Appendix A Supplementary data of primers

Primer Name	ID	Foword primers(5’-3’)	Tm(℃)	Reverse primers(5’-3’)	Tm(℃)	Pr S
ES1	GD116879	GGTGGTCAAATTGCACGGTA	61.7	CCTTCACCGTAGCATATGTCATTC	61.9	
ES2	GD120609	CACGAGGGGCATCTTTAGTTC	61.0	AATGACTGCTTTCATGGTTTGAA	60.9	
ES3	GD053433	GATGCTGAAATCGCGTGTATTG	62.8	CCCGCGCCTTTAACATAGAAAT	63.4	
ES4	GD108881	GCACGAGGTATGATTGAACTTCTT	60.9	TTTATTTGAATCCCTTTTGGGG	61.2	
ES5	GD130947	GCACGAGGGAGAGAGAGAGAGA	62.6	AAAAGAACGGGTGGAGAGGG	62.6	
ES6	GD089751	GCACGAGGGAGAGAGAGAGAGA	62.6	CGCAAGAGAGCCAAAGGAGTAG	62.7	
ES7	GD076037	AAGGAAAATGTGCTTCTCCCTTCT	62.8	CAAATGCCGATTTAGACAAACCA	63.1	
ES8	GD080319	ACGGGCCCTTCAATGTCTAGTA	62.1	GGAGCGAAAAACTCTTTTGAAACT	61.4	
ES9	GD053569	CTGAGGCACTGAGTCCATTTTG	62.1	TCGTTCGAAAATAGAGACTTCCAA	61.4	
ES10	GD072399	TCGGACCCTTCTCCATCACTT	63.2	TGGGAATTGGTGTTACATGAAGG	63.0	
ES11	GD076983	TCCTTCCACTAAGAACCTCTCTGG	62.3	CCCTCAAGAATTCCCTCCATCT	62.8	
ES12	GD133175	AGAAGGGCAGAGAGAGAGACCA	62.0	GCGCAAATATATGTGTTTGTGAGA	61.2	
ES13	GD130266	CATTCAAATCGCACAAAATTGG	62.4	TTGGATGGGAAGTGACTGGATT	62.9	
ES14	GD128393	GCACGAGGGAAAATCATATTACAA	61.3	TTGACATCGTGCATCACAAAAC	61.9	
ES15	BM067867	AAAGCATATCAGCAGAAGCCAT	60.3	TGTCTTAAGAGCACAAATGATGGA	61.0	
ES16	BM067382	CCGCTAAAGCCTTTTTGTGAAA	62.6	AACGGTTAACCAGCCAAACTTAGA	62.3	
ES17	GD061499	TGCAATTTTCGATGATTTGTTTG	62.0	ACGAGATGGAGCTGTCGTAAGG	62.9	
ES18	GD104142	ACGAGATGGAGCTGTCGTAAGG	62.9	TGCAATTTTCGATGATTTGTTTG	62.0	
ES19	BM064026	TGAAGCGATGTGTTTTTATTGAGA	61.0	GAGAAGCTGGGGTACTAGAAGTGA	60.3	
ES20	GD071818	CATATTTCTTCGTACACGCAAAGG	62.0	TCCAGTGTCGCCGACTACATAA	62.8	
ES21	BM062907	CAAATGAACATGCAAGGAGCTG	62.9	CACACGTTCGCGTTTTGTTAAT	62.1	
ES22	GD123510	TTCACAGAAATGATACAACCCGA	61.6	CTTGGGAAGATTTTGAGCTCCT	61.1	
ES23	GD128734	GGTGGGAAAGGAGAGTGATGAA	62.6	TCCCCCTAACTGACGTAGCAAA	63.0	

ES24	GD072875	ATTCCGAATGGGTTTGGAAAAA	63.6	ACAAGCATCACCACGGATTTCT	63.0
ES25	GD095208	GGGGTCGCTCTCTCTCTATATCTC	61.0	TCTCTTTCTCTTTCTTTCCCTTCC	60.7
ES26	GD088905	TTCAAAACAATTTGCATGGTGTG	62.9	TGTGCGTCTAATGCACAAATCA	62.5
ES27	GD072113	CAATACCCACATGCTTCTTCAGT	60.4	AAAATAAAAAGGGGTTGATTGAGC	60.8
ES28	GD069136	TTTCCCTTTTACGGCTGATGTG	63.3	TAGATGAAGAAACGGGGTGGAG	62.5
ES29	GD116227	GCACGAGGCTCTTACGCTATCA	63.9	AATCCCTCAAGAATTCCCTCCA	63.2
ES30	GD117017	GCGGATGGTCGGTTTATTTTA	61.0	TTCATTTGATCGGTAAAACTGTTG	60.3
ES31	GD082709	ACGAGGGTTAACTCAAAGGTTGC	62.8	AGCAGAAGCCATAATTGGCTGA	63.3
ES32	GD113317	ACAAAACCGGAAAACGATTTGA	62.7	GCCTTTTTGATTGCGCTGATAA	63.5
ES33	GD087785	TTTATTGTCCAGCCTTCCCAAA	62.8	GGAAGCAACATGAGAGCCTTTT	61.9
ES34	GD134263	GCACGAGGTTTTAGATGAAATGGT	62.6	GATGATCCATAGCCTCTACTCCCA	62.8
ES35	GD101345	TCGCAAAATGATTTAGGTGTGG	62.1	TTTTACCCCGCCAGATTTGTTA	62.6
ES36	GD099413	GCACGAGGTTTTGAAGCAACAT	63.6	AACCCTGTGCAACACGAAAACT	63.1
ES37	GD120275	CATCTTACTTCCCCAGATCCCA	62.4	GGCCATTACGCGTTAATAATTCC	62.7
ES38	GD054130	GGCACGGAGAGAGAGAGAGAGA	62.6	GAAAACGGAGACCAGCTTGAGA	63.0
ES39	GD078806	CTTTTTAACGCTTTTCGCGTTT	61.8	TTCTTGTATGCATTTTTACTGCCA	60.8
ES40	GD089042	CGAGGAATACCCATCTACGCAC	62.9	TGCGTCTAATGCACAAATCACA	62.5
ES41	GD093127	CGAGGAGAGAATGTGTAGTTTTGG	61.4	GGTCATTTCTATCCGACCGATT	61.4
ES42	GD092254	GCACGAGGGAGAGAGAGAGAGA	62.6	GCGAGAGAGCTCGAGAAAAGC	63.2
ES43	GD068844	TGGCTCGATTTTCATTTCACCT	63.0	TTTCCTTGAAGTGGCTAAGGGA	62.2
ES44	GD092899	GCACGAGGGAGAGAGAGAGAGA	62.6	GAGGGGTGTGTATGTGAAAACAAA	62.2
ES45	GD097605	GCACGAGGGAGAGAGAGAGAGA	62.6	CACACACGCACACAGAGAGAGA	62.7
ES46	GD130644	GCACGAGGGAGAGAGAGAGAGA	62.6	AGAAAGAAGGAGGGTCACCTCG	63.2
ES47	GD079563	GGTCTGCTTGACCTCTCCAATG	63.4	CGGGAACAGAAATGGTGTCAAC	63.8
ES48	GD068665	TTGGCAGCTACAATAGCACAAGAA	63.2	TGGGCAAAGGCCTCTAGCTTAT	63.4
ES49	GD070542	CGGTAAGTGAGTCTCTGCACCA	62.7	ACCATCACCAGCATTCATAGGG	63.2

