

SUPPLEMENTAL FIGURES

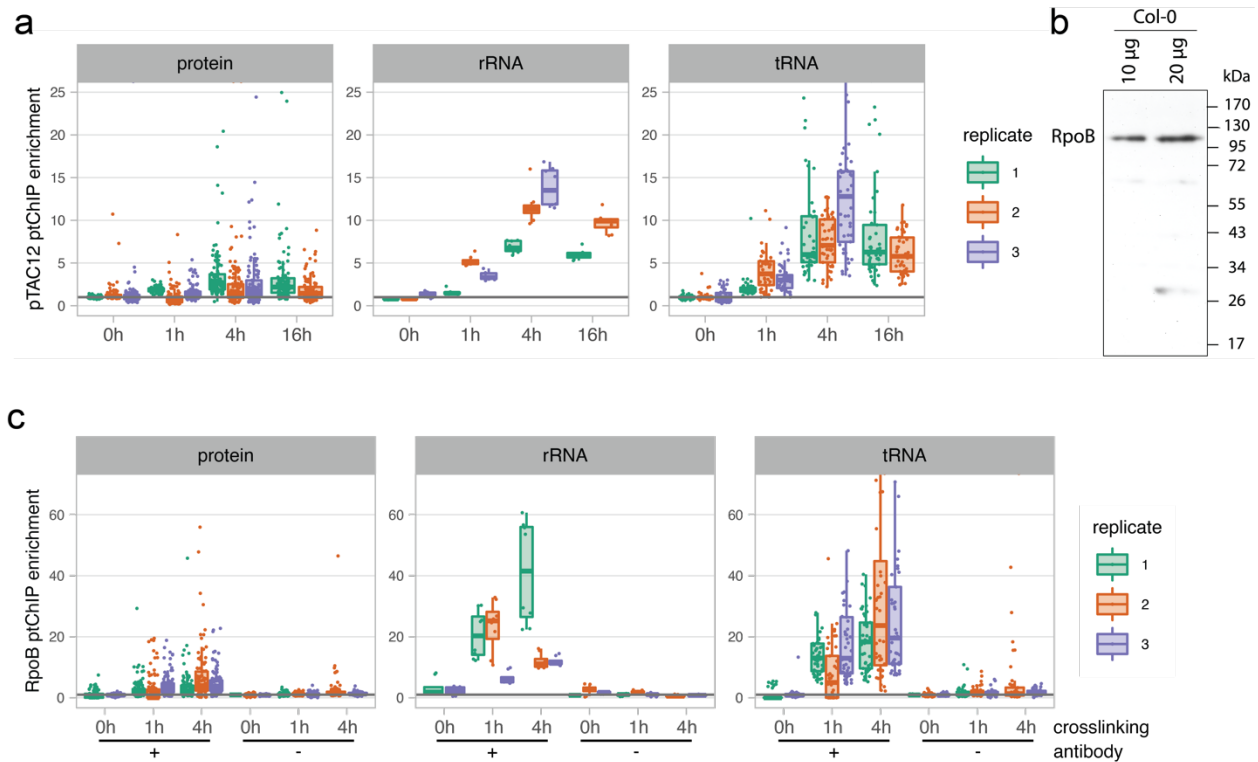


Figure S1. Detection of PEP binding to DNA using ptChIP-seq. Individual biological replicates of data shown in Fig. 1.

- A. Optimization of formaldehyde crosslinking duration in ptChIP-seq. Individual biological replicates of ptChIP-seq performed using α HA antibody in plants expressing pTAC12-HA shown in Fig. 1A.
- B. Western blot indicating that the polyclonal anti-RpoB antibody used in this study recognizes a protein of the expected size.
- C. Optimization of formaldehyde crosslinking duration and negative controls in ptChIP-seq. Individual biological replicates of ptChIP-seq using α RpoB antibody in Col-0 wild-type plants shown in Fig. 1B.

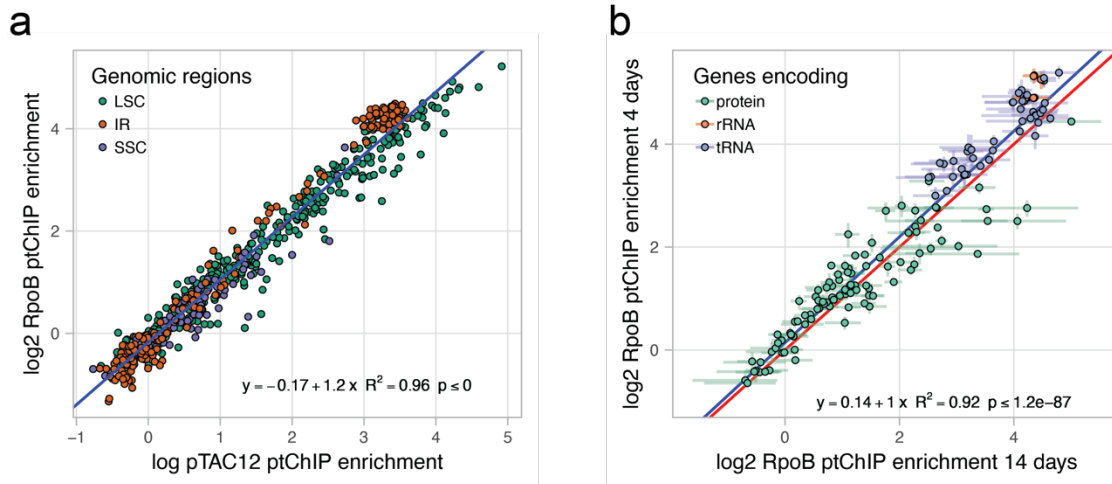


Figure S2. Specificity of ptChIP-seq with α RpoB antibody.

