Table S2. 92 *Arabidopsis* miRNA loci.

family	gene	chromosome	begin	end	strand	miRNA sequence
156	156a	chr2	10625079	10625099	-	UGACAGAAGAGAGUGAGCACA
156	156b	chr4	14039438	14039458	+	UGACAGAAGAGAGUGAGCACA
156	156c	chr4	14379983	14380003	-	UGACAGAAGAGAGUGAGCACA
156	156d	chr5	3456710	3456730	-	UGACAGAAGAGAGUGAGCACA
156	156e	chr5	3867209	3867229	+	UGACAGAAGAGAGUGAGCACA
156	156f	chr5	9111868	9111888	+	UGACAGAAGAGAGUGAGCACA
156	156f	chr5	22310993	22311013	-	UUGACAGAAGAAAGAGAGCAC
156	156g	chr2	8361137	8361157	-	CGACAGAAGAGAGUGAGCACA
156	157a	chr1	24565188	24565208	-	UUGACAGAAGAUAGAGAGCAC
156	157b	chr1	24573016	24573036	+	UUGACAGAAGAUAGAGAGCAC
156	157c	chr3	6244670	6244690	-	UUGACAGAAGAUAGAGAGCAC
156	157d	chr1	17614552	17614572	-	cUGACAGAAGAUAGAGAGCAC
158	158a	chr3	3366356	3366375	-	ucccaaauguagacaaagca
158	158b	chr1	20359823	20359842	+	ccccaaauguagacaaagca
159/JAW	159a	chr1	27365144	27365164	-	uuuggauugaagggagcucua
159/JAW	159b	chr1	6220814	6220834	+	uuuggauugaagggagcucuu
159/JAW	159c	chr2	18943365	18943385	+	UUUGGAUUGAAGGGAGCUCCU
159/JAW	319a	chr4	11317607	11317626	+	UUGGACUGAAGGGAGCUCCC
159/JAW	319b	chr5	16374378	16374397	-	UUGGACUGAAGGGAGCUCCC
159/JAW	319c	chr2	16978412	16978432	+	uuggacugaagggagcuccu
160	160a	chr2	16288826	16288846	+	uGCCUGGCUCCCUGUAUGCCA
160	160b	chr4	8853486	8853506	+	UGCCUGGCUCCCUGUAUGCCA
160	160c	chr5	18723065	18723085	-	UGCCUGGCUCCCUGUAUGCCA
161	161	chr1	17413291	17413311	+	uugaaagugacuacaucgggg
162	162a	chr5	2634935	2634955	-	UCGAUAAACCUCUGCAUCCAG
162	162b	chr5	7716352	7716372	-	UCGAUAAACCUCUGCAUCCAG
163	163	chr1	24536271	24536294	+	uugaagaggacuuggaacuucgau
164	164a	chr2	19469303	19469323	+	UGGAGAAGCAGGGCACGUGCA
164	164b	chr5	287583	287603	+	UGGAGAAGCAGGGCACGUGCA
164	164c	chr5	9809605	9809625	+	UGGAGAAGCAGGGCACGUGCG
166	165a	chr1	78932	78952	-	UCGGACCAGGCUUCAUCCCCC
166	165b	chr4	368856	368876	-	UCGGACCAGGCUUCAUCCCCC
166	166a	chr2	19124776	19124796	+	UCGGACCAGGCUUCAUUCCCC
166	166b	chr3	22931260	22931280	+	UCGGACCAGGCUUCAUUCCCC
166	166c	chr5	2838736	2838756	+	UCGGACCAGGCUUCAUUCCCC
166	166d	chr5	2840707	2840727	+	ucggaccaggcuucauucccc
166	166e	chr5	16489432	16489452	-	UCGGACCAGGCUUCAUUCCCC
166	166f	chr5	17230285	17230305	+	UCGGACCAGGCUUCAUUCCCC
166	166g	chr5	25218788	25218808	+	UCGGACCAGGCUUCAUUCCCC
167	167a	chr3	8108078	8108098	+	UGAAGCUGCCAGCAUGAUCUA
167	167b	chr3	23415136	23415156	+	UGAAGCUGCCAGCAUGAUCUA
167	167c	chr3	1306759	1306779	-	UUAAGCUGCCAGCAUGAUCUU
167	167d	chr1	11137674	11137694	+	ugaagcugccagcaugaucug
168	168a	chr4	9543150	9543170	+	UCGCUUGGUGCAGGUCGGGAA
168	168b	chr5	18072780	18072800	-	UCGCUUGGUGCAGGUCGGGAA
169	169a	chr3	4359019	4359039	-	CAGCCAAGGAUGACUUGCCGA
169	169b	chr5	8503253	8503273	+	CAGCCAAGGAUGACUUGCCGG
169	169c	chr5	15584776	15584796	-	CAGCCAAGGAUGACUUGCCGG
169	169e	chr1	19629133	19629153	+	GAGCCAAGGAUGACUUGCCGA
169	169f	chr3	4805800	4805820	-	GAGCCAAGGAUGACUUGCCGG
169	169f	chr1	19627101	19627121	-	GAGCCAAGGAUGACUUGCCGA

