

TABLE S1 **ChIP-Seq Peaks Called with MACS**

MACS was used to call peaks of significant enrichment for the Sir protein ChIP-Seq datasets. The “Sir” column indicates the Sir protein dataset (either Sir2, Sir3 or Sir4) that the peak was identified in. The start and end coordinates indicate the chromosomal coordinate of the peak as identified by MACS. A “yes” in columns 5-7 indicate that the peak was detected in that dataset for the particular Sir protein and a “No” indicates that the peak was not called in that dataset. The “Genome Features” column indicates the genome features within the starting and ending coordinates of the peak as annotated in SGD.

Sir	Telomere	start	end	Sonication Replicate 1	Sonication Replicate 2	MNase	Genome Features
Sir2	<i>TEL01-L</i>	1	3165	Yes	Yes	Yes	TR, X element, <i>PAU8</i>
Sir3	<i>TEL01-L</i>	1	3204	Yes	Yes	Yes	TR, X element, <i>PAU8</i>
Sir4	<i>TEL01-L</i>	1	3211	Yes	Yes	Yes	TR, X element, <i>PAU8</i>
Sir2	<i>TEL01-L</i>	1	1905	No	Yes	Yes	Y'
Sir3	<i>TEL02-L</i>	1	8824	No	Yes	Yes	X-Y', <i>PAU9</i>
Sir4	<i>TEL02-L</i>	1	8824	Yes	Yes	Yes	X-Y', <i>PAU9</i>
Sir2	<i>TEL02-L</i>	4924	8824	Yes	Yes	Yes	X element, <i>PAU9</i>
Sir2	<i>TEL03-L</i>	1	18568	Yes	Yes	Yes	TR, X element, <i>YCL076W</i> , <i>YCL075W</i> , <i>YCL074W</i> , <i>GEX1</i> , <i>VBA3</i> , <i>YCL068C</i> , <i>YCL065W</i> , <i>HML</i> , <i>CHA1</i>
Sir3	<i>TEL03-L</i>	1	18622	Yes	Yes	Yes	TR, X element, <i>YCL076W</i> , <i>YCL075W</i> , <i>YCL074W</i> , <i>GEX1</i> , <i>VBA3</i> , <i>YCL068C</i> , <i>YCL065W</i> , <i>HML</i> , <i>CHA1</i>
Sir4	<i>TEL03-L</i>	1	15202	Yes	Yes	Yes	TR, X element, <i>YCL076W</i> , <i>YCL075W</i> , <i>YCL074W</i> , <i>GEX1</i> , <i>VBA3</i> , <i>YCL068C</i> , <i>YCL065W</i> , <i>HML</i>
Sir4	<i>TEL03-L</i>	15460	18178	Yes	Yes	Yes	<i>HML</i>
Sir4	<i>TEL03-R</i>	312518	315021	Yes	Yes	Yes	TR, X element
Sir2	<i>TEL03-R</i>	313064	315102	Yes	Yes	Yes	TR, X element
Sir2	<i>TEL04-L</i>	1	1725	Yes	Yes	Yes	TR, X element
Sir3	<i>TEL04-L</i>	1	1800	Yes	Yes	Yes	TR, X element
Sir4	<i>TEL04-L</i>	1	1731	Yes	Yes	Yes	TR, X element
Sir4	<i>TEL04-R</i>	1521508	1525877	No	Yes	Yes	X element, <i>PAU10</i>
Sir3	<i>TEL04-R</i>	1522260	1526289	Yes	Yes	Yes	X element, <i>PAU10</i>
Sir2	<i>TEL04-R</i>	1522281	1526268	Yes	Yes	Yes	X element, <i>PAU10</i>

Sir3	TEL04-R	1526513	1529507	No	Yes	Yes	Y'
Sir2	TEL09-L	1	5882	Yes	Yes	Yes	Y'
Sir3	TEL09-L	1	5999	Yes	Yes	Yes	Y'
Sir4	TEL09-L	1	7027	Yes	Yes	Yes	Y'
Sir2	TEL09-L	6054	9980	Yes	Yes	Yes	X element, PAU14
Sir3	TEL09-L	6057	10087	Yes	Yes	Yes	X element, PAU14
Sir4	TEL09-L	7049	9980	Yes	Yes	Yes	X element, PAU14
Sir4	TEL09-L	16947	18692	No	Yes	Yes	IMA3
Sir4	TEL09-R	437481	439152	No	Yes	Yes	X element
Sir2	TEL09-R	437501	439339	No	Yes	Yes	X element
Sir2	TEL05-L	1	7618	Yes	Yes	Yes	X-Y'
Sir3	TEL05-L	1	7804	Yes	Yes	Yes	X-Y'
Sir4	TEL05-L	1	7826	Yes	No	Yes	X-Y'
Sir4	TEL05-R	567524	571291	No	Yes	Yes	X element
Sir2	TEL05-R	568755	571249	No	Yes	Yes	X element
Sir3	TEL05-R	568818	571793	No	Yes	Yes	X element
Sir4	TEL06-L	1	7113	Yes	Yes	Yes	X-Y', YFL063W, COS4, YFL058W
Sir3	TEL06-L	1	7067	No	Yes	Yes	X-Y', YFL063W, COS4, YFL058W
Sir2	TEL06-L	374	8410	No	Yes	Yes	X-Y', YFL063W, COS4, YFL058W
Sir4	TEL06-R	263978	265355	Yes	Yes	No	IRC7
Sir3	TEL06-R	263993	265339	Yes	Yes	Yes	IRC7
Sir2	TEL06-R	264026	265321	Yes	No	Yes	IRC7
Sir3	TEL07-L	1	875	Yes	Yes	No	TR, X-element
Sir4	TEL07-R	1081144	1083523	No	Yes	Yes	COS6
Sir2	TEL07-R	1082655	1085210	Yes	Yes	Yes	X element
Sir3	TEL07-R	1083258	1085832	No	Yes	Yes	X element
Sir3	TEL07-R	1085851	1087178	No	Yes	Yes	Y'
Sir2	TEL08-L	1	2478	Yes	Yes	Yes	X element
Sir3	TEL08-L	1	2476	Yes	Yes	Yes	X element
Sir4	TEL08-L	1	6631	Yes	Yes	Yes	X-Y'
Sir3	TEL08-L	4505	6572	No	Yes	Yes	X element
Sir2	TEL08-L	4521	6542	Yes	Yes	Yes	X element
Sir4	TEL08-R	552041	558152	Yes	Yes	No	X element, Y', IMD2
Sir3	TEL08-R	552750	562261	No	Yes	Yes	X element, Y', IMD2
Sir2	TEL08-R	552885	557851	Yes	Yes	Yes	X element, Y', IMD2
Sir2	TEL10-L	1	5942	Yes	Yes	Yes	Y'
Sir3	TEL10-L	1	7045	Yes	Yes	Yes	Y'
Sir4	TEL10-L	1	10006	Yes	Yes	Yes	X-Y'
Si, Y'L10-L	6061	9999	Yes	Yes	Yes	X element	