- A. pTAC12 and RpoB ptChIP-seq signals are highly correlated. Enrichment levels on 250 bp genomic bins were compared between ptChIP-seq experiments using α HA antibody in plants expressing pTAC12-HA and using α RpoB antibody in Col-0 wild-type plants. Data points are color-coded by location of bins within the LSC, IR or SSC. Blue line represents the linear regression model.
- B. RpoB ptChIP-seq signals are highly correlated between 4-day-old plants and 14-day-old plants. Enrichment levels on annotated genes from ptChIP-seq using α RpoB antibody in Col-0 wild-type plants were compared between 4-day-old and 14-day-old plants. Data points are color-coded by the function of the corresponding genes and show averages from three independent replicates. Error bars indicate standard deviations. Blue line represents the linear regression model. Red line represents values that are equal between both conditions.

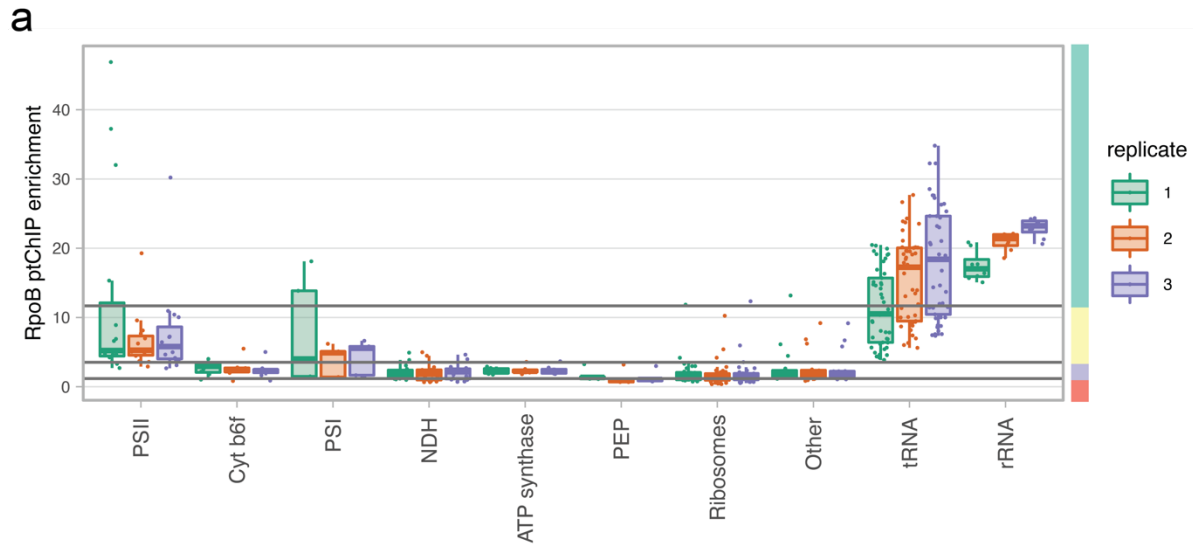


Figure S3. Complex pattern of PEP binding to plastid DNA. Individual biological replicates of data shown in Fig. 3C.

A. PEP binding to DNA of genes classified by function. Enrichment levels of ptChIP-seq using α RpoB antibody in Col-0 wild-type were plotted on annotated genes split by the function of gene products (Chotewutmontri and Barkan, 2018). PEP binding level groups are indicated on the right. Colors indicate data from independent replicates.

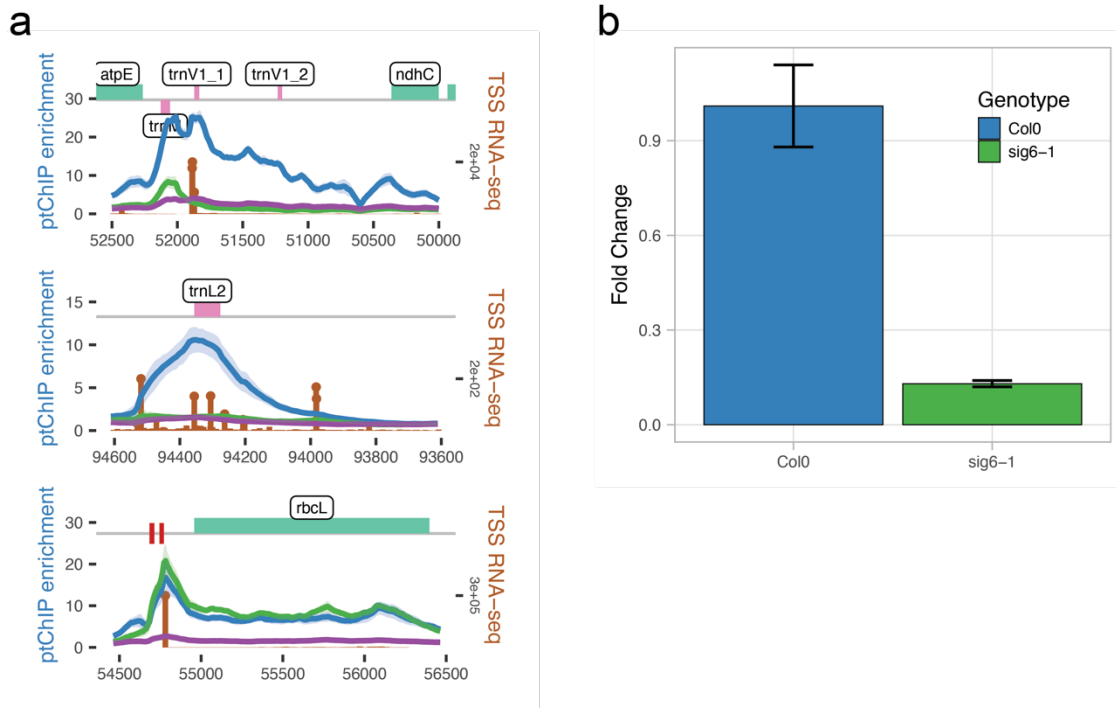
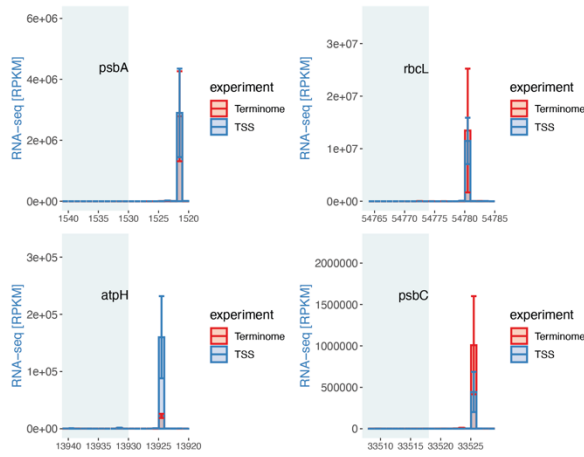


