

		20		40		60	
VSD21+fbpA	ACAGATAAAT	TAAAACGGTT	CCGTGAGTTT	TTTGCTAGAC	CTACTCAAGC	AAGTTTAACC	60
VSD5+fbpA	ACAGATAAAT	TAAAACGGTT	CCGTGAGTTT	TTTGCTAGAC	CTACTCAAGC	AAGTTTAACC	60
VSD9+fbpA	ACAGATAAAT	TAAAACGGTT	CCGTGAGTTT	TTTGCTAGAC	CTACTCAAGC	AAGTTTAACC	60
VSD23+fbpA	ACAGATAAAT	TAAAACGGTT	CCGTGAGTTT	TTTGCTAGAC	CTACTCAAGC	AAGTTTAACC	60
VSD24+fbpA	ACAGATAAAT	TAAAACGGTT	CCGTGAGTTT	TTTGCTAGAC	CTACTCAAGC	AAGTTTAACC	60
VSD13+fbpA	ACAGATAAAT	TAAAACGGTT	CCGTGAGTTT	TTTGCTAGAC	CTACTCAAGC	AAGTTTAACC	60
COI289+fbpA	ACAGACAAAT	TAAAACGGTT	CCGTGAGTTT	TTTGCTAGAC	CTACTCAAGC	AAGTTTAACC	60
SDSE GGS124	ACAGACAAAT	TAAAACGGTT	CCGTGAGTTT	TTTGCTAGAC	CTACTCAAGC	AAGTTTAACC	60
HSM53+fbpA	ACAGACAAAT	TAAAACGGTT	CCGTGAGTTT	TTTGCTAGAC	CTACTCAAGC	AAGTTTAACC	60
Consensus	ACAGATAAAT	TAAAACGGTT	CCGTGAGTTT	TTTGCTAGAC	CTACTCAAGC	AAGTTTAACC	
Sequence logo							
		80		100		120	
VSD21+fbpA	AATACCTCTT	TTGCACCAGT	TCTTTTCTCA	GAGAGCCAAG	CAACGTTTGA	GACTTTATCA	120
VSD5+fbpA	AATACCTCTT	TTGCACCAGT	TCTTTTCTCA	GAGAGCCAAG	CAACGTTTGA	GACTTTATCA	120
VSD9+fbpA	AATACCTCTT	TTGCACCAGT	TCTTTTCTCA	GAGAGCCAAG	CAACGTTTGA	GACTTTATCA	120
VSD23+fbpA	AATACCTCTT	TTGCACCAGT	TCTTTTCTCA	GAGAGCCAAG	CAACGTTTGA	GACTTTATCA	120
VSD24+fbpA	AATACCTCTT	TTGCACCAGT	TCTTTTCTCA	GAGAGCCAAG	CAACGTTTGA	GACTTTATCA	120
VSD13+fbpA	AATACCTCTT	TTGCACCAGT	TCTTTTCTCA	GAGAGCCAAG	CAACGTTTGA	GACTTTATCA	120
COI289+fbpA	AATACCTCTT	TTGCACCAGT	TCTTTTCTCA	GAGAGCCAAG	TGACGTTTGA	GACTTTATCT	120
SDSE GGS124	AATACCTCTT	TTGCACCAGT	TCTTTTCTCA	GAGAGCCAAG	TGACGTTTGA	GACTTTATCT	120
HSM53+fbpA	AATACCTCTT	TTGCACCAGT	TCTTTTCTCA	GAGAGTCAAG	TGACGTTTGA	GACTTTATCT	120
Consensus	AATACCTCTT	TTGCACCAGT	TCTTTTCTCA	GAGAGCCAAG	CAACGTTTGA	GACTTTATCA	
Sequence logo							
		140		160		180	
VSD21+fbpA	GAGATGCTTG	ATCACCTTTA	TCAAGATAAA	GCTGAGCGTG	ACCGTATCAA	TCAACAAGCG	180
