

**Table S1:** ANOVA table for the subtrait DISTANCE. The table contains effects of replicate (P) and genotype (G), i.e.,  $Mi\{ET1\}$  vs  $w^{1118}$ . P-values are adjusted for multiple testing using a false-discovery rate (FDR). Significance levels are indicated by asterisks; \*\*\*: FDR adjusted P-value < 0.001, \*\*: FDR adjusted P-value < 0.01, \*: FDR adjusted P-value < 0.05, ns: FDR adjusted P-value > 0.05.  $Mi\{ET1\}$  in bold indicates a significant phenotypic effect (FDR adjusted P-value<0.05) of disrupting the target gene.

$Mi\{ET1\}$	Effect	Df	F value	Pr(>F)	FDR
<b>23767</b>	P	43	4.99	2.2E-16	***
	G	1	24.63	1.2E-06	***
24213	P	43	4.36	3.3E-14	***
	G	1	0.49	0.48	ns
24228	P	43	3.23	3.1E-09	***
	G	1	0.76	0.38	ns
<b>24240</b>	P	43	3.17	5.3E-09	***
	G	1	12.91	3.9E-04	***
24283	P	43	4.62	2.8E-15	***
	G	1	0.37	0.54	ns
<b>24687</b>	P	43	3.32	9.5E-10	***
	G	1	25.38	8.4E-07	***
<b>25509</b>	P	43	3.40	4.6E-10	***
	G	1	14.46	18E-04	***
<b>25518</b>	P	43	3.99	9.6E-13	***
	G	1	15.00	1.3E-04	***
<b>25519</b>	P	43	4.13	2.7E-13	***
	G	1	35.21	8.7E-09	***
25547	P	43	4.28	6.7E-14	***
	G	1	2.05	0.15	ns
<b>26103</b>	P	43	3.74	1.8E-11	***
	G	1	6.70	8.6E-03	*
27790	P	43	4.02	8.6E-13	***
	G	1	1.09	0.29	ns
<b>29073</b>	P	43	4.28	6.0E-14	***
	G	1	41.76	4.6E-10	***
<b>29924</b>	P	43	4.63	1.5E-15	***
	G	1	15.07	1.3E-4	***

**Table S2:** ANOVA table for the subtrait PROPORTION TIME SPENT IN CENTER. The table contains effects of replicate (P) and genotype (G), i.e.,  $Mi\{ET1\}$  vs  $w^{1118}$ . P-values are adjusted for multiple testing using a false-discovery rate (FDR). Significance levels are indicated by asterisks; \*\*\*: FDR adjusted P-value < 0.001, \*\*: FDR adjusted P-value < 0.01, \*: FDR adjusted P-value < 0.05, ns: FDR adjusted P-value > 0.05.  $Mi\{ET1\}$  in bold indicates a significant phenotypic effect (FDR adjusted P-value<0.05) of disrupting the target gene.

$Mi\{ET1\}$	Effect	Df	F value	Pr(>F)	FDR
23767	P	43	2.53	3.0E-06	***
	G	1	2.79	0.10	ns
24213	P	43	1.87	1.6E-03	**
	G	1	1.38	0.24	ns
<b>24228</b>	P	43	1.88	1.4E-03	**
	G	1	10.43	1.4E-03	**
24240	P	43	1.59	0.015	ns
	G	1	1.25	0.26	ns
<b>24283</b>	P	43	2.61	1.5E-06	***
	G	1	19.83	1.2E-05	***
24687	P	43	2.24	5.1E-05	***
	G	1	3.22	0.074	ns
<b>25509</b>	P	43	3.37	6.2E-10	***
	G	1	16.90	5.2E-05	***
25518	P	43	2.38	1.4E-05	***
	G	1	4.77	0.030	ns
<b>25519</b>	P	43	2.41	1.0E-05	***
	G	1	5.45	2.0E-02	*
<b>25547</b>	P	43	2.02	4.2E-04	***
	G	1	5.50	2.0E-02	*
26103	P	43	1.98	5.9E-04	***
	G	1	1.31	0.25	ns
<b>27790</b>	P	43	2.51	3.9E-06	***
	G	1	20.50	8.8E-06	***
29073	P	43	2.68	7.2E-07	***
	G	1	2.59	0.11	ns
<b>29924</b>	P	43	2.92	6.4E-08	***
	G	1	9.52	2.2E-03	**

