

APPENDIX (Blank et al)

TABLE OF CONTENTS

ITEM	Pages
Appendix Table 1. Oligonucleotides	2-3
Appendix Table 2. <i>S. cerevisiae</i> strains	4
Appendix Table 3. 5'- and 3'ends of mRNAs under periodic translational control in the cell cycle	5-7
Appendix Figure 1. Acc1p-TAP levels drop as cells exit mitosis and re-enter a new cell cycle	8
Appendix Figure 2. The <i>ACC1</i> uORF is conserved in the indicated genomic regions of <i>sensu stricto Saccharomyces</i> species	9
Appendix Figure 3. Ribosome occupancy of the <i>ACC1</i> uORF in the cell cycle	10
Appendix File 1. Composite file of all sequencing data for the 17 mRNAs under periodic translational control. This file contains the following information: 1) File names of the 48 libraries analyzed in this study. 2) The Coverage of the Ribosome Profile (RP) and Transcriptional Profile (TP--RNAseq) reads detected mapping to the annotated CDS of each mRNAs in question and for each cell size point analyzed. 3) The combined length distribution of the Ribosome Profile footprints (RP-footprints) we observed in the CDS corresponding to each locus in question. In every case we included a similar analysis of the original ribosome profiling data from Ingolia (Ingolia et al., 2009), as controls.	11-47

Appendix Table 1. Oligonucleotides

NAME	SEQUENCE	USE
miRNA linker	/5rApp/CTGTAGGCACCATCAAT/3ddC/	Ribosome footprint libraries
RT primer-RiboSeq	/5Phos/AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTA GATCTCGGTGGTCGC/iSp18/CACTCA/iSp18/TTCAGACGTG TGCTCTCCGATCTATTGATGGTGCCTACAG	Ribosome footprint libraries
rRNAsub-1	/5BiotinTEG/CAGGATCGGTCGATTGTGCACCTCTT	rRNA depletion
rRNAsub-2	/5BiotinTEG/CCGCTTCATTGAATAAGTAAAGAACTA	rRNA depletion
rRNAsub-3	/5BiotinTEG/GACGCCTTATTCGTATCCATCTATATT	rRNA depletion
FWD-library-PCR	AATGATACGGCGACCACCGAGATCTACAC	Ribosome footprint libraries
INDEXED-1-REV	CAAGCAGAAGACGGCATAACGAGATAGTCGTGTGACTGGAGT TCAGACGTGTGCTCTTCCG	Ribosome footprint libraries
INDEXED-2-REV	CAAGCAGAAGACGGCATAACGAGATACTGATGTGACTGGAGT TCAGACGTGTGCTCTTCCG	Ribosome footprint libraries
INDEXED-3-REV	CAAGCAGAAGACGGCATAACGAGATATGCTGGTACTGGAGT TCAGACGTGTGCTCTTCCG	Ribosome footprint libraries
INDEXED-4-REV	CAAGCAGAAGACGGCATAACGAGATACGTCGGTACTGGAGT TCAGACGTGTGCTCTTCCG	Ribosome footprint libraries
INDEXED-5-REV	CAAGCAGAAGACGGCATAACGAGATAGCTGCGTACTGGAGT TCAGACGTGTGCTCTTCCG	Ribosome footprint libraries
INDEXED-6-REV	CAAGCAGAAGACGGCATAACGAGATATCGTAGTACTGGAGT	Ribosome footprint

	TCAGACGTGTGCTCTTCCG	libraries
INDEXED-7-REV	CAAGCAGAAGACGGCATAACGAGATCGTCAGGTGACTGGAGT TCAGACGTGTGCTCTTCCG	Ribosome footprint libraries
INDEXED-8-REV	CAAGCAGAAGACGGCATAACGAGATCGTAGCGTGACTGGAGT TCAGACGTGTGCTCTTCCG	Ribosome footprint libraries
XIV662193-F1	GCCCCATATGCGTTGACGTTATCCAAAGGGGAATGCTTCATC TTGTTGAACGGATCCCCGGGTTAATTAA	Strain construction
XIV662093-R1	GATTTTAAACGGGCGCAACGATTCGGTGGGCAGTGGAATTG TTGGGCGTTGAATTCGAGCTCGTTTAAAC	Strain construction
XIV662374-FWD	GCGCATGCATCGACGTCAC	Strain construction
XIV661899-FWD	CGGTTCTACAATTGTTCTGCT	Strain construction
XIV661552-REV	GTGGAGAAGAAAAGGGAAG	Strain construction
ACC1-(TG-340A)- REV	GGGCAGAGGGAAAAGTTCGTATAGTAGAATGAATAAACTTT TATAAACATTTGCACCGATCACTCACAGAG	Strain construction
ACC1-CTAP-FWD	CTGAAGTTATCAAGATGTTATCTACCGATGATAAAGAAAAT TGTTGAAGACTTTGAAATCCATGGAAAAGAGAAG	Strain construction
ACC1-CTAP-REV	TTATATTAGCAACTAAATTAATTACATCAATACTATTTTTTTT TTTTACTTTACAAGGTTACGACTCACTATAGGG	Strain construction
ACC1(+2)-FWD	TGAGCGAAGAAAGCTTATTCG	RNA surveillance
ACC1(+495)-REV	CTGGGACAATTTTTAGGCA	RNA surveillance
PGK1-FWD	AACGGTGAAAGAAACGAAAAA	RNA surveillance
PGK1-REV	TCCAAAACCTTCTGAAGGTG	RNA surveillance

Appendix Table 2. *S. cerevisiae* strains

NAME	GENOTYPE	SOURCE	FIGURE USED IN
BY4743	<i>MATa/α, his3Δ1/his3Δ1, leu2Δ0/leu2Δ0, LYS2/lys2Δ0, met15Δ0/MET15, ura3Δ0/ura3Δ0</i>	Yeast Deletion Project	1; EV1; Appendix Figures 3-20
BY4741	<i>MATα, his3Δ1, leu2Δ0, ura3Δ0, met15Δ0</i>	Yeast Deletion Project	7
YL01	<i>ChrXIV:662143::kanMX6</i> (BY4741 otherwise)	This study	6; 7
SCMSP232	<i>ChrXIV:662143::kanMX6, (TG-340→AA)-ACC1/+</i> (BY4743 otherwise)	This study	N/A
SCMSP233-C	<i>ChrXIV:662143::kanMX6, (TG-340→AA)-ACC1</i> (<i>MATa</i> segregant of SCMSP232)	This study	6; 7
SCMSP234	<i>ACC1-TAP::URA3</i> (YL01 otherwise)	This study	4A; 5C,D; EV2A; EV3; EV4; Appendix Fig. 1
SCMSP236	<i>ACC1-TAP::URA3</i> (SCMSP233-C otherwise)	This study	5B,C,D; EV2B; EV3; EV4
YSC1178- 202232118	<i>FAS1-TAP::HIS3</i> (BY4741 otherwise)	GE Healthcare	4B
YSC1178- 202233787	<i>FAS2-TAP::HIS3</i> (BY4741 otherwise)	GE Healthcare	4C
JD186	<i>sch9::HIS3</i> (BY4742 otherwise)	Kennedy lab collection	7

Appendix Table 3. 5'- and 3'ends of mRNAs under periodic translational control in the cell cycle^a

Standard Name	Systematic Name	Chromosome Identifier	Strand	CDS Start Position	CDS End Position	Transcript Start Position	Transcript End Position	5'-leader length	3'-leader length	Reference	ΔG^b (5'leader+48)	%GC
<i>ACC1</i>	YNR016C	chrXIV	Crick	661374	654673	661909		535		(Kang, Lai et al., 2015)	-81.0	40.0
<i>DSK2</i>	YMR276W	chrXIII	Watson	818827	819948	818749	820057	78	109	(Kang et al., 2015)	-16.3	26.7
<i>DYN1</i>	YKR054C	chrXI	Crick	547925	535647							46.7
<i>FAS1</i>	YKL182W	chrXI	Watson	100671	106826							53.3
<i>FAS2</i>	YPL231W	chrXVI	Watson	108652	114315	108613		39		(Kang et al., 2015)	-14.5	53.3
<i>GAT2</i>	YMR136W	chrXIII	Watson	541199	542881	541101	542967	98	86	(Pelechano, Wei et al., 2013)	-16.3	53.3
<i>GCV3</i>	YAL044C	chrI	Crick	58462	57950	58486	57824	24	126	(Kang et al., 2015)	-6.2	40.0
<i>GND1</i>	YHR183W	chrVIII	Watson	470960	472429	470880	472553	80	124	(Kang et al., 2015, Nagalakshmi, Wang et al., 2008)	-19.8	46.7
<i>HHF1</i>	YBR009C	chrII	Crick	255684	255373	255728	255004	44	369	(Pelechano et al.,	-6.7	46.7

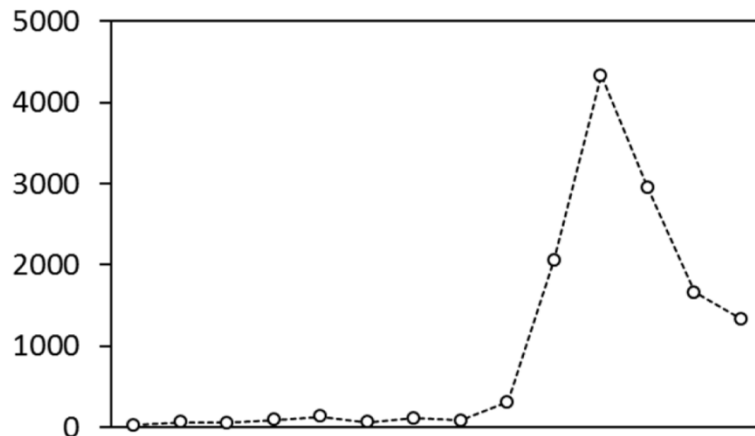
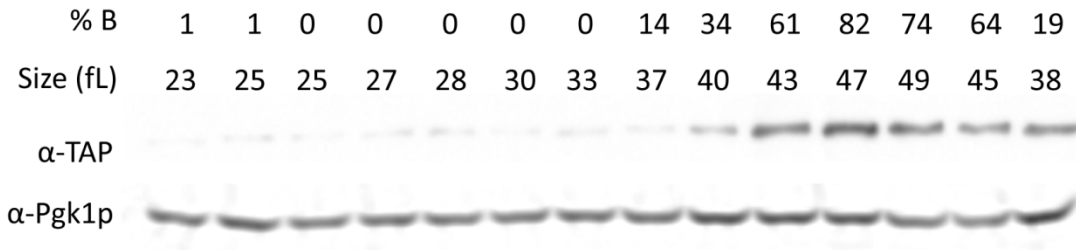
										2013)		
<i>MPS1</i>	YDL028C	chrIV	Crick	403291	400997	403424	400847	133	150	(Poch, Schwob et al., 1994)	-22.9	33.3
<i>MSC1</i>	YML128C	chrXIII	Crick	16676	15135	16800	14956	124	179	(Pelechano et al., 2013)	-28.5	33.3
<i>NQM1</i>	YGR043C	chrVII	Crick	581436	580435							46.7
<i>PCT1</i>	YGR202C	chrVII	Crick	904748	903474	904775	903345	27	129	(Kang et al., 2015)	-12.3	46.7
<i>RTN2</i>	YDL204W	chrIV	Watson	94605	95786	94107	95965	498	179	(Nagalakshmi et al., 2008, Zhang & Dietrich, 2005)	-128.1	33.3
<i>TIP1</i>	YBR067C	chrII	Crick	372735	372103	372972	371870	237	233	(Pelechano et al., 2013)	-49.0	40.0
<i>YRO2</i>	YBR054W	chrII	Watson	343101	344135	342781	344496	320	361	(Nagalakshmi et al., 2008, Zhang & Dietrich, 2005)	-42.4	26.7
	YKR018C	chrXI	Crick	475900	473723	475949	473546	49	177	(Pelechano et al., 2013)	-26.7	26.7

^aIf different isoforms for the indicated mRNA have been reported, we show the nucleotide positions that correspond to the longest mRNA isoforms at either end.

^aThe folding free energy change (ΔG) for the 5'-leader and the first 48 nucleotides of the mRNA was calculated with the RNAstructure 5.8 software package (Bellaousov, Reuter et al., 2013)..

