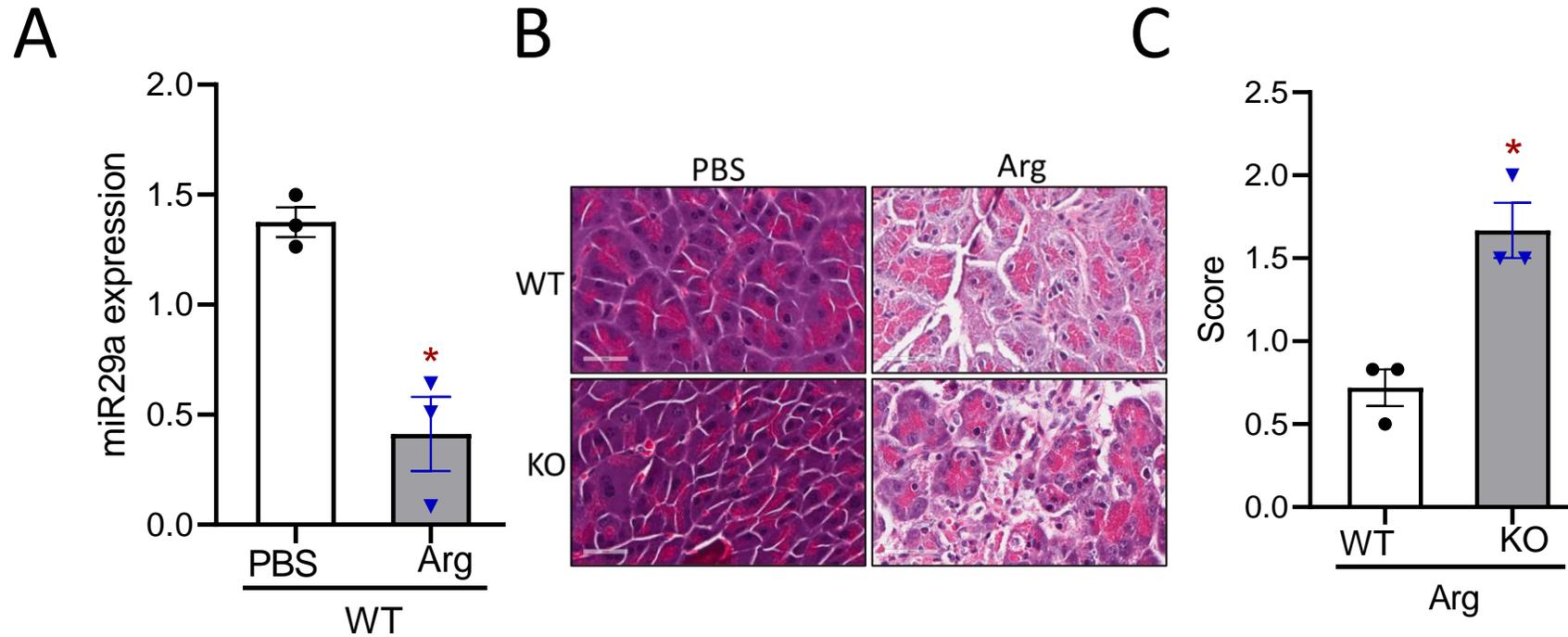
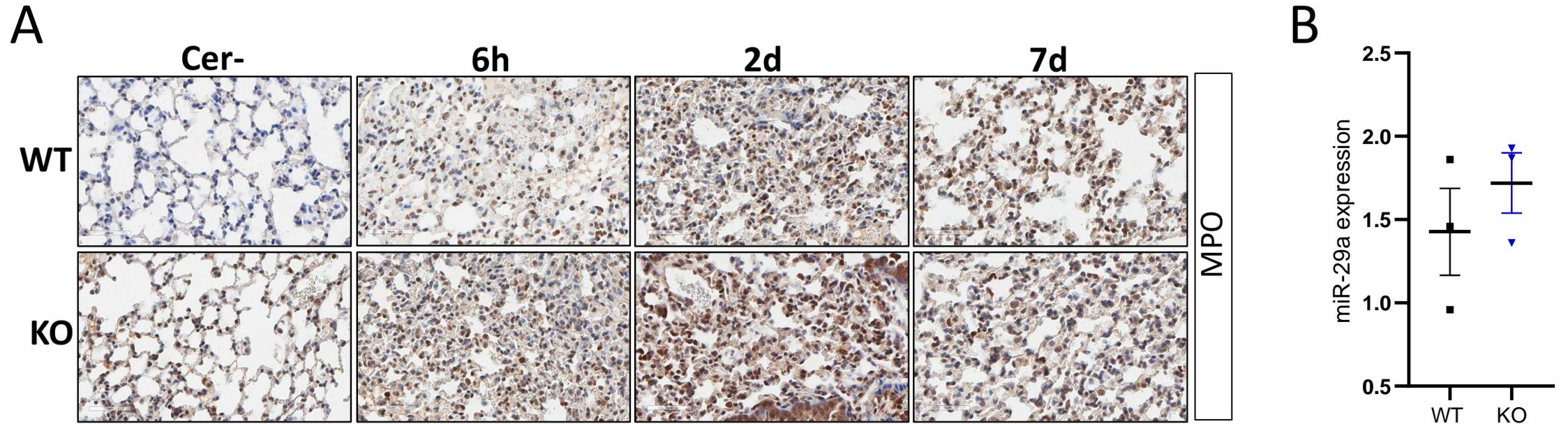


