

Name	Sense	Sequence (5' -> 3')	IGR size	PCR size
5S	forward reverse	CGACCTGGTGGTTCTGG AGACCTGGCAGCGACCTACT	120	120
5Sint	forward reverse	CGTTCCCATTCGGAACAC GACCTACTCTCCCGCGTCTT	120	76
sra01	forward reverse	TATCCAGTCCGCGTCAATCT TGATAAGGCGGGACAAAAAC	400	293
sra02	forward reverse	CAAAGGCTCCTGTCAGTTCC ACTTTCAGCCGAATCGTCAA	306	161
sra03	forward reverse	GGTCGGCCTATCCTTGAAAT CTCTTTGAAAGCGGGACAAA	332	160
sra04	forward reverse	GTCATCCGCAGCACCTTT GCCACCTGTCCATCCTTCT	320	175
sra05 (4.5S)	forward reverse	AGGCTTGGCTTGCATTTG CTGCTTCCTTCCGGACCT	161	101
sra05Bis (4.5S)	forward reverse	GCATTTGCTGCGGATATTG CGACAGGACGGAGAAGGTG	161	148
sra06	forward reverse	GTATTGTAAAGGGCGCCACA GGGAGGCTTCAAAGAAAACC	227	199
sra07	forward reverse	GGAGGGGCTACTTCTGCC GATGAGGCCCTCCCTAA	162	138
sra08	forward reverse	CTTGCCTTACCGTCACCG CACCGCGTCTTCTTCGAC	214	144
sra09	forward reverse	GGGCGGCTTTCCTTTTT TCCAGCGTTAAGAACGGC	180	133
sra10A	forward reverse	GATTGACCTTGCCACGCT AAAGCCCAAAGTCACCCC	448	388
sra10B	forward reverse	CGAGACGATAAAACCGGG TGGCGGCCTCATCTTTA	417	365
sra11	forward reverse	ATTACTGCCAGCCAACATC AAGAAATGCCTTCGCTTCA	179	160
sra12A	forward reverse	GCTGGCACTAGCAGTCCTTC TCGTCGCGAGACACTTTATG	689	178
sra12BFAR	forward reverse	TAGTGTGGCGGTTACTTTG TCGTCGCGAGACACTTTATG	689	550
sra13	forward reverse	CGAAACGACCGGTTTGAC CCAACTCCGGGAATTGA	137	130
sra14A	forward reverse	CGGAGCAGGTGATAAAGCTC GGGTGTACTIONGGCGTCAGTT	773	230
sra14B	forward reverse	CAAAGACACGCATTCCATCA CATCCATTGCAAACGGTTA	773	567
sra15	forward reverse	AGCTTAGCGGGTGCATCG CACGCGAATGAGGCTGT	210	150
sra16	forward reverse	GAATCGCAGACGACACAAGA CCGGAATCGCTAAAATTCAA	566	216
sra17A	forward reverse	GTTACTCCGCGTTGTTTGCT TTTCGTTGCAGATCAGTTGC	686	211
sra17BFAR	forward reverse	TTTCGTTGCAGATCAGTTGC GGCCTTCCGGGAGTATTG	686	385
sra17AFBR	forward	CGAGTATCAGGACGCGAATC	686	456

	reverse	GTTACTCCGCGTTGTTTGCT		
sra18	forward	CTCTCGGCCAAAGAACCA	247	190
	reverse	CGGTAATCTTGCGTGGGA		
sra19	forward	CCTTCTGCTTCTGGGTTGAG	449	213
	reverse	TCGGGGTCTTTCACTTGTCT		
sra20	forward	CATTAACATTTGCCGGGTG	139	99
	reverse	TGCAGCGGATCTGAGACA		
sra21	forward	AATCACGGCATTGTGATCG	234	154
	reverse	GAAAGCATTCCGGACTTCAA		
sra22A	forward	TCGATCAGACCCTTGTGTTG	497	247
	reverse	GGCACCTTGAGTGTCCCTCAT		
sra22B	forward	TTTCTGGAATCGGATGTCGT	497	249
	reverse	TTTCTGCTTCAAGGCTGGTT		
