


**A**

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**m5-10**



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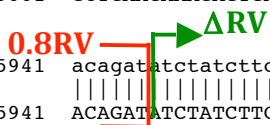
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m5-5

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Seq_1	6061	atctcgtgtgccagtttgtaagcaaaatacagaaaacaacattgagtgggtggctggcttc	6120
Seq_2	6061	ATCTCGTGTGCCAGTTTGTAAAGCAAAATACAGAAAACAACATTGAGTGGTGGCTGGCTTC	6120
Seq_1	6121	gtgcaccatctaagcccaaggaaggaagtgtttctggctgggttgttgcctggggaaggc	6180
Seq_2	6121	GTGCACCATCTAAGCCCAAGGAAGGAAGTGTCTTCTGGCTGGGTGTGCTTGGGGAAGGC	6180
Seq_1	6181	cagcttttccctctcgggaagggcctgctgattatattatggggattaattttatcctcaa	6240
Seq_2	6181	CAGCTTTTCCCTCTCGGGAAGGGCCTGCTGATTATTTATGGGGATTAATTTTATCCTCAA	6240
Seq_1	6241	atctctgtgaatgtaaaagggattggcgaggtctgtctgatttcccctatgcttcaacc	6300
Seq_2	6241	ATCTCTGTGAATGTAAAAGGGATTGGCGAGGTCTGTCTGGATTTCCCTATGCTTCAACC	6300
Seq_1	6301	agagatgcaggtctcaaccggcttccagcttccagtcctgcaccaaggttgaggttgc	6360
Seq_2	6301	AGAGATGCAGGCTCTCAACCGCTTTCAGCTTTCAGTCTGCACCCAAGGTTGAGGTTGC	6360
Seq_1	6361	ctctctgttcaaccccaaaggctttctagctgactttttagaagcgcgtgacgaaggtgt	6420
Seq_2	6361	CTCTCTGTTCAACCCCAAAGGCTTTCAGCTGACTTTTTAGAAAGCGGTGACGAAGGTGT	6420
Seq_1	6421	ttgcacaaataaatagctggccttgccagggtctgtgtgaaaacagacctggaaactag	6480
Seq_2	6421	TTGCACAAATAAATAGCTGGCCTTGCCAGGGTCTGTGTGAAAACAGACCTGGAAACTAG	6480
Seq_1	6481	agagtggggttgccctagctgccccacgcttacaactgcaaagtccactgaagttttt	6540
Seq_2	6481	AGAGTGGGGTTGCCCTAGCTGCCCCACGCTTACAAC TCAAAGTCCACTGAAGTTTTT	6540
Seq_1	6541	gcaagggcagcctgcaaattttgcagccacagaggctacaatgttgcggagtcctatgg	6600
Seq_2	6541	GCAAGGGCAGCCTGCAAATTTGTCAGCCACAGAGGCTACAATGTTGCCGGAGTCCTATGG	6600
Seq_1	6601	gctc	6660
Seq_2	6601	GCTC	6660



