

Supplementary data

Phytohormones as regulators of mitochondrial gene expression in *Arabidopsis thaliana*

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Table S1. Effect of phytohormone treatment on relative gene expression values of mitochondrial and nuclear genes. *A. thaliana*. wild-type and *rpotmp* mutant plants were grown on MS medium in Petri dishes at an illumination of 50 $\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$, a temperature of 23 °C with a 16 h photoperiod. 10-day-old seedlings were treated with the solutions of hormones and collected after 3 h of exposure. Total RNAs were isolated from seedlings and analyzed by relative quantitative RT-PCR using *UBQ10* and *PP2A* as internal standards. The data presented in the table are the mean values ($n \geq 3$). Error bars represent SEs. Different letters denote statistically significant differences between variants within the same genotype at $p < 0.05$ (ANOVA with post hoc Tukey's multiple-comparison test), asterisks indicate statistically significant differences between the control variants of mutants and the wild type at $p < 0.05$ (t-test).

	MS	TZ	IAA	BL	GA3	ACC	ABA	MetJa	SA
<i>nad6</i>									
WT	1.000 $\pm$ 0.096 ^b	2.520 $\pm$ 0.311 ^c	2.426 $\pm$ 0.199 ^c	2.040 $\pm$ 0.217 ^c	2.624 $\pm$ 0.285 ^c	2.255 $\pm$ 0.233 ^c	2.279 $\pm$ 0.219 ^c	0.431 $\pm$ 0.051 ^a	1.739 $\pm$ 0.144 ^c
<i>rpotmp-2</i>	0.392 $\pm$ 0.040 ^{b*}	0.151 $\pm$ 0.016 ^a	0.291 $\pm$ 0.032 ^b	0.280 $\pm$ 0.025 ^b	0.313 $\pm$ 0.026 ^b	0.575 $\pm$ 0.066 ^c	0.118 $\pm$ 0.009 ^a	0.184 $\pm$ 0.022 ^{ab}	0.426 $\pm$ 0.051 ^c
<i>nad3</i>									
WT	1.000 $\pm$ 0.141 ^b	1.398 $\pm$ 0.161 ^{bc}	1.388 $\pm$ 0.135 ^{bc}	1.427 $\pm$ 0.156 ^{bc}	1.547 $\pm$ 0.174 ^c	1.751 $\pm$ 0.189 ^c	1.265 $\pm$ 0.142 ^b	0.378 $\pm$ 0.044 ^a	0.913 $\pm$ 0.107 ^b
<i>rpotmp-2</i>	2.975 $\pm$ 0.329 ^{b*}	2.590 $\pm$ 0.301 ^a	3.506 $\pm$ 0.151 ^b	4.367 $\pm$ 0.514 ^b	2.835 $\pm$ 0.298 ^b	4.141 $\pm$ 0.423 ^c	2.133 $\pm$ 0.222 ^a	1.372 $\pm$ 0.142 ^{ab}	4.112 $\pm$ 0.399 ^c
<i>cob</i>									
WT	1.000 $\pm$ 0.119 ^b	2.004 $\pm$ 0.195 ^c	1.569 $\pm$ 0.163 ^c	1.892 $\pm$ 0.232 ^c	1.849 $\pm$ 0.202 ^c	1.894 $\pm$ 0.202 ^c	1.587 $\pm$ 0.211 ^c	0.132 $\pm$ 0.255 ^a	1.363 $\pm$ 0.152 ^{bc}
<i>rpotmp-2</i>	1.401 $\pm$ 0.135 ^{c*}	0.971 $\pm$ 0.089 ^b	0.644 $\pm$ 0.065 ^a	1.055 $\pm$ 0.120 ^b	0.870 $\pm$ 0.096 ^b	1.838 $\pm$ 0.204 ^c	0.677 $\pm$ 0.074 ^a	0.550 $\pm$ 0.061 ^a	1.560 $\pm$ 0.125 ^c
<i>cox1</i>									
WT	1.000 $\pm$ 0.125 ^b	2.227 $\pm$ 0.219 ^c	2.135 $\pm$ 0.191 ^c	1.929 $\pm$ 0.265 ^c	1.992 $\pm$ 0.213 ^c	2.128 $\pm$ 0.215 ^c	1.246 $\pm$ 0.089 ^b	0.376 $\pm$ 0.40 ^a	1.854 $\pm$ 0.177 ^c
<i>rpotmp-2</i>	0.651 $\pm$ 0.055 ^{b*}	0.515 $\pm$ 0.042 ^b	0.439 $\pm$ 0.051 ^b	0.433 $\pm$ 0.047 ^b	0.503 $\pm$ 0.050 ^b	1.082 $\pm$ 0.119 ^c	0.215 $\pm$ 0.031 ^a	0.312 $\pm$ 0.041 ^a	0.912 $\pm$ 0.083 ^c