sra23	forward	CCAGTGAGGTTTCGCCAT	179	101
	reverse	AGAGCTTGACCTCCGCCT		
sra24	forward	TCCCTGCCGATCTAAGAATG	446	214
	reverse	AATGCCATTCACCTCCTCAGC		
sra25	forward	CGTCAACGAACAGAAAGGAAG	277	154
	reverse	ATGAGCTTTGGCCTCACAAT		
sra26	forward	AACGTTCGATCCCATCTTCAG	222	212
	reverse	TCAACGCATCAATCCATCTC		
sra27	forward	TTGAAATCCGGACGTGAAAT	444	181
	reverse	CGCTCGTCTTATGGATGTGA		
sra28A	forward	CGAACCCAAAACATTTTCGTC	907	254
	reverse	TAATAGGTGGGCTCGCTGGT		
sra28B	forward	CGATCGTTCCTCCAACAACCT	907	298
	reverse	GCCGCCATTATTGTGTTTTT		
sra29	forward	TGAGAGCCGGCAAGAAAG	283	198
	reverse	GACACCAATCCGACGAGG		
sra30	forward	GACGCGCGGGAACAGTAG	164	150
	reverse	ATGATGCGCCGGTTTTGT		
sra31	forward	ATGCCGCCAAAAGTGT	96	89
	reverse	CTGAGGCCTAGGACATAAAGC		
sra32A	forward	GAAGTCTTCGCCGTAATGT	570	195
	reverse	ATTTTCGGCTCACAAAACAGG		
sra32B	forward	TTGGTCTTCCTGCCTGTTTT	570	249
	reverse	AGCGTTCATAGCCGCTTC		
sra33	forward	GCCGGGGTAAGCACATC	346	245
	reverse	GGTTGCAGCACGAGGAAT		
sra34	forward	ACGCTTTTTGAAGCGGTG	287	197
	reverse	GTGAAACCTTTGCGCGTT		
sra35	forward	GCGTAAGCCAATAGGAATGG	221	207
	reverse	TCTGCCTTTCACTGCTCCTT		
sra36	forward	CGCCTCTTTTGACCGTT	205	172
	reverse	CGACCCCGTCAATCAAT		
sra37	forward	CGATTCAGCAACACATTTCC	230	154
	reverse	TGACGGCACACAACTCACT		
sra38A	forward	GTTTGAGCCGGGATTACAGA	1338	217
	reverse	GCCTCAACGCCATCATCTAT		
sra38D	forward	AATAATGGGCAAGTGGATCG	1338	449

	reverse	GCTTGAGGCTCCTTAGCAGA		
sra39A	forward	GACAAATTCGAGCCCCCT	448	409
	reverse	TATGGGCGAAGGACAGGA		
sra39B	forward	TATCTTCTCCCCGACGGC	366	310
	reverse	CATAGCGGCGCAAGAAAT		
sra40A	forward	ATACGGGAGCTGCACTTGAT	908	161
	reverse	CGATTGCCCGCATAGAGTAT		
sra40B	forward	TTTGTGTACCGTCGGTTGAA	908	371
	reverse	GACAGCCCTCTTGCGATG		
sra41	forward	AGGAAGCGGGCCATAAAC	592	396
	reverse	ATGATTGCCGATAGCCCA		
sra42	forward	AATGGCAGAGGCCTACCC	327	277
	reverse	TCTCCAAGAGCGAGGTG		
sra43AFBR	forward	TACATCTTTCGCCGATTTC	765	550
	reverse	CGTTACCTGAGTGAAATATACC		
sra43BFAR	forward	GGAGTTGAGCGATGAACCAG	765	445
	reverse	CCAGCCAAGAGCCTTATGAC		
sra44	forward	CGGCAGCTTGTC AATACG	94	81
	reverse	CTTGGCAAATGGGGTGAA		
sra45	forward	GTAAACCGGCAAAGAAGCAG	274	164
	reverse	ACCACCCAATCGCAAAATTA		
sra46	forward	CGCCTTCCCGAATAGCTT	237	157
	reverse	ATATGCCGCCGTCAGGT		
sra47AFBR	forward	GAAGAATGCTCCGGAATCAA	647	450
	reverse	CCTGGGTCACAGTAGCGAAT		