References

- Bellaousov S, Reuter JS, Seetin MG, Mathews DH (2013) RNAstructure: Web servers for RNA secondary structure prediction and analysis. *Nucleic acids research* 41: W471-4
- Kang YN, Lai DP, Ooi HS, Shen TT, Kou Y, Tian J, Czajkowsky DM, Shao Z, Zhao X (2015) Genome-wide profiling of untranslated regions by paired-end ditag sequencing reveals unexpected transcriptome complexity in yeast. *Molecular genetics and genomics* : MGG 290: 217-24
- Nagalakshmi U, Wang Z, Waern K, Shou C, Raha D, Gerstein M, Snyder M (2008) The transcriptional landscape of the yeast genome defined by RNA sequencing. *Science* 320: 1344-9
- Pelechano V, Wei W, Steinmetz LM (2013) Extensive transcriptional heterogeneity revealed by isoform profiling. *Nature* 497: 127-31
- Poch O, Schwob E, de Fraipont F, Camasses A, Bordonne R, Martin RP (1994) RPK1, an essential yeast protein kinase involved in the regulation of the onset of mitosis, shows homology to mammalian dual-specificity kinases. *Molecular & general genetics* : MGG 243: 641-53
- Zhang Z, Dietrich FS (2005) Mapping of transcription start sites in *Saccharomyces cerevisiae* using 5' SAGE. *Nucleic acids research* 33: 2838-51

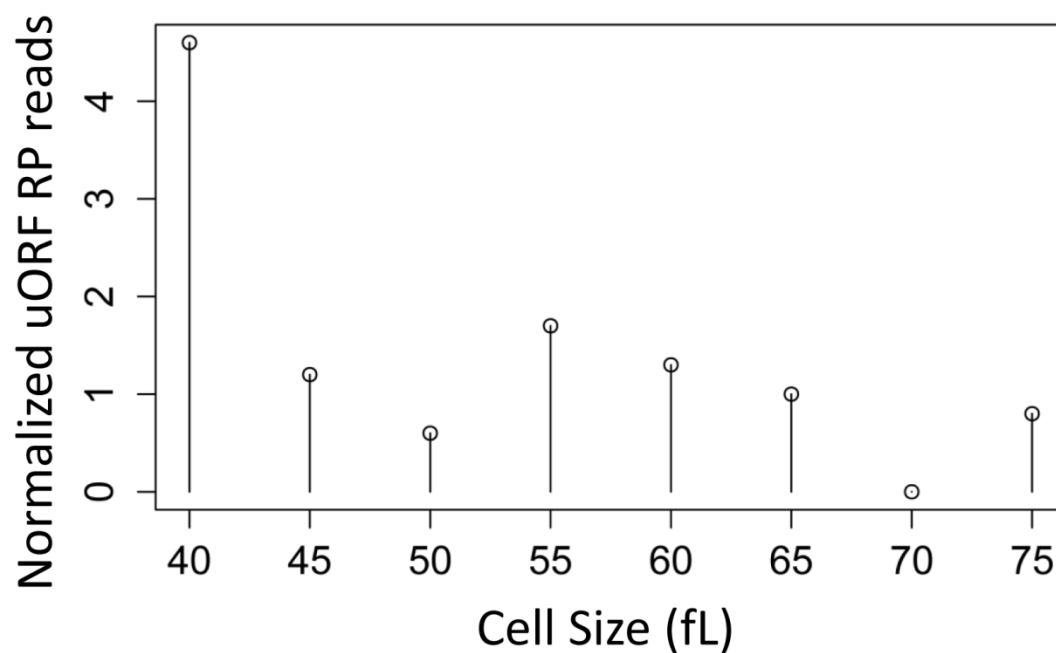


APPENDIX FIGURE 1. Acc1p-TAP levels drop as cells exit mitosis and re-enter a new cell cycle.

The experiment was done as in Fig. 4, except that α -factor was added when cells reached 50% budding index, to maintain synchrony between mother and daughter cells, ensuring that large mother cells stayed in the subsequent G1 phase and did not quickly initiate a new round of DNA replication. In the graph shown at the bottom, on the y-axis are Acc1p-TAP levels, normalized against Pgk1, for every sample examined on the immunoblots shown on the top (x-axis).

		<u>MetCysLeu</u> *	
SGD_Scer_ACC1/YNR016C	-348	TCGGTGCATGTGTTTATAA-AAG	-327
MIT_Smik_c642_18747	-340	CCGGTGCATGTGTTTATAGCAAG	-318
MIT_Spar_c258_19381	-337	TCAGTGCATGTGTTTATAG-AAG	-315
WashU_Sbay_Contig655.32	-364	TCGGTGCATGTGCTTATAG-AAG	-343

APPENDIX FIGURE 2. The ACC1 uORF is conserved in the indicated genomic regions of *sensu stricto Saccharomyces* species. The positions shown are numbered relative to the start of the ACC1 main ORF (position +1) in each case. The figure was generated using the “Fungal Sequence Alignment” function of the Saccharomyces Genome Database (Cherry, Hong et al., 2012).



APPENDIX FIGURE 3. Ribosome occupancy of the *ACC1* uORF in the cell cycle. Line plots showing the ratio of the ribosome footprint (RP) reads mapping to the *ACC1* uORF normalized against the ribosome footprint reads mapping to the main *ACC1* ORF (y-axis; expressed as [uORF ribosome footprint reads/ ribosome footprint reads mapping to the main *ACC1* ORF] $\times 1000$), at the indicated cell sizes (x-axis).

Appendix File 01

Contents

1	GEO File Names	
1.1	Table 04: Next Generation Sequencing Data	
2	<i>ACC1</i> (Crick Strand)	
2.1	Table 05: RP and TP Coverage (CDS)	
2.2	<i>ACC1</i> CDS Read Size Distribution	
3	<i>DSK2</i> (Watson Strand)	
3.1	Table 06: RP and TP Coverage (CDS)	
3.2	<i>DSK2</i> CDS Read Size Distribution	
4	<i>DYN1</i> (Crick Strand)	
4.1	Table 07: RP and TP Coverage (CDS)	
4.2	<i>DYN1</i> CDS Read Size Distribution	
5	<i>FAS1</i> (Watson Strand)	
5.1	Table 08: RP and TP Coverage (CDS)	
5.2	<i>FAS1</i> CDS Read Size Distribution	
6	<i>FAS2</i> (Watson Strand)	
6.1	Table 09: RP and TP Coverage (CDS)	
6.2	<i>FAS2</i> CDS Read Size Distribution	
7	<i>GAT2</i> (Watson Strand)	
7.1	Table 10: RP and TP Coverage (CDS)	
7.2	<i>GAT2</i> CDS Read Size Distribution	
8	<i>GCV3</i> (Crick Strand)	
8.1	Table 11: RP and TP Coverage (CDS)	
8.2	<i>GCV3</i> CDS Read Size Distribution	
9	<i>GND1</i> (Watson Strand)	
9.1	Table 12: RP and TP Coverage (CDS)	
9.2	<i>GND1</i> CDS Read Size Distribution	
10	<i>HHF1</i> (Crick Strand)	
10.1	Table 13: RP and TP Coverage (CDS)	
10.2	<i>HHF1</i> CDS Read Size Distribution	
11	<i>MPS1</i> (Crick Strand)	
11.1	Table 14: RP and TP Coverage (CDS)	
11.2	<i>MPS1</i> CDS Read Size Distribution	
12	<i>MSC1</i> (Crick Strand)	
12.1	Table 15: RP and TP Coverage (CDS)	
12.2	<i>MSC1</i> CDS Read Size Distribution	
13	<i>NQM1</i> (Crick Strand)	
13.1	Table 16: RP and TP Coverage (CDS)	
13.2	<i>NQM1</i> CDS Read Size Distribution	

14 *PCT1* (Crick Strand)

- 14.1 Table 17: RP and TP Coverage (CDS)
- 14.2 *PCT1* (Crick Strand) CDS Read Size Distribution

15 *RTN2* (Watson Strand)

- 15.1 Table 18: RP and TP Coverage (CDS)
- 15.2 *RTN2* CDS Read Size Distribution

16 *TIP1* (Crick Strand)

- 16.1 Table 19: RP and TP Coverage (CDS)

- 16.2 *TIP1* CDS Read Size Distribution

17 *YKR018C* (Crick Strand)

- 17.1 Table 20: RP and TP Coverage (CDS)
- 17.2 *YKR018C* CDS Read Size Distribution

18 *YRO2* (Watson Strand)

- 18.1 Table 21: RP and TP Coverage (CDS)
- 18.2 *YRO2* CDS Read Size Distribution

1 GEO File Names

1.1 Table 04: Next Generation Sequencing Data

	Sample Name	Experiment Class and Cell Volume (fL)	Sample Type	Raw Data Files	
01	RP-Sample01A	Ribosome-Profile-40fl	Protected-RNA	1A.01-RP.fq	
02	RP-Sample01B	Ribosome-Profile-40fl	Protected-RNA	1B.01-RP.fq	
03	RP-Sample01C	Ribosome-Profile-40fl	Protected-RNA	1C.01-RP.fq	1C.02-RP.fq
04	RP-Sample02A	Ribosome-Profile-45fl	Protected-RNA	2A.01-RP.fq	
05	RP-Sample02B	Ribosome-Profile-45fl	Protected-RNA	2B.01-RP.fq	
06	RP-Sample02C	Ribosome-Profile-45fl	Protected-RNA	2C.01-RP.fq	2C.02-RP.fq
07	RP-Sample03A	Ribosome-Profile-50fl	Protected-RNA	3A.01-RP.fq	
08	RP-Sample03B	Ribosome-Profile-50fl	Protected-RNA	3B.01-RP.fq	
09	RP-Sample03C	Ribosome-Profile-50fl	Protected-RNA	3C.01-RP.fq	3C.02-RP.fq
10	RP-Sample04A	Ribosome-Profile-55fl	Protected-RNA	4A.01-RP.fq	
11	RP-Sample04B	Ribosome-Profile-55fl	Protected-RNA	4B.01-RP.fq	
12	RP-Sample04C	Ribosome-Profile-55fl	Protected-RNA	4C.01-RP.fq	4C.02-RP.fq
13	RP-Sample05A	Ribosome-Profile-60fl	Protected-RNA	5A.01-RP.fq	
14	RP-Sample05B	Ribosome-Profile-60fl	Protected-RNA	5B.01-RP.fq	
15	RP-Sample05C	Ribosome-Profile-60fl	Protected-RNA	5C.01-RP.fq	5C.02-RP.fq
16	RP-Sample06A	Ribosome-Profile-65fl	Protected-RNA	6A.01-RP.fq	
17	RP-Sample06B	Ribosome-Profile-65fl	Protected-RNA	6B.01-RP.fq	
18	RP-Sample06C	Ribosome-Profile-65fl	Protected-RNA	6C.01-RP.fq	6C.02-RP.fq
19	RP-Sample07A	Ribosome-Profile-70fl	Protected-RNA	7A.01-RP.fq	
20	RP-Sample07B	Ribosome-Profile-70fl	Protected-RNA	7B.01-RP.fq	
21	RP-Sample07C	Ribosome-Profile-70fl	Protected-RNA	7C.01-RP.fq	7C.02-RP.fq
22	RP-Sample08A	Ribosome-Profile-75fl	Protected-RNA	8A.01-RP.fq	
23	RP-Sample08B	Ribosome-Profile-75fl	Protected-RNA	8B.01-RP.fq	
24	RP-Sample08C	Ribosome-Profile-75fl	Protected-RNA	8C.01-RP.fq	8C.02-RP.fq
25	TP-Sample01A	Transcriptional-Profile-40fl	PolyA-RNA	1A.01-TP.fq	
26	TP-Sample01B	Transcriptional-Profile-40fl	PolyA-RNA	1B.01-TP.fq	
27	TP-Sample01C	Transcriptional-Profile-40fl	PolyA-RNA	1C.01-TP.fq	1C.02-TP.fq
28	TP-Sample02A	Transcriptional-Profile-45fl	PolyA-RNA	2A.01-TP.fq	
29	TP-Sample02B	Transcriptional-Profile-45fl	PolyA-RNA	2B.01-TP.fq	
30	TP-Sample02C	Transcriptional-Profile-45fl	PolyA-RNA	2C.01-TP.fq	2C.02-TP.fq
31	TP-Sample03A	Transcriptional-Profile-50fl	PolyA-RNA	3A.01-TP.fq	
32	TP-Sample03B	Transcriptional-Profile-50fl	PolyA-RNA	3B.01-TP.fq	
33	TP-Sample03C	Transcriptional-Profile-50fl	PolyA-RNA	3C.01-TP.fq	3C.02-TP.fq
34	TP-Sample04A	Transcriptional-Profile-55fl	PolyA-RNA	4A.01-TP.fq	
35	TP-Sample04B	Transcriptional-Profile-55fl	PolyA-RNA	4B.01-TP.fq	
36	TP-Sample04C	Transcriptional-Profile-55fl	PolyA-RNA	4C.01-TP.fq	4C.02-TP.fq
37	TP-Sample05A	Transcriptional-Profile-60fl	PolyA-RNA	5A.01-TP.fq	
38	TP-Sample05B	Transcriptional-Profile-60fl	PolyA-RNA	5B.01-TP.fq	
39	TP-Sample05C	Transcriptional-Profile-60fl	PolyA-RNA	5C.01-TP.fq	5C.02-TP.fq
40	TP-Sample06A	Transcriptional-Profile-65fl	PolyA-RNA	6A.01-TP.fq	
41	TP-Sample06B	Transcriptional-Profile-65fl	PolyA-RNA	6B.01-TP.fq	
42	TP-Sample06C	Transcriptional-Profile-65fl	PolyA-RNA	6C.01-TP.fq	6C.02-TP.fq
43	TP-Sample07A	Transcriptional-Profile-70fl	PolyA-RNA	7A.01-TP.fq	
44	TP-Sample07B	Transcriptional-Profile-70fl	PolyA-RNA	7B.01-TP.fq	
45	TP-Sample07C	Transcriptional-Profile-70fl	PolyA-RNA	7C.01-TP.fq	7C.02-TP.fq
46	TP-Sample08A	Transcriptional-Profile-75fl	PolyA-RNA	8A.01-TP.fq	
47	TP-Sample08B	Transcriptional-Profile-75fl	PolyA-RNA	8B.01-TP.fq	
48	TP-Sample08C	Transcriptional-Profile-75fl	PolyA-RNA	8C.01-TP.fq	8C.02-TP.fq

2 *ACC1* (Crick Strand)

2.1 Table 05: RP and TP Coverage (CDS)

CDS: ChrXIV:654673..661374 (6701 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	19	.054	781	5.495
	Crick	12857	51.613	7382	51.481
2	Watson	5	.014	409	2.750
	Crick	15524	60.904	11631	80.428
3	Watson	1	.002	409	2.746
	Crick	1608	6.360	7788	53.939
4	Watson	11	.032	447	3.030
	Crick	30617	122.391	7072	48.809
5	Watson	2	.005	97	.645
	Crick	5235	20.138	2980	20.775
6	Watson	0	0.00	241	1.614
	Crick	3105	12.761	2930	20.316
7	Watson	1	.002	318	2.197
	Crick	1850	7.444	4959	34.916
8	Watson	9	.027	244	1.630
	Crick	9156	37.652	2817	19.504
Control (Ingolia):					
Rich	Watson	4	.016	80	.294
	Crick	1586	6.381	1306	4.726
Starved	Watson	2	.006	18	.064
	Crick	1528	6.012	451	1.636