VSD5+fbpA	GAGATGCTTG	ATCACCTTTA	TCAAGATAAA	GCTGAGCGTG	ACCGTATCAA	TCAACAAGCG	180
VSD9+fbpA	GAGATGCTTG	ATCACCTTTA	TCAAGATAAA	GCTGAGCGTG	ACCGTATCAA	TCAACAAGCG	180
VSD23+fbpA	GAGATGCTTG	ATCACCTTTA	TCAAGATAAA	GCTGAGCGTG	ACCGTATCAA	TCAACAAGCG	180
VSD24+fbpA	GAGATGCTTG	ATCACCTTTA	TCAAGATAAA	GCTGAGCGTG	ACCGTATCAA	TCAACAAGCG	180
VSD13+fbpA	GAGATGCTTG	ATCACCTTTA	TCAAGATAAA	GCTGAGCGTG	ACCGTATCAA	TCAACAAGCG	180
COI289+fbpA	GAGATGCTTG	ATCACCTTTA	TCAAGATAAA	GCTGAGCGTG	ACCGTATCAA	TCAACAAGCG	180
SDSE GGS124	GAGATGCTTG	ATCACCTTTA	TCAAGATAAG	GCTGAGCGTG	ACCGTATCAA	TCAACAAGCG	180
HSM53+fbpA	GAGATGCTTG	ATCACCTTTA	TCAAGATAAG	GCTGAGCGTG	ACCGTATCAA	TCAACAAGCG	180
Consensus	GAGATGCTTG	ATCACCTTTA	TCAAGATAAA	GCTGAGCGTG	ACCGTATCAA	TCAACAAGCG	
Sequence logo							
		200		220		240	
VSD21+fbpA	AGTGACTTGA	TTCACCGTGT	ACAAAAATGAA	CTAGAAAAAA	ATCGCAACAA	ACTAAGAAAA	240
VSD5+fbpA	AGTGACTTGA	TTCACCGTGT	ACAAAAATGAA	CTAGAAAAAA	ATCGCAACAA	ACTAAGAAAA	240
VSD9+fbpA	AGTGACTTGA	TTCACCGTGT	ACAAAAATGAA	CTAGAAAAAA	ATCGCAACAA	ACTAAGAAAA	240
VSD23+fbpA	AGTGACTTGA	TTCACCGTGT	ACAAAAATGAA	CTAGAAAAAA	ATCGCAACAA	ACTAAGAAAA	240
VSD24+fbpA	AGTGACTTGA	TTCACCGTGT	ACAAAAATGAA	CTAGAAAAAA	ATCGCAACAA	ACTAAGAAAA	240
VSD13+fbpA	AGTGACTTGA	TTCACCGTGT	ACAAAAATGAA	CTAGAAAAAA	ATCGCAACAA	ACTAAGAAAA	240
COI289+fbpA	AGTGACTTGA	TTCACCGTGT	GCAAAAATGAA	CTAGAAAAAA	ATCGCAACAA	ACTAAGTAAA	240
SDSE GGS124	AGTGACTTGA	TTCACCGTGT	GCAAAAATGAA	CTAGAAAAAA	ATCGCAACAA	ACTAAGTAAA	240
HSM53+fbpA	AGTGACTTGA	TTCACCGTGT	GCAAAAATGAA	CTAGAAAAAA	ATCGCAACAA	ACTAAGTAAA	240
Consensus	AGTGACTTGA	TTCACCGTGT	ACAAAAATGAA	CTAGAAAAAA	ATCGCAACAA	ACTAAGAAAA	
Sequence logo							
		260		280		300	
VSD21+fbpA	CAAGAAGCTG	AACCTTTTGGC	TACGGAAAAAC	GCTGAGTTGT	TCCGCCAAAA	AGGTGAGCTG	300
VSD5+fbpA	CAAGAAGCTG	AACCTTTTGGC	TACGGAAAAAC	GCTGAGTTGT	TCCGCCAAAA	AGGTGAGCTG	300
