APPENDIX 1

Appendix 1-table 1. List of the 106 DBLaAF forward primer sequences. The GS FLX Titanium primer sequence (i.e., Adaptor) is represented in red (5'-CGTATCGCCTCCCTCGCGCCA-3'), the key in blue (5'-TCAG-3'), the unique 10 bp multiplex identifier in black (5'-MID-'3) in black, and the forward primer sequence in green (DBLαAF, 5'-GCACGMAGTTTYGC-3').

Forward Primer Sequence (5' -> 3'): Adaptor + Key + MID + Primer				
Primer name	Adaptor	Key (Blue)	MID	Primer (Forward)
DBLaAF-MID-1	CGTATCGCCTCCCTCGCGCCA	TCAG	ACGAGTGCGT	GCACGMAGTTTYGC
DBLaAF-MID-2	CGTATCGCCTCCCTCGCGCCA	TCAG	ACGCTCGACA	GCACGMAGTTTYGC
DBLaAF-MID-3	CGTATCGCCTCCCTCGCGCCA	TCAG	AGACGCACTC	GCACGMAGTTTYGC
DBLaAF-MID-4	CGTATCGCCTCCCTCGCGCCA	TCAG	AGCACTGTAG	GCACGMAGTTTYGC
DBLaAF-MID-5	CGTATCGCCTCCCTCGCGCCA	TCAG	ATCAGACACG	GCACGMAGTTTYGC
DBLaAF-MID-6	CGTATCGCCTCCCTCGCGCCA	TCAG	ATATCGCGAG	GCACGMAGTTTYGC
DBLaAF-MID-7	CGTATCGCCTCCCTCGCGCCA	TCAG	CGTGTCTCTA	GCACGMAGTTTYGC
DBLaAF-MID-8	CGTATCGCCTCCCTCGCGCCA	TCAG	CTCGCGTGTC	GCACGMAGTTTYGC
DBLaAF-MID-10	CGTATCGCCTCCCTCGCGCCA	TCAG	TCTCTATGCG	GCACGMAGTTTYGC
DBLaAF-MID-11	CGTATCGCCTCCCTCGCGCCA	TCAG	TGATACGTCT	GCACGMAGTTTYGC
DBLaAF-MID-13	CGTATCGCCTCCCTCGCGCCA	TCAG	CATAGTAGTG	GCACGMAGTTTYGC
DBLaAF-MID-14	CGTATCGCCTCCCTCGCGCCA	TCAG	CGAGAGATAC	GCACGMAGTTTYGC
DBLaAF-MID-15	CGTATCGCCTCCCTCGCGCCA	TCAG	ATACGACGTA	GCACGMAGTTTYGC
DBLaAF-MID-16	CGTATCGCCTCCCTCGCGCCA	TCAG	TCACGTACTA	GCACGMAGTTTYGC
DBLaAF-MID-18	CGTATCGCCTCCCTCGCGCCA	TCAG	TCTACGTAGC	GCACGMAGTTTYGC
DBLaAF-MID-19	CGTATCGCCTCCCTCGCGCCA	TCAG	TGTACTACTC	GCACGMAGTTTYGC
DBLaAF-MID-20	CGTATCGCCTCCCTCGCGCCA	TCAG	ACGACTACAG	GCACGMAGTTTYGC
DBLaAF-MID-21	CGTATCGCCTCCCTCGCGCCA	TCAG	CGTAGACTAG	GCACGMAGTTTYGC
DBLaAF-MID-22	CGTATCGCCTCCCTCGCGCCA	TCAG	TACGAGTATG	GCACGMAGTTTYGC
DBLaAF-MID-23	CGTATCGCCTCCCTCGCGCCA	TCAG	TACTCTCGTG	GCACGMAGTTTYGC
DBLaAF-MID-24	CGTATCGCCTCCCTCGCGCCA	TCAG	TAGAGACGAG	GCACGMAGTTTYGC
DBLaAF-MID-25	CGTATCGCCTCCCTCGCGCCA	TCAG	TCGTCGCTCG	GCACGMAGTTTYGC
DBLaAF-MID-26	CGTATCGCCTCCCTCGCGCCA	TCAG	ACATACGCGT	GCACGMAGTTTYGC