2.2 *ACC1* CDS Read Size Distribution

Ribosome Profiling (RP)

Percentage (y-axis) versus Read Size (nt)(x-axis)

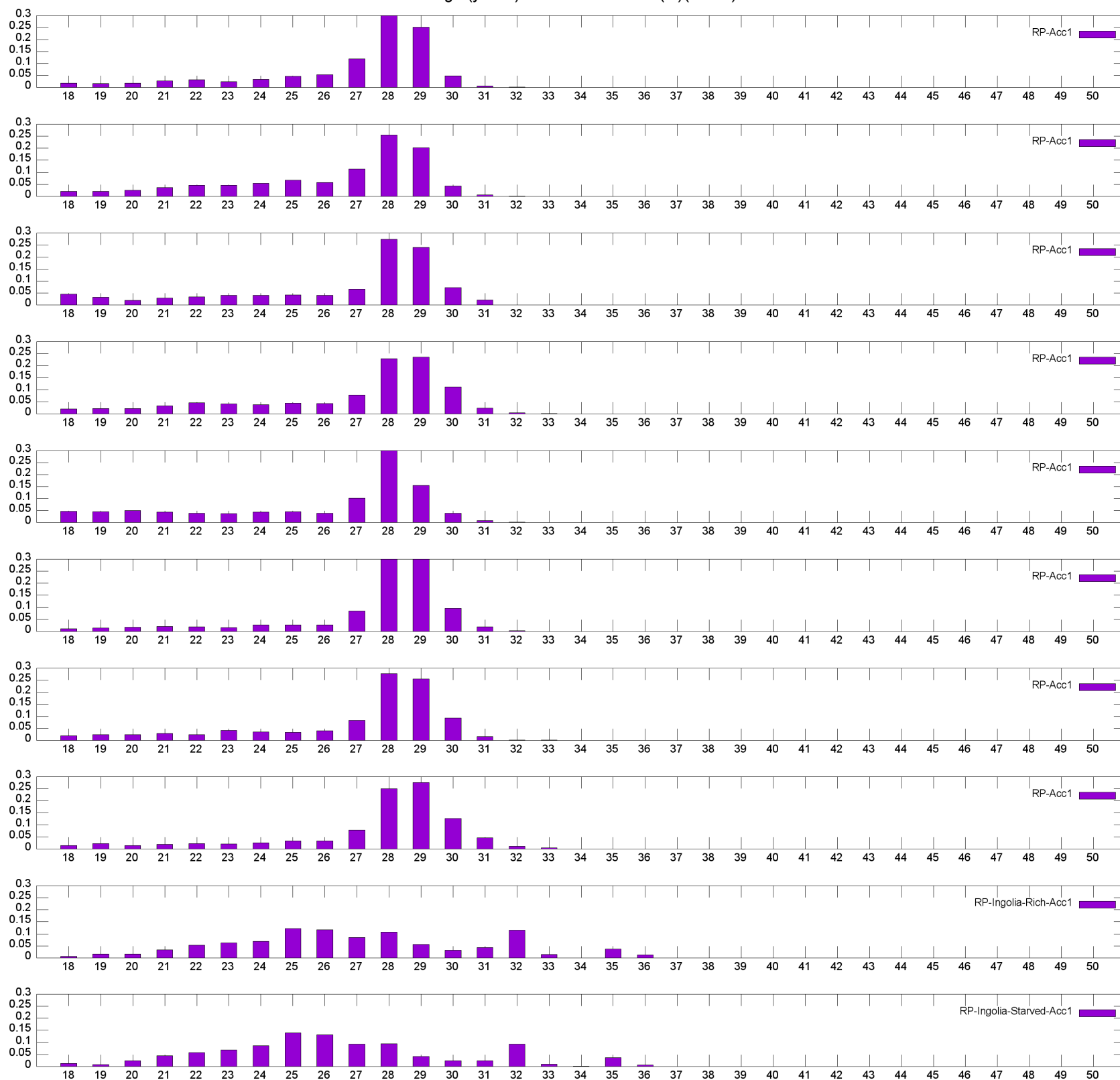


Figure 4: *ACC1* CDS Crick Reads Size Distribution (RP)

3 *DSK2* (Watson Strand)

3.1 Table 06: RP and TP Coverage (CDS)

CDS: ChrXIII:818827..819948 (1121 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	1364	32.756	431	18.232
	Crick	2	.033	96	4.018
2	Watson	1352	31.521	1132	46.761
	Crick	2	.041	87	3.357
3	Watson	297	7.297	1075	43.719
	Crick	0	0.00	65	2.483
4	Watson	2337	55.573	967	40.103
	Crick	6	.132	85	3.443
5	Watson	596	13.776	509	21.057
	Crick	0	0.00	27	1.132
6	Watson	416	10.191	426	17.702
	Crick	0	0.00	50	2.087
7	Watson	279	6.730	559	23.787
	Crick	1	.016	51	2.056
8	Watson	886	22.221	606	25.246
	Crick	15	.251	53	2.059
Control (Ingolia):					
Rich	Watson	385	8.976	463	9.943
	Crick	0	0.00	18	.380
Starved	Watson	540	12.297	239	5.247
	Crick	0	0.00	6	.124

3.2 *DSK2* CDS Read Size Distribution

Ribosome Profiling (RP)

Percentage (y-axis) versus Read Size (nt)(x-axis)

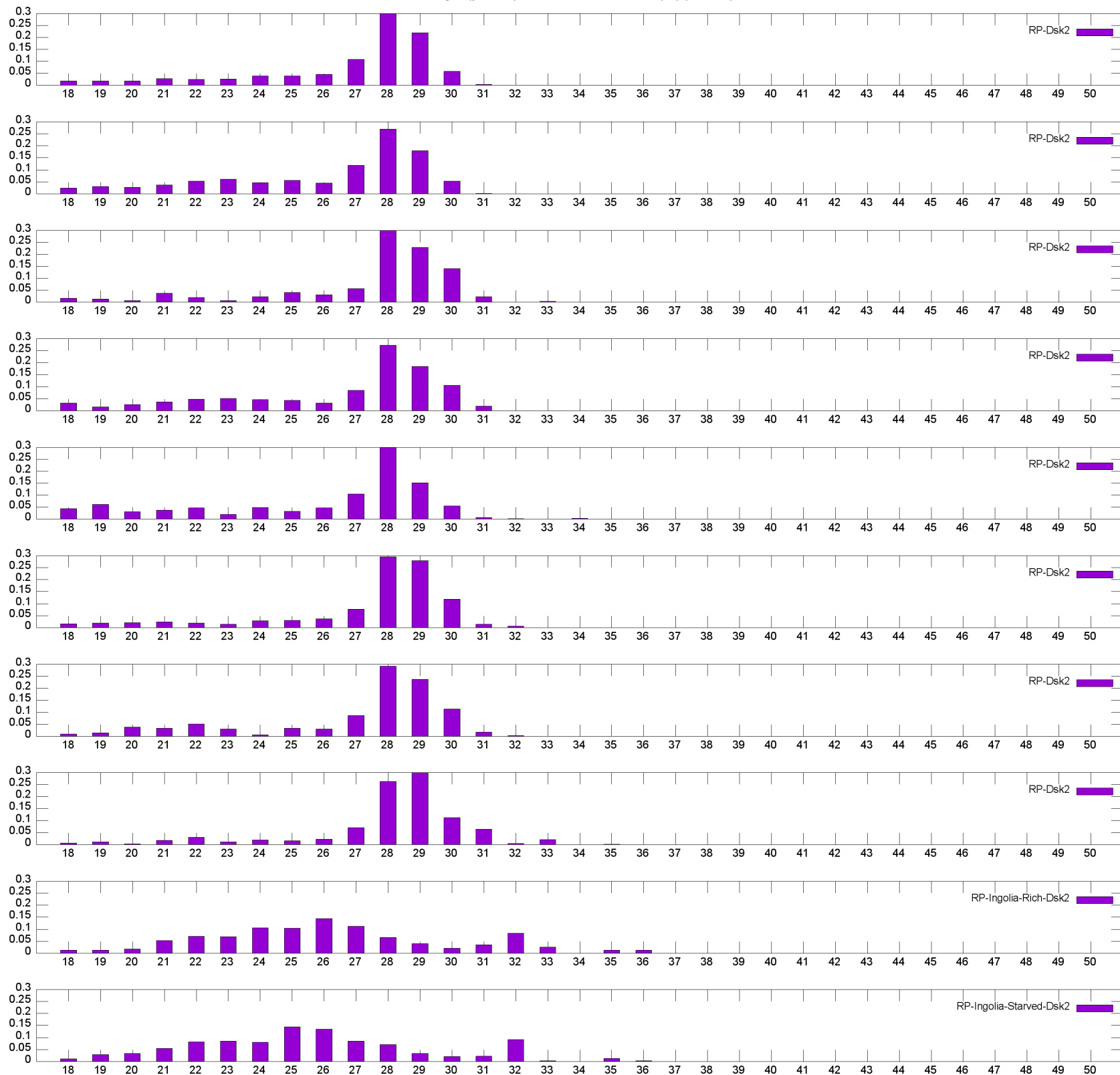


Figure 5: *DSK2* CDS Watson Reads Size Distribution (RP)

4 *DYN1* (Crick Strand)

4.1 Table 07: RP and TP Coverage (CDS)

CDS: ChrXI:535647..547925 (12278 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	24128	52.267	29712	112.780
	Crick	3636	7.734	10853	41.981
2	Watson	17863	37.500	109891	416.161
	Crick	3056	6.348	14458	54.791
3	Watson	4929	11.353	83078	313.598
	Crick	707	1.495	15700	59.701
4	Watson	28152	59.872	64070	240.397
	Crick	4848	10.282	14425	54.797
5	Watson	12223	26.575	52063	197.280
	Crick	1862	3.930	9689	36.744
6	Watson	3345	7.548	50818	188.437
	Crick	814	1.701	15829	59.956
7	Watson	9809	21.276	50407	191.434
	Crick	1101	2.346	13819	53.069
8	Watson	14749	32.332	35169	131.737
	Crick	2645	5.802	10764	40.866
Control (Ingolia):					
Rich	Watson	1444	3.221	8313	16.392
	Crick	680	1.499	3869	7.578
Starved	Watson	1026	2.187	1344	2.657
	Crick	812	1.730	1031	2.036

4.2 *DYN1* CDS Read Size Distribution

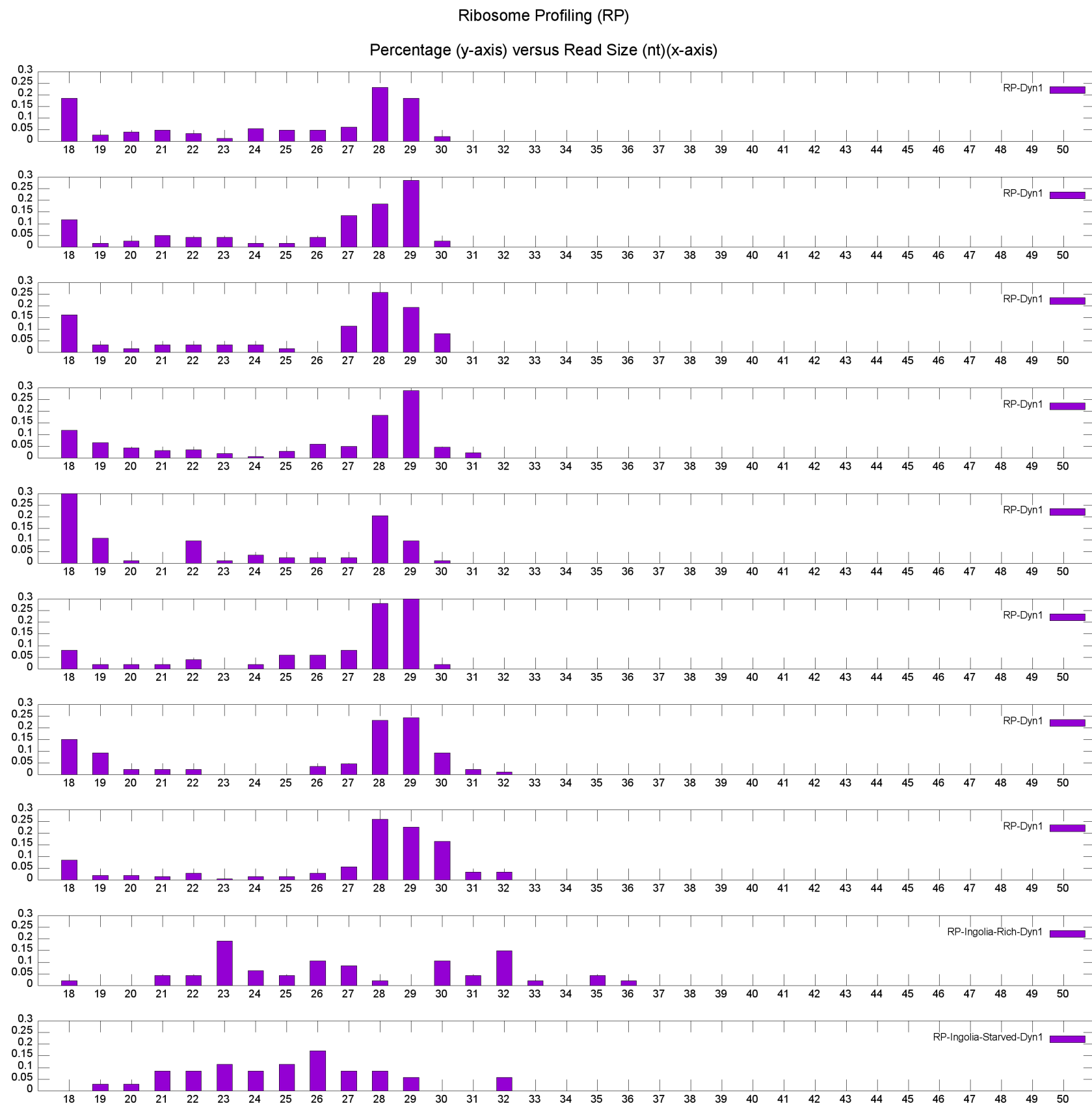


Figure 6: *DYN1* CDS Crick Reads Size Distribution (RP)

