

Additional file 1 Non redundant set of cloned sRNA sequences after filtering.

Clone ID	Sequence 5'→3'	Length (nt)	Frequency	Hit in the genomic trace files and/or EST database
1-1	AGGCGACGGGGAUUCA	16	1	
1-46	GGCUACUUCGGCGAAA	16	1	
1-7	GAGCUUUCUUCGGUCC	16	1	
2-8	UGCGGAAGGAUCAUUG	16	1	
3-15	AUCCGAUGAGGGUGUA	16	1	
4-75	GUGACGCGCAUGAAUG	16	1	
2-67	AGACCCAGUACUACAGC	17	1	
3-13	AGCGUCGAGUGCAGAUC	17	1	
3-21	CUGCUGAGCACGCCAAA	17	1	
3-61	CCAUAUUCGUUCUUUAAA	17	1	
4-53	GAGGUCUGGGGGGUGAG	17	1	
5-40	AGGCUAGCCAGGCGGUG	17	1	
1-15	UCAUGCCCGCUCGUACAA	18	1	
1-16	CUCUCAGUGGAAGCACCA	18	1	
1-74	CUGCUAUACAGCUCCAC	18	1	
2-2	GCCCGCGCAGGUUCGAAA	18	1	
2-61	GCCCCCAUCGUCUAGUGA	18	1	
2-66	CCUGCGGAAGGAUCAUUG	18	1	
3-1	GCGGGGAUAGCUCAGUUG	18	2	
3-46	CAACAGCUAUUCCAUCUA	18	1	
4-55	ACUAUGCCUGAGCAGGGA	18	1	
5-11	GCAUGAACGUUUCAAAC	18	1	
5-54	GUGACGCGCAUGAAUGGA	18	1	
2-23	AUAGACAAAAGUGGUUAU	19	1	
2-70	GUUGGAAGCCUUCGUGGGA	19	2	yes
3-72	UUGGUACACUUGACGCAA	19	1	
4-14	CCCGCCCACCCUGGAAUCG	19	1	
4-31	GGCGGACGUGGCCAAGUGG	19	1	
4-64	GUUGCUUGGUUGAACCCCG	19	1	
5-41	AGUUGGAUCUUGGGUAAAA	19	1	
1-22	AUUGGGACUUGUCUGGGAC	20	1	yes
1-31	CGGAGGUCUGCCCGAGCUGC	20	1	yes
1-39	CGUUUCACGUCGGGUUCACC	20	1	yes
1-41	GCCGGGAUAGCUCAGUUGGA	20	1	
1-63	UUGCUGUGCACUACUAGUA	20	1	yes
2-51	GAGCUUUCUUCGGUCCAAUA	20	1	yes
2-88	UGACAGAAGAGAGUGAGCAC	20	1	yes
2-90	GGCAUUCUGCCAGAGCGUC	20	1	yes
2-93	GCGGGGAUAGCUCAGUAAAA	20	1	
2-95	UAGGGACGGUUGGGGGCAA	20	1	