Supplemental Figure 1. Pancreatic sections of WT and KO mice at 1, 3 and 12 months of age immunostained with antibodies against **(A)** amylase (green)/ counterstained with DAPI (blue), **(B)** insulin (green)/counterstained with DAPI (blue), and **(C)** CK19 (green), photographed at 40X objective (scale bar= 62.2 μm).



Supplemental Figure 2. (A) qPCR analysis of miR-29a expression in pancreata of WT mice 72h post final L-arginine injection. **(B)** Representative H&E images of pancreatic sections of WT and KO mice treated with PBS or L-arginine at 72h post L-arginine administration (scale bars = 40 μ m). **(C)** Quantification of inflammatory cell infiltration from H&E-stained pancreatic sections of L-arginine dosed WT and miR-29a/b1 KO mice 72hrs post final injection. Graphs represent Mean \pm SEM; n=3 mice/group/timepoint, * p < 0.05, 2-tailed Student's t test.



Supplemental Figure 3. (A) Representative images for MPO staining in the lungs of saline (Cer-) or caerulein dosed WT and KO mice at the indicated time-points (Scale bars = 50 μ m). **(B)** miR-29a expression in the lungs of WT and miR-29a KO mice assessed by qPCR analysis. Results represent Mean \pm SEM; n= 3mice/group/timepoint, 2-tailed Student's *t* test.

Supplemental Table 1. Summary of clinical characteristics of human subjects.¹

	Normal	Chronic Pancreatitis (CP)
Pancreas		
Normal	4	0
Pancreatitis	0	4
Sex		
Male	2	3
Female	2	1
Average age at procedure	68.75	66.75
Age Range	61-77	56-76
Race		
Non-Hispanic, White	4	4

¹ Source: Indiana University Simon Cancer Center Tissue Bank and Department of Pathology

Supplemental Table 2. Demographic and clinical characteristics of normal and human chronic pancreatitis patients.¹

ID	Sex	Birth Year	Ethnicity	Race	Procedure Year	Histological Characteristics of pancreas
NP-1	F	1932	Non-Hispanic	White	2006	100% normal pancreas
NP-2	M	1947	Non-Hispanic	White	2010	100% normal pancreas
NP-3	F	1951	Non-Hispanic	White	2012	100% normal pancreas
NP-4	M	1936	Non-Hispanic	White	2013	100% normal pancreas
CP-1	M	1961	Non-Hispanic	White	2010	100% pancreatitis
CP-2	M	1949	Non-Hispanic	White	2010	100% pancreatitis
CP-3	M	1955	Non-Hispanic	White	2011	100% pancreatitis
CP-4	F	1935	Non-Hispanic	White	2011	100% pancreatitis

¹ Source: Indiana University Simon Cancer Center Tissue Bank and Department of Pathology

Supplemental Table 3. miR-29a/b1 KO Strategy using CRISPR/CAS9.

Long ssODN with offset homology:

Color codes: Blue: 5'-homology; Green: loxP; Purple: EcoR1; Black: Floxed miR-29a/b1 genomic region; Red: 3'-homology.

```

ccccacccccactgctagatgaggtcagcataggatcgctgaaattaggaactattgcacggacttcacctccctctataacttcgtatagcatacattatacgaagttatGAATTCcgg
taggaaggccacaaaaacagacgacaaagcttctcaggaagctggtttcatatggtggtttagatttaaatagtgattgctagcaccatttgaatcagtgttcttggggagaactacttcgc
tgccgaccgcacaaagaaatgagtgtagcagccctgaagtaagtgccaggtgctctaaaacaggctaccagagcctgcctcgcacccctgcttacctctgtgttatggatagctgattagtcac
caccgttagaattgcatactgttcatgtaataagccttctctggaagtggactcccatgctcggatgaagacctacatatacagacagattgaaggcctgggccttccagtgacatgacctc
ttgtgacccttagaggatgactgattcttttgggttccagtgtaataagaatttctagcaccatctgaaatcggttataatgattggggaagagcaccgtttagctgactactgttattgctgacg
ttggagccacaggttaagaattaagaacaaatacctcaaaacatgataacttcgtatagcatacattatacgaagttatGAATTCcgaaggtacattttcttctatcttaaaccttgactttcat
    
```

Genomic sequence of miR-29a/b1 (yellow highlight)

