APPENDIX 2

Appendix 2-table 1. List of the 106 DBLαAF forward primer sequences. The Illumina Nextera overhang sequence is represented in red (5'- TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG -3'), the unique 10 bp multiplex identifier in black (5'-MID-'3), and the forward primer sequence in green (DBLαAF, 5'-GCACGMAGTTTYGC-3').

Forward Primer Sequence (5' -> 3'): Forward Nextera overhang + DBLαAF forward primer			
Primer name	Forward Nextera overhang	MID	Primer
DBLaAF-MID-1.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACGAGTGCGT	GCACGMAGTTTYGC
DBLaAF-MID-2.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACGCTCGACA	GCACGMAGTTTYGC
DBLaAF-MID-3.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	AGACGCACTC	GCACGMAGTTTYGC
DBLaAF-MID-4.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	AGCACTGTAG	GCACGMAGTTTYGC
DBLaAF-MID-5.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ATCAGACACG	GCACGMAGTTTYGC
DBLaAF-MID-6.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ATATCGCGAG	GCACGMAGTTTYGC
DBLaAF-MID-7.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CGTGTCTCTA	GCACGMAGTTTYGC
DBLaAF-MID-8.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CTCGCGTGTC	GCACGMAGTTTYGC
DBLaAF-MID-10.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCTCTATGCG	GCACGMAGTTTYGC
DBLaAF-MID-11.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TGATACGTCT	GCACGMAGTTTYGC
DBLaAF-MID-13.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CATAGTAGTG	GCACGMAGTTTYGC
DBLaAF-MID-14.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CGAGAGATAC	GCACGMAGTTTYGC
DBLaAF-MID-15.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ATACGACGTA	GCACGMAGTTTYGC
DBLaAF-MID-16.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCACGTACTA	GCACGMAGTTTYGC
DBLaAF-MID-18.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCTACGTAGC	GCACGMAGTTTYGC
DBLaAF-MID-19.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TGTACTACTC	GCACGMAGTTTYGC
DBLaAF-MID-20.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACGACTACAG	GCACGMAGTTTYGC
DBLaAF-MID-21.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CGTAGACTAG	GCACGMAGTTTYGC
DBLaAF-MID-22.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TACGAGTATG	GCACGMAGTTTYGC
DBLaAF-MID-23.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TACTCTCGTG	GCACGMAGTTTYGC
DBLaAF-MID-24.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TAGAGACGAG	GCACGMAGTTTYGC
DBLaAF-MID-25.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCGTCGCTCG	GCACGMAGTTTYGC
DBLaAF-MID-26.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACATACGCGT	GCACGMAGTTTYGC
DBLaAF-MID-27.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACGCGAGTAT	GCACGMAGTTTYGC

