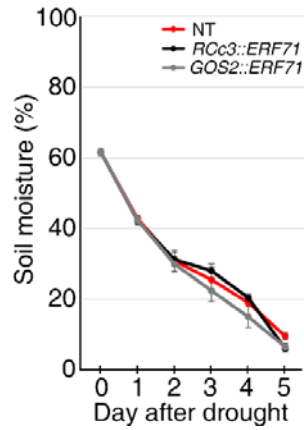1   **SUPPLEMENTAL MATERIALS**

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3   **Figure S1.** Soil moisture during drought treatment at the vegetative growth stage.

4   Soil moisture percentage during drought treatment described in Figure 1C. Values for each

5   time point represent the mean ± SD of 10 soils on the pots for each genotype, measured by

6   SM150 Soil Moisture Sensor (AT Delta-T Devices, Cambridge, England).
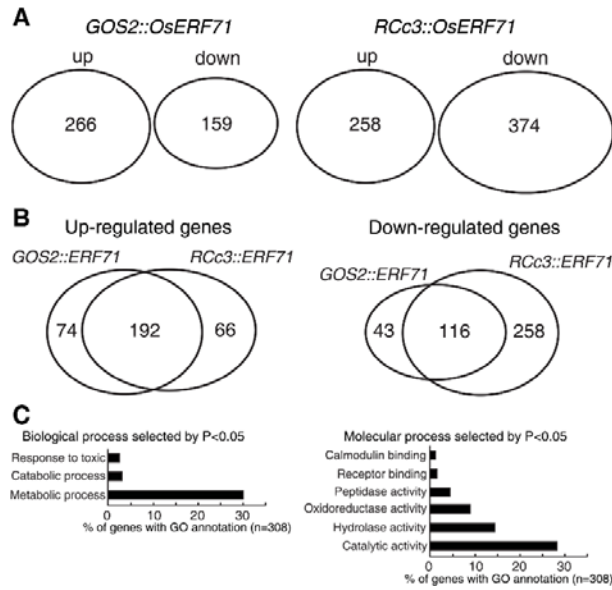
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19 **Figure S2.** *OsERF71*-regulated genes in *GOS2::OsERF71* and *RCc3::OsERF71* roots.

20 A, Venn diagrams of up- (fold change > 3 and *P* value < 0.05) and down- (fold change < -3

21 and *P* value < 0.05) regulated genes based on microarray data from two-week old

22 *GOS2::OsERF71* and *RCc3::OsERF71* roots, compared to NT roots.

23 B, Venn diagrams of differentially regulated genes common to *GOS2::OsERF71* and

24 *RCc3::OsERF71* roots.

25 C, GO analysis (P < 0.05) of the selected 308 genes using the PANTHER Classification
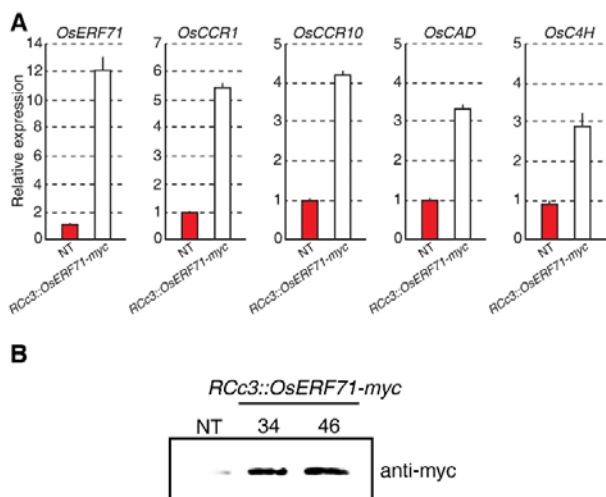
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Figure S3. Expression analysis of *RCc3::OsERF71-myc plants*.

A, Expression level of *OsERF71-myc* and lignin biosynthesis genes in roots of two-week old *RCc3::OsERF71-myc* and NT rice plants by qRT-PCR. *Ubiquitin1* expression was used as an internal control. Data are shown as the mean + SD of three biological and two technical replicates.