9601	CTTCACCTTC	CCCTCTCCGTA	GGAAGGCCAC	AA	AAACAGAC	GACAAAGCTT	CTTCAGGAAG	CTGGTTTCAT	ATGGTGGTTT	AGATTAAAT	AGTGATTGTC
	GAAGTGGAAAG	GGAGAGGCAT	CCTTCCGGTG	TTTT	TGTCTG	CTGTTTCGAA	GAAGTCCTTC	GACCAAAGTA	TACCACCAA	TCTAAATTTA	TCACTAACAG
9701	TAGCACCATT	TGAAATCAGT	GTTCTTGGTG	GAGA	ACTACT	TCGCTCCCGA	CCGCACAAAG	AAATGAGTGT	ACAGCCCTGA	AGTAAAGTGC	CAGTGTCTAA
	ATCGTGGTAA	ACTTTAGTCA	CAAGA	ACCAC	CITITGAIGA	AGCGACGGCT	GGCGTGTTC	TTTACTCACA	TGTCGGGACT	TCATTACAG	GTCACAGATT
9801	AACAGGCTAC	CAGAGCCTGC	CCTCGCCAC	CCTG	CTTACC	TCTGTGTTAT	GGATAGCTGA	TTAGTCAACC	ACCGTTAGAA	TTCATACTT	GTTCATGTAA
	TTGTCCGATG	GTCTCGGACG	GGAGCGGGTG	GGAC	GAATGG	AGACACAATA	CCTATCGACT	AATCAGTTGG	TGGCAATCTT	AACGTATGAA	CAAGTACAIT
9901	TAAGCCTTCT	CTGGAAGTGG	ACTCCACCAT	GCTC	GGATGA	AGACCTACAT	ATACGACAGA	TTGAAGGCCT	GGGCCTTCCC	AGTGACATG	ACCTCTTGTG
	ATTCGGAAGA	GACCTTCACC	TGAGGTGGA	CGAG	CCTACT	TCTGGATGTA	TATGCTGTCT	AACTTCCGGA	CCCGGAAGGG	TCACGTGTAC	TGGAGAACAC
0001	ACCCCTTAGA	GGATGACTGA	TTTCTTTTGG	TGTT	CAGAGT	CAATAGAATT	TTCTAGCACC	ATCTGAAATC	GGTTATAATG	ATTGGGGAG	AGCACCGTTC
	TGGGGAATCT	CCTACTGACT	AAAGAAAACC	ACA	AGTCTCA	GTTATCTTAA	AAGATCGTGG	TAGACTTTAG	CCAATATTAC	TAACCCCTTC	TCGTGGCAAG
0101	AGCTGACTAC	GTTATTGCTG	ACGTTGGAGC	CACAG	GTAAG	AATTAAGAA	CAAATACCAA	AACATGCTAA	GGTACATTTT	CITCCTAICT	TAAACTTGAC
	TCGACTGATG	CAATAACGAC	TGCAACCTCG	GTGTC	CAATC	TTAATCTTT	GTTTATGTTT	TGTACGATT	CCAATGAAAA	GAAGGATAGA	ATTGAAGTGC

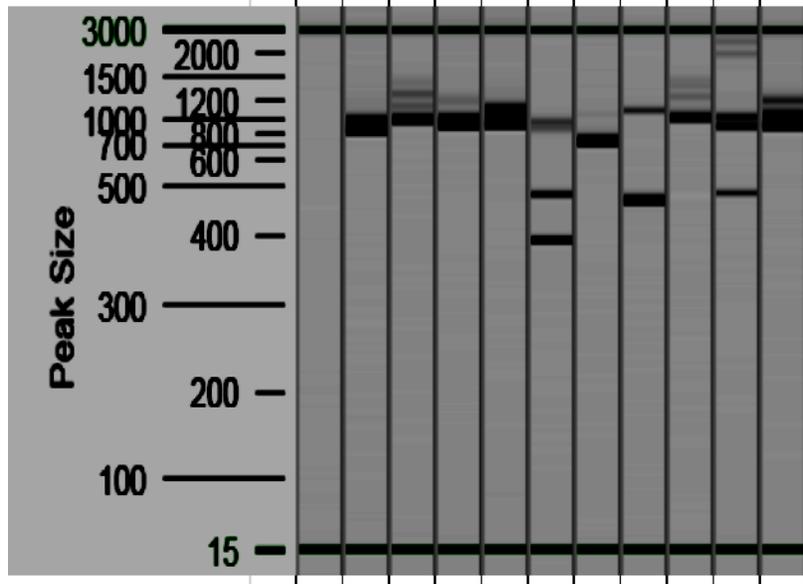
Cut

Cut

Supplemental Table 4. PCR confirmation of founder line with expected deletion.

Sample	Exdel	Seq candidate
CR1646-1	NO	
CR1646-2	NO	
CR1646-3	NO	
CR1646-4	YES	
CR1646-5	NO	
CR1646-6	YES	YES
CR1646-7	NO	
CR1646-8	YES	
CR1646-9	NO	

Sample ID	Assay	Well
NTC	Mir29a/Mir29b-1	A:1
WT	5529	A:2
CR1646-1	5F/3R	A:3
CR1646-2		A:4
CR1646-3		A:5
CR1646-4		A:6
CR1646-5		A:7
CR1646-6		A:8
CR1646-7		A:9
CR1646-8		A:10
CR1646-9		A:11



Supplemental Table 5. Sequence confirmation of founder line with expected homologous recombination.

