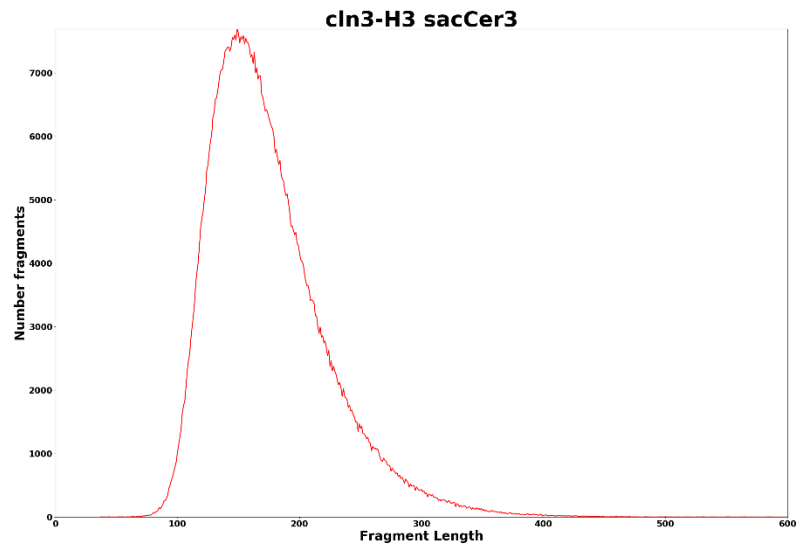
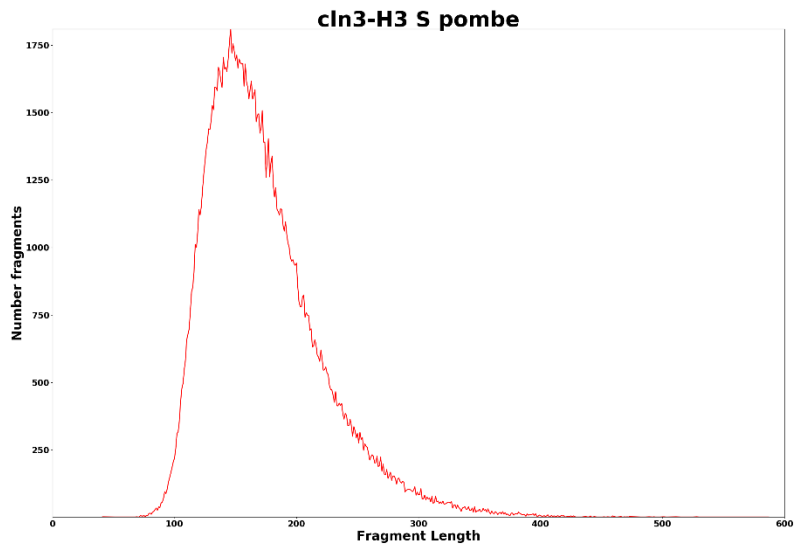
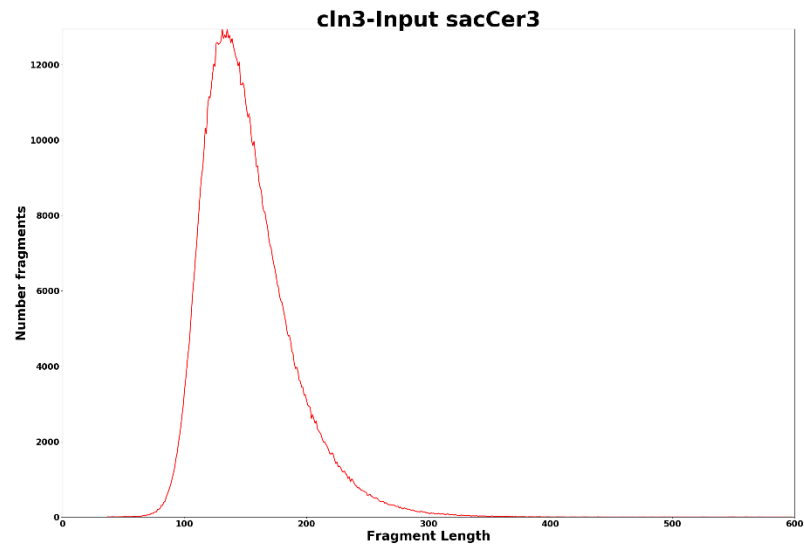
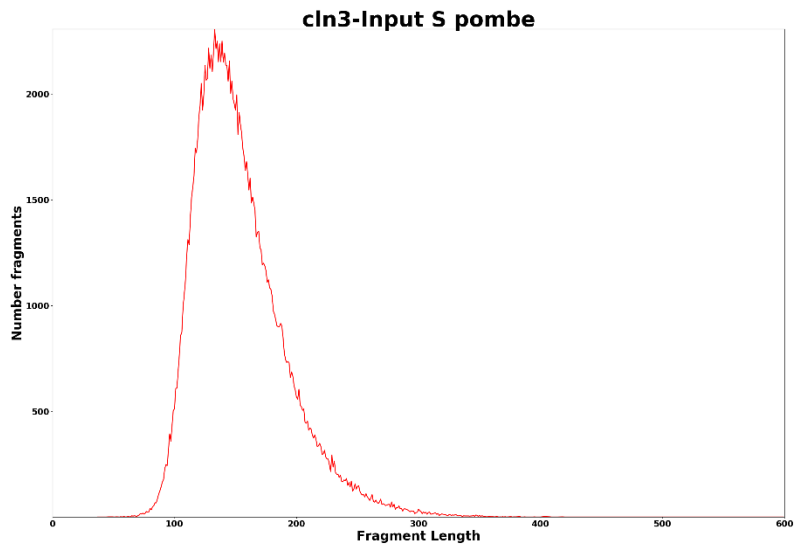
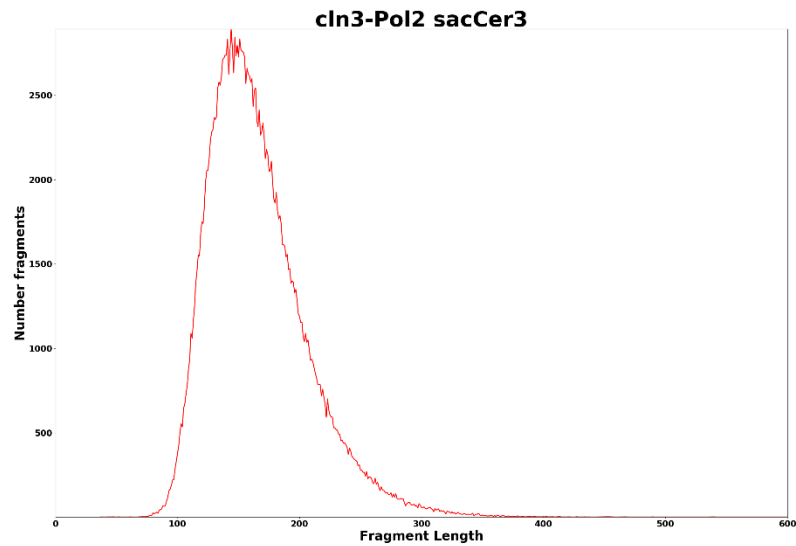
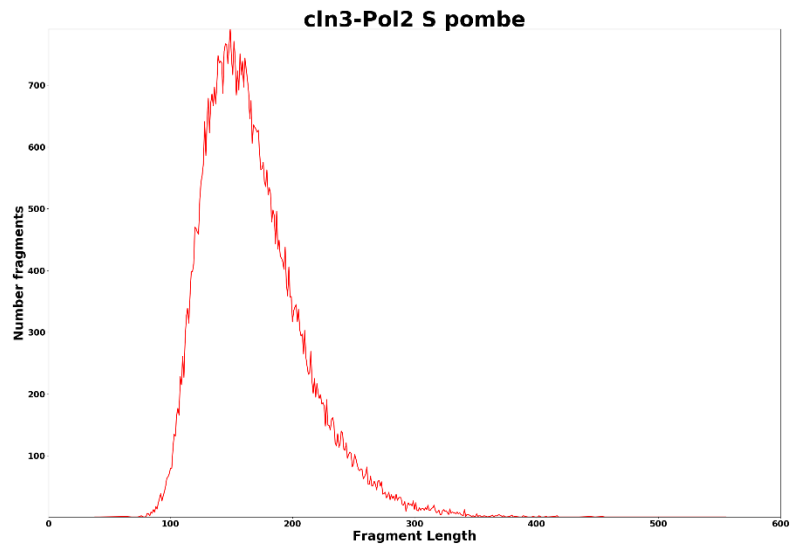


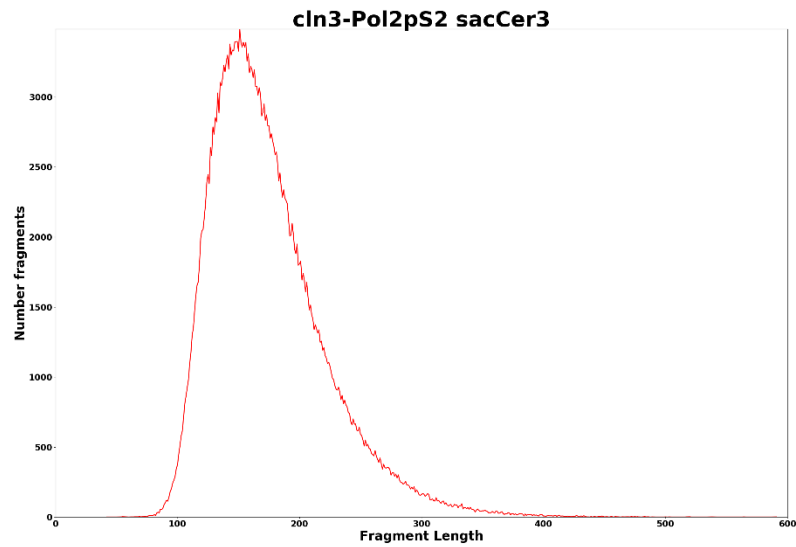
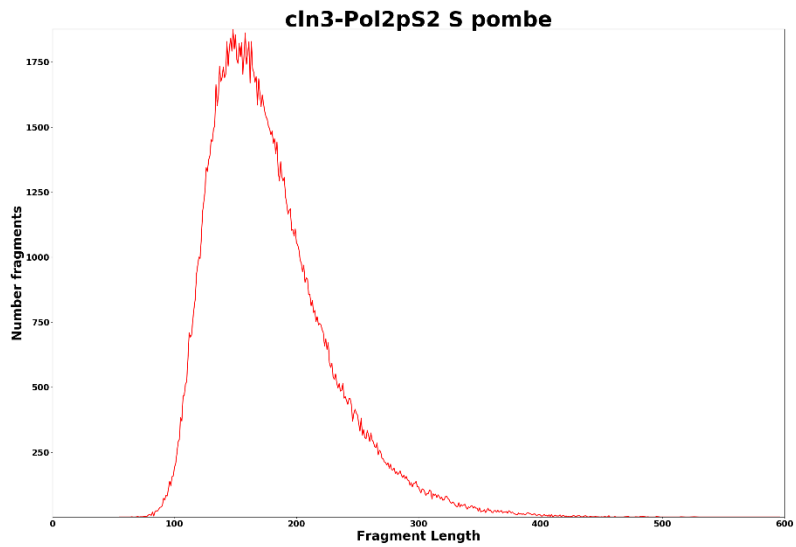
Dataset stats

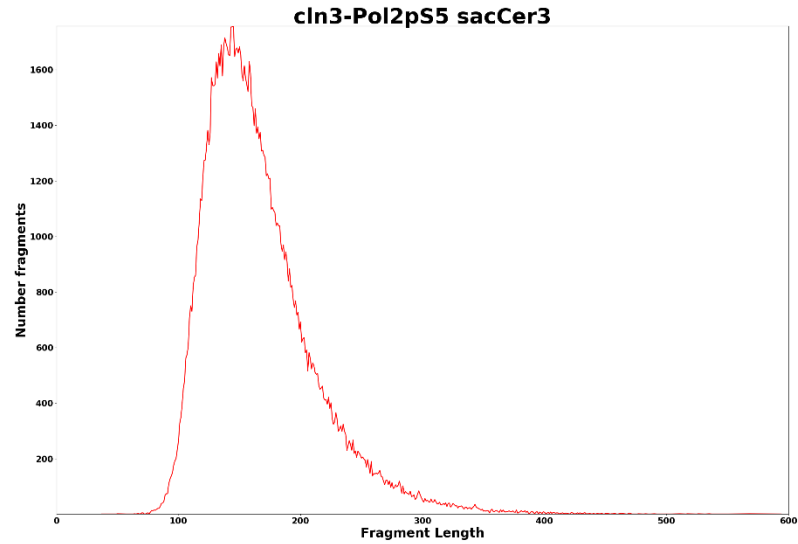
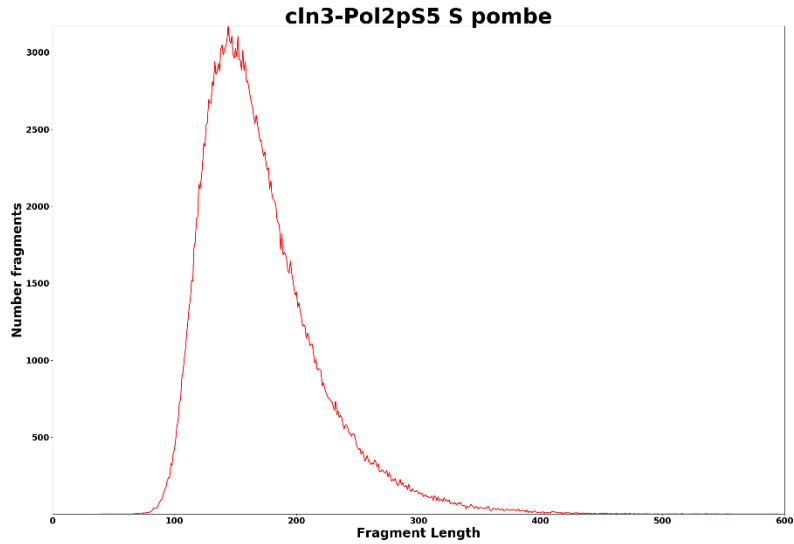
Library	Raw fragments	Species	2x36mers		1x36mers		Mappability Corrected RPKM
			Unique non-chrM reads	Complexity	Unique non-chrM reads	Complexity	
WT-H3	1,064,508	sacCer3	1,064,528	0.97	536,713	0.96	69.66
	1,064,508	S.pombe	264,160	0.99	133,460	0.99	16.43
WT-Input	615,834	sacCer3	805,132	0.98	404,907	0.98	74.01
	615,834	S.pombe	141,106	0.99	70,949	0.99	12.30
WT-Pol2	812,719	sacCer3	772,936	0.96	390,550	0.96	69.45
	812,719	S.pombe	195,266	0.98	98,571	0.98	16.63
WT-Pol2pS2	724,576	sacCer3	577,786	0.96	293,261	0.96	56.75
	724,576	S.pombe	308,428	0.97	156,231	0.97	28.67
WT-Pol2pS25	840,788	sacCer3	471,840	0.97	238,486	0.97	33.35
	840,788	S.pombe	760,898	0.96	383,524	0.96	50.87
cln3-H3	1,436,625	sacCer3	1,509,632	0.97	760,729	0.96	71.20
	1,436,625	S.pombe	334,466	0.99	168,538	0.99	14.96
cln3-Input	1,796,984	sacCer3	1,936,920	0.97	976,332	0.96	73.97
	1,796,984	S.pombe	341,372	0.99	171,789	0.99	12.34
cln3-Pol2	434,701	sacCer3	482,620	0.98	243,009	0.98	68.21
	434,701	S.pombe	132,890	0.99	66,860	0.99	17.80
cln3-Pol2pS2	671,364	sacCer3	654,598	0.97	330,625	0.97	55.77
	671,364	S.pombe	366,916	0.97	184,985	0.97	29.60
cln3-Pol2pS25	610,734	sacCer3	300,588	0.98	152,613	0.98	30.12
	610,734	S.pombe	569,874	0.96	288,067	0.96	53.93
whi5-H3	1,201,314	sacCer3	1,138,238	0.97	574,493	0.96	61.24
	1,201,314	S.pombe	478,280	0.99	241,492	0.99	24.42
whi5-Input	2,229,447	sacCer3	2,426,126	0.96	1,224,910	0.95	72.07
	2,229,447	S.pombe	502,180	0.99	253,399	0.99	14.14
whi5-Pol2	918,837	sacCer3	960,044	0.95	485,651	0.95	70.70
	918,837	S.pombe	221,524	0.97	111,824	0.98	15.44
whi5-Pol2pS2	1,430,630	sacCer3	965,332	0.94	489,313	0.94	64.43
	1,430,630	S.pombe	339,026	0.95	171,278	0.96	21.39
whi5-Pol2pS25	1,433,030	sacCer3	678,682	0.96	345,660	0.96	38.63
	1,433,030	S.pombe	852,574	0.95	432,639	0.94	45.86

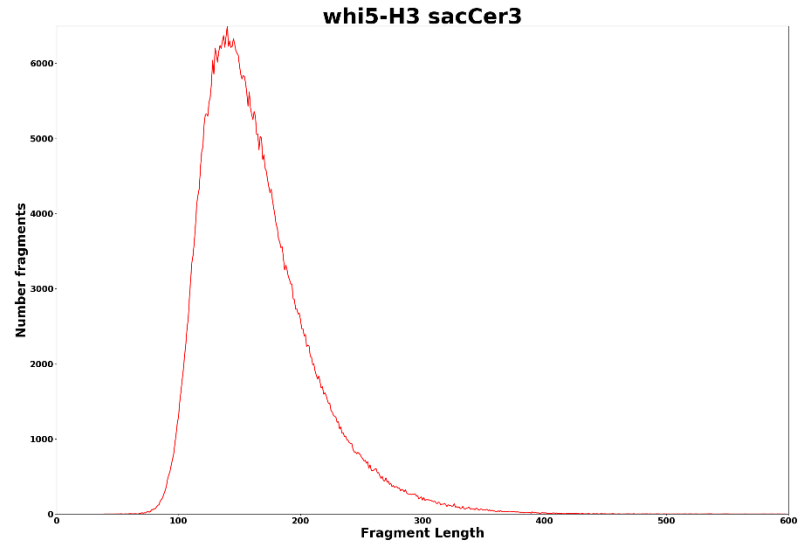
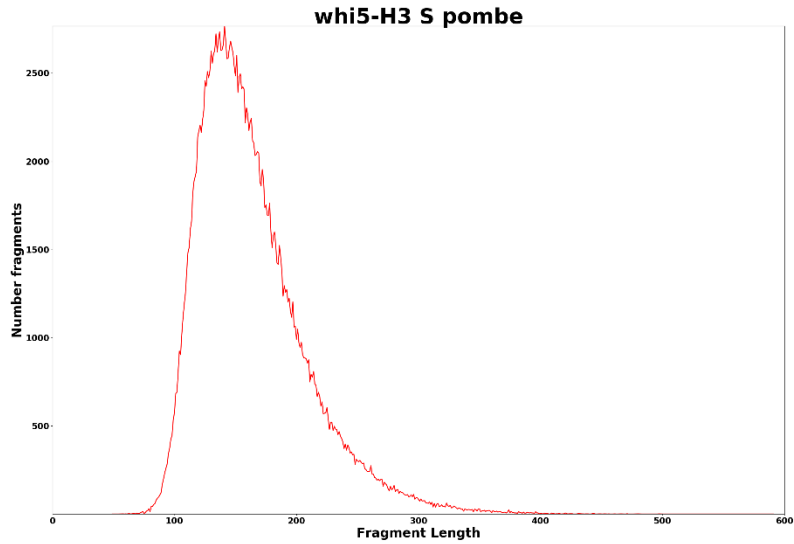


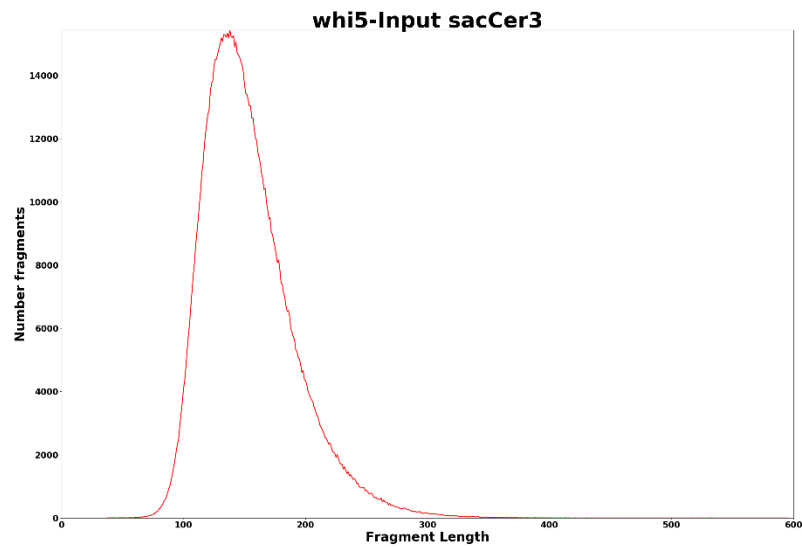
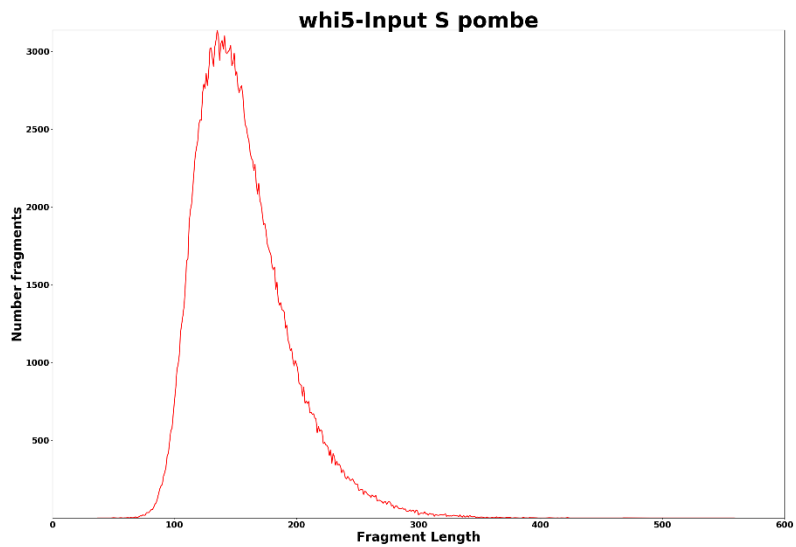


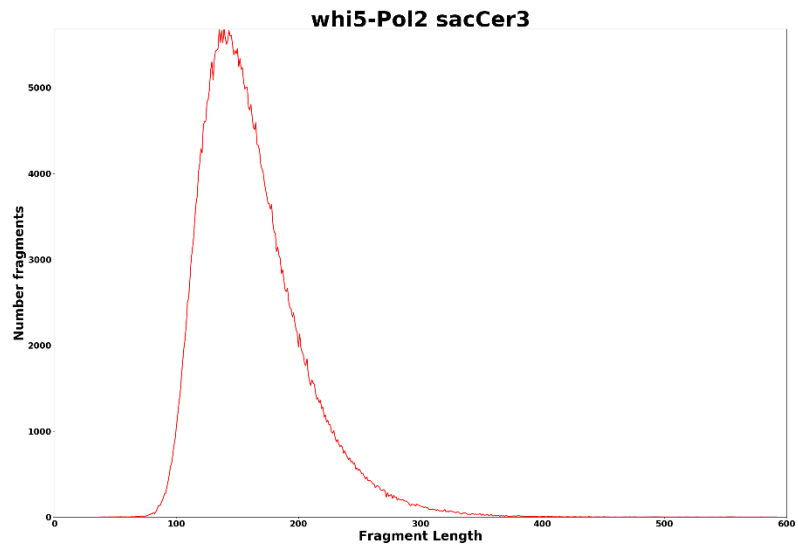
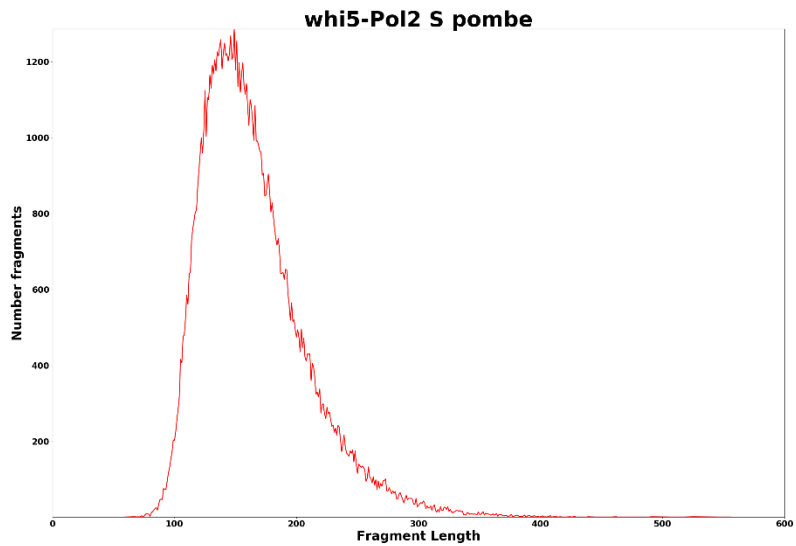