5 *FAS1* (Watson Strand)

5.1 Table 08: RP and TP Coverage (CDS)

CDS: ChrXI:100671..106826 (6155 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	33337	144.293	12240	93.916
	Crick	1434	6.227	3979	30.463
2	Watson	30841	130.579	16778	125.081
	Crick	1273	5.418	4916	37.027
3	Watson	3972	16.970	12690	94.499
	Crick	344	1.496	5838	43.973
4	Watson	58210	251.243	12980	96.820
	Crick	1919	8.145	4760	35.807
5	Watson	9859	40.927	8948	67.435
	Crick	439	1.830	4341	32.749
6	Watson	6498	28.625	11265	84.395
	Crick	432	1.931	5828	44.262
7	Watson	5577	23.873	12578	95.729
	Crick	432	1.881	5996	45.974
8	Watson	20378	90.265	7529	56.065
	Crick	1347	5.982	3136	23.658
Control (Ingolia):					
Rich	Watson	3227	14.165	5640	22.276
	Crick	194	.852	1466	5.783
Starved	Watson	2030	8.656	815	3.221
	Crick	326	1.360	333	1.344

5.2 *FAS1* CDS Read Size Distribution

Ribosome Profiling (RP)

Percentage (y-axis) versus Read Size (nt)(x-axis)

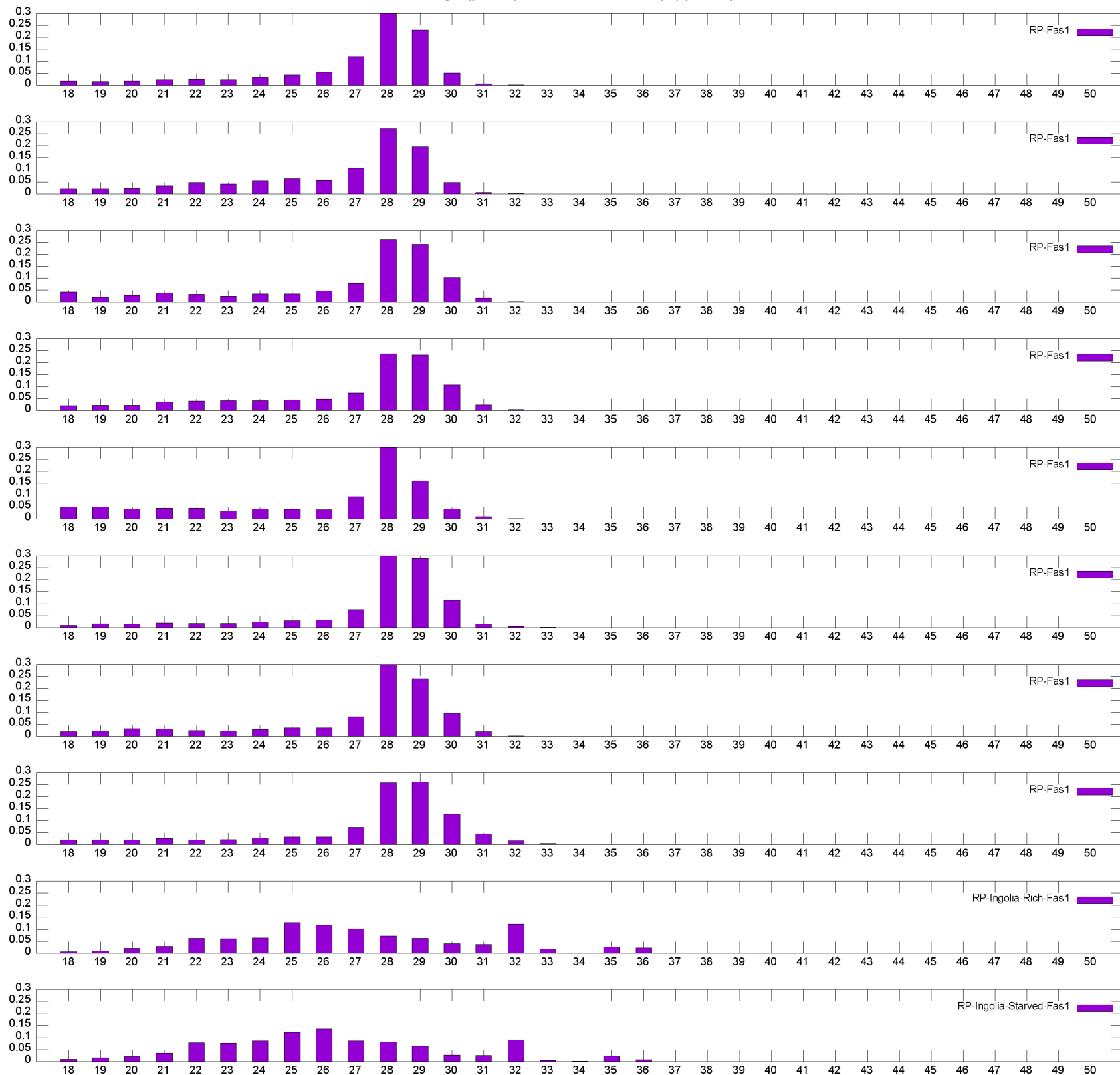


Figure 7: *FAS1* CDS Watson Reads Size Distribution (RP)

6 *FAS2* (Watson Strand)

6.1 Table 09: RP and TP Coverage (CDS)

CDS: ChrXVI:108652..114315 (5663 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	24546	116.979	3111	26.002
	Crick	71	.232	174	1.413
2	Watson	19706	91.612	3782	30.757
	Crick	14	.045	122	.988
3	Watson	1668	7.927	2704	22.048
	Crick	6	.019	102	.806
4	Watson	38613	182.812	2730	22.261
	Crick	4	.013	112	.933
5	Watson	6365	28.871	1053	8.652
	Crick	7	.022	26	.201
6	Watson	4217	20.440	1106	9.011
	Crick	1	.003	55	.443
7	Watson	2416	11.492	2335	19.466
	Crick	4	.013	106	.876
8	Watson	11262	54.757	1657	13.678
	Crick	23	.076	138	1.139
Control (Ingolia):					
Rich	Watson	2067	9.829	1602	6.806
	Crick	1	.003	8	.029
Starved	Watson	1882	8.669	464	1.999
	Crick	1	.004	3	.010

6.2 *FAS2* CDS Read Size Distribution

Ribosome Profiling (RP)

Percentage (y-axis) versus Read Size (nt)(x-axis)

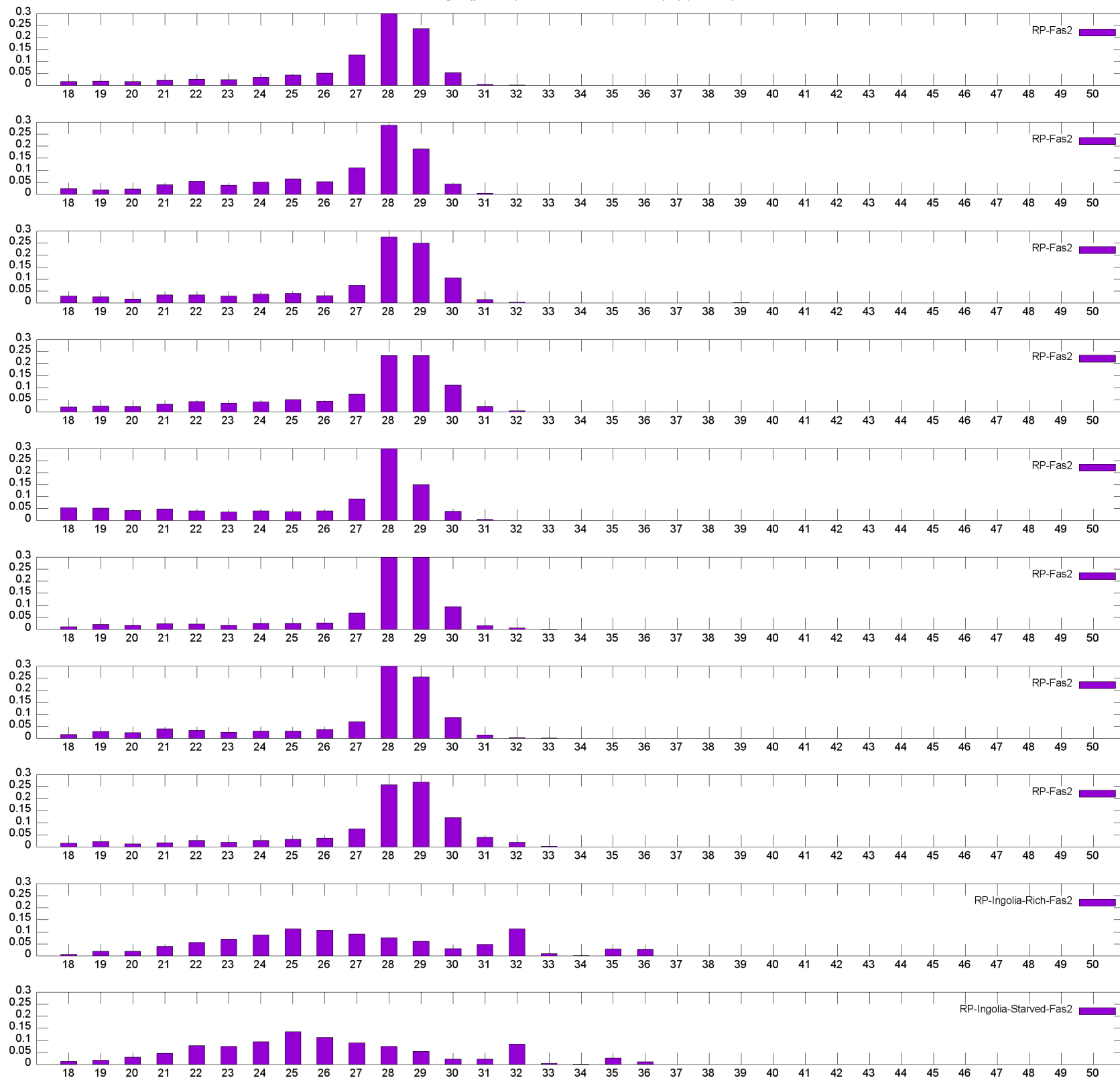


Figure 8: *FAS2* CDS Watson Reads Size Distribution (RP)

7 *GAT2* (Watson Strand)

7.1 Table 10: RP and TP Coverage (CDS)

CDS: ChrXIII:541199..542881 (1682 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	1491	23.903	876	24.442
	Crick	4	.045	63	1.763
2	Watson	732	11.403	1593	44.008
	Crick	4	.043	72	1.960
3	Watson	71	1.131	2122	58.486
	Crick	1	.010	105	2.876
4	Watson	221	3.419	2244	62.400
	Crick	1	.010	148	4.089
5	Watson	54	.826	1327	36.879
	Crick	2	.021	54	1.462
6	Watson	71	1.152	2116	58.702
	Crick	0	0.00	64	1.750
7	Watson	91	1.480	2287	64.146
	Crick	0	0.00	76	2.088
8	Watson	506	8.366	2187	60.840
	Crick	3	.035	110	3.055
Control (Ingolia):					
Rich	Watson	22	.345	111	1.577
	Crick	0	0.00	8	.110
Starved	Watson	65	.997	29	.398
	Crick	4	.049	0	0.00