ES50	CA514549	GACGTCGTTTCAAGTCCCAATC	63.0	GGTTAGGGGTTTTGGTCAGCTC	63.2
ES51	GD055940	TTCACTACCCTAATTCACCATCCC	62.4	TTTGGTGGGAATTCTTCAATGG	63.1
ES52	GD060568	CAGCAAAAGCAAATCAAGTGGA	62.5	ATCACCACAAGCTCCACACAGA	63.1
ES53	EB084990	ACTAGGCTTTCAACCCCATCGT	63.2	TGACAACGAAAGGAGCATGTGT	62.9
ES54	GD094178	GCACGAGGGAGAGAGAGAGAGA	62.6	AAAAAGGGGAAGAGGGAGAGAGA	62.9
ES55	GD110266	CCCACCAGCTTCTCGTTATCAG	63.2	GACTGAAGAGGATGGTGCCACT	62.9
ES56	GD095271	GGGCAGTTTCTCCTCTTGGG	63.3	AGCAAGGCTCTTCAGCACACTT	62.8
ES57	GD133560	CGAGGCTCCAACAAAATCCTC	63.2	TGAGACCAATTATGGAGAACCACA	62.8
ES58	GD121301	ATGGATGAAGCGGAGGATGTAA	62.9	CAGGAGTAACAGCAGGGAAAACA	62.7
ES59	GD092092	TTCAGTTGAATTCTCCGCCTCT	62.5	GGCTAATTGTACTTCCATCCTCCA	62.6
ES60	GD108161	GCGAGCAGCTGTAAAAAGAGGA	63.2	GATGGTGGTGGTGGTATAGAAGGT	62.4
ES61	GD100614	CACTTTCCCACTTCCCCTTTTC	63.2	AATCCCACAACCCCACAAATTA	62.4
ES62	GD070087	TGGATGCCATTGAAGAAGAAGA	62.0	TGGCAAGAGAGTGAGAACGAAA	62.3
ES63	GD070619	CTTGCATTTTATTTGGCCACTG	61.7	TTCTCATAAACCAAACTTGTTGGC	61.5
ES64	GD119015	TTCGGCTATTTGAACAGAAGCA	62.1	TGATCCCTTCTTGTTTGATTTTTG	61.5
ES65	CA518410	CTTGATCCCAAAACCAAAACCA	63.1	AATTAAGCTGGCCACACAGCAC	63.6
ES66	GD096617	TACCAAGTATCCCCCTTCCCTC	62.5	TGCCCCAAAAAGAACAAGAATG	63.3
ES67	GD128705	AGCAGCAACTCTAACCACCACC	62.8	GTTGGGTTCGGATCTGGTGA	63.2
ES68	GD054950	TCCCCGCTAGCTATATATTGGATG	62.5	GCTGTTGCTACTCGCAATGATG	63.1
ES69	CA523694	ATGCATTGGAATGGACTTTGGA	63.7	CTTCCACATTACCAGGACCAGC	63.0
ES70	GD117752	GGGATCACTGAGTACCACTGCC	63.1	AGTCGAAAACCGATTTGTGCAT	62.9
ES71	GD060445	TTCCGAGTTGGGAGTCTCAGTC	63.0	TGTGGCAGTTTATTCATGGTGG	62.9
ES72	BM059634	GCACGGGAGAGAGAGATATGAGA	62.1	CCAGAGGCAACAAAGAGTGTCA	62.7
ES73	GD096841	GGCATTCCAGTAGGCAATAAGATG	63.0	GCCACCATAGCGCATTTAGACT	62.6
ES74	GD070184	CTTTTCGTTGTCGTTGTTGCAG	63.0	AGCTCCAGATGGTGAACTTGCT	62.6
ES75	BM067882	CCACCCTGAGAAAAATCCCTTC	63.2	GCTCAGCCCTTGAGAATTTATGAC	62.5

ES76	GD125560	CGAGGCCTCTCTCTAACTCTCTCT	61.1	ATTTTCCGGAGGAGGAGGAC	61.7
ES77	GD081353	CATATACCCACCTGGTAAAAATCG	60.7	AAAAACTTCCCCAACCAAAGAC	60.6
ES78	GD055838	CACGGCTCTCTCTCTCTCTCTC	60.0	TCTCTCTCACACACACACACACTC	60.5
ES79	GD130763	GCTGCACTTAATTCAACAATGCC	63.0	GCACGAGGGTCTCTCTCTCTCTC	63.3
ES80	CA516698	AGAAGAAGAATCCGGCGAAGAG	63.3	AAGAAGAATCTTGAGGTGGTGGC	63.0
ES81	CA524696	GAGAGTTGGATCCCTCTTCTTCG	62.8	GGGTTGTACGATTTGGGATGAA	63.0
ES82	GD071825	TCACCTACTCCTGTTACCCCCA	62.9	TGCTTCTTTCCAGAACCAGGAG	63.0
ES83	GD120872	GCACGAGGAAATGGAGAAAATG	63.0	AAGACTCTGGTGAGAAATGGCG	62.9
ES84	GD063634	TCCGTGAAAAATCTCAAATGGC	63.3	TCCTTTGGCAGCTACAATAGCAC	62.8
ES85	GD117052	TTGCCTCAGGGACAGATCTAGG	62.9	CCTCTGTGGGAGTACACTGGGT	62.7
ES86	GD066353	TTCCTTCTGCATCAATAACCCC	62.4	TGGGATCTGAAACAACACAACTTT	62.0
ES87	BM066619	CACCGGAAAATTACTCAGCCAC	62.9	GCAAAGCTAATGGCCTCTGATG	63.3
ES88	GD070759	CGAGGCCTCCACAATGTTTTAG	63.0	TGGTGAAGAGTGAGCAACAACAA	63.1
ES89	GD102494	GGTTCAACCACCTACCCCTGTT	63.4	CTCCTTAGCTTTTTGCCTTTGGA	63.0
ES90	GD102474	CCTCAACTACCCCTACCCCATC	63.0	GCTGCTTCTCCGGCTAATTGTA	62.8
ES91	GD093444	TATACTATACAGGCACGCCGCA	62.7	CAGCGAATTCTTCGACCATTCT	62.8
ES92	GD112751	CGAGGAAAAATCTCAAATGGCTT	62.8	TCCTTTGGCAGCTACAATAGCAC	62.8
ES93	GD058849	GGAAAATCAACCAAGATTGCCA	63.2	TGGCTCTGGTGGCTTTTGATTA	64.0
ES94	GD121044	AAGCGTCCTGTTGATTCTGACG	63.8	ACCACGAGAACCACCACCTCT	63.2
ES95	GD101906	GCTCCTCTCTCTCTCTCTCTCGC	62.8	ATCGTGGACTCCGAGCATTTT	63.1
ES96	GD125484	TAAATGGGTCGAAGAACATGGC	63.2	TCATCATGTTTACATACGCGTCG	63.0
ES97	CA516572	CCAGTTGTACAAAAGGAAGCCG	63.0	CTGTAGCCGGTGGCTCTACTGT	62.9
ES98	GD117393	TGGCGCGTTGAATTATAGAGAA	61.9	AGAAGTCGATGGAGTGCTGCTT	62.7
ES99	GD114065	CCACCCCCTCCTCAATATTTTC	62.8	ACCAGTATTATTTGGTGGCGGA	62.6
ES100	CO909413	AACACTGCTCCGCCTTATTCC	62.7	TCACCATGAACATCATCACCCT	62.5
ES101	GD069627	TCGTCAAACATATCATCGGGTG	62.9	AATCCACTTCCACAACAACCTTTT	62.1