B, Western bot analysis of the expression of the OsERF71-myc protein in roots of two-week old *RCc3::OsERF71-myc* and NT rice plants.

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Overexpression constructs

GOS2::OsERF71

RCc3::OsERF71

Promoter analysis constructs

GOS2::GFP

RCc3::GFP

OsERF71::GFP

ChIP analysis construct

RCc3::OsERF71-myc

RNAi construct

GOS2::OsERF71RNAi

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59 **Figure S4.** Vector maps for *GOS2::OsERF71*, *RCc3::OsERF71*, *GOS2::GFP*, *RCc3::GFP*,

60 *OsERF71::GFP*, *RCc3::OsERF71-myc*, and *GOS2::ERF71^{RNAi}*.
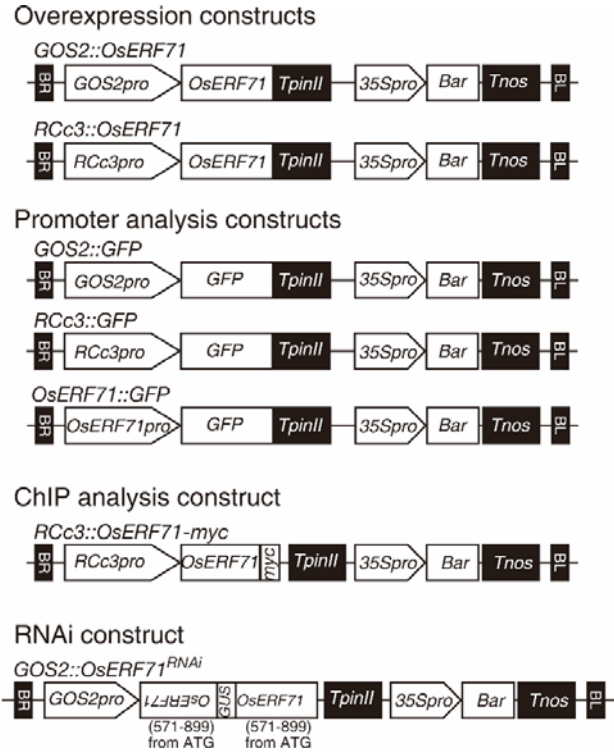
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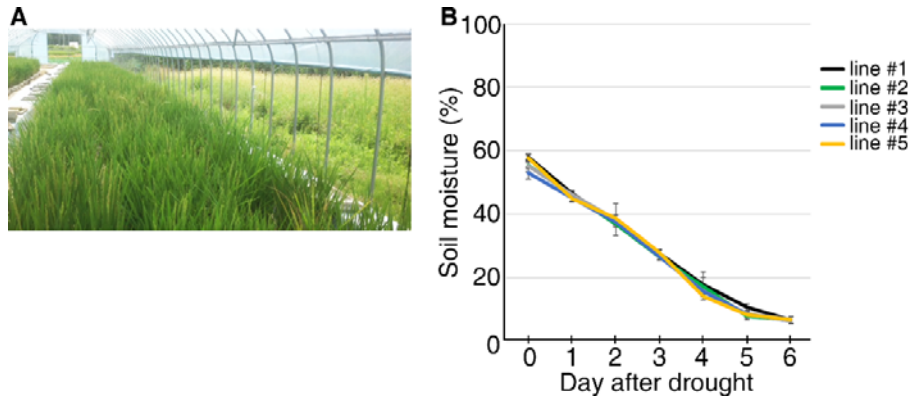
Figure S5. Photograph of the field experiments and water content in soils during drought treatment in the field.

A, Photograph of a rain-off shelter to cover rice plants before drought treatment.

B, Soil moisture percentage during drought treatment in the field. Rice plants for each genotype were randomly located on 5 different lines in a rain-off shelter. Rice plants at a transition stage from vegetative to reproductive development were exposed to drought stress conditions by removing water. During the drought stress, water contents in soils were monitored by randomly selected 20 soil spots on each line for each time point. Values for each time point represent the mean ± SD of randomly selected 20 soil spots on each line. Soil moisture was measured by SM150 Soil Moisture Sensor (AT Delta-T Devices, Cambridge, England).