Seq_1	6661	tccagtccttggctctaaggatgtagtttctaattagagtc ccagaaaagactccctgta	6720
Seq_2	6661	TCCAGTCCTTGGCTCTAAGGATG TAGTTTCTAATTAGAGTCC CAGAAAAGACTCCCTGTA	6720
Seq_1	6721	cttagagaatacaaggaagctgaagagggaaacagaatgtgatttggggcatttgtttca	6780
Seq_2	6721	CTTAGAGAATACAAGGAAGCTGAAGAGGGAAACAGAATGTGATTGGGGCATTGTTTCA	6780
Seq_1	6781	agcaacattctgtgcttctcccggcctggttctgcttacagcaagagctacttccagtgc	6840
Seq_2	6781	AGCAACATTCTGTGCTTGTCCCGCCTGGTCTGCTTACAGCAAGAGCTACTTCCAGTGC	6840
Seq_1	6841	ctctgctgtgggctgcttttattcaccctctgaactgcagacttcagagaggctaagggc	6900
Seq_2	6841	CTCTGCTGTGGGCTGCTTTTATTACCCCTCTGAAC TGCAGACTTCAGAGAGGCTAAGGGC	6900
Seq_1	6901	aggccaaggagtgtgagcagctgaacccccagccagcctcagtgactgattattttaa	6960
Seq_2	6901	AGGCCAAGGAGTGTGGCAGCTGAAACCC CAGCCAGCCCTCAGTGACTGATTATTTTAA	6960
Seq_1	6961	taaaactgggcactgctctgtgtacactccagtgtgtgtcttgaggagggggcacacaca	7020
Seq_2	6961	TAAAAC TGGGC ACTGCTCTGTGTACACTCCAGTGTGTGCTTGAGGAGGGGGCACACACA	7020
Seq_1	7021	acaatttcttggcatctttgatcttgggtcccccacctaaggcaccttctcccccaagt	7080
Seq_2	7021	ACAATTTCTTGGCATCTTTGATCTTGGT TCCCCATCCTAAGGCACCTTCTCCCCAAGT	7080
Seq_1	7081	cctagagagccttgagtgaggtagggtagggtaggggacaatgagtctgaagtggaggagatg	7140
Seq_2	7081	CCTAGAGAGCCTTGAGTGGGTAGGGTAGGGGACAATGAGTCTGAAGTGGAGGAGAGATG	7140
Seq_1	7141	tcaaggcagctagtcctggctctgcaaggggccaggcagggtcacaccactctctgtctg	7200
Seq_2	7141	TCAAGGCAGCTAGTCTGGCTCTGCAAGGGGCCAGGCAGGGT CACACC ACTCTCTGTCTG	7200
Seq_1	7201	aggtcagcattggagacagaaatcgggtagggctgcagaggcccatgggtgtgtgcacac	7260
Seq_2	7201	AGGTCAGCATTGGAGACAGAAATCGGGT GAGGCTGCAGAGGCCCATGGGTGTGTGCACAC	7260
Seq_1	7261	gcctaatacatccagtcttgggtctctgcagggtgggccattgaaattgctgggctccc	7320
Seq_2	7261	GCCTAATGATCCAGTCTTGGTCTCTGCAGGGCTGGGCCATTGAAATTGCTGGGCTCCC	7320
Seq_1	7321	agagttctgccttgattactgtagcttgcctgcctgccttccttcttcttcttcttctt	7380
Seq_2	7321	AGAGTTCTGCCTTGATTACTGTAGCTTGCTGCCTGCCTTCCTTCTTCTTCTTCTTCTT	7380
Seq_1	7381	ccttccttcccttcccttcccttcccttcccttcccttcttcttcttcttcttcttcttctt	7440
Seq_2	7381	CCTT	7440
Seq_1	7441	cactggctcagagcagtcacagagatggaaggagggtaaagaggatgggaagtggaaaag	7500
Seq_2	7441	CACTGGCTCAGAGCAGTCAACAGAGATGGAAGGAGGGTAAAGAGGATGGGAAGTGGAAAAG	7500
Seq_1	7501	ggagtggggggtggggaatcagcaggctctatagtggttcaagagtttggggtatatctag	7560
Seq_2	7501	GGAGTGGGGGTGGGGAATCAGCAGGTCTATAGTGGTTC AAGAGTTTGGGGTATATCTAG	7560
Seq_1	7561	tgagaaagtgggaaagtggtgggaggaggaggaggaggaggagagagacacacacacac	7620
Seq_2	7561	TGAGAAAGTGGGAAAGTGGTGGGAGGAGGGAGGGAGGGAGGAGAGGACACACACACAC	7620