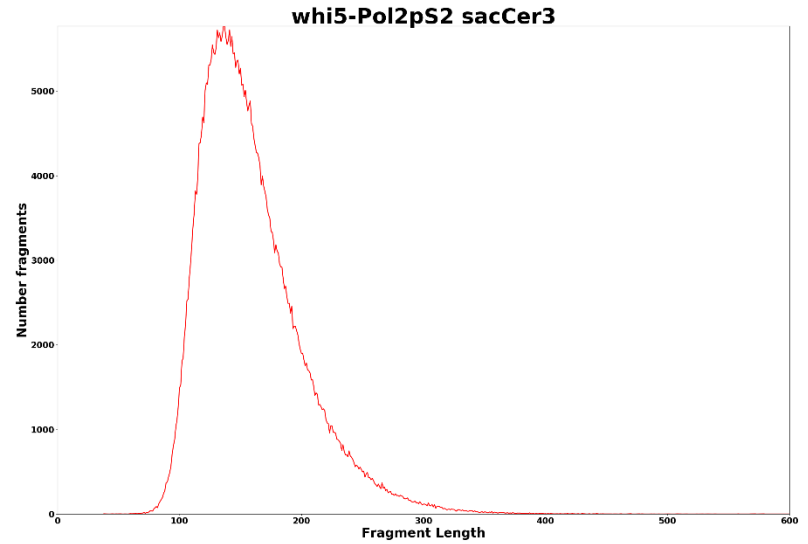
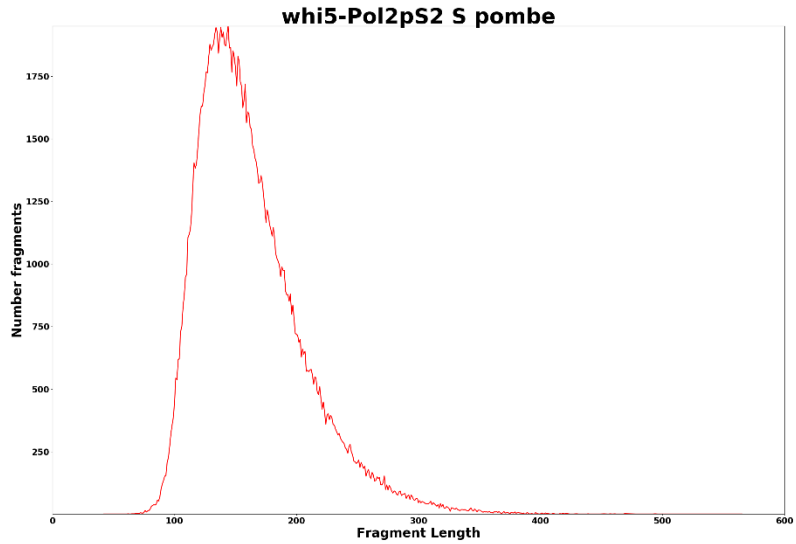


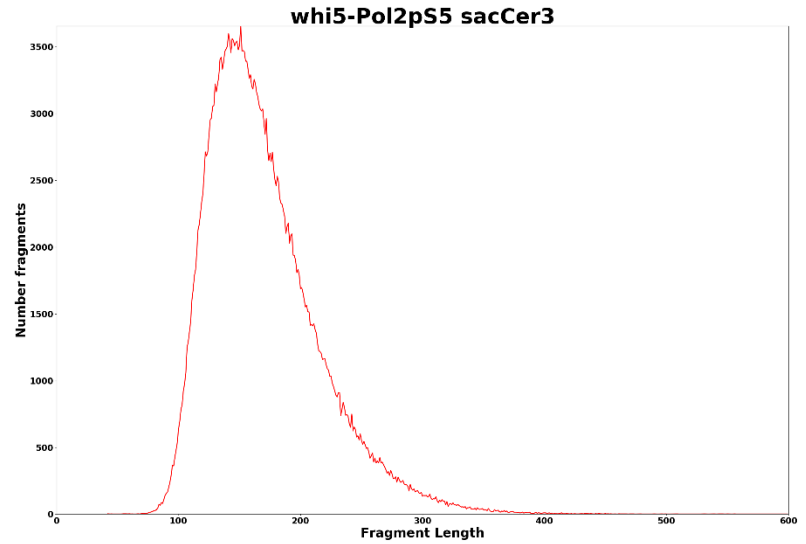
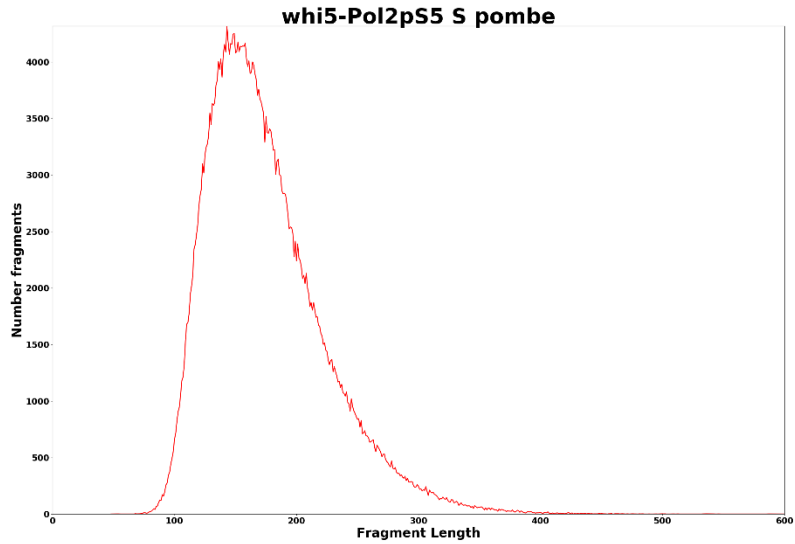


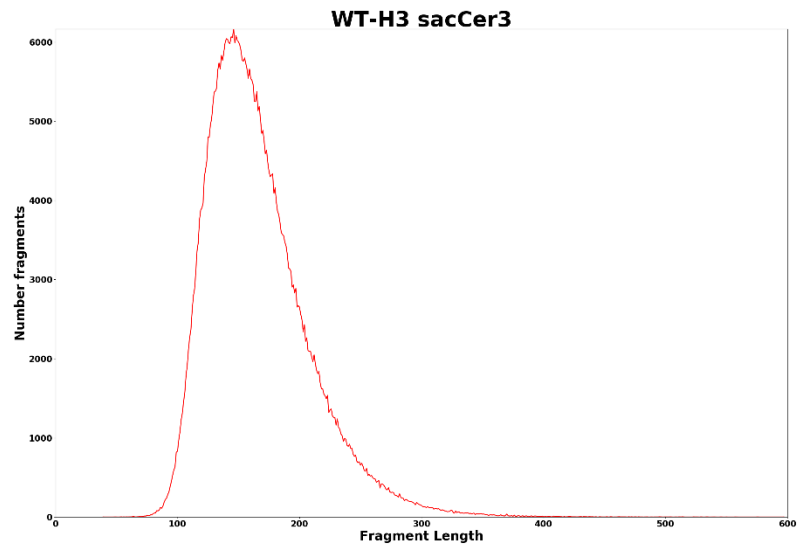
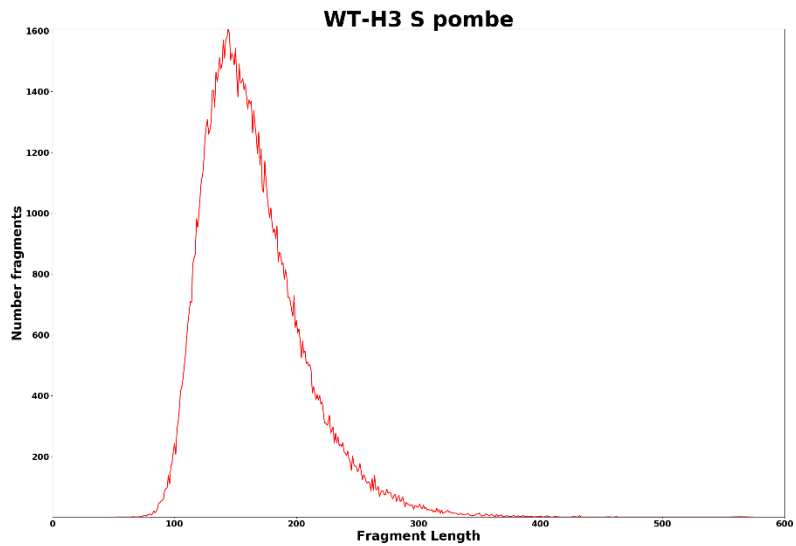


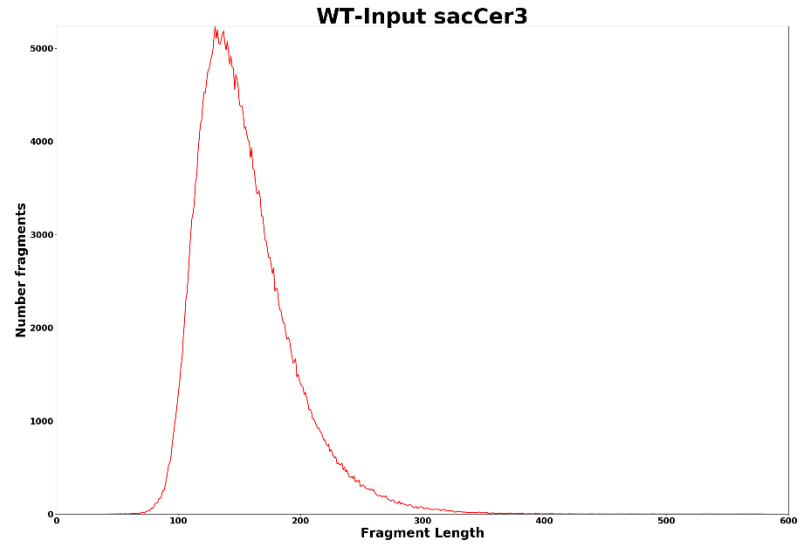
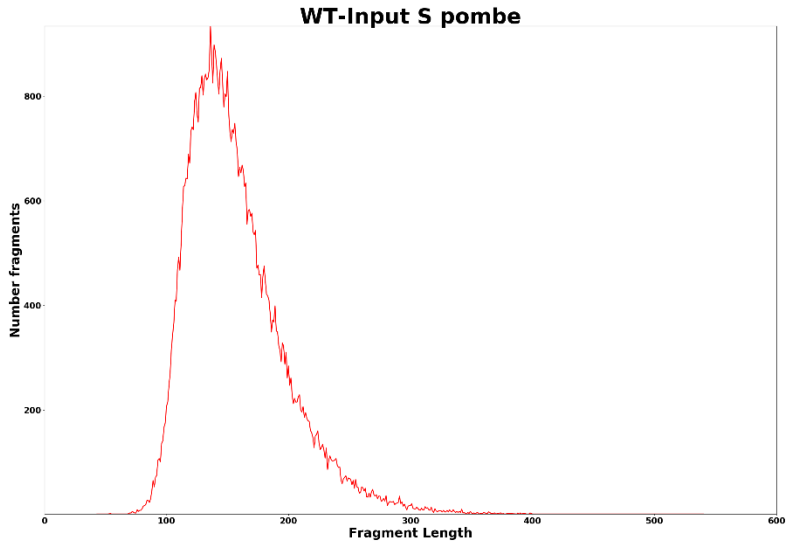


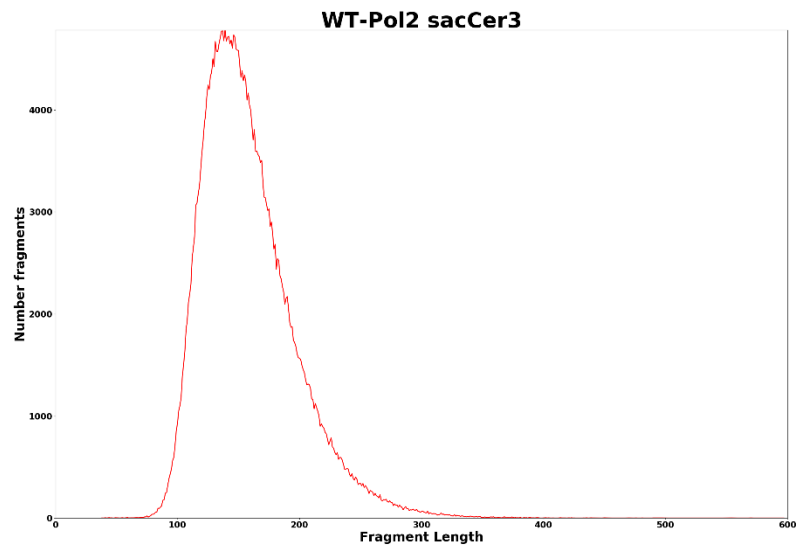
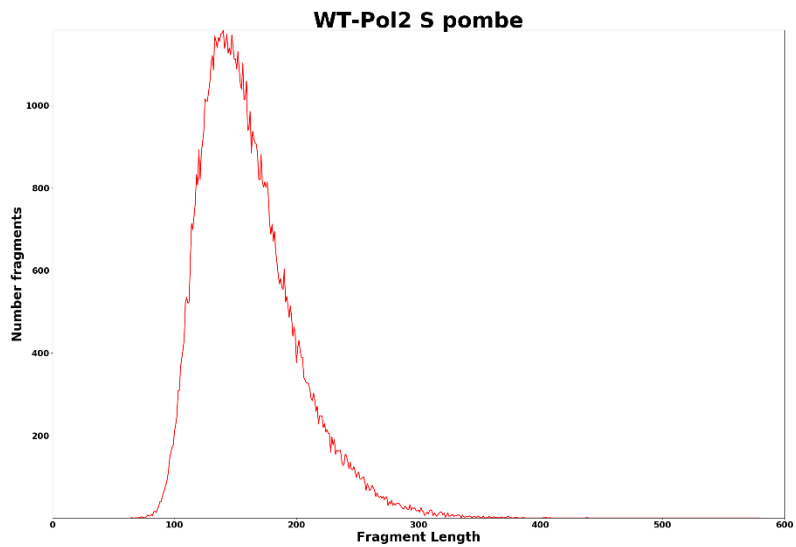


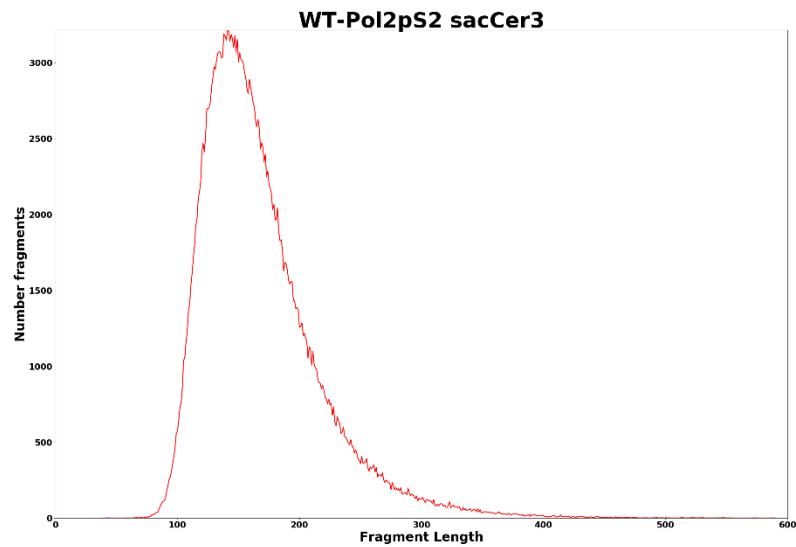
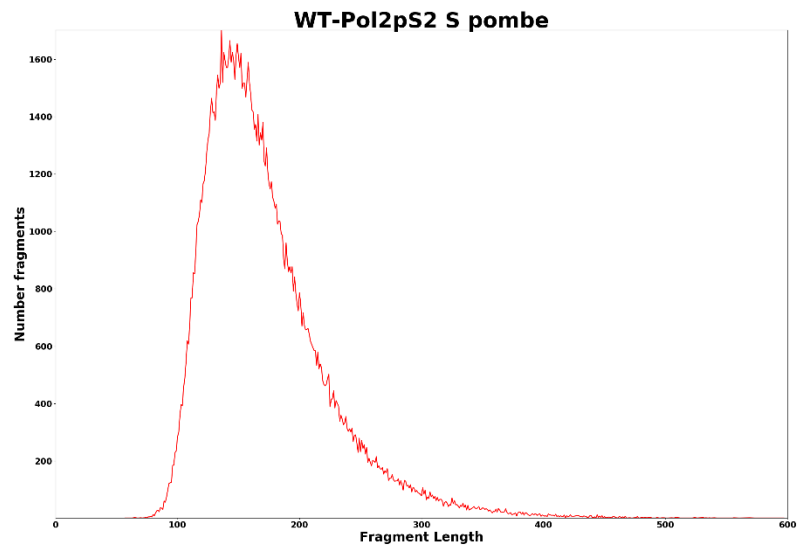


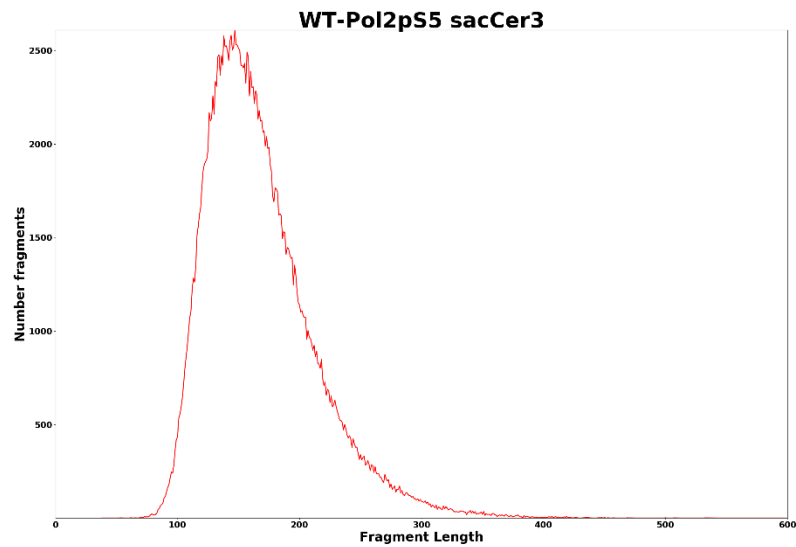
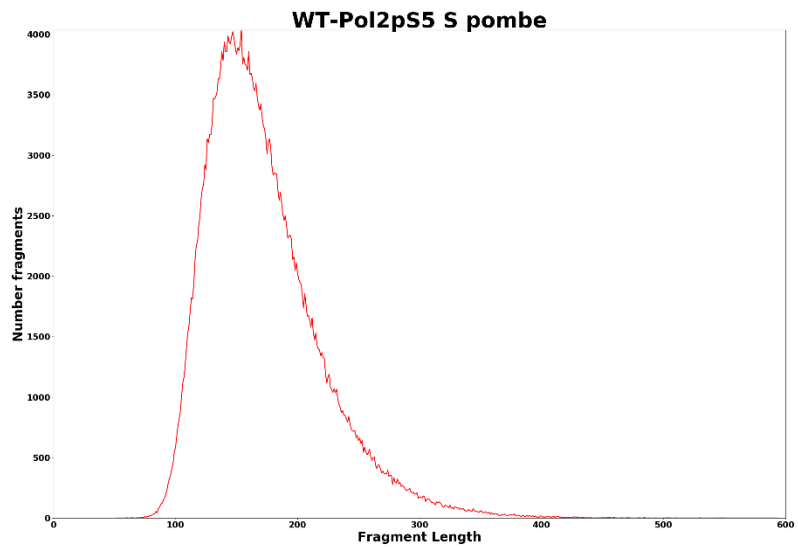








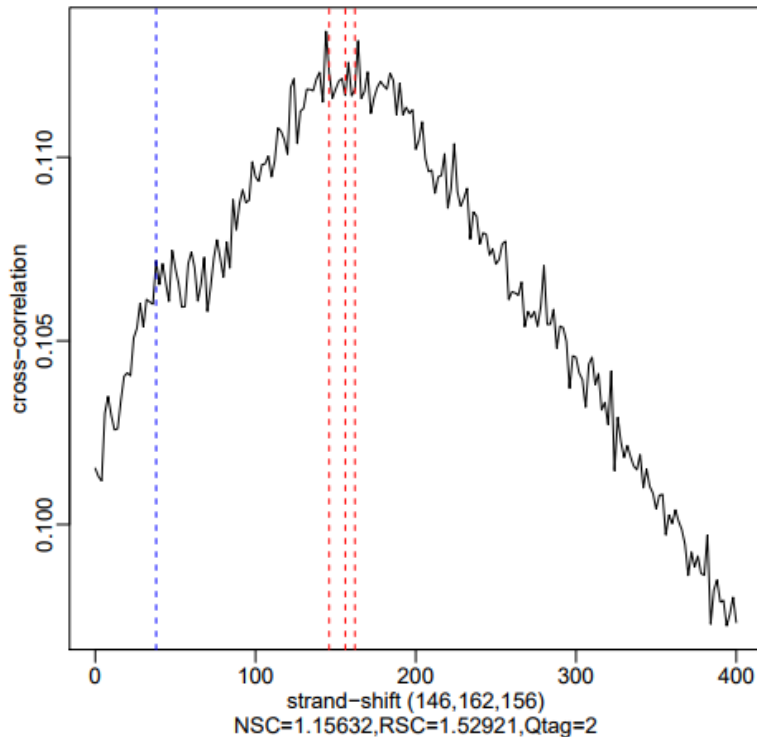




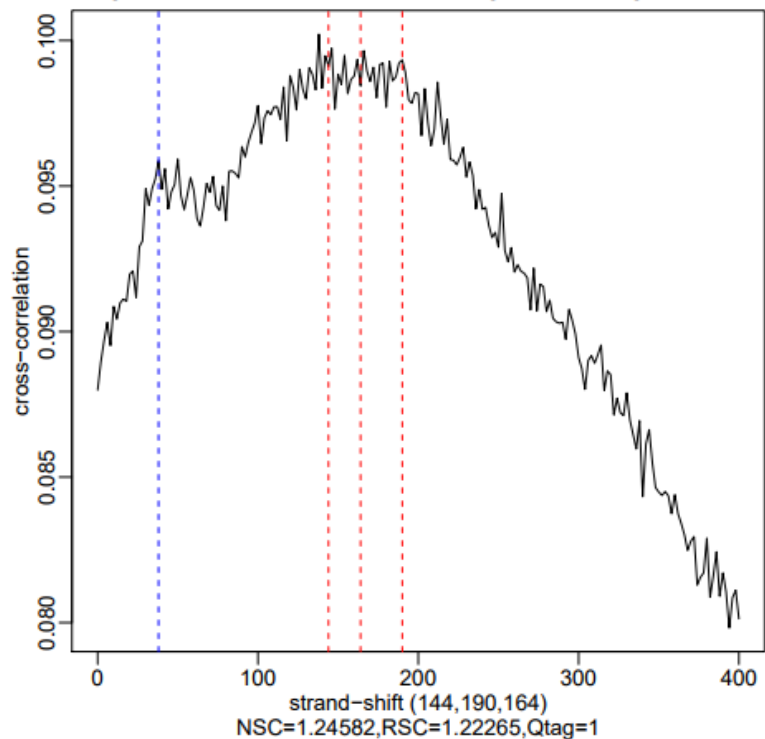
Cross-correlation profiles

Note: these are not very informative in yeast because of the small and compact genome