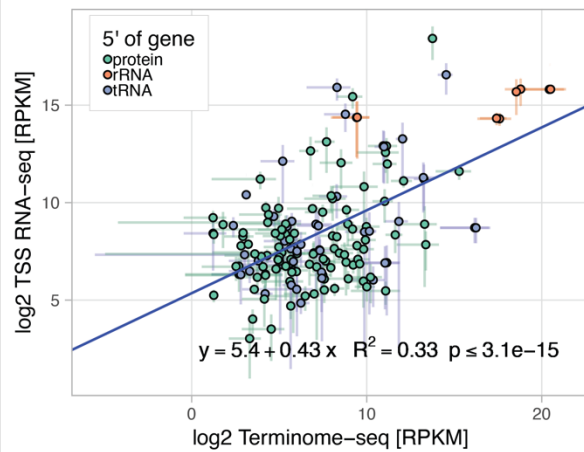
Figure S4. Dual impact of *sig2* and *sig6* mutants on PEP binding to plastid DNA.

- A. Reduction of PEP binding to DNA in *sig2* and *sig6* on *trnV*, *ndhC*, *trnL* and *rbcL*. Signal enrichments from ptChIP-seq using α RpoB antibody in Col-0 wild-type, *sig2* and *sig6* plants were calculated in 10 bp genomic bins and plotted at the relevant locus. Color-coding of ptChIP-seq data corresponds to data shown in Fig. 4A. Average enrichments from three independent biological replicates are shown. Ribbons indicates standard deviations. Brown vertical lines indicate sense strand data from three combined replicates of TSS RNA-seq. Genome annotation is shown on top.
- B. Reduction of the tRNA product of *trnI1* (tRNA-Ile-CAU) in the *sig6* mutant. Accumulation of the tRNA was assayed using RT-qPCR. The average and standard deviation from three biological replicates are shown.

a



b



c

Gene	Sequence	Position relative to translation start site	Ref.
<i>psbA</i>	TTTACATTGGTT GACA TGGCTATATAAGTCATGT---T ATACT GTTTCAT A CAAGCTCTCAA	-66	1,2
<i>trnQ</i>	TCATTTTGAAT TGACG AACAACCAATAGGAATAT---T ACTCT TTTAGT A GTCCTGAATAAAA	-8	3
<i>atpH</i>	TTGGTTTACAT TATGTA AAGAAACACTTGTATA-----T GTGAT ATT G ATATGCCTAGGTAT	-403	4
<i>atpI</i>	AGGGCCGTT CTAGCT AATACAATAAATCTTGATT---A ATAAT AAGATA AAT TAATCA ATTTT	-215	5
<i>petN</i>	TCCCTTTTT TTGACT CTGCACCAGTGATTTCCAC---T ATTAT TAGT G CAATAATGGAATA	-39	6
<i>trnE</i>	TTTCATTATAT TGACA ATTTAAAAAACTGATCA---T ACTAT GAT C TG TATGA TGGCGGT	-12	3,7
<i>psbD</i>	ACCTAACCCAT TCGA ATCATGACTATATCCAC-----T ATTCT GATAT G AAATTCGATAGAG	-934	7,8
<i>psbD</i>	GAAACTCTCAT TTACAG TTTCCCTATAATTTTATT---T AAAT ATTGAAT A AAATATAAATAAG	-527	8,9
<i>psbD</i>	CATCCGACAAT TCATG ATTTAGATTCACACTACT---T ATACT TATTAAT A AACTAATAGCAA	-244	7
<i>psbD</i>	ACAAATTGAG TTGAT CCGTTTACCTAAGTAAGGACCAAT AAAT CAAAAATTT GAT CTTCGAA	-173	8,9
<i>psaA</i>	AAAGGGTCCG TTGAG CACCCCTATGGATATGT-----C ATAAT AGAT CCG AACACTTGCCCCA	-175	6,10
<i>rps4</i>	TTTATATATAT TGTAT ATACAATAAAAAAATCTG---T TATAT GAGAGAATATATCTTCTTAC	-109	5
<i>trnV1</i>	AATATTAATCT TGACA AAGAAATTAATCTACATGA---T AGATA AAAAT GTG TATCACAAACAC	-2	7
<i>trnM</i>	TTTATTGGTAT TGCTT AGAAATAATATGGATT---T ATAAT CCAT TCG ATGTGATAGGTAT	-31	3
<i>atpB</i>	AAAATCACT CTTGAC AGTAATATCTGTTGTATA----T GTAAT CCTAGAT ATG ACAATATGC	-451	6
<i>atpB</i>	TTTTGAATCT TTGACT TTTTATAAATCCAATATT---T AATAT TAAAAT T AAAT A TTAATAA	-508	5
<i>rbcL</i>	AAGTATTAG GTGCG CTATACATATGAAAGAATA---T ACAATA AT GAT GTATTGGCG ATC	-164	7,11
<i>ycf4</i>	TTTTAAAAA CTCGAT TCGATAAGACCCATTTGG---T AGAAT GTTGT A ACACATAGATTTC	-314	12
<i>psbE</i>	TCAAAT TGCGT GTGCTGTGTCAGAAGAAGGATAGC---T ATACT GATT CGG TAGACTCTAAAAA	-112	6,13
<i>psaJ</i>	CTTAATTACAT GTACAT CTGTAATTATATATAT---T ACTAT ATATA T GTAATACAATAAA	-23	14
<i>psbB</i>	TTAACCC ATTCGAT ATTTGGTACTATCGGATA---T AGAATA GAT CCG CTCCCTTTTTTT	-158	6
<i>psbN</i>	TCTGTTGAC TTGTAT ACCATTCCGTTGTAAA-----T AAATG ATCTTAGCAT AGAT CC GTG	-22	4
<i>rm16</i>	GCTCGTGGGAT TGACG TGAGGGGGTAGGGGTAGC---T TATAT TCT GGAG CC ACT CCATGC	-102	15
<i>ndhF</i>	GTGGAATCT TTGTT CTATTCTTAATATATGTA---T ATAAAT TAT TGTAAT TGGAATTAT	-305	12
<i>tic214</i>	ATTTCTATAT TGGAA AGTTGCAAAATCATCA-----T ATAAT ATCC G AAATGAAATAGA	-20	5