Forward:

TGCNCGTGAATGTGTAAGCCTCGTGCTCACTGTCCCACGTCTGCTCTCGGGTGAGGGCTCAGTTACCATTTGGAGGGAAGAATGCCATGAGTGACCGACATGTCACA
CCCCACCCCACCTGCTAGATGAGGTCAGCATAGGATCGCCTGAAATTAGGAACTATTGCACGGACTTCACCTTCCCTCTATAAATTTCGTATAGCATAATTATACGA
AGTTATGAATTCCCGTAGGAAGGCCACAAAACAGACGACAAAGCTTCTTCAGGAAGCTGGTTTCATATGGTGGTTTAGATTTAATAGTGATTGTCTAGCACCATT
TGAAATCAGTGTCTTGGTGGAGAATACTTCGCTGCCGACCGACAAAGAAATGAGTGTACAGCCCTGAAGTAAGTGTCCAGTGTCTAAAACAGGCTACCGAGC
CTGCCCTCGCCACCCTGCTTACCTCTGTGTTATGGATAGCTGATTAGTCAACCACCGTTAGAATTGCATACTTGTTTCATGTAATAAGCCTTCTCTGGAAGTGGACTCC
ACCATGCTCGGATGAAGACCTACATATACGACAGATTGAAGGCCTGGGCCTTCCCAGTGCACATGACCTCTTGACCCCTTAGAGGATGACTGATTTCTTTTGTGT
TNNNANNNAANANNNTNTCTAGCACCATCTGAAATCGGTTANNATGANTGNTGACA



Reverse:

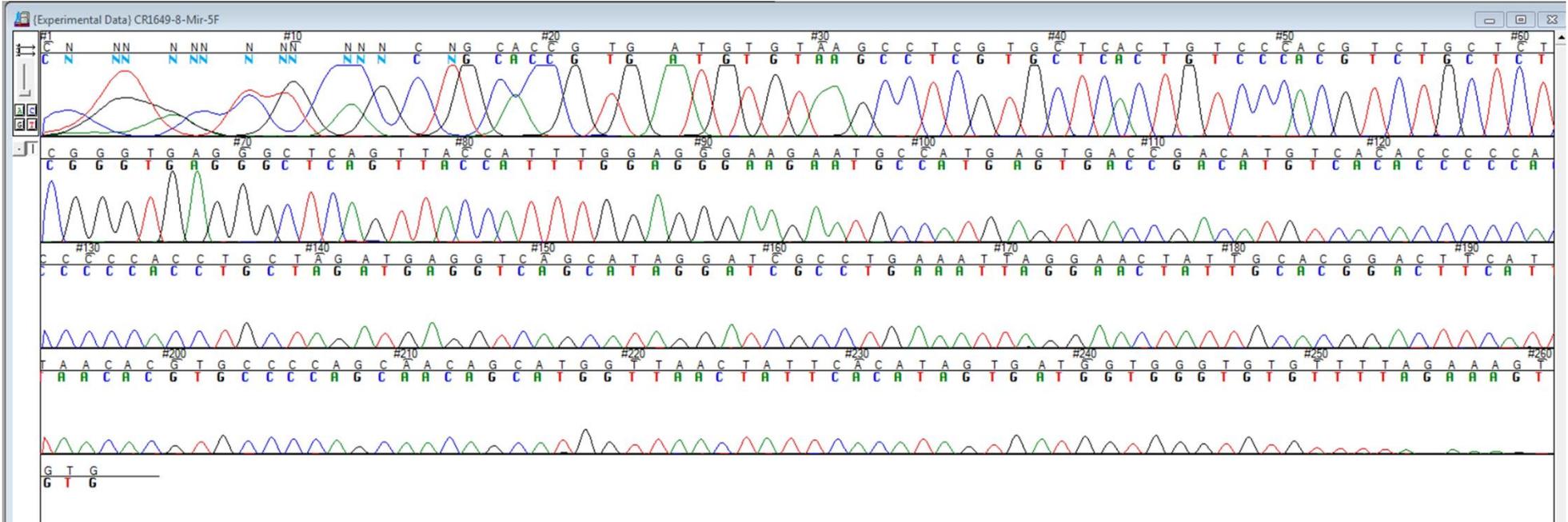
NGGCAGGCTAGGTGACTATCCCTATGTGAGCTGTTAGAACCTTATAGAAGTAAATATCCCCTGCTCCTCTCACATTGACTGGTCAGTCATTGGTTTGGCCCTTATCCT
CTAGTTACCGTCAAATCTGCAACCCATACACACTTTCTAAAACACACCCACCATCACTATGTGAATAGTTAACCATGCTGTTGCTGGGGCACGTGTTAATGAAAGTCA
AGTTTAAGATAGGAAGAAAATGTACCTTAGGAATTCATAACTTCGTATAATGTATGCTATACGAAGTTATCATGTTTTGGTATTTGTTTCTTAATTCTTACCTGTGGCT
CCAACGTCAGCAATAACGTAGTCAGCTGAACGGTGTCTTCCCAATCATTATAACCGATTTTCAGATGGTGCTAGAAAATTCTATTGACTCTGAACACCAAAGAAAT
CAGTCATCCTCTAAGGGGTCACAAGAGGTCATGTGCACTGGGAAGGCCAGGCCTTCAATCTGTCGTATATGTAGGTCTTCATCCGAGCATGGTGGAGTCCACTTCC
AGAGAAGGCTTATTACATGAACAAGTATGCAATTCTAACGGTGGTTGACTAATCAGCTATCCATAACACAGAGGTAAGCNGGGTGGGCGAGGGCAGGCTCTGGTA
GCCTGTTTTAGACTGGACTTACTTCAGGGCTGTACTACTATTTCTTTGTGCGGTCGGCAGCGAANTAGTTCTCCACCAAGAACACTGATTTCAATGGTGCTAG
ACATCACTATTANTCTAAACCACCATATGAAACCANNTCTGNNAAAGCTNTGTGCACTGTTNNGTCG