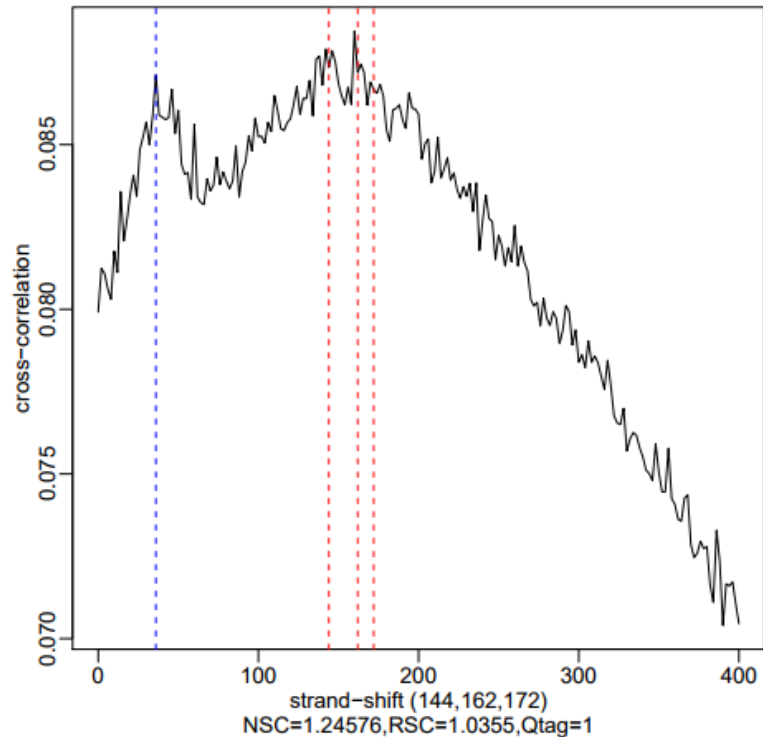
WT-Pol2pS25.1x36mers.S.cerevisiae+S.pombe.unique.nochrM



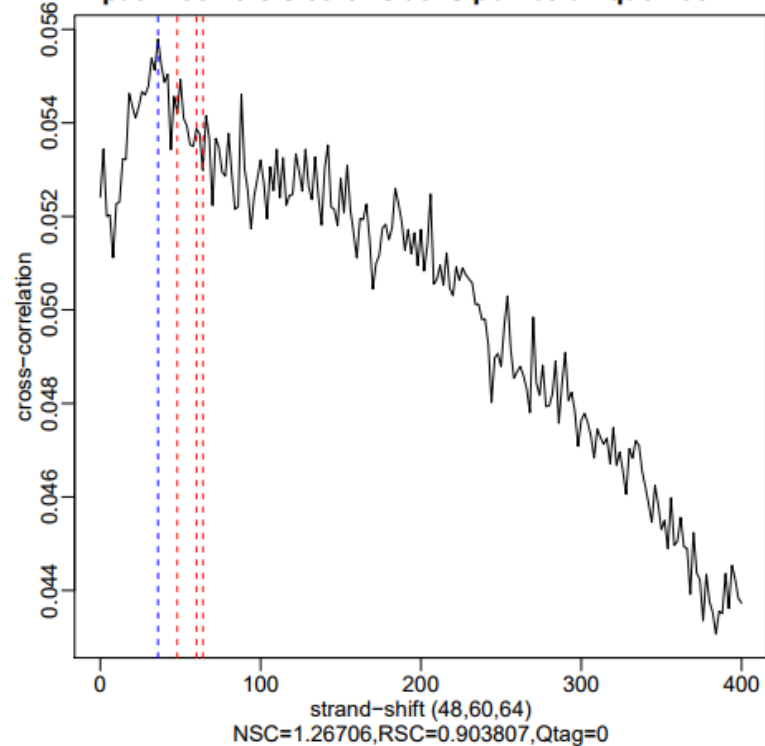
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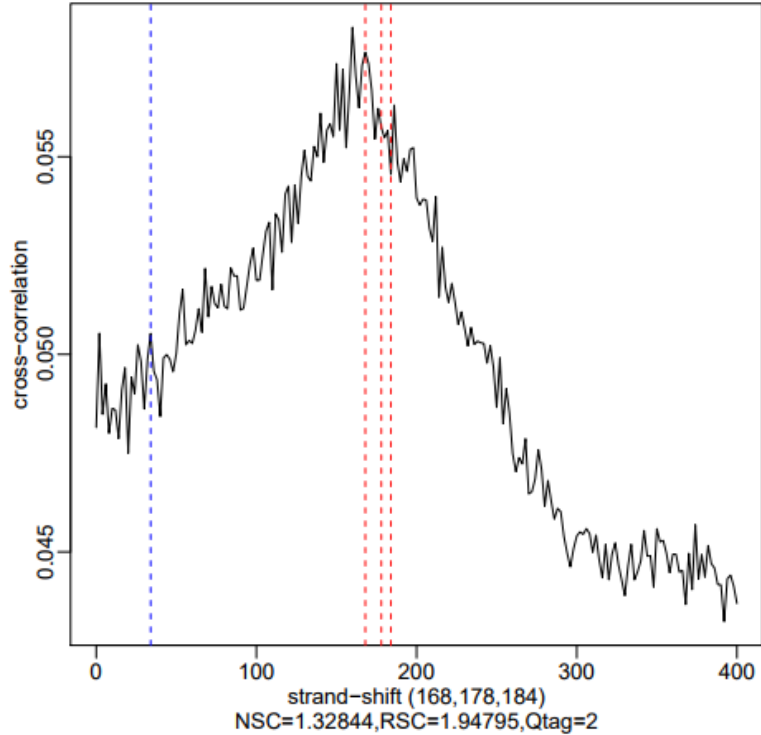
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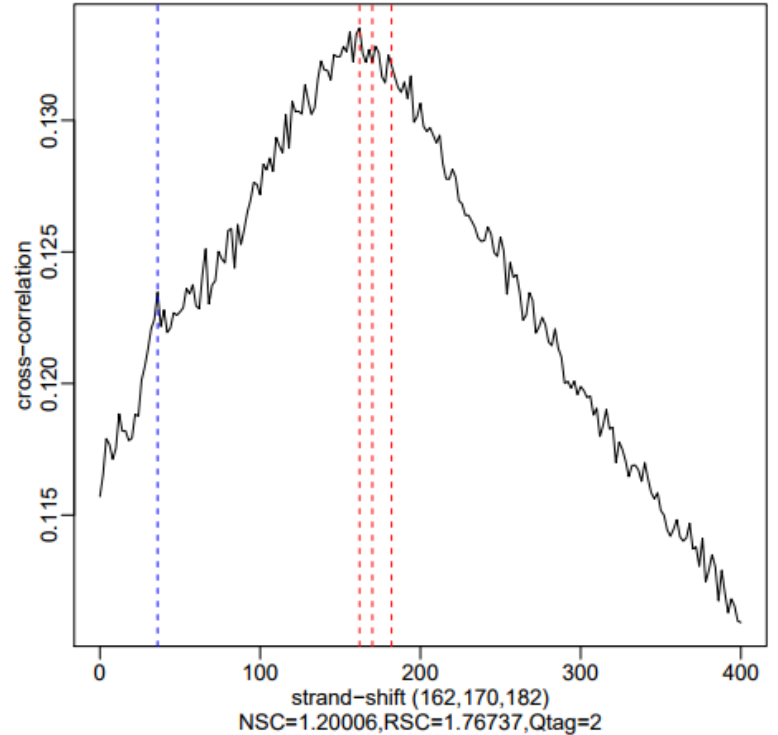
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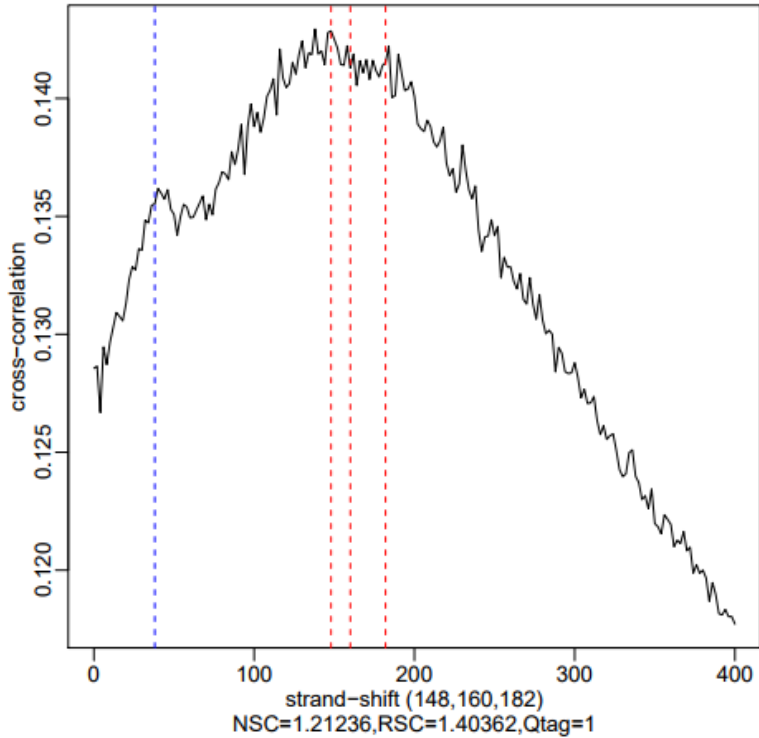
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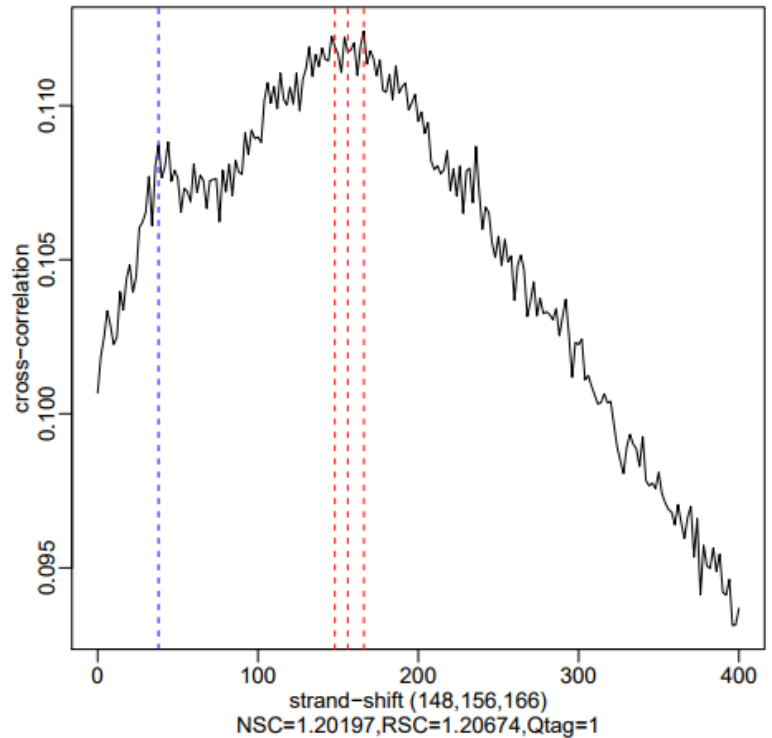
whi5-Pol2pS25.1x36mers.S.cerevisiae+S.pombe.unique.nochrI



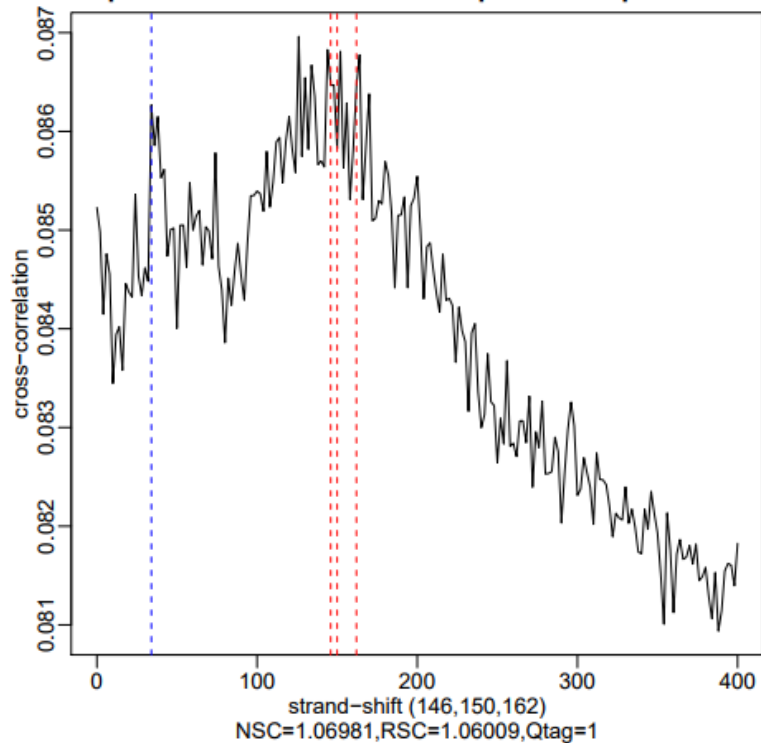
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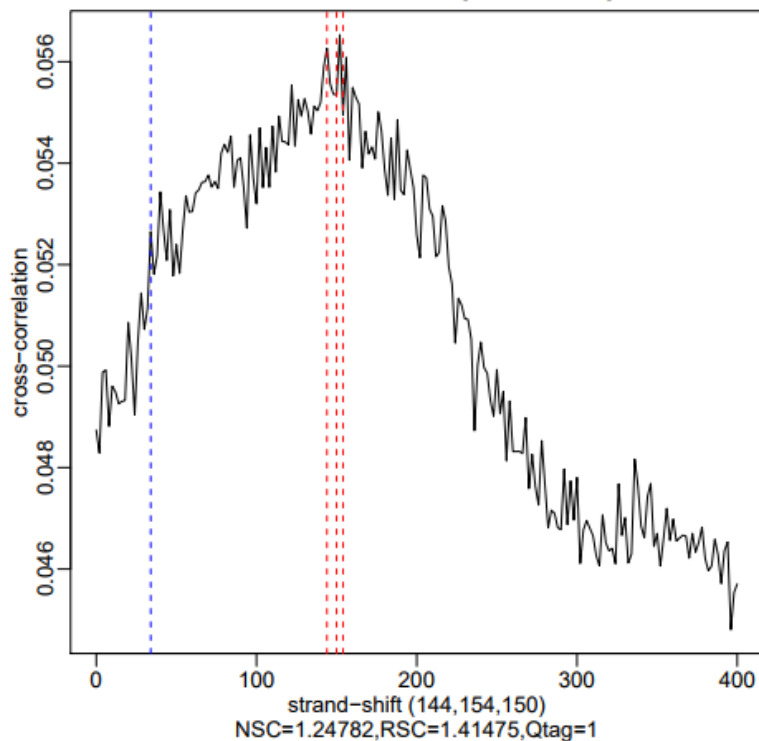
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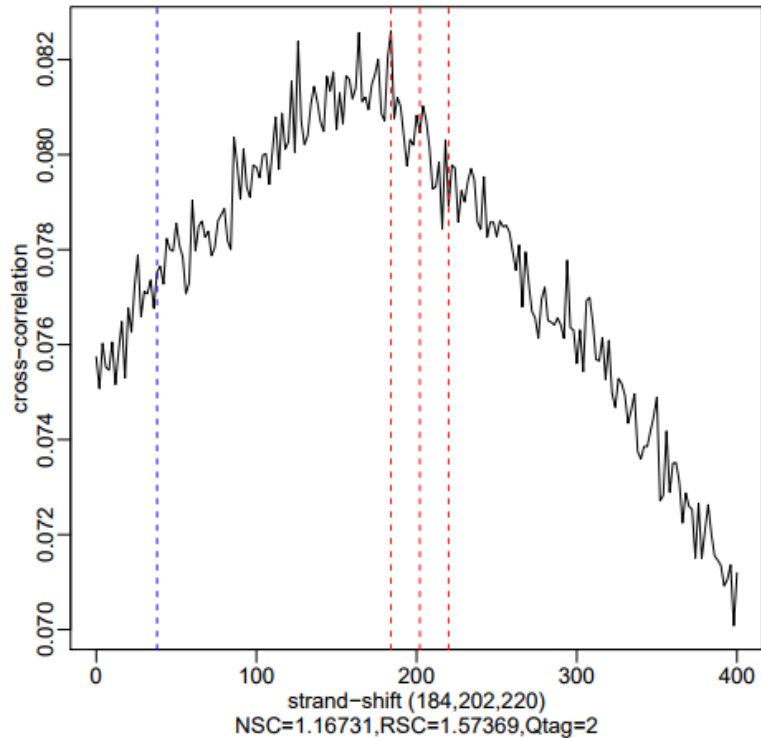
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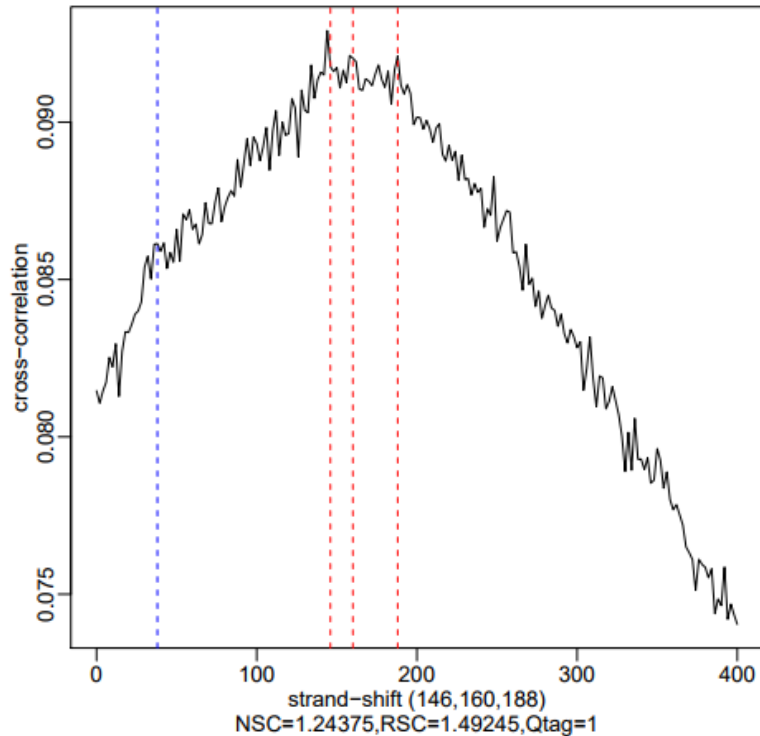
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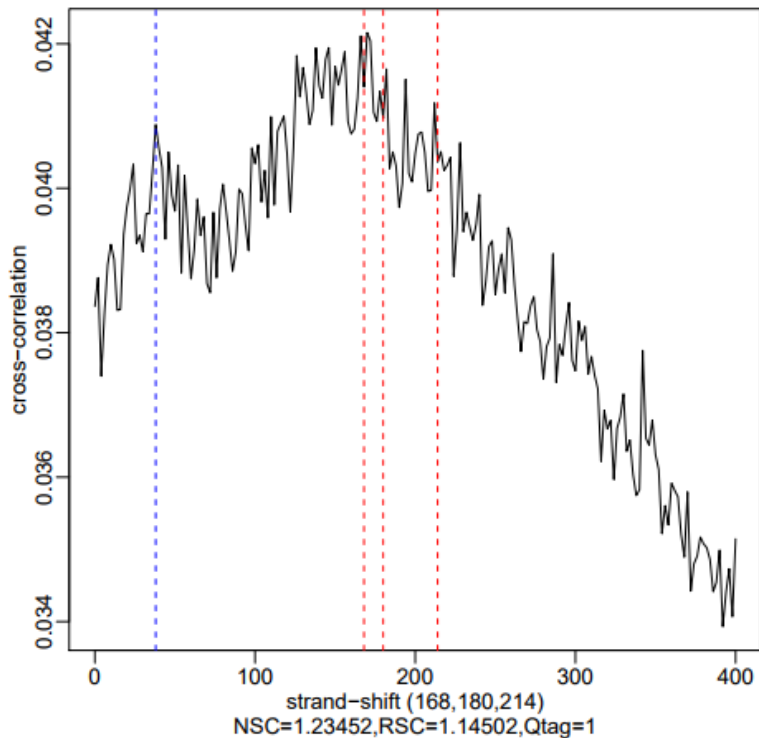
cln3-Pol2pS25.1x36mers.S.cerevisiae+S.pombe.unique.nochrM



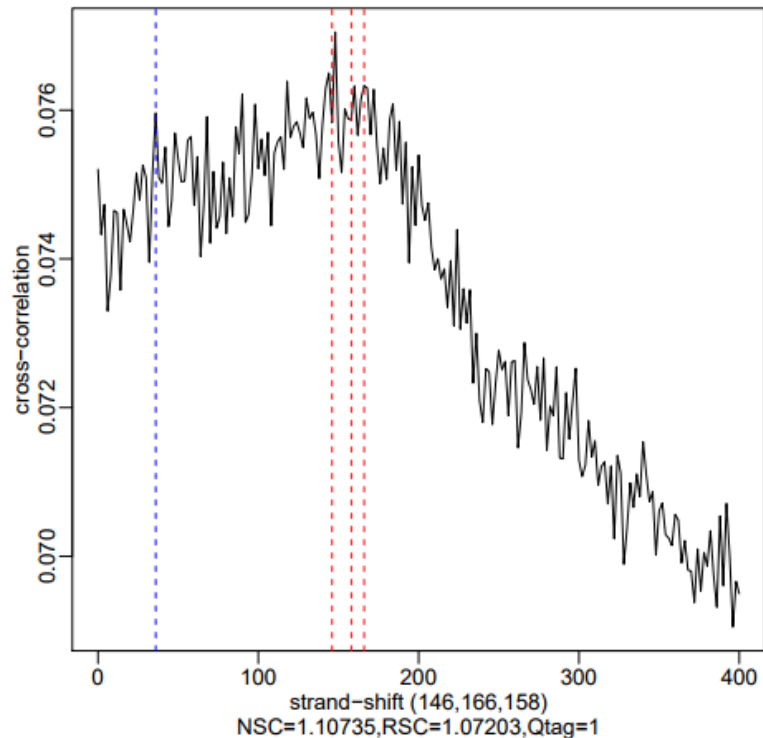
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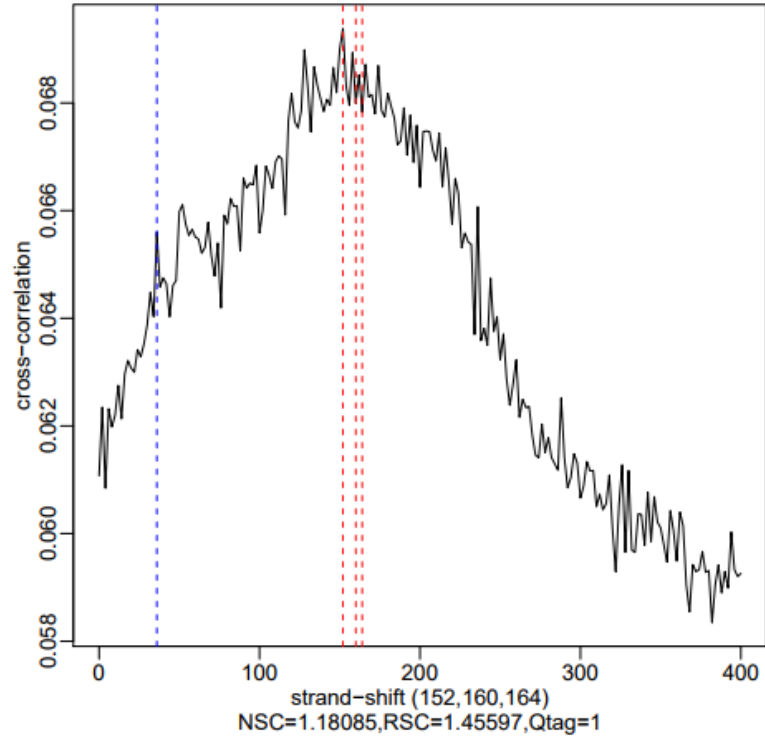
cln3-Pol2.1x36mers.S.cerevisiae+S.pombe.unique.nochrM.t