<i>atp6-1</i>									
WT	1.000 ± 0.096 ^c	1.508 ± 0.111 ^d	0.944 ± 0.066 ^c	0.942 ± 0.055 ^c	0.964 ± 0.059 ^c	1.197 ± 0.088 ^c	1.002 ± 0.049 ^c	0.091 ± 0.014 ^a	0.609 ± 0.057 ^b
<i>rpotmp-2</i>	1.854 ± 0.145 ^{c*}	1.039 ± 0.092 ^b	0.626 ± 0.052 ^a	1.633 ± 0.152 ^c	1.149 ± 0.083 ^b	2.010 ± 0.274 ^c	0.599 ± 0.051 ^a	0.660 ± 0.042 ^a	1.499 ± 0.154 ^{bc}
<i>ccMc</i>									
WT	1.000 ± 0.121 ^b	1.861 ± 0.121 ^c	1.662 ± 0.066 ^c	2.075 ± 0.169 ^c	1.621 ± 0.078 ^c	1.442 ± 0.104 ^{bc}	1.674 ± 0.099 ^c	0.170 ± 0.009 ^a	1.251 ± 0.107 ^b
<i>rpotmp-2</i>	0.738 ± 0.069 ^{b*}	0.423 ± 0.020 ^a	0.394 ± 0.022 ^a	0.681 ± 0.050 ^b	0.448 ± 0.023 ^a	0.537 ± 0.074 ^{ab}	0.389 ± 0.032 ^a	0.321 ± 0.017 ^a	0.756 ± 0.054 ^b
<i>ccMFc</i>									
WT	1.000 ± 0.114 ^b	1.760 ± 0.116 ^c	1.609 ± 0.135 ^c	1.909 ± 0.180 ^c	1.744 ± 0.145 ^c	2.087 ± 0.211 ^c	1.628 ± 0.148 ^c	0.141 ± 0.011 ^a	1.114 ± 0.096 ^b
<i>rpotmp-2</i>	5.965 ± 0.611 ^{b*}	3.872 ± 0.415 ^a	2.989 ± 0.167 ^a	6.423 ± 0.711 ^b	4.103 ± 0.325 ^{ab}	9.996 ± 1.006 ^c	3.316 ± 0.298 ^a	2.687 ± 0.213 ^a	6.634 ± 0.550 ^b
<i>rps4</i>									
WT	1.000 ± 0.121 ^b	1.520 ± 0.141 ^c	1.322 ± 0.127 ^{bc}	1.591 ± 0.172 ^c	0.984 ± 0.101 ^b	0.704 ± 0.082 ^b	0.868 ± 0.091 ^b	0.072 ± 0.010 ^a	0.806 ± 0.077 ^b
<i>rpotmp-2</i>	0.057 ± 0.007 ^{b*}	0.056 ± 0.004 ^b	0.070 ± 0.009 ^b	0.083 ± 0.009 ^b	0.052 ± 0.006 ^b	0.050 ± 0.004 ^b	0.023 ± 0.002 ^a	0.022 ± 0.003 ^a	0.051 ± 0.006 ^b
<i>mttB</i>									
WT	1.000 ± 0.113 ^b	1.922 ± 0.188 ^c	2.133 ± 0.201 ^c	2.228 ± 0.195 ^c	2.223 ± 0.195 ^c	1.983 ± 0.204 ^c	1.831 ± 0.197 ^c	0.580 ± 0.061 ^a	1.253 ± 0.135 ^b