**Table S3:** ANOVA table for the subtrait NUMBER OF CLOCKWISE MOVEMENTS. The table contains effects of replicate (P) and genotype (G), i.e.,  $Mi\{ET1\}$  vs  $w^{1118}$ . P-values are adjusted for multiple testing using a false-discovery rate (FDR). Significance levels are indicated by asterisks; \*\*\*: FDR adjusted P-value < 0.001, \*\*: FDR adjusted P-value < 0.01, \*: FDR adjusted P-value < 0.05, ns: FDR adjusted P-value > 0.05.  $Mi\{ET1\}$  in bold indicates a significant phenotypic effect (FDR adjusted P-value<0.05) of disrupting the target gene.

$Mi\{ET1\}$	Effect	Df	F value	Pr(>F)	FDR
<b>23767</b>	P	43	1.51	2.7E-02	*
	G	1	21.94	4.4E-06	***
24213	P	43	1.83	2.2E-03	**
	G	1	0.98	0.32	ns
24228	P	43	1.48	3.4E-02	*
	G	1	2.59	0.11	ns
24240	P	43	1.54	2.2E-02	*
	G	1	0.82	0.37	ns
24283	P	43	1.94	8.4E-04	**
	G	1	2.44	0.12	ns
<b>24687</b>	P	43	1.81	2.4E-03	**
	G	1	18.82	2.0E-05	***
25509	P	43	1.81	2.5E-03	**
	G	1	4.38	0.04	ns
<b>25518</b>	P	43	1.39	0.06	ns
	G	1	7.32	7.2E-03	*
<b>25519</b>	P	43	2.25	4.7E-05	***
	G	1	14.70	1.6E-04	***
25547	P	43	2.12	1.7E-04	**
	G	1	0.97	0.32	ns
26103	P	43	1.99	5.7E-04	**
	G	1	0.002	0.96	ns
27790	P	43	1.82	2.4E-03	**
	G	1	2.54	0.11	ns
<b>29073</b>	P	43	1.72	5.4E-03	**
	G	1	21.03	6.9E-06	***
<b>29924</b>	P	43	1.44	4.6E-02	*
	G	1	7.28	7.4E-03	*

**Table S4:** ANOVA table for the subtrait NUMBER OF COUNTER-CLOCKWISE MOVEMENTS. The table contains effects of replicate (P) and genotype (G), i.e., *Mi{ET1}* vs *w*<sup>1118</sup>. P-values are adjusted for multiple testing using a false-discovery rate (FDR). Significance levels are indicated by asterisks; \*\*\*: FDR adjusted P-value < 0.001, \*\*: FDR adjusted P-value < 0.01, \*: FDR adjusted P-value < 0.05, ns: FDR adjusted P-value > 0.05. *Mi{ET1}* in bold indicates a significant phenotypic effect (FDR adjusted P-value<0.05) of disrupting the target gene.