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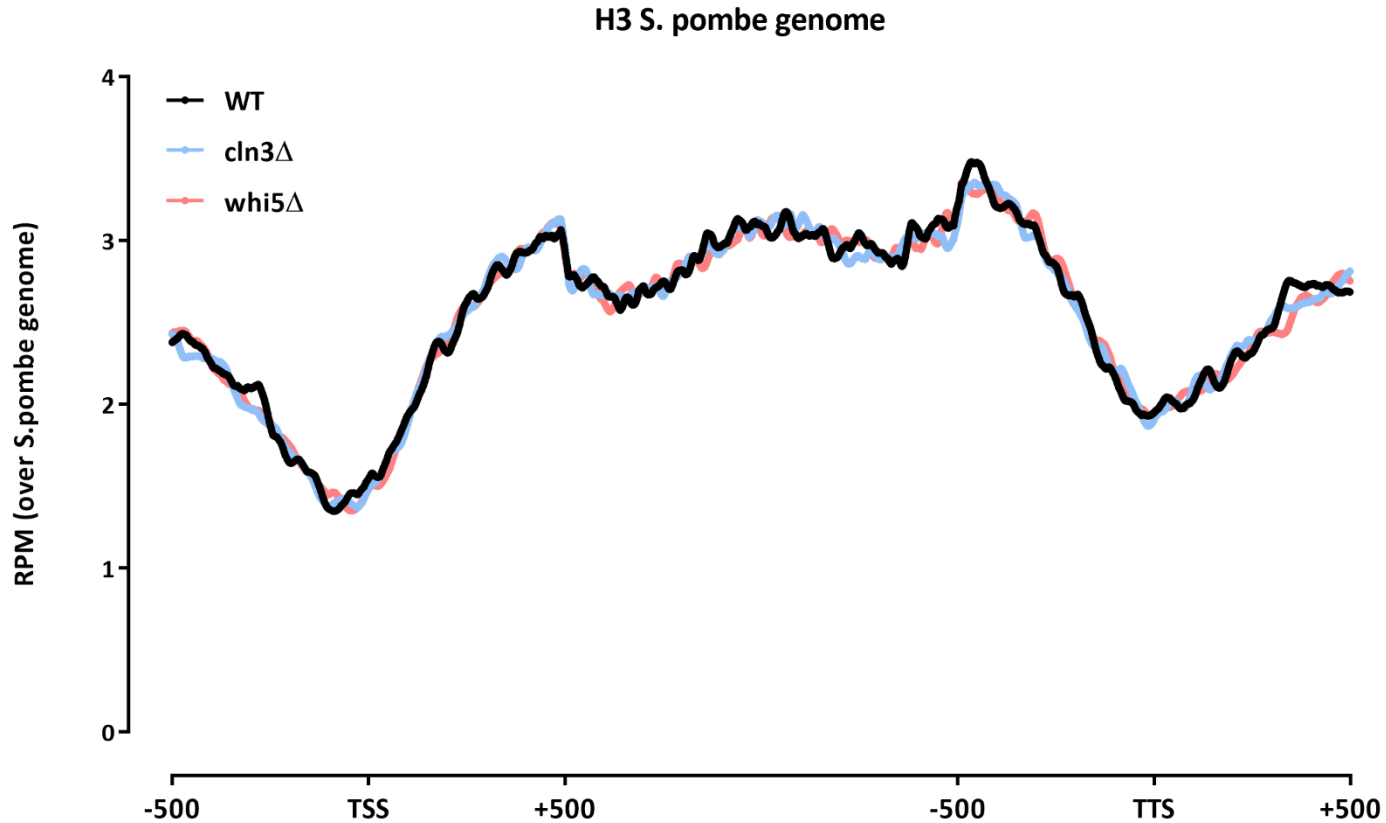


cln3-H3.1x36mers.S.cerevisiae+S.pombe.unique.nochrM.b:

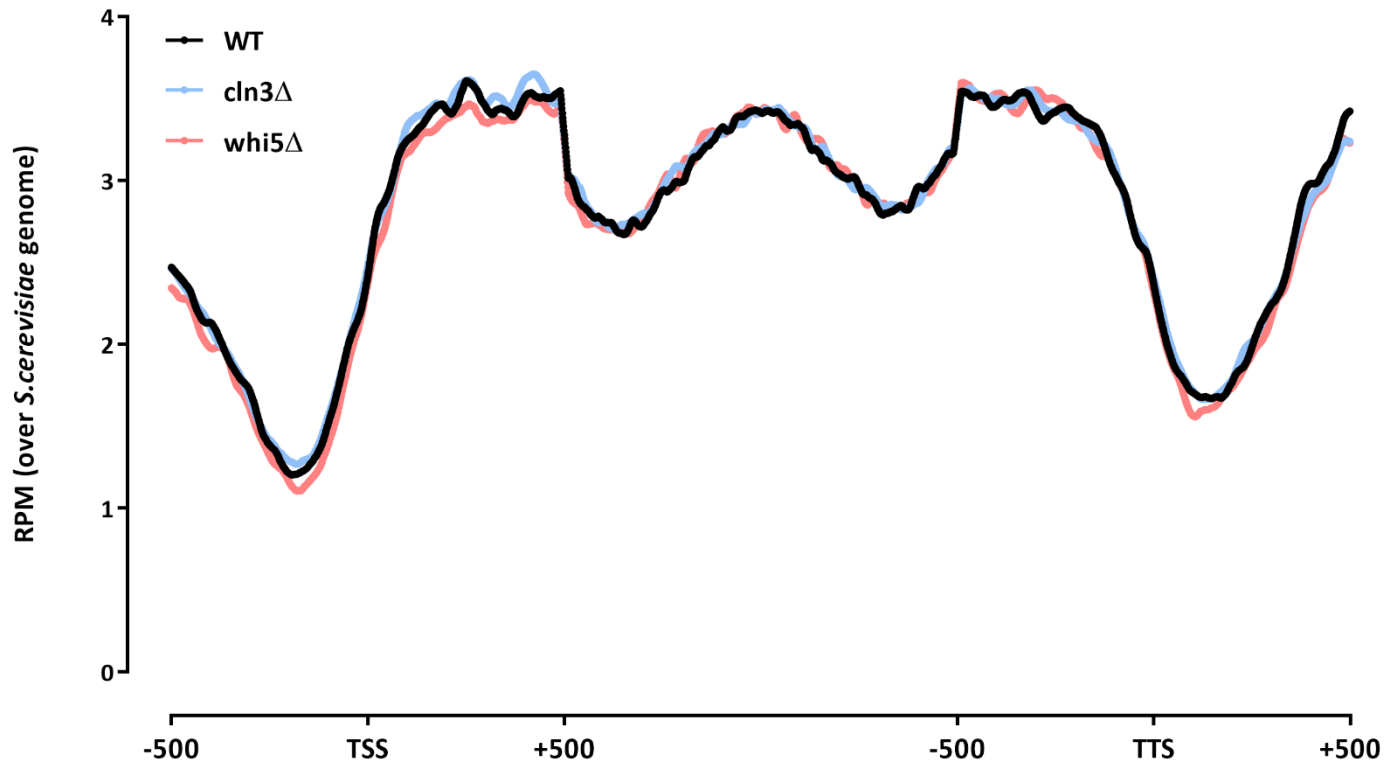


Sanity check on the ChIP itself

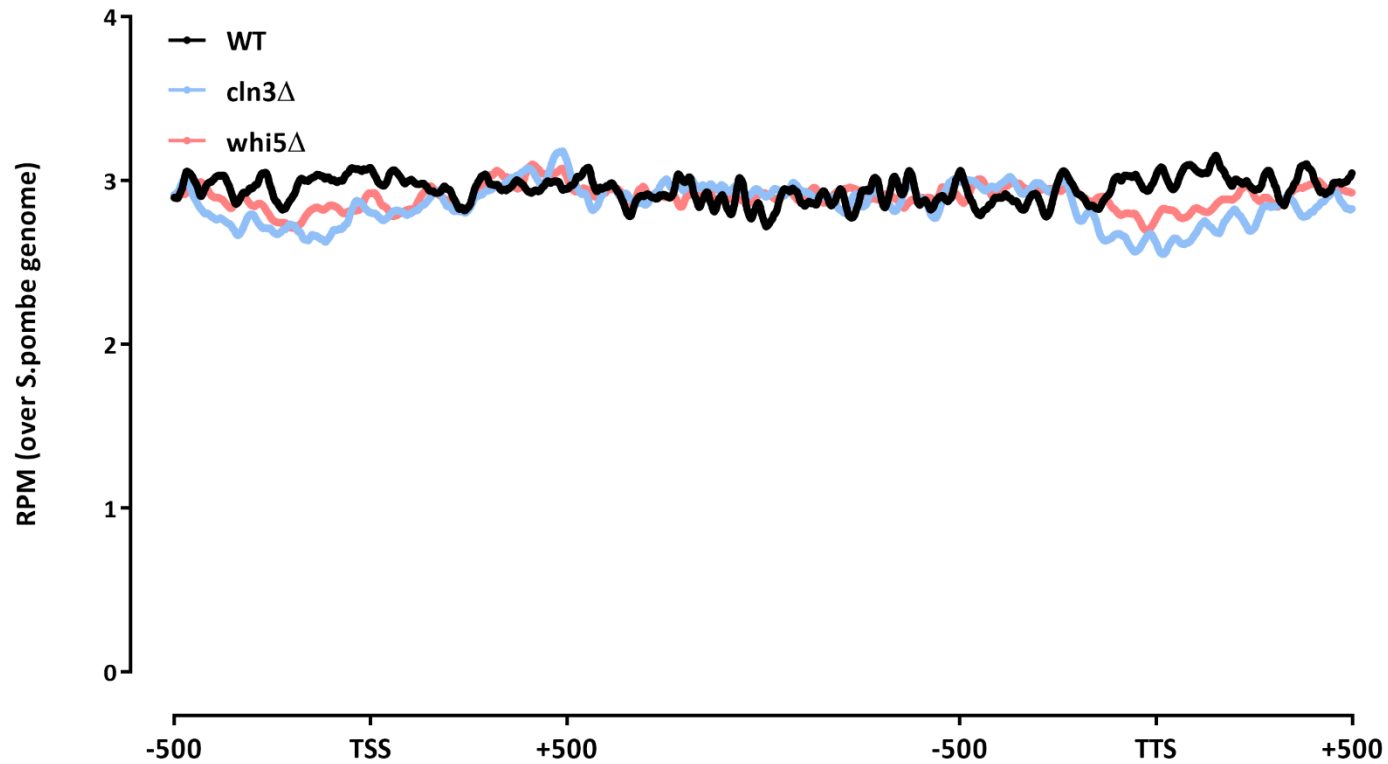
Average gene profiles without renormalization, to see if the ChIP-seq behaves as expected