Sir3	TEL10-L	7070	10068	Yes	Yes	Yes	X element
Sir2	TEL11-L	1	3067	Yes	Yes	Yes	TR, X element, PAU16
Sir3	TEL11-L	1	3107	Yes	Yes	Yes	TR, X element, PAU16
Sir4	TEL11-L	1	3117	Yes	Yes	Yes	TR, X element, PAU16
Sir4	TEL11-R	658211	660866	Yes	Yes	Yes	VBA5
Sir3	TEL11-R	658212	660806	Yes	Yes	Yes	VBA5
Sir2	TEL11-R	658227	660267	Yes	Yes	Yes	VBA5
Sir3	TEL11-R	660881	663222	Yes	Yes	No	GEX2
Sir2	TEL11-R	661907	664824	X	No	Yes	GEX2
Sir3	TEL12-L	1	4543	No	Yes	Yes	Y'
Sir2	TEL12-L	1	4537	Yes	Yes	Yes	Y'
Sir4	TEL12-L	1	14200	Yes	Yes	Yes	X-Y'
Sir3	TEL12-L	4752	10100	Yes	Yes	Yes	X-Y'
Sir2	TEL12-L	4786	10091	Yes	Yes	Yes	X-Y'
Sir3	TEL12-L	10354	14187	No	Yes	Yes	X-Y'
Sir2	TEL12-L	10392	14195	Yes	Yes	Yes	X-Y'
Sir3	TEL12-R	1061965	1066024	No	Yes	Yes	X element, PAU4
Sir4	TEL12-R	1061988	1072866	Yes	Yes	No	X element, PAU4
Sir2	TEL12-R	1062036	1066015	Yes	Yes	Yes	X element, PAU4
Sir3	TEL12-R	1066129	1072549	No	Yes	Yes	Y'
Sir2	TEL12-R	1066155	1072450	Yes	Yes	Yes	Y'
Sir3	TEL12-R	1072672	1077188	No	Yes	Yes	Y'
Sir2	TEL13-L	1	4459	Yes	Yes	Yes	Y'
Sir3	TEL13-L	1	4429	Yes	Yes	Yes	Y'
Sir4	TEL13-L	1	7494	Yes	Yes	Yes	X-Y'
Sir3	TEL13-L	4617	7435	Yes	Yes	Yes	X element
Sir2	TEL13-L	4658	7401	Yes	Yes	Yes	X element
Sir2	TEL14-L	1	5012	Yes	Yes	Yes	Y'
Sir3	TEL14-L	1	5265	No	Yes	Yes	Y'
Sir4	TEL14-L	1	8603	Yes	Yes	Yes	X-Y'
Sir2	TEL14-L	5748	8491	Yes	Yes	Yes	X element
Sir3	TEL14-L	5748	8575	Yes	Yes	Yes	X element
Sir2	TEL15-L	1	2868	Yes	Yes	Yes	X element, AAD15
Sir4	TEL15-L	1	2883	Yes	Yes	Yes	X element, AAD15
Sir3	TEL15-L	1	2924	Yes	Yes	Yes	X element, AAD15
Sir4	TEL15-L	10818	12699	Yes	Yes	No	PAU20
Sir3	TEL15-L	10840	12798	Yes	Yes	No	PAU20
Sir3	TEL15-R	1082035	1085505	No	Yes	Yes	X element, PAU21
Sir2	TEL15-R	1082045	1085443	Yes	Yes	Yes	X element, PAU21
Sir3	TEL15-R	1085649	1090020	No	Yes	Yes	Y'

Sir2	TEL16-L	1	4519	Yes	Yes	Yes	Y'
Sir3	TEL16-L	1	5215	No	Yes	Yes	Y'
Sir4	TEL16-L	1	8760	Yes	Yes	Yes	Y'
Sir2	TEL16-L	5594	9094	Yes	Yes	Yes	X element
Sir3	TEL16-L	5648	9097	No	Yes	Yes	X element
Sir3	TEL16-R	941574	945387	No	Yes	Yes	X element
Sir2	TEL16-R	942173	944929	No	Yes	Yes	X element
Sir2	TEL16-R	945624	947502	No	Yes	Yes	Y'

TABLE S2 Percent Reads Mapped of RNA-Seq Data

Strain	Alias	Replicate	Total Reads	Reads Mapped	% Reads Mapped	% Mapped Non-uniquely
JRY9316	Wild type	A	15,747,860	14,480,231	92	6.94
JRY9316	Wild type	B	20,204,590	18,636,063	92	6.76
JRY9316	Wild type	C	19,988,764	18,323,263	91.7	8.98
JRY9720	<i>sir2Δ</i>	A	13,176,140	12,290,225	93	7.58
JRY9721	<i>sir2Δ</i>	B	13,865,402	12,737,081	92	6.10
JRY9722	<i>sir2Δ</i>	C	12,505,868	11,519,936	92.1	6.71
JRY9723	<i>sir3Δ</i>	A	19,925,570	18,454,658	92.6	6.8
JRY9724	<i>sir3Δ</i>	B	20,806,146	19,352,189	93	6.45
JRY9725	<i>sir3Δ</i>	C	19,655,418	18,102,386	92.1	6.43
JRY9726	<i>sir4Δ</i>	A	14,217,780	12,973,038	91	5.51
JRY9727	<i>sir4Δ</i>	B	15,272,748	14,043,542	92	6.20
JRY9728	<i>sir4Δ</i>	C	13,785,048	12,561,860	91	5.85

TABLE S3 Reads Mapped to Y' Elements

Strain	Alias	% Reads Mapped to Y'	% Of Total Y' Reads Uniquely Mapped
JRY9316	Wild type	0.044	18.8
JRY9316	Wild type	0.055	17.3
JRY9316	Wild type	0.058	18.9
JRY9720	<i>sir2Δ</i>	0.053	20.0
JRY9721	<i>sir2Δ</i>	0.056	19.9
JRY9722	<i>sir2Δ</i>	0.052	19.4
JRY9723	<i>sir3Δ</i>	0.011	19.2
JRY9724	<i>sir3Δ</i>	0.010	19.2
JRY9725	<i>sir3Δ</i>	0.010	18.7
JRY9726	<i>sir4Δ</i>	0.048	18.8
JRY9727	<i>sir4Δ</i>	0.050	18.3
JRY9728	<i>sir4Δ</i>	0.056	18.9

Average % Uniquely-Mapped Y' reads: 18.95%

TABLE S4 Normalized Read Counts Of Uniquely-Mapped Reads at Y' Elements

Y' Element	Wild type	<i>sir2Δ</i>	<i>sir3Δ</i>	<i>sir4Δ</i>
<i>TEL04R-YP</i>	0.0	0.0	0.0	0.0
<i>TEL16L-YP</i>	0.0	0.0	0.0	0.0
<i>TEL08L-YP</i>	130.6	185.8	159.0	174.1
<i>TEL07R-YP</i>	0.0	0.0	0.0	0.0
<i>TEL06L-YP</i>	61.8	76.6	94.3	70.9
<i>TEL05R-YP</i>	23.7	17.4	24.6	22.4
<i>TEL13L-YP</i>	3.9	3.3	5.2	5.4
<i>TEL05L-YP</i>	209.6	199.5	206.2	203.1
<i>TEL12R-YP2</i>	16.0	20.6	17.3	15.8
<i>TEL12-R YP1</i>	0.0	0.0	0.0	0.0
<i>TEL14L-YP</i>	0.0	0.0	0.0	0.0
<i>TEL15R-YP</i>	0.0	0.0	0.0	0.0
<i>TEL16R-YP</i>	78.2	61.7	53.2	56.3
<i>TEL08R-YP</i>	4.3	6.5	13.1	8.4
<i>TEL10L-YP</i>	10.5	6.2	15.3	4.8
<i>TEL12L-YP2</i>	16.1	15.6	13.4	20.0
<i>TEL09L-YP</i>	0.5	0.0	0.0	0.0
<i>TEL02L-YP</i>	140.5	168.3	147.4	167.7
<i>TEL12L-YP1</i>	0.8	0.0	0.3	0.4