<i>rpotmp-2</i>	1.463 ± 0.142 ^{b*}	1.334 ± 0.125 ^b	1.772 ± 0.132 ^{bc}	2.578 ± 0.287 ^c	1.532 ± 0.092 ^b	1.962 ± 0.177 ^c	1.440 ± 0.152 ^b	0.676 ± 0.059 ^a	2.004 ± 0.187 ^c
<i>matR</i>									
WT	1.000 ± 0.100 ^b	1.598 ± 0.159 ^c	1.328 ± 0.097 ^{bc}	1.639 ± 0.171 ^c	1.557 ± 0.149 ^c	0.818 ± 0.087 ^b	1.507 ± 0.119 ^c	0.140 ± 0.012 ^a	1.081 ± 0.102 ^b
<i>rpotmp-2</i>	0.174 ± 0.019 ^{c*}	0.123 ± 0.018 ^b	0.173 ± 0.004 ^c	0.164 ± 0.027 ^c	0.182 ± 0.019 ^c	0.216 ± 0.011 ^c	0.109 ± 0.012 ^b	0.065 ± 0.008 ^a	0.173 ± 0.014 ^c
<i>rrn26</i>									
WT	1.000 ± 0.133 ^b	1.110 ± 0.121 ^b	1.361 ± 0.142 ^b	0.956 ± 0.088 ^b	1.188 ± 0.122 ^b	2.114 ± 0.319 ^c	1.049 ± 0.101 ^b	0.225 ± 0.020 ^a	0.842 ± 0.103 ^b
<i>rpotmp-2</i>	4.312 ± 0.511 ^{d*}	3.110 ± 0.325 ^c	2.980 ± 0.204 ^c	3.669 ± 0.421 ^c	3.329 ± 0.325 ^c	7.559 ± 0.811 ^e	0.979 ± 0.101 ^a	1.907 ± 0.185 ^b	4.496 ± 0.447 ^d
<i>rrn4</i>									
WT	1.000 ± 0.101 ^b	1.974 ± 0.214 ^c	2.541 ± 0.311 ^c	1.702 ± 0.102 ^c	1.107 ± 0.099 ^b	0.901 ± 0.088 ^b	0.614 ± 0.055 ^a	0.517 ± 0.054 ^a	0.989 ± 0.099 ^b
<i>rpotmp-2</i>	0.913 ± 0.087 ^b	0.712 ± 0.068 ^b	0.811 ± 0.063 ^b	0.815 ± 0.091 ^b	0.804 ± 0.075 ^b	0.831 ± 0.107 ^b	0.479 ± 0.051 ^a	0.498 ± 0.012 ^a	0.810 ± 0.074 ^b
<i>mTERF15</i>									
WT	1.000 ± 0.098 ^c	1.678 ± 0.168 ^d	5.966 ± 0.601 ^e	2.357 ± 0.213 ^d	1.755 ± 0.134 ^d	3.009 ± 0.288 ^d	0.551 ± 0.060 ^b	0.245 ± 0.022 ^a	0.442 ± 0.039 ^b
<i>rpotmp-2</i>	0.485 ±	0.856 ±	2.002 ±	1.022 ±	0.610 ±	0.904 ±	0.202 ±	0.131 ±	0.300 ±

