

# Primers and allele-specific oligonucleotides

## Primers

### VNTR amplification primers

Name	Sequence
INS-1296	CTGCTGAGGACTTGCTGCTTG
INS-23+	CAGAAGGACAGTGATCTGGGT
INS-23-	CAGAAGGACAGTGATCTGGGA

### MVR-PCR primers

Name	Sequence
TAG	TCATGCGTCCATGGTCCGGA
INS-MA	TCATGCGTCCATGGTCCGGAACCCCTGTCCCCAC
INS-MB	TCATGCGTCCATGGTCCGGAACCCCTGTCCCCAGG
INS-MC	TCATGCGTCCATGGTCCGGAACCCCTGTCCCCAG
INS-ME	TCATGCGTCCATGGTCCGGAACCCCTATCCCCAC
INS-MF	TCATGCGTCCATGGTCCGGAACCCCTGTCCCCGGG
INS-MH	TCATGCGTCCATGGTCCGGAACCCCTGTCCCCAC

### Primers for fragmenting large alleles

Name	Sequence
INS-MBR	CTGCTGAGGACTTGCTGCTTGGGGGACAGGGGTCCCT
INS-MEF	CAGAAGGACAGTGATCTGGGATCCCCACACCCCTA
INS-MER	CTGCTGAGGACTTGCTGCTTGCAGGGGTGTGGGGAT
INS-MFF	CAGAAGGACAGTGATCTGGGAACCCCTGTCCCCGGG
INS-MFR	CTGCTGAGGACTTGCTGCTTGGGGGACAGGGGTCCC
INS-MHF	CAGAAGGACAGTGATCTGGGACCCACACCCCTGTG
INS-MHR	CTGCTGAGGACTTGCTGCTTGCAGGGGTGTGGGC

### Sequencing primers

Name	Sequence
5F1	GAGCAGGGCTGGACCTGTGA
5F2	CCCGGCAGTCTCTAGTGGAA
5F3	GCACCTGCTTCTCAGCGCAA
5F4	TCCCAGCCCTTGAGAGAAAACA
5F5	GGGTGTCTCTGAAGGGCTGT
5F6	CTGGTGCTAAGAGGCAGGTA
5R1	GCCGCCATGGATGGGCCAA
3F1	CCTCCAGCTCTCCTGGTCTA
3F2	GACGTGGCTGGGCTCGTGAA
3R4	GCACACTAGGTAGAGAGCTTC
3F8	GAGGCTTCTTCTACACACCCAA
3F3	TCCCTGTGGCCAGTCAGAA
3F4	GTGGGTGACCCTCCCTCTAA
3F5	GGGTGCCACAGGTGCCAA
3F6	GCCCAGGTCCAGCCAGACA
3F6-NEST	CCACTGGTGCCTTGGAGGAA
3R5	TGCAATCCTCAGGGCCTCAT
3R3	TGCTTCTCCTGGGCTGCAATC
3F7	TGCTGGAGCTGAGGTATGTGA

3R2 ACAGCTTGGCCGATGGCTGA  
 3R1-NEST GGAGCAGTTAGATGGACCCAA  
 3R1 CTTGTGACTGGGGAGCAGTTA

## Allele-specific oligonucleotides

SNP	Allele	Sequence
INS-1	C	5'-CCCCTGGCTGCAGCAGCC-3'
	T	5'-CCCCTGGTTGCAGCAGCC-3'
INS-2	A	5'-TGAGGACATCCTGTGGAA-3'
	G	5'-TGAGGACGTCCTGTGGAA-3'
INS-3	C	5'-CCCCCTGCCCTGGGATGG-3'
	T	5'-CCCCCTGTCCTGGGATGG-3'
INS-4	C	5'-GAGCCACCGTGAAGGTGG-3'
	T	5'-GAGCCACTGTGAAGGTGG-3'
INS-5	C	5'-CCATCGACGTGCTGGACA-3'
	T	5'-CCATCGATGTGCTGGACA-3'
INS-6	A	5'-AATCACCATCACAATAAA-3'
	G	5'-AATCACCGTCACAATAAA-3'
INS-7	C	5'-CCACAGACACAGACCCTG-3'
	G	5'-CCACAGAGACAGACCCTG-3'
INS-9	A	5'-GGCCTGGAAGGGAGCAGG-3'
	C	5'-GGCCTGGCAGGGAGCAGG-3'
INS-10	C	5'-CACTACACGCTGCTGGGA-3'
	T	5'-CACTACATGCTGCTGGGA-3'
INS-11	C	5'-AGCTCCCCGGCCGACAAC-3'
	T	5'-AGCTCCCTGGCCGACAAC-3'
INS-12	C	5'-CTCCCCCATCCAGCCTC-3'
	T	5'-CTCCCCCTATCCAGCCTC-3'
INS-14	C	5'-GAAAGGGCGGAAGGGAGG-3'
	T	5'-GAAAGGGTGAAGGGAGG-3'
INS-16	A	5'-AGGCTAAGGCCAGGGTGG-3'
	G	5'-AGGCTGAGGCCAGGGTGG-3'
INS-17	A	5'-GGTGTCAAGGGACCTGGC-3'
	T	5'-GGTGTGTCATGGGACCTGGC-3'
INS-18	A	5'-TGCCGCCACCCCAGATC-3'
	G	5'-TGCCGCCGCCCCAGATC-3'
INS-19	C	5'-GATCACACGGAAGATGAG-3'
	T	5'-GATCACATGGAAGATGAG-3'
INS-20	C	5'-CAGGTCCCCAGGTCATGC-3'
	T	5'-CAGGTCTCAGGTCATGC-3'