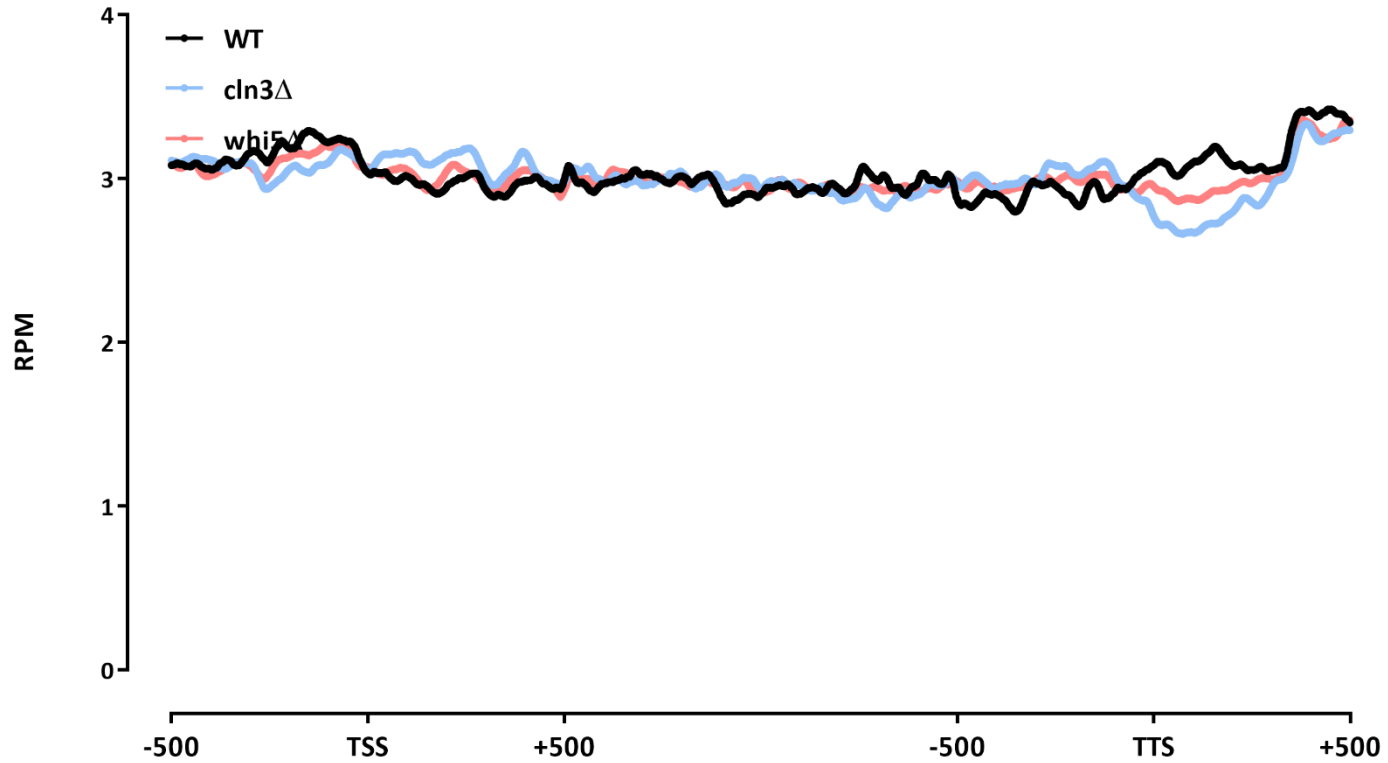
H3 *S. cerevisiae* genome



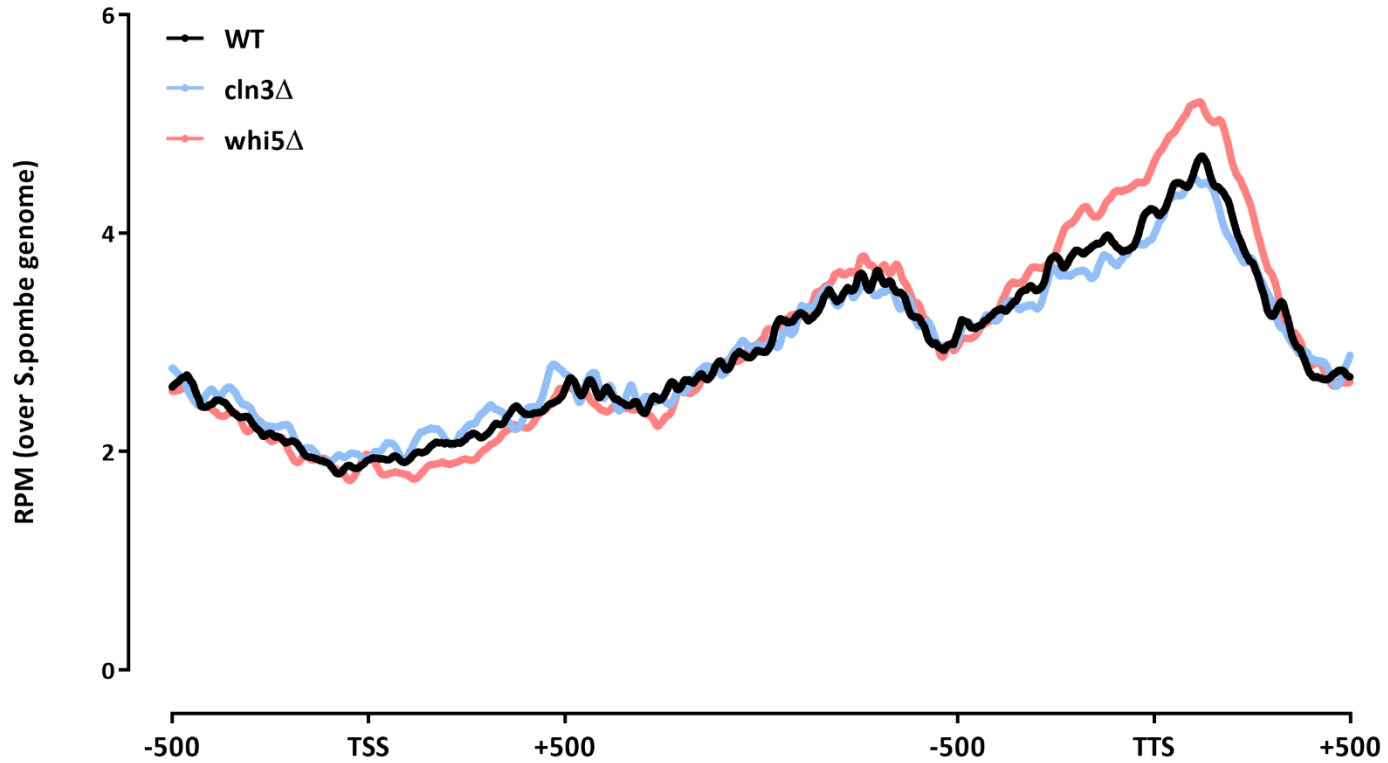
Input *S. pombe* genome



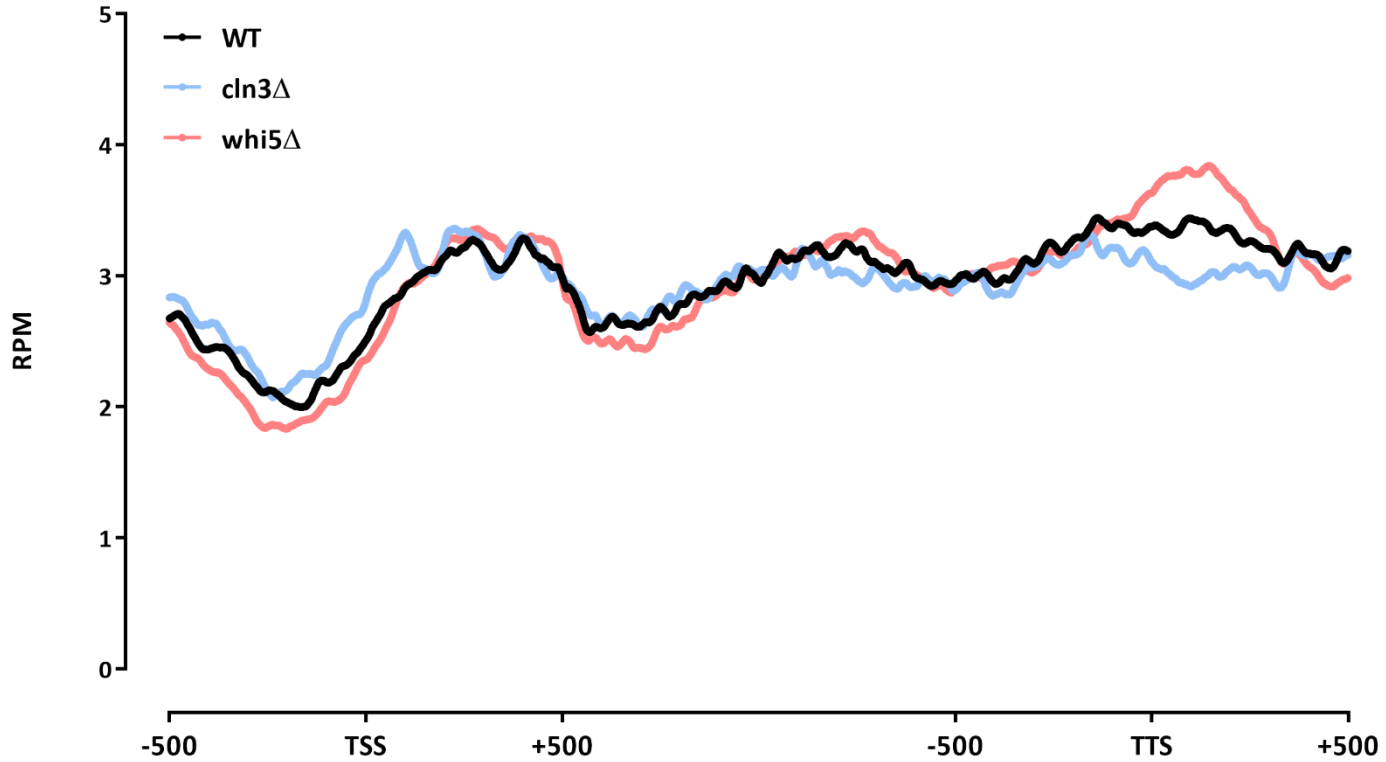
Input *S. cerevisiae* genome



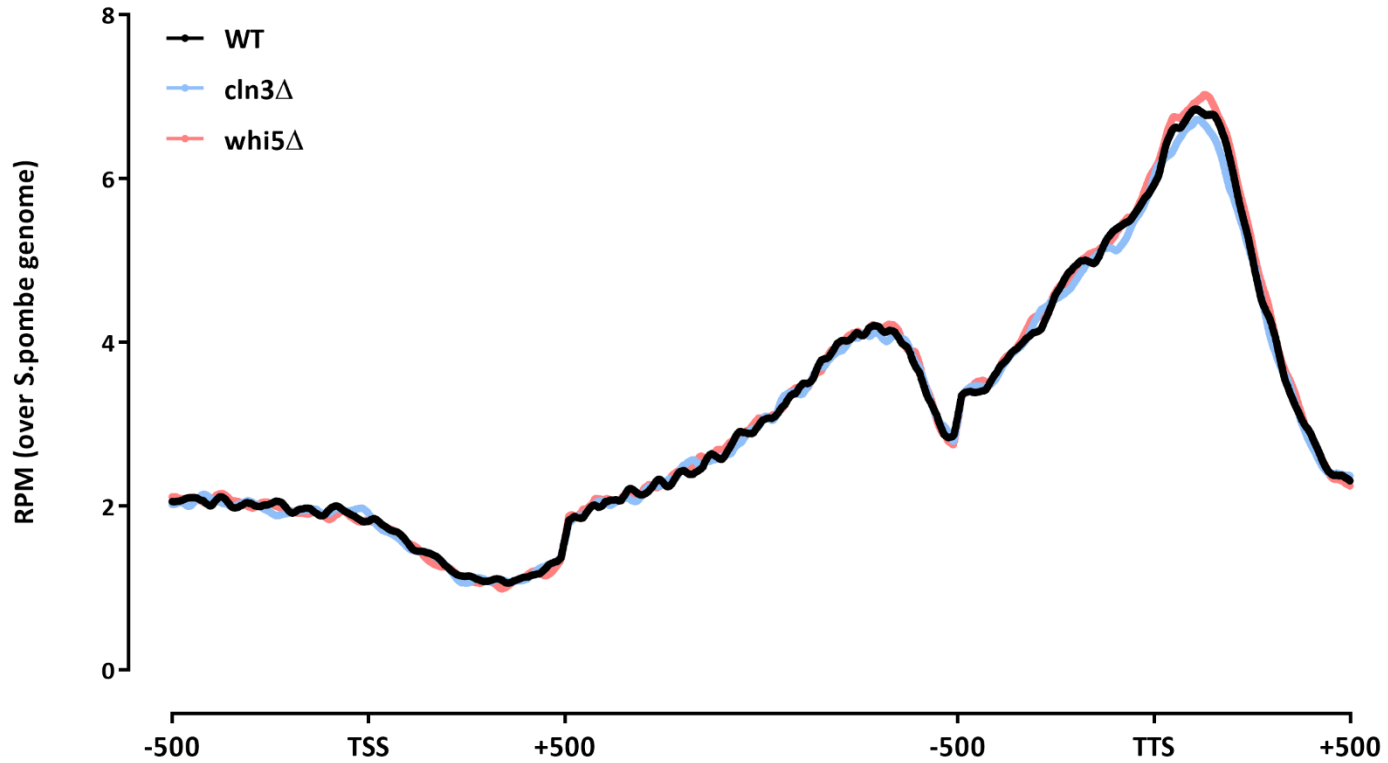
Pol2 S. pombe genome



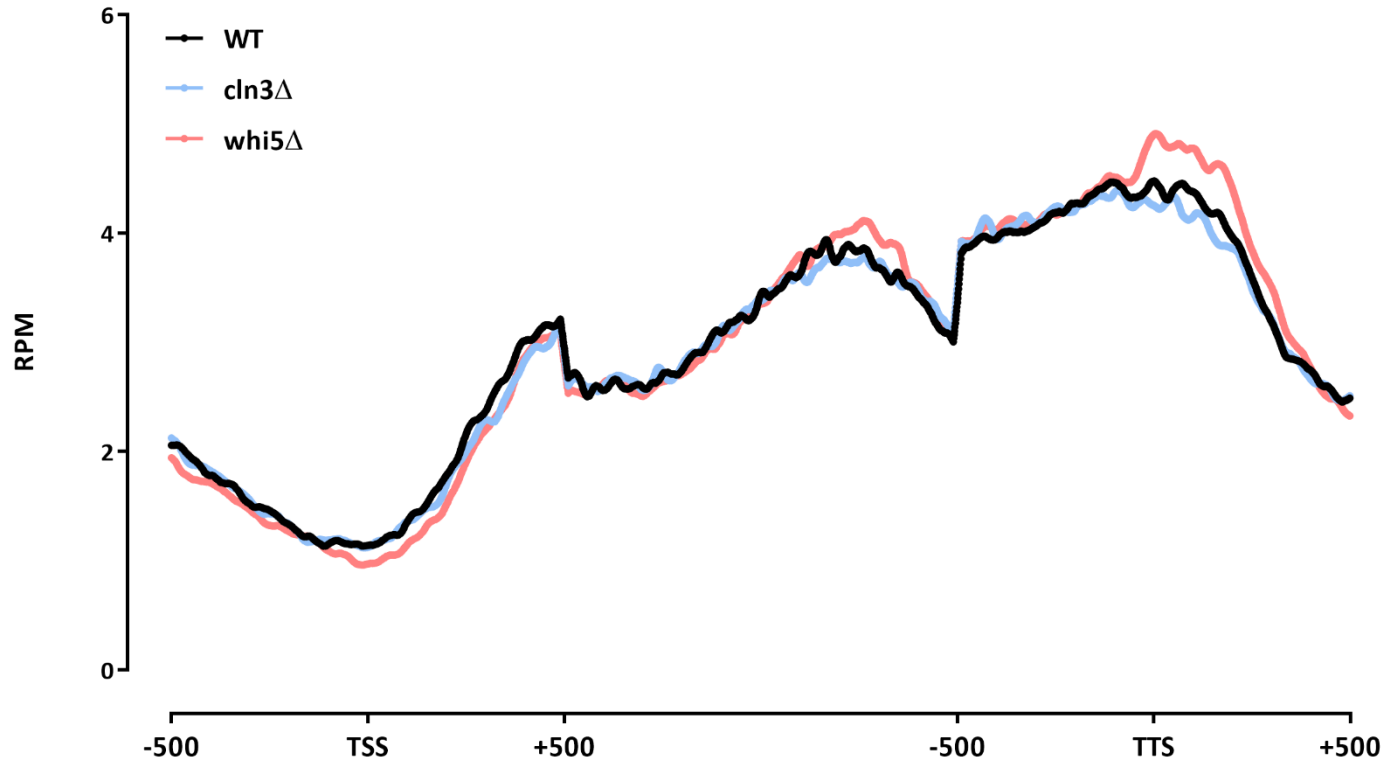
Pol2 *S. cerevisiae* genome



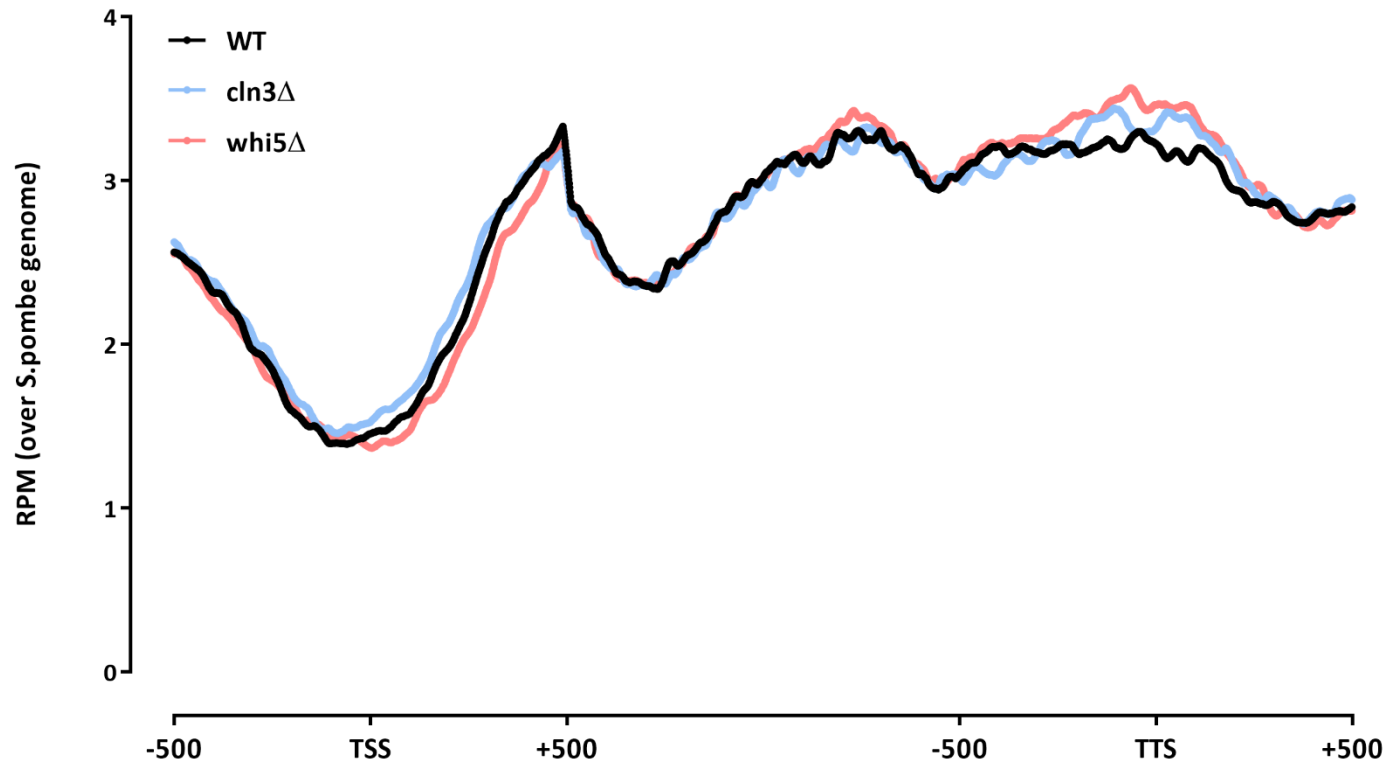
Pol2pS2 S. pombe genome



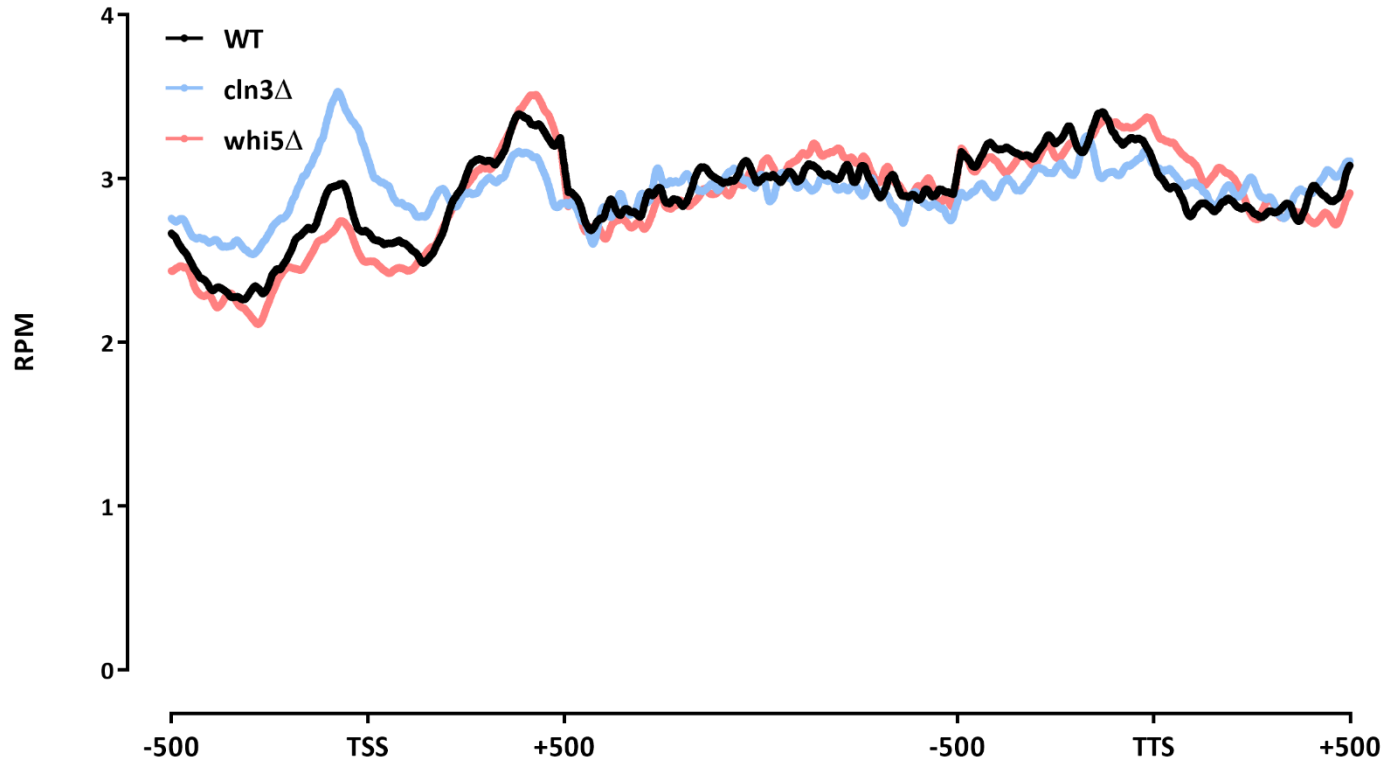
Pol2pS2 *S. cerevisiae* genome



Pol2pS5 S. pombe genome

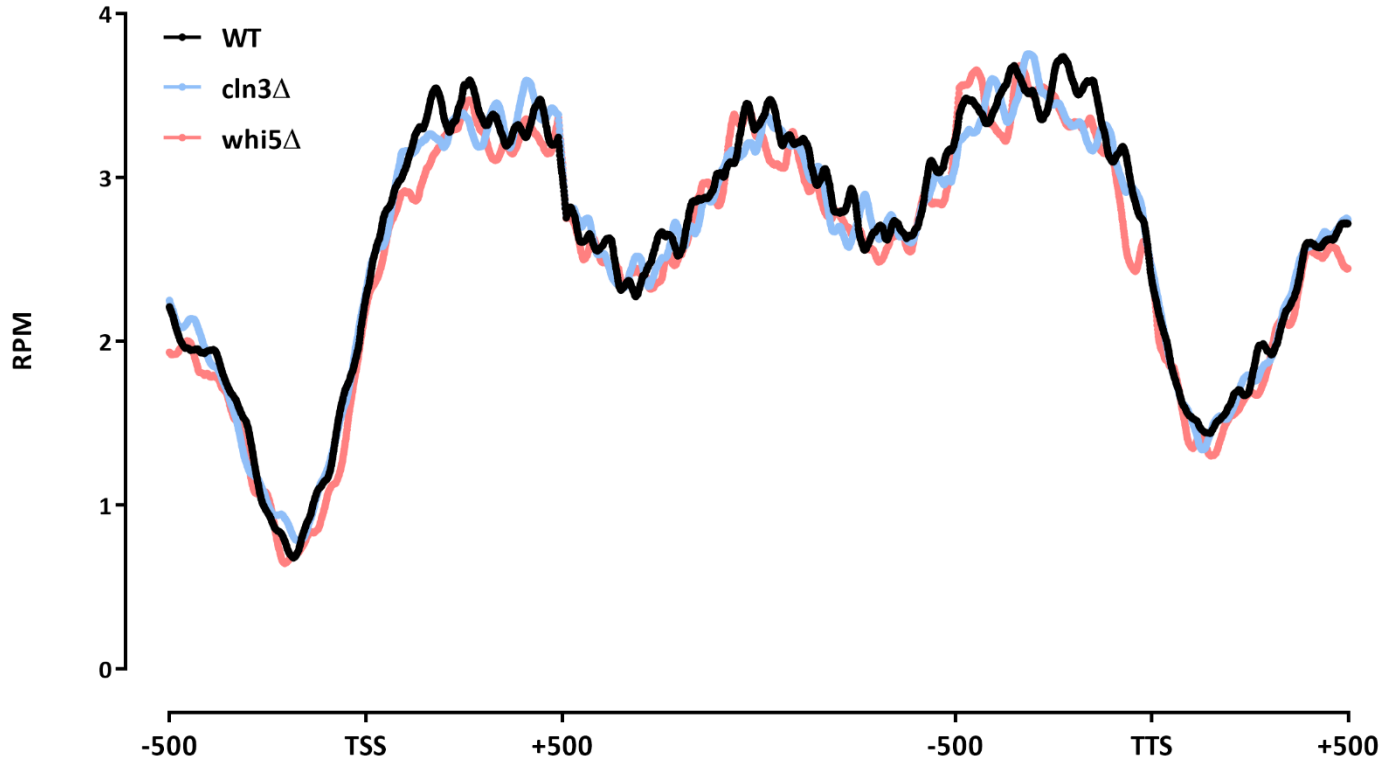


Pol2pS5 *S. cerevisiae* genome

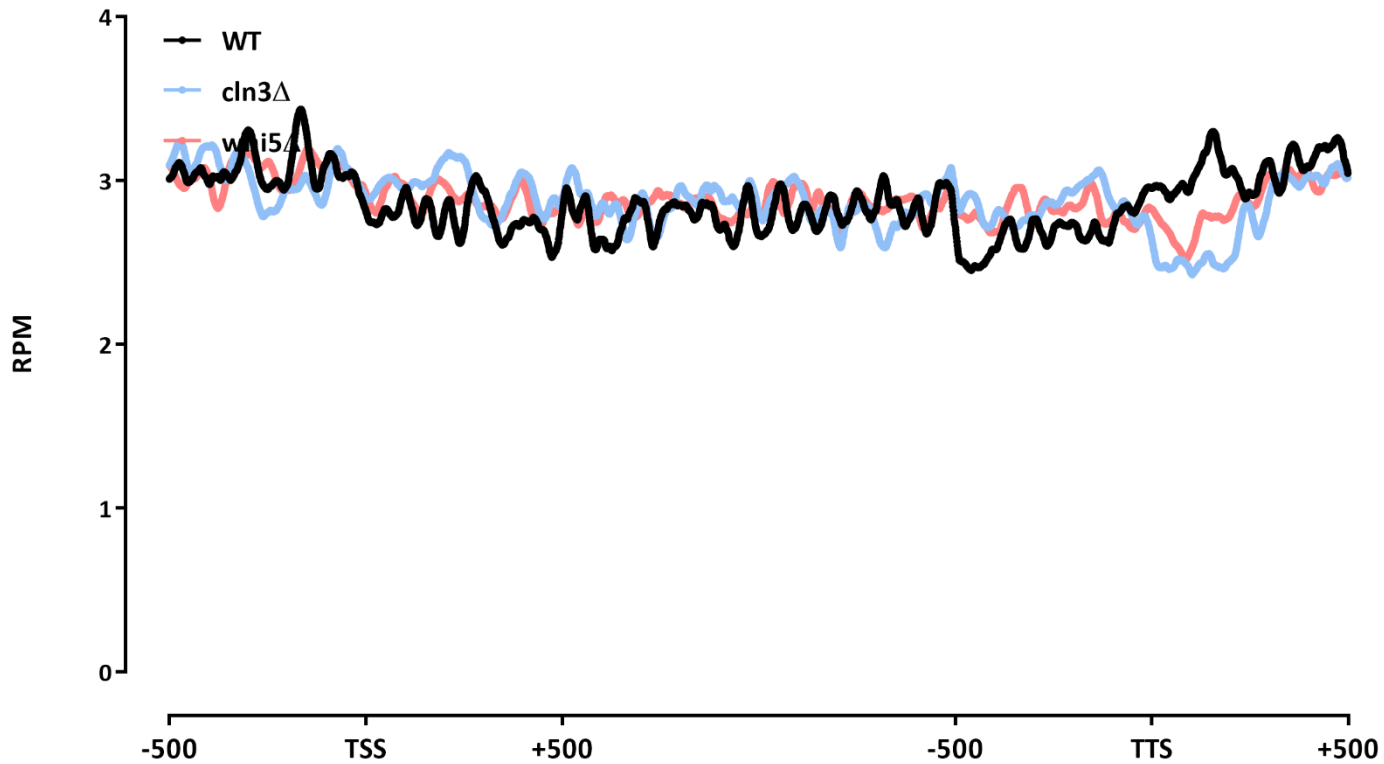


Splitting by expression levels

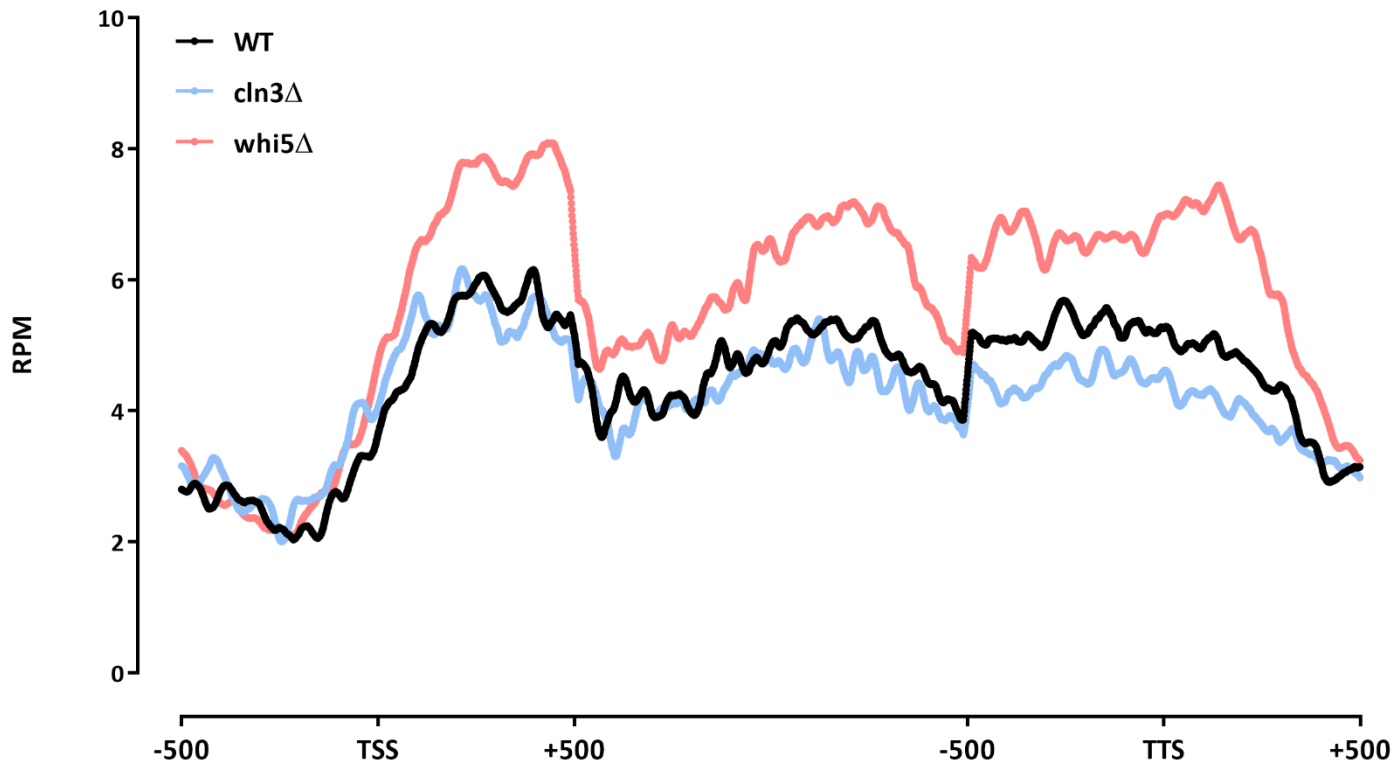
H3 *S. cerevisiae* genome top expression quintiles



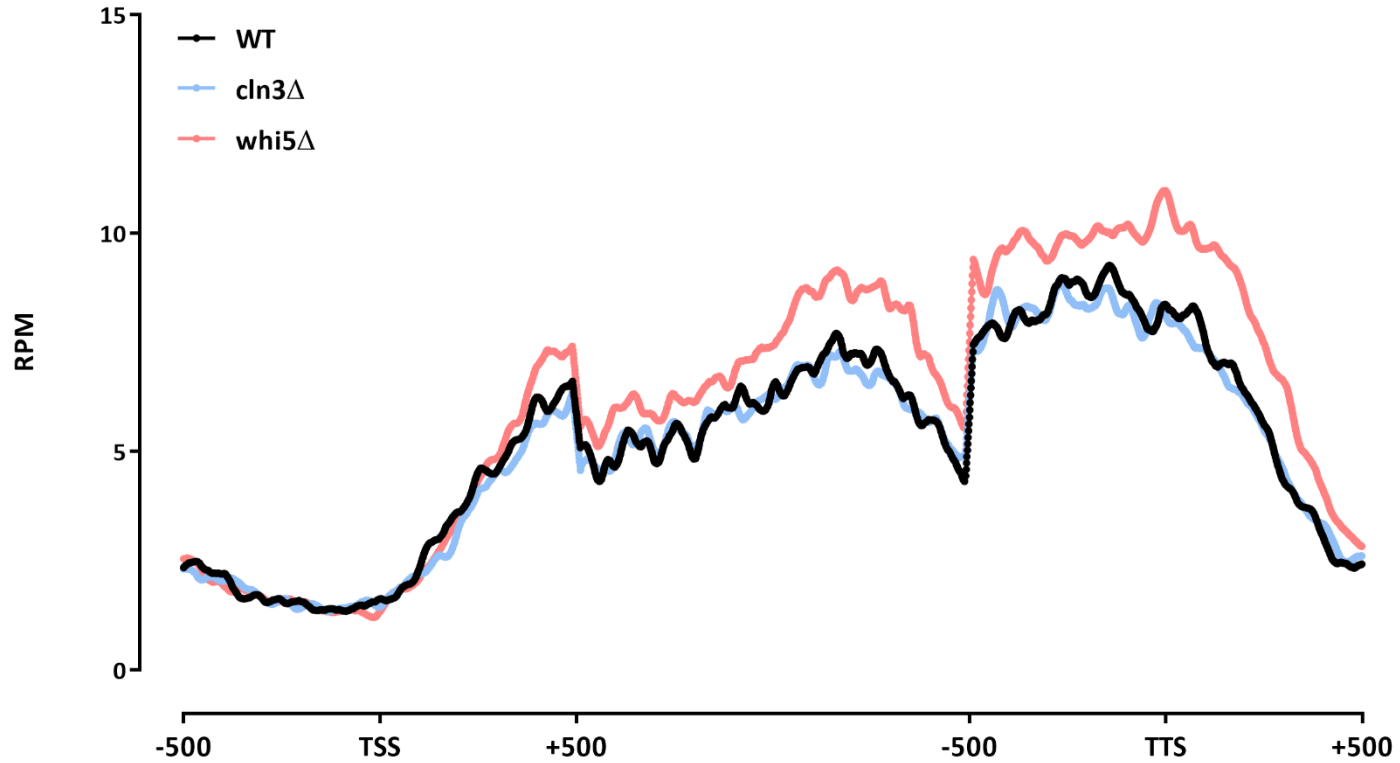
Input *S. cerevisiae* genome top expression quintiles



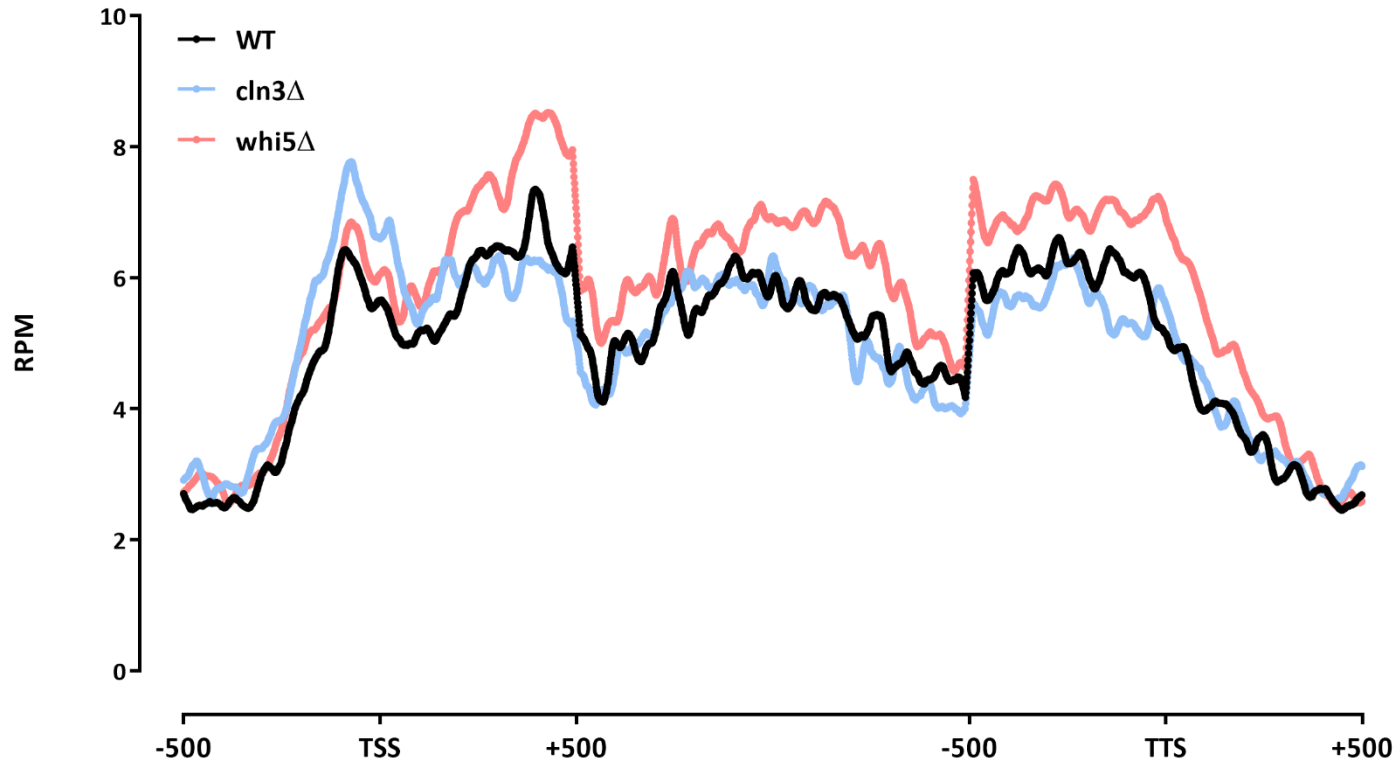
Pol2 *S. cerevisiae* genome top expression quintiles