	0.057 ^c	0.107 ^d	0.176 ^e	0.099 ^d	0.063 ^{cd}	0.087 ^d	0.018 ^b	0.010 ^a	0.034 ^b
<i>mTERF17</i>									
WT	1.000 ± 0.120 ^d	2.427 ± 0.255 ^e	6.277 ± 0.581 ^f	2.066 ± 0.204 ^e	2.184 ± 0.191 ^e	0.713 ± 0.069 ^c	0.503 ± 0.048 ^c	0.184 ± 0.021 ^a	0.321 ± 0.035 ^b
<i>rpotmp-2</i>	0.526 ± 0.053 ^c	0.511 ± 0.049 ^c	1.148 ± 0.131 ^d	0.809 ± 0.087 ^d	0.912 ± 0.085 ^d	0.395 ± 0.040 ^b	0.305 ± 0.040 ^b	0.222 ± 0.025 ^a	0.328 ± 0.036 ^b
<i>mTERF18</i>									
WT	1.000 ± 0.087 ^c	1.596 ± 0.161 ^d	3.171 ± 0.320 ^e	1.821 ± 0.199 ^d	1.331 ± 0.128 ^{cd}	2.158 ± 0.209 ^{de}	0.851 ± 0.069 ^{bc}	0.236 ± 0.031 ^a	0.684 ± 0.066 ^b
<i>rpotmp-2</i>	1.213 ± 0.113 ^c	2.425 ± 0.251 ^e	2.990 ± 0.266 ^e	1.777 ± 0.164 ^d	1.796 ± 0.149 ^d	1.676 ± 0.157 ^{cd}	0.329 ± 0.044 ^b	0.159 ± 0.017 ^a	0.859 ± 0.073 ^c
<i>At2g37320</i>									
WT	1.000 ± 0.144 ^c	1.404 ± 0.161 ^c	6.649 ± 0.320 ^e	2.894 ± 0.186 ^d	2.168 ± 0.175 ^d	3.322 ± 0.360 ^d	0.374 ± 0.029 ^b	0.148 ± 0.011 ^a	0.552 ± 0.049 ^b
<i>rpotmp-2</i>	0.738 ± 0.063 ^c	1.417 ± 0.150 ^d	3.611 ± 0.369 ^e	1.319 ± 0.164 ^d	1.837 ± 0.171 ^d	1.681 ± 0.160 ^d	0.090 ± 0.006 ^a	0.084 ± 0.009 ^a	0.359 ± 0.034 ^b
<i>At1g09190</i>									
WT	1.000 ± 0.108 ^c	1.790 ± 0.139 ^d	3.017 ± 0.287 ^e	1.825 ± 0.175 ^d	1.316 ± 0.120 ^d	2.863 ± 0.293 ^e	0.841 ± 0.067 ^{bc}	0.230 ± 0.020 ^a	0.537 ± 0.055 ^b
<i>rpotmp-2</i>	1.396 ± 0.142 ^d	2.004 ± 0.196 ^{de}	2.671 ± 0.282 ^e	1.769 ± 0.169 ^d	1.788 ± 0.155 ^d	1.720 ± 0.163 ^d	0.356 ± 0.042 ^b	0.140 ± 0.013 ^a	0.710 ± 0.088 ^c
<i>SWIB5</i>									
WT	1.000 ± 0.123 ^c	3.142 ± 0.307 ^d	9.815 ± 1.005 ^e	6.386 ± 0.701 ^d	5.809 ± 0.602 ^d	6.225 ± 0.519 ^d	0.675 ± 0.074 ^{bc}	0.311 ± 0.029 ^a	0.502 ± 0.058 ^b
<i>rpotmp-2</i>	1.444 ± 0.148 ^c	2.993 ± 0.311 ^d	6.190 ± 0.717 ^e	5.364 ± 0.549 ^e	6.191 ± 0.593 ^e	3.410 ± 0.299 ^d	0.602 ± 0.059 ^b	0.376 ± 0.040 ^a	0.666 ± 0.074 ^b