TABLE S5 Strains Used In This Study

Name	Genotype	Source
JRY9316	<i>matΔ::HygMX can1-100 his3-11 leu2-3,112 lys2- trp1-1 ura3-52</i>	TEYTELMAN <i>et al.</i> 2013
JRY9720	<i>matΔ::HygMX can1-100 his3-11 leu2-3,112 lys2- trp1-1 ura3-52 sir2Δ::KanMX</i>	This study
JRY9721	<i>matΔ::HygMX can1-100 his3-11 leu2-3,112 lys2- trp1-1 ura3-52 sir2Δ::KanMX</i>	This study
JRY9722	<i>matΔ::HygMX can1-100 his3-11 leu2-3,112 lys2- trp1-1 ura3-52 sir2Δ::KanMX</i>	This study
JRY9723	<i>matΔ::HygMX can1-100 his3-11 leu2-3,112 lys2- trp1-1 ura3-52 sir3Δ::KanMX</i>	This study
JRY9724	<i>matΔ::HygMX can1-100 his3-11 leu2-3,112 lys2- trp1-1 ura3-52 sir3Δ::KanMX</i>	This study
JRY9725	<i>matΔ::HygMX can1-100 his3-11 leu2-3,112 lys2- trp1-1 ura3-52 sir3Δ::KanMX</i>	This study
JRY9726	<i>matΔ::HygMX can1-100 his3-11 leu2-3,112 lys2- trp1-1 ura3-52 sir4Δ::KanMX</i>	This study
JRY9727	<i>matΔ::HygMX can1-100 his3-11 leu2-3,112 lys2- trp1-1 ura3-52 sir4Δ::KanMX</i>	This study
JRY9728	<i>matΔ::HygMX can1-100 his3-11 leu2-3,112 lys2- trp1-1 ura3-52 sir4Δ::KanMX</i>	This study
JRY9741	<i>matΔ::HygMX can1-100 his3-11 leu2-3,112 lys2- trp1-1 ura3-52 sir2Δ::KanMX hmlΔ::SpHIS5MX</i>	This study

TABLE S6 Oligos Used in qRT-PCR Expression Analysis

Gene	Forward	Reverse
<i>ACT1</i>	ggcatcataccttctacaacg	ctaccggaagagtacaaggacaaaac
<i>STE14</i>	gaagaccaagaaggagtccg	gtagctgagtccaattgcc
<i>TOS1</i>	gccaagtgacaccagcggttct	ttggccgtcatggatgtgtgag
<i>AXL2</i>	acggaatcactcccacaacaatgtc	ggtcttctgtctggttccatgc
<i>MHF2</i>	tcattgatgaggcgggtgctg	cttgatgcgataacttaaggac
<i>STE2</i>	gataggtttatccaggcacgctg	ttgaactcgtagggtgggcaactg
<i>HO</i>	gaaatcatgtcaggctgctg	ccatagcatctagcacatactc
<i>YGL193C</i>	ccttcctatagctccagcg	ccggtcacataaattgacgg

TABLE S7 Complete List of Genes Increasing in Expression in *sir2Δ*, *sir3Δ*, and *sir4Δ*

Shown below are expression levels in FPKM for the 107 genes that significantly increased in expression across all three *sir* mutants (*sir2Δ*, *sir3Δ*, and *sir4Δ*). Genes are listed in alphabetical order by gene name. Expression changes were filtered based on a p-value < 0.05 and a false-discovery rate of < 0.10. Forty-two genes (bold-faced type) showed expression changes of 2-fold or greater in *sir* mutants relative to wild type as analyzed by DESeq in terms of read counts (NOT FPKM). Transcript quantification in terms of FPKM was done with Cufflinks.

Gene	Systematic Name	Wild type	<i>sir2Δ</i>	<i>sir3Δ</i>	<i>sir4Δ</i>
AAD15	YOL165C	2.1	7.2	10.1	10.4
ADH7	YCR105W	11	15.1	15.3	15.3
ADI1	YMR009W	146.4	182.5	264.1	287.1
AHP1	YLR109W	218.2	480.6	438.6	526.6
ARO9	YHR137W	62.4	75.7	116.2	91.7
BNA2	YJR078W	7.7	11.2	14.1	12.5
BNA4	YBL098W	27.3	37.9	42.7	45.7
BNA5	YLR231C	26.8	44.2	71	69.8
CAR1	YPL111W	47.6	84.3	73.4	83.5
CHA1	YCL064C	51.2	148	229.4	242.2
CMC4	YMR194C-B	12.5	14.8	20.7	23.5
COA2	YPL189C-A	64.4	152.4	128	140.4
COS1	YNL336W	134	191.3	252.7	302.1
COS4	YFL062W	5	12.5	15.3	18.1
COS7	YDL248W	36	51.3	67.6	71.9
COS8	YHL048W	115.6	161.5	233.2	266.9
COX5A	YNL052W	198.4	240.4	394.7	248.9
COX6	YHR051W	175.9	235.6	255.3	243.4
COX7	YMR256C	204.3	322.7	408.4	286.6
CRC1	YOR100C	1.4	3.3	3.2	3.1
CYB5	YNL111C	146.4	254.6	572	316.5
CYC1	YJR048W	130.8	444.2	513.5	267.8
CYC7	YEL039C	11.2	26.8	99.7	62.9
CYT1	YOR065W	55.5	82.3	172.5	105.1
DLD1	YDL174C	31	40	49.8	47
EDC1	YGL222C	17.4	21.9	23.2	23.6
ERG13	YML126C	302.4	372.5	544	388
ERG6	YML008C	161.4	188.7	219.9	206.6
ERG8	YMR220W	49.2	60.6	71.6	61.8
FDH1	YOR388C	1.4	2.7	2.5	2.7
FMP43	YGR243W	1.3	10.4	8.5	8.3