d

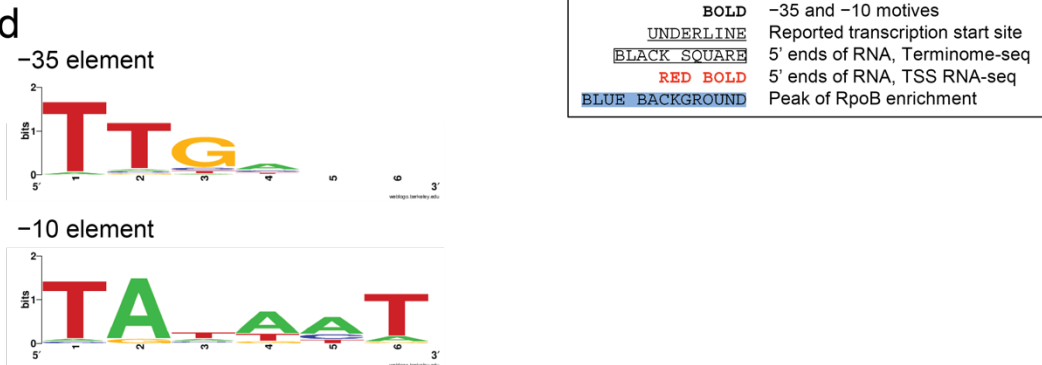


Figure S5. PEP promoters identified in Arabidopsis.

- A. TSS RNA-seq (this study) and Terminome-seq (Castandet *et al.*, 2019) identify similar subsets of RNA 5' ends. Bars indicate averages and standard deviations from three (TSS RNA-seq) or two (Terminome-seq) experiments. The light-blue areas in the plot represent the promoter positions.
- B. Signal levels of 5' ends identified using TSS RNA-seq (this study) and Terminome-seq (Castandet *et al.*, 2019) are significantly correlated. Signal levels were counted on regions spanning 100 bp around 5' ends of annotated genes. Error bars indicate standard deviations from three (TSS RNA-seq) or two (Terminome-seq) experiments.
- C. Alignment of PEP promoters. Positions of the last nucleotides (20 nt from the -10 element) relative to translation start sites are indicated. Transcription start sites reported previously using primer extension, nuclease protection or Terminome-seq and using TSS RNA-seq in this study are represented with underlines, black squares, and red colors, respectively. Blue background indicates the position with highest RpoB enrichment downstream of each -10 element. ¹Liere *et al.*, 1995; ²Shen *et al.*, 2001; ³Kanamaru *et al.*, 2001; ⁴Zghidi *et al.*, 2007; ⁵Swiatecka-Hagenbruch *et al.*, 2007; ⁶Ishizaki *et al.*, 2005; ⁷Hanaoka *et al.*, 2003; ⁸Hoffer and Christopher, 1997; ⁹Shimmura *et al.*, 2008; ¹⁰Fey *et al.*, 2005; ¹¹Hakimi *et al.*, 2000; ¹²Favory *et al.*, 2005; ¹³Demarsy *et al.*, 2012; ¹⁴Nagashima *et al.*, 2004; ¹⁵Sriraman *et al.*, 1998.
- D. Sequence logos for -35 and -10 elements of PEP promoters listed in A. Images were generated by using WebLogo (<https://weblogo.berkeley.edu/logo.cgi>) with default settings.

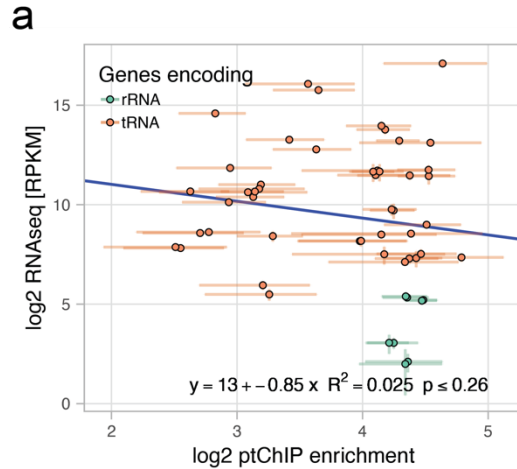


Figure S6. Correlation of PEP binding with steady-state levels of RNA.