sra47BFAR	forward	CTTCGCCTGCCTCTTCGT	647	307
	reverse	GCGCTAGAGAGTCCTTCGTG		
sra48	forward	GAATCCACAGGGGCGAC	411	339
	reverse	CTCTGGCTGGAACGCCT		
sra49 (tmRNA)	forward	[39]		206
	reverse	[39]		206
sra50A	forward	CCGCACATACTCGCAC	377	350
	reverse	GGCAAAGCACGTTTCCTG		
sra50B	forward	TCTGTATGGCTCCGCCTC	377	396
	reverse	CGCCGGTCGTTTAATGAG		
sra51A	forward	TGAATACGCGAGTCAAACG	529	250
	reverse	ATTGAGGAAAGGGTCCTGGT		
sra51B	forward	TTGAGCCGGCAATATATCCT	529	281
	reverse	TTGCGTCTTCTCATTGCTCA		
sra52	forward	TGATCTCCAACAACCCGAAT	273	208
	reverse	TATCGCGTGACAAAACCAA		
sra53A	forward	AGAAATGAACCACGCCTCAC	881	334
	reverse	ATGGCTGACAGAGGACCAAC		
sra53B	forward	CCTCTGTCAGCCATTGGAGT	881	324
	reverse	TTTCCTTATTGCGCGTTTTG		
sra54	forward	GCATCCCGCTCTAACTCCTT	410	238
	reverse	ACTCGTAAATGCGCGAAAGT		
sra55	forward	CGCACGGTCGTGAGTAAGAT	224	159
	reverse	GAGTGCACCTTATCGGCTTC		
sra56	forward	GTCCGGCCAGGGACAGT	224	153

	reverse	TGCGATTTTCGCAGAAATTAT		
sra57	forward	CAAGCAACTGAAGCCGAGAC	292	170
	reverse	CCTCAACACCTTCAGCCAAT		
sra58	forward	CTCGCTCTGACCAAGCATTC	234	151
	reverse	GGTGCTTCCCTTCTTGACAC		
sra59	forward	TTCCGGCAATGAAGGTGT	526	364
	reverse	GGTAGACGGGTCTCCGGT		
sra60A	forward	CCCTTGGTTTTTACGGGTTT	944	341
	reverse	AACGGAGTGGCGAATACTTG		
sra60B	forward	CACGACTCCGATCAACATTC	944	277
	reverse	TCCGATCTTCTACGCGAAAC		
sra61	forward	TTTGGCTTATCCCATTGAGC	359	207
	reverse	CATATTGCTCCAGCCACTCA		
sra62A	forward	CGCGCTCGAACTAAGATTG	721	337
	reverse	ACGTGAAAGAGCCCAAAAAG		
sra62B	forward	ACGTAAGGCGTCAGCTTTGT	721	321
	reverse	AAGCCAAACCACAGTCCATC		
sra63A	forward	AATGCTCTTCACTGCCATCC	2018	350
	reverse	GCTTTCACTGCCATCTGCAC		
sra63B	forward	GCCAAATCGTTTCGGTAACAT	2018	350
	reverse	GACGTCACCAGCCTGTTCTC		
sra63C	forward	CGATGCAAGGCTGAAGAAAC	2018	321
	reverse	ACCGGTATCCTGCGATATGA		
sra63D	forward	GAGATCGAAGGCACTCATCC	2018	329
	reverse	GACGTCCCTCAAGGCCAGA		
sra64	forward	CTTGGTTTTGGACCAAGCAT	592	349
	reverse	GCGTGGAAGTCAGCCACTAT		
sra65A	forward	GCTTCACGTGTCACGATTTC	964	340
	reverse	GATGTAGTCCGCTTGCCTTG		
sra65B	forward	TCCGTAAACTGGCAGCAGTA	964	350
	reverse	CCAGAGGGCAGGTGAGAATA		
sra66	forward	TGCACGAAGCCAATGTAGAC	728	236
	reverse	CTCCGAGTGTGCAATCTTCA		
sra67	forward	GCACCGCAAGGTTCAAAA	70	54
	reverse	GTTGGGTATCGCCCCATC		
sra67Bis	forward	CCGGTAGCGCTCTAAAACAG	135	129
	reverse	GGTTCTTCCCTCCAGACATGC		