169	169g	chr4	10447592	10447612	-	GAGCCAAGGAUGACUUGCCGG
169	169h	chr1	6695544	6695564	-	UAGCCAAGGAUGACUUgccug
169	169i	chr3	9873334	9873354	-	UAGCCAAGGAUGACUUgccug
169	169j	chr3	9873711	9873731	-	UAGCCAAGGAUGACUUgccug
169	169k	chr3	9876903	9876923	-	UAGCCAAGGAUGACUUgccug
169	169l	chr3	9877268	9877288	-	UAGCCAAGGAUGACUUgccug
169	169m	chr3	9879546	9879566	-	UAGCCAAGGAUGACUUgccug
169	169n	chr3	9879918	9879938	-	UAGCCAAGGAUGACUUgccug
171	170	chr5	26125500	26125520	-	UGAUUGAGCCGUGUCAAUAUC
171	171a	chr3	19082475	19082495	+	UGAUUGAGCCGCGCCAAUAUC
171	171b	chr1	3961372	3961392	-	CGAUUGAGCCGUGCCAAUAUC
171	171c	chr1	22582009	22582029	-	UGAUUGAGCCGUGCCAAUAUC
172	172a	chr2	11891460	11891480	-	AGAAUCUUGAUGAUGCUGCAU
172	172b	chr5	1188210	1188230	-	AGAAUCUUGAUGAUGCUGCAU
172	172c	chr3	3599799	3599819	-	AGAAUCUUGAUGAUGCUGCAG
172	172d	chr3	20596954	20596974	+	AGAAUCUUGAUGAUGCUGCAG
172	172e	chr5	23702472	23702492	+	gGAAUCUUGAUGAUGCUGCAU
173	173	chr3	8236149	8236170	+	uucgcuugcagagagaaaucac
393	393a	chr2	16600655	16600675	+	UCCAAAGGGAUCGCAUUGAUC
393	393b	chr3	20700620	20700640	+	UCCAAAGGGAUCGCAUUGAUC
394	394a	chr1	7058203	7058223	+	UUGGCAUUCUGUCCACCUCC
394	394b	chr1	28221960	28221980	+	UUGGCAUUCUGUCCACCUCC
395	395a	chr1	9363152	9363172	-	CUGAAGUGUUUGGGGGAACUC
395	395b	chr1	9364486	9364506	+	CUGAAGUGUUUGGGGGGACUC
395	395c	chr1	9367096	9367116	+	CUGAAGUGUUUGGGGGGACUC
395	395d	chr1	25921892	25921912	-	CUGAAGUGUUUGGGGGAACUC
395	395e	chr1	25924689	25924709	-	CUGAAGUGUUUGGGGGAACUC
395	395f	chr1	25925842	25925862	+	CUGAAGUGUUUGGGGGGACUC
396	396a	chr2	4090996	4091016	-	UUCCACAGCUUUCUUGAACUg
396	396b	chr5	13325718	13325738	+	UUCCACAGCUUUCUUGAACUU
397	397a	chr4	2624964	2624984	+	ucauugagugcagcguugaug
397	397b	chr4	6843213	6843233	-	UCAUUGAGUGCAUCGUUGAUG
398	398a	chr2	1040008	1040028	+	UGUGUUCUCAGGUCACCCCUU
398	398b	chr5	4691108	4691128	+	UGUGUUCUCAGGUCACCCCUG
398	398c	chr5	4694779	4694799	+	UGUGUUCUCAGGUCACCCCUG
399	399a	chr1	10227285	10227305	+	UGCCAAAGGAGAUUUGCCCUG
399	399b	chr1	22997300	22997320	-	UGCCAAAGGAGAGUUGCCCUG
399	399c	chr5	24676474	24676494	+	UGCCAAAGGAGAGUUGCCCUG
399	399d	chr2	14391531	14391551	-	UGCCAAAGGAGAUUUGCCCCG
399	399e	chr2	14392125	14392145	+	UGCCAAAGGAGAUUUGCCUCG
399	399f	chr2	14393627	14393647	+	UGCCAAAGGAGAUUUGCCCGG

All *Arabdiopsis* miRNAs identified by cloning, computational prediction, and homology to validated miRNAs a
as are the portions of each locus computationally predicted to have miRNA encoding potential. Nucleotides ir
region are in lowercase. For miRNA families that have not been cloned, the 5' end of the sequence is determi
mobility on a Northern blot. For miRNA loci that are related to a cloned miRNA, the 5' and 3' ends are inferrec
miRNAs have heterogeneity at either the 5' or 3' end, the ends of the sequences listed should be considered
sequence length containing the miRNA, miRNA*, and intervening sequence.