DBLaAF-MID-27	CGTATCGCCTCCCTCGCGCCA	TCAG	ACGCGAGTAT	GCACGMAGTTTYGC

DBLaAF-MID-28	CGTATCGCCTCCCTCGCGCCA	TCAG	ACTACTATGT	GCACGMAGTTTYGC
DBLaAF-MID-29	CGTATCGCCTCCCTCGCGCCA	TCAG	ACTGTACAGT	GCACGMAGTTTYGC
DBLaAF-MID-30	CGTATCGCCTCCCTCGCGCCA	TCAG	AGACTATACT	GCACGMAGTTTYGC
DBLaAF-MID-31	CGTATCGCCTCCCTCGCGCCA	TCAG	AGCGTCGTCT	GCACGMAGTTTYGC
DBLaAF-MID-32	CGTATCGCCTCCCTCGCGCCA	TCAG	AGTACGCTAT	GCACGMAGTTTYGC
DBLaAF-MID-33	CGTATCGCCTCCCTCGCGCCA	TCAG	ATAGAGTACT	GCACGMAGTTTYGC
DBLaAF-MID-34	CGTATCGCCTCCCTCGCGCCA	TCAG	CACGCTACGT	GCACGMAGTTTYGC
DBLaAF-MID-35	CGTATCGCCTCCCTCGCGCCA	TCAG	CAGTAGACGT	GCACGMAGTTTYGC
DBLaAF-MID-36	CGTATCGCCTCCCTCGCGCCA	TCAG	CGACGTGACT	GCACGMAGTTTYGC
DBLaAF-MID-37	CGTATCGCCTCCCTCGCGCCA	TCAG	TACACACACT	GCACGMAGTTTYGC
DBLaAF-MID-38	CGTATCGCCTCCCTCGCGCCA	TCAG	TACACGTGAT	GCACGMAGTTTYGC
DBLaAF-MID-39	CGTATCGCCTCCCTCGCGCCA	TCAG	TACAGATCGT	GCACGMAGTTTYGC
DBLaAF-MID-40	CGTATCGCCTCCCTCGCGCCA	TCAG	TACGCTGTCT	GCACGMAGTTTYGC
DBLaAF-MID-41	CGTATCGCCTCCCTCGCGCCA	TCAG	TAGTGTAGAT	GCACGMAGTTTYGC
DBLaAF-MID-42	CGTATCGCCTCCCTCGCGCCA	TCAG	TCGATCACGT	GCACGMAGTTTYGC
DBLaAF-MID-43	CGTATCGCCTCCCTCGCGCCA	TCAG	TCGCACTAGT	GCACGMAGTTTYGC
DBLaAF-MID-44	CGTATCGCCTCCCTCGCGCCA	TCAG	TCTAGCGACT	GCACGMAGTTTYGC
DBLaAF-MID-45	CGTATCGCCTCCCTCGCGCCA	TCAG	TCTATACTAT	GCACGMAGTTTYGC
DBLaAF-MID-46	CGTATCGCCTCCCTCGCGCCA	TCAG	TGACGTATGT	GCACGMAGTTTYGC
DBLaAF-MID-47	CGTATCGCCTCCCTCGCGCCA	TCAG	TGTGAGTAGT	GCACGMAGTTTYGC
DBLaAF-MID-48	CGTATCGCCTCCCTCGCGCCA	TCAG	ACAGTATATA	GCACGMAGTTTYGC
DBLaAF-MID-49	CGTATCGCCTCCCTCGCGCCA	TCAG	ACGCGATCGA	GCACGMAGTTTYGC
DBLaAF-MID-50	CGTATCGCCTCCCTCGCGCCA	TCAG	ACTAGCAGTA	GCACGMAGTTTYGC
DBLaAF-MID-51	CGTATCGCCTCCCTCGCGCCA	TCAG	AGCTCACGTA	GCACGMAGTTTYGC
DBLaAF-MID-53	CGTATCGCCTCCCTCGCGCCA	TCAG	AGTCGAGAGA	GCACGMAGTTTYGC
DBLaAF-MID-54	CGTATCGCCTCCCTCGCGCCA	TCAG	AGTGCTACGA	GCACGMAGTTTYGC
DBLaAF-MID-55	CGTATCGCCTCCCTCGCGCCA	TCAG	CGATCGTATA	GCACGMAGTTTYGC
DBLaAF-MID-56	CGTATCGCCTCCCTCGCGCCA	TCAG	CGCAGTACGA	GCACGMAGTTTYGC