3-29	ACCAAUACCAGGUCCAUAUAG	20	1	yes
3-42	AGGAGGGCGUGGGGGUCGUG	20	1	yes
3-51	CAUCAUGUUAGUCAGCCUGG	20	1	yes
3-6	UUGGAAGAGCAGAUCGAAUU	20	1	
3-91	GCUGUGUUCUUGUACCUGGG	20	1	yes
3-96	UACCUGGUUGAUCCUGCCAG	20	1	yes
4-28	CCUGCGGAAGGAUCAUUGAA	20	1	yes
4-33	CUGAAGACCGCCUUUACAAA	20	1	
4-65	GCGCUUUUAGUUCAGUCUGG	20	1	yes
4-68	GUCGAUAUGGCCGAGAAAAA	20	1	
5-21	UCUUGUCAAUGUUUAGGGGC	20	1	yes
5-28	AACGUGAUAGGACUCUGAAA	20	1	
5-33	UUGAGGUGUUUCUACAGGCU	20	1	yes
5-51	CGAACAGCCGGUUUUAAGU	20	1	yes
5-70	UGCCGAAGCUGUGGGAUGUC	20	1	yes
1-36	GUUGGGCCUAGGGGUCUGUGA	21	1	yes
1-50	UGGCUGAGUCGAAGGUUGUGC	21	7	yes
1-67	UCCAGGCCCGGACAACGUAA	21	1	
2-28	CGCUGUCCAUAUCUGAGCAUUG	21	1	yes
2-31	UGACAACGAGAGAGAGCACGC	21	9	yes
2-33	UCGAGUCCGCUUGUCUCCACC	21	1	yes
2-38	ACAGACCGAGAGAUUUGAACA	21	1	yes
2-44	CAAGUCCAGGAUAGCCCACCA	21	1	yes
2-86	CCUUAGAGUCGUAGGCCUCUG	21	1	yes
2-92	ACUAAGGCAUGCCAAACAUUA	21	1	yes
3-14	GCUAGGCAGUGCACAGCGAUA	21	4	yes
3-49	CCCUCGUCGGCCCUUGAAAAA	21	1	
3-62	AACUGAGAUACAUCGCAAUCG	21	1	yes
3-71	CCUUAGGCUCGGAGGUCUGCA	21	1	
3-79	UCAUCCAGGGAGCCAGACAGA	21	1	
4-12	GGUAAAGUGGCGGCUAGGUUA	21	1	yes
4-19	CCAUGGCCGACUCUGAGCAGC	21	1	yes
4-27	CUGCGGAAGGAUCAUUGAAAA	21	1	yes
4-29	GGAGAGAUGGCCGAGUGGCUU	21	1	yes
4-34	CGUGGGACAGCAUAGAAUGCG	21	1	yes
4-45	CGGAGGUCUGCCCGAGCUGCU	21	1	yes
4-72	UUGAGCCGCGCCAAUAUCACA	21	1	yes
4-9	GGUGGCUGUAGUUUAGAAAAA	21	1	
5-27	UCCUGCCAGAGCGUCAUCAA	21	1	
5-42	UCCAUUUAGCAGCUUCACGAC	21	1	
5-50	GCUACAGCAGCUCCACCAAAA	21	1	
1-68	AGACACGACGACGGCCCAUAUC	22	1	
1-81	UGGCUGAGUCGAAGGUUGUGAA	22	1	
2-1	GUAGCUUAGCGAGGUGUUGGUA	22	1	yes