Table S1. Agronomic traits of *RCc3::OsERF71* and *GOS2::OsERF71* transgenic rice plants grown in the field.

Genotypes	Grain filling rate (%)						Total grain weight (g)					
	2009 (T_5)		2010 (T_6)		2011 (T_7)		2009 (T_5)		2010 (T_6)		2011 (T_7)	
	N^a	D^b	N^a	D^b	N^a	D^b	N^a	D^b	N^a	D^b	N^a	D^b
NT(Nipponbare)	87.57	49.78	81.39	47.61	86.83	46.83	22.39	8.46	29.05	11.56	24.01	13.13
RCc3::ERF71-12	88.60	**54.99**	80.78	**55.55**	87.29	**57.51**	22.43	**10.75**	29.92	**14.60**	25.09	**16.79**
P value^c	0.843	0.013	0.73	0.011	0.739	0.001	0.975	0.014	0.589	0.024	0.433	0.009
RCc3::ERF71-34	87.99	**59.71**	80.49	52.02	82.42	**58.37**	22.72	**10.99**	30.90	**15.30**	23.66	**17.10**
P value^c	0.91	0.016	0.609	0.003	0.811	0.000	0.782	0.007	0.249	0.006	0.054	0.004
RCc3::ERF71-49	88.84	**61.55**	81.99	**55.26**	87.18	**53.79**	21.40	**10.50**	31.58	**15.15**	25.96	**16.20**
P value^c	0.276	0.004	0.73	0.000	0.80	0.028	0.403	0.027	0.114	0.008	0.159	0.027
GOS2::ERF71-20	88.03	45.71	81.30	43.74	86.57	45.20	23.27	8.33	31.70	10.63	26.54	13.34
P value^c	0.14	0.319	0.961	0.083	0.85	0.61	0.459	0.885	0.098	0.492	0.068	0.875
GOS2::ERF71-34	86.77	49.81	81.71	39.22	88.72	47.09	20.82	8.05	29.01	10.89	26.62	13.80
P value^c	0.142	0.995	0.852	0.111	0.176	0.933	0.188	0.654	0.978	0.62	0.059	0.627
GOS2::ERF71-49	88.96	47.19	80.94	47.52	85.59	47.20	23.91	7.69	31.62	10.63	25.98	12.57
P value^c	0.132	0.525	0.8	0.33	0.373	0.905	0.204	0.398	0.11	0.49	0.15	0.687

Genotypes	Culm length (cm)						Panicle length (cm)					
	2009 (T_5)		2010 (T_6)		2011 (T_7)		2009 (T_5)		2010 (T_6)		2011 (T_7)	
	N^a	D^b	N^a	D^b	N^a	D^b	N^a	D^b	N^a	D^b	N^a	D^b
NT(Nipponbare)	71.89	67.04	89.50	56.47	79.27	66.72	19.68	19.04	21.03	18.58	19.83	20.12
RCc3::ERF71-12	72.97	**71.12**	**97.56**	53.31	**87.07**	**73.60**	**21.30**	19.60	**22.48**	**22.78**	19.70	**18.88**
P value^c	0.07	0.00	0.00	0.05	0.00	0.00	0.00	0.48	0.00	0.00	0.56	0.01
RCc3::ERF71-34	71.88	**75.23**	**94.53**	**60.67**	**82.17**	69.86	19.65	19.57	**22.73**	**23.11**	19.93	19.99
P value^c	0.99	0.00	0.00	0.01	0.00	0.09	0.94	0.52	0.00	0.00	0.66	0.76
RCc3::ERF71-49	71.77	**72.13**	**94.87**	**61.83**	**83.80**	65.43	20.17	19.00	21.20	19.50	19.67	**19.12**
P value^c	0.83	0.00	0.00	0.00	0.00	0.49	0.12	0.96	0.63	0.15	0.47	0.02
GOS2::ERF71-20	72.85	**72.04**	89.80	58.94	**88.77**	65.26	**20.63**	19.07	21.43	**19.94**	**19.07**	**19.06**
P value^c	0.12	0.00	0.75	0.13	0.00	0.43	0.00	0.98	0.24	0.03	0.00	0.02
GOS2::ERF71-34	**74.22**	**71.67**	**94.23**	55.14	**83.03**	69.51	**21.15**	18.56	**21.87**	19.06	19.63	20.13
P value^c	0.00	0.00	0.00	0.40	0.00	0.13	0.00	0.55	0.02	0.45	0.38	0.99
GOS2::ERF71-49	**74.70**	68.98	90.53	**59.94**	**84.90**	65.08	20.20	18.92	21.23	19.64	20.07	19.93
P value^c	0.00	0.11	0.28	0.03	0.00	0.38	0.10	0.88	0.56	0.10	0.31	0.66