ES102	GD111124	TGGAGGAAGATCAAGATCAAGAAG	61.1	TCAATGTGTGATTTTGTCTGAAGC	61.4
ES103	GD054155	GCACGAGAGAGAGAGAGAGAGAGA	61.1	GTTCCTCGTCCGACATGTTTT	61.3
ES104	CA515656	CAAATGGAGGGTCCTTAGTTTTC	60.2	TGAACAAAGAAAGATGAAGAAGCA	60.4
ES105	GD080546	CGCATCTACATCAAGAATCAACCA	63.4	GATGTAGAACAAGGAAGCAGGGG	63.3
ES106	GD086903	AGGATGACCAATGTTTTGCCTC	62.5	TACGGTTCCTCATCCCAGAAGA	63.1
ES107	GD064848	ACGAGGGGTCACTCCTTTTCTC	63.1	ACCACTCACAATGAGCTGTGGA	63.1
ES108	GD105227	CACGAGGAGACAGCTCCAGG	63.5	AGTATGCGCATCTCCTTCTTGG	62.8
ES109	CA524051	TTTTCAAATGGCTTCTGTTGAGG	62.6	TGAATAGTCCGAACAACGGAAAA	62.8
ES110	GD084122	TACGGTTCCTCATCCCAGAAGA	63.1	AGGATGACCAATGTTTTGCCTC	62.5
ES111	GD075425	TTTACAAAACCTCGGAGGAGCA	63.1	GCAGCAGCAAAGCATATGGTAA	62.5
ES112	GD115843	CCCGCCATTGAAAGTTATCATC	62.7	TGGACCAATGAATTTAGCAAAGG	62.3
ES113	GD055816	TCGCATCTACATCAAGAATCAACC	62.5	GTGTAGAACAAGGAAGCAGGGG	62.2
ES114	GD067226	ATTCCCTGCAAATGGGAGTTTT	63.0	CTGACACAGCTAAATTTGGTCCAG	62.2
ES115	GD110370	GGAGCCGAAATAAACGTCATCA	63.4	GGAATATCCCTCGATTCCTTCG	63.1
ES116	CO910028	TAGGCAATAGCTCACATGCCCT	63.2	CCAACCCAAATATTCGTTGAACA	62.9
ES117	GD070041	GCAGCTTCTCGTTATCAGCACA	62.9	GACTGAAGAGGATGGTGCCACT	62.9
ES118	GD078403	GCACGAGGAAGACTTGACAGCTA	63.2	TTGGTGTGCATAGGTGCAGATT	62.7
ES119	GD079474	AGATTTTCATCAAAACTGCGGC	62.6	ACAAAGCATGAAATCACCCTCC	62.5
ES120	GD134715	GCGGCCTTTTGATTCATACAAT	62.3	CGTTTTACTGCCCTATCTGCTTG	62.2
ES121	CO909126	AAGCGTACCACGCATTGAAATAA	62.8	GGTGGGGCCTACCTAATGTGTA	62.2
ES122	GD063980	AAAGCAGAAGCCTACATTACATGG	60.9	AACTGGTGGGTTGTCTTGTTCA	61.8
ES123	GD066539	GGGGGATTGACTCTCGGTAAAG	63.2	TAAAGTCTTTTCCCCCGAGCTG	63.8
ES124	CA522816	TCTTCGTGGCTCTAGGGATCAG	63.0	ACCAGGGAACCAATTAACGAGG	63.4
ES125	BM068195	TAAAGTCTTTTCCCCCGAGCTG	63.8	GGGGGATTGACTCTCGGTAAAG	63.2
ES126	GD119556	CGATTTTGCGATCTTCAGCACT	63.8	CACAAATCCCAGTTCAAACAAACA	63.1
ES127	GD133231	GCAATTCTCCGCTCTTGTAAGC	62.5	ACGAAGCATTGGTAATGATGGG	63.1

ES128	GD070189	AAGGACCATCACCAGCATTCAT	62.9	TCAATAGAGCAAACACGCTCCA	63.1
ES129	GD099721	GCACGAGGATAGAGTCAACAGC	61.3	TCGATGAAAAGTCCTTCAGAAACA	62.3
ES130	GD123264	TCCTCGACTCAAAACAGATGGA	62.1	GCCTTTTACCTGACTTCATGGC	62.2
ES131	GD064745	TTTCCAATTGCTCAAGATTCAGTT	61.3	ACATTTTCTCAGCTTGGCATGA	62.0
ES132	GD098891	TCATTTACAAAGCACAATGACGAA	61.7	ACCAGAAGTCTTGCAGGTTTCC	61.9
ES133	GD107978	TTTTGGGGTTCAATAAAGCTGTG	62.3	TTCAACAAGATCATCAATTCACCA	61.6
ES134	GD127960	TGGTTTGCTTGGTGGTGAAG	62.1	TCCAAGAAATACCACACCCAAA	61.5
ES135	GD080007	GCACGAGGGTTATCAGCACACT	63.7	GACTGAAGAGGATGGTGCCACT	62.9
ES136	GD107543	AGCCTCCCTTTTGTTCATTCGT	63.3	CTTTGGCTCGAGCTTTCACTTC	62.7
ES137	GD121462	CTTCTCACTAACCAAAACTGGACG	61.4	CTGACCCTGATGAAGAAGGTCC	62.3
ES138	GD110124	CGGATCAAGATCTGGAAATGG	61.7	CAAACATCCATTTACCAAAAACCA	61.9
ES139	CA514770	AATCTTCGAGTTCCGGGAAGAG	63.1	TGTGTACGAACTTCAGGAGCGA	63.2
ES140	CA525246	TCGTCGGAGAGAGGAGAGAGAA	63.0	GACTGTAGCTGCTGATGACACCAT	62.9
ES141	CO776559	GCGGGTCGTAGTCAAGAACAAG	63.3	CACTCAATGGACGCATAGTTCG	62.8
ES142	CO912315	TAGGCAATAGCTCACATGCCCT	63.2	CCAAATATGTCGTTGAACAAGCC	62.7
ES143	GD096675	GCACGAGGGAGAGAGAGAGAGA	62.6	CATGCAGATGCAGAAGGAGAAA	62.7
ES144	GD130763	TCCAGAAATGAAGCTATATCCCGA	63.1	TTTGTTTCTCGTGCAGAATTGG	62.4
ES145	GD113627	CTTTTCGTCCTCTTGCCTCATC	62.5	CTCCTGCAACACCGTTCACTAT	61.5
ES146	GD122450	CTCCACCATCACCTTCTTCTTC	60.1	CTTCAGCACTGTGAACCTCAAA	60.5
ES147	GD107836	CTATTATTGGGGGCATGTCTCA	61.0	ACAGTCATATGGTATCAACCCCA	60.4
ES148	GD052819	GGCCTCTGTATAACAATTCAACGG	62.9	CATCGATGGAGAATGGAGTGCT	63.7
ES149	GD100635	TCATGCACTTTCTGTGAGGATGA	63.0	AGGCGATAGAGGCAAAATTGGT	63.2
ES150	BM066440	CCATCTTCACCAATGTGACCAA	63.0	CTGTTCCGATAACCGAAAGCTG	63.1
ES151	CA524230	AGGCGATAGAGGCAAAATTGGT	63.2	TCATGCACTTTCTGTGAGGATGA	63.0
ES152	GD059115	CCACATGCCTCTCTAATAGGGGT	62.7	CCACCAAGAATAACGTTTGAACC	61.8
ES153	GD085299	GATGACCAATGTTTTGCCTCAA	62.1	GGTTCCTCATCCCAGAAGAATC	61.2