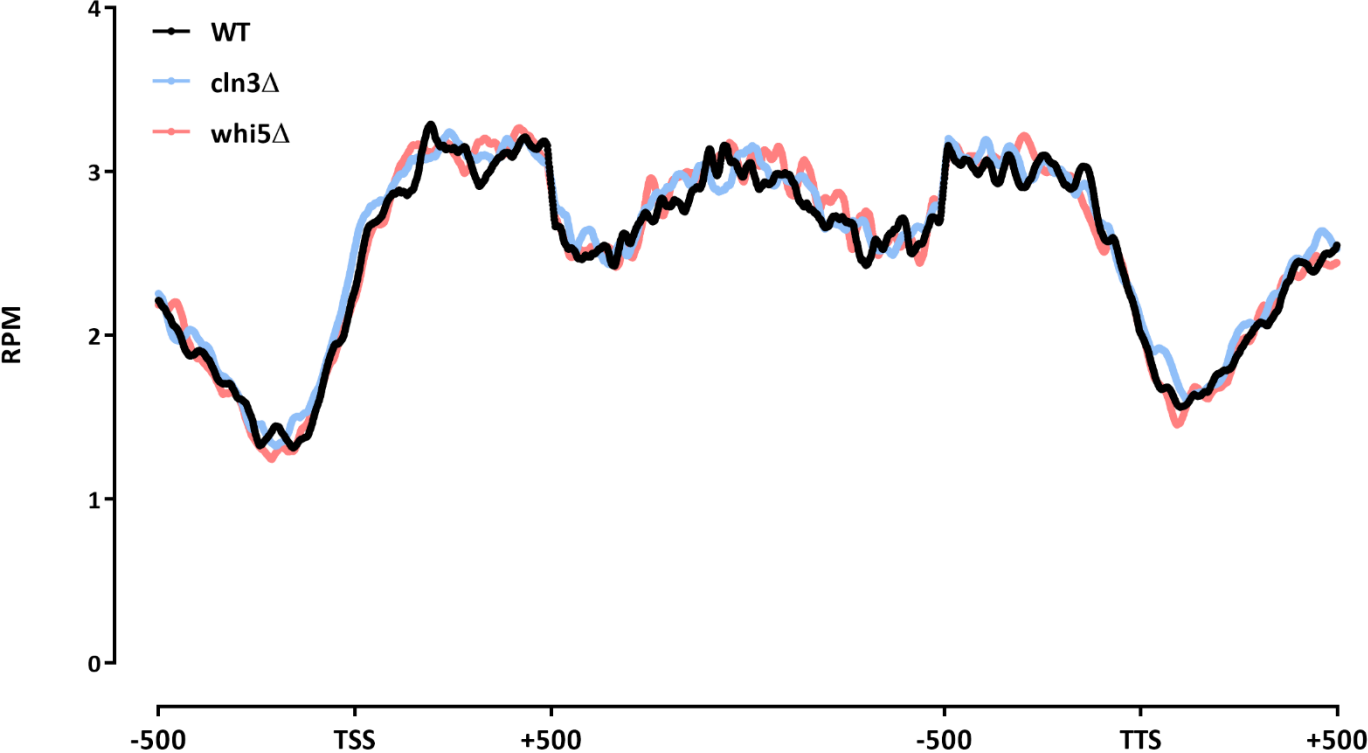
Pol2pS2 *S. cerevisiae* genome top expression quintiles



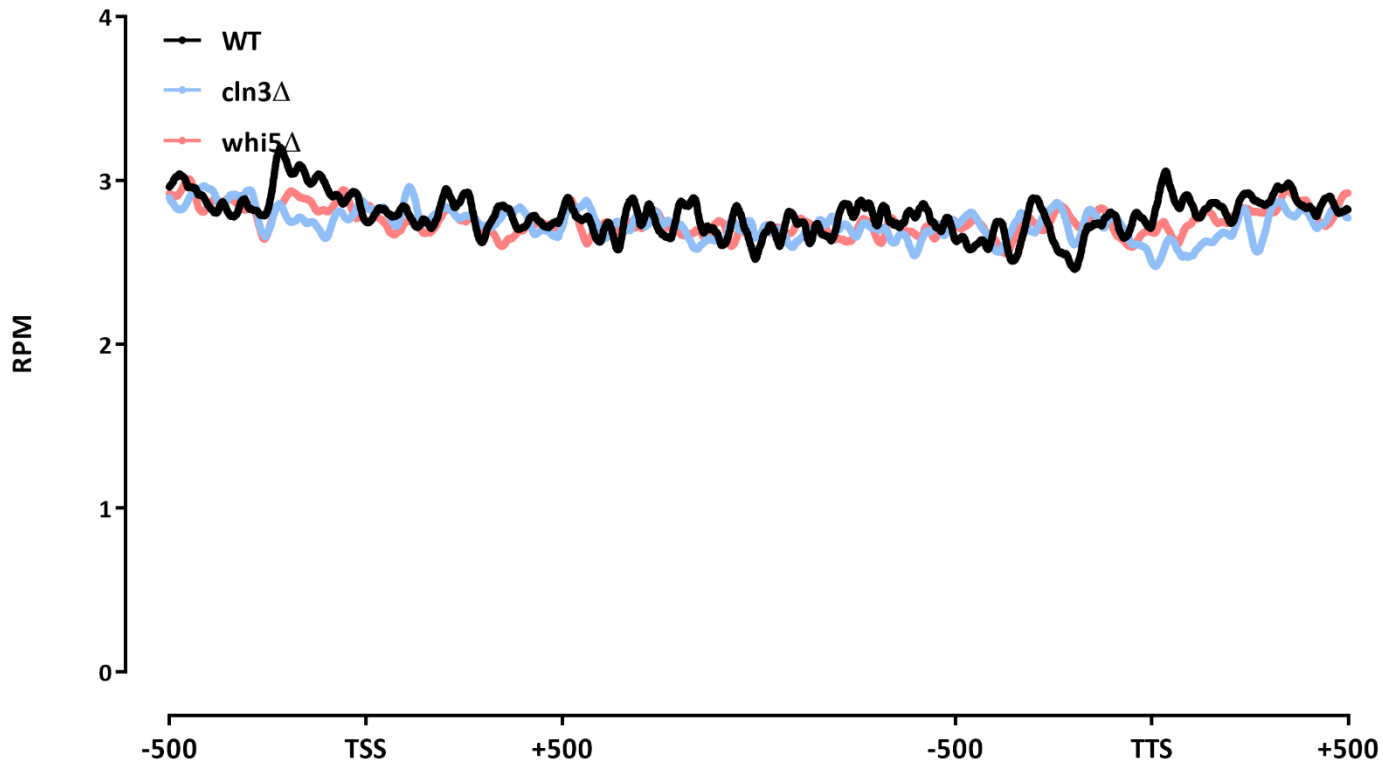
Pol2pS5 *S. cerevisiae* genome top expression quintiles



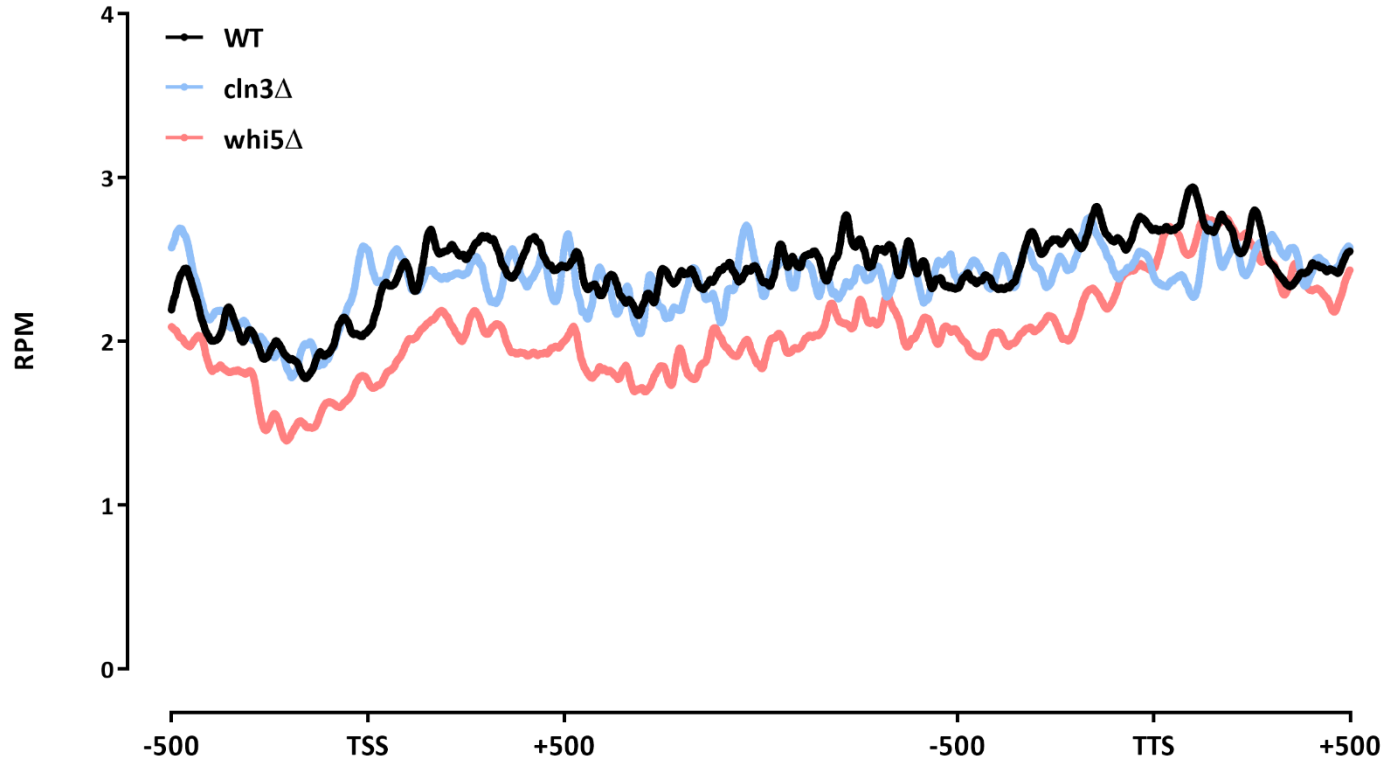
H3 *S. cerevisiae* genome bottom expression quintiles



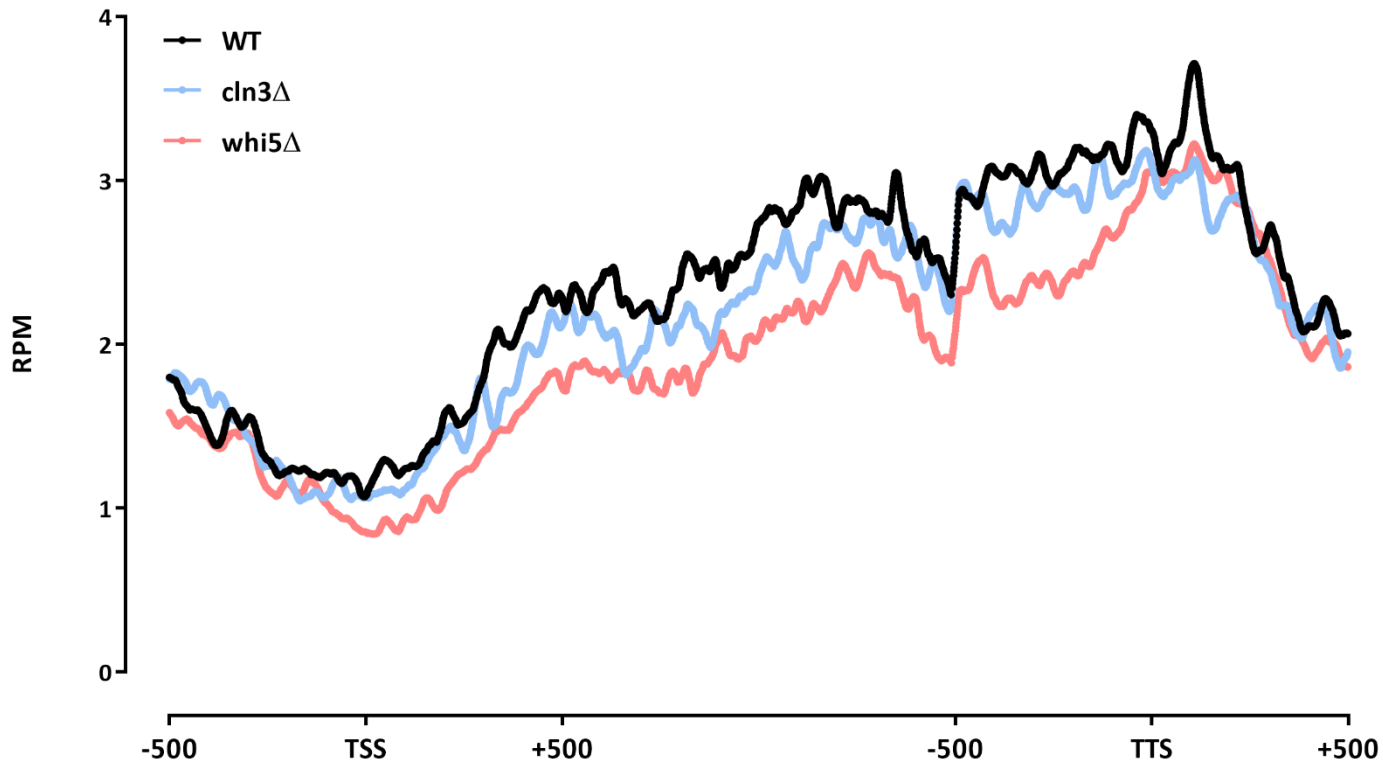
Input *S. cerevisiae* genome bottom expression quintiles



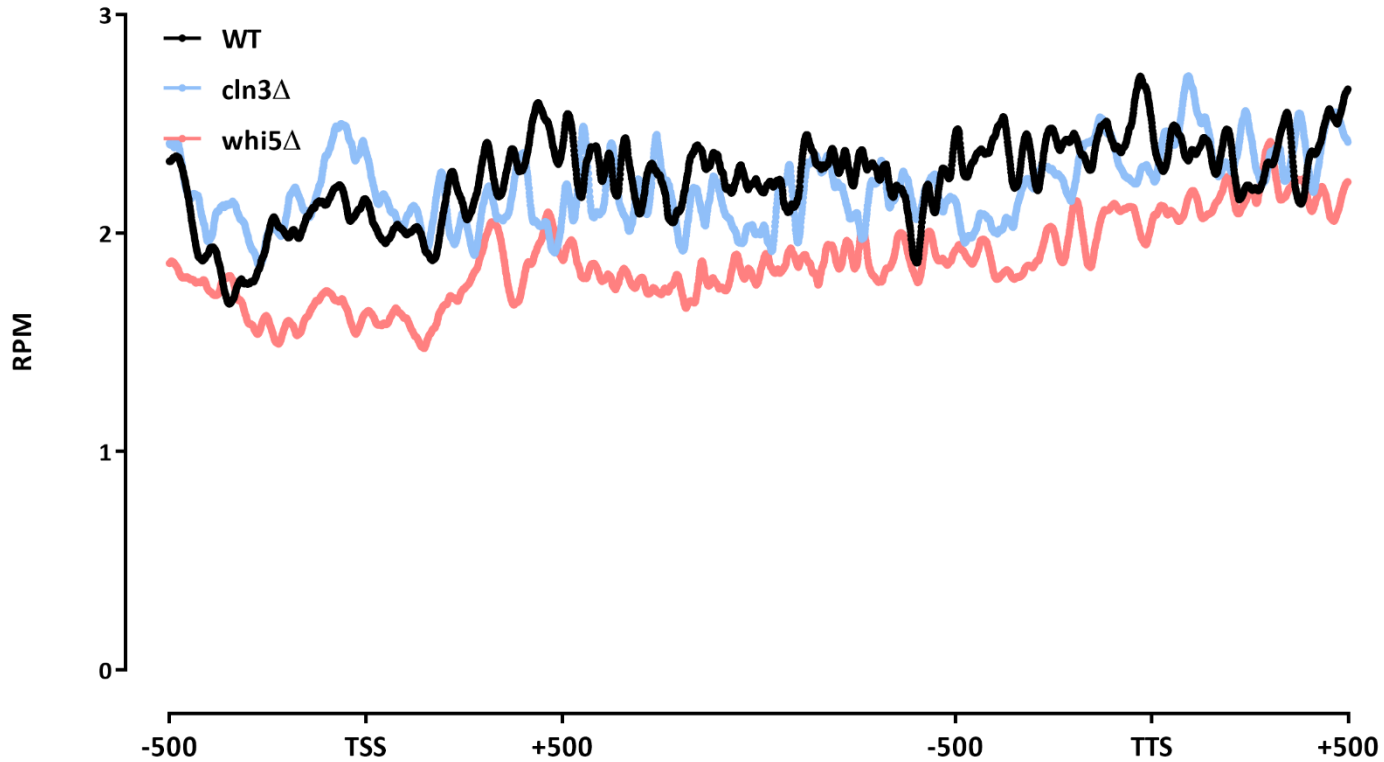
Pol2 *S. cerevisiae* genome bottom expression quintiles



Pol2pS2 *S. cerevisiae* genome bottom expression quintiles



Pol2pS5 *S. cerevisiae* genome bottom expression quintiles

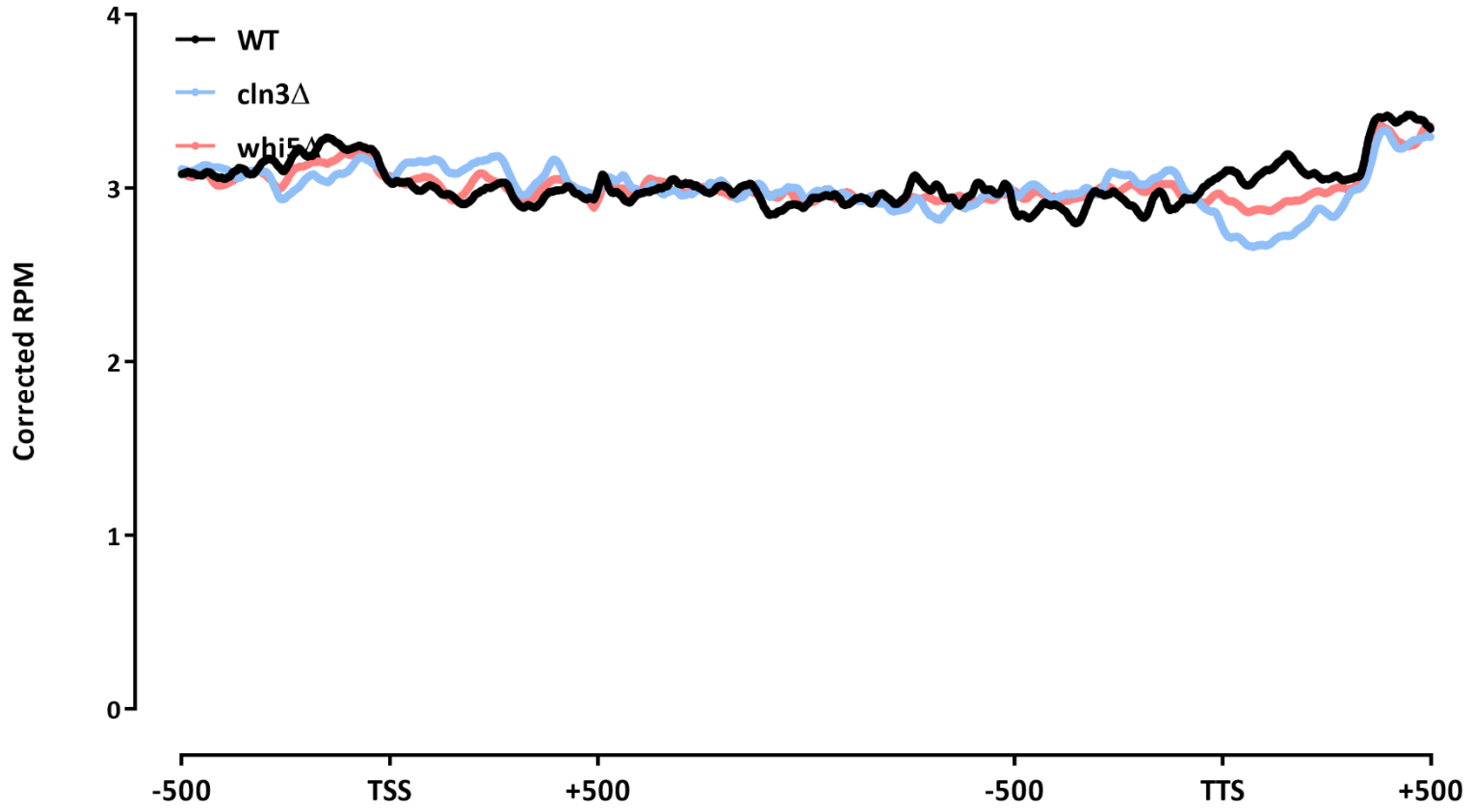


Normalization

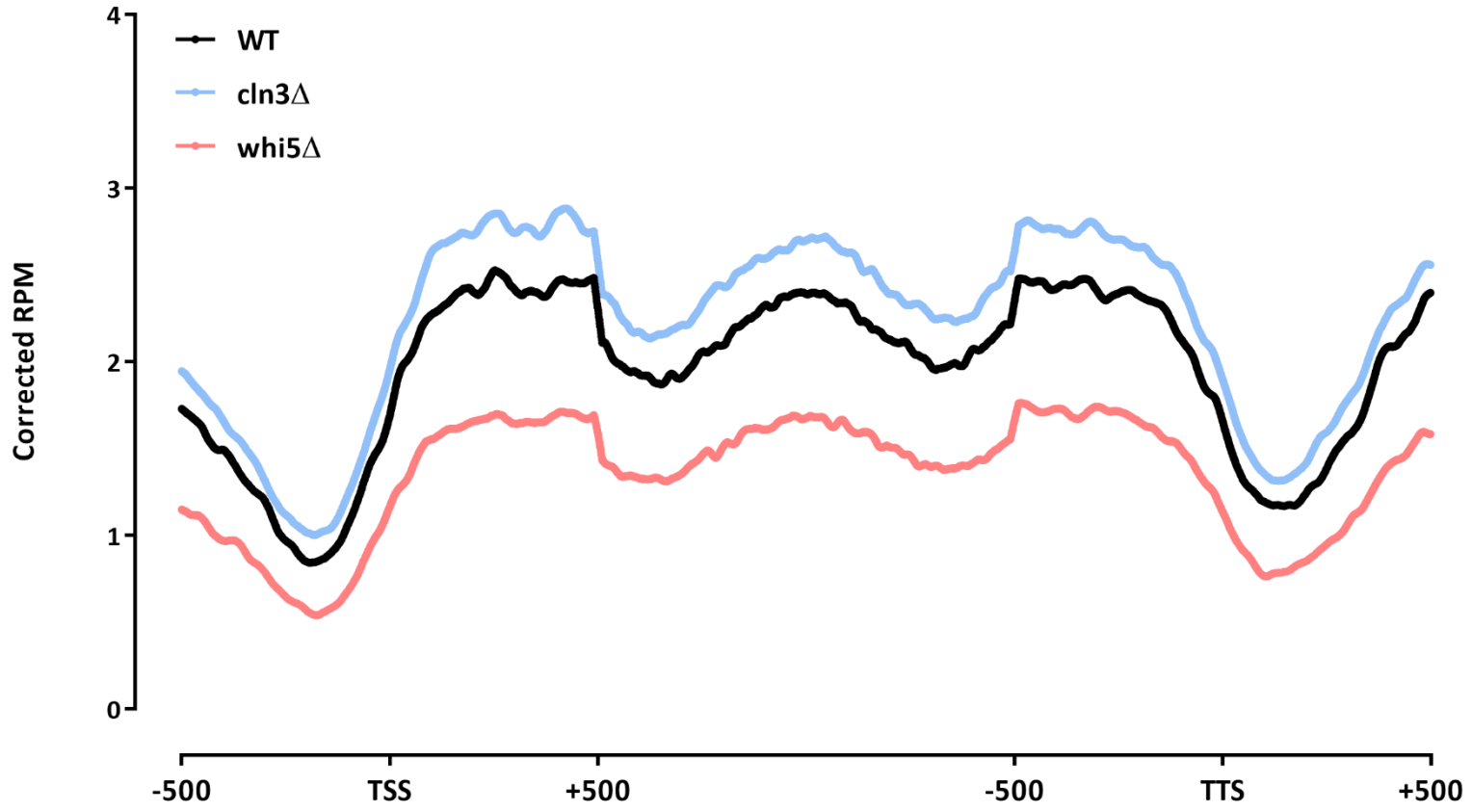
Note: this is much better done for large genomes and/or point-source factors, where we can calculate FRiP values for peaks in the control genome and use that for normalization. The nature of the data here is such that makes it impossible though