GEX1	YCL073C	0.1	0.4	0.5	0.5
GTO3	YMR251W	3.7	7.6	8.5	10.6
HAP4	YKL109W	53.7	96.6	124.1	92.8
HMLALPHA1	YCL066W	0	20.7	16.6	14.1
HMLALPHA2	YCL067C	0	38.7	32.3	48.9
HMRA1	YCR097W	0	40.6	33.4	39.5
HMRA2	YCR096C	0.1	31.9	23.9	39.5
HMX1	YLR205C	6.7	29.3	44	24.5
HOR2	YER062C	52.9	98.8	137.2	133.8
HPF1	YOL155C	61.2	82.2	114.6	118.9
HSP12	YFL014W	51.7	126	113.8	80.1
HSP31	YDR533C	38.9	50.6	59.5	51.9
ICY1	YMR195W	97.8	209.9	154.8	175.8
IDH2	YOR136W	131.4	170.1	228.2	205.1
IDI1	YPL117C	97.6	140.3	143.1	128.8
IMD1	YAR073W	0.1	1.1	1.1	1.1
IMD2	YHR216W	61.5	234.2	331.9	352.5
JID1	YPR061C	3.2	9.1	8.3	8.5
MCR1	YKL150W	126.7	171.6	266	258.6
MET10	YFR030W	18.4	24.5	37.1	29.2
MET14	YKL001C	69.2	119	151.7	129.4
MET3	YJR010W	25.7	40.1	81.4	56.8
MMP1	YLL061W	17.1	22.8	43.6	34.9
MTH1	YDR277C	6.8	14.3	18.8	16.6
MVD1	YNR043W	202.2	242.2	333.8	252.7
NCA3	YJL116C	10.1	24.4	28.4	25.8
NDE1	YMR145C	204.4	523.2	487.4	351
NSG2	YNL156C	69.4	97.9	121.2	101
PAU4	YLR461W	0.5	1.1	1.6	1.9
PDH1	YPR002W	2.1	3.4	4.7	3.2
PET10	YKR046C	229.5	282.1	381.2	322.5
PRX1	YBL064C	32.5	39.7	46.3	54.7
PUT4	YOR348C	4.8	12.2	13.2	9.3
QCR10	YHR001W-A	72.4	103.2	222.3	142.1
QCR2	YPR191W	76.7	97.3	149.9	110.3
QCR6	YFR033C	149.3	247.8	247.8	233.7
QCR7	YDR529C	200.4	255.1	390.8	288
QCR8	YJL166W	193.6	289.7	396.2	318.6
QCR9	YGR183C	238.2	301	606	344.7
REX3	YLR107W	20.5	33.5	28.5	31.6
ROX1	YPR065W	20.5	35.1	95	57.5

RSB1	YOR049C	21.9	45.5	45.6	49.3
SER1	YOR184W	148.1	195.8	192.6	198.8
SER3	YER081W	102.3	135.7	131.3	160.3
SFC1	YJR095W	0.8	1.6	1.4	1.8
TGL2	YDR058C	9	12.4	13.5	15.4
THI5	YFL058W	1.3	4.4	3.8	3.1
UBX6	YJL048C	86.8	119.6	218.7	162.9
VBA3	YCL069W	0.4	3.5	3.9	4.5
YAR075W	YAR075W	1.6	26	21.9	25
YBR284W	YBR284W	2.1	3	3.7	4
YCL065W	YCL065W	0	14.9	9.1	9.2
YCL068C	YCL068C	0.1	4.8	0.5	7.4
YCL074W	YCL074W	0	4.5	6.5	4.9
YCL075W	YCL075W	0	1.9	2.6	2.8
YCL076W	YCL076W	0	3.3	2.8	3.5
YCR097W-A	YCR097W-A	0	8.8	5.6	6.2
YDR018C	YDR018C	2.2	4.2	4.1	4.5
YDR042C	YDR042C	4.6	19.4	14.6	10.7
YDR119W-A	YDR119W-A	27	70.8	145.3	136.2
YER053C-A	YER053C-A	0	777.5	1640.7	371.2
YFL063W	YFL063W	0	1.7	1.2	0.4
YFR057W	YFR057W	0.2	12	9.7	10.8
YGL258W-A	YGL258W-A	3.4	13.1	27.8	29.7
YGR182C	YGR182C	44.8	55.8	48.5	56.5
YILO14C-A	YILO14C-A	19.4	28.6	29	23.5
YJL047C-A	YJL047C-A	0	39.2	9.5	11.8
YJL133C-A	YJL133C-A	67.2	183.8	152	303.5
YJR115W	YJR115W	11.2	20.9	21.3	24.5
YKR075C	YKR075C	8.1	24.6	36.1	38.5
YLR312C	YLR312C	2	3.6	4.8	5.4
YLR460C	YLR460C	2	3.5	4.4	4.1
YMR206W	YMR206W	2.2	4.9	4.9	6
YNL337W	YNL337W	0	2.2	0.4	0.6
YNR064C	YNR064C	6.1	9.5	9.1	10.7
YPC1	YBR183W	53.8	101.6	150.1	130.5
YPS5	YGL259W	0.2	2.9	3.3	2.7