CR1649-8

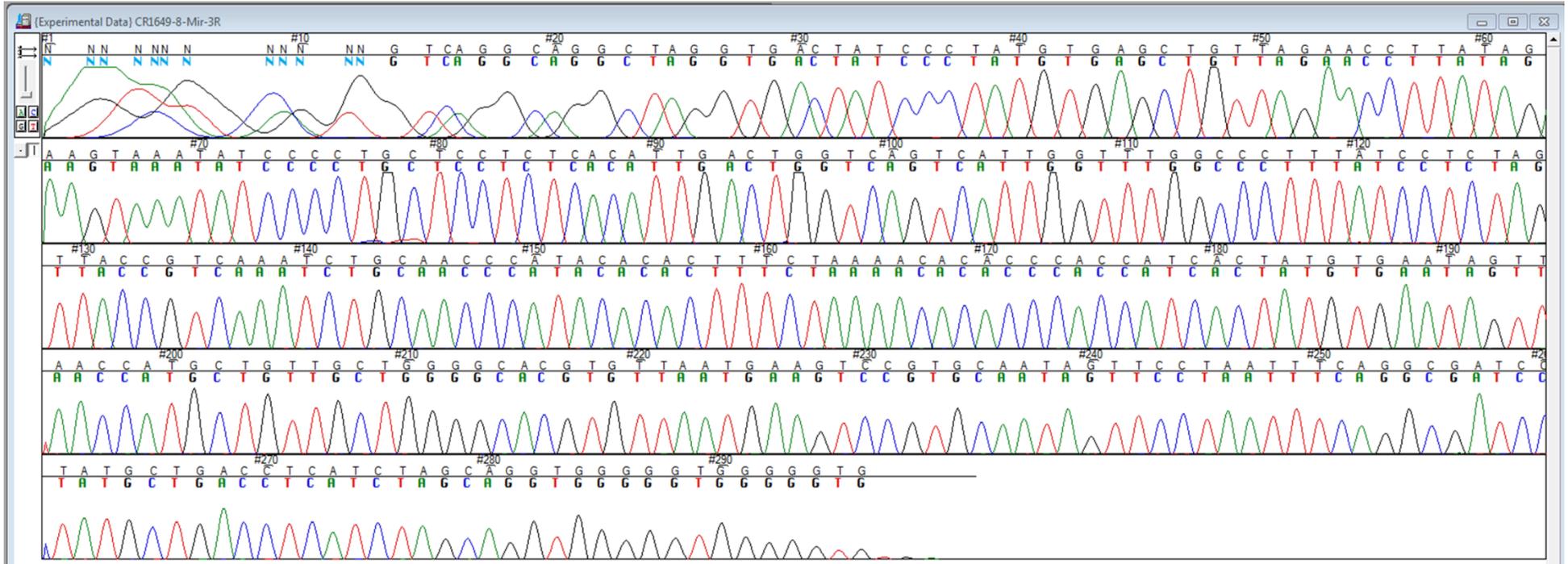
Forward:

CNGCACCGTGATGTGTAAGCCTCGTGCTCACTGTCCCACGCTGCTCTCGGGTGAGGGCTCAGTTACCATTTGGAGGGAAGAATGCCATGAGTGACCGACATGTCAC
ACCCCCACCCACCTGCTAGATGAGGTCAGCATAGGATCGCCTGAAATTAGGAACTATTGCACGGACTTCATTAACACGTGCCCCAGCAACAGCATGGTAACTATT
CACATAGTGATGGTGGGTGTGTTTTAGAAAGTGTG



Reverse:

