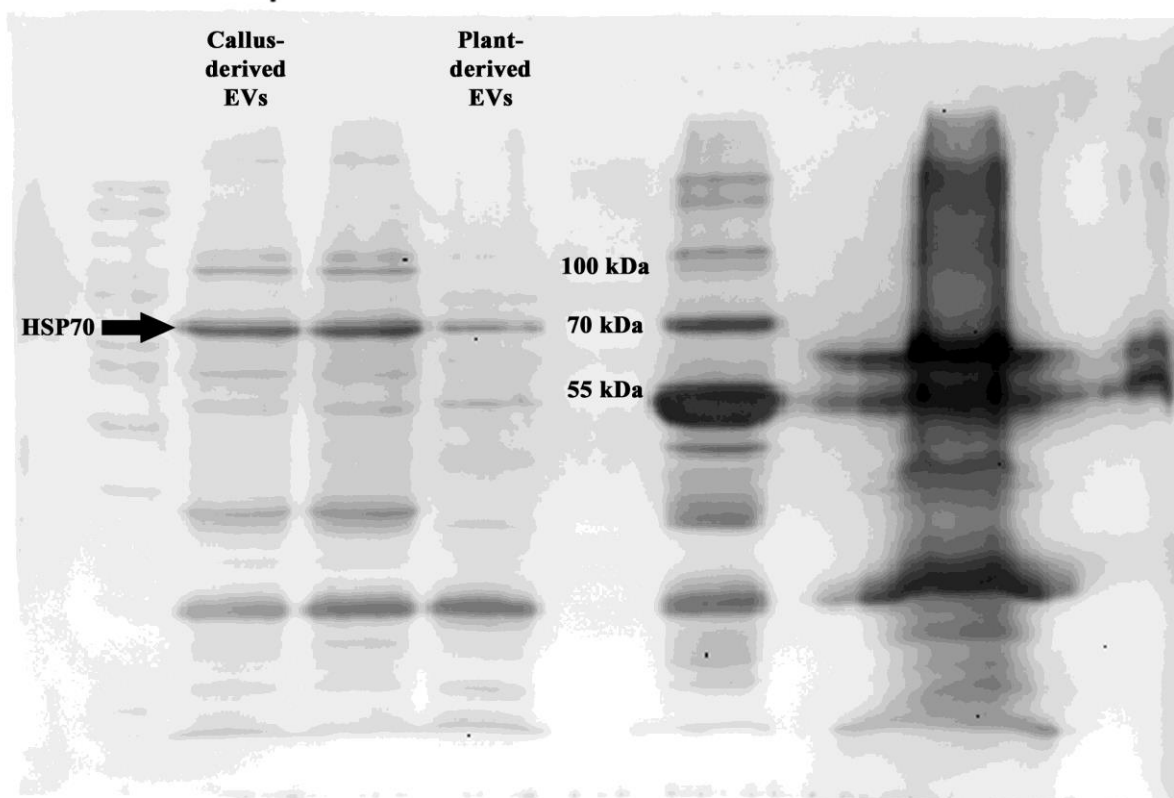
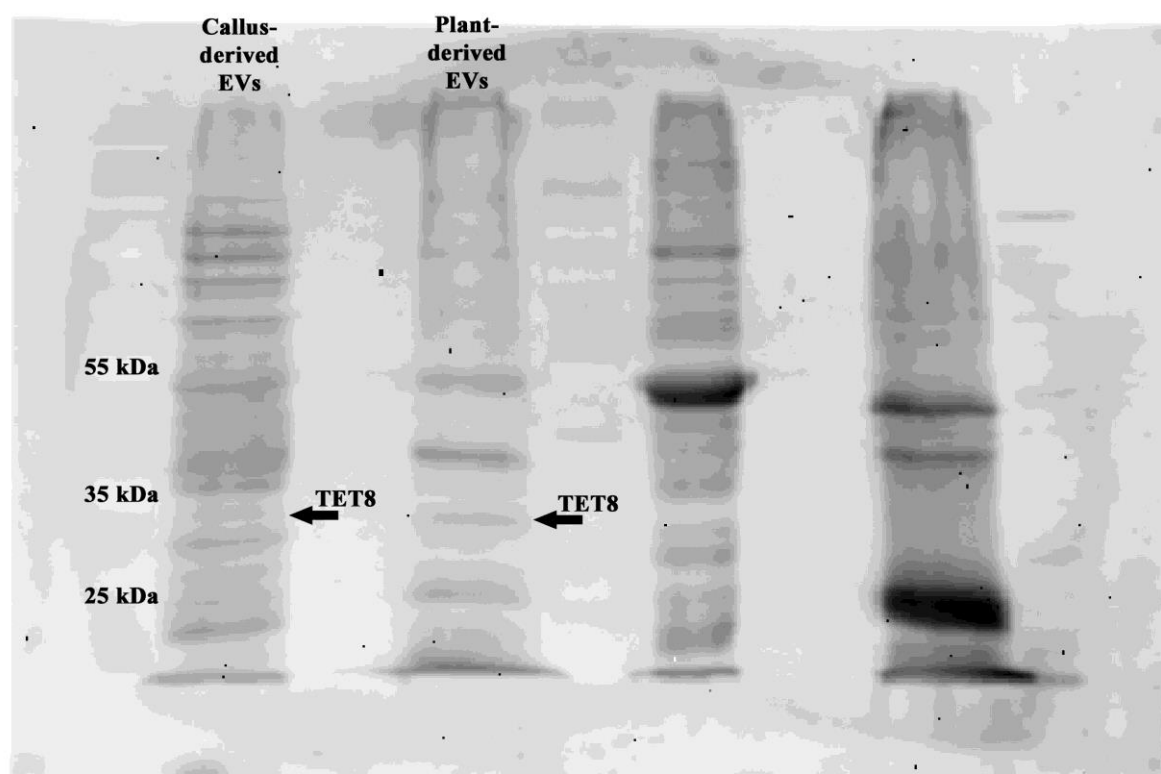