7.2 *GAT2* CDS Read Size Distribution

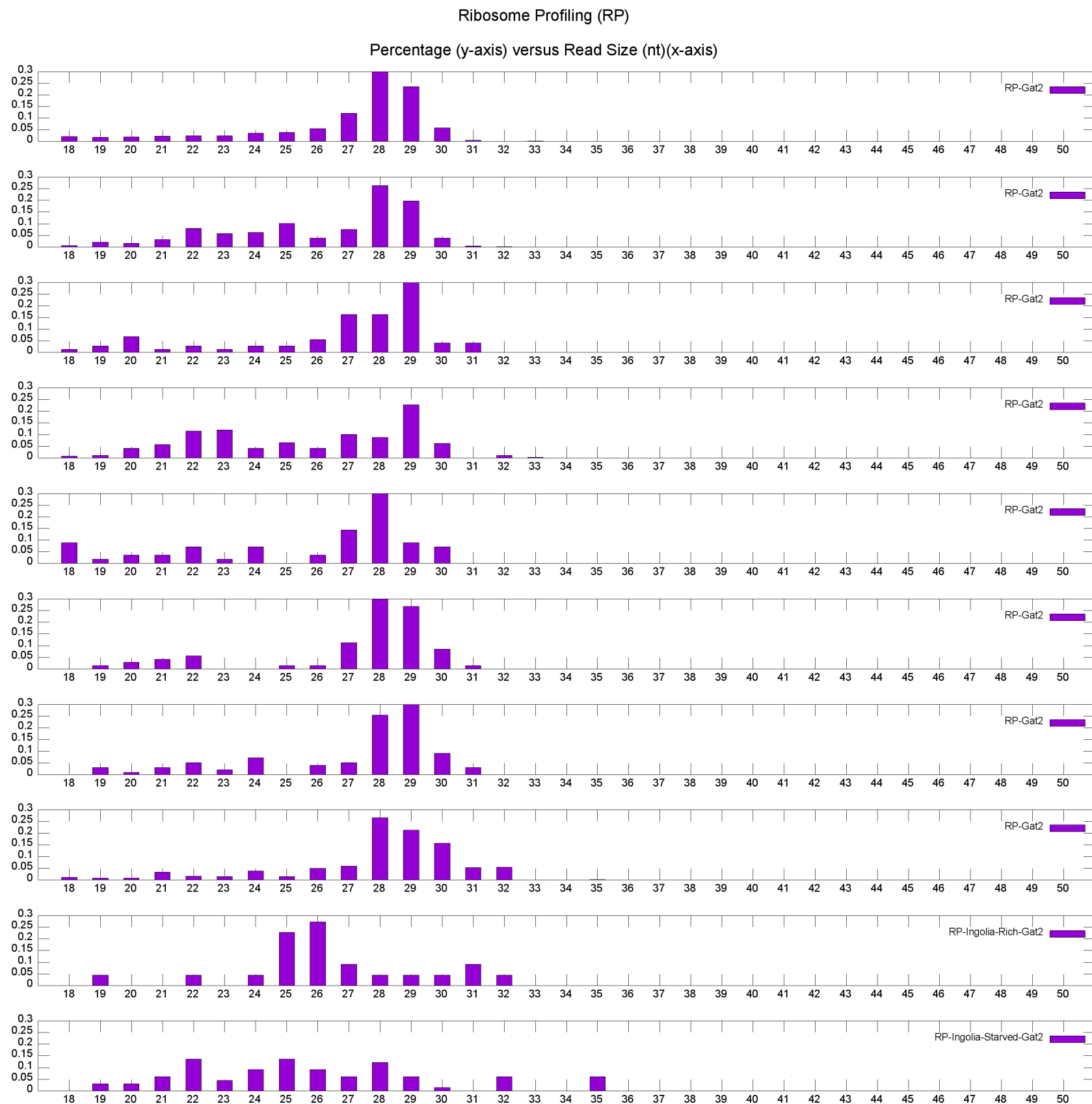


Figure 9: *GAT2* CDS Watson Reads Size Distribution (RP)

8 *GCV3* (Crick Strand)

8.1 Table 11: RP and TP Coverage (CDS)

CDS: ChrI:57950..58462 (512 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	2	.074	160	14.937
	Crick	2276	119.234	856	78.460
2	Watson	6	.232	55	4.962
	Crick	1408	72.341	1415	126.492
3	Watson	1	.035	75	6.849
	Crick	340	17.974	1903	171.355
4	Watson	6	.226	75	6.808
	Crick	1767	92.855	1196	107.787
5	Watson	2	.076	35	3.117
	Crick	385	19.458	1234	111.179
6	Watson	0	0.00	88	8.097
	Crick	385	20.638	1807	161.476
7	Watson	2	.072	129	11.871
	Crick	422	22.226	2990	273.955
8	Watson	2	.072	108	10.099
	Crick	1402	75.898	1173	103.712
Control (Ingolia):					
Rich	Watson	1	.044	22	.978
	Crick	490	25.541	1808	83.992
Starved	Watson	2	.074	3	.105
	Crick	1016	51.451	1350	63.576

8.2 *GCV3* CDS Read Size Distribution

Ribosome Profiling (RP)

Percentage (y-axis) versus Read Size (nt)(x-axis)

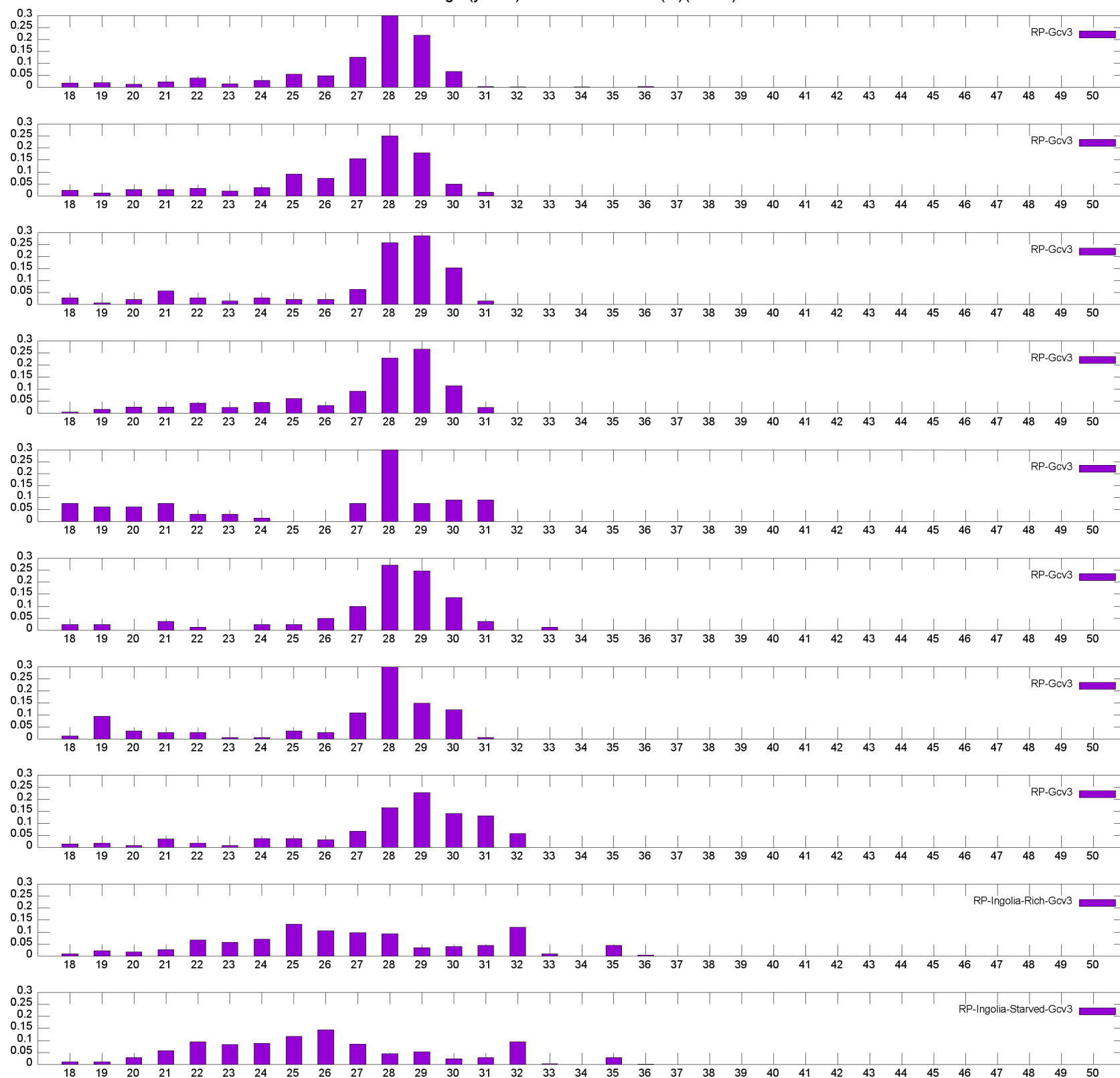


Figure 10: *GCV3* CDS Crick Reads Size Distribution (RP)

9 *GND1* (Watson Strand)

9.1 Table 12: RP and TP Coverage (CDS)

CDS: ChrVIII:470960..472429 (1469 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	4722	86.353	1864	59.553
	Crick	2	.025	65	2.122
2	Watson	4003	71.579	1255	39.409
	Crick	1	.014	44	1.448
3	Watson	958	17.775	1270	40.281
	Crick	1	.014	58	1.875
4	Watson	8574	155.800	998	31.489
	Crick	7	.093	39	1.258
5	Watson	1612	27.514	631	20.110
	Crick	0	0.00	19	.632
6	Watson	1214	22.631	913	28.886
	Crick	0	0.00	21	.691
7	Watson	934	16.560	1218	39.006
	Crick	0	0.00	41	1.331
8	Watson	4123	77.605	520	16.493
	Crick	54	.748	42	1.351
Control (Ingolia):					
Rich	Watson	918	16.870	1688	27.923
	Crick	0	0.00	6	.089
Starved	Watson	1289	22.698	608	9.987
	Crick	0	0.00	3	.039

9.2 *GND1* CDS Read Size Distribution

Ribosome Profiling (RP)

Percentage (y-axis) versus Read Size (nt)(x-axis)

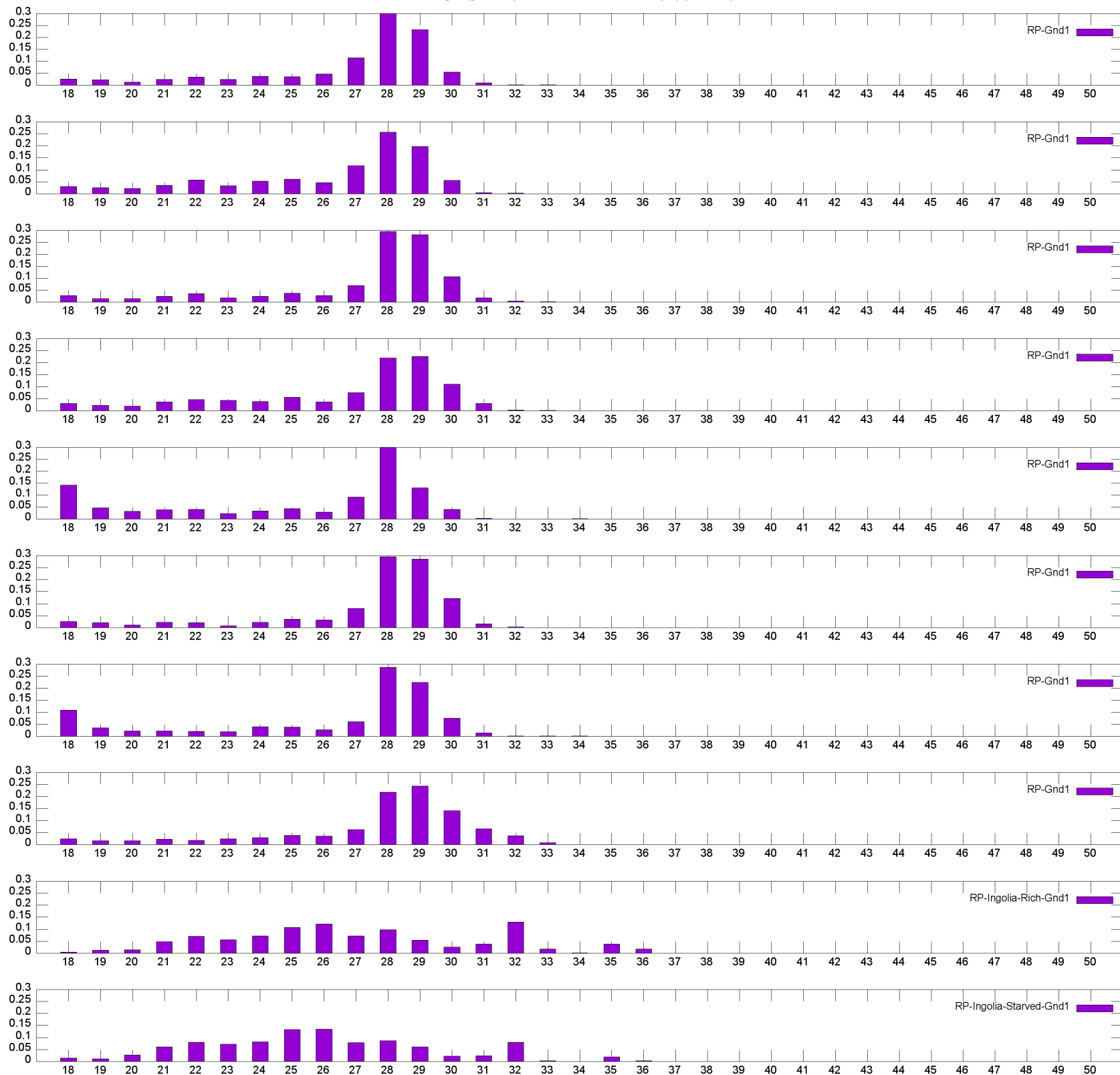


Figure 11: *GND1* CDS Watson Reads Size Distribution (RP)

10 *HHF1* (Crick Strand)

10.1 Table 13: RP and TP Coverage (CDS)

CDS: ChrII:255373..255684 (311 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	8	.720	28	4.302
	Crick	760	65.038	620	91.900
2	Watson	6	.511	21	3.093
	Crick	789	67.405	1374	201.061
3	Watson	0	0.00	81	12.115
	Crick	531	46.231	2300	338.816
4	Watson	2	.141	265	39.684
	Crick	1834	154.758	5599	819.421
5	Watson	3	.270	177	26.205
	Crick	408	33.196	8981	1327.652
6	Watson	3	.215	275	40.530
	Crick	153	13.408	11675	1728.212
7	Watson	7	.614	108	16.218
	Crick	699	60.819	7487	1119.292
8	Watson	4	.344	153	22.971
	Crick	1197	106.694	2320	340.990
Control (Ingolia):					
Rich	Watson	1	.083	7	.553
	Crick	532	45.218	5617	436.061
Starved	Watson	2	.183	2	.176
	Crick	463	39.032	343	26.434