Table S2. Effect of CK treatment on relative gene expression values of mitochondrial and nuclear genes. Seeds of *A. thaliana*. wild-type were germinated in the dark for 4 days on full MS medium with or without cytokinin (1 μ M *trans*-zeatin). Total RNAs were isolated from seedlings and analyzed by relative quantitative RT-PCR using *UBQ10* and *PP2A* as internal standards. The data presented in the table are the mean values ($n \geq 3$). Error bars represent SEs. Different letters denote statistically significant differences between variants within the same genotype at $p < 0.05$ (ANOVA with post hoc Tukey's multiple-comparison test), asterisks indicate statistically significant differences between the control variants of mutants and the wild type at $p < 0.05$ (t-test).

Gene	MS	1 μ M TZ
<i>RPOTm</i>	1.000 $\pm$ 0.019 ^a	1.041 $\pm$ 0.209 ^a
<i>RPOTmp</i>	1.000 $\pm$ 0.190 ^a	0.084 $\pm$ 0.012 ^b
<i>nad3</i>	1.000 $\pm$ 0.145	0.213 $\pm$ 0.023 ^b
<i>nad6</i>	1.000 $\pm$ 0.158 ^a	0.529 $\pm$ 0.090 ^b
<i>cob</i>	1.000 $\pm$ 0.217 ^a	0.366 $\pm$ 0.039 ^b
<i>cox1</i>	1.000 $\pm$ 0.152 ^a	0.119 $\pm$ 0.026 ^b
<i>rps12</i>	1.000 $\pm$ 0.169 ^a	1.894 $\pm$ 0.270 ^b
<i>rrn26</i>	1.000 $\pm$ 0.209 ^a	0.544 $\pm$ 0.108 ^b
<i>atp6-1</i>	1.000 $\pm$ 0.228 ^a	0.397 $\pm$ 0.055 ^b
<i>mTERF15</i>	1.000 $\pm$ 0.104 ^a	0.622 $\pm$ 0.225 ^b
<i>mTERF18</i>	1.000 $\pm$ 0.090 ^a	0.446 $\pm$ 0.043 ^b
<i>At1g09190</i>	1.000 $\pm$ 0.234 ^a	0.374 $\pm$ 0.091 ^b
<i>At2g37320</i>	1.000 $\pm$ 0.035 ^a	0.483 $\pm$ 0.032 ^b
<i>SWIB5</i>	1.000 $\pm$ 0.121 ^a	0.622 $\pm$ 0.132 ^b

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RAV1
 AAAATCCTAAACGCTCCATTCAAACCTCAAATCCAAACCATTAGCTATATAGACGACTTAGATCCCCAAAACCCAACGAAGATCACT
 CGATCATCGACCAACAGAAGTATCARR-BAGATCCTCGAGCAAAAAACCCAGCAGAAGAACAACGAAAGTGGCCACAAAGGAACCAAAAC
 TCAGGTAGAAATCAATCGGAAGCTACGCAATCAGCTAGCCTGGAGTTGGAGCAAARR-BAGATTCTGAACCTTTGGATCAGTAATTAGTAATT
 TACCTCAACAAB3VP1AB3VP1AGCTTCGTCTTTTGTAGTAACACGAAGAAGAGAGAGATAGAGAGAGAGACCTAATACAATTTCT
 TTGTAGCTTCAGTTCCGAGGAAAGGAAACAAATCAGGCTTGTACTTCTCAGACAAAARFAGTTAAGGGGTAAATGGTAATATATTAA
 AACTATGAGGTGGAACGATCAAATTTGGAGCGAATAATCAGGTGTGAGTTATCATTGGTGAAACACAACCTAGCAACCCCAACCACT
 AGTCGACACATCCCAAGAAAAATAGATTTTGTAGTCCAAATTTATTTACAAATAATAGACTAGAATAATTATTATTAACACAAATTG
 ATATTGTTGACCAAAAAATAAAARFATCCAAGTGAATTATTCATACAAAAATCTAAATATTTTAATTATATTTCGGCATTGTAATTGGG
 TTCCACCTTTTTTTGTTGTTGATTAATTGGGTTCCACTAAAAAGTTGTATGAAATGGTAAAAATAATAGAAGAACTATAATAAAAA
 TTCATTTTGTATATATATATTTTAACTAATTGGGCTCCATAAATTCGTCAAGCCTTTTTCATATTAAGACACTTTGGCCGTTAT
 TAGAGGCCTTAATCAGATACTTCCARRFARR-BGGGTCGGGTAAAGATCCTCTATACGGGTGCAATTTAGGGTAGATATTTTAAATTTATTTT
 TAATTGTTTGAATMYC2 RD22 REF6REF6TAAAGAAAGCAAGGGTTTTTAAGCGAGGTTTA
 GGC-boxAGGCGGTTTCGTCTGTACGCTTCACTCACATTGTTTTTATTTTCTTCGGTCTATGAAACTCTTCCCAATTTGCCATTTTCTT
 TGCTCATGCGATCGAATTTATTCATCTCGAGTTGGTTATTGTTCTGGTTTATCGATTTTACTCAATTTTAAAGTTCGATTGATG
 CCAGTGCTCAAACCCCACTGTTCTTGGCAAATCAGACTAAGGTATT