<i>Mi{ET1}</i>	Effect	Df	F value	Pr(>F)	FDR
23767	P	43	1.60	1.4E-02	*
	G	1	0.03	0.86	ns
24213	P	43	1.70	6.4E-03	*
	G	1	0.81	0.37	ns
24228	P	43	1.46	4.0E-02	*
	G	1	1.94	0.16	ns
24240	P	43	1.55	2.0E-02	*
	G	1	2.85	0.09	ns
24283	P	43	1.95	8.1E-04	**
	G	1	4.07	0.04	ns
24687	P	43	1.30	0.11	ns
	G	1	0.38	0.54	ns
25509	P	43	1.34	0.09	ns
	G	1	0.11	0.74	ns
25518	P	43	2.11	1.7E-04	**
	G	1	1.11	0.29	ns
25519	P	43	1.61	1.3E-02	*
	G	1	1.90	0.17	ns
25547	P	43	1.72	5.4E-03	*
	G	1	0.0001	0.99	ns
26103	P	43	1.58	1.7E-02	*
	G	1	3.61	0.06	ns
27790	P	43	1.67	7.9E-03	*
	G	1	2.82	0.09	ns
29073	P	43	2.14	1.3E-04	**
	G	1	0.61	0.43	ns
29924	P	43	2.07	2.6E-04	**
	G	1	0.76	0.38	ns

**Table S5:** ANOVA table for the subtrait NUMBER STATE SHIFTS. The table contains effects of replicate (P) and genotype (G), i.e.,  $Mi\{ET1\}$  vs  $w^{1118}$ . P-values are adjusted for multiple testing using a false-discovery rate (FDR). Significance levels are indicated by asterisks; \*\*\*: FDR adjusted P-value < 0.001, \*\*: FDR adjusted P-value < 0.01, \*: FDR adjusted P-value < 0.05, ns: FDR adjusted P-value > 0.05.  $Mi\{ET1\}$  in bold indicates a significant phenotypic effect (FDR adjusted P-value<0.05) of disrupting the target gene.

$Mi\{ET1\}$	Effect	Df	F value	Pr(>F)	FDR
<b>23767</b>	P	43	2.70	5.5E-07	***
	G	1	13.63	2.7E-04	**
24213	P	43	1.55	2.0E-02	*
	G	1	2.07	0.15	ns
<b>24228</b>	P	43	2.34	2.0E-05	***
	G	1	9.34	2.5E-03	*
24240	P	43	1.73	5.1E-03	**
	G	1	0.01	0.93	ns
<b>24283</b>	P	43	1.65	9.9E-03	*
	G	1	15.44	1.1E-04	**
24687	P	43	2.21	6.6E-05	***
	G	1	0.69	0.41	ns
25509	P	43	2.03	3.7E-04	***
	G	1	2.67	0.10	ns
25518	P	43	3.26	1.8E-09	***
	G	1	4.76	0.03	ns
25519	P	43	1.94	8.0E-04	**
	G	1	0.13	0.72	ns
25547	P	43	1.63	1.1E-02	*
	G	1	0.004	0.95	ns
26103	P	43	2.01	4.8E-04	***
	G	1	0.93	0.34	ns
<b>27790</b>	P	43	2.73	4.6E-07	***
	G	1	13.53	2.8E-04	**
29073	P	43	3.18	4.5E-09	***
	G	1	2.03	0.16	ns
29924	P	43	2.39	1.2E-05	***
	G	1	0.65	0.42	ns

**Table S6:** ANOVA table for the subtrait MEAN TIME INACTIVE. The table contains effects of replicate (P) and genotype (G), i.e.,  $Mi\{ET1\}$  vs  $w^{1118}$ . P-values are adjusted for multiple testing using a false-discovery rate (FDR). Significance levels are indicated by asterisks; \*\*\*: FDR adjusted P-value < 0.001, \*\*: FDR adjusted P-value < 0.01, \*: FDR adjusted P-value < 0.05, ns: FDR adjusted P-value > 0.05.  $Mi\{ET1\}$  in bold indicates a significant phenotypic effect (FDR adjusted P-value<0.05) of disrupting the target gene.