2-15	UGACAACGAGAGAGAGUACGCU	22	1	
2-4	UCGAGUCCGCUUGUCUCCACCA	22	2	yes
2-84	CAACUGCAGGUGCAGGACCAUG	22	1	
2-85	CAUCGCCGCAAUACCUIAAAGUU	22	1	yes
2-96	CCCGAAGUCGUUACCCUAACAA	22	1	yes
3-22	CUGAUCAUGCCCGGUCGUACAA	22	1	yes
3-36	GCUACUUCGGCGGGACAAGAGA	22	1	yes
3-40	UGACAGAAGAGAGUGAGCACAU	22	1	
3-52	GUGGGACGUGUGGACGAAAAAA	22	1	
3-60	UUCGUGCCAAGCUGUGUGCAAC	22	5	yes
3-78	UGAAUGCAACACUCCUACGCAA	22	1	yes
4-43	GCAACCAGACUCUCUCACAAAA	22	1	
4-58	CUCACCGUCCCAACGAUUUGUA	22	1	yes
4-67	AUCGUGCCAAGCUUUGUGCUUU	22	1	yes
4-70	CUAAUGAAACUGUUAUACACC	22	1	yes
5-23	GCAGACACGCGCGGCCCAUAUC	22	1	yes
5-48	GAACGAGACCUCAGCCUGAAAA	22	1	
5-90	GGCGGACGUGGCCAAGUGGAAA	22	1	
3-20	GUUCGAGUCCGCUUGUCUCCACC	23	4	yes
3-5	UGAUCAAGUGGAAACUCAGCAAA	23	1	yes
4-16	AACACCAACGGCGAAAGCACUAA	23	1	yes
4-66	ACGAAGGUCUGCAUCAUAGCCAA	23	1	yes
5-3	UUUUCGGUGAAAAGUGACUCUGC	23	1	yes
5-5	GUUCAAGUCCUACCUGGGGAGCC	23	2	
5-58	UUCGUUUCUCGCAGUGCCCCCA	23	1	
5-63	AUGGUUCAAGAAGAGACACGUGG	23	1	yes
1-55	GUGGGUGACUGCCCCCUGCCUCA	24	1	yes
2-68	CAAAAGAAUAGCUGCCCAACACAA	24	1	
3-44	UCGGAAGCCUUUGUGGGAGAGGAA	24	1	
3-54	CUUGGACUGAAGGGAGCUUUUUUU	24	1	
4-1	CUUGAUACUCUAUUGACCAUUAAC	24	1	
5-19	GAUUCGAAUUCCCCUGGGGGGACC	24	1	
5-86	GGUUCAAGUGCAGGAUAGCCCACC	24	1	
1-21	GAUUCGAAUUCCCCUGGGGGCUACC	25	1	
1-29	GACCGUGCAGCUGGAACCUUGUACA	25	1	yes
1-51	GAUUCGAAUUCCCCUGGGGGUUAACC	25	1	
1-57	GUUCAAGUGCACCUAGGGGAGACCA	25	1	
2-19	GGUUCGAGUCCAGGAUAGCCCACCA	25	1	
2-42	GUCAAUUUGGCCGAGUGGUUAAGGC	25	1	yes
2-45	UUCGGAAUUUCAGUGUUCGGACAGG	25	1	yes
2-82	GGUUCAAGUCCAGGGUAGCCCACCA	25	1	
4-23	UCAUAGCCGCACCAAUGAAUAAGAA	25	1	yes
4-26	GCGUUUGUAGUCCAACGGUUAAGAU	25	1	yes
4-60	CAUUAAGCCUUGCGAGCAGUACUA	25	1	yes

5-30	UGCUGCACCAGCUGCUGAGGAAAAG	25	1	yes
1-54	GUUCAAGUCCAGGUUAUACGUCCCACC	26	1	
2-24	UGUACACACCGCCCCGUCAAAAAAAAA	26	1	
2-7	AGGGAGGGAUGGUUAUGCAAAAAAAAA	26	1	
3-39	AAAUUCAAAUUCCCCCUGGGGGUUAAC	26	1	
3-59	UCGAAUGGGGACCUAUCGCAGAAAAA	26	1	yes
3-90	UGAGUUCAGCUCUCAGUGGAAGCACC	26	1	
4-40	CGGCGGCGACCGCAGCUAACAGGCUA	26	1	yes
4-57	CUUAUUUUUUUUCUAAGUGUCAUUCUA	26	1	
5-57	UGUUUCGGUGCGGGCUGCGAAAAAAA	26	1	
1-65	CAUGACUUUUGGAAUAUUGCCAUUCAG	27	1	yes
2-57	AAGAUAGAGGAGUUCAAGAAAAAAAAA	27	1	
3-47	UGCAGGCAGUGCAGCCCCAAAAAAAAA	27	1	
3-87	AAGCGGGAGGUCCUGAGUUCUCUCUCA	27	1	
4-44	UCGAAUUCCCCUGGGGGUACCAAAAAA	27	1	
4-79	CUUAUUUUUUUUCUAAGUGUCAUUCUAU	27	1	
5-12	CUUAUUUUUUUUCUAAGUGUCAUUCUAA	27	1	
5-4	GAUUACUGAUGAUGCCCGGUCGUACAA	27	1	yes
5-52	GAUUACGAAUUAACCCUGGGGGUACC	27	1	
5-72	UAAGAUUGGUGCCCCAGUAUGGAACAA	27	1	
2-14	AUCCUAACCAGCACCGAGAGAUUUGAAC	28	1	
1-23	GAUUCGAAUUACCCACUGGGGGUACCAAAA	30	1	
5-44	GAUUACGAAUUCCCCUGGGGGUACCAAGAA	30	1	
1-73	ACCUUGGCUGUCACUCAAUCCGUUGUAGUCUAG	34	1	