- A. There is no correlation on rRNA and tRNA genes between RpoB ptChIP-seq enrichments and total RNA-seq signals. Enrichment levels of RpoB ptChIP-seq in 14-day-old Col-0 wild-type plants (this study) and RPKM normalized total RNA-seq signals from a similar developmental stage (Thieffry *et al.*, 2020) were compared on annotated rRNA and tRNA genes. Data points are color-coded by function of the corresponding genes and show averages from three independent replicates. Error bars indicate standard deviations. Blue line represents the linear regression model.

Table S1. High throughput sequencing datasets generated in this study.

Experiment	Genotype and treatment	Repl.	Numbers of paired end sequencing reads			Plastid genome coverage	GEO accession	
			Raw	Mapped to whole genome	Mapped to plastid genome			
ptChIP-seq in Col-0	α RpoB ptChIP Col-0, 14do IP	1	4054606	3143903	1209796	2349.5	GSM5751803	
		2	2882681	2416142	917690	1782.2	GSM5751804	
		3	2433915	2176001	1304195	2532.8	GSM5751805	
	α RpoB ptChIP Col-0, 14do input	1	2658090	2112848	726098	1410.1	GSM5751806	
		2	2198631	1937278	1124582	2184.0	GSM5751807	
		3	4179457	4012193	2169404	4213.1	GSM5751808	
ptChIP-seq in sigma factor mutants	α RpoB ptChIP Col-0, 4do IP	1	3178254	2738462	2406332	4673.2	GSM5751809	
		2	4290851	3644708	2987565	5802.0	GSM5751810	
		3	4022836	3625185	2993794	5814.1	GSM5751811	
	α RpoB ptChIP Col-0, 4do input	1	3054715	2892619	1638568	3182.2	GSM5751812	
		2	3512602	3344462	1735754	3370.9	GSM5751813	
		3	2213601	2106974	1272387	2471.0	GSM5751814	
	α RpoB ptChIP <i>sig2-2</i> , 4do IP	1	5124923	3438873	1886483	3663.6	GSM5751815	
		2	5461169	4243874	2833197	5502.2	GSM5751816	
		3	5449395	4558063	3226441	6265.9	GSM5751817	
	α RpoB ptChIP <i>sig2-2</i> , 4do input	1	3275658	3081156	2026055	3934.7	GSM5751818	
		2	2835440	2686028	1732618	3364.8	GSM5751819	
		3	2321023	2207212	1541574	2993.8	GSM5751820	
	α RpoB ptChIP <i>sig6-1</i> , 4do IP	1	2270376	1611802	771552	1498.4	GSM5751821	
		2	4898113	3653232	1670993	3284.0	GSM5751822	
		3	4337287	3587995	2136859	4149.9	GSM5751823	
	α RpoB ptChIP <i>sig6-1</i> , 4do input	1	3409410	3163122	1955323	3797.3	GSM5751824	
		2	2733495	2521338	1286623	2498.7	GSM5751825	
		3	3314878	3162046	2050470	3982.1	GSM5751826	
	ptChIP xlinking optimization α HA	α HA ptChIP Col-0, 14do IP, 0h xlinking	1	920851	63211	36351	70.6	GSM5751827
			2	1795101	967635	564879	1097.0	GSM5751831
			3	1257078	492658	298718	580.1	GSM5751835
		α HA ptChIP Col-0, 14do IP, 1h xlinking	1	1400807	375440	20968	40.7	GSM5751829
			2	1371708	1039486	28528	55.4	GSM5751833
			3	1454561	1274143	26604	51.7	GSM5751836
α HA ptChIP Col-0, 14do IP, 4h xlinking		1	863247	491943	18762	36.4	GSM5751830	
		2	1097756	576260	22844	44.4	GSM5751834	
		3	1378762	1223467	256851	498.8	GSM5751837	
α HA ptChIP Col-0, 14do IP, 16h xlinking		1	1280235	505963	62808	122.0	GSM5751828	
		2	859243	463860	23227	45.1	GSM5751832	
α HA ptChIP pTAC12-HA, 14do IP, 0h xlinking		1	1044721	154740	90663	176.1	GSM5751838	
		2	861576	107061	56040	108.8	GSM5751842	
		3	1274177	236643	141322	274.5	GSM5751846	
α HA ptChIP pTAC12-HA, 14do IP, 1h xlinking		1	1523025	880460	156886	304.7	GSM5751840	
		2	921045	613309	180805	351.1	GSM5751844	
		3	1075036	955224	64285	105.4	GSM5751847	
α HA ptChIP pTAC12-HA, 14do IP, 4h xlinking		1	1865224	945349	512855	996.0	GSM5751841	
		2	2386408	2145698	1661482	3326.7	GSM5751845	
		3	1305128	1106074	677949	1316.6	GSM5751848	
α HA ptChIP pTAC12-HA, 14do IP, 16h xlinking		1	1773357	1286948	863110	1676.2	GSM5751839	
		2	3405511	3187074	2882288	5597.5	GSM5751843	
ptChIP xlinking optimization α RpoB		α RpoB ptChIP Col-0, 14do IP, 0h xlinking	1	101564	59924	26451	51.4	GSM5751849
			3	1311600	728344	490235	913.2	GSM5751854
		1	1290652	858857	523683	1017.0	GSM5751850	