ES154	GD111046	TTCATAGAAGAAAAGCATGGACAA	60.1	CTCCATTTTCCATTTTCAACCTT	60.5
ES155	EB084431	GCATGCACGATTCCCTATTCTC	63.0	ATCGCAACCCCGACATTTTTA	63.6
ES156	GD073405	AGGGTGAGATGGAGTCATCAGG	62.7	AAGAACAGAAACCCAATCCGCT	63.3
ES157	GD094066	GGTATGGAGGATTACCTCGCAA	62.4	TCCATCCATAGTAACTGAATGGGG	63.2
ES158	CO910439	TAGGCAATAGCTCACATGCCCT	63.2	CCAAATATTCGTTGAACAAGCCA	63.1
ES159	EL813007	GCAGCAGCAAAGCATATGGTAA	62.5	TTTACAAAACCTCGGAGGAGCA	63.1
ES160	CA523065	CCAGTTGTACAAAAGGAAGCCG	63.0	TAGCCGCTGGCTCTACTGTTTC	63.1
ES161	GD126953	TTTACAAAACCTCGGAGGAGCA	63.1	TGGTAACGAAATCCATATCCGC	63.0
ES162	BM063920	ATGCCAGGTAATAGGGTGGCTT	63.0	TCACTAATTCCTCGGATTTTGCAT	63.0
ES163	GD132071	GCACGAGGCTCTCTCTCTCTCT	61.9	CACATCCACACAAACCCAAAAA	62.8
ES164	CO911508	TAGGCAATAGCTCACATGCCCT	63.2	CCCAATATTCGTTGAACAAGCC	62.7
ES165	GD134570	AATGGAAATGAAATGTGGTAGGGA	62.7	TGCATGAGCTTCGCTCCTTAAT	63.4
ES166	CA524075	GCCAAATGGAGGGTCCTTAGTT	62.7	TGAAGAAGCACCCGTAGAAGGA	63.3
ES167	GD114375	CGCGATTCGATTGCTAAATCTC	63.2	CTAATTTCCCAGTTGCGTCTGC	63.2
ES168	FE193349	ACGACAGCCTCGCTCAAGTAAC	63.1	AAACTGTGTTTGCTCCTGCTCC	62.9
ES169	CA518916	TCATTTCTGAATTTTCACTACGCC	61.6	CCATTGTCTTCAATCCCGAACT	62.4
ES170	GD093321	ACATGATCAAGATCACGCTGGA	62.9	TTTCCATCCAACTTTCTCAGCA	62.0
ES171	EB084628	GGCGTTTCACTCGAACAACACT	63.7	AACGGTGGGATGAATGGTTACA	63.5
ES172	CO906480	CTATCTTCACCATCTGCGACGA	62.6	CTTTTTGAAACCGATCGGAGG	63.0
ES173	GD068486	CCCACACGTATATCTCAACCATCA	63.0	CGTTCATAGAGCCCACAAATCC	62.9
ES174	GD131502	TGGAGAAAATGCTACTGATGCG	62.5	AAGACTCTGGTGAGAAATGGCG	62.9
ES175	GD088168	CTCGACGATCAGAGGCAGATTT	63.0	CGGCACGAGGGAGAGAACTA	62.8
ES176	CA524477	ACTGGAAGACCAAGAGAGGTGG	62.0	CTGATACGCCACTTGAACCAGA	62.5
ES177	GD055720	AGCAGCCGTTGTATCATGGAAT	62.9	CCTCTTGTGGAACAAGTGACCA	62.4
ES178	GD093998	TGCAATTTTGTGGAGAGCTTTG	62.5	ACAGTGGCATCTGCATTTTTGT	61.8
ES179	GD128647	CCTTTTGGAAGACTCTTACCCATT	61.0	AATCCCAACATATTCACAGAATGC	61.3

ES180	GD099517	CGCCTATCAACAATGGCAAATAC	62.7	CTCGACGATCAGAGGCAGATTT	63.0
ES181	GD079479	CACGAGGCTGGTATAGGTGGAG	63.1	CTTTTCGTTGTCGTTGTTGCAG	63.0
ES182	GD127828	ACAAAGCATGAAATCACCCTCC	62.5	AGATTTTCATCAGAACTGCGGC	62.8
ES183	BM063625	CTCGACGATCAGAGGCAGATTT	63.0	CGCCTATCAACAATGGCAAATAC	62.7
ES184	GD062273	GGATGCCGACAACAAAATTGA	63.0	GAACACATCAAGATTTTCCCCACT	62.6
ES185	GD076607	GTGGACTTCGGAACAAGCTGAT	62.8	CAGCATCTCAGGTTCTACCGTTT	61.9
ES186	GD129429	TTGGGCCGATGTAAGCAGACTA	64.0	CGCAAGGGAAAAGAAAACTCGT	63.8
ES187	BM068544	TGGGCCTTTCCTATTTTGGTTT	62.9	GCTAACAGCGAATAAAAGGGGG	63.1
ES188	GD053834	TATTCCGCACGGAGAAAGTTCA	64.0	GCTAACAGCCTGCCGAATAATG	63.1
ES189	BM062480	TTTGGTGGTTGTTTTCCCAATC	63.0	ACACCTGGTTTGGATACATGGG	63.0
ES190	CA513842	CATAATCGGAAAATGACGTGGG	63.4	CACAAAACTTTGCACCAGCAAG	63.0
ES191	GD079897	GCAAACACTTGGAATTATGCAGAT	61.5	ACACGGGTCATGCTCCTCTAGT	62.4
ES192	GD120757	GGGCAAATTGAGTCTGCCTAAC	62.2	GTTTTGGGGGCATATACTGCAT	62.1
ES193	GD080045	CACGAGGTGAGAGCTTCTGCTT	63.4	GAACCCACATCATCATCCGTTC	63.7
ES194	GD102258	TTCCCATAGTTGAAGAGCCTGC	62.8	CGGCCAAATTATTTTTCCCAGT	63.2
ES195	GD131799	CAATTGATGCTGCTAGGCTTGA	62.6	GCGTAGGTTTTCTACGCGGAC	63.2
ES196	DY635274	AGTCCCAACTAAACAATCCACCC	62.5	CAACGACATCGTATCGGTTCAA	63.1
ES197	CA513929	CGAATCAACACCAGCACCAGTA	63.3	ACAGCAGGTTCTTCTGTAGCCG	63.1
ES198	CA522848	CAGCCCCAGTTGTAGAAAAGGA	62.7	CTCTACTGTTTCTGGCAGCCGT	63.1
ES199	EC911948	AACATCCTTACCACAAGTCCGATT	62.1	GCAGTTTCTCCTCTTTTGGGGT	63.0
ES200	GD089757	AGCGTCTTCCCTGACGATACAC	62.8	CGGTTTGACATCTAACTGCACG	62.8
ES201	GD100216	CGGCCAAATTATTTTTCCCAGT	63.2	TTCCCATAGTTGAAGAGCCTGC	62.8
ES202	GD063306	ATTCTGTACACTGCGCCAAAGG	63.6	CCTGAATTAACAAAGGCATGTGG	62.7
ES203	GD065124	GCACGAGGCTTCTATTATCTGAGC	62.8	ATGATTGAACTCCTTTGGCAGC	62.7
ES204	GD095551	GCGTAGGTTTTCTACGCGGAC	63.2	CAATTGATGCTGCTAGGCTTGA	62.6
ES205	GD076944	GGTCACAATTTGAGTGGGACAA	62.1	TGATTTCTCAAATTCCATGCACA	62.6