**Supplementary Table S1.** List of primers used in this study.

Gene (GenBank accession no.)	Forward (5'–3')	Reverse (5'–3')
GAPDH (AT1G13440)	TTGGTGACAACAGGTCAAGC	AACTTGTCGCTCAATGCAAT C
TET8 (AT2G23810)	ACTTGGTGATTACTCTACTTG	AGGTTTGGCAGTCTGGATTA
PEN1 (AT3G11820)	TCGTCCGAGTATAGAGAAAC	AGCACGGCCATGTCTAGAA
Universal stem-loop primer	GAAAGAAGGCGAGGAGCAGATCGAGGAAGAAGACGGAAGA ATGTGCGTCTCGCCTTCTTTCNNNNNNNN	
Universal reverse primer	-	CGAGGAAGAAGAAGACGGA AGAAT
miR157c (AT3G18217)	CGAGGAAGAAGAAGACGGAA G	-
miR167a (AT3G22886)	TTGAAGCTGCCAGCATGATC	-
miR167c (AT3G04765)	TTGAAGCTGCCAGCATGATC	-
miR168a (AT4G19395)	TCGCTTGGTGCAGGTCGG	-
miR172e (AT5G59505)	ATGGAATCTTGATGATGCTGC	-
miR390b (AT5G58465)	CGAAGCTCAGGAGGGATAG	-
miR394b (AT1G76135)	ATTGGCATTCTGTCCACCTC	-
miR408 (AT2G47015)	ATGCACTGCCTCTTCCCTG	-
miR8175 (AT2G05455)	GATCCCCGGCAACGGCC	-
VPS37-1 (At3g53120)	ATTCTACTCCCCTGGTTCTC	CGTCGATGATAGGTAGTAC G
VPS36 (AT5G04920)	AGGAACATCTACTATCTGCAG	CCGTATGTCCCAAACCTCCTT
VPS2-1 (AT2G06530)	GTATCGACATCAACCAAGAG	TCTATACCTCCACTGTCCTC
VPS4 (AT4G26750)	CCTTCTCACTACCAAAACCC	TGATGAGTAAGGTGGAGGA G
BRO1 (AT1G15130)	TGAGGGCCTGAAGTTCTATG	TATGGGCCGGAGCTTCTATG
TOL2 (AT1G06210)	GAAAGCCAAATCACACAGAG	TCAGATGCAGAGCCTCGAA C
FREE1 (AT1G20110)	GTTTGAGGGAAGGATCTGGG	TCAATGTGCGCTAACGAGG A

**A****B**

**Supplementary Figure S1.** Western blot analysis of EVs isolated from *A. thaliana* callus culture and apoplast washing fluid. Proteins (40  $\mu$ g) were resolved using a 10% SDS-PAGE gel. EVs marker proteins detected were: (A) HSP70 (71/72 kDa) and (B) TET8 (31 kDa).