10.2 *HHF1* CDS Read Size Distribution

Ribosome Profiling (RP)

Percentage (y-axis) versus Read Size (nt)(x-axis)

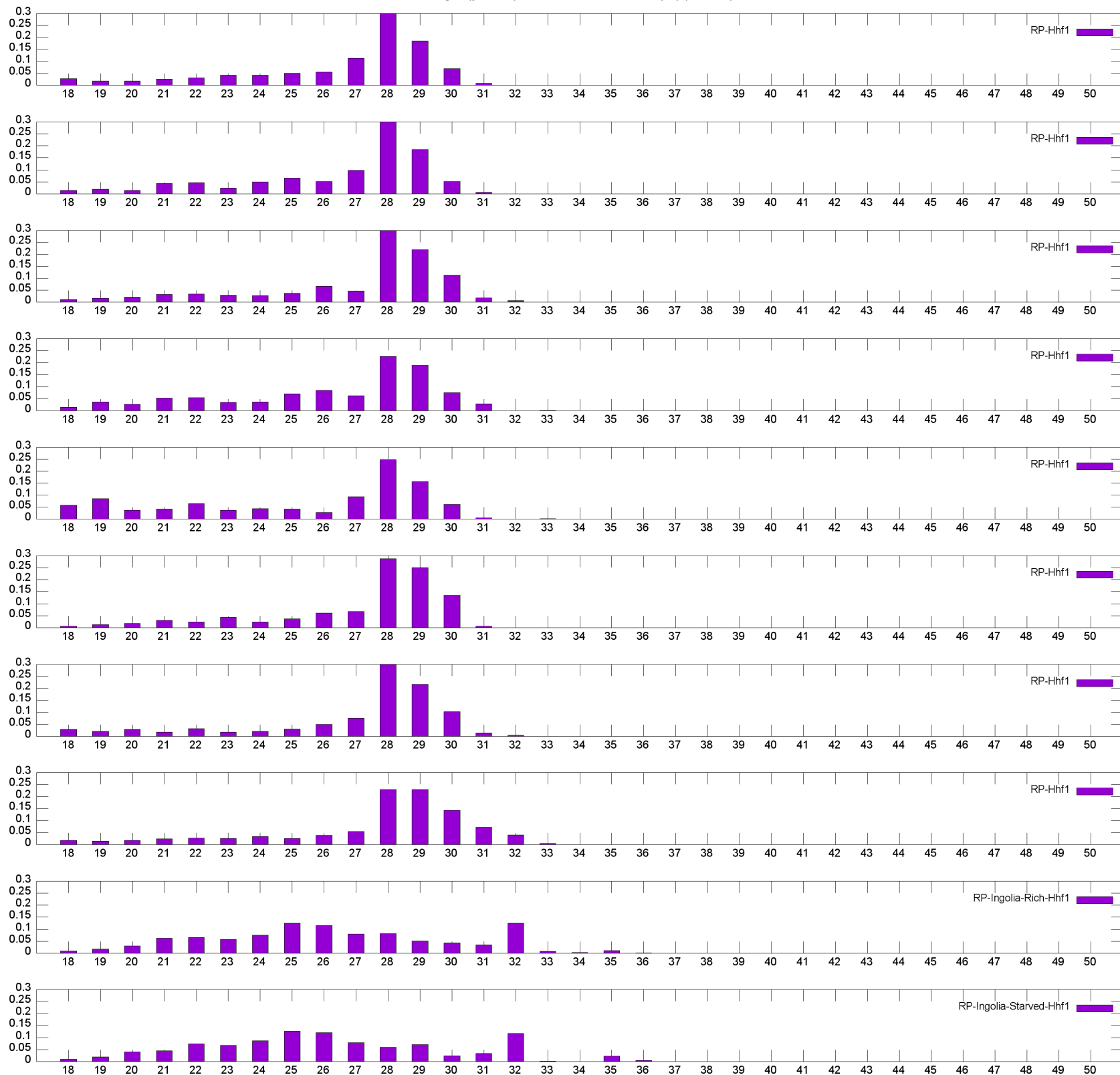


Figure 12: *HHF1* CDS Crick Reads Size Distribution (RP)

11 *MPS1* (Crick Strand)

11.1 Table 14: RP and TP Coverage (CDS)

CDS: ChrIV:400997..403291 (2294 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	1	.007	39	.819
	Crick	283	2.683	442	9.043
2	Watson	2	.016	30	.595
	Crick	90	.905	997	19.870
3	Watson	0	0.00	41	.834
	Crick	39	.433	1058	21.165
4	Watson	1	.007	39	.792
	Crick	146	1.649	1214	24.256
5	Watson	0	0.00	13	.273
	Crick	36	.390	1018	20.396
6	Watson	0	0.00	58	1.183
	Crick	28	.307	1497	30.223
7	Watson	0	0.00	67	1.395
	Crick	47	.509	1156	23.814
8	Watson	0	0.00	31	.618
	Crick	105	1.193	827	16.603
Control (Ingolia):					
Rich	Watson	0	0.00	3	.028
	Crick	25	.284	185	1.965
Starved	Watson	0	0.00	0	0.00
	Crick	40	.466	45	.465

11.2 *MPS1* CDS Read Size Distribution

Ribosome Profiling (RP)

Percentage (y-axis) versus Read Size (nt)(x-axis)



Figure 13: *MPS1* CDS Crick Reads Size Distribution (RP)

12 *MSC1* (Crick Strand)

12.1 Table 15: RP and TP Coverage (CDS)

CDS: ChrXIII:15135..16676 (1541 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	10	.151	118	3.572
	Crick	903	15.726	1746	53.791
2	Watson	5	.075	80	2.292
	Crick	977	16.728	2701	81.744
3	Watson	2	.027	192	5.828
	Crick	361	6.154	6950	211.451
4	Watson	20	.313	137	4.138
	Crick	3064	53.199	3390	102.968
5	Watson	4	.052	39	1.157
	Crick	1806	30.214	3948	120.262
6	Watson	5	.083	26	.687
	Crick	3623	64.798	1584	48.296
7	Watson	4	.068	36	1.071
	Crick	372	6.470	2386	73.232
8	Watson	7	.112	45	1.348
	Crick	1374	24.730	688	20.929
Control (Ingolia):					
Rich	Watson	2	.031	17	.265
	Crick	6	.101	207	3.205
Starved	Watson	0	0.00	3	.040
	Crick	1017	17.294	613	9.963

12.2 *MSC1* CDS Read Size Distribution

Ribosome Profiling (RP)

Percentage (y-axis) versus Read Size (nt)(x-axis)

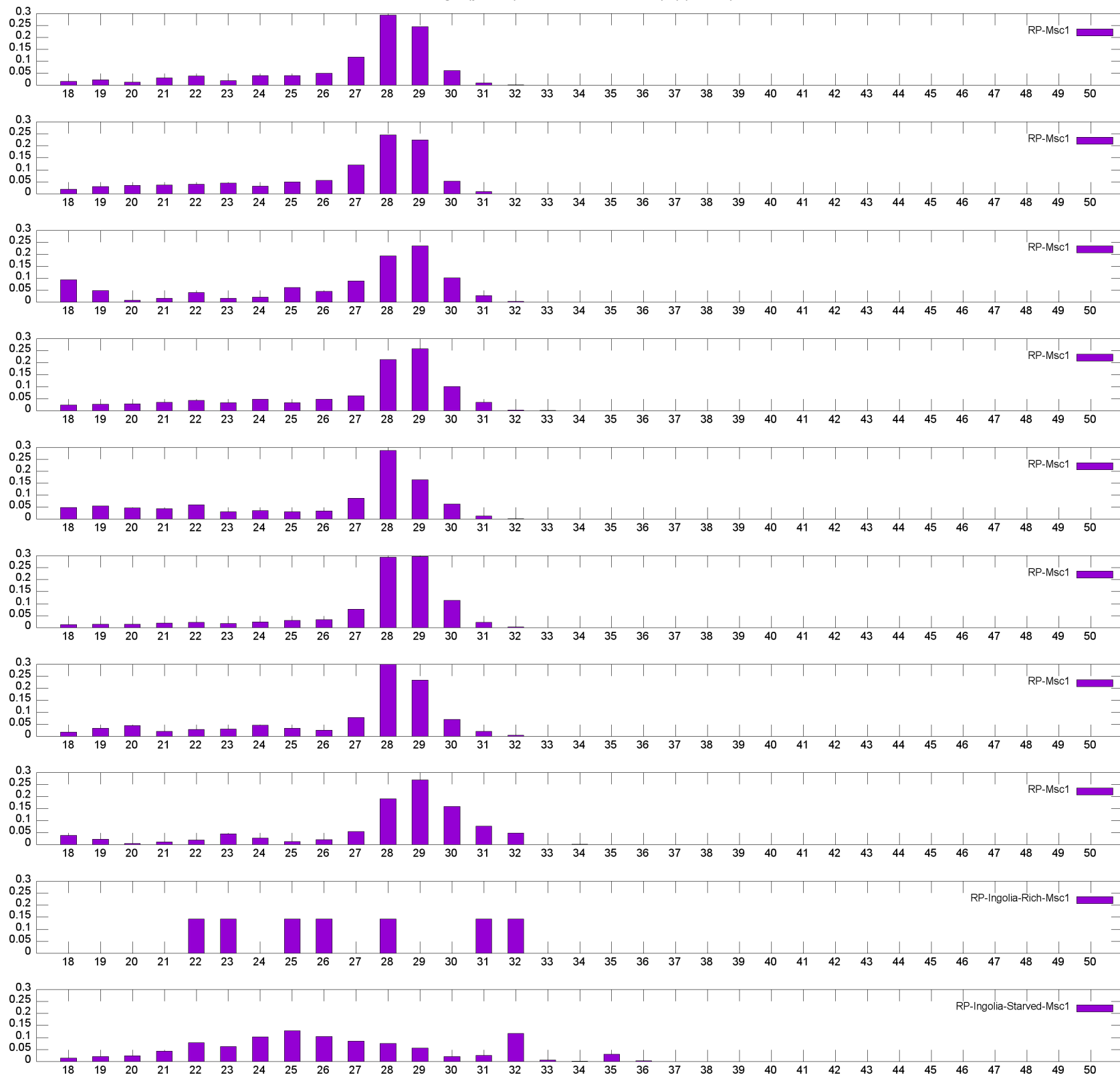


Figure 14: *MSC1* CDS Crick Reads Size Distribution (RP)

13 *NQM1* (Crick Strand)

13.1 Table 16: RP and TP Coverage (CDS)

CDS: ChrVII:580435..581436 (1001 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	32	.603	55	2.564
	Crick	78	2.131	362	16.961
2	Watson	10	.179	41	1.814
	Crick	123	3.332	681	31.436
3	Watson	4	.071	298	13.700
	Crick	41	1.130	5268	245.445
4	Watson	44	.794	219	9.936
	Crick	343	9.156	2197	102.013
5	Watson	94	1.691	53	2.367
	Crick	162	4.205	2247	105.074
6	Watson	3	.053	41	1.919
	Crick	578	15.888	892	41.498
7	Watson	38	.684	61	2.898
	Crick	52	1.389	611	28.764
8	Watson	55	.989	12	.556
	Crick	206	5.648	325	15.037
Control (Ingolia):					
Rich	Watson	0	0.00	6	.125
	Crick	0	0.00	55	1.312
Starved	Watson	0	0.00	14	.280
	Crick	83	2.185	106	2.649

13.2 *NQM1* CDS Read Size Distribution

Ribosome Profiling (RP)

Percentage (y-axis) versus Read Size (nt)(x-axis)

