

Table S1. Primer sequences used in this study

Primer	Sequence (5' to 3')
<i>rnIA</i> -forward	GGCGCTGGTGAAATAGTAAG
<i>rnIA</i> -reverse	TCTTTAGAAGGTTACCGCCC
<i>macA</i> -forward	CAAATAGTTTAGAATATTTAAATCCTTTTAATATATCTTC
<i>macA</i> -reverse	CATATTGTAAAAAATTGGAGGATCCATTTG
Fragment 1-forward	CAGTCACAACCATCTCCGATG
Fragment 1-reverse	GCAACTGAAGATTCACAACC
Fragment 2-forward	TGGGTCAGAACATCTATCTC
Fragment 2-reverse	CGTTCATTTAAGAGTGGTCG
Fragment 3-forward	GTGTATCACCATTGGAGGCAG
Fragment 3-reverse	CCTTCAATGGTAATACCAGC
Fragment 4-forward	AGTCCTACCAACTTCTTTAC
Fragment 4-reverse	CTACCAGTTCAACTTTAATCGG
Fragment 5-forward	CTGCTGCCACTACCTGAAG
Fragment 5-reverse	CTCTCAGTAATTGAGTTCTCC

Table S2. Detection of MacA peptides in crude membrane fractions<sup>a</sup>

#	Peptide	Position		Type-I		Type-II		Type-III	
	Sequence	start	end	FC	ICL	FC	ICL	FC	ICL
1	YPTTLNSPSFIINK	50	63	4.5	2.8	1.7	1.5	2.5	2.4
2	SQPCEQYTFSNMNPISINK	65	82	1.5	0.9	-	-	-	-
3	SNSYWNEMIEQIK	180	192	3.0	1.9	-	-	0.8	0.8
4	LIINNFILNSQPPIPK	193	208	1.5	1.9	-	-	-	-
5	NIQSLLSPIDPLILSDPLK	209	227	-	5.7	-	-	-	-
6	SIESNLFLISNLIK	373	386	-	5.7	-	-	-	-
7	ITFEDICYCR	446	455	-	0.9	-	-	0.8	-
8	FITSSLFSNVVK	507	518	3.0	4.7	-	1.5	0.8	1.6
9	DIPENTIASFLLSNGK	598	613	7.4	5.7	-	-	-	-
10	IGISPFPCPYLCGLPK	614	628	-	1.9	-	-	-	-
11	LGFGSNGITDSCLVTPK	678	694	-	0.9	-	-	-	-
12	YQLIFTNSDYNSPR	695	708	4.5	2.8	-	-	1.7	1.6
13	NILPTDFLNR	709	718	-	1.9	-	-	-	0.8
14	ATTIEMWLK	719	727	-	0.9	-	-	-	-
15	TITPSITNPSTQQIIFK	761	777	1.5	2.8	1.7	1.5	1.7	1.6
16	ISFMIDEFK	839	847	-	0.9	0.9	-	-	-
17	EFVVNGGLNYCLSK	911	924	-	0.9	-	-	-	-
18	NLNDPSQCDCIDGEFK	932	947	1.5	0.9	-	-	1.7	1.6
19	SDNYYSNNIDK	965	975	-	-	-	-	0.8	0.8
20	ISITPLPNPTTMK	1045	1057	-	-	-	-	1.7	0.8
21	STLPLQANQIDIDYETVSPK	1080	1099	4.5	1.9	-	-	-	2.4
22	SVVPFACIACPTMPTFK	1100	1116	-	0.9	-	-	-	-
23	ESPSSLSYIYPPTSLLPR	1117	1134	4.5	6.6	-	-	-	0.8
24	NEINSCGCFGR	1135	1145	-	-	-	0.7	1.7	1.6
25	SSFSCMPPLPAPTFTLPSGSYK	1151	1172	-	0.9	-	-	-	-
26	LSSDVASSIYK	1233	1243	4.5	2.8	0.9	0.7	-	-
27	AIGCINQACSR	1441	1451	-	-	0.9	-	0.8	0.8
28	LTFDFDQLLPTIK	1459	1471	-	4.7	-	-	-	-
29	TLYQYTLIK	1496	1504	1.5	0.9	-	-	0.8	-
30	FSISAIDCPK	1637	1646	1.5	-	0.9	-	1.7	1.6
31	DFICSEPSNSEIILR	1647	1661	-	-	-	-	0.8	0.8
32	ANSNILDFIYTVEK	1744	1757	5.9	6.6	-	-	-	-
33	YLRPNKPIINPGQGGYLDK	1758	1776	4.5	1.9	-	-	-	0.8
34	SNIPLLLIDAIK	1808	1818	3.0	2.8	-	-	1.7	1.6
35	FILYEYYLK	2015	2023	-	0.9	-	-	-	-
			Total	57.9	75.9	7.0	5.9	20.3	22.3