	αRpoB ptChIP Col-0, 14do IP, 1h xlinking	2	2344827	874776	443673	861.6	GSM5751852
		3	2118397	1907385	655533	1273.1	GSM5751855
	αRpoB ptChIP Col-0, 14do IP, 4h xlinking	1	1494376	1341752	862853	1675.7	GSM5751851
		2	1407565	1300862	715731	1390.0	GSM5751853
		3	1989369	1841830	1496908	2907.1	GSM5751856
	αRpoB ptChIP Col-0, 14do input, 0h xlinking	1	1946086	1868107	1254291	2435.9	GSM5751857
		2	1314300	1128562	788860	1532.0	GSM5751860
		3	1904283	1786188	1125708	2186.2	GSM5751863
	αRpoB ptChIP Col-0, 14do input, 1h xlinking	1	2017339	1908754	1343661	2609.4	GSM5751858
		2	2353928	1868689	1099790	2135.8	GSM5751861
		3	2630442	2524112	1484385	2882.7	GSM5751864
	αRpoB ptChIP Col-0, 14do input, 4h xlinking	1	857691	720821	538286	1047.3	GSM5751859
		2	2235821	1132373	696053	1351.8	GSM5751862
		3	2041195	1637617	980754	1904.7	GSM5751865
	noAB ptChIP Col-0, 14do IP, 0h xlinking	1	1390386	967246	646014	1254.6	GSM5751866
		2	1609455	200103	112500	218.5	GSM5751868
		3	1729661	1034151	631310	1226.0	GSM5751871
	noAB ptChIP Col-0, 14do IP, 1h xlinking	1	2003662	1791505	75438	146.5	GSM5751867
		2	1846817	1704905	35527	69.0	GSM5751869
3		2264948	2077787	81503	138.9	GSM5751872	
noAB ptChIP Col-0, 14do IP, 4h xlinking	2	2119540	1866929	132512	257.3	GSM5751870	
	3	3974954	3171658	202329	382.9	GSM5751873	
TSS RNA-seq	TSS RNA-seq Col-0, 14do	1	37708807	33877020	8078124	3922.0	GSM5751874
		2	24176101	20318827	9007260	4373.1	GSM5751875
		3	21521488	16821098	5901521	2865.2	GSM5751876

Table S2. Annotation of plastid-encoded genes in Arabidopsis used in this study.

chr	start	end	strand	type	name	long name	gene ID
Pt	4	76	-	tRNA	trnH	tRNA-His-GUG	ATCG00010
Pt	383	1444	-	protein	psbA	PSII D1 protein	ATCG00020
Pt	1717	1751	-	tRNA	trnK_2	tRNA-Lys-UUU	ATCG00030
Pt	2056	3570	-	protein	matK	Splicing factor	ATCG00040
Pt	4311	4347	-	tRNA	trnK_1	tRNA-Lys-UUU	ATCG00030
Pt	5084	5283	-	protein	rps16_2	30S Ribosomal protein CS16	ATCG00050
Pt	6149	6188	-	protein	rps16_1	30S Ribosomal protein CS16	ATCG00050
Pt	6616	6687	-	tRNA	trnQ	tRNA-Gln-UUG	ATCG00060
Pt	7017	7202	+	protein	psbK	PSII K protein	ATCG00070
Pt	7583	7693	+	protein	psbI	PSII I protein	ATCG00080
Pt	7785	7872	+	tRNA	trnS1	tRNA-Ser-GCU	ATCG00090
Pt	8646	8668	+	tRNA	trnG1_1	tRNA-Gly-UCC	ATCG00100
Pt	9383	9431	+	tRNA	trnG1_2	tRNA-Gly-UCC	ATCG00100
Pt	9590	9661	+	tRNA	trnR1	tRNA-Arg-UCU	ATCG00110
Pt	9938	11461	-	protein	atpA	ATP synthase subunit CF1 alpha	ATCG00120
Pt	11529	11938	-	protein	atpF_2	ATP synthase subunit CFo I	ATCG00130
Pt	12654	12798	-	protein	atpF_1	ATP synthase subunit CFo I	ATCG00130
Pt	13262	13507	-	protein	atpH	ATP synthase subunit CFo III	ATCG00140
Pt	14021	14770	-	protein	atpI	ATP synthase subunit CFo IV	ATCG00150
Pt	15013	15723	-	protein	rps2	30S Ribosomal protein CS2	ATCG00160
Pt	15938	20068	-	protein	rpoC2	PEP subunit beta prime prime	ATCG00170
Pt	20251	21861	-	protein	rpoC1_2	PEP subunit beta prime	ATCG00180
Pt	22653	23084	-	protein	rpoC1_1	PEP subunit beta prime	ATCG00180
Pt	23111	26329	-	protein	rpoB	PEP subunit beta	ATCG00190
Pt	27373	27443	+	tRNA	trnC	tRNA-Cys-GCA	ATCG00200
Pt	28089	28178	+	protein	petN	Cytochrome b6/f complex subunit N	ATCG00210
Pt	28707	28811	-	protein	psbM	PSII M protein	ATCG00220
Pt	29801	29874	-	tRNA	trnD	tRNA-Asp-GUC	ATCG00230
Pt	30323	30406	-	tRNA	trnY	tRNA-Tyr-GUA	ATCG00240

