

NAT PCR and Sequencing Primers		
NAT1		
2856 bp	Oligonucleotide	5'-3' Sequence
	-1182_F	GCCAAGCACTGGTCCTAGAG
	-455_R	CAAAGTTTCCCCTCAAAGA
	-574F	AAGCACTAGAACAGTAGGAA
	-194_R	CCCAGAATCCTGTGAGAAATG
	-78_F	GCCATAATTAGCCTACTCAA
	+301_R	GTGAATCATGCCAGTGCTGT
	+473_F	CTGGTATCTAGACCAAATC
	+933_F	CCTATCATGTATCTTCTGTAC
	+1387_F	TGCCATACAAGAATGAACATGA
	+1420_R	GGATTTCAACTCAGATCTAC
	+2066_R	AGCTGGAAAAGGCCAGTACA
NAT2		
3064 bp	Oligonucleotide	5'-3' Sequence
	-1134_F	TCCTACATAGTTTATGTGAC
	-545_F	ACACATCAAGAGTATTCTGT
	-443_R	GACCCACTTGATTTCCCATTT
	-77_R	GGATCTGGTGCTCAAGAATG
	-15_F	CTTGCTTAGGGGATCATGGACA
	+702_F	GTGGGCTTCATCCTCACCTAT
	+779_R	CAGCACTTCTTCAACCTCTTCC
	+1320_F	AATAGAGTCTTCTCTCATC
	+1373_R	TGTGGCAAAGTATGGATGGA
	+1812_F	ACTGCAGATTTGTTCTTAAC
	+2412_R	ATTCGCTTCCAGGTTGAAG
NATP1		
3000 bp	Oligonucleotide	5'-3' Sequence
	-1204_F	GGCATTACTGCCTAGAGCATTTT
	-1160_F	TCAAACCTACCAATGACATTCTGC
	-577_R	GCAGATAACCTACAGAGTGGGA
	-631_F	TGGGACTCAAACCTAAAGTGCTTGTA
	-60_F	CAAGGGAATCTAAGGGCAAAAAG
	-14_R	TTGTTTAAGGGATCATGG
	+535_F	TGATCTCCGGAAGAAAAGAAA
	+555_R	CCTTACTCCTGAATCCTGAACA
	+1080_F	CCTGTGATTATCTTGGGAACCAT
	+1112_R	TGTGAGAAAATATTTAATGCGGG
	+1500_F	CAGTGCCAGACCTGGAGTAAA
	+1655_R	ATCTGCCTGCTTCTTCTTG
	+1860_R	CCTGTGATTATCTTGGGAACCAT
<p>*All primer numbering is with respect to the +1=ATG . <i>NATP1</i> ATG start was inferred according to consensus alignment with <i>NAT1</i> and <i>NAT2</i> F and R denote Forward and Reverse Primers, respectively.</p>		