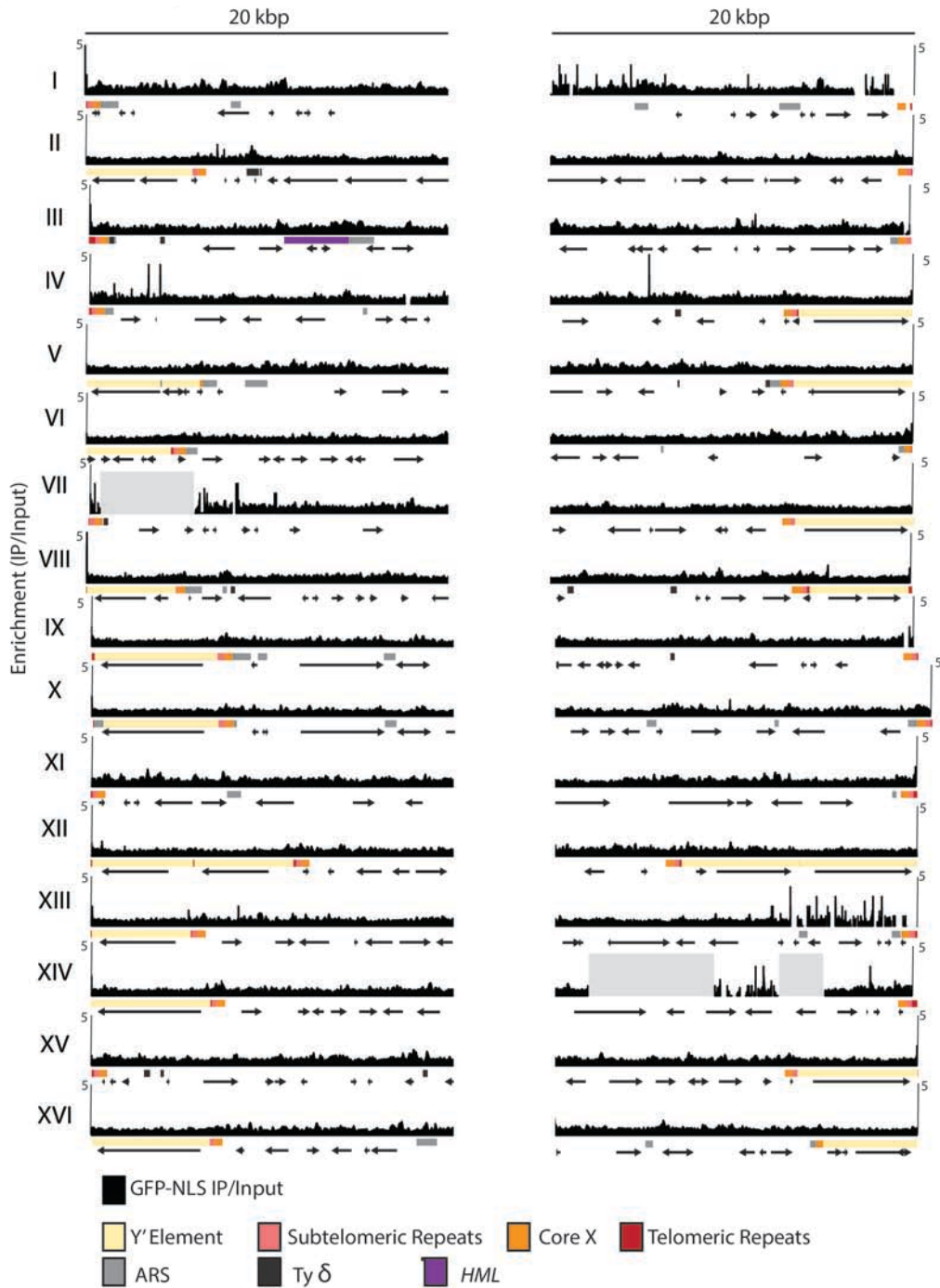


Figure S1. GFP-NLS ChIP-Seq control at all thirty-two yeast telomers. The IP/Input enrichment values of the GFP-NLS ChIP-Seq dataset from (TEYTELMAN *et al.* 2013) was mapped at all thirty-two *S. cerevisiae* telomers. 20 kbp for each telomere is shown. Salient features as annotated in SGD are indicated below the X-axis for each telomere as in Figure 2. The light gray rectangles indicate regions deleted in the sequenced W303 derived lab strain relative to the SGD sacCer2 reference genome.

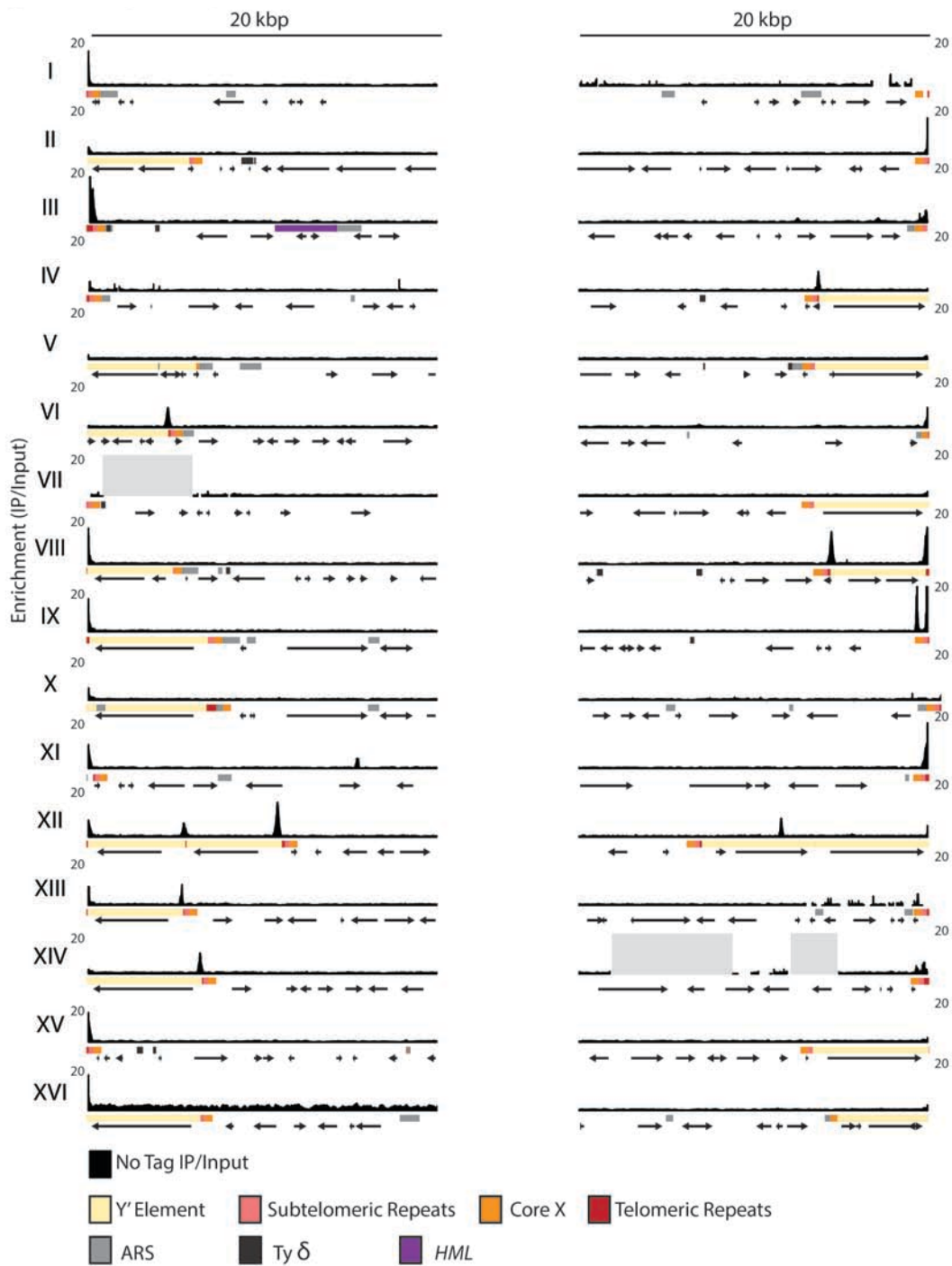


Figure S2. No tag ChIP-Seq control at all thirty-two yeast telomeres. The IP/Input enrichment values of the no tag ChIP-Seq dataset from (THURTLÉ and RINE 2014) was mapped at all thirty-two *S. cerevisiae* telomeres. 20 kbp for each telomere is shown. Salient features as annotated in SGD are indicated below the X-axis for each telomere as in Figure 2. The light gray rectangles indicate regions deleted in the sequenced W303 derived lab strain relative to the SGD sacCer2 reference genome.