ES206	GD088061	GGAAAAAGAATTCCCGGAGAGA	62.8	CCGCGGGTCAATAAAAATAAAA	62.0
ES207	GD077736	CAAGGTTCAAGATTGGAGAGCAA	62.8	TGGTTTTTCCTGCTCTTTCACA	62.0
ES208	BM060557	TTTACGTTGAAAAGAGGAAAAAGG	60.0	TGAGAAATCGACAAACTCCCAT	60.9
ES209	GD068812	CCTTTGGCAGCTACAATAGCAC	61.1	TCAAATGGCTTCTCTTGTTCTTCT	60.7
ES210	GD132325	GCACGAGGATTTCGCATTTTT	63.5	CGTTTCCGTTCTGTGGTTCTTC	63.1
ES211	GD080045	CACGAGGTGAGAGCTTCTGCTT	63.4	AACCCACATCATCATCCGTTCT	62.8
ES212	GD128442	CCCTTCCCTTTTCTCCCTTCTT	63.1	CCAGAAACAGCCATTGATGATG	62.7
ES213	GD112171	GCAGGAGCACTTGAAAAACTCAA	62.9	TGAGTCCATCAGCTTCAGTTGG	62.7
ES214	GD053802	GCACGGAGAGAGAGAGAGAGAGA	61.9	GAGCGAACCTAGCGTGCTCTAT	62.2
ES215	GD115942	CCCTCTTTCTTCAATGGCTTCA	62.8	GTGCGAAATGTGACCGGATACT	63.4
ES216	GD075468	TGTGAGCATTGGTATTGAGGGA	62.7	GCAAATGTCCCCATCACTTCAT	63.2
ES217	GD121875	TCATATATGCAACCGCCAAGC	63.1	CAAGGAGCAAAACGAAGGAAGA	62.9
ES218	GD118633	ACACACTGGAGGCATTGTTGAA	62.8	ACGATGGAGATGAAGAAGACGG	62.8
ES219	GD125480	TTTTTGGTCATTGTTCACCTTCAA	62.7	TGCCATGCATGCAAAAATAAAT	62.3
ES220	BM063990	TGAACAGGATCCAAATAGAAAGGA	61.1	TAACGATCCCTGAAAAAGGCTC	61.7
ES221	BM059678	CTGCTCAAGCTTCCCTCAAGAA	63.2	TGGGATTGATGATGGGAGTAGG	63.2
ES222	GD060928	CTCCCTTCATTGCCATTAGTCG	63.0	AGATGGAGATGCTGAGGACCAG	63.0
ES223	GD100965	TTCCACACAATGGAACATCCC	62.9	TGATCGATCGTTTCATTTTCGAT	62.8
ES224	GD119278	CCCATCATCGCTAAACGGTAAA	63.1	TCCAGGTCCAATAGAAGCAAGC	62.8
ES225	GD111935	CCAAAAGATGCCCAATACCAAA	63.0	TGCAAATAGCCAAGGCTTAGGA	63.1
ES226	GD117434	AGGTTTTTCCCGATTGTTCTGA	62.0	AAAGGTGCCACATGTCCTTACC	62.4
ES227	BM062560	GGATATCCCATGTTATTTGCCG	62.4	AGGTGGTGGAGGACATGGTG	63.2
ES228	BM063444	TGGCAATTAAGCCTCTTCAAGTTT	62.5	GTGCAGCATCAATGCCAATTT	63.2
ES229	GD134675	AGCCATGTCATTCACCTCCATT	62.9	ATTCCGACTCCGCCTCTAGTTC	63.1
ES230	DV643160	AGCGATTTTGAAGGAGGAGGAG	63.2	CGGTTCTTACACACATTGCAGC	62.9
ES231	GD055426	TAGCACATTTCCACGTTCCCTT	62.9	GCAGGCTTCTCTTCAACCTGAG	62.8

ES232	CO910971	TTGCTTCCACAAACCCTATAATGA	61.8	TGTGGAAAATGGGACCATACAA	62.2
ES233	CO776234	TGTGGAAAATGGGACCATACAA	62.2	TTGCTTCCACAAACCCTATAATGA	61.8
ES234	GD111974	ACCATCAATTTTGACCCTCATCA	62.7	AGTGGCTGTGAGGAGTGGGAT	63.4
ES235	GD101584	ACAGCAGGTTCTTCTGTAGCCG	63.1	CGAATCAACACCAGCACCAGTA	63.3
ES236	GD061744	ACGAGGGAAAGCATCAGAATCA	63.2	GAAACATGGTTCAATGCCAACA	62.9
ES237	GD135286	CTACCACTACCACCCAACCACC	62.7	GCCAATCTGGACTTACCCATGA	63.3
ES238	GD094823	GGGCTTTCCACAACACTACACC	62.9	CGTCAGCAGATCTTTCGCTTTT	63.1
ES239	GD093760	AGGTGCCCAAAACAAAAGTTCA	62.9	TTGCATGAATGAAGCTCCAAAA	62.8
ES240	GD112449	ACGCACACACAGTGAGTTTGAA	61.8	TCCCTCTCTCGCTGTCTCTCTC	62.6
ES241	CO906654	CGGAAGTTGGTGAGGACCTTAG	62.2	TCAATTTTTCAAAAGATGGTGGTC	61.4
ES242	GD097448	ACGTTCTTCATGCAGTGCTCCT	63.5	CGTAATGCTCCTTGAAACAGGC	63.2
ES243	GD094462	CCTCCACTACCTGTAGCCTCACC	63.4	CCACTGGTGGTAGAAGTGGAGG	63.1
ES244	GD074031	CAAAATACAACCCCCATACCCC	63.3	TGGAGTTGAAAACGGTGGAGAT	63.0
ES245	CA847557	CCAGTTCAACTTCCGACCTGTT	62.7	TCCTGAAAATCAGCAGCAAAGTC	62.9
ES246	BM063090	CCTTGCCTATGTTGAAGCTTTTG	62.2	AGATATTCGGCCTCAACAGCAG	62.8
ES247	GD085183	CTTTGACACTGCCAATCTTCCA	62.5	TGCATGCTGGATCCAAATTAAG	62.2
ES248	GD068494	CATTGATTCGATTGATCGGTTG	62.5	TGAATCACATCATATGCACACCTT	61.5
ES249	CO910027	CACATGCCCTATAAATACCACCA	60.8	CAAATATTCGTTGAACAAGCCATT	61.4
ES250	GD053948	GAGAGAGCGAGAGAGAGAGAGAGA	60.3	GTAGAATGGGGGTACCCGTAGA	61.3
ES251	BM063971	TTCGTCATCCATTTTTCTCAACAA	62.8	ATATTAAGGCTAGCCCTGCCGA	63.2
ES252	CO910026	CAAGAAGTCAGTGCCGAAGACA	62.8	CCCTCAGATAGCGAAATGATGTG	63.0
ES253	CA520406	CGAAAATGAAAATGGTAAAGCGA	62.3	GGCGATGGTGAGAGTCTCTGTT	63.0
ES254	GD075589	TTTATGGCCTCATCTTCTCCCA	63.0	AGATGACGAAGAGCAACAAGGG	62.9
ES255	GD079657	CCCTCAGATAGCGAAATGATGTG	63.0	CAAGAAGTCAGTGCCGAAGACA	62.8
ES256	GD110337	GCTTGCAAAGTGCATTCATGTC	63.0	AATAATTTGGAAAGAACGTGCAGC	62.7
ES257	CO911135	CTATCTTCACCATCTGCGACGA	62.6	GATCGGAGGAAGAGGAAGAACA	62.0