Pt	30466	30538	-	tRNA	trnE	tRNA-Glu-UUC	ATCG00250
Pt	31369	31440	+	tRNA	trnT1	tRNA-Thr-GGU	ATCG00260
Pt	32711	33772	+	protein	psbD	PSII D2 protein	ATCG00270
Pt	33720	35141	+	protein	psbC	PSII CP43 protein	ATCG00280
Pt	35312	35403	-	tRNA	trnS2	tRNA-Set-UGA	ATCG00290
Pt	35751	35939	+	protein	psbZ	PSII Z protein	ATCG00300
Pt	36490	36560	+	tRNA	trnG2	tRNA-Gly-GCC	ATCG00310
Pt	36704	36777	-	tRNA	trnFM	tRNA-fMet-CAU	ATCG00320
Pt	36938	37240	-	protein	rps14	30S Ribosomal protein CS14	ATCG00330
Pt	37375	39579	-	protein	psaB	PSI PsaB protein	ATCG00340
Pt	39605	41857	-	protein	psaA	PSI PsaA protein	ATCG00350
Pt	42584	42736	-	protein	ycf3_3	PSI assembly	ATCG00360
Pt	43524	43751	-	protein	ycf3_2	PSI assembly	ATCG00360
Pt	44466	44591	-	protein	ycf3_1	PSI assembly	ATCG00360
Pt	44827	44913	+	tRNA	trnS3	tRNA-Ser-GGA	ATCG00370
Pt	45223	45828	-	protein	rps4	30S Ribosomal protein CS4	ATCG00380
Pt	46213	46285	-	tRNA	trnT2	tRNA-Thr-UGU	ATCG00390
Pt	46894	46928	+	tRNA	trnL1_1	tRNA-Leu-UAA	ATCG00400
Pt	47441	47490	+	tRNA	trnL1_2	tRNA-Leu-UAA	ATCG00400
Pt	48175	48247	+	tRNA	trnF	tRNA-Phe-GAA	ATCG00410
Pt	48677	49153	-	protein	ndhJ	NDH complex subunit J	ATCG00420
Pt	49257	49934	-	protein	ndhK	NDH complex subunit K	ATCG00430
Pt	50001	50363	-	protein	ndhC	NDH complex subunit C	ATCG00440
Pt	51199	51233	-	tRNA	trnV1_2	tRNA-Val-UAC	ATCG00450
Pt	51833	51871	-	tRNA	trnV1_1	tRNA-Val-UAC	ATCG00450
Pt	52056	52128	+	tRNA	trnM	tRNA-Met-CAU	ATCG00460
Pt	52265	52663	-	protein	atpE	ATP synthase subunit CF1 epsilon	ATCG00470
Pt	52660	54156	-	protein	atpB	ATP synthase subunit CF1 beta	ATCG00480
Pt	54958	56397	+	protein	rbcl	Rubisco large subunit	ATCG00490
Pt	57075	58541	+	protein	accD	Acetyl-CoA carboxylase beta subunit	ATCG00500
Pt	59247	59360	+	protein	psal	PSI I protein	ATCG00510
Pt	59772	60326	+	protein	ycf4	PSI assembly	ATCG00520
Pt	60741	61430	+	protein	cemA	Inner envelope protein	ATCG00530
Pt	61657	62619	+	protein	petA	Cytochrome b6/f complex cytochrome f	ATCG00540
Pt	63538	63660	-	protein	psbJ	PSII J protein	ATCG00550
Pt	63804	63920	-	protein	psbL	PSII L protein	ATCG00560
Pt	63942	64061	-	protein	psbF	PSII cytochrome b559 beta subunit	ATCG00570
Pt	64071	64322	-	protein	psbE	PSII cytochrome b559 alpha subunit	ATCG00580
Pt	65712	65807	+	protein	petL	Cytochrome b6/f complex subunit L	ATCG00590
Pt	65998	66111	+	protein	petG	Cytochrome b6/f complex subunit G	ATCG00600
Pt	66229	66302	-	tRNA	trnW	tRNA-Trp-CCA	ATCG00610
Pt	66490	66563	-	tRNA	trnP	tRNA-Pro-UGG	ATCG00620
Pt	66929	67063	+	protein	psaJ	PSI J protein	ATCG00630
Pt	67488	67688	+	protein	rpl33	50S ribosomal protein CL33	ATCG00640
Pt	67917	68222	+	protein	rps18	30S ribosomal protein CS18	ATCG00650
Pt	68512	68865	-	protein	rpl20	50S ribosomal protein CL20	ATCG00660
Pt	69611	69724	-	protein	rps12_1	30S ribosomal protein CS12	ATCG00665
Pt	69910	70137	-	protein	clpP_3	ATP-dependent Clp protease	ATCG00670
Pt	70653	70944	-	protein	clpP_2	ATP-dependent Clp protease	ATCG00670
Pt	71812	71882	-	protein	clpP_1	ATP-dependent Clp protease	ATCG00670
Pt	72371	73897	+	protein	psbB	PSII CP47 protein	ATCG00680
Pt	74082	74183	+	protein	psbT	PSII T protein	ATCG00690
Pt	74249	74380	-	protein	psbN	PSII N protein	ATCG00700
Pt	74485	74706	+	protein	psbH	PSII H protein	ATCG00710
Pt	74841	74846	+	protein	petB_1	Cytochrome b6/f complex cytochrome b6	ATCG00720
Pt	75651	76292	+	protein	petB_2	Cytochrome b6/f complex cytochrome b6	ATCG00720
Pt	76481	76488	+	protein	petD_1	Cytochrome b6/f complex subunit IV	ATCG00730
Pt	77198	77672	+	protein	petD_2	Cytochrome b6/f complex subunit IV	ATCG00730
Pt	77901	78890	-	protein	rpoA	PEP subunit alpha	ATCG00740