sequence predicted to encode miRNA	hairpin arm	hairpin length	hairpin sequ
AACUGACAGAAGAGAGUGAGCACACAA	5'	82	GCAAAGA
AACUGACAGAAGAGAGUGAGCACAUGC	5'	80	CAGAGAA
AACUGACAGAAGAGAGUGAGCACACAA	5'	83	GCAUAGA
UGACAGAAGAGAGUGAGCACACAAAGGG	5'	86	GAAAAGA
GGUGACAGAAGAGAGUGAGCACACAUGGUGG	5'	96	AAUUAGG
UGGUGACAGAAGAGAGUGAGCACACAUGGUGG	5'	90	GAAUUGA
UUGACAGAAGAAAGAGAGCAC	5'	86	AUGAAAA
GGCGACAGAAGAGAGUGAGCACACAUGGCU	5'	83	AUAACGA
GUUGACAGAAGAUAGAGAGCACA	5'	91	AUUGAUA
UGUUGACAGAAGAUAGAGAGCACA	5'	91	AUUGAUA
UUGUUGACAGAAGAUAGAGAGCAC	5'	165	AUGUUGG
UGACAGAAGAUAGAGAGCAC	5'	172	AGUGUGG
	3'	65	AUCUCUG
	3'	65	AUCUCUG
	3'	182	ACGAUGG
	3'	186	GAAGAAG
CGUUUGGAUUGAAGGGAGCUCCUU	3'	205	GUGUAAC
UUGAUUGGACUGAAGGGAGCUCCC	3'	170	UAUAUGU
CUAUGCUUGGACUGAAGGGAGCUCCC	3'	170	GGUGGAG
	3'	179	UAGAUAU
GCCUGGCUCCCUGUAUGCCAUAU	5'	79	UAUAUAU
GUCGUGCCUGGCUCCCUGUAUGCCACAAG	5'	81	AUAAUAG
CGUUAUGCCUGGCUCCCUGUAUGCCACGAG	5'	81	UUUGUCG
	5'	90	GAUCAAU
UGAAUAGAUCGAUAAACCUCUGCAUCCAGC	3'	85	GUGAGAG
GAAUCGAUCGAUAAACCUCUGCAUCCAGC	3'	88	AGUGAAG
	3'	303	GGUGGAU
CCAUGUUGGAGAAGCAGGGCACGUGCAAAC	5'	78	AUCUCCA
AAGAUGGAGAAGCAGGGCACGUGCA	5'	149	AUGAGCA
CUUGAUGGAGAAGCAGGGCACGUGCGA	5'	82	UAACACU
GUAUCCUCGGACCAGGCUUCAUCCCCC	3'	101	UUUCAGU
UCGGACCAGGCUUCAUCCCCC	3'	136	UUUCUGU
UCGGACCAGGCUUCAUUCCCC	3'	136	UCUCUUU
UCGGACCAGGCUUCAUUCCCC	3'	112	UUUCUUU
UCGGACCAGGCUUCAUUCCCC	3'	108	UUAGUGU
	3'	101	UUAGGGU
UCGGACCAGGCUUCAUUCCCCUCAA	3'	135	UUCCUUU
UCGGACCAGGCUUCAUUCCCCUCAACU	3'	91	CAAAAGU
UCGGACCAGGCUUCAUUCCCCUCAAC	3'	90	UUAGGGU
CUGAUGAAGCUGCCAGCAUGAUCUAAUUA	5'	101	CGGCAUC
AAGUGAAGCUGCCAGCAUGAUCUAUCUUUG	5'	91	AGGGAAC