ES258	CA522143	TCGATTCTTTCACTCTCCCAAA	61.1	AACTTCCCCAACCAAAGACAAA	61.9
ES259	GD129571	GCTGAAAGTACCAGATTCCATTCC	62.3	CTATGGGTGAGTTTTGCATTCG	61.7
ES260	CA524381	TGTCAACAAGCAGTTGGCTCAT	63.1	GGTGAAGGCTTGAGGAATAGGG	63.3
ES261	CA524647	TTGTAGAAAAGGAAGCCGAGGTC	63.0	CTGTACTGTTTCTGCAGCCGTG	63.2
ES262	GD071776	GCACGAGGTATTGCTACACTGC	62.1	AGAAAGCCGCCGTTTAATCTTC	62.9
ES263	GD099145	TAAGGGTGGTGAAAAGGGGATT	62.9	AATTCGCCCAAGATGAAAAACA	62.8
ES264	GD128266	CGAGGCCTCTCTTTAACTCTCTCT	61.0	GGGGAATAGGGTGAGGGAAG	61.9
ES265	GD134193	GCACCGAAGTTTTCCCTTCATA	62.5	TTTCTGTTCTGTTGGCAAATTCA	61.9
ES266	CO907045	TCCCAGTGCCTTTTTCGTATTC	62.5	GCACGACCATTTGTCGATTACA	63.1
ES267	GD108981	GGCCCATTGTTCTGATCTCAAT	62.4	AAAGGTGCCACATGTCCTTACC	62.4
ES268	GD111026	TTTCGTGTATGTGTCATCCATTG	60.7	AATTATGGATATGGATATGGGCAG	60.2
ES269	GD053120	TGGAACTTGAGCTGCTTTCACA	63.3	CAACTTATTTCCATGAAGGCGG	62.8
ES270	GD100215	TGGTGACTATGGAATGGTGGTG	62.9	TCACAACCCATCATTTCTCTGTG	62.2
ES271	GD127105	TTCCTTAGCTGCACATCTGGTG	62.6	CGAAACTAGTGAGCGATCGGTAT	61.8
ES272	GD126095	CACGAGGCCTTATCAGCACACT	63.8	CGACAGCCTTCACCATTTTTGT	63.5
ES273	GD119474	TTTGGTTTGCGTGAGTCTTGAA	62.9	TTTGTTGGTTGATGTTCCTCCC	63.2
ES274	GD066318	CAGCATGAGCTCTCTCGTTCAA	63.1	TGCGCATGTTCATCCTTAGAGA	63.1
ES275	GD081301	GGAAGGGCTGTGCGTTATTGTA	63.4	ACAGACCAAAGGGGATAACGGT	63.0
ES276	GD073812	GCACGAGGAATAGTCATAAACCA	60.4	CTTGAGCAATAATTGGACCAGC	61.0
ES277	GD073314	CACACTTCTCCCCCTTTACCCT	62.8	CCCATATTGCCAACGAGATACG	63.6
ES278	GD105955	GGGCTTCTCGTTATCAGCACAC	63.3	CGACAGCCTTCACCATTTTTGT	63.5
ES279	GD093879	CAGTGTAGCTCTTGTGGGTGGA	62.6	CAACTGTTCGGACACAGCAAAA	63.4
ES280	GD056998	TGCGTAGCTAGTTTGCCGGTAT	63.1	GAATTAAAGGCGGCTATAGATGGG	63.1
ES281	GD095867	TATCCCAACCCATCATTTCCCT	63.6	CACATCTAACATGGTCGGGTCA	63.0
ES282	GD079399	GCACGAGGCTCAACTTCACTTC	63.6	CTCCATCTCCTCTACCACCCCT	62.9
ES283	GD130184	GCACGAGGGAGAGAGAGAGAGA	62.6	AAGTGTGAGTGTGAGTGTGTGTGG	62.5

ES284	GD104862	CCCTATTTAGGCCTTGAGTTTGG	62.2	GCTCTGTCATCTCCTGCTCCAT	63.1
ES285	GD127041	GCACGAGGCAACAAAAGAGAAT	62.8	CGCTGAGCGAGACAGAGAGAG	63.1
ES286	GD055528	TTCAACCGACTGACGGAGATTT	63.1	CACCAATAGAGAATTCACCAAGCA	62.5
ES287	GD094425	TTTACAAAACCTCGGAGGAGCA	63.1	TATCAAGTCTCCAGCAGCAGCA	63.4
ES288	GD116751	CGATAATTTTGACGGAATTGGC	62.6	CGGATCAAAGCTTACCATCCAA	63.3
ES289	GD123815	CATAACCTGTCTGGTCGGGAAC	62.9	CATTGACGGATTCGGAGGTAAA	63.2
ES290	GD061076	CACGAGGGTTTTTCCATTTTCC	63.8	CGTTTCCGTTCTGTGGTTCTTC	63.1
ES291	GD096388	CCACCCATCCTTGGAAACAA	63.0	CTTGACTGGTCTGAATGCTCCA	62.7
ES292	GD080083	TCCCATTTCGCAAGAAAGAAAA	63.0	TCCGATACAGCTGCAGTAGAAAAA	62.4
ES293	GD135382	GCACGAGGCAAAAGGTGTTTAT	62.5	ACATTAAGGTTCGGTGGAGGTG	62.4
ES294	GD060955	GCACGAGGTTCACATTTCATTTC	62.9	AGCAAATGTTGAGCTTGAACCC	62.7
ES295	GD095674	CAAAAGTTGATAACCACTTGCTGA	60.5	TGGTAGCAAATTTGTGATGGGT	61.5
ES296	CA516371	AGGCTTTGAACAGCAGCTATGG	62.9	GTCACATTTGGTGGAACTTCGC	63.9
ES297	GD074431	TCAGCGATTAAGAATGCGATTG	62.4	CCAAATTGCCCTCTCTCTTCCT	63.1
ES298	GD131824	TGTTGGTTCATCATCATCGTCA	62.3	GGATCGCCAAATTATTGCTCAG	62.9
ES299	GD056515	GCACGGCTCTCTCTACTCGC	62.7	TGCAGAGTAACGTCGCTACGAG	62.9
ES300	GD063946	AATGTTCTCAGTGATACGGGCG	63.5	AGCTGTTGGAAACGATACAGGG	62.6
ES301	GD090986	TTTGGTGGCAACTGTTACATGG	62.9	CAGCCCCTCAGATCCTGGTA	62.5
ES302	GD090239	AGATTCGCCTTCACTTACCGTC	61.8	TGAAGGAATAAGATGTGACACGG	61.3
ES303	GD130120	CCCTCAGATAGCGAAATGATGTG	63.0	GCCGAAGACATTAAGGCACAGA	63.7
ES304	CO907044	AAAGTAGACAGCTCCAGGGAGGA	62.8	CGACTGAAAAGCTTGCCAAAAG	63.4
ES305	CA847465	GGCACGAGGAAAGAGAGAGACA	63.2	ATCAACGGATTCAGTCTTCCCA	63.0
ES306	GD070887	CGACCTGTAAAGAAAGCTGTGTCC	63.5	GCAGAAGCAAACTTGTCAAAGGA	62.9
ES307	GD105404	TTCTGTTTCGAAATCACCACCC	63.3	GATTTGGACAATGACCTGGACC	62.8
ES308	CA522652	CCTCCCTCTTCTTTTTCTTCCAA	62.1	AAATTTGCAATTAAATCCTCGGC	62.5
ES309	CA522666	CATTTTTCAAATGGCTTCTGTTG	60.8	AAGTGTCAACAATGCTGCTAGTGA	61.2