VSD9+fbpA	CAAGAAGCTG	AACCTTTTGGC	TACGGAAAAAC	GCTGAGTTGT	TCCGCCAAAA	AGGTGAGCTG	300
VSD23+fbpA	CAAGAAGCTG	AACCTTTTGGC	TACGGAAAAAC	GCTGAGTTGT	TCCGCCAAAA	AGGTGAGCTG	300
VSD24+fbpA	CAAGAAGCTG	AACCTTTTGGC	TACGGAAAAAC	GCTGAGTTGT	TCCGCCAAAA	AGGTGAGCTG	300
VSD13+fbpA	CAAGAAGCTG	AACCTTTTGGC	TACGGAAAAAC	GCTGAGTTGT	TCCGCCAAAA	AGGTGAGCTG	300
COI289+fbpA	CAAGAAGCTG	AACCTTTTGGC	TACGGAAAAAC	GCTGAGTTGT	TCCGTCAAAA	AGGAGAGCTG	300
SDSE GGS124	CAAGAAGCTG	AACCTTTTGGC	TACGGAAAAAC	GCTGAGTTGT	TCCGTCAAAA	AGGAGAGCTG	300
HSM53+fbpA	CAAGAAGCTG	AACCTTTTGGC	TACGGAAAAAC	GCTGAGTTGT	TCCGTCAAAA	AGGAGAGCTG	300
Consensus	CAAGAAGCTG	AACCTTTTGGC	TACGGAAAAAC	GCTGAGTTGT	TCCGCCAAAA	AGGTGAGCTG	
Sequence logo							
		320		340		360	
VSD21+fbpA	TAAACCACTT	ACCTCAGTAT	GGTTCCTAAT	AACCAGGACT	CCGTGGTGT	AGACAATTAT	360
VSD5+fbpA	TAAACCACTT	ACCTCAGTAT	GGTTCCTAAT	AACCAGGACT	CCGTGGTGT	AGACAATTAT	360
VSD9+fbpA	TAAACCACTT	ACCTCAGTAT	GGTTCCTAAT	AACCAGGACT	CCGTGGTGT	AGACAATTAT	360
VSD23+fbpA	TAAACCACTT	ACCTCAGTAT	GGTTCCTAAT	AACCAGGACT	CCGTGGTGT	AGACAATTAT	360
VSD24+fbpA	TAAACCACTT	ACCTCAGTAT	GGTTCCTAAT	AACCAGGACT	CCGTGGTGT	AGACAATTAT	360
VSD13+fbpA	TAAACCACTT	ACCTCAGTAT	GGTTCCTAAT	AACCAGGACT	CCGTGGTGT	AGACAATTAT	360
COI289+fbpA	TAAACCACTT	ACATCAGTAT	GGTTCCTAAT	AACCAAGACT	CCGTGGTATT	AGACAATTAT	360
SDSE GGS124	TAAACCACTT	ACATCAGTAT	GGTTCCTAAT	AACCAAGACT	CCGTGGTATT	AGACAATTAT	360
HSM53+fbpA	TAAACCACTT	ACATCAGTAT	GGTTCCTAAT	AACCAAGACT	CCGTGGTATT	AGACAATTAT	360
Consensus	TAAACCACTT	ACCTCAGTAT	GGTTCCTAAT	AACCAGGACT	CCGTGGTGT	AGACAATTAT	
Sequence logo							

		380		400		420	
VSD21+fbpA	TACACAGGCG	AAAAGATTGA	GATTGCCTTA	GACAAGGCAC	TAAACCCCAA	TCAAAATGCT	420
VSD5+fbpA	TACACAGGCG	AAAAGATTGA	GATTGCCTTA	GACAAGGCAC	TAAACCCCAA	TCAAAATGCT	420
VSD9+fbpA	TACACAGGCG	AAAAGATTGA	GATTGCCTTA	GACAAGGCAC	TAAACCCCAA	TCAAAATGCT	420