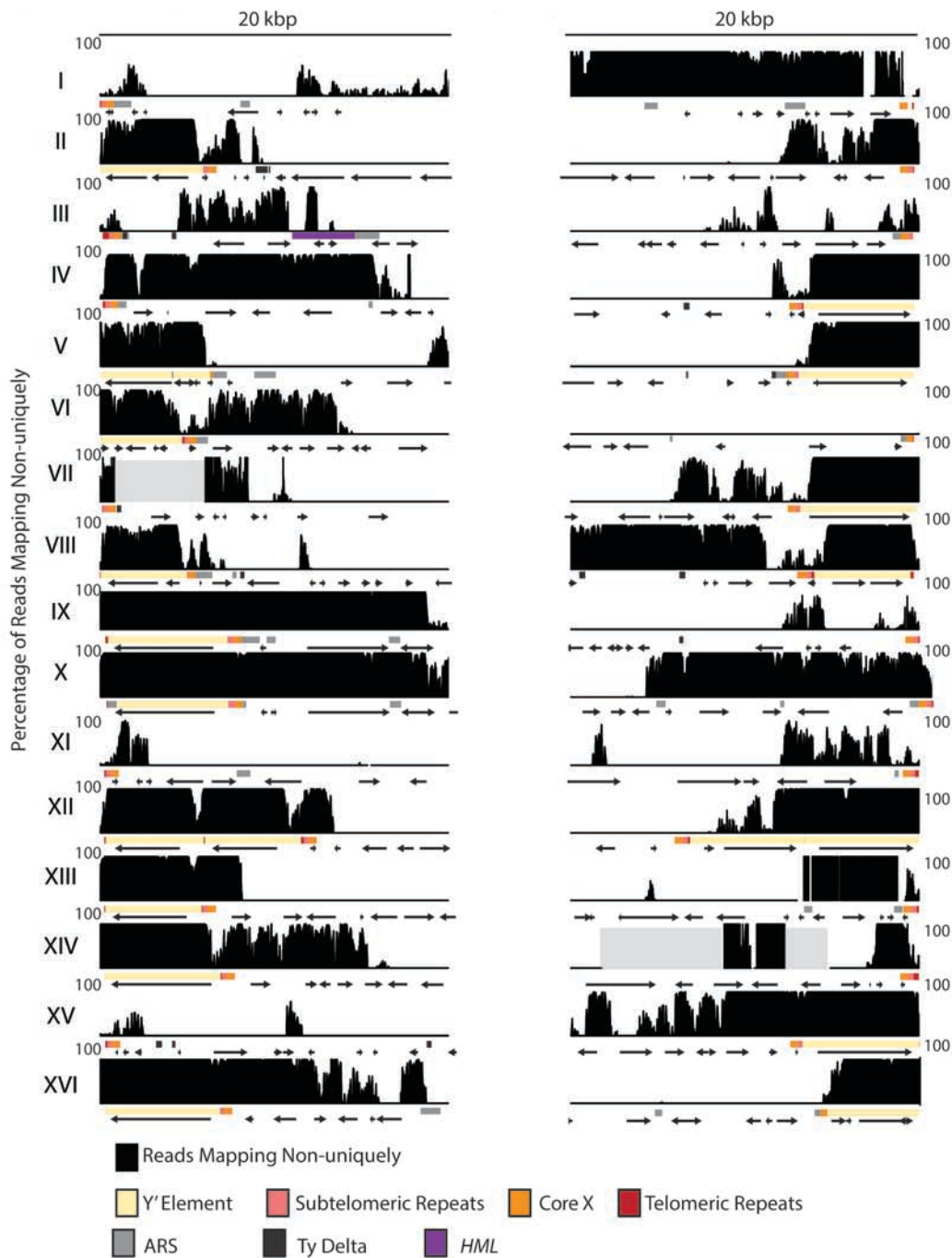


Figure S3. Percentage of non-uniquely mapping reads from ChIP-Seq experiments at all thirty-two telomeres. Reads that mapped non-uniquely in the Sir4 input dataset from (THURTLER and RINE 2014) were determined by those reads with a MAPQ flag of 0. The number of reads that mapped non-uniquely at that base-pair position was determined and divided by the total number of reads that mapped at that position. This percentage of non-uniquely mapped reads was plotted for each telomere. 20 kbp for each telomere is shown. Salient features as annotated in SGD are indicated below the X-axis for each telomere as in Figure 2. The light gray rectangles indicate regions deleted in the sequenced W303 derived lab strain relative to the SGD *sacCer2* reference genome.

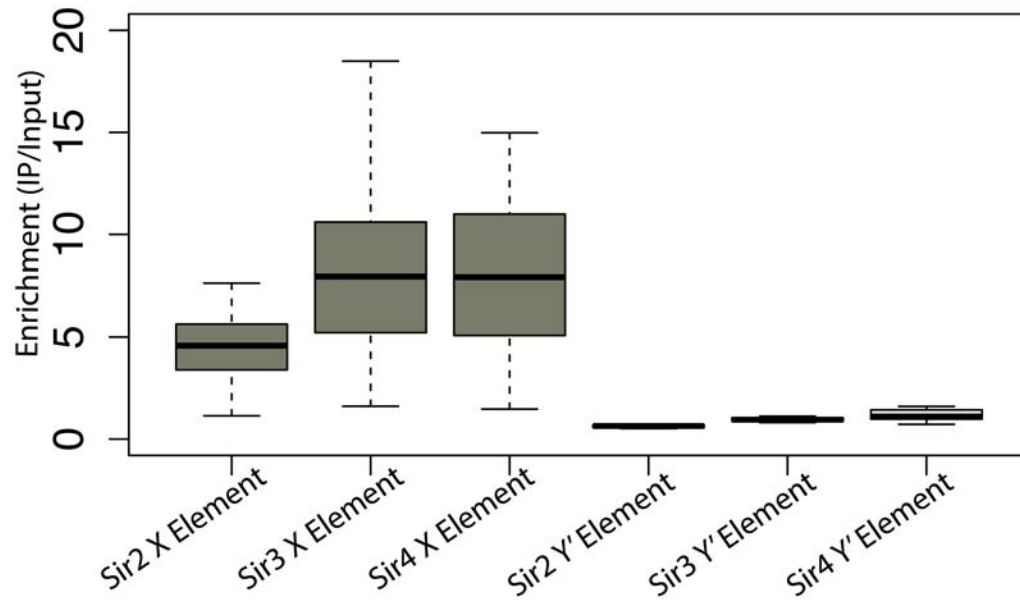


Figure S4. Sir proteins are not enriched at Y' elements. Average enrichment for all annotated X elements and Y' elements was calculated for all three Sir proteins. Enrichment was determined by the average IP/Input for that sample for the X elements and Y' elements for each chromosome as defined in SGD.

