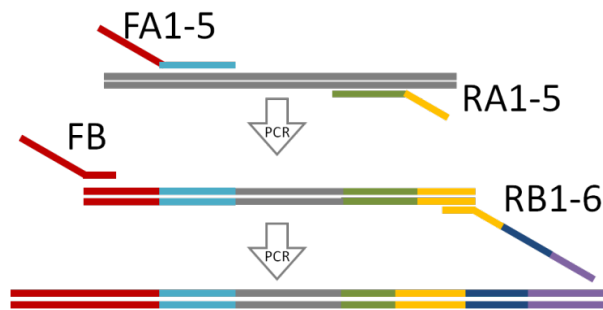


S4 Table. Illumina primer design. Conserved framework positions with regions or sites having low diversity, as is the case with conserved framework positions, require additional considerations during sample preparation to ensure a high level of accuracy during the MiSeq run. The inclusion of variable length degenerate sequence (N_{4-8}) at 5' and 3' ends allow the conserved sites to be offset. Based on TruSeq guidelines, adapter indices are designed to have balanced G/T and C/A content, the following 6 adapter index tags were selected: AD005,6,12,14,18,19. Schematic below demonstrates the two-step PCR used for amplicon library construction. Colored regions of schematic indicate (from left to right) TruSeq universal adapter (red), target primer (cyan), gene of interest (gray), reverse target primer (green), multiplex primer 2.0 (yellow), Illumina index (blue), and Illumina PCR primer (purple). Table at bottom lists individual sequences with item names corresponding to PCR schematic.



Item Name	Length	Sequence
RB1	59	caagcagaagacggcatacagagat CACTGT gtgactggagttcagacgtgtgctcttcc
RB2	59	caagcagaagacggcatacagagat ATTGGC gtgactggagttcagacgtgtgctcttcc
RB3	59	caagcagaagacggcatacagagat TACAAG gtgactggagttcagacgtgtgctcttcc
RB4	59	caagcagaagacggcatacagagat TTTCAC gtgactggagttcagacgtgtgctcttcc
RB5	59	caagcagaagacggcatacagagat GGAAC Tgtgactggagttcagacgtgtgctcttcc
RB6	59	caagcagaagacggcatacagagat GCGGAC gtgactggagttcagacgtgtgctcttcc
FB	51	aatgatacggcgaccaccgagatctacactctttccctacacgacgctctt
RA1	49	G TTCAGACGTGTGCTCTTCCGATCTN N N N N N A A A G C T T T T G T T C G G A T C C
RA2	50	G TTCAGACGTGTGCTCTTCCGATCTN N N N N N A A A G C T T T T G T T C G G A T C C
RA3	51	G TTCAGACGTGTGCTCTTCCGATCTN N N N N N N A A A G C T T T T G T T C G G A T C C
RA4	52	G TTCAGACGTGTGCTCTTCCGATCTN N N N N N N N A A A G C T T T T G T T C G G A T C C
RA5	53	G TTCAGACGTGTGCTCTTCCGATCTN N N N N N N N N A A A G C T T T T G T T C G G A T C C
FA1	51	T T T C C C T A C A C G A C G C T C T T C C G A T C T N N N N N A C T A C G C T C T G C A G G C T A G T
FA2	52	T T T C C C T A C A C G A C G C T C T T C C G A T C T N N N N N A C T A C G C T C T G C A G G C T A G T
FA3	53	T T T C C C T A C A C G A C G C T C T T C C G A T C T N N N N N N A C T A C G C T C T G C A G G C T A G T
FA4	54	T T T C C C T A C A C G A C G C T C T T C C G A T C T N N N N N N N A C T A C G C T C T G C A G G C T A G T
FA5	55	T T T C C C T A C A C G A C G C T C T T C C G A T C T N N N N N N N N A C T A C G C T C T G C A G G C T A G T

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