GTCAGGCAGGCTAGGTGACTATCCCTATGTGAGCTGTTAGAACCTTATAGAAGTAAATATCCCCTGCTCCTCTCACATTGACTGGTCAGTCATTGGTTTGGCCCTTTAT
CCTCTAGTTACCGTCAAATCTGCAACCCATACACACTTTCTAAAACACACCCACCATCACTATGTGAATAGTTAACCATGCTGTTGCTGGGGCAGTGTTAATGAAGTC
CGTGCAATAGTTCTAATTCAGGCGATCCTATGCTGACCTCATCTAGCAGGTGGGGGTGGGGGTG



CR1646-6 FWD (5'):

Query	1	TGAGCTCTGCCACGCTGCACCGTGAATGTGTAAGCCTCGTGCTCACTGTCCCACGTCTGC	60
Sbjct	1	TG-----CNCG-----TGAATGTGTAAGCCTCGTGCTCACTGTCCCACGTCTGC	44
Query	61	TCTCGGGTGAGGGCTCAGTTACCATTTGGAGGGGAAGAATGCCATGAGTGACCGACATGTC	120
Sbjct	45	TCTCGGGTGAGGGCTCAGTTACCATTTGGAGGGGAAGAATGCCATGAGTGACCGACATGTC	104
Query	121	ACACCCCCACCCCCACCTGCTAGATGAGGTGAGCATAGGATCGCCTGAAATTAGGAACTA	180
Sbjct	105	ACACCCCCACCCCCACCTGCTAGATGAGGTGAGCATAGGATCGCCTGAAATTAGGAACTA	164
Query	181	TTGCACGGACTTCACCTTCCCTCTATAA CTTCGTATAGCATACATTATACGAAGTT ATGA	240
Sbjct	165	TTGCACGGACTTCACCTTCCCTCTATAA CTTCGTATAGCATACATTATACGAAGTT ATGA	224
Query	241	ATTCCCGTAGGAAGGCCACAAAAACAGACGACAAAGCTTCTTCAGGAAGCTGGTTTCATA	300
Sbjct	225	ATTCCCGTAGGAAGGCCACAAAAACAGACGACAAAGCTTCTTCAGGAAGCTGGTTTCATA	284
Query	301	TGGTGGTTTAGATTTAAATAGTGATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGTGG	360
Sbjct	285	TGGTGGTTTAGATTTAAATAGTGATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGTGG	344
Query	361	AGAACTACTTCGCTGCCGACCGCACAAAGAAATGAGTGTACAGCCCTGAAGTAAGTGTC	420
Sbjct	345	AGAACTACTTCGCTGCCGACCGCACAAAGAAATGAGTGTACAGCCCTGAAGTAAGTGTC	404
Query	421	AGTGTCTAAAACAGGCTACCAGAGCCTGCCCTCGCCACCCCTGCTTACCTCTGTGTTATG	480
Sbjct	405	AGTGTCTAAAACAGGCTACCAGAGCCTGCCCTCGCCACCCCTGCTTACCTCTGTGTTATG	464
Query	481	GATAGCTGATTAGTCAACCACCGTTAGAATTGCATACTTGTTTCATGTAATAAGCCTTCTC	540
Sbjct	465	GATAGCTGATTAGTCAACCACCGTTAGAATTGCATACTTGTTTCATGTAATAAGCCTTCTC	524
Query	541	TGGAAGTGGACTCCACCATGCTCGGATGAAGACCTACATATACGACAGATTGAAGGCCTG	600
Sbjct	525	TGGAAGTGGACTCCACCATGCTCGGATGAAGACCTACATATACGACAGATTGAAGGCCTG	584
Query	601	GGCCTTCCCAGTGACATGACCTCTTGTGACCCCTTAGAGGATGACTGATTTCTTTTGGT	660
Sbjct	585	GGCCTTCCCAGTGACATGACCTCTTGTGACCCCTTAGAGGATGACTGATTTCTTTTGN	644

CR1646-6 REV (3')