Figure S1. Nucleotide sequence (-1,200/+ 50 bp) of the *RpoTnp* gene from *Arabidopsis thaliana* with distribution of *cis*-regulatory elements located with PLAN [3], AGRIS [5], PLACE [2], PlantTFDB v5.0 [4]. The motifs for CREs (see Table 1) were searched in the 1,200 bp upstream of the translation initiation codon (bold). The 5'-UTR sequence (for *At5g15700.1* transcript) is shown in italics and marked with grey. Partial coding sequence is shown in grey letters (+ 50 bp). TATA boxes indicated in the frame and transcriptional start sites (TSS) printed in bold red letters were determined using the TSSPlant tool PlantProm DB [6] on SoftBerry platform (<https://www.softberry.com/>). Significant motifs with the highest nucleotide similarity to previously identified transcription factor binding sites are shown in bold and the name of the corresponding transcription factor is given above the motif. The start position of the 5'-deletion fragment P958 is indicated by an arrow relative to ATG.

Table S3. Putative *cis*-regulatory elements for MYB and MY-related identified in the 1,200 bp Arabidopsis *RPOTmp* promoter sequence relative to ATG *in silico* (based on the results of analysis by PlantRegMap/PlantTFDB v5.0).

Motif	Family	Seq ID	Position	Strand	Matched sequence
AT3G47600	MYB	At5g15700	503-521	-	CGACTAGTGGTTGGGTTGC
AT2G02820	MYB	At5g15700	6-20	+	cctaaacgctccatt
AT1G08810	MYB	At5g15700	503-521	+	gcaaccaaccactagtcg
AT5G62470	MYB	At5g15700	497-514	-	TGGTTGGGTTGCTAGTTG
AT3G23250	MYB	At5g15700	1148-1168	-	AACCAGAACAATAACCAACTC
AT1G66370	MYB	At5g15700	1148-1158	+	gagttgggttat
AT3G28910	MYB	At5g15700	505-519	+	aaccaaccactagt
AT5G02320	MYB	At5g15700	845-859	+	gacttgggcccgtta
AT2G32460	MYB	At5g15700	1148-1162	-	AACAATAACCAACTC
AT5G11510	MYB	At5g15700	846-860	+	acttgggcccgttat
AT5G40330	MYB	At5g15700	275-285	-	AAGCTTGTTGC
AT1G74650	MYB	At5g15700	468-482	-	TAAC TCACACCTGAT
AT5G62470	MYB	At5g15700	465-482	+	ataatcaggtgtgagtta
AT5G06100	MYB	At5g15700	1148-1158	-	ATAACCAACTC
AT4G32730	MYB	At5g15700	846-860	+	acttgggcccgttat
AT1G09540	MYB	At5g15700	507-521	+	cccaaccactagtcg
AT5G02840	MYB_related	At5g15700	926-935	+	agatatatttt
AT4G01280	MYB_related	At5g15700	926-936	+	agatatatttta
AT1G18330	MYB_related	At5g15700	924-935	-	AAAAATATCTAC
AT5G52660	MYB_related	At5g15700	926-936	+	agatatatttta
AT3G09600	MYB_related	At5g15700	926-937	+	agatatattttaa
AT1G01060	MYB_related	At5g15700	926-935	+	agatatatttt
AT5G17300	MYB_related	At5g15700	924-937	-	TTAAAAATATCTAC
AT5G67580	MYB_related	At5g15700	915-933	-	AAATATCTACCCTAAATTC
AT1G18960	MYB_related	At5g15700	697-718	-	CCAATTAATCAACAACAAAAAA
AT3G10113	MYB_related	At5g15700	924-938	-	ATTAAAAATATCTAC
AT2G46830	MYB_related	At5g15700	926-933	-	AAATATCT