Seq_1	8521	tccctggatcctggcaagggttccggagggtttctccctatggctggccgcgaatgggag	8580
Seq_2	8521	TCCCTGGATCCTGGCAAGGGTTCCGGAGGGTTTCTCCCTATGGCTGGCCGCGAATGGGAG	8580
Seq_1	8581	agcgtatgtggggctccagccctgttttctttggtatgagaagatcatgggggatccca	8640
Seq_2	8581	AGCGTATGTGGGGCTCCAGCCCTGTTTTCTTTGTTATGAGAAGATCATGGGGGATCCCA	8640
Seq_1	8641	tggcagttttccccaagctcctaaggccagaggaagaagaattgggcctcagaaacgat	8700
Seq_2	8641	TGGCAGTTTTCCCAAGCTCCTAAGGCCAGAGGAAGAAGAATTGGGCCTCAGAAACGAT	8700
Seq_1	8701	ctgtggcgggttaggtctcaggccgcttcaaacaggctggtatgcaggcttctttgcct	8760
Seq_2	8701	CTGTGGCGGTTTAGGTCTCAGGCCGCTTCAAACAGGCTGGTATGCAGGCTTCTTTGCCT	8760
Seq_1	8761	aagaagctgctaaaactgtggaagccatctcttacttgaggtctgctggtgttttgagg	8820
Seq_2	8761	AAGAAGCTGCTAAAACGTGGAAGCCATCTCTTACTTGAGGTCTGCTGGTGTTTGAGG	8820
Seq_1	8821	tagaggcagtggtagaaatcctcccttgaggaagggggtgaactaagaatttcaactgc	8880
Seq_2	8821	TAGAGGCAGTGGTAGAAATCCTCCCTTGAGGAAGGGGTTGAACTAAGAATTTCAACTGC	8880
Seq_1	8881	ttgcttcatcttcttctggtgaacactcggggctgcctaccaatgtacctcctcccta	8940
Seq_2	8881	TTGCTTCATCTTCTTCTGTTGAACACTCGGGGCTGCCCTACCAATGTACCTCCTCCCTA	8940
Seq_1	8941	gcagtccactgaatgtctgcagcccagaatttatctgggactgatttaggctgtccgac	9000
Seq_2	8941	GCAGTCCACTGAATGTCTGCAGCCCAGAATTTATCTGGGACTGATTTTAGGCTGTCCGAC	9000
Seq_1	9001	tgggagccaggctggcagtttgagttagccagccccgttgaagctcaagacattccctt	9060
Seq_2	9001	TGGGAGCCAGGCTGGCAGTTTGAGTTAGCCAGCCCCGTTGAAGCTCAAAGACATTCCCTT	9060
Seq_1	9061	tagcttgattactccacgaaaacgcctgcaccaccgccccccccactctcccag	9120
Seq_2	9061	TAGCTTGATTACTCCACGAAAACGCCTGCACCACCGCCCCCCCCACTCTCCCGCAG	9120
Seq_1	9121	ccagccgatctgaaaagatccgtgagggtagacagccccgccaccggcagtgagagtcag	9180
Seq_2	9121	CCAGCCGATCTGAAAAGATCCGTGAGGGTACAGCCCCGCCACCGCAGTGAGAGTCAG	9180
Seq_1	9181	ccaccgagttgtaggcccctctctgatttgatctacctccagctctccctggctacttt	9240
Seq_2	9181	CCACCAGTTGTAGGCCCTCTCTGATTTGGATCTACCTCCAGCTCTCCCTGGCTACTTT	9240
Seq_1	9241	atattttattttattttattttattttattttattttattttattttccattggtattgctt	9300
Seq_2	9241	ATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTTCCATTGGTATTGCTT	9300
Seq_1	9301	aggcttgggagaggtggttcatthtaaatgcctgtaacagatgatgagagggttattat	9360
Seq_2	9301	AGGCTTGGGAGAGGCTGTTTCATTTAATGCCTGTAACAGATGATGAGAGGGTTATTAT	9360
Seq_1	9361	cctctatcctccgggtatatactctttctcccctgttttttatttttgaagacgcggtt	9420
Seq_2	9361	CCTCTATCCTCCGGGTATATCTCTTTCTCCCCTGTTTTTATTTTGAAGACGCGGTT	9420
Seq_1	9421	attctgggccttttctctattgtagaaaaataacgtctcttaggaggtttcatttttaa	9480
Seq_2	9421	ATTCTGGGCCTTTTCTCTATTGTAGAAAAATAACGTCTCTTAGGAGGTTTCATTTTTAA	9480