DBLaAF-MID-57	CGTATCGCCTCCCTCGCGCCA	TCAG	CGCGTATACA	GCACGMAGTTTYGC
DBLaAF-MID-58	CGTATCGCCTCCCTCGCGCCA	TCAG	CGTACAGTCA	GCACGMAGTTTYGC

DBLaAF-MID-59	CGTATCGCCTCCCTCGCGCCA	TCAG	CGTACTCAGA	GCACGMAGTTTYGC
DBLaAF-MID-60	CGTATCGCCTCCCTCGCGCCA	TCAG	CTACGCTCTA	GCACGMAGTTTYGC
DBLaAF-MID-61	CGTATCGCCTCCCTCGCGCCA	TCAG	CTATAGCGTA	GCACGMAGTTTYGC
DBLaAF-MID-62	CGTATCGCCTCCCTCGCGCCA	TCAG	TACGTCATCA	GCACGMAGTTTYGC
DBLaAF-MID-63	CGTATCGCCTCCCTCGCGCCA	TCAG	TAGTCGCATA	GCACGMAGTTTYGC
DBLaAF-MID-64	CGTATCGCCTCCCTCGCGCCA	TCAG	TATATATACA	GCACGMAGTTTYGC
DBLaAF-MID-65	CGTATCGCCTCCCTCGCGCCA	TCAG	TATGCTAGTA	GCACGMAGTTTYGC
DBLaAF-MID-66	CGTATCGCCTCCCTCGCGCCA	TCAG	TCACGCGAGA	GCACGMAGTTTYGC
DBLaAF-MID-67	CGTATCGCCTCCCTCGCGCCA	TCAG	TCGATAGTGA	GCACGMAGTTTYGC
DBLaAF-MID-68	CGTATCGCCTCCCTCGCGCCA	TCAG	TCGCTGCGTA	GCACGMAGTTTYGC
DBLaAF-MID-69	CGTATCGCCTCCCTCGCGCCA	TCAG	TCTGACGTCA	GCACGMAGTTTYGC
DBLaAF-MID-70	CGTATCGCCTCCCTCGCGCCA	TCAG	TGAGTCAGTA	GCACGMAGTTTYGC
DBLaAF-MID-71	CGTATCGCCTCCCTCGCGCCA	TCAG	TGTAGTGTGA	GCACGMAGTTTYGC
DBLaAF-MID-72	CGTATCGCCTCCCTCGCGCCA	TCAG	TGTCACACGA	GCACGMAGTTTYGC
DBLaAF-MID-73	CGTATCGCCTCCCTCGCGCCA	TCAG	TGTCGTCGCA	GCACGMAGTTTYGC
DBLaAF-MID-74	CGTATCGCCTCCCTCGCGCCA	TCAG	ACACATACGC	GCACGMAGTTTYGC
DBLaAF-MID-75	CGTATCGCCTCCCTCGCGCCA	TCAG	ACAGTCGTGC	GCACGMAGTTTYGC
DBLaAF-MID-76	CGTATCGCCTCCCTCGCGCCA	TCAG	ACATGACGAC	GCACGMAGTTTYGC
DBLaAF-MID-77	CGTATCGCCTCCCTCGCGCCA	TCAG	ACGACAGCTC	GCACGMAGTTTYGC
DBLaAF-MID-78	CGTATCGCCTCCCTCGCGCCA	TCAG	ACGTCTCATC	GCACGMAGTTTYGC
DBLaAF-MID-79	CGTATCGCCTCCCTCGCGCCA	TCAG	ACTCATCTAC	GCACGMAGTTTYGC
DBLaAF-MID-80	CGTATCGCCTCCCTCGCGCCA	TCAG	ACTCGCGCAC	GCACGMAGTTTYGC
DBLaAF-MID-81	CGTATCGCCTCCCTCGCGCCA	TCAG	AGAGCGTCAC	GCACGMAGTTTYGC
DBLaAF-MID-82	CGTATCGCCTCCCTCGCGCCA	TCAG	AGCGACTAGC	GCACGMAGTTTYGC
DBLaAF-MID-83	CGTATCGCCTCCCTCGCGCCA	TCAG	AGTAGTGATC	GCACGMAGTTTYGC
DBLaAF-MID-84	CGTATCGCCTCCCTCGCGCCA	TCAG	AGTGACACAC	GCACGMAGTTTYGC
DBLaAF-MID-85	CGTATCGCCTCCCTCGCGCCA	TCAG	AGTGTATGTC	GCACGMAGTTTYGC
DBLaAF-MID-86	CGTATCGCCTCCCTCGCGCCA	TCAG	ATAGATAGAC	GCACGMAGTTTYGC