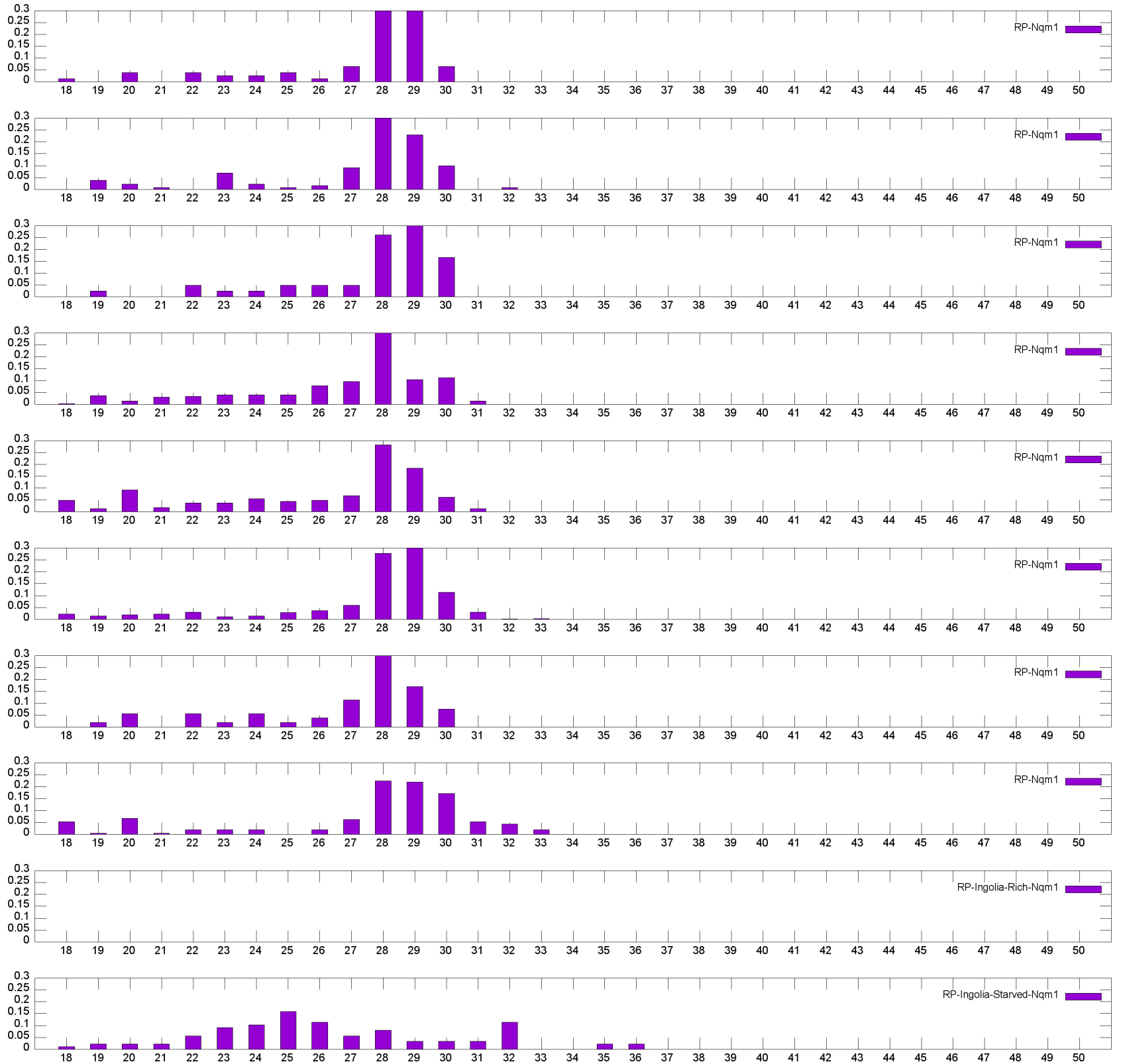


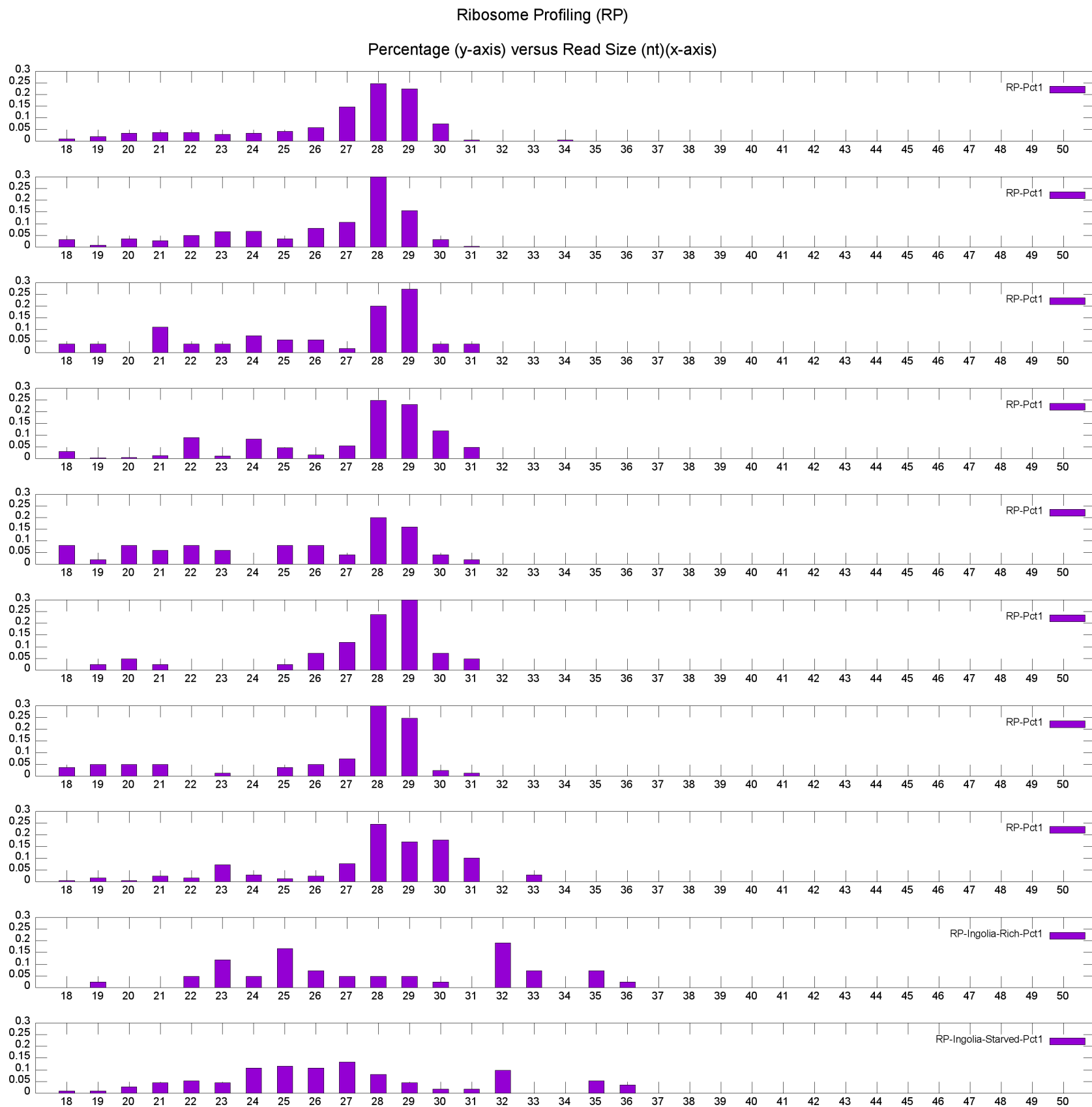
Figure 15: *NQM1* CDS Crick Reads Size Distribution (RP)

14 *PCT1* (Crick Strand)

14.1 Table 17: RP and TP Coverage (CDS)

CDS: ChrVII:903474..904748 (1274 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	2	.028	42	1.559
	Crick	432	9.043	265	9.809
2	Watson	0	0.00	15	.544
	Crick	387	7.916	630	22.964
3	Watson	0	0.00	39	1.415
	Crick	45	.914	787	28.598
4	Watson	4	.059	42	1.569
	Crick	323	6.835	825	30.107
5	Watson	1	.014	19	.667
	Crick	46	.898	553	20.210
6	Watson	1	.014	23	.819
	Crick	38	.816	629	22.824
7	Watson	0	0.00	47	1.657
	Crick	70	1.437	856	31.631
8	Watson	0	0.00	52	1.864
	Crick	226	4.940	762	27.623
Control (Ingolia):					
Rich	Watson	0	0.00	5	.094
	Crick	41	.895	372	6.959
Starved	Watson	0	0.00	1	.016
	Crick	105	2.208	108	2.100

14.2 *PCT1* (Crick Strand) CDS Read Size DistributionFigure 16: *PCT1* CDS Crick Reads Size Distribution (RP)

15 *RTN2* (Watson Strand)

15.1 Table 18: RP and TP Coverage (CDS)

CDS: ChrIV:94605..95786 (1181 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	201	4.536	370	14.755
	Crick	33	.503	63	2.433
2	Watson	272	5.972	958	37.486
	Crick	21	.320	75	2.961
3	Watson	94	2.093	3997	157.508
	Crick	12	.182	200	7.893
4	Watson	852	19.054	2488	97.808
	Crick	91	1.386	196	7.731
5	Watson	588	12.743	2247	88.870
	Crick	263	4.010	22	.791
6	Watson	1309	30.558	594	23.303
	Crick	5	.076	28	1.061
7	Watson	83	1.887	1051	42.035
	Crick	139	2.119	53	2.141
8	Watson	331	7.678	424	16.723
	Crick	43	.655	37	1.480
Control (Ingolia):					
Rich	Watson	1	.023	59	1.176
	Crick	0	0.00	1	.015
Starved	Watson	98	2.206	20	.411
	Crick	0	0.00	0	0.00

15.2 *RTN2* CDS Read Size Distribution

Ribosome Profiling (RP)

Percentage (y-axis) versus Read Size (nt)(x-axis)

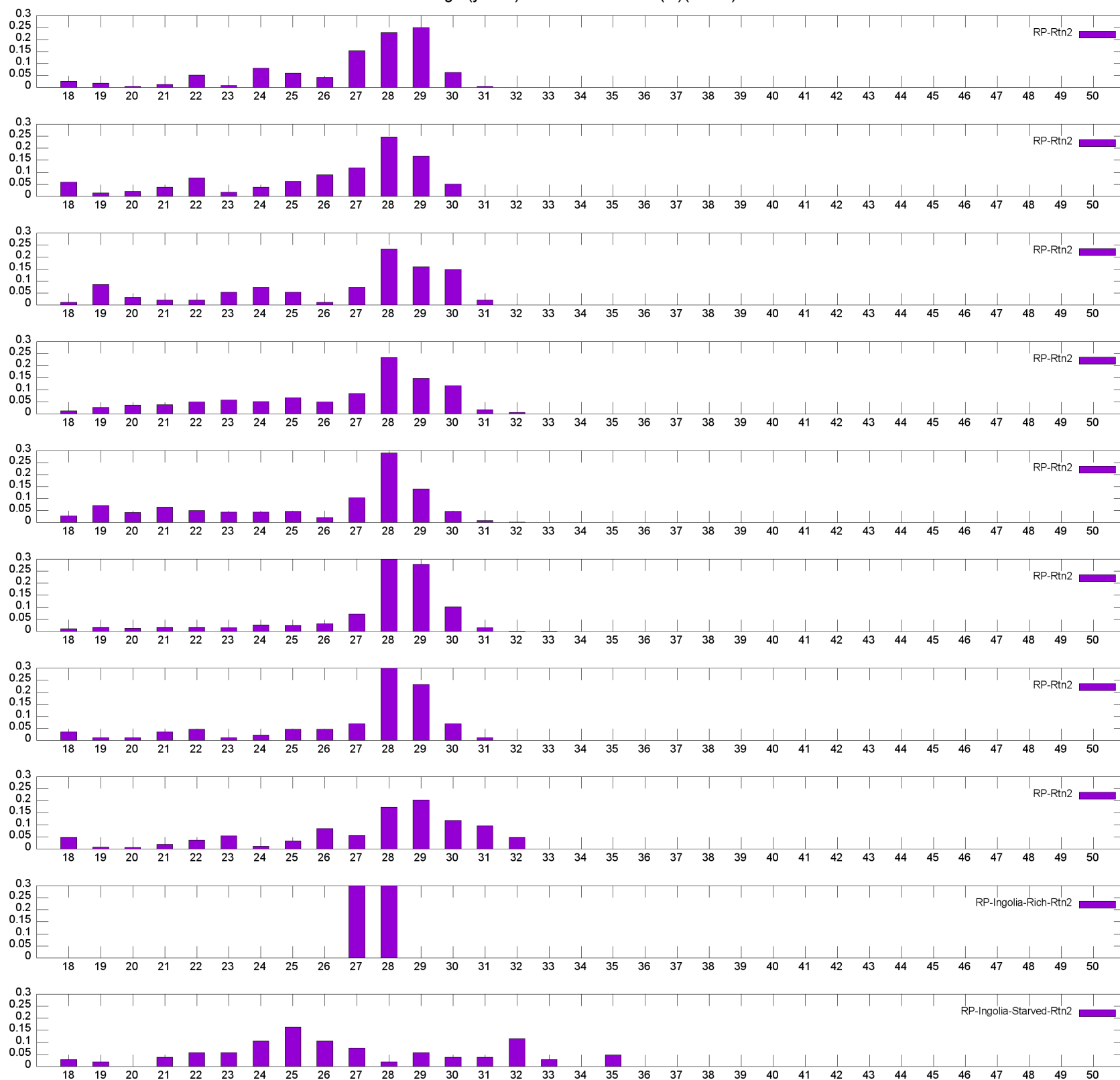


Figure 17: *RTN2* CDS Watson Reads Size Distribution (RP)

16 *TIP1* (Crick Strand)

16.1 Table 19: RP and TP Coverage (CDS)

CDS: ChrII:372103..372735 (632 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	2	.061	170	12.704
	Crick	28950	1242.158	2798	208.827
2	Watson	0	0.00	88	6.542
	Crick	20662	866.569	2658	194.045
3	Watson	0	0.00	72	5.305
	Crick	479	20.096	1330	97.743
4	Watson	1	.031	114	8.034
	Crick	24816	1058.814	1547	113.952
5	Watson	3	.125	34	2.493
	Crick	2935	121.330	332	24.762
6	Watson	1	.028	105	7.851
	Crick	1699	73.789	279	20.759
7	Watson	1	.028	66	4.935
	Crick	745	32.041	720	53.784
8	Watson	3	.088	100	7.352
	Crick	6262	273.340	920	68.463
Control (Ingolia):					
Rich	Watson	0	0.00	65	2.420
	Crick	300	12.598	849	32.642
Starved	Watson	2	.077	12	.449
	Crick	443	18.216	117	4.517

16.2 *TIP1* CDS Read Size Distribution

Ribosome Profiling (RP)

Percentage (y-axis) versus Read Size (nt)(x-axis)