Query	1	CAGGCAGGCTAGGTGACTATCCCTATGTGAGCTGTTAGAACCTTATAGAAGTAAATATCC	60
Sbjct	1	N-GGCAGGCTAGGTGACTATCCCTATGTGAGCTGTTAGAACCTTATAGAAGTAAATATCC	59
Query	61	CCTGCTCCTCTCACATTGACTGGTCAGTCATTGGTTTGGCCCTTTATCCTCTAGTTACCG	120
Sbjct	60	CCTGCTCCTCTCACATTGACTGGTCAGTCATTGGTTTGGCCCTTTATCCTCTAGTTACCG	119
Query	121	TCAAATCTGCAACCCATACACACTTTCTAAAACACACCCACCATCACTATGTGAATAGTT	180
Sbjct	120	TCAAATCTGCAACCCATACACACTTTCTAAAACACACCCACCATCACTATGTGAATAGTT	179
Query	181	AACCATGCTGTTGCTGGGGCACGTGTTAATGAAAGTCAAGTTTAAAGATAGGAAGAAAATG	240
Sbjct	180	AACCATGCTGTTGCTGGGGCACGTGTTAATGAAAGTCAAGTTTAAAGATAGGAAGAAAATG	239
Query	241	TACCTTAGGAATTCACTAATTCGTATAATGTATGCTATACGAAGTTATCATGTTTTGGTA	300
Sbjct	240	TACCTTAGGAATTCACTAATTCGTATAATGTATGCTATACGAAGTTATCATGTTTTGGTA	299
Query	301	TTTGTTCCTTAATTCCTTACCTGTGGCTCCAACGTCAAGCAATAACGTAGTCAGCTGAACGG	360
Sbjct	300	TTTGTTCCTTAATTCCTTACCTGTGGCTCCAACGTCAAGCAATAACGTAGTCAGCTGAACGG	359
Query	361	TGCTCTTCCCAATCATTATAAACCATTTCAGATGGTGCTAGAAAATTCTATTGACTCTG	420
Sbjct	360	TGCTCTTCCCAATCATTATAAACCATTTCAGATGGTGCTAGAAAATTCTATTGACTCTG	419
Query	421	AACACCAAAAGAAATCAGTCATCCTCTAAGGGGTCAACAAGAGGTATGTGCACTGGGAAG	480
Sbjct	420	AACACCAAAAGAAATCAGTCATCCTCTAAGGGGTCAACAAGAGGTATGTGCACTGGGAAG	479
Query	481	GCCCAGGCCTTCAATCTGTCGTATATGTAGGTCTTCATCCGAGCATGGTGGAGTCCACTT	540
Sbjct	480	GCCCAGGCCTTCAATCTGTCGTATATGTAGGTCTTCATCCGAGCATGGTGGAGTCCACTT	539
Query	541	CCAGAGAAGGCTTATTACATGAACAAGTATGCAATTCTAACGGTGGTTGACTAATCAGCT	600
Sbjct	540	CCAGAGAAGGCTTATTACATGAACAAGTATGCAATTCTAACGGTGGTTGACTAATCAGCT	599
Query	601	ATCCATAACACAGAGGTAAGCAGGGTGGGCGAGGGCAGGCTCTGGTAGCCTGTTTTAGAC	660
Sbjct	600	ATCCATAACACAGAGGTAAGCAGGGTGGGCGAGGGCAGGCTCTGGTAGCCTGTTTTAGAC	659
Query	661	ACTGGACACTTACTTCAGGGCTGTACACTCATTTCCTTTGTGCGGTCGGCAGCGAAGTAGT	720
Sbjct	660	ACTGGACACTTACTTCAGGGCTGTACACTCATTTCCTTTGTGCGGTCGGCAGCGAANTAGT	719
Query	721	TCTCCACCAAGAACAAGTATTTCAAATGGTGCTAGACAATCACTATTTAAATCTAAACCA	780
Sbjct	720	TCTCCACCAAGAACAAGTATTTCAAATGGTGCTAGACA-TCACTATT--ANTCTAAACCA	776

CR1649-8 (5') NOTE: appears to have sequence from the deletion. REPEAT NECESSARY.

```
Query 1   TGAGCTCTGCCACGCTGCACCGTGAATGTGTAAGCCTCGTGCTCACTGTCCCACGCTCTGC 60
Sbjct 1   CNGCACCGTGA-TGTGTAAGCCTCGTGCTCACTGTCCCACGCTCTGC 45
Query 61  TCTCGGGTGAGGGGCTCAGTTACCATTTGGAGGGGAAGAATGCCATGAGTGACCGACATGTC 120
Sbjct 46  TCTCGGGTGAGGGGCTCAGTTACCATTTGGAGGGGAAGAATGCCATGAGTGACCGACATGTC 105
Query 121 ACACCCCCACCCACCTGCTAGATGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 180
Sbjct 106 ACACCCCCACCCACCTGCTAGATGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 165
Query 181 TTGCACGGACTTCACCTTCCCTCTATAACTTCGTATAGCATAACATTATACGAAGTTATGA 240
Sbjct 166 TTGCACGGACTTCA----- 179
Query 241 ATTCCCGTAGGAAGGCCACAAAAACAGACGACAAAGCTTCTTCAGGAAGCTGGTTTCATA 300
Sbjct -----
Query 301 TGGTGGTTTAGATTTAAATAGTGATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGTGG 360
Sbjct -----
Query 361 AGAACTACTTCGCTGCCGACCGCACAAAGAAATGAGTGTACAGCCCTGAAGTAAAGTGCC 420
Sbjct -----
Query 421 AGTGTCTAAAACAGGCTACCAGAGCCTGCCCTCGCCACCCCTGCTTACCTCTGTGTATG 480
Sbjct -----
Query 481 GATAGCTGATTAGTCAACCACCGTTAGAATTGCATACTTGTTCATGTAATAAGCCTTCTC 540
Sbjct -----
Query 541 TGGAAAGTGGACTCCACCATGCTCGGATGAAGACCTACATATACGACAGATTGAAGGCCTG 600
Sbjct -----
Query 601 GGCCTTCCCAGTGACATGACCTCTTGTGACCCCTTAGAGGATGACTGATTTCTTTGGT 660
Sbjct -----
Query 661 GTTCAGAGTCAATAGAATTTCTAGCACCATCTGAAATCGGTTATAATGATTGGGGAAGA 720
Sbjct -----
Query 721 GCACCGTTCAGCTGACTACGTTATTGCTGACGTTGGAGCCACAGGTAAGAATTAAGAAAC 780
Sbjct -----
Query 781 AAATACCAAAACATGATAACTTCGTATAGCATAACATTATACGAAGTTATGAATTCCTAAG 840
Sbjct -----
Query 841 GTACATTTCTTCTATCTTAACTTGACTTTCATTAAACACGTGCCCCAGCAACAGCATG 900
Sbjct 180 -----TTAACACGTGCCCCAGCAACAGCATG 205
Query 901 GTTAACTATTACATAGTATGATGGTGGGTGTGTTTTAGAAAAGTGTATGGGTTGCAGATT 960
Sbjct 206 GTTAACTATTACATAGTATGATGGTGGGTGTGTTTTAGAAAAGTGTG 250
```