Library	Raw fragments	Species	2x36mers		1x36mers		Mappability Corrected RPKM	S.cerevisiae/S.pombe ratio	Correction factor
			Unique non-chrM reads	Complexity	Unique non-chrM reads	Complexity			
WT-H3	1,064,508	sacCer3	1,064,528	0.97	536,713	0.96	69.66	4.24	0.70
	1,064,508	S.pombe	264,160	0.99	133,460	0.99	16.43		
WT-Input	615,834	sacCer3	805,132	0.98	404,907	0.98	74.01	6.02	1.00
	615,834	S.pombe	141,106	0.99	70,949	0.99	12.30		
WT-Pol2	812,719	sacCer3	772,936	0.96	390,550	0.96	69.45	4.18	0.69
	812,719	S.pombe	195,266	0.98	98,571	0.98	16.63		
WT-Pol2pS2	724,576	sacCer3	577,786	0.96	293,261	0.96	56.75	1.98	0.33
	724,576	S.pombe	308,428	0.97	156,231	0.97	28.67		
WT-Pol2pS25	840,788	sacCer3	471,840	0.97	238,486	0.97	33.35	0.66	0.11
	840,788	S.pombe	760,898	0.96	383,524	0.96	50.87		
cln3-H3	1,436,625	sacCer3	1,509,632	0.97	760,729	0.96	71.20	4.76	0.79
	1,436,625	S.pombe	334,466	0.99	168,538	0.99	14.96		
cln3-Input	1,796,984	sacCer3	1,936,920	0.97	976,332	0.96	73.97	5.99	1.00
	1,796,984	S.pombe	341,372	0.99	171,789	0.99	12.34		
cln3-Pol2	434,701	sacCer3	482,620	0.98	243,009	0.98	68.21	3.83	0.64
	434,701	S.pombe	132,890	0.99	66,860	0.99	17.80		
cln3-Pol2pS2	671,364	sacCer3	654,598	0.97	330,625	0.97	55.77	1.88	0.31
	671,364	S.pombe	366,916	0.97	184,985	0.97	29.60		
cln3-Pol2pS25	610,734	sacCer3	300,588	0.98	152,613	0.98	30.12	0.56	0.09
	610,734	S.pombe	569,874	0.96	288,067	0.96	53.93		
whi5-H3	1,201,314	sacCer3	1,138,238	0.97	574,493	0.96	61.24	2.51	0.49
	1,201,314	S.pombe	478,280	0.99	241,492	0.99	24.42		
whi5-Input	2,229,447	sacCer3	2,426,126	0.96	1,224,910	0.95	72.07	5.10	1.00
	2,229,447	S.pombe	502,180	0.99	253,399	0.99	14.14		
whi5-Pol2	918,837	sacCer3	960,044	0.95	485,651	0.95	70.70	4.58	0.90
	918,837	S.pombe	221,524	0.97	111,824	0.98	15.44		
whi5-Pol2pS2	1,430,630	sacCer3	965,332	0.94	489,313	0.94	64.43	3.01	0.59
	1,430,630	S.pombe	339,026	0.95	171,278	0.96	21.39		
whi5-Pol2pS25	1,433,030	sacCer3	678,682	0.96	345,660	0.96	38.63	0.84	0.17
	1,433,030	S.pombe	852,574	0.95	432,639	0.94	45.86		

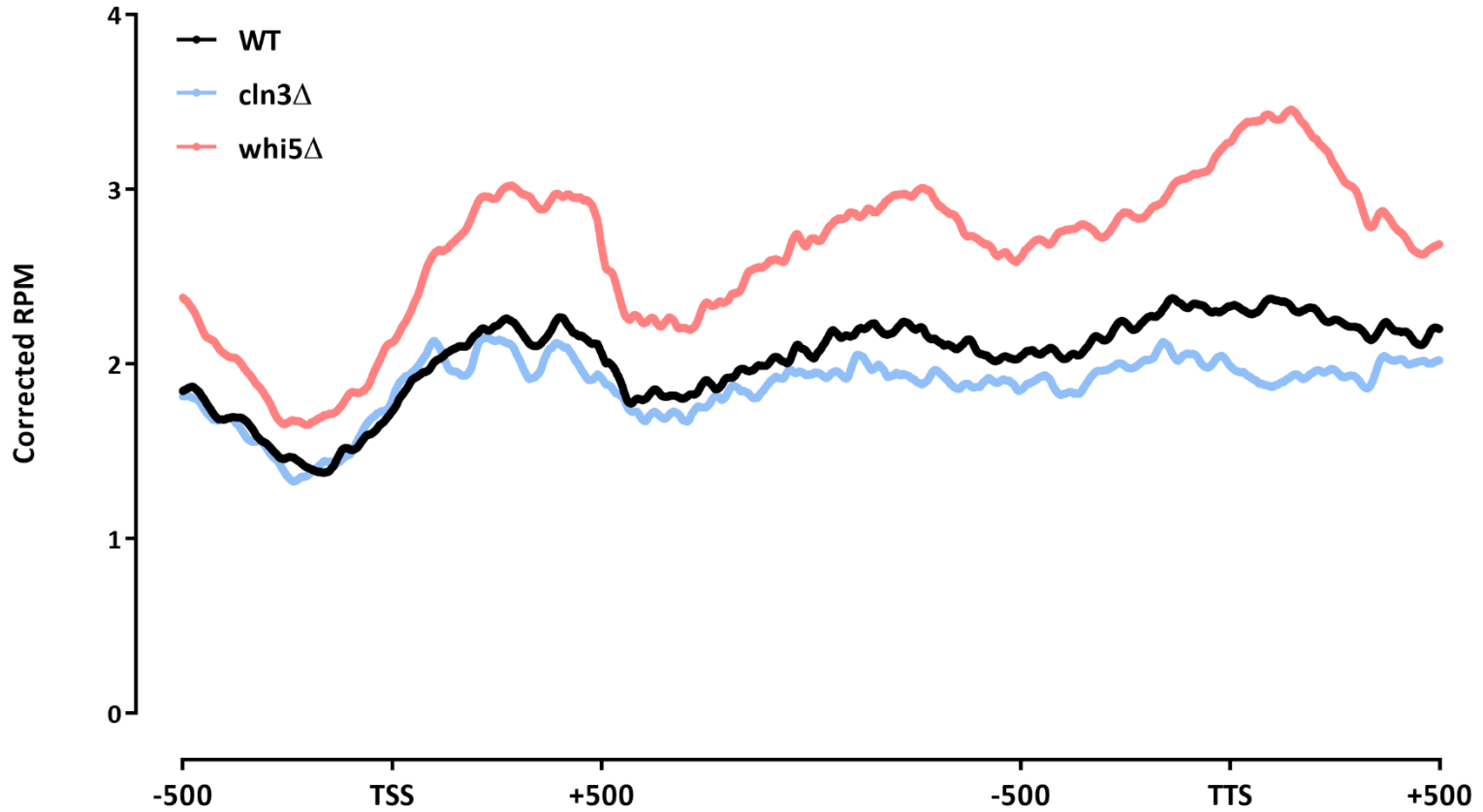
Input *S. cerevisiae* corrected



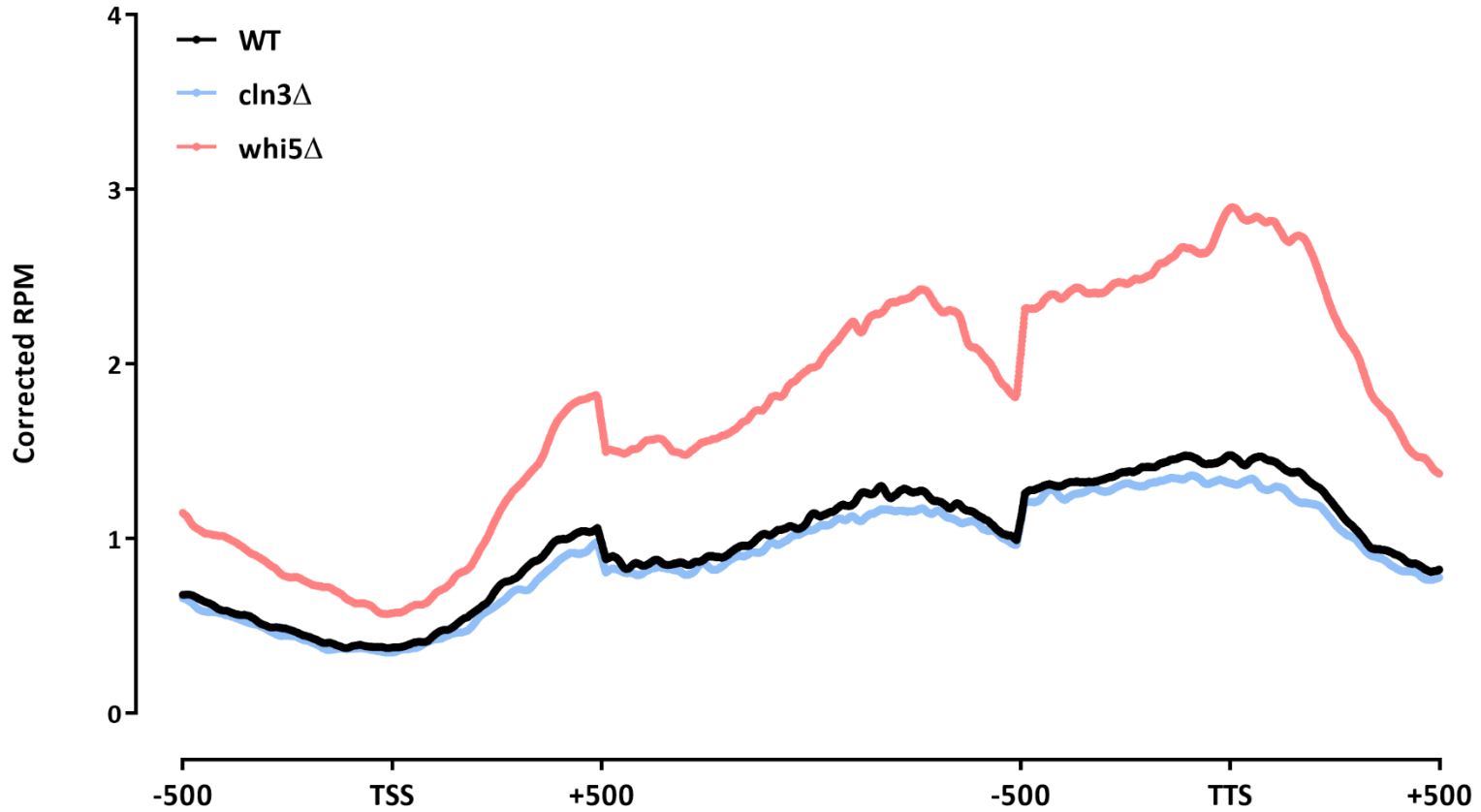
H3 *S. cerevisiae* corrected



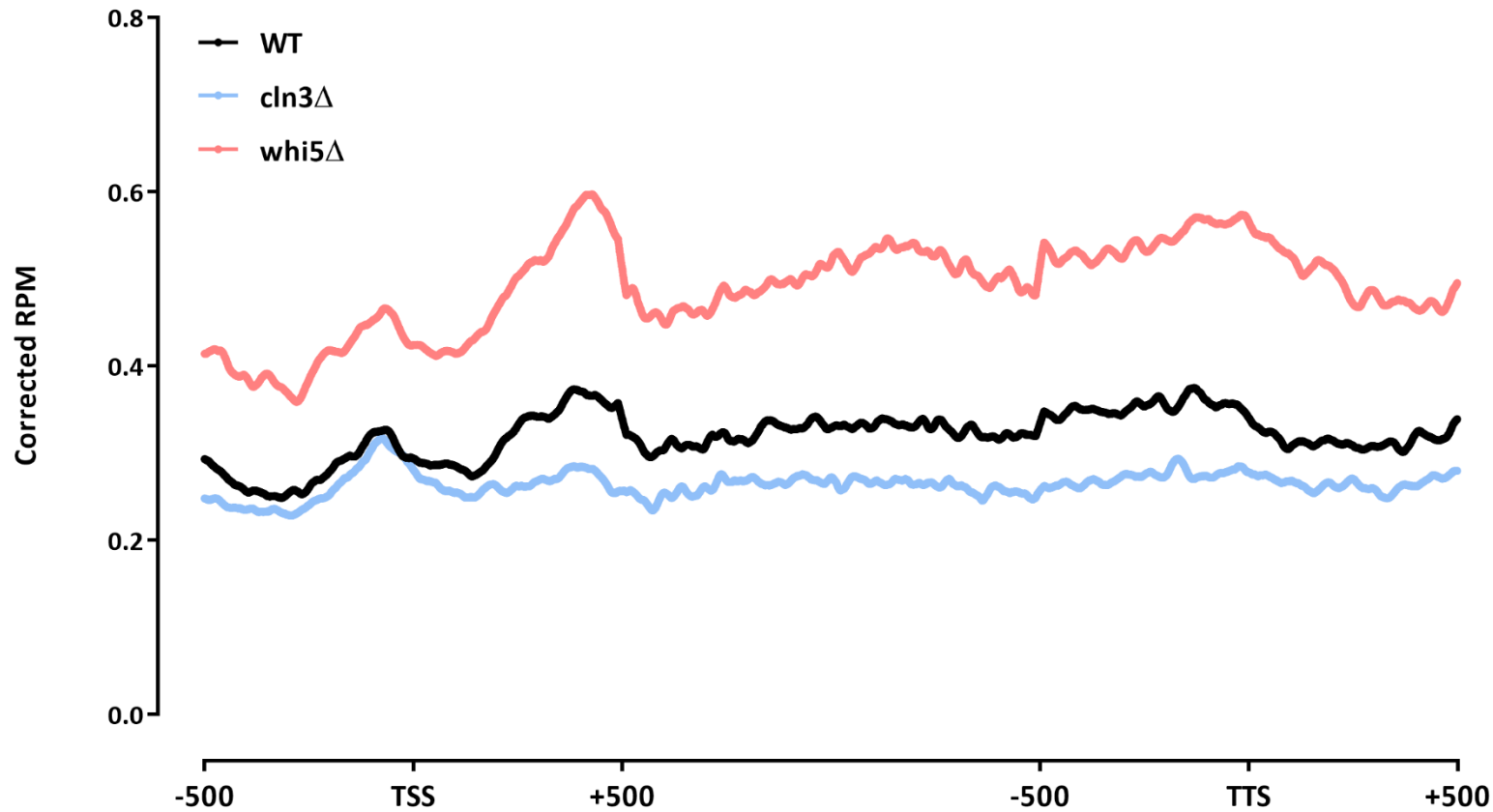
Pol2 *S. cerevisiae* corrected



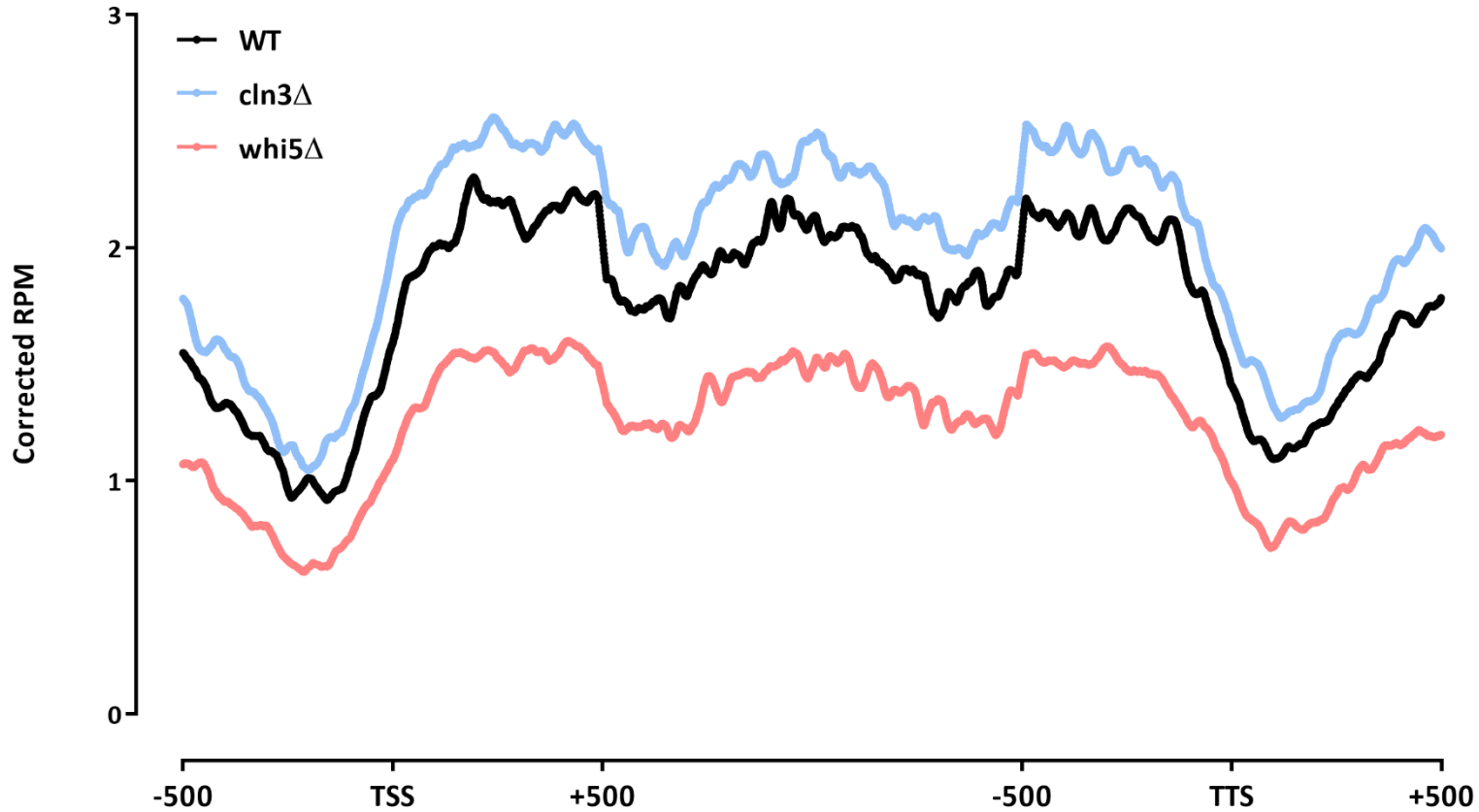
Pol2pS2 *S. cerevisiae* corrected



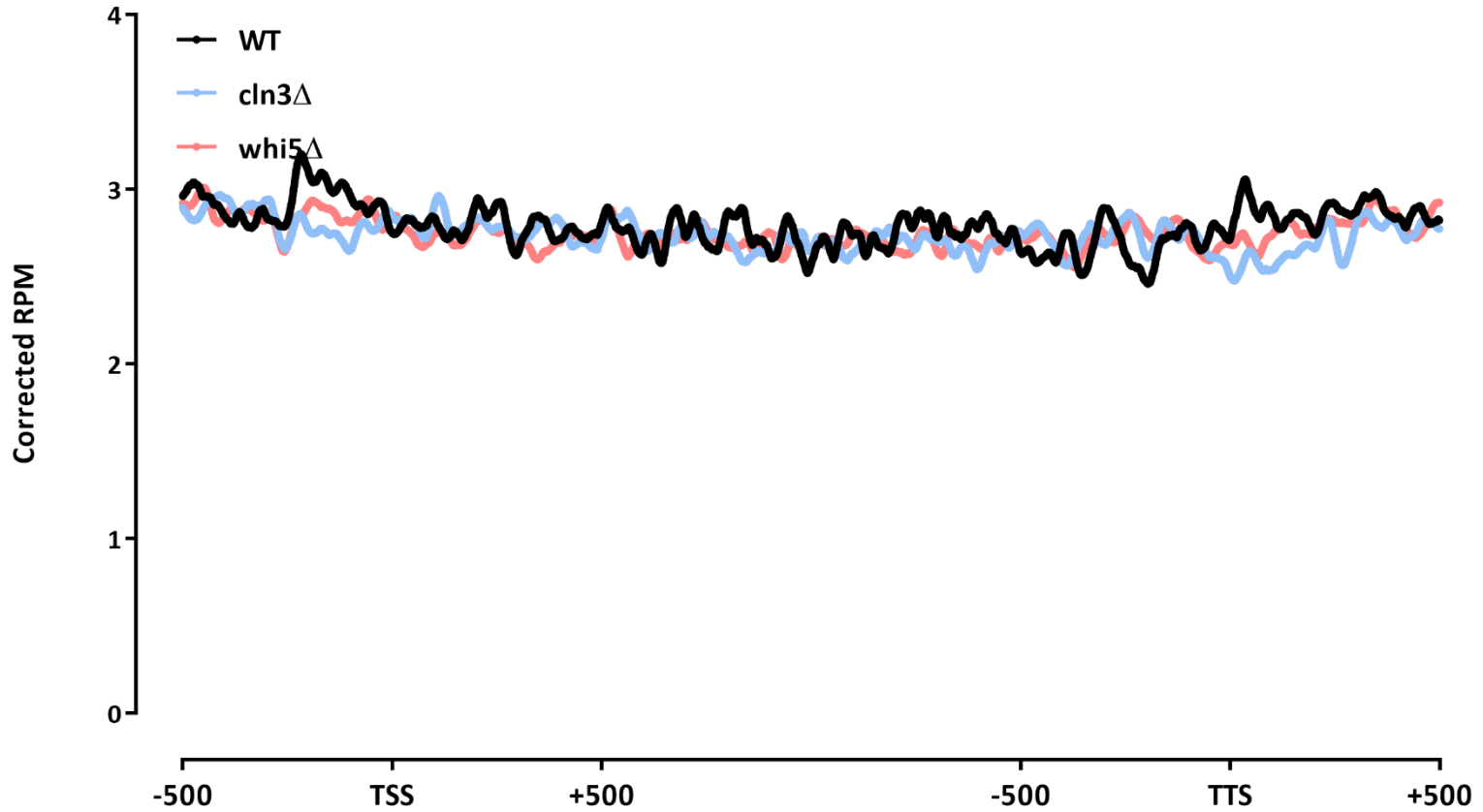
Pol2pS5 *S. cerevisiae* corrected



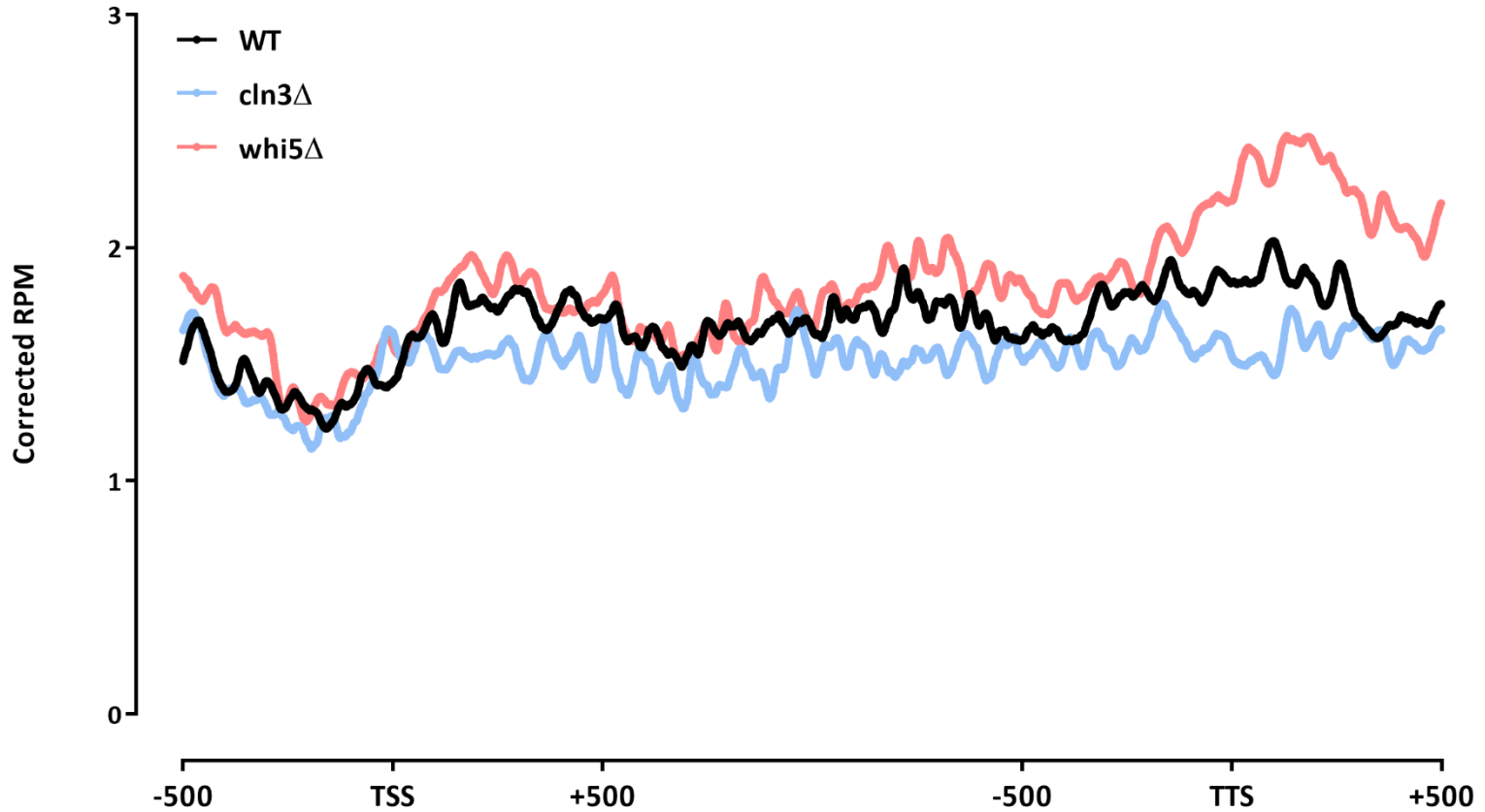
H3 *S. cerevisiae* bottom expression quintile corrected