VSD23+fbpA	TACACAGGCG	AAAAGATTGA	GATTGCCTTA	GACAAGGCAC	TAAACCCCAA	TCAAAATGCT	420
VSD24+fbpA	TACACAGGCG	AAAAGATTGA	GATTGCCTTA	GACAAGGCAC	TAAACCCCAA	TCAAAATGCT	420
VSD13+fbpA	TACACAGGCG	AAAAGATTGA	GATTGCCTTA	GACAAGGCAC	TAAACCCCAA	TCAAAATGCT	420
COI289+fbpA	TACACGGGCG	AAAAGCTTGA	GATTGCCCTA	GACAAGGCAC	TAAACCTTAA	TCAAAATGCT	420
SDSE GGS124	TACACGGGCG	AAAAGCTTGA	GATTGCCCTA	GACAAGGCAC	TAAACCTTAA	TCAAAATGCT	420
HSM53+fbpA	TACACGGGCG	AAAAGCTTGA	AATTGCCCTA	GACAAGGCAC	TAAAGCTTAA	TCAAAATGCT	420
Consensus	TACACAGGCG	AAAAGATTGA	GATTGCCTTA	GACAAGGCAC	TAAACCCCAA	TCAAAATGCT	
Sequence logo							
		440		460		480	
VSD21+fbpA	CAACGTTATT	TTAAAAAATA	CCAAAAGCTA	AAAGAAGCTG	TCAAACACTT	ATCTGGATTG	480
VSD5+fbpA	CAACGTTATT	TTAAAAAATA	CCAAAAGCTA	AAAGAAGCTG	TCAAACACTT	ATCTGGATTG	480
VSD9+fbpA	CAACGTTATT	TTAAAAAATA	CCAAAAGCTA	AAAGAAGCTG	TCAAACACTT	ATCTGGATTG	480
VSD23+fbpA	CAACGTTATT	TTAAAAAATA	CCAAAAGCTA	AAAGAAGCTG	TCAAACACTT	ATCTGGATTG	480
VSD24+fbpA	CAACGTTATT	TTAAAAAATA	CCAAAAGCTA	AAAGAAGCTG	TCAAACACTT	ATCTGGATTG	480
VSD13+fbpA	CAACGTTATT	TTAAAAAATA	CCAAAAGCTA	AAAGAAGCTG	TCAAACACTT	ATCTGGATTG	480
COI289+fbpA	CAACGTTATT	TTAAAAAATA	CCAAAAGCTA	AAAGAAGCTG	TCAAACACTT	ATCTGGATTG	480
SDSE GGS124	CAACGTTATT	TTAAAAAATA	CCAAAAGCTA	AAAGAAGCTG	TCAAACACTT	ATCTGGATTG	480
HSM53+fbpA	CAACGTTATT	TTAAAAAATA	CCAAAAGCTA	AAAGAAGCTG	TCAAACACTT	ATCTGGATTG	480
Consensus	CAACGTTATT	TTAAAAAATA	CCAAAAGCTA	AAAGAAGCTG	TCAAACACTT	ATCTGGATTG	
Sequence logo							
		500		520		540	
VSD21+fbpA	ATTACCGATA	CCAAGCAAAG	TATTGCGTAT	TTTGAGAGTG	TGGACTACAA	TTTGTCCCAA	540
VSD5+fbpA	ATTACCGATA	CCAAGCAAAG	TATTGCGTAT	TTTGAGAGTG	TGGACTACAA	TTTGTCCCAA	540
VSD9+fbpA	ATTACCGATA	CCAAGCAAAG	TATTGCGTAT	TTTGAGAGTG	TGGACTACAA	TTTGTCCCAA	540
VSD23+fbpA	ATTACCGATA	CCAAGCAAAG	TATTGCGTAT	TTTGAGAGTG	TGGACTACAA	TTTGTCCCAA	540