Table S4. Primers for plasmid constructions, sequencing and qRT-PCR

Name/ Purpose	Primer Name	Primer sequence* (5'→ 3')
P336/cloning P336::GUS	15700-336 Bam HI	ATT <u>GGA TCC</u> AGG CCT TAA TCA GAT ACT TC
P530/cloning p530::GUS	15700-530 Bam HI	ATT <u>GGA TCC</u> ATT CGG CAT TGT AAT TGG GTT
p958/cloning P958::GUS	15700-958 Bam HI	ATT <u>GGA TCC</u> ATC AGT AAT TAG TAA TTT ACC TCA
cloning <i>Pro::GUS</i> general primer	15700-R1 Pst I	AAT <u>CTG CAG</u> AAT CGA ACT TAA AAA TTG AG
ARR5/qRT-PCR	ARR5_F	TAT CTA CTC GCA GCT AAA ACG C
	ARR5_R	GTA AGC CGA AAG AAT CAG GAC AT
GUS/PCR and qRT-PCR	GUS_F	CCT CGC ATT ACC CTT ACG CT
	GUS_R	AAG ACA GCT GAA AGC CGA CA
RPOTm/qRT-PCR	RPOTm_F	ATA TGC CAA ACT CAT GCT CG
	RPOTm_R	CTG TTT GAC CAG CTT TCT GTC
RPOTmp/qRT-PCR	RPOTmp_F	CGT TTC CTC ATT TAG ACT TTC CTC C
	RPOTmp_R	CCT TCT CTC TGT CTG CGT CTC TGT
nad6/qRT-PCR	nad6_F	TAT GCC GGA AAG GTA CGA AG
	nad6_R	GTG AGT GGG TCA GTC GTC CT
nad3/qRT-PCR	nad3_F	ACC TTT TTC TTT CCT TGG GCA GT
	nad3_R	CGA AGC ACC CCT TTT CCA TTC A
cob/qRT-PCR	cob_F	TGC CGC AAT GGT ATT TCC TA
	cob_R	GCC AAA AGC AAC CAA AAC AT
cox1/qRT-PCR	cox1_F	AGT CAT TCT GGA GGA GCA GTT GA
	cox1_R	ACG GAC CAC ACA AAT AGG GGT AA
atp6-1/qRT-PCR	atp6-1_F	TCT TTT GCG AGT CAA TGC AC
	atp6-1_R	TCT CGC GTA TCT CAC ATT GC
ccMc/qRT-PCR	ccMc_F	AGC TAC GCG CAA ATT CTC AT
	ccMc_R	GCC GTG GCG ATA TAA ACA AT
ccMF/qRT-PCR	ccMF_F	CAC ATG GAG GAG TGT GCA TC
	ccMF_R	GTG GGT CCA TGT AAA TGA TCG
rps4/qRT-PCR	rps4_F	ACC CAT CAC AGA GAT GCA CA
	rps4_R	TCA CAC AAA CCC TTC GAT GA
mttB/qRT-PCR	mttB_F	GGG GTC TTT CTT TGG AAA CC
	mttB_R	TCT CCC TCA TTC CAC TCG TC
matR/qRT-PCR	matR_F	AAT TTT TGC GAG AGC TGG AA
	matR_R	TTG AAC CCC GTC CTG TAG AC
rrn26/qRT-PCR	rrn26_F	GAC GAG ACT TTC GCC TTT TG
	rrn26_R	CTT GGA GCG AAT TGG ATG AT
mTERF15/qRT-PCR	mTERF15_F	TCG TGC TGG GTT TGA AGT GAA
	mTERF15_R	ACC CTC GGC TCT TTC CAT AC
mTERF17/qRT-PCR	mTERF17_F	TCT TTA GTT GCC GTC TTG TCC T
	mTERF17_R	TCT ATC GCG GGT TTG ATC TT