CAGUUAAGCUGCCAGCAUGAUCUUGUC	5'	140	CCAGUAG
	5'	341	UUUUAGA
CUCGGAUUCGCUUGGUGCAGGUCGGGAACC	5'	104	GGGCUCG
CUCGGAUUCGCUUGGUGCAGGUCGGGAAC	5'	89	GGUCUCG
AGUGUGCAGCCAAGGAUGACUUGCCGAUU	5'	191	AAGUAGU
AUAAUGCAGCCAAGGAUGACUUGCCGGAAC	5'	101	GAGUAUA
GUUCAGCCAAGGAUGACUUGCCGGUA	5'	214	CAUUGUU
GAUUGAGCCAAGGAUGACUUGCCGAU	5'	73	AAAUGAG
UUGAGCCAAGGAUGACUUGCCGGUU	5'	103	GAAUGGA
GAUUGAGCCAAGGAUGACUUGCCGAU	5'	74	GAAUGAG

GGUUGAGCCAAGGAUGACUUGCCGGGUU	5'	81	GAAUGAG
GUGUGGUAGCCAAGGAUGACUU	5'	101	ACUUGUG
AUUUGGUAGCCAAGGAUGACUU	5'	126	UCAUAUU
UUUAGUAGCCAAGGAUGACUU	5'	146	UCAUGUU
AUUUGGUAGCCAAGGAUGACUU	5'	126	CAAUAUU
UUAAUAGCCAAGGAUGACUU	5'	147	UCAUGUU
AUUUGGUAGCCAAGGAUGACUU	5'	128	UCAUAUU
UUUAGUAGCCAAGGAUGACUU	5'	147	UCAUGUU
UGAUUGAGCCGUGUCAAUAUCUC	3'	64	GAGUCCC
UUAUCUGAUUGAGCCGCGCCAAUAUCUCAGU	3'	92	GAGUCCC
UGUUCGAUUGAGCCGUGCCAAUAUCACGCG	3'	80	GGUAACG
UUAUUUGAUUGAGCCGUGCCAAUAUCAC	3'	79	UCAAAUA
AAUGAGAAUCUUGAUGAUGCUGCAUCGGCA	3'	96	UUGUUGG
UAUGAGAAUCUUGAUGAUGCUGCAUC	3'	89	UUGUUUG
UAUGAGAAUCUUGAUGAUGCUGCAGCUGCAA	3'	103	CUGUUCG
GUUUGAGAAUCUUGAUGAUGCUGCAGCGGCAA	3'	93	UUGUUUG
GAAUCUUGAUGAUGCUGCAUC	3'	105	GUAGUCG
	5'	86	AUUAAGU
GAGGAAGGAUCCAAAGGGAUCGCAUUGAUCCUAA	5'	113	AGAGGAA
GAAAGGAUCCAAAGGGAUCGCAUUGAUCCU	5'	140	AGAGAAA
AUCUUUGGCAUUCUGUCCACCUCCUUC	5'	97	CUUACAG
CAGAGAUCUUUGGCAUUCUGUCCACCUCCUCU	5'	101	CUUACAG
CACUGAAGUGUUUGGGGGAACUCCCGGA	3'	73	AUGUCUC
ACUGAAGUGUUUGGGGGGACUCUUG	3'	80	AUGUCCC
ACUGAAGUGUUUGGGGGGACUCUU	3'	80	AUGUCCA
CACUGAAGUGUUUGGGGGAACUCCCGA	3'	80	AUGUCCU
CUACUGAAGUGUUUGGGGGAACUCCC	3'	75	AUGUUUU
ACUGAAGUGUUUGGGGGGACUCUAGGUGACA	3'	92	AUGUCCC
UUCCACAGCUUUCUUGAACU	5'	131	CUCUGUA