DBLaAF-MID-87	CGTATCGCCTCCCTCGCGCCA	TCAG	ATATAGTCGC	GCACGMAGTTTYGC
DBLaAF-MID-88	CGTATCGCCTCCCTCGCGCCA	TCAG	ATCTACTGAC	GCACGMAGTTTYGC

DBLaAF-MID-89	CGTATCGCCTCCCTCGCGCCA	TCAG	CACGTAGATC	GCACGMAGTTTYGC
DBLaAF-MID-90	CGTATCGCCTCCCTCGCGCCA	TCAG	CACGTGTCGC	GCACGMAGTTTYGC
DBLaAF-MID-91	CGTATCGCCTCCCTCGCGCCA	TCAG	CATACTCTAC	GCACGMAGTTTYGC
DBLaAF-MID-92	CGTATCGCCTCCCTCGCGCCA	TCAG	CGACACTATC	GCACGMAGTTTYGC
DBLaAF-MID-93	CGTATCGCCTCCCTCGCGCCA	TCAG	CGAGACGCGC	GCACGMAGTTTYGC
DBLaAF-MID-94	CGTATCGCCTCCCTCGCGCCA	TCAG	CGTATGCGAC	GCACGMAGTTTYGC
DBLaAF-MID-95	CGTATCGCCTCCCTCGCGCCA	TCAG	CGTCGATCTC	GCACGMAGTTTYGC
DBLaAF-MID-96	CGTATCGCCTCCCTCGCGCCA	TCAG	CTACGACTGC	GCACGMAGTTTYGC
DBLaAF-MID-97	CGTATCGCCTCCCTCGCGCCA	TCAG	CTAGTCACTC	GCACGMAGTTTYGC
DBLaAF-MID-98	CGTATCGCCTCCCTCGCGCCA	TCAG	CTCTACGCTC	GCACGMAGTTTYGC
DBLaAF-MID-99	CGTATCGCCTCCCTCGCGCCA	TCAG	CTGTACATAC	GCACGMAGTTTYGC
DBLaAF-MID-100	CGTATCGCCTCCCTCGCGCCA	TCAG	TAGACTGCAC	GCACGMAGTTTYGC
DBLaAF-MID-101	CGTATCGCCTCCCTCGCGCCA	TCAG	TAGCGCGCGC	GCACGMAGTTTYGC
DBLaAF-MID-102	CGTATCGCCTCCCTCGCGCCA	TCAG	TAGCTCTATC	GCACGMAGTTTYGC
DBLaAF-MID-103	CGTATCGCCTCCCTCGCGCCA	TCAG	TATAGACATC	GCACGMAGTTTYGC
DBLaAF-MID-104	CGTATCGCCTCCCTCGCGCCA	TCAG	TATGATACGC	GCACGMAGTTTYGC
DBLaAF-MID-105	CGTATCGCCTCCCTCGCGCCA	TCAG	TCACTCATAC	GCACGMAGTTTYGC
DBLaAF-MID-106	CGTATCGCCTCCCTCGCGCCA	TCAG	TCATCGAGTC	GCACGMAGTTTYGC
DBLaAF-MID-107	CGTATCGCCTCCCTCGCGCCA	TCAG	TCGAGCTCTC	GCACGMAGTTTYGC
DBLaAF-MID-108	CGTATCGCCTCCCTCGCGCCA	TCAG	TCGCAGACAC	GCACGMAGTTTYGC
DBLaAF-MID-109	CGTATCGCCTCCCTCGCGCCA	TCAG	TCTGTCTCGC	GCACGMAGTTTYGC
DBLaAF-MID-110	CGTATCGCCTCCCTCGCGCCA	TCAG	TGAGTGACGC	GCACGMAGTTTYGC

Appendix 1-table 2 List of the 106 DBLaBR reverse primer sequences. The GS FLX Titanium primer sequence (i.e., Adaptor) is represented in red (5'-CTATGCGCCTTGCCAGCCCGC-3'), the key in blue (5'-TCAG-3'), the unique 10 bp multiplex identifier in black (5'-MID-'3) in black, and the forward primer sequence in green (DBLαAF, 5'-GCCCATTCSTCGAACCA -3').