<i>mTERF18</i> /qRT-PCR	<i>mTERF18_F</i>	GAG TGC CGT CGA AAT ACA AGT
	<i>mTERF18_R</i>	GGT GGT GTG GAG ATA GTC TGT A
<i>At2g37320</i> /qRT-PCR	<i>At2g37320_F</i>	AAG CGG AAC AAA GCC AGA TG
	<i>At2g37320_R</i>	CCG TGT TCC GCC ATC AAA T
<i>At1g09190</i> /qRT-PCR	<i>At1g09190_F</i>	ACA GGT CAG GTG GAG AGA GGA GA
	<i>At1g09190_R</i>	CGT AAT GCT CGG TTC TCG CCT
<i>SWIB5</i> /qRT-PCR	<i>SWIB5_F</i>	ATG GCG GGA ATT TCT AGG GT
	<i>SWIB5_R</i>	GCT ACA GTA ACG GCC TCA ACA
<i>IAA19</i> /qRT-PCR	<i>IAA19_F</i>	ACG AAG ACA AAG ATG GAG ACT GGA
	<i>IAA19_R</i>	GTC ATC ATC ACT CGT CTA CTC CTC T
<i>DWF4</i> /qRT-PCR	<i>DWF4_F</i>	GTT GGC CAT TTC TTG GTG AAA
	<i>DWF4_R</i>	TGG CGG TGT ACG GTT TAA GAT
<i>ERF-1</i> /qRT-PCR	<i>ERF-1_F</i>	ATT AGG GTT TGG CTC GGG AC
	<i>ERF-1_R</i>	GAC TCT TGA ACT CTC TCC GCC G
<i>GA3</i> /qRT-PCR	<i>GA3_F</i>	AGTCTCTTCGGGCTACCTGT
	<i>GA3_R</i>	CGGAAATCGTTGAGAGGCG
<i>RD29</i> /qRT-PCR	<i>RD29_F</i>	AGG AAC CAC CAC TCA ACA CAC
	<i>RD29_R</i>	GCT CGT CAT CAT CAT CAT CTT C
<i>ARR5</i> /qRT-PCR	<i>ARR5_F</i>	CTA CTC GCA GCT AAA ACG C
	<i>ARR5_R</i>	GCC GAA AGA ATC AGG ACA
<i>PR1</i> /qRT-PCR	<i>PR1_F</i>	TTC ACA ACC AGG CAC GAG GA
	<i>PR1_R</i>	CCA GCG TAG TTG TAG TTA GCC TTC
<i>Phas2a</i> /qRT-PCR	<i>Phas2a_F</i>	ACT GCA TCT AAA GAC AGA GTT CCA
	<i>Phas2a_R</i>	CCA CAA GCC CAG GAC GAA T
<i>UBQ10</i> /qRT-PCR	<i>UBQ10_F</i>	GCG TCT TCG TGG TGG TTT CTAA
	<i>UBQ10_R</i>	GAA AGA GAT AAC AGG AAC GGA AAC A

*Sequences for restriction sites Bam HI and Pst I are underlined.

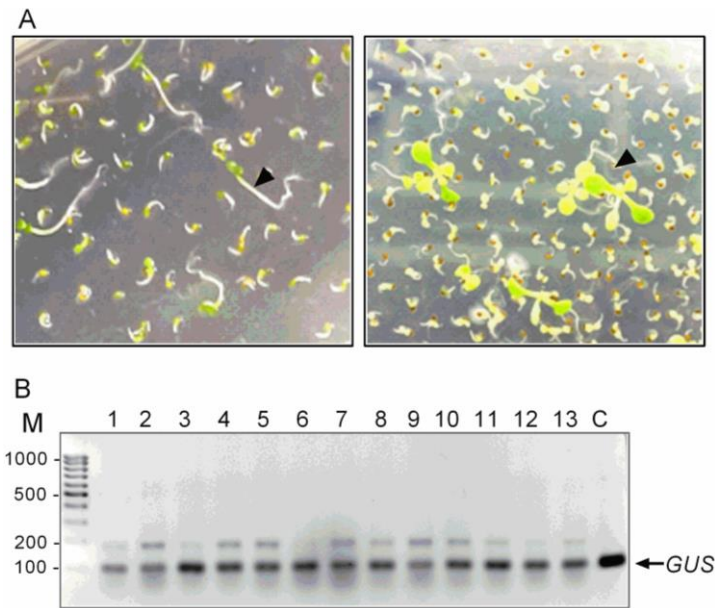


Figure S2. Generation of *RPOTmp pro::GUS* transgenic *Arabidopsis* plants. (A) Selection of T0-seedlings carrying the P336, P530, and P958 constructs on $\frac{1}{2}$ MS medium containing 0.8% (w/v) phyto agar (Duchefa Biochemie) and 30 mg/L hygromycin (Hyg). Hyg-resistant seedlings (left photo) had more elongated hypocotyl after 3 days of growth in darkness compared to untransformed plants. Phenotype of 10-days-old transgenic seedlings (right panel) used for further analysis. (B) PCR analysis of genomic DNA extracted from rosette leaves of P958 transgenic plants using *GUS*-specific primers (Table S1), where C is the control for PCR with pCambia-35SGUS plasmid. The position of the *GUS* gene fragment (100 bp) is indicated by an arrow. M – 100 bp DNA marker (SybEnzyme, Russia).