic midgut	5.09E-15	587
posterior endoderm primordium	5.20E-14	299
dorsal prothoracic pharyngeal muscle	1.13E-12	220
head mesoderm primordium P2	1.76E-09	253
embryonic/larval muscle system	3.69E-09	277
head mesoderm primordium	8.15E-09	153
posterior endoderm primordium P2	2.19E-08	218
anterior endoderm anlage	6.20E-08	205
faint ubiquitous	1.26E-07	437

BDGP Term Enrichment	p-value	# genes
ventral nerve cord	1.19E-24	452
ventral epidermis primordium	5.92E-24	159
dorsal ectoderm primordium	9.17E-23	152
dorsal ectoderm anlage in statu nascendi	3.07E-22	137
ventral ectoderm anlage in statu nascendi	1.25E-20	125
embryonic brain	1.14E-19	431
dorsal epidermis primordium	2.17E-19	167
procephalic ectoderm anlage in statu nascendi	5.27E-19	123
ventral ectoderm primordium P2	2.40E-18	169
ventral ectoderm primordium	7.18E-17	139
gap	6.36E-13	56
embryonic ventral epidermis	1.43E-12	245
procephalic ectoderm anlage	1.44E-12	140
embryonic dorsal epidermis	2.56E-12	266
tracheal primordium	7.27E-12	90







Target	Sequence
2s	CTTACAACCCTCAACCATATGTAGTCCAAGCAGC
18s	CAATAATGATCCTTCCGCAGGTT
5.8s	CAGCATGGACTGCGATATGCGTTC
28s alpha	ATTTTCGCTTTCGCCTTGAAC
28s Beta	TCGAATCATCAAGCAAAGGATAAGC
28s	GTGTTAATTAGCTATAAATAGCTAAAAAACTAATC
28s	CAGGTTACGGAATTGGAACCGTATTCCCTTTCGTT
28s	CAATCTTCAGAGCCAATCCTTATCCCGAAGTTACG
28s	GCCCGTTCCTTGGCTGTGGTTTCGCTAG
18s	GAACAGAGGTCTTATTTTATTATCCCATGCACAGA
18s	CGGTACAAGACCATACGATCTGCATGTTATCTAGA
18s	TTTAATTGCATGTATTAGCTCTAGAATTACCACAG
5s	AAGTTGTGGACGAGGCCAACACGCGGTGTTCCC
5'_end_of_rRNA	TATTCCTATTATCCGCGGAG
5'_end_of_rRNA	CCATTCTGAATACGGCCATT
nodavirus RNA1	ACCTCCGCCCTTTCGGGCTAGAAC
nodavirus RNA2	ACCTTAGTCGGCTGACTTAACTGTC
totivirus SW-2009a	CGACTATATCTTCTGCGTTATCCAGC
oligo dT	TTTTTTTTTTTTTT