Reverse Primer Sequence (5' -> 3'): Adaptor + Key + MID + Primer				
Primer name	Adaptor	Key	MID	Primer (Reverse)
DBLaBR-MID-1	CTATGCGCCTTGCCAGCCCGC	TCAG	ACGAGTGCGT	GCCCATTCSTCGAACCA
DBLaBR-MID-2	CTATGCGCCTTGCCAGCCCGC	TCAG	ACGCTCGACA	GCCCATTCSTCGAACCA
DBLaBR-MID-3	CTATGCGCCTTGCCAGCCCGC	TCAG	AGACGCACTC	GCCCATTCSTCGAACCA
DBLaBR-MID-4	CTATGCGCCTTGCCAGCCCGC	TCAG	AGCACTGTAG	GCCCATTCSTCGAACCA
DBLaBR-MID-5	CTATGCGCCTTGCCAGCCCGC	TCAG	ATCAGACACG	GCCCATTCSTCGAACCA
DBLaBR-MID-6	CTATGCGCCTTGCCAGCCCGC	TCAG	ATATCGCGAG	GCCCATTCSTCGAACCA
DBLaBR-MID-7	CTATGCGCCTTGCCAGCCCGC	TCAG	CGTGTCTCTA	GCCCATTCSTCGAACCA
DBLaBR-MID-8	CTATGCGCCTTGCCAGCCCGC	TCAG	CTCGCGTGTC	GCCCATTCSTCGAACCA
DBLaBR-MID-10	CTATGCGCCTTGCCAGCCCGC	TCAG	TCTCTATGCG	GCCCATTCSTCGAACCA
DBLaBR-MID-11	CTATGCGCCTTGCCAGCCCGC	TCAG	TGATACGTCT	GCCCATTCSTCGAACCA
DBLaBR-MID-13	CTATGCGCCTTGCCAGCCCGC	TCAG	CATAGTAGTG	GCCCATTCSTCGAACCA
DBLaBR-MID-14	CTATGCGCCTTGCCAGCCCGC	TCAG	CGAGAGATAC	GCCCATTCSTCGAACCA
DBLaBR-MID-15	CTATGCGCCTTGCCAGCCCGC	TCAG	ATACGACGTA	GCCCATTCSTCGAACCA
DBLaBR-MID-16	CTATGCGCCTTGCCAGCCCGC	TCAG	TCACGTACTA	GCCCATTCSTCGAACCA
DBLaBR-MID-18	CTATGCGCCTTGCCAGCCCGC	TCAG	TCTACGTAGC	GCCCATTCSTCGAACCA
DBLaBR-MID-19	CTATGCGCCTTGCCAGCCCGC	TCAG	TGTACTACTC	GCCCATTCSTCGAACCA
DBLaBR-MID-20	CTATGCGCCTTGCCAGCCCGC	TCAG	ACGACTACAG	GCCCATTCSTCGAACCA
DBLaBR-MID-21	CTATGCGCCTTGCCAGCCCGC	TCAG	CGTAGACTAG	GCCCATTCSTCGAACCA
DBLaBR-MID-22	CTATGCGCCTTGCCAGCCCGC	TCAG	TACGAGTATG	GCCCATTCSTCGAACCA
DBLaBR-MID-23	CTATGCGCCTTGCCAGCCCGC	TCAG	TACTCTCGTG	GCCCATTCSTCGAACCA
DBLaBR-MID-24	CTATGCGCCTTGCCAGCCCGC	TCAG	TAGAGACGAG	GCCCATTCSTCGAACCA
DBLaBR-MID-25	CTATGCGCCTTGCCAGCCCGC	TCAG	TCGTCGCTCG	GCCCATTCSTCGAACCA
DBLaBR-MID-26	CTATGCGCCTTGCCAGCCCGC	TCAG	ACATACGCGT	GCCCATTCSTCGAACCA
DBLaBR-MID-27	CTATGCGCCTTGCCAGCCCGC	TCAG	ACGCGAGTAT	GCCCATTCSTCGAACCA
DBLaBR-MID-28	CTATGCGCCTTGCCAGCCCGC	TCAG	ACTACTATGT	GCCCATTCSTCGAACCA

