Table S1. List of parameters used in the model, related to **Figure 2A**.

Parameter	Meaning	Value
g_L	Leak conductance	0.0025 1/s
V_L	Rest potential	-90 mV
g_{C1}	Initial cation channel conductance	0.0125 1/s
g_{C2}	Final cation channel conductance	0.003125 1/s
δ_C	Cation channel decay rate	0.025 1/s
V_0	Cation Nernst potential when $C = C_e$	1 mV
C_e	Extracellular cation concentration	2 mM
α_{in}	Import rate	0.075 1/s
α_{out}	Export rate	0.075 1/s
F	Conductance coefficient	0.0067 mM/mV
β_T	ThT input rate	0.01 mM/s
δ_{hyp}	ThT export rate under hyperpolarization	0.00025 1/s
δ_{dep}	ThT export rate under depolarization	0.005 1/s
V_S	Steepness of the ThT response function	0.1 mV

Table S2. Proteins enriched uniquely in the L22* mutant, related to **Figure 5**.

Proteins marked in bold are ion transporters. The table lists a description of overexpressed proteins and its expression level in wild-type in the presence of spectinomycin (Spec), ΔyhdP, ΔL34, and L22* mutant normalized to wild-type (WT) expression level.

Protein	**Description**	**WT**	**Spec**	**ΔyhdP**	**ΔL34**	**L22***
YodF	Uncharacterized symporter, similar to amino acid permease	1	0.83	0.69	0.87	1.94
MgtE	Magnesium transporter MgtE	1	0.94	0.57	0.99	1.87
YybJ	Uncharacterized ABC transporter ATP-binding protein	1	0.91	1.04	0.92	1.77
YoaB	2-oxoglutarate permease (proton symporter)	1	0.77	0.73	0.87	1.68
YhdP	Magnesium efflux pump	1	0.93	0.27	1.09	1.57
YbeC	Probable amino acid-proton symporter	1	1.06	0.72	0.97	1.56
NtdC	Glucose-6-phosphate 3-dehydrogenase	1	0.68	0.51	0.67	6.25
NtdA	3-oxo-glucose-6-phosphate:glutamate aminotransferase	1	0.69	0.55	0.66	5.02
NtdB	Kanosamine-6-phosphate phosphatase	1	0.70	0.57	0.62	4.90
YqjL	General stress protein, putative hydrolase involved in oxidative stress resistance	1	0.92	1.09	1.00	2.31
YdiP	Similar to DNA-3-methyladenine glycosidase II	1	0.94	0.93	0.87	1.90
EpsN	UDP-2,6-dideoxy 2-acetamido 4-keto glucose aminotransferase	1	0.66	0.83	0.71	1.75
BioD	ATP-dependent dethiobiotin synthetase	1	0.87	1.00	0.94	1.71
YokE	SPBc2 prophage-derived uncharacterized protein	1	1.07	1.09	1.06	1.68
MtnK	Methylthioribose kinase	1	0.69	0.96	0.96	1.65
PxpC	5-oxoprolinase subunit C	1	1.05	0.98	0.87	1.65
YvyE	IMPACT family member	1	1.02	0.97	1.07	1.57
KipR	HTH-type transcriptional regulator KipR	1	0.91	0.85	0.71	1.56
RapG	Response regulator aspartate phosphatase G	1	0.99	0.97	1.05	1.54
MtnA	Methylthioribose-1-phosphate isomerase	1	0.95	1.03	0.90	1.51

Table S3. Summary values of parameters measured at the population level for the conditions listed, related to **Figure 7**.

The table lists mean ThT level with its standard deviation (ThT std), hyperpolarized cell fraction and its confidence interval (CI), and number of analyzed cells.

Condition	**ThT mean (a.u.)**	**ThT std**	**Hyperpolarized cell fraction**	**CI**	**Number of cells**
WT	211.39	20.15	3.68	0.03	1,459,602
WT Spec	229.56	42.41	28.54	0.07	1,404,264
WT Kan	219.89	34.24	15.76	0.06	1,298,188
WT Cm	219.44	41.03	23.41	0.07	1,415,308
WT+20 mM Mg^{2+}	191.36	31.98	2.94	0.04	781,747
L22*	197.35	15.35	0.29	0.01	896,718
L22* Spec	197.6	17.05	0.36	0.01	1,279,746
∆L34	237.09	47.30	35.22	0.07	1,741,790
∆L34+100 mM Mg^{2+}	184.42	21.53	2.3	0.03	1,249,549

Table S4. Summary values of parameters measured at the single-cell level for the conditions listed, related to **Figure 7**.

The table lists the elongation rate with its standard error (SE), mean number of surviving generations with its standard error (SE), and number of analyzed cells.

Condition	**Elongation rate (h^{-1})**	**SE**	**Surviving generations**	**SE**	**Number of cells**
WT	0.19	0.01	2.85	0.18	102
WT Spec	0.06	0.01	1.22	0.08	174
WT Kan	0.19	0.01	1.56	0.12	134
WT Cm	0.04	0.01	1.31	0.13	35
WT+20 mM Mg^{2+}	0.19	0.02	3.58	0.10	50
L22*	0.26	0.01	4.02	0.31	51
L22* Spec	0.17	0.01	2.52	0.14	100
∆L34	0.09	0.02	1.29	0.28	35
∆L34+100 mM Mg^{2+}	0.23	0.02	2.56	0.34	35