

Additional file 1.

Table 1. Bioinformatic compilation of putative HHRs and retrozymes found in Phytozome v10.0 and GenBank (Aug 15 2014) sequence databases of plants (see Materials and Methods section for more information).

Plant sp. ⁱ	Acc. number	# HHRs	# Retrozymes (~RNA size)
<i>Actinidia chinensis</i>	AONS00000000.1	2	-
<i>Arabidopsis halleri</i>	BASO00000000.1	13	3 (454-602 nt)
<i>Arabidopsis lyrata</i> <small>subsp. lyrata</small>	NZ_ADBK00000000.1	10	2 (567-602 nt)
<i>Arabidopsis lyrata</i> <small>subsp. petraea</small>	BASP00000000.1	10	2 (582-744 nt)
<i>Arabidopsis thaliana</i> ⁱⁱ	GCA_000001735	2	-
<i>Artemisia annua</i> ⁱⁱⁱ	txid35608	3 ^{vi}	1 (503 nt)
<i>Azadirachta indica</i>	AMWY00000000.2	108	8 (757-776 nt)
<i>Camelina sativa</i>	JFZQ00000000.1	6	-
<i>Capsella rubella</i>	ANNY00000000.1	18	8 (584-606 nt)
<i>Chlamydomonas reinhardtii</i>	NZ_ABCN00000000.1	24 ^{vi}	6 (~2,000 nt)
<i>Chorispora bungeana</i> ⁱⁱⁱ	txid238895	4	-
<i>Citrus clementina</i>	AMZM00000000.1	19	13 (663-692 nt)
<i>Citrullus lanatus</i>	AGCB00000000.1	2	-
<i>Citrus sinensis</i>	AJPS00000000.1	10	11 (665-694 nt)
<i>Citrus latifolia</i> ⁱⁱⁱ	txid200541	2	-
<i>Dahlia pinnata</i> ⁱⁱⁱ	txid101596	5	-
<i>Daucus carota</i>	LNRQ00000000.1	1	-
<i>Dianthus caryophyllus</i> ^v	BAUD00000000.1	1 ^{vi} , 1	Retroviroid
<i>Eucalyptus camaldulensis</i>	BADO00000000.1	101	26 (900-1034 nt)
<i>Eucalyptus grandis</i>	AUSX00000000.1	132	56 (908-1024 nt)
<i>Fragaria ananassa</i>	BATT00000000.1	72	8 (673-701 nt)
<i>Helianthus argophyllus</i> ⁱⁱⁱ	txid73275	2	1 (772 nt)
<i>Helianthus paradoxus</i> ⁱⁱⁱ	txid73304	3	-
<i>Helianthus tuberosus</i> ⁱⁱⁱ	txid4233	1	-
<i>Ipomoea batatas</i> ⁱⁱⁱ	txid4120	1	-
<i>Ipomoea purpurea</i> ⁱⁱⁱ	txid4121	5	-
<i>Jatropha curcas</i>	AFEW00000000.1	30	24 (693-790)
<i>Lactuca perennis</i> ⁱⁱⁱ	txid43195	3	1 (432 nt)
<i>Lactuca sativa</i>	AFSA00000000.1	10	8 (643-652 nt)
<i>Mangifera indica</i> ⁱⁱⁱ	txid29780	3	-
<i>Manihot esculenta</i> <small>ssp. Flabellifolia (W14)</small>	JPQE00000000.1	40	34 (659-739 nt)
<i>Manihot esculenta</i> Crantz <small>(KU50)</small>	JPQF00000000.1	28	9 (660-719 nt)
<i>Erythranthe guttata</i>	APLE00000000.1	3	-
<i>Morus notabilis</i>	ATGF00000000.1	2	-
<i>Nicotiana benthamiana</i>	CBMM00000000.1	1	-
<i>Nicotiana tabacum</i>	AYMY00000000.1	2 ^{vi}	1 (641 nt)
<i>Oryza sativa</i>	GCA_000005425.2	2	1 (466 nt)
<i>Pachycladon fastigiatum</i> ⁱⁱⁱ	txid106774	1	1 (626 nt)
<i>Penstemon centranthifolius</i>	JPFH00000000.1	2	1 (678 nt)
<i>Physcomitrella patens</i> <small>mitDNA</small>	NC_007945.1	2	-
<i>Picrorhiza kurroa</i> ⁱⁱⁱ	txid195120	1	-
<i>Selaginella moellendorffii</i> ^v	NZ_ADFJ00000000.1	111 ^{vi}	4 (757-994 nt)
<i>Solanum melongena</i>	BAUE00000000.1	152	18 (664-672 nt)
<i>Solanum torvum</i> ⁱⁱⁱ	txid119830	2	-
<i>Vitis vinifera</i>	CAAP00000000.3	7	7 (794-866 nt)

ⁱ Plant species not included in this table did not show the presence of HHR/retrozyme motifs at the moment of the analysis

ⁱⁱ (Przybilski et al., 2005)

ⁱⁱⁱ Based on ESTs and Transcriptome Shotgun Assembly (TSA) sequences

^{iv} (Daros and Flores, 1995)

^v (Cervera and De la Peña, 2014)

^{vi} Type I HHRs