DBLaBR-MID-29	CTATGCGCCTTGCCAGCCCGC	TCAG	ACTGTACAGT	GCCCATTCSTCGAACCA
DBLaBR-MID-30	CTATGCGCCTTGCCAGCCCGC	TCAG	AGACTATACT	GCCCATTCSTCGAACCA
DBLaBR-MID-31	CTATGCGCCTTGCCAGCCCGC	TCAG	AGCGTCGTCT	GCCCATTCSTCGAACCA
DBLaBR-MID-32	CTATGCGCCTTGCCAGCCCGC	TCAG	AGTACGCTAT	GCCCATTCSTCGAACCA
DBLaBR-MID-33	CTATGCGCCTTGCCAGCCCGC	TCAG	ATAGAGTACT	GCCCATTCSTCGAACCA
DBLaBR-MID-34	CTATGCGCCTTGCCAGCCCGC	TCAG	CACGCTACGT	GCCCATTCSTCGAACCA
DBLaBR-MID-35	CTATGCGCCTTGCCAGCCCGC	TCAG	CAGTAGACGT	GCCCATTCSTCGAACCA
DBLaBR-MID-36	CTATGCGCCTTGCCAGCCCGC	TCAG	CGACGTGACT	GCCCATTCSTCGAACCA
DBLaBR-MID-37	CTATGCGCCTTGCCAGCCCGC	TCAG	TACACACACT	GCCCATTCSTCGAACCA
DBLaBR-MID-38	CTATGCGCCTTGCCAGCCCGC	TCAG	TACACGTGAT	GCCCATTCSTCGAACCA
DBLaBR-MID-39	CTATGCGCCTTGCCAGCCCGC	TCAG	TACAGATCGT	GCCCATTCSTCGAACCA
DBLaBR-MID-40	CTATGCGCCTTGCCAGCCCGC	TCAG	TACGCTGTCT	GCCCATTCSTCGAACCA
DBLaBR-MID-41	CTATGCGCCTTGCCAGCCCGC	TCAG	TAGTGTAGAT	GCCCATTCSTCGAACCA
DBLaBR-MID-42	CTATGCGCCTTGCCAGCCCGC	TCAG	TCGATCACGT	GCCCATTCSTCGAACCA
DBLaBR-MID-43	CTATGCGCCTTGCCAGCCCGC	TCAG	TCGCACTAGT	GCCCATTCSTCGAACCA
DBLaBR-MID-44	CTATGCGCCTTGCCAGCCCGC	TCAG	TCTAGCGACT	GCCCATTCSTCGAACCA
DBLaBR-MID-45	CTATGCGCCTTGCCAGCCCGC	TCAG	TCTATACTAT	GCCCATTCSTCGAACCA
DBLaBR-MID-46	CTATGCGCCTTGCCAGCCCGC	TCAG	TGACGTATGT	GCCCATTCSTCGAACCA
DBLaBR-MID-47	CTATGCGCCTTGCCAGCCCGC	TCAG	TGTGAGTAGT	GCCCATTCSTCGAACCA
DBLaBR-MID-48	CTATGCGCCTTGCCAGCCCGC	TCAG	ACAGTATATA	GCCCATTCSTCGAACCA
DBLaBR-MID-49	CTATGCGCCTTGCCAGCCCGC	TCAG	ACGCGATCGA	GCCCATTCSTCGAACCA
DBLaBR-MID-50	CTATGCGCCTTGCCAGCCCGC	TCAG	ACTAGCAGTA	GCCCATTCSTCGAACCA
DBLaBR-MID-51	CTATGCGCCTTGCCAGCCCGC	TCAG	AGCTCACGTA	GCCCATTCSTCGAACCA
DBLaBR-MID-53	CTATGCGCCTTGCCAGCCCGC	TCAG	AGTCGAGAGA	GCCCATTCSTCGAACCA
DBLaBR-MID-54	CTATGCGCCTTGCCAGCCCGC	TCAG	AGTGCTACGA	GCCCATTCSTCGAACCA
DBLaBR-MID-55	CTATGCGCCTTGCCAGCCCGC	TCAG	CGATCGTATA	GCCCATTCSTCGAACCA
DBLaBR-MID-56	CTATGCGCCTTGCCAGCCCGC	TCAG	CGCAGTACGA	GCCCATTCSTCGAACCA