Pt	78960	79376	-	protein	rps11	30S ribosomal protein CS11	ATCG00750
Pt	79489	79602	-	protein	rpl36	50S ribosomal protein CL36	ATCG00760
Pt	80068	80472	-	protein	rps8	30S ribosomal protein CS8	ATCG00770
Pt	80696	81064	-	protein	rpl14	50S ribosomal protein CL14	ATCG00780
Pt	81189	81587	-	protein	rpl16_2	50S ribosomal protein CL16	ATCG00790
Pt	82644	82652	-	protein	rpl16_1	50S ribosomal protein CL16	ATCG00790
Pt	82826	83482	-	protein	rps3	30S ribosomal protein CS3	ATCG00800
Pt	83467	83949	-	protein	rpl22	50S ribosomal protein CL22	ATCG00810
Pt	84005	84283	-	protein	rps19	30S ribosomal protein CS19	ATCG00820
Pt	84337	84771	-	protein	rpl2_2	50S ribosomal protein CL2	ATCG00830
Pt	85454	85843	-	protein	rpl2_1	50S ribosomal protein CL2	ATCG00830
Pt	85862	86143	-	protein	rpl23	50S ribosomal protein CL23	ATCG00840
Pt	86312	86385	-	tRNA	trnI1	tRNA-Ile-CAU	ATCG00850
Pt	86474	93358	+	protein	ftsHi	AAA-protease	ATCG00860
Pt	94276	94356	-	tRNA	trnL2	tRNA-Leu-CAA	ATCG00880
Pt	94941	95702	-	protein	ndhB_2	NDH complex subunit B	ATCG00890
Pt	96388	97164	-	protein	ndhB_1	NDH complex subunit B	ATCG00890
Pt	97478	97945	-	protein	rps7	30S ribosomal protein CS7	ATCG00900
Pt	97999	98024	-	protein	rps12_3	30S ribosomal protein CS12	ATCG00905
Pt	98562	98793	-	protein	rps12_2	30S ribosomal protein CS12	ATCG00905
Pt	100709	100780	+	tRNA	trnV2	tRNA-Val-GAC	ATCG00910
Pt	101012	102502	+	rRNA	rrn16	16S rRNA	ATCG00920
Pt	102801	102837	+	tRNA	trnI2_1	tRNA-Ile-GAU	ATCG00930
Pt	103567	103601	+	tRNA	trnI2_2	tRNA-Ile-GAU	ATCG00930
Pt	103665	103702	+	tRNA	trnA_1	tRNA-Ala-UGC	ATCG00940
Pt	104504	104538	+	tRNA	trnA_2	tRNA-Ala-UGC	ATCG00940
Pt	104691	107500	+	rRNA	rrn23	23S rRNA	ATCG00950
Pt	107599	107701	+	rRNA	rrn4.5	4.5S rRNA	ATCG00960
Pt	107949	108069	+	rRNA	rrn5	5S rRNA	ATCG00970
Pt	108302	108375	+	tRNA	trnR2	tRNA-Arg-ACG	ATCG00980
Pt	109013	109084	-	tRNA	trnN	tRNA-Asn-GUU	ATCG00990
Pt	109405	110436	+	protein	tic214	TIC214 Partial	ATCG01000
Pt	110398	112638	-	protein	ndhF	NDH complex subunit F	ATCG01010
Pt	113449	113607	+	protein	rpl32	50S ribosomal protein CL32	ATCG01020
Pt	114270	114349	+	tRNA	trnL3	tRNA-Leu-UAG	ATCG01030
Pt	114461	115447	+	protein	ccsA	Cytochrome c6 biosynthesis protein	ATCG01040
Pt	115665	117167	-	protein	ndhD	NDH complex subunit D	ATCG01050
Pt	117318	117563	-	protein	psaC	PSI PsaC protein	ATCG01060
Pt	117804	118109	-	protein	ndhE	NDH complex subunit E	ATCG01070
Pt	118377	118907	-	protein	ndhG	NDH complex subunit G	ATCG01080
Pt	119244	119762	-	protein	ndhI	NDH complex subunit I	ATCG01090
Pt	119847	120376	-	protein	ndhA_2	NDH complex subunit A	ATCG01100
Pt	121457	122009	-	protein	ndhA_1	NDH complex subunit A	ATCG01100
Pt	122011	123192	-	protein	ndhH	NDH complex subunit H	ATCG01110
Pt	123296	123562	-	protein	rps15	30S ribosomal protein CS15	ATCG01120
Pt	123884	129244	-	protein	tic214	Translocon subunit TIC214	ATCG01130
Pt	129565	129636	+	tRNA	trnN	tRNA-Asn-GUU	ATCG01140
Pt	130274	130347	-	tRNA	trnR2	tRNA-Arg-ACG	ATCG01150
Pt	130580	130700	-	rRNA	rrn5	5S rRNA	ATCG01160
Pt	130948	131050	-	rRNA	rrn4.5	4.5S rRNA	ATCG01170
Pt	131149	133958	-	rRNA	rrn23	23S rRNA	ATCG01180
Pt	134111	134145	-	tRNA	trnA_2	tRNA-Ala-UGC	ATCG01190
Pt	134947	134984	-	tRNA	trnA_1	tRNA-Ala-UGC	ATCG01190
Pt	135048	135082	-	tRNA	trnI2_2	tRNA-Ile-GAU	ATCG01200
Pt	135812	135848	-	tRNA	trnI2_1	tRNA-Ile-GAU	ATCG01200
Pt	136147	137637	-	rRNA	rrn16	16S rRNA	ATCG01210
Pt	137869	137940	-	tRNA	trnV2	tRNA-Val-GAC	ATCG01220
Pt	139856	140087	+	protein	rps12_2	30S ribosomal protein CS12	ATCG01230
Pt	140625	140650	+	protein	rps12_3	30S ribosomal protein CS12	ATCG01230

Pt	140704	141171	+	protein	rps7	30S ribosomal protein CS7	ATCG01240
Pt	141485	142261	+	protein	ndhB_1	NDH complex subunit B	ATCG01250
Pt	142947	143708	+	protein	ndhB_2	NDH complex subunit B	ATCG01250
Pt	144293	144373	+	tRNA	trnL2	tRNA-Leu-CAA	ATCG01260
Pt	145291	152175	-	protein	ftsHi	AAA-protease	ATCG01280
Pt	152264	152337	+	tRNA	trnI1	tRNA-Ile-CAU	ATCG01290
Pt	152506	152787	+	protein	rpl23	50S ribosomal protein CL23	ATCG01300
Pt	152806	153195	+	protein	rpl2_1	50S ribosomal protein CL2	ATCG01310
Pt	153878	154312	+	protein	rpl2_2	50S ribosomal protein CL2	ATCG01310

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