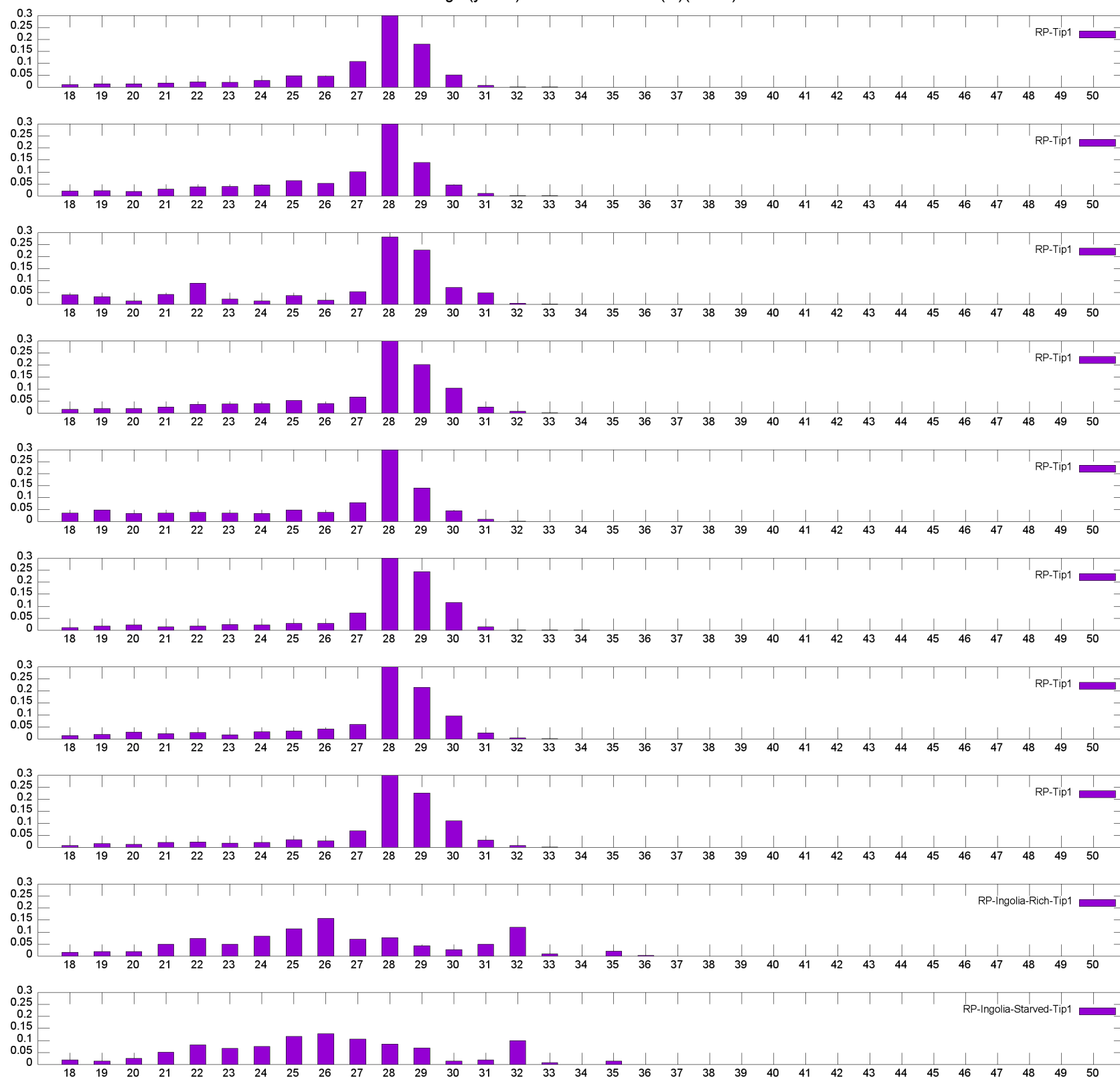


Figure 18: *TIP1* CDS Crick Reads Size Distribution (RP)

17 *YKR018C* (Crick Strand)

17.1 Table 20: RP and TP Coverage (CDS)

CDS: ChrXI:473723..475900 (2177 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	75	.881	620	13.587
	Crick	594	7.390	878	18.805
2	Watson	63	.753	878	18.904
	Crick	646	7.681	1381	28.854
3	Watson	18	.223	1711	37.110
	Crick	176	2.163	1767	37.099
4	Watson	233	2.796	1732	37.329
	Crick	1351	16.355	1457	30.408
5	Watson	69	.779	1837	39.736
	Crick	401	4.709	1396	29.395
6	Watson	29	.355	1395	30.112
	Crick	421	5.328	1852	39.086
7	Watson	45	.538	1463	31.963
	Crick	199	2.429	1782	38.167
8	Watson	94	1.186	845	18.306
	Crick	635	8.126	897	18.663
Control (Ingolia):					
Rich	Watson	40	.524	280	3.067
	Crick	127	1.633	606	6.729
Starved	Watson	33	.396	87	.948
	Crick	250	3.091	385	4.276

17.2 *YKR018C* CDS Read Size Distribution

Ribosome Profiling (RP)

Percentage (y-axis) versus Read Size (nt)(x-axis)

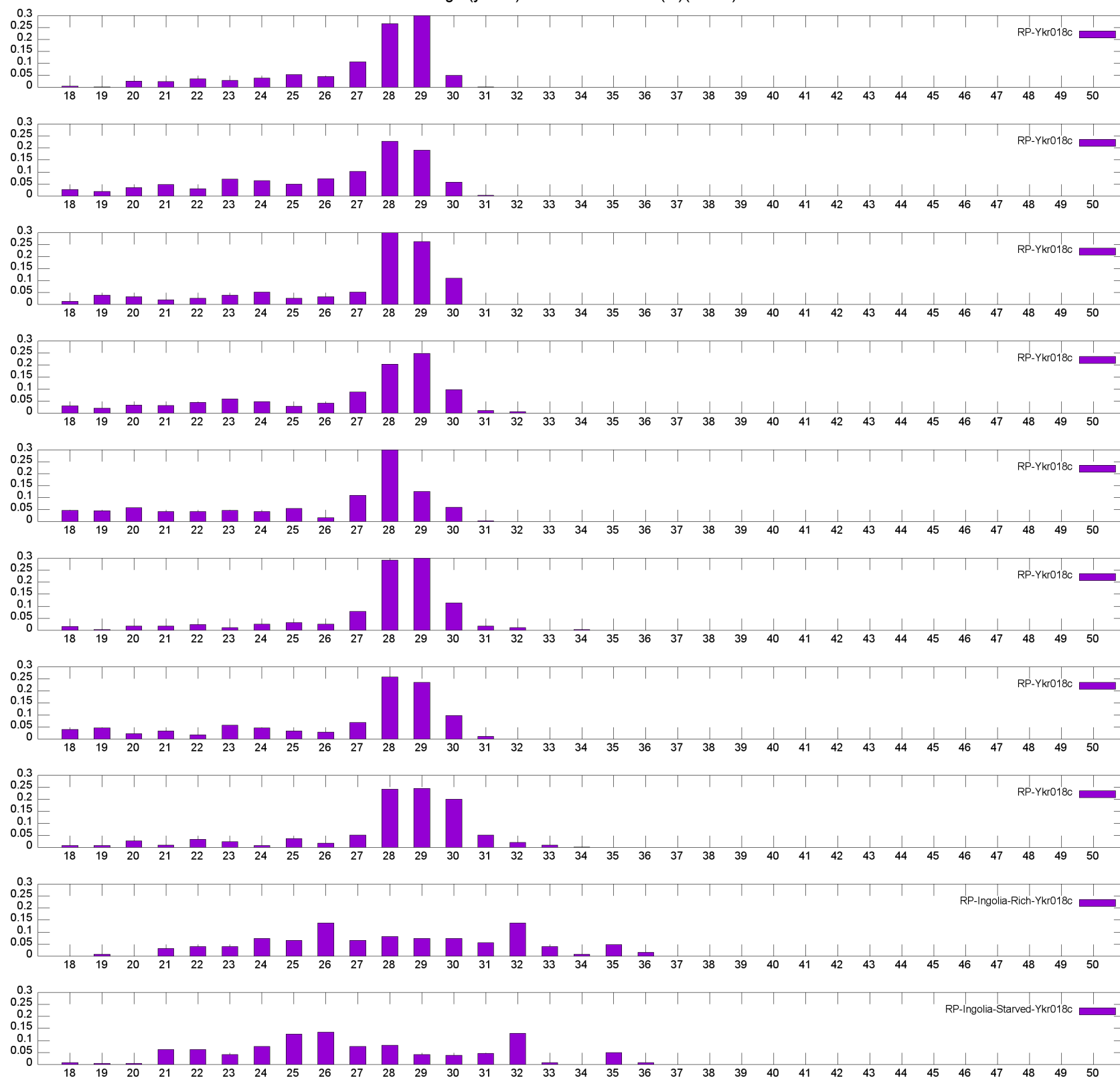


Figure 19: *YKR018C* CDS Crick Reads Size Distribution (RP)

18 *YRO2* (Watson Strand)

18.1 Table 21: RP and TP Coverage (CDS)

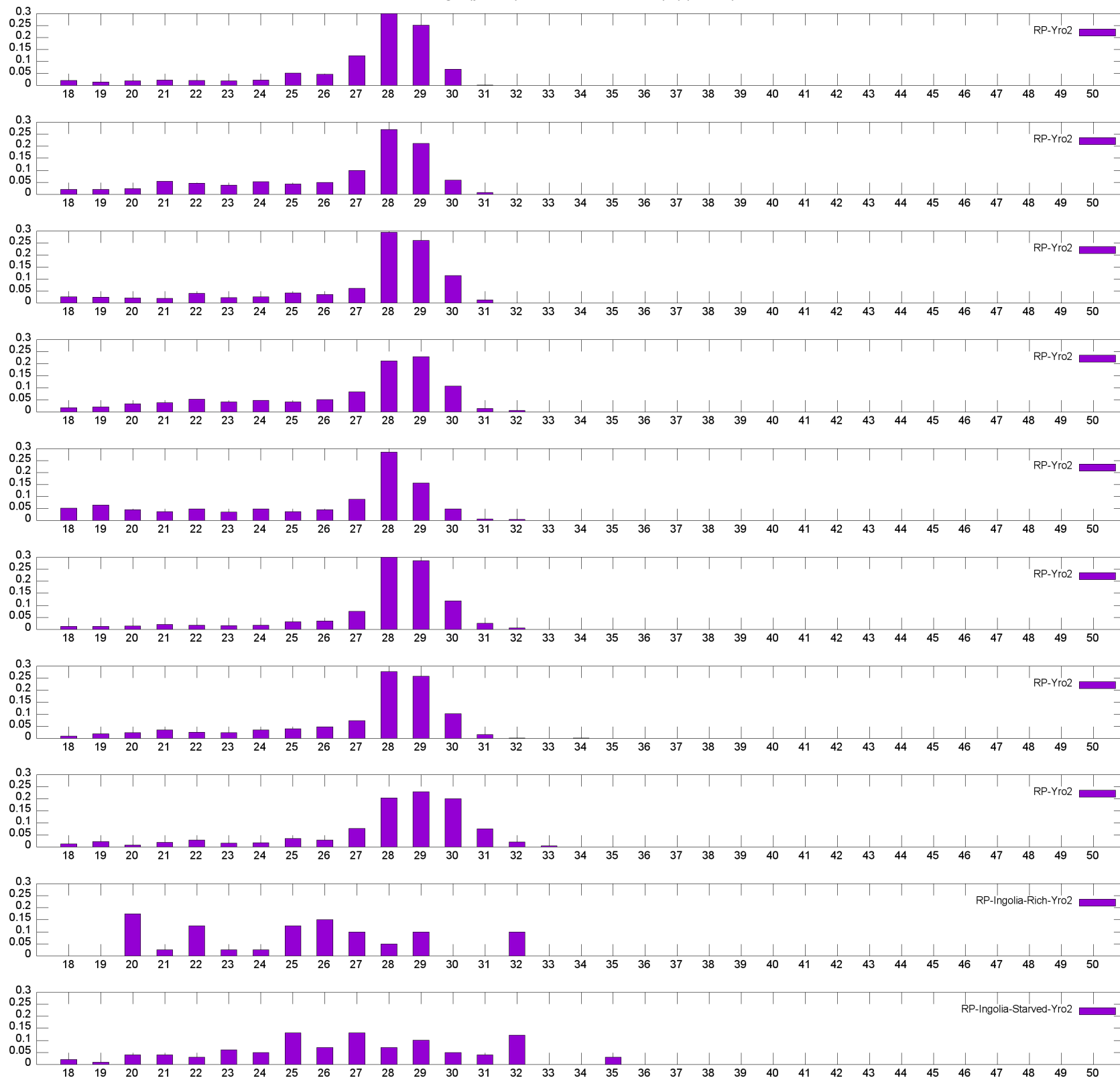
CDS: ChrII:343101..344135 (1034 bp)

Experimental:	Strand	Ribosome Profiling (RP)		Transcriptional Profiling (TP)	
		Number of Reads	Coverage	Number of Reads	Coverage
1	Watson	1686	44.113	2935	131.536
	Crick	0	0.00	217	10.076
2	Watson	1331	33.912	6197	275.793
	Crick	1	.017	114	5.176
3	Watson	576	15.059	6664	295.917
	Crick	0	0.00	177	8.049
4	Watson	6928	178.094	3635	161.989
	Crick	0	0.00	138	6.144
5	Watson	1475	36.560	2979	134.828
	Crick	0	0.00	21	.968
6	Watson	2703	72.179	5884	263.935
	Crick	0	0.00	109	4.888
7	Watson	408	10.701	1753	79.817
	Crick	0	0.00	40	1.787
8	Watson	2631	70.811	1318	58.019
	Crick	0	0.00	51	2.333
Control (Ingolia):					
Rich	Watson	36	.879	116	2.748
	Crick	0	0.00	50	1.168
Starved	Watson	94	2.414	18	.446
	Crick	2	.050	2	.038

18.2 *YRO2* CDS Read Size Distribution

Ribosome Profiling (RP)

Percentage (y-axis) versus Read Size (nt)(x-axis)

Figure 20: *YRO2* CDS Watson Reads Size Distribution (RP)