DBLaBR-MID-57	CTATGCGCCTTGCCAGCCCGC	TCAG	CGCGTATACA	GCCCATTCSTCGAACCA
DBLaBR-MID-58	CTATGCGCCTTGCCAGCCCGC	TCAG	CGTACAGTCA	GCCCATTCSTCGAACCA
DBLaBR-MID-59	CTATGCGCCTTGCCAGCCCGC	TCAG	CGTACTCAGA	GCCCATTCSTCGAACCA

DBLaBR-MID-60	CTATGCGCCTTGCCAGCCCGC	TCAG	CTACGCTCTA	GCCCATTCSTCGAACCA
DBLaBR-MID-61	CTATGCGCCTTGCCAGCCCGC	TCAG	CTATAGCGTA	GCCCATTCSTCGAACCA
DBLaBR-MID-62	CTATGCGCCTTGCCAGCCCGC	TCAG	TACGTCATCA	GCCCATTCSTCGAACCA
DBLaBR-MID-63	CTATGCGCCTTGCCAGCCCGC	TCAG	TAGTCGCATA	GCCCATTCSTCGAACCA
DBLaBR-MID-64	CTATGCGCCTTGCCAGCCCGC	TCAG	TATATATACA	GCCCATTCSTCGAACCA
DBLaBR-MID-65	CTATGCGCCTTGCCAGCCCGC	TCAG	TATGCTAGTA	GCCCATTCSTCGAACCA
DBLaBR-MID-66	CTATGCGCCTTGCCAGCCCGC	TCAG	TCACGCGAGA	GCCCATTCSTCGAACCA
DBLaBR-MID-67	CTATGCGCCTTGCCAGCCCGC	TCAG	TCGATAGTGA	GCCCATTCSTCGAACCA
DBLaBR-MID-68	CTATGCGCCTTGCCAGCCCGC	TCAG	TCGCTGCGTA	GCCCATTCSTCGAACCA
DBLaBR-MID-69	CTATGCGCCTTGCCAGCCCGC	TCAG	TCTGACGTCA	GCCCATTCSTCGAACCA
DBLaBR-MID-70	CTATGCGCCTTGCCAGCCCGC	TCAG	TGAGTCAGTA	GCCCATTCSTCGAACCA
DBLaBR-MID-71	CTATGCGCCTTGCCAGCCCGC	TCAG	TGTAGTGTGA	GCCCATTCSTCGAACCA
DBLaBR-MID-72	CTATGCGCCTTGCCAGCCCGC	TCAG	TGTCACACGA	GCCCATTCSTCGAACCA
DBLaBR-MID-73	CTATGCGCCTTGCCAGCCCGC	TCAG	TGTCGTCGCA	GCCCATTCSTCGAACCA
DBLaBR-MID-74	CTATGCGCCTTGCCAGCCCGC	TCAG	ACACATACGC	GCCCATTCSTCGAACCA
DBLaBR-MID-75	CTATGCGCCTTGCCAGCCCGC	TCAG	ACAGTCGTGC	GCCCATTCSTCGAACCA
DBLaBR-MID-76	CTATGCGCCTTGCCAGCCCGC	TCAG	ACATGACGAC	GCCCATTCSTCGAACCA
DBLaBR-MID-77	CTATGCGCCTTGCCAGCCCGC	TCAG	ACGACAGCTC	GCCCATTCSTCGAACCA
DBLaBR-MID-78	CTATGCGCCTTGCCAGCCCGC	TCAG	ACGTCTCATC	GCCCATTCSTCGAACCA
DBLaBR-MID-79	CTATGCGCCTTGCCAGCCCGC	TCAG	ACTCATCTAC	GCCCATTCSTCGAACCA
DBLaBR-MID-80	CTATGCGCCTTGCCAGCCCGC	TCAG	ACTCGCGCAC	GCCCATTCSTCGAACCA
DBLaBR-MID-81	CTATGCGCCTTGCCAGCCCGC	TCAG	AGAGCGTCAC	GCCCATTCSTCGAACCA
DBLaBR-MID-82	CTATGCGCCTTGCCAGCCCGC	TCAG	AGCGACTAGC	GCCCATTCSTCGAACCA
DBLaBR-MID-83	CTATGCGCCTTGCCAGCCCGC	TCAG	AGTAGTGATC	GCCCATTCSTCGAACCA