VSD24+fbpA	ATTACCGATA	CCAAGCAAAG	TATTGCGTAT	TTTGAGAGTG	TGGACTACAA	TTTGTCCCAA	540
VSD13+fbpA	ATTACCGATA	CCAAGCAAAG	TATTGCGTAT	TTTGAGAGTG	TGGACTACAA	TTTGTCCCAA	540
COI289+fbpA	ATTGCCGATA	CCAAGCAAAG	TATTGCTTAC	TTTGAGAGCG	TGGACTACAA	TTTATCCCAA	540
SDSE GGS124	ATTGCCGATA	CCAAGCAAAG	TATTGCTTAC	TTTGAGAGCG	TGGACTACAA	TTTATCCCAA	540
HSM53+fbpA	ATTGCCGATA	CCAAGCAAAG	TATTGCTTAC	TTTGAGAGCG	TGGACTACAA	TTTATCCCAA	540
Consensus	ATTACCGATA	CCAAGCAAAG	TATTGCGTAT	TTTGAGAGTG	TGGACTACAA	TTTGTCCCAA	
Sequence logo							
		560		580		600	
VSD21+fbpA	GTAAGTATCG	AAGATATTGA	AGATATTCCG	GAAGAGTTAT	ATCAAGCTGG	CTTTTTGAAA	600
VSD5+fbpA	GTAAGTATCG	AAGATATTGA	AGATATTCCG	GAAGAGTTAT	ATCAAGCTGG	CTTTTTGAAA	600
VSD9+fbpA	GTAAGTATCG	AAGATATTGA	AGATATTCCG	GAAGAGTTAT	ATCAAGCTGG	CTTTTTGAAA	600
VSD23+fbpA	GTAAGTATCG	AAGATATTGA	AGATATTCCG	GAAGAGTTAT	ATCAAGCTGG	CTTTTTGAAA	600
VSD24+fbpA	GTAAGTATCG	AAGATATTGA	AGATATTCCG	GAAGAGTTAT	ATCAAGCTGG	CTTTTTGAAA	600
VSD13+fbpA	GTAAGTATCG	AAGATATTGA	AGATATTCCG	GAAGAGTTAT	ATCAAGCTGG	CTTTTTGAAA	600
COI289+fbpA	GCAAGTATCG	AAGATATTGA	AGATATTCCG	GAAGAGTTAT	ATCAGGCTGG	CTTTTTGAAG	600
SDSE GGS124	GCAAGTATCG	AAGATATTGA	AGATATTCCG	GAAGAGTTAT	ATCAGGCTGG	CTTTTTGAAG	600
HSM53+fbpA	GCAAGTATCG	AAGATATTGA	AGATATTCCG	GAAGAGTTAT	ATCAGGCTGG	CTTTTTGAAG	600
Consensus	GTAAGTATCG	AAGATATTGA	AGATATTCCG	GAAGAGTTAT	ATCAAGCTGG	CTTTTTGAAA	
Sequence logo							
		620					
VSD21+fbpA	AGTCGCCACC	GTGATAAACG	620				
VSD5+fbpA	AGTCGCCACC	GTGATAAACG	620				
VSD9+fbpA	AGTCGCCACC	GTGATAAACG	620				
VSD23+fbpA	AGTCGCCACC	GTGATAAACG	620				
VSD24+fbpA	AGTCGCCACC	GTGATAAACG	620				
VSD13+fbpA	AGTCGCCACC	GTGATAAACG	620				
COI289+fbpA	AGTCGCCACC	GTGATAAACG	620				
SDSE GGS124	AGTCGCCACC	GTGATAAACG	620				
HSM53+fbpA	AGTCGCCACC	GTGATAAACG	620				
Consensus	AGTCGCCACC	GTGATAAACG					
Sequence logo							