<sup>a</sup>Normalized to 50,000 hits

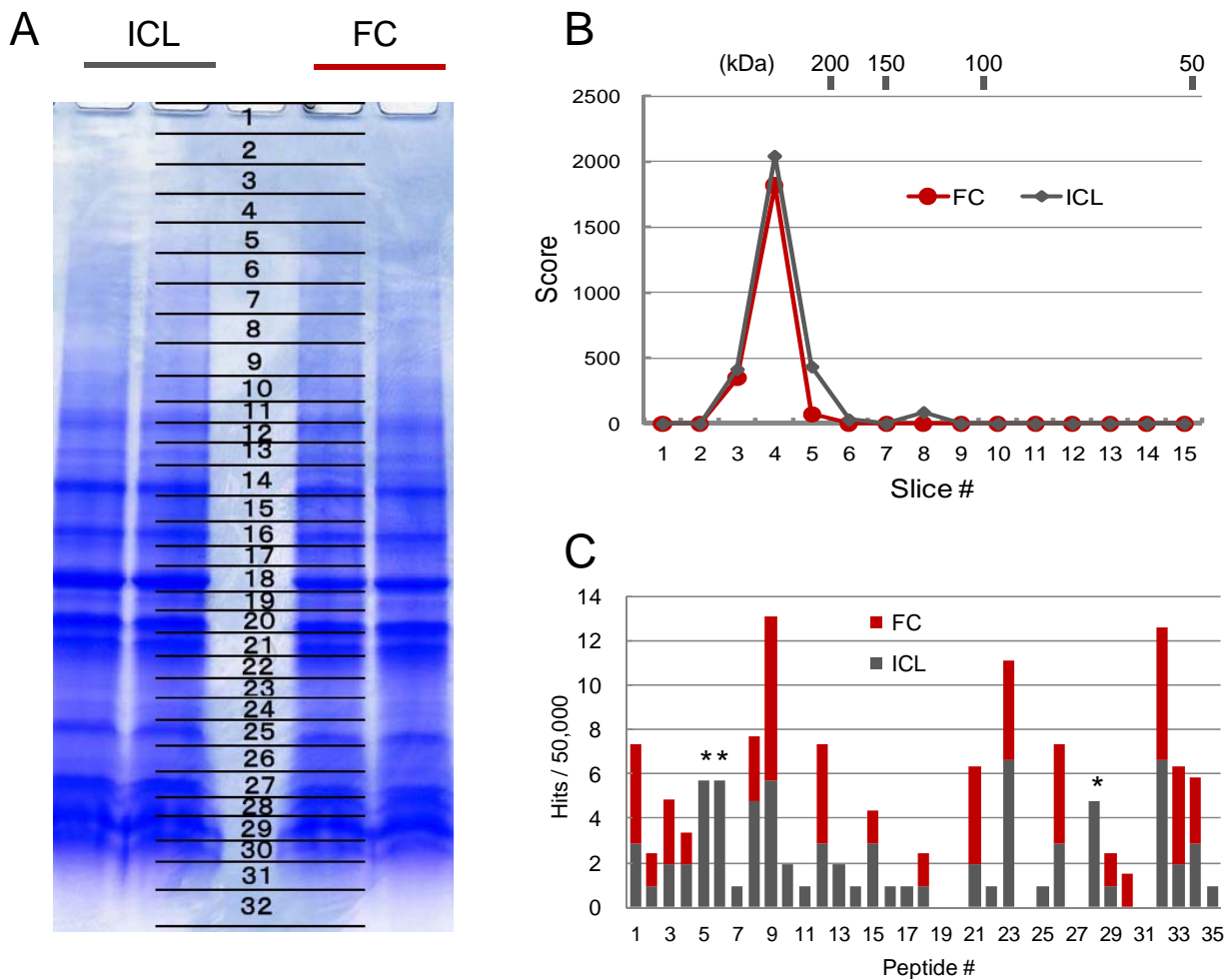


Fig. S1. Detection of the *macA* product. **A**: Crude membrane fractions were prepared from KAX3 FC and ICL cells and their proteins were separated by SDS-PAGE. The gel was horizontally sliced in 32 pieces for proteome analyses by LC/MS/MS. **B**: Scores of the hits to the *MacA*-derived peptides were plotted against the gel slice number. No hits were obtained beyond the 9<sup>th</sup> slice. **C**: Hits to the individual peptides are shown. The peptides were numbered from the N- to C-terminus of the *MacA* sequence (Table S2). The asterisks indicate peptides detected 4/50000 or more in ICL but none in FC cells.