Seq_1	9481	aaattgctggcatggtctcttggatttgacaaagaccatttctcaaaggggcacaaggtt	9540
Seq_2	9481	AAATTGCTGGCATGGTCTCTTGGATTTGACAAAGACCATTCTCAAAGGGGCACAAGGTT	9540
Seq_1	9541	tttgtttctgttttgtttgggtttctaccgatggcttccaaaaataccgacgcctta	9600
Seq_2	9541	TTTGTTTTCTGTTTTGTTTTGGGTTTCTACCCGATGGCTTCCAAAAATACCGACGCCTTA	9600
Seq_1	9601	tctttattggctcttccaggagttcagacaaatttgacggacagctctcttatcaccag	9660
Seq_2	9601	TCTTTATTGGCTCTTCCAGGAGTTCAGACAAATTTGACGGACAGCTCTCTTATCACCAG	9660
Seq_1	9661	agcctgtgcaggggagatgtgggggaccttccgcctcctcctgtctgaagcgggtctt	9720
Seq_2	9661	AGCCTGTGCAGGGGAGATGTGGGGGACCTTGCCGCCTCCTCCTGTCTGAAGCGGGTCTT	9720
Seq_1	9721	tcgcaagcgggtggtgctggtcggaagtataacaataaaaaagactttctgaagcctc	9780
Seq_2	9721	TCGCAAGCGGTGGTGCCTGGTGGTGGAAAGTATAACAATAAAAAAGACTTTCTGAAGCCTC	9780
Seq_1	9781	cttcagcttggagtgaaggggtcaaacagcttgtcccctatgtcgctagacactctccaac	9840
Seq_2	9781	CTTCAGCTTGGAGTGAAGGGTCAAACAGCTTGTCCCCTATGTCGCTAGACACTCTCCAAC	9840
Seq_1	9841	tccctctcttgcctcagaatagaaacctcgcgcgggcacaggaaccctgcgaccatgg	9900
Seq_2	9841	TCCCTCTCTTGTCTCAGAAATAGAACTCGCGCGGGCACAGGAACCCCTGCGCACCATGG	9900
Seq_1	9901	ccgatacagatgagggtcttggcctggcgcgacgcctctggagcctgattccaaagaca	9960
Seq_2	9901	CCGATACAGATGAGGGCTTTGGCCTGGCGCGCACGCCTCTGGAGCCTGATTCCAAAGACA	9960
Seq_1	9961	ggtcttgcgattcgaaacctgagagtgtcttgggggtcccagcaagtctccatcatccc	10020
Seq_2	9961	GGTCTTGCGATTTCGAAACCTGAGAGTGCTCTGGGGGTCCCAGCAAGTCTCCATCATCCC	10020
Seq_1	10021	cgagcgtgccttaccagcaggttaagaaaagccggcccagcggcaggcgtagaccgag	10080
Seq_2	10021	CGCAGCTGCCTTACCCAGCAGGTAAGAAAAGCCGCCAGCGGCAGGCGTAGACCAGAG	10080
Seq_1	10081	gactgagcccagctctctgtaaacggtgcaggggggtgggcagggccagctattcctct	10140
Seq_2	10081	GACTGAGCCCAGCTCTCTGTAACGGTGCAGGGGGTGGGCAGGGCCAGCTATTCCCTCT	10140
Seq_1	10141	atctcctggctagtctcaccaaatctcccccaattccactctatcccaatccactttatc	10200
Seq_2	10141	ATTCCTGGCTAGTCTACCAAATCTCCCCAATTCACACTCTATCCCAATCCACTTTATC	10200
Seq_1	10201	gagcgtttatctttatggcctgctattttagaaacctatttadattattggagagctc	10260
Seq_2	10201	GAGCGTTTTATCTTTATGGCCTGCGTATTTTAGAAACCTATT-----	10242
Seq_1	10261	tcaattatccgactatttggggtcagctaacaacgggccagataattctctcccagctgc	10320
Seq_2	10243	-----	10242
Seq_1	10321	cctgggtatgccttattaagggtcgggtcagcggccgcttcaggccggcatgagcgtga	10380
Seq_2	10243	-----	10242
Seq_1	10381	cttgaccctccttagatctttcttagccttcgctcggctcgcctgctctgcgaacccg	10440
Seq_2	10243	-----	10242