$Mi\{ET1\}$	Effect	Df	F value	Pr(>F)	FDR
<b>23767</b>	P	43	2.49	4.6E-06	***
	G	1	10.63	1.2E-03	**
24213	P	43	3.37	7.2E-10	***
	G	1	1.73	0.19	ns
24228	P	43	2.91	7.9E-08	***
	G	1	1.67	0.20	ns
<b>24240</b>	P	43	3.60	6.6E-11	***
	G	1	17.95	3.1E-05	***
<b>24283</b>	P	43	2.40	1.2E-05	***
	G	1	18.01	3.0E-05	***
<b>24687</b>	P	43	2.30	2.8E-05	***
	G	1	5.55	1.9E-02	*
<b>25509</b>	P	43	2.64	9.9E-07	***
	G	1	12.43	4.9E-04	**
<b>25518</b>	P	43	2.09	2.1E-04	***
	G	1	24.07	1.6E-06	***
25519	P	43	2.13	1.5E-04	***
	G	1	2.22	0.14	ns
25547	P	43	1.99	5.6E-04	***
	G	1	1.32	0.25	ns
26103	P	43	3.04	2.1E-08	***
	G	1	3.18	0.08	ns
<b>27790</b>	P	43	2.42	9.0E-06	***
	G	1	15.24	1.2E-04	***
<b>29073</b>	P	43	2.20	7.6E-05	***
	G	1	29.65	1.1E-07	***
29924	P	43	2.06	2.7E-04	***
	G	1	1.77	0.18	ns

**Table S7:** ANOVA table for the subtrait MEAN TIME ACTIVE. The table contains effects of replicate (P) and genotype (G), i.e.,  $Mi\{ET1\}$  vs  $w^{1118}$ . P-values are adjusted for multiple testing using a false-discovery rate (FDR). Significance levels are indicated by asterisks; \*\*\*: FDR adjusted P-value < 0.001, \*\*: FDR adjusted P-value < 0.01, \*: FDR adjusted P-value < 0.05, ns: FDR adjusted P-value > 0.05.  $Mi\{ET1\}$  in bold indicates a significant phenotypic effect (FDR adjusted P-value<0.05) of disrupting the target gene.

$Mi\{ET1\}$	Effect	Df	F value	Pr(>F)	FDR
<b>23767</b>	P	43	3.11	9E-09	***
	G	1	28.47	2E-07	***
24213	P	43	2.06	3E-04	***
	G	1	0.29	0.59	ns
<b>24228</b>	P	43	2.34	2E-05	***
	G	1	6.14	1E-02	*
24240	P	43	1.85	2E-03	**
	G	1	1.53	0.22	ns
<b>24283</b>	P	43	3.41	5E-10	***
	G	1	18.84	2E-05	***
<b>24687</b>	P	43	2.77	3E-07	***
	G	1	5.77	2E-02	*
25509	P	43	2.38	1E-05	***
	G	1	0.09	0.77	ns
25518	P	43	3.53	1E-10	***
	G	1	0.04	0.83	ns
25519	P	43	2.75	4E-07	***
	G	1	3.03	0.08	ns
25547	P	43	2.85	1E-07	***
	G	1	0.16	0.69	ns
26103	P	43	2.33	2E-05	***
	G	1	1.74	0.19	ns
27790	P	43	3.02	2E-08	***
	G	1	4.90	0.03	ns
<b>29073</b>	P	43	3.59	7E-11	***
	G	1	14.47	2E-04	***
<b>29924</b>	P	43	3.06	1E-08	***
	G	1	6.58	1E-02	*

**Table S8:** ANOVA table for the subtrait MAX TIME INACTIVE. The table contains effects of replicate (P) and genotype (G), i.e.,  $Mi\{ET1\}$  vs  $w^{1118}$ . P-values are adjusted for multiple testing using a false-discovery rate (FDR). Significance levels are indicated by asterisks; \*\*\*: FDR adjusted P-value < 0.001, \*\*: FDR adjusted P-value < 0.01, \*: FDR adjusted P-value < 0.05, ns: FDR adjusted P-value > 0.05.  $Mi\{ET1\}$  in bold indicates a significant phenotypic effect (FDR adjusted P-value<0.05) of disrupting the target gene.