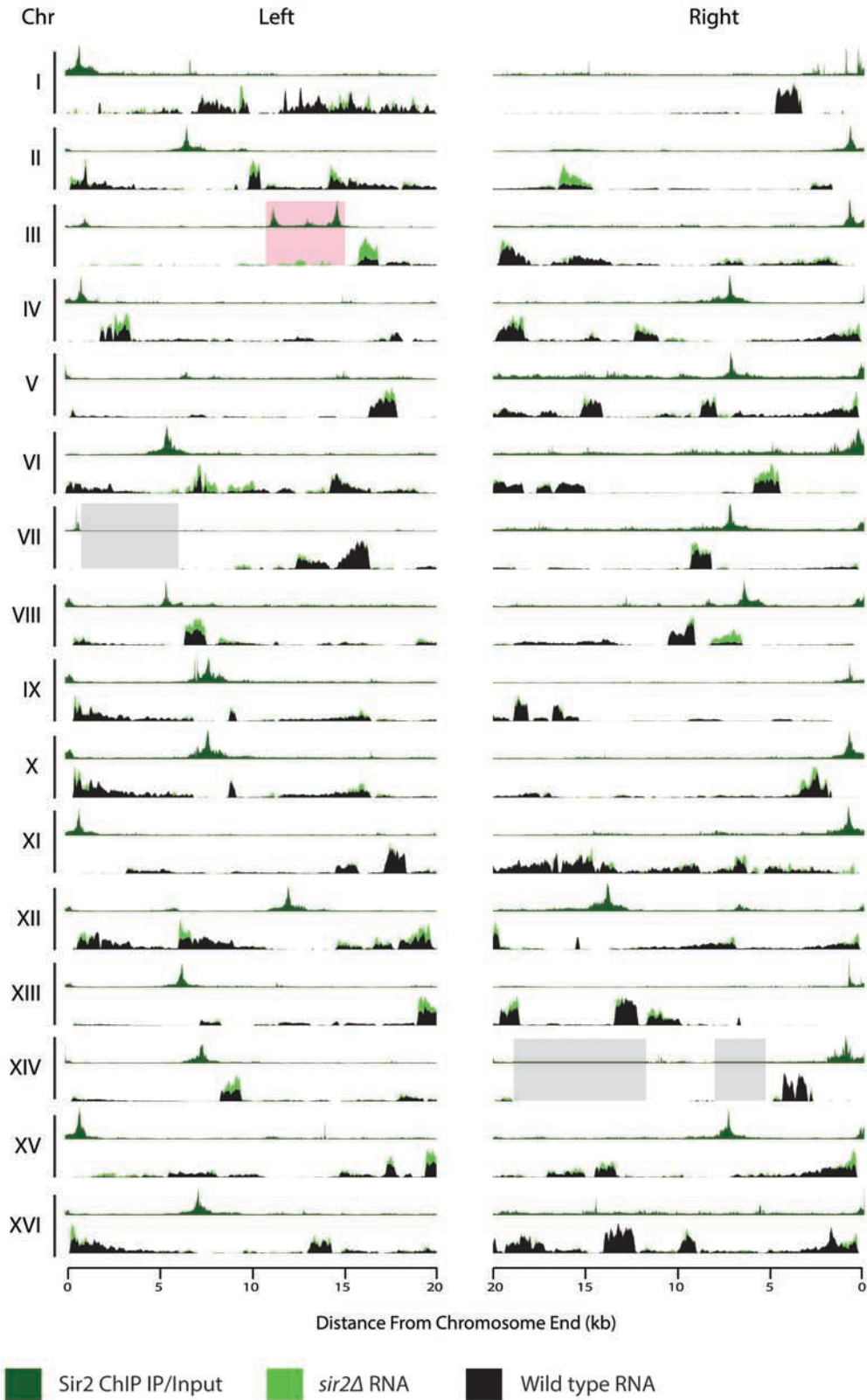


Figure S5. Transcription occurs in subtelomeric genes adjacent to peaks of Sir2 protein. For each telomere arm, top axis shows Sir2 IP/input (dark green) and lower axis shows transcription in the form of RNA read pileups in wild type (black) *sir2Δ* (light green).

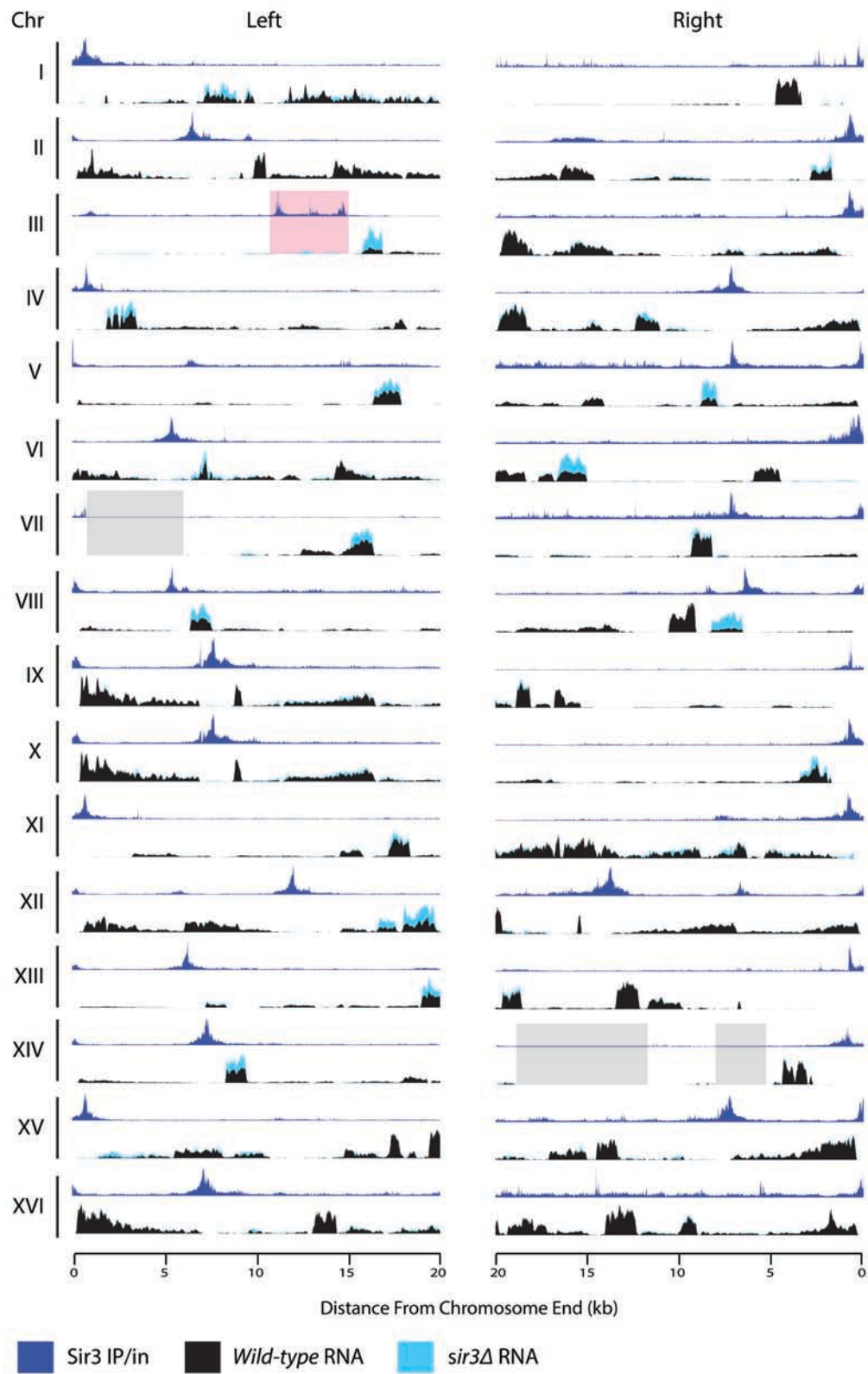


Figure S6. A comparison of Sir3 protein association and expression in wild type *sir3Δ*. For each telomere arm, top axis shows Sir3 IP/input (dark blue) and lower axis displays transcription as RNA read pileups in wild type (black) and *sir3Δ* (light blue).