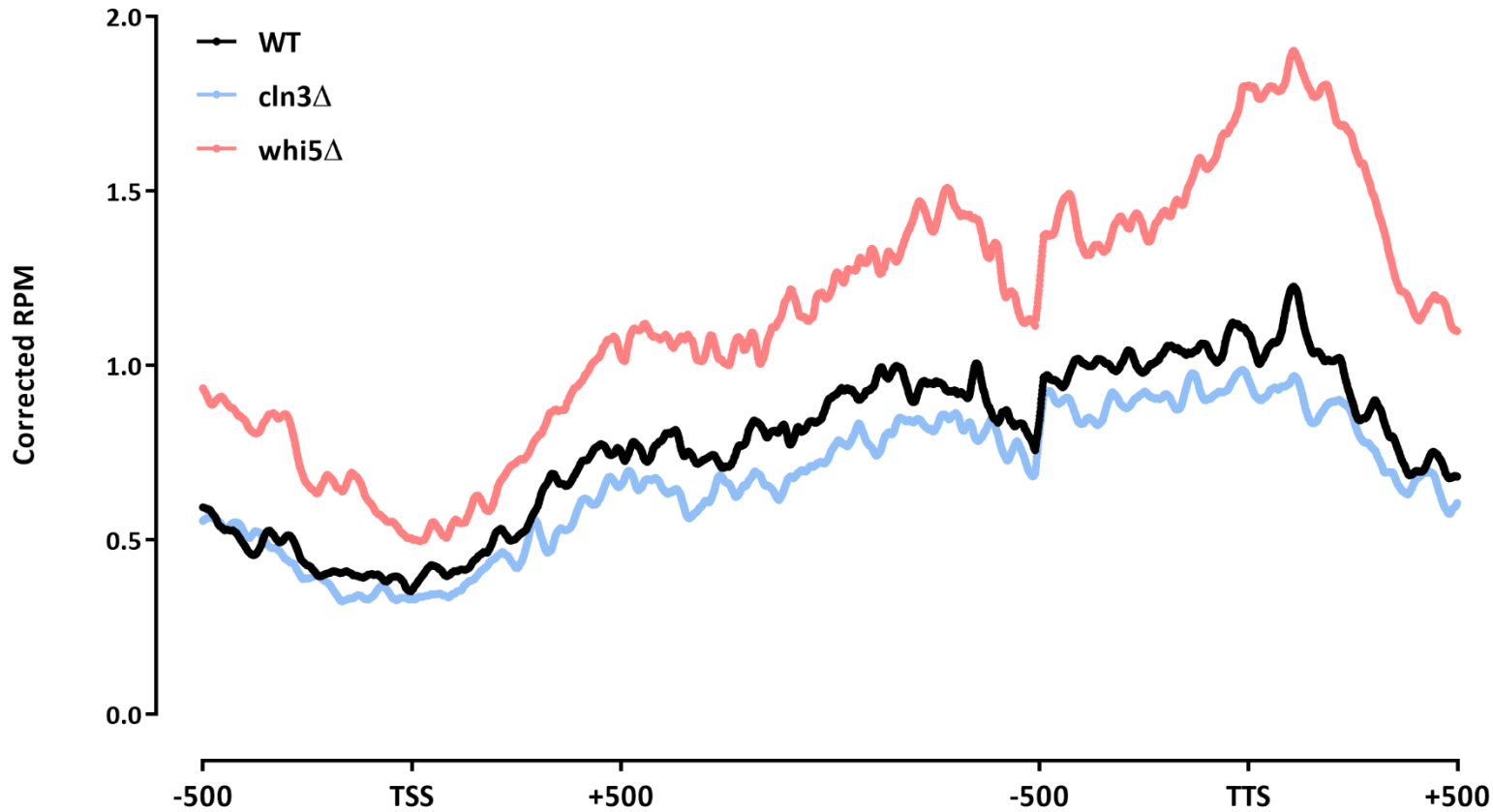
Input *S. cerevisiae* bottom expression quintile corrected



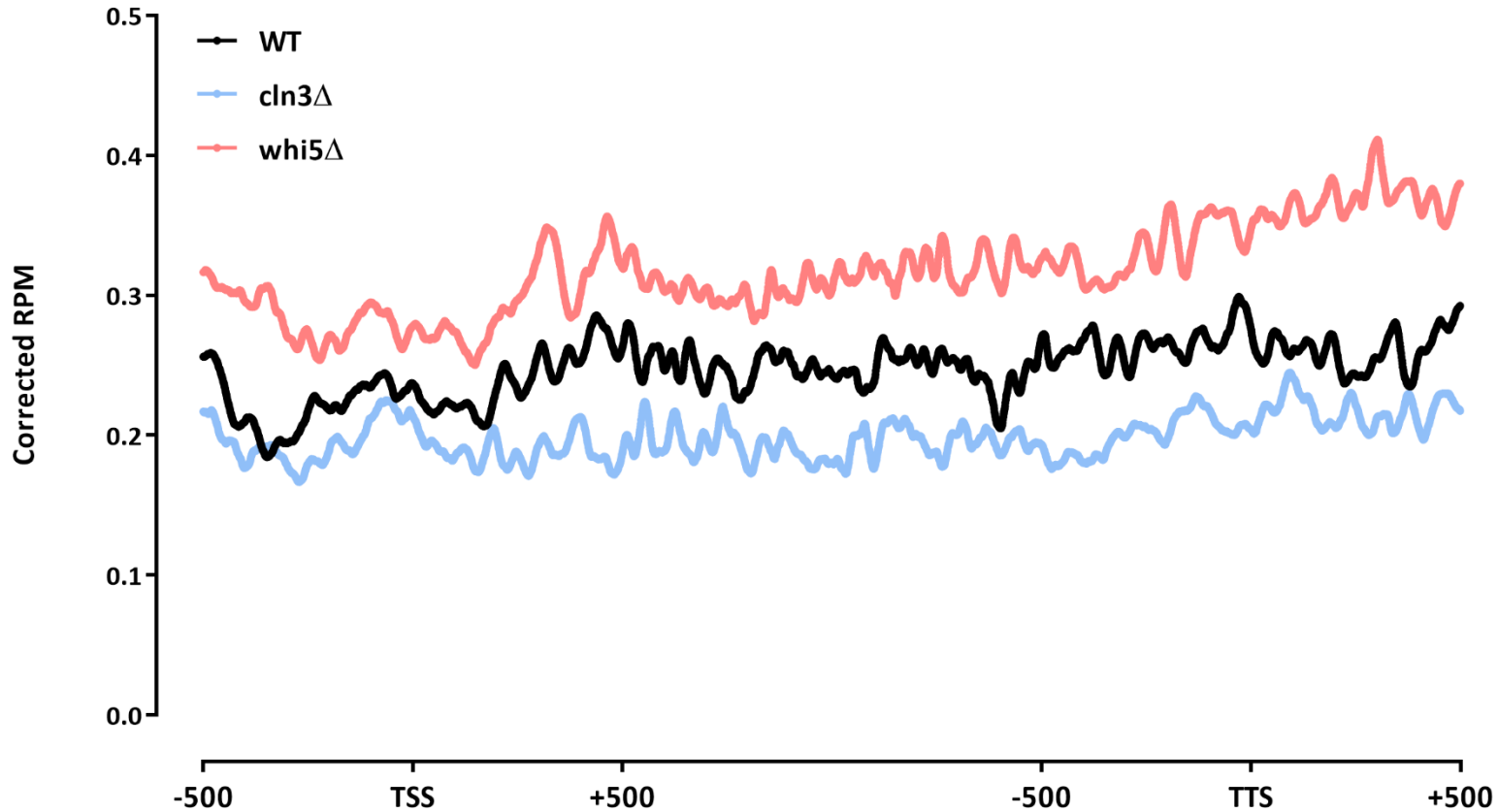
Pol2 *S. cerevisiae* bottom expression quintile corrected



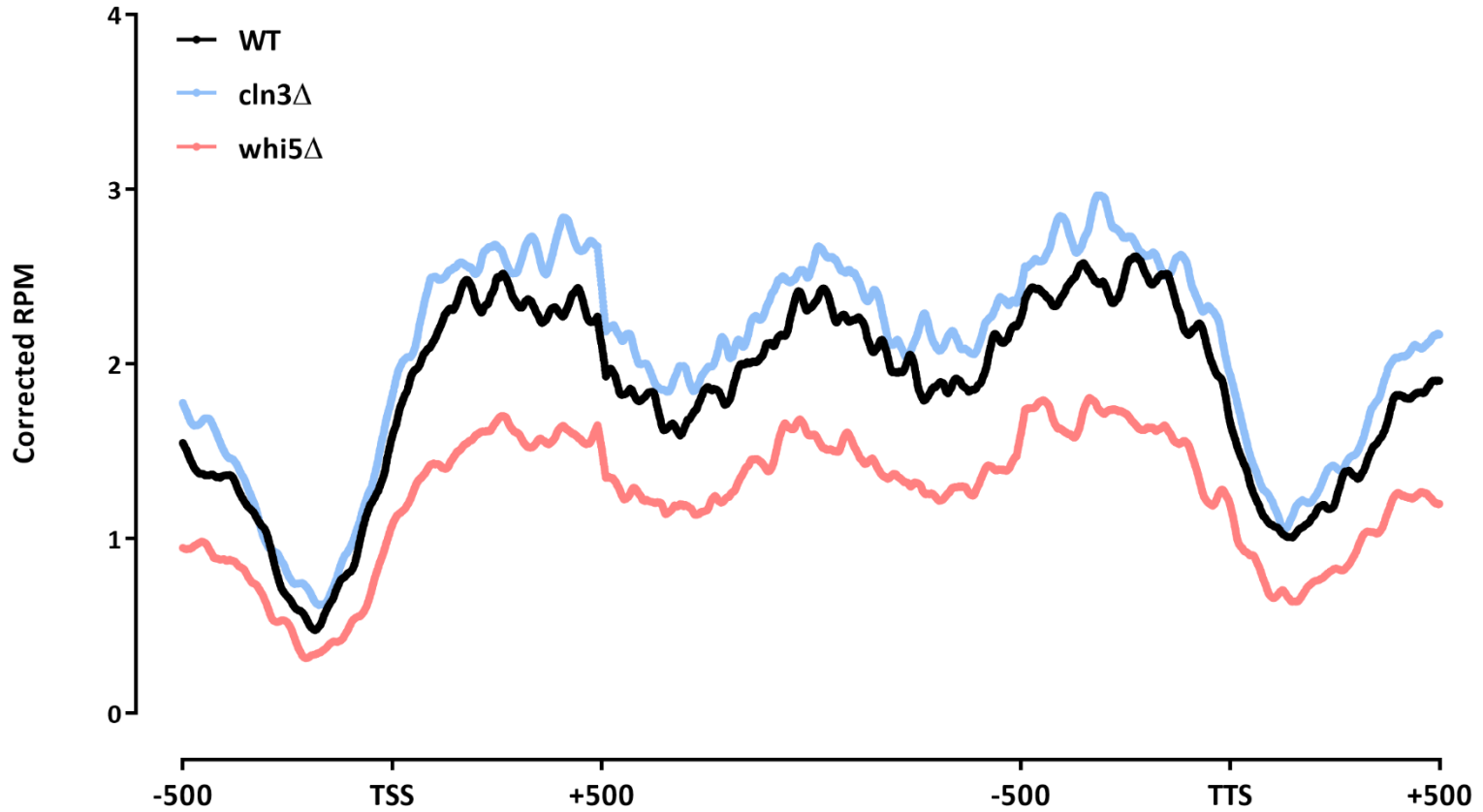
Pol2pS2 *S. cerevisiae* bottom expression quintile corrected



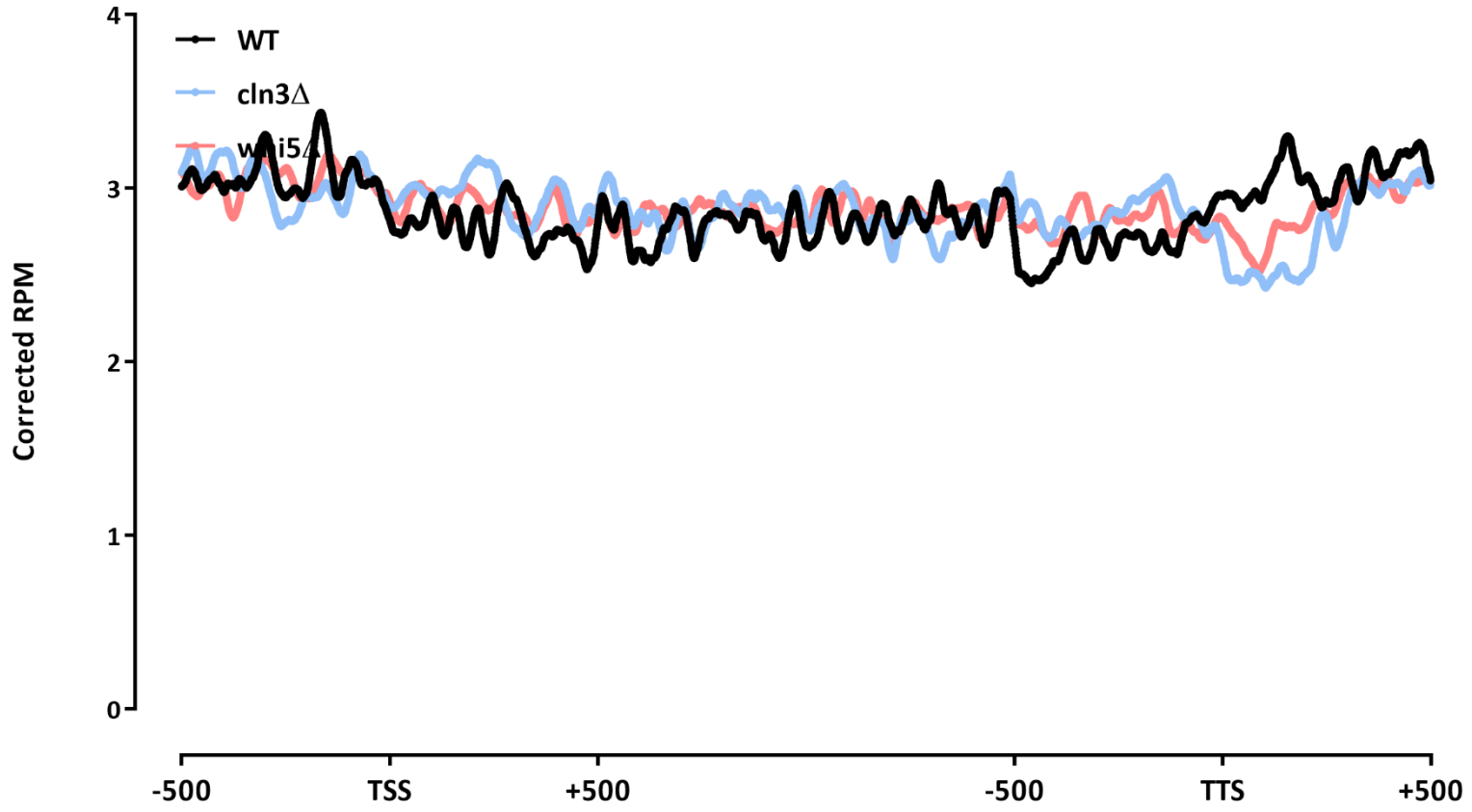
Pol2pS5 *S. cerevisiae* bottom expression quintile corrected



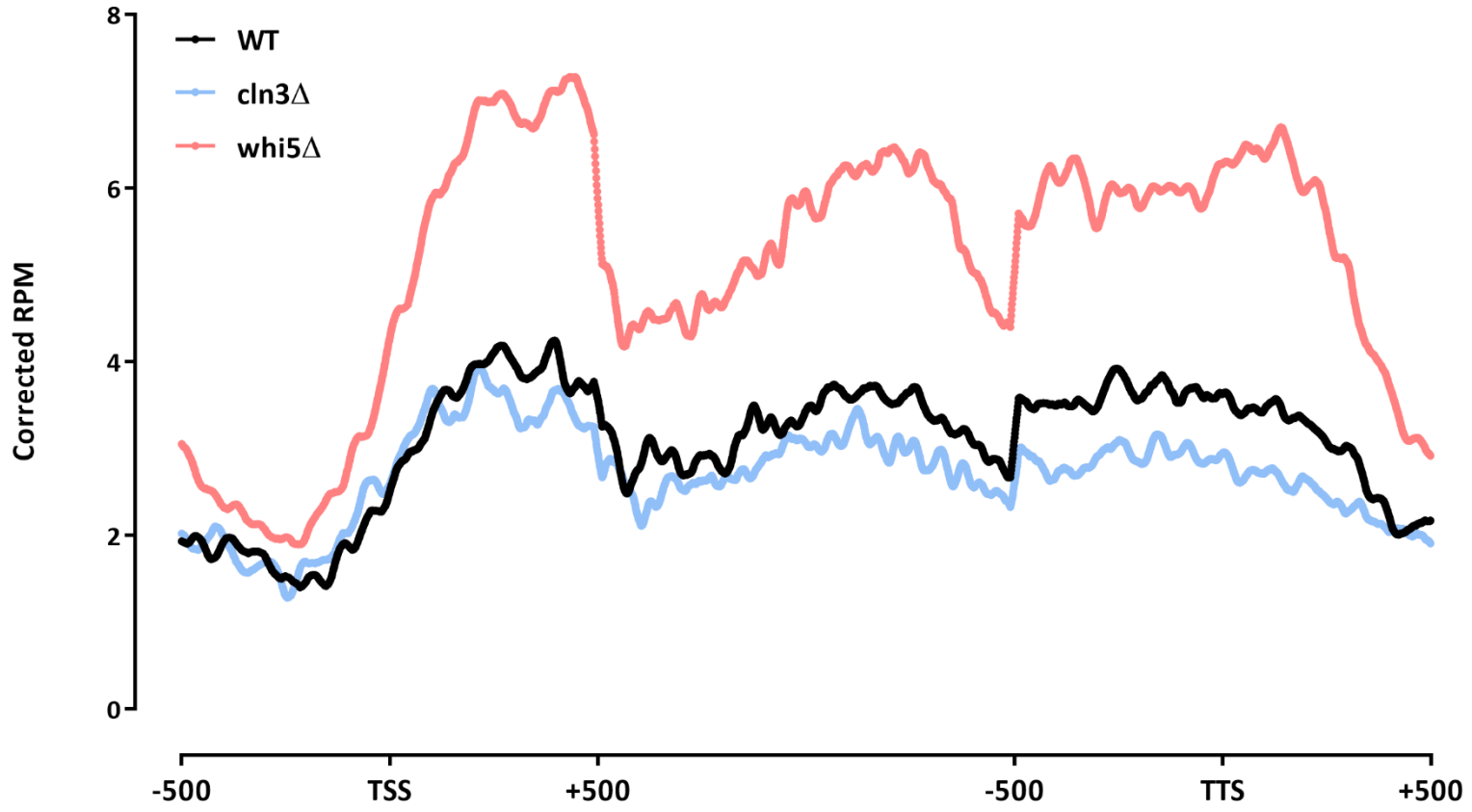
H3 *S. cerevisiae* top expression quintile corrected



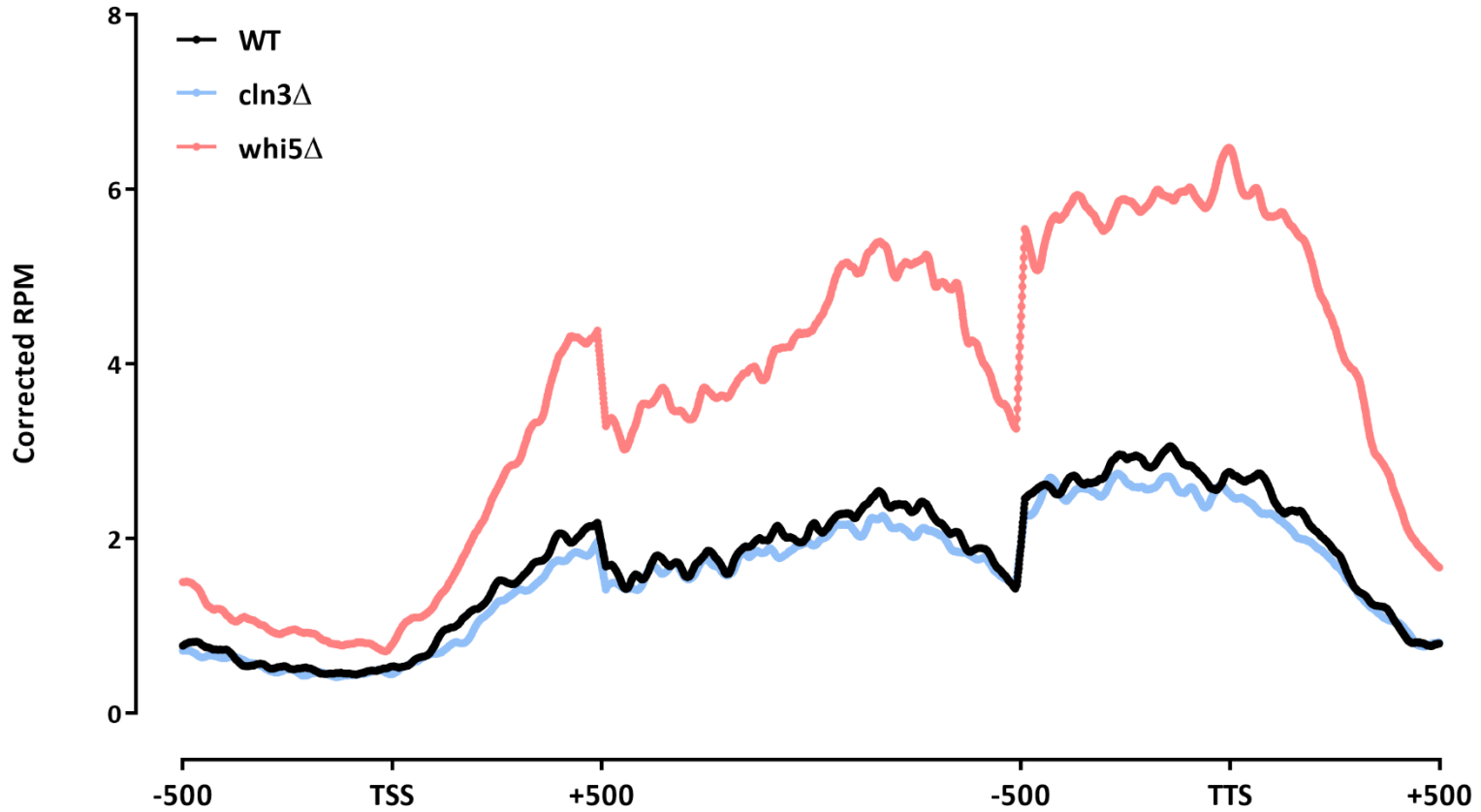
Input *S. cerevisiae* top expression quintile corrected



Pol2 *S. cerevisiae* top expression quintile corrected



Pol2pS2 *S. cerevisiae* top expression quintile corrected



Pol2pS5 *S. cerevisiae* top expression quintile corrected