ES310	GD104941	ACCAAAGCACTCGATCCTCCTT	63.5	CGTGAAGTGCTCCTTCTTTGGT	62.9
ES311	GD074296	CAAACCTTGCAAGCTACAGGCT	63.0	GTGAGTATGGTCCCATGGAAATG	62.6
ES312	CA524139	GCCACTCACTTTCTCTCCCCTT	63.2	AAATACCCACAACCCACCAACA	63.3
ES313	GD090003	ATGCTTGTCGCTCATTTTCACA	63.0	CCCATCATCGCTAAACGGTAAA	63.1
ES314	CO907277	GTCGTCTCCGATCAATCAATCC	63.0	ACACAGCCTTACCTCGTGCTTC	63.0
ES315	GD072597	TTGAAGGAGCAGAATTTTTCCA	61.1	TCATATTCACCATCTCCTTGATGA	60.7
ES316	EL813578	GAAGCCTTGGAAAAGGACCAAA	63.7	CCGGGCAGGTACAGTGGTTAAT	64.3
ES317	EL812991	CCGGGCAGGTACAGTGGTTA	63.1	AAAGCCTTGGAAAAGGACCAAA	63.2
ES318	EL813010	AAAGCCTTGGAAAAGGACCAAA	63.2	CCGGGCAGGTACAGTGGTTA	63.1
ES319	BM061457	AATGCGGAGGAAGAAGAGGAAG	63.2	ATGCGACAATCGACAAACAATG	63.1
ES320	GD083407	GACCGGAAAGATCATTGTGGAG	63.0	GCCTCACCAACCTTTTATTCCC	63.0
ES321	GD123159	ACGAGGTCCACTTCCCCATTAT	63.0	TTAGAGAAGGAATAACCGGCAGC	62.9
ES322	GD110372	CACCTGTCACATTTTCACTGCC	62.8	ACGAAGATCACCACCACACTGA	62.9
ES323	GD119220	ACGAAGATCACCACCACACTGA	62.9	CACCTGTCACATTTTCACTGCC	62.8
ES324	GD054212	GTGTGAGCGAGAGAGAGAGAGAGA	61.9	ACTTTTCCGATCCCCATTTTTC	62.5
ES325	GD074521	ACGAGGATCGTTTTCTCCTTCC	63.0	TATACTGCAAGTTTTGGGGGCA	63.7
ES326	GD135034	CACGAGGCCCAATACAAATCAT	63.1	AAACGATCACGGAGAAAGCAAA	63.1
ES327	GD055107	TTTTTAACACAACAAAAGGGGG	60.1	TTGCTCTGTATGTCTTCCGAGTC	60.8
ES328	GD100617	TTGGTGGTAATCCAATCTCCAAA	62.6	GGAGAGGAGTACAAGGAGGGGA	63.1
ES329	GD065695	TCCTCACCTTCACCTTCTCAAA	61.2	AAATGGTTGCTTGTCCTCATAGTG	61.6
ES330	GD117528	GTAGCCATGGCAGAATTGGAAG	63.0	TTCAGCAGGTTCTGGTTCTGGT	63.4
ES331	GD126700	ATAGTATAAGCGCCAGTGCCGA	63.1	TACGTTTCAAATCATCCGCTCC	63.4
ES332	GD056160	GCCTAGAGGCCCCAAATAAATG	63.0	AAACCCTTGGGCTTCTCATTG	62.5
ES333	GD084654	GCAAAAAGTTTGTTCCAATCCA	61.2	TTCCTCATCCCAGAAGAATCAG	60.6
ES334	CA514614	TATCCACTTCCCCATTATCCCC	63.1	TTAGAGAAGGAATAACCGGCAGC	62.9
ES335	GD073514	GCACGAGGCATTATCCCCTG	65.0	CGATTAGAGAAGGAATAACCGGCA	64.6

ES336	GD128916	ACCACCACCACCATAACAACAA	62.2	GGTGGGGTAGTAGGTGTAGGGG	62.9
ES337	BM067337	GCAGCAGCAAAGCATATGGTAA	62.5	TGCCGATGTTGAAGCTTTTGTA	62.9
ES338	GD086677	AGATCCCGTGCTGTTAAATGGA	62.9	TCAATGAGAATTCATGACCCCA	62.5
ES339	BM063089	TGCCGATGTTGAAGCTTTTGTA	62.9	GCAGCAGCAAAGCATATGGTAA	62.5
ES340	GD113030	ATTTTAGTGCATCGATTGGGC	61.2	GGCACTTGTCCAAGTCCAAA	61.1
ES341	BM062406	GCACTTGTCCAAGTCCAAAACC	63.0	ATTTTAGTGCATCGATTGGGCA	63.7
ES342	GD132347	CACGAGGAAGTAACAGCATCCC	63.1	AGGTTTTGGTGGGTGGAAAGAG	63.6
ES343	GD086888	AAAATGGCAGAAGCAGGACAAG	62.8	ATCTTCATGGGATTTGGCAATG	63.1
ES344	GD117914	ATTTTAGTGCATCGATTGGGCA	63.7	GCACTTGTCCAAGTCCAAAACC	63.0
ES345	GD099659	TAAGGGTGGTGAAAAGGGGATT	62.9	ACAACAAGAGTGAAATGACCTCCA	62.2
ES346	GD133095	GGTGATGATGGGCTTTTTCGTA	63.2	CACAACCCATCATTTCTCTGTGG	63.8
ES347	GD077924	TTTTTCCCTTTCATTTCCCCAC	63.3	TTTTTAAACTTTGGGGCGGG	63.1
ES348	GD080841	CGAGGGTTGAAGCTTTTGTAGC	62.4	GCAGCAGCAAAGCATATGGTAA	62.5
ES349	GD061029	ACGAGGCTTCCCCATTATCC	62.4	GAGAAGGAATAACCGGCAGCTA	61.9
ES350	CA516531	GGGATTTCTCCGATCTCAACAA	62.5	TCCTGAAAATCAGCAGCAAAGTC	62.9
ES351	CA514547	CGAATCAACACCAGCACCAGTA	63.3	CTCTACTGTTTCTGCAGCCGTG	62.4
ES352	GD101976	TTTTATGAACTTTGCGGCTGG	62.3	TTTCACTTACATATCCCAATCCCA	61.6
ES353	GD054248	GCCCTTGGTTCATATGCTTCAC	62.9	TTGTTTCGTTCATTACGGGAGG	63.2
ES354	GD118620	GCACGAGGACCAAGTATCTTGAA	62.7	AGCTCGAGATGGGTATGCGTAA	63.2
ES355	CO906426	TGAAGACGATCCAGATGACCAA	62.9	GTTTCTTCCTCTCCTTCAGGGC	62.8
ES356	GD090172	GGGAAAACAAATTAATATCAGCCG	61.9	TAACGACCAATGGGCTTCTCTC	62.7
ES357	GD072274	GAGGCATCAGCCTCCCTCAC	64.6	GGTGTCATGGTGGTGTTGGTTT	64.1
ES358	CA523162	GCTTTGTGCACATTTCGTTTCTT	62.7	TTCGATCATGAGGTACATCGCT	61.9
ES359	GD075156	TCCAACAACCTAGGAAACTGTGC	62.6	GAGATGAATCCCATTTCACCCA	63.2
ES360	CO906426	GCCCTGAAGGAGAGGAAGAAAC	62.8	TTCTTTGGTGGCTGAATTGCTT	63.1
ES361	GD093605	CACAGGATGAGGTCAGTATGGG	61.7	TGATGTTGTTCTCTACTGACGGTG	61.5

