A	Gene	AT	IPC	Expansion	B. p-Value	C. E	pres	ssion								
Root cell	SOS1	1	7	0.001			28.17	38.58	31.44	32.13	18.27	19.69	24.55	20.59	23.02	SOS1
	GLRS	20	40	8.35E-06			6.04	5.74	5.17	5.08	11.52	11.72	10.08	6.71	5.73	GLRS
	CNGCs	20	26	1		20.53	17.94	22.28	19.66	20.37	19.23	20.44	25.06	19.37	18.63	CNGCs
	HKT2	0	0	1		24.81	47.66	44 61	32.16	29.45	1.57	1.54	5.07	1.28	1.73	AKT1
	AKT1	1	4	0.005												
	HAK5	1	7	2.60E-04					11.65				10.69	-		HAK5
	LCT1	0	0	1		1231.09	816.82	759.58	688.34	488.53	313.19	193.76	174.63	178.55	155.49	PIP2;1
	PIP2;1	1	2	0.341		29.12	24.35	21.32	20.64	15.47	16.29	19.11	17.63	15.10	14.85	GORK
	GORK	1	1	1		2.62	4.01	2.38	2.44	2.29	2.83	3.12	2.94	4.56	5.97	NHX8
	NHX8	1	3	0.093		43.27	15.75	16.52	10.64	16.31	6.45	6.40	6.38	4.11	3.99	HKT5
Root to xylem	HKT1/HKT1;1	1	0	0.341	•	13.11	15.31	14.05	12.93	14.46	8.10	8.90	10.40	6.65	7.47	ccc
	HKT5/HKT1;5	0	1	0		3.77	1.25	1.35	1.14	1,44	0.42	0.23	0.45	0.38	10000	SV/TCP1
	CCC	1	3	0.093	•		7.000		20.00				2,000,00	100000000000000000000000000000000000000		
Leaf Vacuole	SV/TCP1	1	6	0.001	•	5.29	19.60	7.76	5.43	6.67	3.61	4.17	4.00	4.52	4.21	TPK
	TPK	6	5	0.714	10	27.80	22.48	33.03	24.91	25.51	21.71	22.46	26.93	22.16	21.50	NHX1/NH
	NHX1/NHX2	2	4	0.163	•	23.35	18.00	25.72	18.93	18.90	20.65	20.86	24.16	20.57	18.16	KEAs
Chloroplast	KEA	5	8	0.178	•	22.25	18.54	16.52	7.79	9.64	3.30	3.97	3.39	2.10	2.17	HKT famil
	HKT family	1	2	0.341	•	22.01	19.24	27.78	22.41	22.14	17.03	16.87	20.94	18.47	19.11	NHX fami
	NHX family	8	32	8.15E-12												CNGC
	CNGC family	20	26	0.3674												
	V-ATP ase	28	50	3.88E-05	•	77.80	75.66	79.26	86.40	75.42	51.57	53.07	68.18	61.48	68.60	V-ATPase
	NHX6	1	4	0.023	•	40.40	39.43	43.35	37.57	34.26	26.75	29.45	32.39	29.35	32.06	NHX6
	Shaker type	9	26	2.49E-07		22.89	29.87	22.86	23.06	20.78	26.92	29.55	30.99	36.75	40.90	Shaker ty

Figure S8. Expansion and expression analysis of genes involved in ions uptake, transportation, and sequestration in IPC. (A) Comparison of the number of genes identified in Arabidopsis (AT) and IPC. (B) The p-value for the expansion analysis. (C) Average expression levels of different gene categories. Gene expansion in IPC is denoted by a significant, corrected p-value (P < 0.01), determined through a Chi-square test for overrepresentation, using all annotated genes as the background.