CAUACUUUUCCACAGCUUUCUUGAACUUUC	5'	115	GGUCAUA
	5'	87	UGAAUGA
ACAUCAUUGAGUGCAUCGUUGAUGUA	5'	89	UGAAUGA
UUGUGUUCUCAGGUCACCCCUUUGAA	3'	85	UGAAAUU
CAUGUGUUCUCAGGUCACCCCUGCUG	3'	96	UGGAUCU
AUGUGUUCUCAGGUCACCCCUGCUG	3'	95	UGGAUCU
AUCUGCCAAAGGAGAUUUGCCCUGU	3'	103	AAAUGCA
ACCUGCCAAAGGAGAGUUGCCCUGAAACUGGU	3'	115	UCACUAG
CUUGCCAAAGGAGAGUUGCCCUGUCA	3'	94	GGAGCAG
CUCUGCCAAAGGAGAUUUGCCCCGCAAUUCA	3'	80	GGUUGGA
UCCUCUGCCAAAGGAGAUUUGCCUCGC	3'	89	GAAAGCA
UGAGCUCUCUGCCAAAGGAGAUUUGCCCGGUAA	3'	98	AUAUGCA

are listed . The sequences of the mature miRNAs are shown,
the mature miRNAs outside of the computationally predicted
ined by PCR of the miRNA and the length is inferred from
d from the ends of the cloned homolog. Because many plant
to be approximations. Hairpin length is defined as the minimal

uence
AACugacagaagagagugagcacaCAAAGGCAAUUUGCAUAUCAUUGCACUUGCUUCUCUUGCGUGCUCAC
AACugacagaagagagugagcacaUGCAGGCACUGUUAUGUGUCUAUAACUUUGCGUGUGCGUGCUCACCU
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GUGuugacagaagauagagagcacAGAUGAUGAGAUACAAUUCGGAGCAUGUUCUUUGCAUCUUACUCCUU
GUGuugacagaagauagagagcacAGAUGAUAAGAUACAAUUCCUCGCAGCUUCUUUGCAUCUUACUCCUU
UUGuugacagaagauagagagcacUAAGGAUGACAUGCAAGUACAUACAUAUAUAUCAUCACACCGCAUGUC
UUGcugacagaagauagagagcacUAAGGAUGCUAUGCAAAACAGACACAGAUAUGUGUUUCUAAUUGUAU
UGCUUCUUUGUCUACAAUUUUGGAAAAAGUGAUGACGCCAUUGCUCUUucccaaauguagacaaagcaAUA
UGCUUCUUUGUCUACACUUUUGGAAAAGGUGAUGAUAUCAUUGCUUUUccccaaauguagacaaagcaAUA
AAGUAGAGCUCCUUAAAGUUCAAACAUGAGUUGAGCAGGGUAAAGAAAAGCUGCUAAGCUAUGGAUC
AGGAAGAGCUCCUUGAAGUUCAAUGGAGGGUUUAGCAGGGUGAAGUAAAGCUGCUAAGCUAUGGAU