$Mi\{ET1\}$	Effect	Df	F value	Pr(>F)	FDR
<b>23767</b>	P	43	2.25	4.7E-05	***
	G	1	19.60	1.4E-05	***
24213	P	43	2.25	5.0E-05	***
	G	1	1.98	0.16	ns
24228	P	43	1.79	3.0E-03	**
	G	1	2.10	0.15	ns
<b>24240</b>	P	43	2.48	5.2E-06	***
	G	1	15.82	8.9E-05	***
24283	P	43	2.44	8.5E-06	***
	G	1	1.20	0.27	ns
<b>24687</b>	P	43	2.35	1.8E-05	***
	G	1	9.19	2.7E-03	**
<b>25509</b>	P	43	2.37	1.5E-05	***
	G	1	6.33	1.2E-02	*
<b>25518</b>	P	43	1.66	8.7E-03	**
	G	1	15.30	1.1E-04	***
<b>25519</b>	P	43	2.15	1.3E-04	***
	G	1	5.21	2.3E-02	*
25547	P	43	2.04	3.5E-04	***
	G	1	1.00	0.32	ns
26103	P	43	2.17	1.1E-04	***
	G	1	1.05	0.31	ns
<b>27790</b>	P	43	1.71	6.0E-03	**
	G	1	6.11	1.4E-02	*
<b>29073</b>	P	43	1.96	6.8E-04	***
	G	1	26.56	4.9E-07	***
<b>29924</b>	P	43	1.92	1.0E-03	**
	G	1	14.04	2.2E-04	***



**Table S9:** ANOVA table for the subtrait MAX TIME ACTIVE. The table contains effects of replicate (P) and genotype (G), i.e.,  $Mi\{ET1\}$  vs  $w^{1118}$ . P-values are adjusted for multiple testing using a false-discovery rate (FDR). Significance levels are indicated by asterisks; \*\*\*: FDR adjusted P-value < 0.001, \*\*: FDR adjusted P-value < 0.01, \*: FDR adjusted P-value < 0.05, ns: FDR adjusted P-value > 0.05.  $Mi\{ET1\}$  in bold indicates a significant phenotypic effect (FDR adjusted P-value<0.05) of disrupting the target gene.

$Mi\{ET1\}$	Effect	Df	F value	Pr(>F)	FDR
<b>23767</b>	P	43	3.21	3.1E-09	***
	G	1	45.23	9.7E-11	***
24213	P	43	2.07	2.6E-04	***
	G	1	1.24	0.27	ns
24228	P	43	2.03	3.7E-04	***
	G	1	2.99	0.09	ns
24240	P	43	1.73	5.2E-03	**
	G	1	2.19	0.14	ns
<b>24283</b>	P	43	3.13	8.8E-09	***
	G	1	6.87	9.3E-03	*
<b>24687</b>	P	43	1.90	1.2E-03	**
	G	1	13.06	3.6E-04	**
<b>25509</b>	P	43	1.92	9.5E-04	**
	G	1	5.51	2.0E-02	*
25518	P	43	2.43	8.4E-06	***
	G	1	0.33	0.56	ns
25519	P	43	2.51	3.7E-06	***
	G	1	1.04	0.31	ns
25547	P	43	2.37	1.5E-05	***
	G	1	0.01	0.94	ns
26103	P	43	1.89	1.4E-03	**
	G	1	1.95	0.16	ns
<b>27790</b>	P	43	2.26	4.2E-05	***
	G	1	8.01	5.0E-03	*
<b>29073</b>	P	43	2.69	6.4E-07	***
	G	1	8.91	3.1E-03	*
29924	P	43	2.48	5.3E-06	***
	G	1	3.41	0.07	ns

**Table S10:** ANOVA table for the subtrait PRINCIPAL COMPONENT SCORE 1. The table contains effects of replicate (P) and genotype (G), i.e.,  $Mi\{ET1\}$  vs  $w^{1118}$ . P-values are adjusted for multiple testing using a false-discovery rate (FDR). Significance levels are indicated by asterisks; \*\*\*: FDR adjusted P-value < 0.001, \*\*: FDR adjusted P-value < 0.01, \*: FDR adjusted P-value < 0.05, ns: FDR adjusted P-value > 0.05.  $Mi\{ET1\}$  in bold indicates a significant phenotypic effect (FDR adjusted P-value<0.05) of disrupting the target gene.