**Supplementary Table S2.** Protein composition of EVs isolated from callus culture of *A. thaliana*.

Name of protein	Score	Mass	Peptides	Unique peptides	Observed mass/sequences
Heat shock 70 kDa protein (HSP70)	159	72946	8	6	1417.6941 [K.EVDEVLLVGGMTR.V]; 1453.6907 [R.EAELHAQKDKER.K]; 1550.7545 [K.AVVTVPAYFNDAQR.Q]; 1581.7806 [R.EAELHAQKDKERK.E]; 1613.8314 [R.SRFETLVNHLIER.T]; 1821.8857 [K.SQVFSTAADNQTQVGIR.V]
GDSL esterase/lipase (ESM1)	89	44032	6	6	1038.4021 [R.SYFFFDGR.H]; 1367.6017 [K.DLPQTYWPY GK.S]; 1408.6409 [R.ELIVYPTGETMR.E]; 1794.9683 [K.FVVQLLAPLGCLPIVR.Q] + Carbamidomethyl (C); 2100.9444 [K.ANPNADASAQQA FVTNVINR.L]; 2570.1685 [K.AQEEMAHLLYGADPDVVQPM TVR.E]
Myrosinase 2 (BGL37)	39	62692	4	4	1301.5325 [R.GLNVWDGFTHR.Y]; 1301.6966 [R.GLNVWDGFTHR.Y]; 1327.7294 [K.ASGLWYQSFLR.D]; 2153.1903 [R.GINEDGINYYSG LIDGLIAR.N]
Germin-like protein subfamily 3 member 1 (GL31)	42	21545	4	4	1436.3863 [A.SVQDFCVANLKR.A]; 1799.8546 [R.AETPAGYPCIRPIHVK.A] + [+47.9847 at C9]; 1808.8865 [R.AETPAGYPCIRPIHVK.A]; 1964.9722 [K.RAETPAGYPCIRPIHVK.A]
Vegetative storage protein 1 (VSP1)	60	30243	3	2	1536.7026 [R.VFKLPNPLY YVPS]; 1388.9514 [K.GYNIVGNIGDQWADLVEDTPGR.V]; 2517.0282 [K.KGYNIVGNIGDQWADLVEDTPGR.V]
Beta carbonic anhydrase 1 (BCA1)	57	37426	1	1	1906.1378 [R.EAVNVSLANLLTYPFVR.E]
UDP-arabinopyranose mutase 1 (RGP1)	140	40602	14	4	1178.5557 [K.TGLPYIYH SK.A]; 1444.5257 [R.YDDMWAGWCIK.V] + [+57.0215 at C9]; 1460.5184 [R.YDDMWAGWCIK.V] + [+72.9952 at I10]; 1606.6586 [K.YIFTIDDDCFVAK.D] + [+57.0215 at C9]; 1729.6889 [K.GTLFPMC GMNLA FDR.E] + [+57.0215 at M6]; 1742.7338 [K.GTLFPMC GMNLA FDR.E] + [+70.0419 at C7]; 1745.6852 [K.GTLFPMC GMNLA FDR.E] + [+72.9952 at L3]; 1786.7728 [K.TIAVPEGFDYELYNR.N]; 1925.8777 [K.GIFWQEDIIPFFQSAK.L]; 2121.9427 [R.ELIGPAMYFGLMGD GQPIGR.Y]; 2137.9395 [R.ELIGPAMYFGLMGD GQPIGR.Y] + [+15.9949 at Y8]; 2365.0337 [K.NLLCPSTPFFFN TLYDPYR.E; + [+57.0215 at C4]; 3035.4605 [R.EGVSTAVSHGLWLNIPDYDAPTQLVKP