AGAAGGAGCUCCCUUCCUCCAAAACGAAGAGGACAAGAUUUGAGGAACUAAAAUGCAGAAUCUAAGA
AGAGAGAGCUUCCUUGAGUCCAUUCACAGGUCGUGAUAUGAUUCAAUUAGCUUCCGACUCAUUCAU
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UCGugccuggcucccuguaugccaCAAGAAAACAUCGAUUUAGUUUCAAAAUCGAUCACUAGUGGCGUACAG
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GCAuugaaagugacuacaucggggUUCCGAUUUUUUUUGUUCUUCAUAUGAUGAAGCGGAAACAGUAAUCA
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UGAGGGGAAUGUUGUCUGGCACGAGGCCCUUAACUUAGAUCUAUAUUUGAUUAUAUAUAUAUGUCU
UCAGGUGAAUGAUGCCUGGCUCGAGACCAUUCAAUCUCAUGAUCUCAUGAUUAUAACGAUGAUGAUC
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AAGugaagcugccagcaugaucuaUCUUUGGUUAAGAGAUGAAUGUGGAAACAUAUUGCUUAAACCCAAGCU
CAGuuaagcugccagcaugaucuuGUCUUCCUCUCUUAGGUUUCAUAUAUAGUUAAUAAAUAUUUUAUAUAU
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AUUgagccaaggaugacuugccggUUUAAACCCAACCGGUUUAUGACCAUUGAUUUGGUCUCAUUCACAAUC
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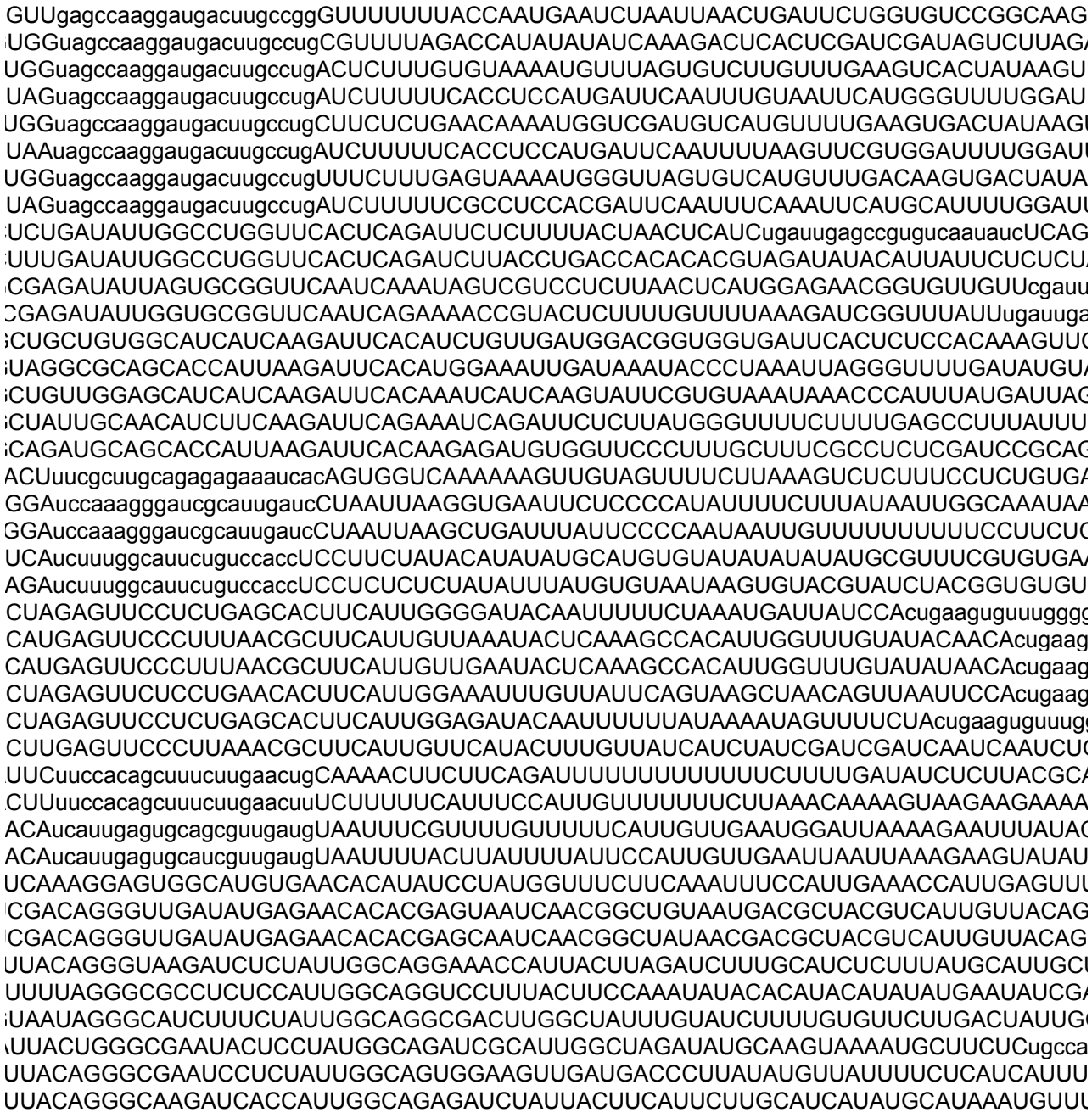

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JCUCUUUCUGUCAGUUGCCUAUC
ACUGCUCUAUCUGUCAGAUUCCGGCU
GCUCACUCUCUUUUUGUCAUAACUUCUCC
AGCUAUGUGUGCUUACUCUCUCUCUGUCACCCCUUCUCU
GUGUGCUCACUCUCUAUCCGUCACCCCCUUCUC
CUCUCUUUCCUUCUGCCACCAUCAUUGCG
JACUCUCUUCUUGUCUCCUGCUCUCU
IUGUGCUCUCUAGCCUUCUGUCAUCACCUUUUAU
UGUGCUCUCUAGCCUUCUGUCAUCACCCGUUAU
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ACCCUGGUUUAGUCACUUUCACUGCAUUAAUC
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GGAAUUUUGUGAUAUAGAUGUGUGUGUGUGUUGAGUGUGAUGAUAUGGAUGAGUUAGUUCUUCAUG
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