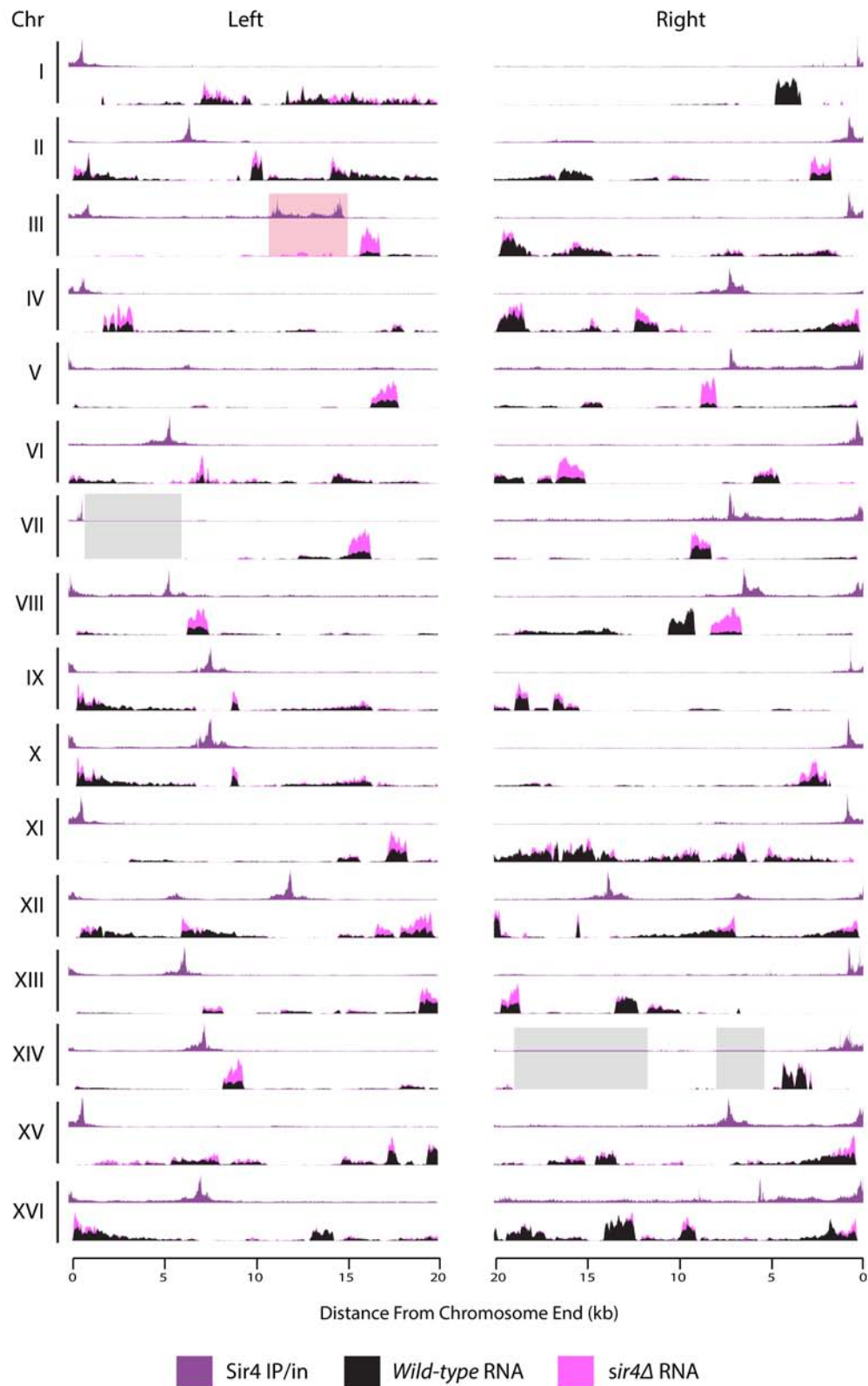


Figure S7. Comparison of Sir4 protein association and expression in wild type and *sir4Δ*. For each telomere arm, top axis shows Sir4 IP/input (dark purple) and lower axis shows transcription as RNA read pileups in wild type (black) and *sir4Δ* (pink).

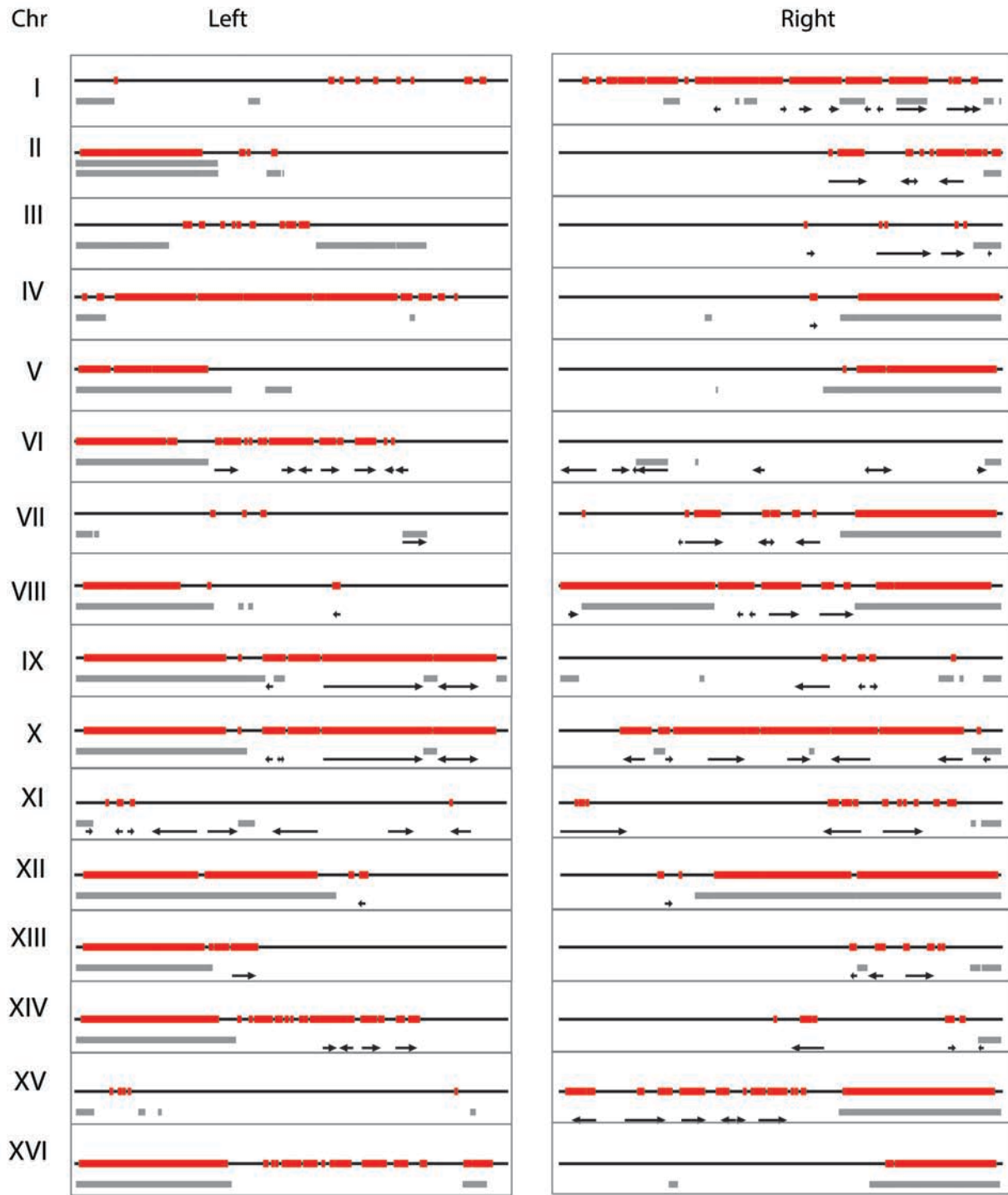


Figure S8. Positions of non-uniquely mapping reads across all thirty-two telomeres from RNA-Seq experiments. Shown in red are regions of all thirty-two telomeres that contribute non-uniquely mapping reads in RNA-Seq experiments. Positions of annotated Y' elements, Ty δ elements, telomeric repeats, and X elements are shown in gray boxes. Black arrows depict ORFs.