					K.E]; 3217.6721 [M.VEPANTVGIPVNHIPLLKDELDIVIPTIR. N] + [+42.0470 at K18]
UDP- arabinopyranose mutase 2 (RGP2)	53	40864	13	5	1178.5557 [K.TGLPYIYHSK.A]; 1444.5257 [R.YDDMWAGWCIK.V] + [+57.0215 at C9]; 1460.5184 [R.YDDMWAGWCIK.V] + [+72.9952 at I10]; 1606.6586 [K.YIFTIDDDCFVAK.D] + [+57.0215 at C9]; 1729.6889 [K.GTLFPMCGMNLAFFDR.E] + [+57.0215 at M6]; 1742.7338 [K.GTLFPMCGMNLAFFDR]; 1745.6852 [K.GTLFPMCGMNLAFFDR.D] + [+72.9952 at L3]; 1767.7332 [K.IHVPEGYDYELYNR.N]; 1895.8272 [K.KIHVPEGYDYELYNR.N]; 2107.9247 [R.DLIGPAMYFGLMGDGPGR.Y]; 2137.9395 [R.DLIGPAMYFGLMGDGPGR.Y] + [+29.9742 at Y8]; 2351,0200 [K.NLLCPSSPFFNTLYDPYR.E] + [+57.0215 at N-term N]; 3035.4605 [R.EGVSTAVSHGLWLNIPDYDAPTQLVKP K.E]
UDP-ara binopyranose mutase 3 (RGP3)	96	41254	7	2	1444.5257 [R.YDDMWAGWCVK.V; + [+71.0371 at C9]; 1460.5184 [R.YDDMWAGWCVK.V] + [+87.0143 at C-term K]; 1729.6889 [K.GTLFPMCGMNLAFFDR.E] + [+57.0215 at M6]; 1742.7338 [K.GTLFPMCGMNLAFFDR.E] + [+70.0419 at C7]; 1745.6852 [K.GTLFPMCGMNLAFFDR.E] + [+72.9952 at L3]; 2121.9427 [R.ELIGPAMYFGLMGDGPGR.Y]; 2137.9395 [R.ELIGPAMYFGLMGDGPGR.Y] + [+15.9949 at Y8]
EP1-like glycoprotein 3 (EP1L3)	61	49020	2	2	960.5236 [R.WVWEANR.G]; 2287.1975 [R.VVNEGGYTDYSPIEYNPDVR.G]
Nitrilase 1 (NRL1)	90	38128	3	3	1603.8037 [K.YHASAIHVPGPVAR.L]; 1821.9265 [K.GAELVLFPEFFIGGYPR.G]
Nitrilase 2 (NRL2)	52	37130	1	1	1837.9168 [K.GSELVVFPEAFIGGYPR.G]
Polygalacturonase inhibitor 1 (PGIP1)	113	36666	3	3	1078.3897 [K.TTWSIDLSR.N]; 1649.5307 [K.LQTFDSYSYFHNK.C]; 2076.8239 [K.LTGSIPESFGSFGTVPDLR.L]
Phosphoglycerate kinase 3 (PGKY3)	28	42105	1	1	1465.6484 [K.FLKPSVAGFLMQK.E]
Probable xyloglucan endotransglucosyla se/hydrolase protein 11 (XTH11)	36	31919	1	1	2182.1109 [K.NSGSGFESQLIYGSGYFNVR.I]
Alpha-xylosidase 1	41	10233	3	3	1376.6194 [K.TVSWWGDEIKR.F]; 1471.6440

(XYL1)					[R.WIEVGAFYPFSR.D]; 1681.6702 [R.QELYQWDTVADSAR.N]
Beta-glucosidase 22 (BGL22)	27	59743	6	4	1714.6510 [R.CSGHNADVAVDFFHR.Y] + Pyro-carbamidomethyl (N-term C); 1731.6862 [R.CSGHNADVAVDFFHR.Y] + [+57.0215 at S2]; 2689.2577 [R.SGYEAYLVSHNLLNAHAEAVEVFR.Q]; 2888.3468 [K.IGIAHSPAWFEPHDLKDSNDVPTVSR.V]
Putative CCR4- associated factor 1 homolog 4 (CAF1D)	35	34840	2	2	1075.4448 [K.IAESCGLSSR.F]; 1237.5222 [K.KIAESCGLSSR.F]
Beta-glucosidase 23 (BGL23)	82	59683	6	6	950.6664 [K.NLNTDAFR.M]; 1250.8489 [R.GPALWDIYCR.R] + Carbamidomethyl (C); 2251.4879 [K.NAQNYAIGSKPLTAALNVYSR.G]; 2706.6729 [R.SGYEAYLVTHNLLISHAEAVEAYR.K]; 2834.7679 [R.SGYEAYLVTHNLLISHAEAVEAYRK.C]; 3169.8278 [K.ASTDFVGLNYYTSVFSNHLEKPDPSKPR. W]
Probable UDP- arabinopyranose mutase 4 (RGP4)	37	41839	2	2	1767.8936 [K.IRVPEGYDYELYNR.N] + [- 19.0422 at R2]; 1786.9365 [K.IRVPEGYDYELYNR.N]
Sucrose synthase 4 (SUS4)	59	92944	7	7	1021.6264 [R.WISSQMNR.V]; 1043.6218 [K.GGAFFEFLR.S]; 1053.6574 [R.SFTLPGLYR.V]; 1267.8453 [R.IKQQGLNITPR.I]; 1282.7649 [K.YIGDGVEFLNR.H]; 1463.9367 [R.IQNLNTLQHNL.R.K]; 1539.0409 [R.LRELVNLVVVGDR.R]
Glyceraldehyde-3- phosphate dehydrogenase GAPC1 (G3PC1)	25	36891	2	2	[K.LVSWYDNEWGYSSR.V]; [K.GILGYTEDDVVSTDFVGDNR.S]