DBLaAF-MID-28.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACTACTATGT	GCACGMAGTTTYGC
DBLaAF-MID-29.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACTGTACAGT	GCACGMAGTTTYGC
DBLaAF-MID-30.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	AGACTATACT	GCACGMAGTTTYGC
DBLaAF-MID-31.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	AGCGTCGTCT	GCACGMAGTTTYGC
DBLaAF-MID-32.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	AGTACGCTAT	GCACGMAGTTTYGC
DBLaAF-MID-33.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ATAGAGTACT	GCACGMAGTTTYGC
DBLaAF-MID-34.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CACGCTACGT	GCACGMAGTTTYGC
DBLaAF-MID-35.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CAGTAGACGT	GCACGMAGTTTYGC
DBLaAF-MID-36.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CGACGTGACT	GCACGMAGTTTYGC
DBLaAF-MID-37.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TACACACACT	GCACGMAGTTTYGC
DBLaAF-MID-38.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TACACGTGAT	GCACGMAGTTTYGC
DBLaAF-MID-39.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TACAGATCGT	GCACGMAGTTTYGC
DBLaAF-MID-40.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TACGCTGTCT	GCACGMAGTTTYGC
DBLaAF-MID-41.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TAGTGTAGAT	GCACGMAGTTTYGC
DBLaAF-MID-42.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCGATCACGT	GCACGMAGTTTYGC
DBLaAF-MID-43.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCGCACTAGT	GCACGMAGTTTYGC
DBLaAF-MID-44.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCTAGCGACT	GCACGMAGTTTYGC
DBLaAF-MID-45.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCTATACTAT	GCACGMAGTTTYGC
DBLaAF-MID-46.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TGACGTATGT	GCACGMAGTTTYGC
DBLaAF-MID-47.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TGTGAGTAGT	GCACGMAGTTTYGC
DBLaAF-MID-48.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACAGTATATA	GCACGMAGTTTYGC
DBLaAF-MID-49.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACGCGATCGA	GCACGMAGTTTYGC
DBLaAF-MID-50.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACTAGCAGTA	GCACGMAGTTTYGC
DBLaAF-MID-51.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	AGCTCACGTA	GCACGMAGTTTYGC
DBLaAF-MID-53.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	AGTCGAGAGA	GCACGMAGTTTYGC
DBLaAF-MID-54.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	AGTGCTACGA	GCACGMAGTTTYGC
DBLaAF-MID-55.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CGATCGTATA	GCACGMAGTTTYGC
DBLaAF-MID-56.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CGCAGTACGA	GCACGMAGTTTYGC
DBLaAF-MID-57.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CGCGTATACA	GCACGMAGTTTYGC
DBLaAF-MID-58.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CGTACAGTCA	GCACGMAGTTTYGC
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DBLaAF-MID-59.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CGTACTCAGA	GCACGMAGTTTYGC
DBLaAF-MID-60.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CTACGCTCTA	GCACGMAGTTTYGC
DBLaAF-MID-61.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CTATAGCGTA	GCACGMAGTTTYGC
DBLaAF-MID-62.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TACGTCATCA	GCACGMAGTTTYGC
DBLaAF-MID-63.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TAGTCGCATA	GCACGMAGTTTYGC
DBLaAF-MID-64.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TATATATACA	GCACGMAGTTTYGC
DBLaAF-MID-65.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TATGCTAGTA	GCACGMAGTTTYGC
DBLaAF-MID-66.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCACGCGAGA	GCACGMAGTTTYGC
DBLaAF-MID-67.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCGATAGTGA	GCACGMAGTTTYGC
DBLaAF-MID-68.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCGCTGCGTA	GCACGMAGTTTYGC
DBLaAF-MID-69.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCTGACGTCA	GCACGMAGTTTYGC
DBLaAF-MID-70.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TGAGTCAGTA	GCACGMAGTTTYGC
DBLaAF-MID-71.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TGTAGTGTGA	GCACGMAGTTTYGC
DBLaAF-MID-72.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TGTCACACGA	GCACGMAGTTTYGC
DBLaAF-MID-73.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TGTCGTCGCA	GCACGMAGTTTYGC
DBLaAF-MID-74.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACACATACGC	GCACGMAGTTTYGC
DBLaAF-MID-75.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACAGTCGTGC	GCACGMAGTTTYGC
DBLaAF-MID-76.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACATGACGAC	GCACGMAGTTTYGC
DBLaAF-MID-77.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACGACAGCTC	GCACGMAGTTTYGC
DBLaAF-MID-78.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACGTCTCATC	GCACGMAGTTTYGC
DBLaAF-MID-79.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACTCATCTAC	GCACGMAGTTTYGC
DBLaAF-MID-80.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ACTCGCGCAC	GCACGMAGTTTYGC
DBLaAF-MID-81.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	AGAGCGTCAC	GCACGMAGTTTYGC
DBLaAF-MID-82.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	AGCGACTAGC	GCACGMAGTTTYGC
DBLaAF-MID-83.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	AGTAGTGATC	GCACGMAGTTTYGC
DBLaAF-MID-84.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	AGTGACACAC	GCACGMAGTTTYGC
DBLaAF-MID-85.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	AGTGTATGTC	GCACGMAGTTTYGC
DBLaAF-MID-86.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ATAGATAGAC	GCACGMAGTTTYGC
DBLaAF-MID-87.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ATATAGTCGC	GCACGMAGTTTYGC
DBLaAF-MID-88.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	ATCTACTGAC	GCACGMAGTTTYGC

DBLaAF-MID-89.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CACGTAGATC	GCACGMAGTTTYGC
DBLaAF-MID-90.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CACGTGTCGC	GCACGMAGTTTYGC
DBLaAF-MID-91.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CATACTCTAC	GCACGMAGTTTYGC
DBLaAF-MID-92.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CGACACTATC	GCACGMAGTTTYGC
DBLaAF-MID-93.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CGAGACGCGC	GCACGMAGTTTYGC
DBLaAF-MID-94.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CGTATGCGAC	GCACGMAGTTTYGC
DBLaAF-MID-95.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CGTCGATCTC	GCACGMAGTTTYGC
DBLaAF-MID-96.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CTACGACTGC	GCACGMAGTTTYGC
DBLaAF-MID-97.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CTAGTCACTC	GCACGMAGTTTYGC
DBLaAF-MID-98.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CTCTACGCTC	GCACGMAGTTTYGC
DBLaAF-MID-99.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	CTGTACATAC	GCACGMAGTTTYGC
DBLaAF-MID-100.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TAGACTGCAC	GCACGMAGTTTYGC
DBLaAF-MID-101.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TAGCGCGCGC	GCACGMAGTTTYGC
DBLaAF-MID-102.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TAGCTCTATC	GCACGMAGTTTYGC
DBLaAF-MID-103.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TATAGACATC	GCACGMAGTTTYGC
DBLaAF-MID-104.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TATGATACGC	GCACGMAGTTTYGC
DBLaAF-MID-105.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCACTCATAC	GCACGMAGTTTYGC
DBLaAF-MID-106.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCATCGAGTC	GCACGMAGTTTYGC
DBLaAF-MID-107.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCGAGCTCTC	GCACGMAGTTTYGC
DBLaAF-MID-108.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCGCAGACAC	GCACGMAGTTTYGC
DBLaAF-MID-109.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TCTGTCTCGC	GCACGMAGTTTYGC
DBLaAF-MID-110.v2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	TGAGTGACGC	GCACGMAGTTTYGC

Appendix 2-table 2. The single DBL α BR reverse primer sequence. The Illumina Nextera overhang sequence is represented in red (5'-GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG-3') and the reverse primer sequence in green (DBL α BR, 5'-GCCCATTCSTCGAACCA-3'). The reverse primer sequence is not barcoded (i.e. no multiplex identifier (MID)).

Reverse Primer Sequence (5' -> 3'): Reverse Nextera overhang + DBLαBR reverse primer			
Primer name	Reverse Nextera overhang	MID	Primer
DBLaBR.v2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG	N/A	GCCCATTCSTCGAACCA