DBLaBR-MID-84	CTATGCGCCTTGCCAGCCCGC	TCAG	AGTGACACAC	GCCCATTCSTCGAACCA
DBLaBR-MID-85	CTATGCGCCTTGCCAGCCCGC	TCAG	AGTGTATGTC	GCCCATTCSTCGAACCA
DBLaBR-MID-86	CTATGCGCCTTGCCAGCCCGC	TCAG	ATAGATAGAC	GCCCATTCSTCGAACCA
DBLaBR-MID-87	CTATGCGCCTTGCCAGCCCGC	TCAG	ATATAGTCGC	GCCCATTCSTCGAACCA
DBLaBR-MID-88	CTATGCGCCTTGCCAGCCCGC	TCAG	ATCTACTGAC	GCCCATTCSTCGAACCA
DBLaBR-MID-89	CTATGCGCCTTGCCAGCCCGC	TCAG	CACGTAGATC	GCCCATTCSTCGAACCA

DBLaBR-MID-90	CTATGCGCCTTGCCAGCCCGC	TCAG	CACGTGTCGC	GCCCATTCSTCGAACCA
DBLaBR-MID-91	CTATGCGCCTTGCCAGCCCGC	TCAG	CATACTCTAC	GCCCATTCSTCGAACCA
DBLaBR-MID-92	CTATGCGCCTTGCCAGCCCGC	TCAG	CGACACTATC	GCCCATTCSTCGAACCA
DBLaBR-MID-93	CTATGCGCCTTGCCAGCCCGC	TCAG	CGAGACGCGC	GCCCATTCSTCGAACCA
DBLaBR-MID-94	CTATGCGCCTTGCCAGCCCGC	TCAG	CGTATGCGAC	GCCCATTCSTCGAACCA
DBLaBR-MID-95	CTATGCGCCTTGCCAGCCCGC	TCAG	CGTCGATCTC	GCCCATTCSTCGAACCA
DBLaBR-MID-96	CTATGCGCCTTGCCAGCCCGC	TCAG	CTACGACTGC	GCCCATTCSTCGAACCA
DBLaBR-MID-97	CTATGCGCCTTGCCAGCCCGC	TCAG	CTAGTCACTC	GCCCATTCSTCGAACCA
DBLaBR-MID-98	CTATGCGCCTTGCCAGCCCGC	TCAG	CTCTACGCTC	GCCCATTCSTCGAACCA
DBLaBR-MID-99	CTATGCGCCTTGCCAGCCCGC	TCAG	CTGTACATAC	GCCCATTCSTCGAACCA
DBLaBR-MID-100	CTATGCGCCTTGCCAGCCCGC	TCAG	TAGACTGCAC	GCCCATTCSTCGAACCA
DBLaBR-MID-101	CTATGCGCCTTGCCAGCCCGC	TCAG	TAGCGCGCGC	GCCCATTCSTCGAACCA
DBLaBR-MID-102	CTATGCGCCTTGCCAGCCCGC	TCAG	TAGCTCTATC	GCCCATTCSTCGAACCA
DBLaBR-MID-103	CTATGCGCCTTGCCAGCCCGC	TCAG	TATAGACATC	GCCCATTCSTCGAACCA
DBLaBR-MID-104	CTATGCGCCTTGCCAGCCCGC	TCAG	TATGATACGC	GCCCATTCSTCGAACCA
DBLaBR-MID-105	CTATGCGCCTTGCCAGCCCGC	TCAG	TCACTCATAC	GCCCATTCSTCGAACCA
DBLaBR-MID-106	CTATGCGCCTTGCCAGCCCGC	TCAG	TCATCGAGTC	GCCCATTCSTCGAACCA
DBLaBR-MID-107	CTATGCGCCTTGCCAGCCCGC	TCAG	TCGAGCTCTC	GCCCATTCSTCGAACCA
DBLaBR-MID-108	CTATGCGCCTTGCCAGCCCGC	TCAG	TCGCAGACAC	GCCCATTCSTCGAACCA
DBLaBR-MID-109	CTATGCGCCTTGCCAGCCCGC	TCAG	TCTGTCTCGC	GCCCATTCSTCGAACCA
DBLaBR-MID-110	CTATGCGCCTTGCCAGCCCGC	TCAG	TGAGTGACGC	GCCCATTCSTCGAACCA