Genotypes	Number of panicles per hill						Number of spikelets per panicle					
	2009 (T_5)		2010 (T_6)		2011 (T_7)		2009 (T_5)		2010 (T_6)		2011 (T_7)	
	N^a	D^b	N^a	D^b	N^a	D^b	N^a	D^b	N^a	D^b	N^a	D^b
NT(Nipponbare)	9.71	11.24	13.93	12.06	11.90	15.30	83.28	74.20	107.65	104.75	98.17	87.82
RCc3::ERF71-12	**10.63**	11.39	14.16	11.06	13.10	16.25	90.44	**94.60**	**119.64**	110.44	94.44	84.00
P value^c	0.036	0.753	0.773	0.134	0.063	0.333	0.196	0.000	0.009	0.523	0.428	0.497
RCc3::ERF71-34	9.77	11.79	14.13	12.39	**13.20**	14.63	86.08	78.46	107.14	118.54	91.74	88.21
P value^c	0.903	0.251	0.789	0.616	0.044	0.486	0.625	0.370	0.905	0.123	0.170	0.944
RCc3::ERF71-49	10.37	11.29	**15.67**	11.44	12.80	**18.00**	86.86	**83.78**	112.02	121.32	92.96	78.54
P value^c	0.135	0.911	0.021	0.358	0.163	0.006	0.518	0.045	0.314	0.065	0.266	0.100
GOS2::ERF71-20	10.44	11.54	14.03	13.61	**13.53**	**17.67**	**100.21**	82.44	113.34	106.31	**87.37**	**66.18**
P value^c	0.103	0.528	0.894	0.933	0.012	0.016	0.003	0.084	0.190	0.861	0.022	0.000
GOS2::ERF71-34	**11.33**	**12.73**	**16.07**	**11.89**	11.17	**13.33**	89.03	78.18	103.65	104.97	98.37	82.99
P value^c	0.000	0.003	0.005	0.021	0.255	0.044	0.299	0.413	0.355	0.980	0.967	0.391
GOS2::ERF71-49	**11.27**	**11.00**	14.67	12.08	12.53	**13.29**	**99.15**	**84.77**	107.32	99.15	91.56	91.26
P value^c	0.000	0.621	0.328	0.802	0.325	0.040	0.004	0.027	0.940	0.531	0.158	0.541

Genotypes	Number of panicles per hill						Number of spikelets per panicle					
	2009 (T_5)		2010 (T_6)		2011 (T_7)		2009 (T_5)		2010 (T_6)		2011 (T_7)	
	N^a	D^b	N^a	D^b	N^a	D^b	N^a	D^b	N^a	D^b	N^a	D^b
NT(Nipponbare)	938.62	861.91	1513.20	1239.83	1126.10	1320.70	26.20	20.42	19.55	20.82	20.82	14.64
RCc3::ERF71-12	949.57	**1064.48**	1671.12	1197.50	1217.60	1316.83	26.97	19.94	19.32	21.39	21.39	14.11
P value^c	0.795	0.001	0.112	0.633	0.136	0.963	0.348	0.280	0.623	0.866	0.866	0.913
RCc3::ERF71-34	934.57	914.21	1506.27	**1453.39**	1201.07	1267.45	26.38	20.72	20.15	21.32	21.32	13.75
P value^c	0.928	0.359	0.942	0.017	0.221	0.525	0.833	0.051	0.182	0.882	0.882	0.938
RCc3::ERF71-49	894.27	944.04	**1737.47**	1340.39	1184.47	1366.37	26.83	**19.30**	20.01	26.93	26.93	15.28
P value^c	0.294	0.151	0.019	0.257	0.340	0.585	0.441	0.001	0.304	0.070	0.070	0.807
GOS2::ERF71-20	**1043.48**	953.50	1584.30	1254.22	1174.80	**1152.71**	**22.91**	19.78	**20.57**	21.81	21.81	16.90
P value^c	0.016	0.109	0.452	0.871	0.426	0.046	0.000	0.260	0.024	0.769	0.769	0.557
GOS2::ERF71-34	1007.23	**982.00**	1675.53	**1415.17**	1092.63	**1099.20**	25.65	20.58	**20.45**	21.70	21.70	15.03
P value^c	0.105	0.036	0.087	0.050	0.584	0.009	0.494	0.240	0.047	0.794	0.794	0.596
GOS2::ERF71-49	**984.59**	923.83	1566.47	1148.83	1139.83	1184.04	**24.67**	20.87	**21.45**	20.87	20.87	14.09
P value^c	0.000	0.278	0.573	0.305	0.822	0.104	0.000	0.519	0.000	0.989	0.989	0.903