INS-21	A C	5' -CACTYCCACTCTCCCACC-3' 5' -CACTYCCCCTCTCCCACC-3'
INS-24	C G	5' -GGGTTGACAGGTAGRGA-3' 5' -GGGTTGAGAGGTAGRGA-3'
INS-25	A G	5' -AGGTAGAGGAGATGGGCT-3' 5' -AGGTAGGGGAGATGGGCT-3'
INS-69	+ -	5' -AGGTCTTTGCGTTCCAAG-3' 5' -GCAGGTCTGTTCCAAGGG-3'
INS-26	A G	5' -GCTCARGATTCCAGGGTG-3' 5' -GCTCARGGTTCCAGGGTG-3'
INS-27	A T	5' -GCCTGTCACCCAGATCAC-3' 5' -GCCTGTCTCCCAGATCAC-3'
INS-72	C T	5' -TCACTGTCCTTCTGCCAT-3' 5' -TCACTGTTCTTCTGCCAT-3'
INS-70	A G	5' -TGCTGGCACTGCTGGCCC-3' 5' -TGCTGGCGCTGCTGGCCC-3'
INS-28	C T	5' -AGCCAACCGCCCATTGCT-3' 5' -AGCCAACGCCCATTGCT-3'
INS-31	C T	5' -GTGGGCACGCTCCTYCCT-3' 5' -GTGGGCATGCTCCTYCCT-3'
INS-32	C T	5' -CTGCCTCCGGGCGAACAC-3' 5' -CTGCCTCTGGGCGAACAC-3'
INS-34	C G	5' -ACACCCACTGTGGGTGAC-3' 5' -ACACCCAGTGTGGGTGAC-3'
INS-35	C T	5' -GGGAGTGCGACCTAGGGC-3' 5' -GGGAGTGTGACCTAGGGC-3'
INS-36	A G	5' -CCTCGCCACTGTTCCGGA-3' 5' -CCTCGCCGCTGTTCCGGA-3'
INS-37	C T	5' -CTCTGCGCGGCACGTYCT-3' 5' -CTCTGCGTGGCAGTYCT-3'
INS-38	C T	5' -CGCAGCCCGCAGGCAGCC-3' 5' -CGCAGCCTGCAGGCAGCC-3'
INS-39	A C	5' -CAGCCCCACACCCGCCGC-3' 5' -CAGCCCCCACCAGCCGC-3'
INS-40	C T	5' -TGCCTGTTCGGCTGCCTGC-3' 5' -TGCCTGTTGGCTGCCTGC-3'
INS-41	G T	5' -GGGAGCTGCGGGGTCTC-3' 5' -GGGAGCTTCGGGGTCTC-3'
INS-42	A G	5' -GCCAGGGATGGTGGGGCC-3' 5' -GCCAGGGTGGTGGGGCC-3'

INS-43	C	5´-AGAGACCACGGCCAGGGT-3´
	G	5´-AGAGACCAGGGCCAGGGT-3´
INS-45	C	5´-CTTAGCCCACCCCCTCCC-3´
	T	5´-CTTAGCCTACCCCCTCCC-3´
INS-49	A	5´-GCTCCACCCAGGGCTGGG-3´
	T	5´-GCTCCACCTGGGCTGGG-3´
INS-71	+	5´-GCTGGGCTGGGGATGGCT-3´
	-	5´-ACCCWGGGCTGGGGATGG-3´
INS-51	C	5´-GAGGCCCTTCTGGGAGG-3´
	G	5´-GAGGCCCGTTCTGGGAGG-3´
INS-52	A	5´-GGACCGTATGTTGGAGTG-3´
	G	5´-GGACCGTGTGTTGGAGTG-3´
INS-53	A	5´-CTGGGGGATGAGGAGTGT-3´
	C	5´-CTGGGGGCTGAGGAGTGT-3´
INS-54	C	5´-GTGTCTTCYGAGGGGCCA-3´
	T	5´-GTGTCTTTYGAGGGGCCA-3´
INS-73	C	5´-GCAAGGCCGCCACCCAA-3´
	T	5´-GCAAGGCTGCCACCCAA-3´
INS-56	A	5´-GCCCTGGACCAGAGCTGG-3´
	G	5´-GCCCTGGGCCAGAGCTGG-3´
INS-74	A	5´-CCAGCACCTTGACCCAC-3´
	G	5´-CCAGCGCCTTGACCCAC-3´
INS-57	A	5´-GGAGACCACAGCCAGGGC-3´
	G	5´-GGAGACCGCAGCCAGGGC-3´
INS-60	A	5´-ATRAGAAACAGTTGGCCA-3´
	G	5´-ATRAGAAGCAGTTGGCCA-3´
INS-63	C	5´-GRCAGCCCTTCAGTGTCC-3´
	T	5´-GRCAGCCTTTCAGTGTCC-3´
INS-64	C	5´-GGAGCCTCGGYTTCACAT-3´
	G	5´-GGAGCCTGGGYTTCACAT-3´
INS-65	C	5´-GCCTSGGCTTCACATGCC-3´
	T	5´-GCCTSGGTTCACATGCC-3´
INS-66	C	5´-TGCCACCRGGCTGGCAG-3´
	T	5´-TGCCACTRGGCTGGCAG-3´
INS-67	A	5´-GCCCACYAGGCTGGCAGG-3´
	G	5´-GCCCACYGGGCTGGCAGG-3´
INS-68	A	5´-CAGCCCCAGCGGTCACCC-3´
	G	5´-CAGCCCCGGCGGTCACCC-3´