→ m5-5#3

→ intron2

MscI (a)

MscI (b)



Seq_1	10441	cctcgcccctcatcacagtaccatttatcttctgctccgggctgaggagctccctgacc	10500
Seq_2	10243	-----	10242
Seq_1	10501	gccgaggagagcacacaggggctggaaccaaggcaccagagcccggctgactggaagt	10560
Seq_2	10243	-----	10242
Seq_1	10561	ggtccgagtgaggaggaggtcttctggtctgttatttgagtgccatcgtttttggg	10620
Seq_2	10243	-----GCCATCGTTTTTGGG	10259
Seq_1	10621	ggcgctaagtaggtttaaaactaggtgtcactggaaggcttgaccagagagatgagttt	10680
Seq_2	10260	GGCGCTAAGTAGGTTTAAAAC TAGGTGTCACTGGGAAGGCTTGACCAGAGAGATGAGTTT	10319
Seq_1	10681	gatctagaaatcttgtccaattgatgtgtatagcttttaataaaagcaaagaggctta	10740
Seq_2	10320	GATCTAGAAATCTTGTC CAATTGATGTGTATAGCTTTAATAAAAAGCAAAGAGGCTTA	10379
Seq_1	10741	agaatagtttgggaaattacataacattttggaaaggaaaacaagttcactttttag	10800
Seq_2	10380	AGAATAGTTTGGGAAATTTACATAACATTTGAAAAGGAAAACAAGTTCAC'TTTT TAG	10439
Seq_1	10801	tcggtggtgataaattgtttcacaatgaagagtagtctgactgttttggtattggttt	10860
Seq_2	10440	TCGGTGGTTGATAATTGTTTCACAATGAAGAGTAGTCTGACTGTTTTGGTATTGGTTT	10499
Seq_1	10861	ttagaaataaacttccagtggaagagaaaatgttaaaaggcttaattggtgcccgaagt	10920
Seq_2	10500	TTAGAAATAA'CTCCAGTGGAAAGAGAAAATGT'AAAAGGCTTAATTGGTTGCCCAAGT	10559
Seq_1	10921	caaagaaaaggctggcggtggtgctagataaggcaagagctctgaaagattgtaataata	10980
Seq_2	10560	CAAAGAAAAGGCTGGCGGTGGTCTAGATAAGGCAAGAGCTCGAAAGATTGTTAATATA	10619
Seq_1	10981	gacactgagggggaaaactacttttttggtccttgagaagaaaaacgattttaaaattg	11040
Seq_2	10620	GACTGAGGGGGAAAAC TACTTTTTTGGTCC'TGAGAAGAAAACGATTTTAAAATTG	10679
Seq_1	11041	aaaatttctacatagtggtcaccatgtgttgaatccttagcacttaggaggggtgaggcag	11100
Seq_2	10680	AAAATTTCTACATAGTGGCTCACATGTGT'GGAATCTTAGCACTTAGGAGGGTGAGGCAG	10739
Seq_1	11101	gagggttgccaaagagtttgagaccacttttatgcgctgcatagtgaaattccaggcctgtc	11160
Seq_2	10740	GAGGGTTGCCAAGAGTTTGAGACC ACTTTATGCGCTGCATAGTGAATTCAGGCCTGTC	10799
Seq_1	11161	tgggctgcagagcaagactttgtctccaatattaataacaacaataatattgaaaatttt	11220
Seq_2	10800	TGGGCTGCAGAGCAAGACTTTGTCTCCAATATTAATAACAACAATAATATTGAAAATTTT	10859
Seq_1	11221	tgtatgttcatattagaccagtgatgacggacagcgatgtatttgcatagctgtgtgt	11280
Seq_2	10860	TGTATGTT'CATATTTAGACCCAGTGATGACGGACAGCGATGTATTTGCATAGCTGTGTGT	10919
Seq_1	11281	tttgcactggttgacaatacaaaaatacctagtggttttctagatggatcccctcc	11340
Seq_2	10920	TTTGCATCTGGGTGACAATACAAAATACTTAGTGGGTTTTCTAGATGGATCCCCTCC	10979

#5

intron2 MscI

#6

intron2 MfeI