CR1649-8 (3') NOTE: appears to have sequence from the deletion. REPEAT NECESSARY.

```
Query 1   ATGCAATGGCCAGTGGTCAGGCAGGCTAGGTGACTATCCCTATGTGAGCTGTTAGAACCT 60
Sbjct 1           GTCAGGCAGGCTAGGTGACTATCCCTATGTGAGCTGTTAGAACCT 45
Query 61  TATAGAAGTAAATATCCCTGCTCCTCTCACATTGACTGGTCAGTCATTGGTTTGGCCCT 120
Sbjct 46  TATAGAAGTAAATATCCCTGCTCCTCTCACATTGACTGGTCAGTCATTGGTTTGGCCCT 105
Query 121 TTATCCTCTAGTTACCGTCAAATCTGCAACCCATACACACTTTCTAAAAACACACCCACCA 180
Sbjct 106 TTATCCTCTAGTTACCGTCAAATCTGCAACCCATACACACTTTCTAAAAACACACCCACCA 165
Query 181 TCACTATGTGAATAGTTAACCATGCTGTTGCTGGGGCACGTGTTAATGAAAGTCAAGTTT 240
Sbjct 166 TCACTATGTGAATAGTTAACCATGCTGTTGCTGGGGCACGTGTTAATGAA----- 215
Query 241  AAGATAGGAAGAAAATGTACCTTAGGAATTCATAACTTCGTATAATGTATGCTATACGAA 300
Sbjct  -----
Query 301  GTTATCATGTTTTGGTATTTGTTTCTTAATTCTTACCTGTGGCTCCAACGTCAGCAATAA 360
Sbjct  -----
Query 361  CGTAGTCAGCTGAACGGTGTCTTCCCAATCATTATAACCGATTTTCAGATGGTGTCTAGA 420
Sbjct  -----
Query 421  AAATTCTATTGACTCTGAACACAAAAGAAATCAGTCATCCTCTAAGGGGTCACAAGAGG 480
Sbjct  -----
Query 481  TCATGTGCACTGGGAAGGCCAGGCCTTCAATCTGTCGTATATGTAGGTCTTCATCCGAG 540
Sbjct  -----
Query 541  CATGGTGGAGTCCACTTCCAGAGAAGGCTTATTACATGAACAAGTATGCAATTCTAACGG 600
Sbjct  -----
Query 601  TGGTTGACTAATCAGCTATCCATAACACAGAGGTAAGCAGGGTGGGCGAGGGCAGGCTCT 660
Sbjct  -----
Query 661  GGTAGCCTGTTTTAGACACTGGACACTTACTTCAGGGCTGTACACTCATTCTTTGTGCG 720
Sbjct  -----
Query 721  GTCGGCAGCGAAGTAGTTCTCCACCAAGAACACTGATTTCAAATGGTGTAGACAATCAC 780
Sbjct  -----
Query 781  TATTTAAATCTAAACCACCATATGAAACCAGCTTCTGAAGAAGCTTTGTCGTCTGTTTT 840
Sbjct  -----
Query 841  TGTGGCCTTCTACGGGAATTCATAACTTCGTATAATGTATGCTATACGAAGTTATAGAG 900
Sbjct  -----
Query 901  GGAAGGTGAAGTCCGTGCAATAGTTCTTAATTTTCAGGCGATCCTATGCTGACCTCATCTA 960
Sbjct 216  -----GTCAGGTGCAATAGTTCTTAATTTTCAGGCGATCCTATGCTGACCTCATCTA 265
Query 961  GCAGGTGGGGGTGGGGGTGTGACATGTCGGTCACTCATGGCATTCTTCCCTCAAATGGT 1020
Sbjct 266  GCAGGTGGGGGTGGGGGTG 284
```