$Mi\{ET1\}$	Effect	Df	F value	Pr(>F)	FDR
<b>23767</b>	P	43	4.52	4.7E-15	***
	G	1	37.30	3.3E-09	***
24213	P	43	3.07	1.5E-08	***
	G	1	0.55	0.46	ns
24228	P	43	2.61	1.6E-06	***
	G	1	0.78	0.38	ns
<b>24240</b>	P	43	2.26	4.6E-05	***
	G	1	2.26	4.6E-05	***
<b>24283</b>	P	43	4.71	1.1E-15	***
	G	1	5.01	2.6E-02	*
<b>24687</b>	P	43	3.32	1.0E-09	***
	G	1	13.06	3.6E-04	**
25509	P	43	3.23	2.5E-09	***
	G	1	3.16	0.08	ns
<b>25518</b>	P	43	3.94	1.7E-12	***
	G	1	5.08	2.5E-02	*
<b>25519</b>	P	43	3.83	5.4E-12	***
	G	1	10.12	1.6E-03	**
25547	P	43	3.44	3.5E-10	***
	G	1	0.01	0.91	ns
26103	P	43	3.01	2.9E-08	***
	G	1	3.44	0.06	ns
27790	P	43	3.86	4.5E-12	***
	G	1	0.92	0.34	ns
<b>29073</b>	P	43	4.31	4.7E-14	***
	G	1	27.32	3.4E-07	***
<b>29924</b>	P	43	4.13	2.3E-13	***
	G	1	9.54	2.2E-03	**

**Table S11:** ANOVA table for the subtrait PRINCIPAL COMPONENT SCORE 2. The table contains effects of replicate (P) and genotype (G), i.e.,  $Mi\{ET1\}$  vs  $w^{1118}$ . P-values are adjusted for multiple testing using a false-discovery rate (FDR). Significance levels are indicated by asterisks; \*\*\*: FDR adjusted P-value < 0.001, \*\*: FDR adjusted P-value < 0.01, \*: FDR adjusted P-value < 0.05, ns: FDR adjusted P-value > 0.05.  $Mi\{ET1\}$  in bold indicates a significant phenotypic effect (FDR adjusted P-value<0.05) of disrupting the target gene.

$Mi\{ET1\}$	Effect	Df	F value	Pr(>F)	FDR
23767	P	43	1.50	2.9E-02	*
	G	1	0.002	0.97	ns
24213	P	43	1.94	8.5E-04	**
	G	1	0.53	0.47	ns
24228	P	43	2.08	2.5E-04	**
	G	1	4.46	0.04	ns
24240	P	43	2.15	1.3E-04	**
	G	1	4.54	0.03	ns
<b>24283</b>	P	43	1.71	6.2E-03	*
	G	1	15.21	1.2E-04	***
24687	P	43	1.63	1.1E-02	*
	G	1	1.61	0.21	ns
<b>25509</b>	P	43	1.80	2.7E-03	**
	G	1	6.09	1.4E-02	*
<b>25518</b>	P	43	1.69	6.9E-03	*
	G	1	13.60	2.7E-04	**
25519	P	43	1.44	0.04	ns
	G	1	1.91	0.17	ns
25547	P	43	0.97	0.52	ns
	G	1	0.30	0.58	ns
26103	P	43	1.96	7.0E-04	**
	G	1	0.05	0.82	ns
<b>27790</b>	P	43	1.68	7.5E-03	*
	G	1	15.35	1.1E-04	***
29073	P	43	1.64	9.9E-03	*
	G	1	5.44	0.02	ns
29924	P	43	1.30	0.11	ns
	G	1	1.96	0.16	ns