^{a}Normal growth conditions; ^{b}Drought growth conditions; ^{c}One-way ANOVA. Each parameter value represents the mean (n = 30). Numbers in boldface indicate a significant difference ($P < 0.05$)

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108   **Table S2.** List of up- and down-regulated genes from *GOS2::OsERF71* and *RCc3::OsERF71*

109   microarray compared to NT (fold > 3, fold < -3, *P* < 0.05).

110   **Attached an Excel file**

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112   **Table S3.** List of up- and down-regulated genes common between *RCc3::OsERF71* and

113   *GOS2::OsERF71* (fold > 3, fold < -3, P < 0.05) compared with NT.

114   **Attached an Excel file**

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116   **Table S4.** List of stress inducible and cell wall-associated genes up-regulated (fold > 3) by

117   both *GOS2::OsERF71* and *RCc3::OsERF71* based on microarray data.

Table S4. List of stress inducible and cell wall-associated genes up-regulated (fold > 3) by both *GOS2::OsERF71* and *RCc3::OsERF71* based on microarray data

Gene name[a]	ID	*GOS2::OsERF71*		*RCc3::OsERF71*	
		Fold change	*P* value[b]	Fold change	*P* value[b]
Stress inducible genes					
USP	Os07g0673400	7.03	2.01E-05	7.38	9.74E-06
USP	Os05g0355400	5.87	5.12E-05	4.79	5.07E-05
USP	Os03g0305400	3.08	6.12E-05	3.53	3.79E-05
LEA	Os01g0705200	6.38	4.92E-05	4.97	5.05E-05
LEA	Os05g0349800	4.12	4.91E-05	3.16	5.78E-05
HSP	Os01g0606900	3.60	6.34E-05	3.70	4.70E-05
OSR	Os03g0830500	4.85	2.11E-05	4.57	1.35E-05
ASR1	Os01g0959100	3.13	1.04E-04	4.44	4.95E-05
CYP450	Os10g0515900	5.05	5.19E-05	4.08	5.40E-05
CYP450	Os04g0560100	3.67	4.96E-05	3.85	3.38E-05
CYP450	Os11g0151400	3.39	5.34E-05	3.47	4.00E-05
NCED	Os07g0154100	34.71	3.47E-06	35.87	1.41E-06
Cell wall-associated genes					
EXP	Os10g0542400	4.2	3.59E-05	4.46	2.07E-05
XTH	Os02g0280300	4.61	2.19E-05	5.71	7.68E-06
PE	Os03g0309400	6.46	2.32E-05	4.65	2.53E-05
CHI	Os11g0701000	12.12	9.55E-06	15.44	4.32E-06
CHI	Os11g0701500	10.07	1.68E-05	12.44	6.16E-06
CHI	Os02g0605900	5.83	5.92E-05	4.64	6.09E-05
CHI	Os11g0702100	5.48	1.88E-05	4.60	1.35E-05
CHI	Os11g0701800	5.44	2.97E-05	5.52	1.87E-05
CHI	Os01g0660200	5.37	1.87E-05	4.20	1.48E-05
CHI	Os10g0542900	4.45	5.16E-05	4.44	4.00E-05
CHI	Os08g0518900	3.66	3.93E-05	4.51	1.72E-05
CHI	Os11g0701400	3.64	9.42E-05	3.88	7.16E-05
CHI	Os08g0518800	3.50	4.73E-05	3.02	4.57E-05