ES362	GD128401	CTACTGTTTCTGCAGCCGTGG	63.2	CACCAGCACCAGTAGAAGAGGC	63.5
ES363	BM064029	GAGGAATTTTGGAGCCACACAC	63.0	AGGTGAAATGGGCAGTGGTAGA	63.0
ES364	GD107993	AAATCCACCTCATACAACCCGA	62.7	AGATGCAAACTTTTCAATCCATGA	62.0
ES365	GO545824	TCAAGATTTCCTTGTTTTATCGCA	62.0	TCAGAGCAATGGAATGTGGAAG	62.4
ES366	GD107791	TAGTGTGGGATGTGCTTGATTG	60.9	TGAAAACCTCATCAGAAATCCTTC	60.8
ES367	GD068332	TAACGGTTCGAGTGGTGAGGAT	63.0	CACGACCACAACCCATCAGTAA	63.0
ES368	GD135307	GCACGAGGCAAGGCTTAGTAAC	62.4	TGGGATTGATGATGGGAGTAGG	63.2
ES369	GD112009	ATTCGGCACGAGGACAAGAAT	63.1	CTTTTGACGCTTCCAGGAGAGA	63.1
ES370	GD113307	CACTTTCATGGAGATTGACGGA	62.3	TCATTCTCCGATTACCAGCACA	62.8
ES371	GD128664	GGGATATCATCATCGGCGTATC	62.6	TGACCTAATCCTCCTACATGACCA	61.9
ES372	GD107244	GCACGAGGGAGAGAGAGAGAGA	62.6	ACAGTTGTTGATGCAGTGGACG	63.4
ES373	CO776727	CACCAGCACCAGTAGAAGAGGC	63.5	CTACTGTTTCTGCAGCCGTGG	63.2
ES374	GD119004	CGGCTCTGTGCTTTCCATATTT	62.6	GGAGGGAGAAAGTTGCCAGAAT	63.0
ES375	GD057317	GAAAGCTTCCTTGAGCTCCTCC	63.0	CAGTGTTCATGTTTCGCTTTGC	63.0
ES376	GO509483	GCTGTCGCTAGAGAGGGAAACA	63.2	ACTTGCTGCTCTCGCTTGATCT	63.0
ES377	GD094092	TGATGATGGGCTATGGAGATCA	62.7	GCATCATCATCATCATCATTGGA	62.9
ES378	CO907173	TGCTTCTAAGAAACCCCACAACA	63.0	TGGATTGGAACAAAGAAATGGAA	62.7
ES379	CO910302	CATCATCAGAAACCAAAAGCCC	62.9	CGTCTCCTGGACCATTTTGTTC	63.0
ES380	CA522270	CACCAGCACCAGTAGAAGAGGC	63.5	CTACTGTTTCTGCAGCCTGGGT	62.9
ES381	GD111786	ACGAGGCCAAACCAGCAAAG	64.7	TCTTTTAGGGGACTGAAATGGGAG	63.8
ES382	GD116944	TAGTGTGGCTACGACAGCATGG	63.4	GTTCTTGTTTCCCCTACCTGCC	63.2
ES383	CA523488	CTCATCCCTCAGTTGCAGTCAC	62.2	TGTGGCAGTTTATTCATGGTGG	62.9
ES384	GD102006	TCAGCGATTAAGAATGCGATTG	62.4	CCTCTCATTCCTCCACTTCCG	63.3
ES385	CA516597	TTATAGCACCAGCAGCCAACAA	62.9	CCGTATTCAGTGCGAGGTCTCT	62.9
ES386	CA519104	CCCCCTTTATTTTTCAACCCAA	63.1	GCTCTTCATCACACCTCTGTGG	62.2
ES387	GD115191	AAACTTCACTACTCCACCATCACC	60.7	TGAACAAAGAAAGATGAAGAAGCA	60.4

ES388	CA516290	CCCCTAAGCCTCATAAAGGTGG	63.1	TGGTGGTGGTGAAGAGTGAGAA	63.0
ES389	GD074797	GCACGAGGCTTCATGTCAATTA	62.4	TTCTCACCATTTTTGCAACCCT	62.9
ES390	BM068108	TTCGCTTTCATAGCGTGTTTGA	63.0	CAACTGGCCTCAGTAAATTCTGC	62.3
ES391	CA523402	CGGTAGCTGTCGTGTTCTTGAG	62.3	GGTAAGCGTGAAGTGAAAGGGA	62.7
ES392	GD112198	TTATGCACCAAGCAAACCACTG	63.2	TGGTGGGAGCACTGTAGAATTG	62.3
ES393	GD102245	GCTCTTCATCACACCTCTCTGGA	63.1	CCCCCTTTATTTTTCAACCCAA	63.1
ES394	GD122403	AGAGACGGGTGGGTTTCTAAGG	62.9	GAGGCCTTTACCGATTCACAGA	62.7
ES395	GD070975	TGTAATTAATTGAGGTGCGCGA	62.6	TCTCTGGTTGACAATTAGGCCC	62.6
ES396	GD103134	GCACGAGGAAATTACCGATCTT	61.6	GAAAATTCAAAAGGCTTGGACTG	61.3
ES397	BM062451	GGCTGCAGGGTGAAAAGTCC	64.3	TGAAAAATTTGTTGGAGCTCGG	63.4
ES398	GD111306	TCTTGAATCAATCAACCGGAGAA	63.0	AGCTCGAGATGGGTATGCGTAA	63.2
ES399	GD100634	AGAGCCACGTTATCTTTCGCTG	62.9	AATTGCCGTGAAAAGAGCAGAG	62.9
ES400	BM066135	GGCACGAGGTTCACTCTACAGC	63.5	GTGCACCTGACAGAGAAAAGGG	63.4
ES401	GD112325	ATGGCTTGACTGCTTCATCTCC	62.9	ACGCGTGGGTTGTACTTCATCT	63.1
ES402	GD068316	TTCTCTAATCAGGTTCTTCACGCA	62.4	GACCAGATGCAAAAATTCAGGG	62.9
ES403	GD097429	CTGCTAGGCTTGATCCTTCACC	62.5	TTACATCCTCGTCCTCATCAGC	61.5
ES404	CO911806	CTGTGTGTGTGTGTGTGTGGGT	63.0	CTCCCCCTCCCTCTTTTCTCTC	63.9
ES405	GD112009	CAGGTCTGCAAAATGACCATGA	63.3	TGTACTTGAGCTGTTGGGGTCC	63.6
ES406	GD133198	TGTACTTGAGCTGTTGGGGTCC	63.6	CAGGTCTGCAAAATGACCATGA	63.3
ES407	CF270002	GATCTGTAATACGGCCTGGCAC	62.9	TCCAACCGAGAGCAATAACACA	62.8
ES408	CA520421	TCAAGGGTTCTCTCTCTTGCTTTC	62.5	CAGTTTTACACTGCCTCCCACC	63.0
ES409	CA523960	CTTGCTTCGATCCCATTTCATC	63.0	ACGAGAATCCGAAGAGGAGGAT	62.6
ES410	BM064818	CTCTCTTGTGAGTGCATGTGGC	63.3	GTTGGCTTTGGAGTTGGAGTTG	63.1
ES411	GD072375	GACCCCACAAAGTGGGAATACA	63.1	AAGGCCACGAGGCAAATTAGAT	63.2
ES412	GD094865	TATATGGCAGCTTTCTCTCCGC	62.8	CAATGAACATTGAAATTTGTGCCT	62.2
ES413	CA518084	CGGAAATGATCAATGGTTATGATG	62.4	TTGAGGGTGCATTTGAGTGATG	63.3

ES414	GD094388	CTGGGAGAGTAAGCCCCTGTTT	63.0	CAATACAAACATGGTTTCCTGGG	62.5
ES415	GD070304	CAGCTGCTCCTGTTACCCTGTA	61.7	TGAATCTTGAAATAAGCCACACAA	60.9
ES416	CA514180	ACCTTCTGCATCAAGCCCTTAC	61.8	GCTGGTATAGGTGGAGATGAAACA	61.6
ES417	CA526323	AATGCGGAGGAAGAAGAGGAAG	63.2	TAGTCCTTATCACCGACACGGC	63.5
ES418	CA521556	GATCAATGGTTATGATGACGATGC	62.6	AAGAGTTGAGGGTGCATTGGAG	62.8