[a]Gene name: *USP, Universal stress protein*; *LEA, Late embryogenesis abundant protein*; *HSP, Heat shock protein*; *OSR, Oxidative stress response protein*; *ASR1, Abscisic stress ripening protein 1*; *CYP450, Cytochrome p450*; *NCED, 9-cis-epoxycarotenoid dioxygenase*; *EXP, Expansin*; *XTH, Xyloglucan endotransglycosylase*; *PE, Pectinesterase*; *CHI, Chitinase*. [b]*P*-value was carried by one-way ANOVA.

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121 **Table S5.** List of gene specific primers for qRT-PCR and ChIP-qPCR.

Table S5. List of gene specific primers for qRT-PCR and ChIP-qPCR		
Target gene (ID)	Forward primers	Reverse primers
Gene expression for qRT PCR		
OsERF71 (Os06g0194000)	GACAGGTGTTGATGACTCCGC	GGGTGTCAATCGACTCATCCG
OsCCR1 (Os02g0808800)	GAACCAGAGGCTCAAGGATT	CATAGGACCGCCTCATTCAA
OsCCR10 (Os02g0811800)	TTGTCACGGTGGCACAACAG	ATATGCCGCCGCTGTCATGT
OsCAD (Os04g0612700)	TTCGTCGTCGACATCGGCAA	GGACCTGCAATCCTGCAAAG
OsC4H (Os02g0467000)	TGGTGAGGAGCTTCGAGATG	TGAGTTCAGGCAGAGATGGG
OsPAL (Os04g0518400)	AGTGCCTCAAGGAGTGGAAC	ACAGCATCAGCTAAGCACATC
OsUBI1 (Os06g0681400)	ATGGAGCTGCTGCTGTTCTA	TTCTTCCATGCTGCTCTACC
Promoter amplification for ChIP-qPCR		
OsCCR1-P1	GCTTCGTGATCCCCTCGTC	TCGCCCGCAATACTGGGC
OsCCR1-P2	CGGCCTTGCGATGTGATGC	GGACGACAAGAGGAAGATAGC
OsCCR1-P3	GACGGCACTCCGTTTCGC	TGTGAGACTAGCGTGTCTGG
OsCCR1-P4	TGCAGGTATAAATAGCGGCCG	CGCTGACCAGTTACTGTCAC
OsCCR10-P1	GGAGGAGGAGGGAGTAGATTC	CCGTTGCTCCAGTCTGCAC
OsCCR10-P2	GTGCAGACTGGAGCAACGG	GCATCAGCCATGGAGTGGC
OsCCR10-P3	CCCTCACCAACCCACGAC	GTTCGAGCTCGAGTGAGGC
OsCCR10-P4	GCCTCACTCGAGCTCGAAC	GGACGACATGGTTGATGCTCTG
OsCAD-P1	CGATTCGGTCCCACAATCTTCG	GTACCACGACAGCACGACC
OsCAD-P2	GGTCGTGCTGTCGTGGTAC	TGCGCGCTGACGTCACTC
OsCAD-P3	GCCAACTCGAGAGTGACGTC	AGTAGCCAGTGGCGGCTTG
OsCAD-P4	GCTCAAGACACTGGCGGAG	TCGTCGTCGGCGCCATTG
OsC4H-P1	CGATTCGGTCCCACAATCTTCG	GTACCACGACAGCACGACC
OsC4H-P2	CACGTCTCTCCTCCATTCCG	CAGTACGTGGGAAACGGCTC
OsC4H-P3	TTCGCCGCATCTCTTCGTGC	TGGGTCGGGTGCCGTTGG
OsC4H-P4	CGCTATATAAGCACGCCACGG	CTAGACCCGCTCACTGGC

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