



INK2J00030_SORL1_T947M_B04_AB
15,352 bp

5'
3'

AGCAAATTCCAACAAATGAGCAGATAATATTCAAATATTTCCCTCACAAAGAGCTGTTATTGATGAGGGCGTGGGTTAGTAGGGTT
TCGTTTAAGGTTGTTTACTCGTCTATTATAAGTTTATAAAGGGAGTGTTCTCGACAATAACTACTCCCGCACCCAATCATCCCAA

85

SORL1 >

SORL1-201 >

TGAGTGATTGCTCTTGAGGGGCTGGAGTGCCTACTTTTTGTAATAAATATTTCTGAAGATAATTCAGCAAGGGACAAAACAGTTTG
ACTCACTAACGAGAACTCCCCGACCTCACGGATGAAAACATTATTTATAAAGACTTCTATTAAGTCGTTCCCTGTTTTGTCAAAC

170

SORL1 >

SORL1-201 >

TTTAAAGCCATCTAAACTGGCAGGAAAGCTATTTTTCTTCTACTGGAAGATAGAACAGGGAACGAAGTGGAGAAATCTCATTCC
AAATTTTCGGTAGATTTGACCGTCCTTTTCGATAAAAGAGAAGATGACCTTCTATCTTGTCCCTTGCTTCACCTCTTTAGAGTAAGG

255

SORL1 >

SORL1-201 >

ATTGTGGGCCACCTCCTATGTAAAAGAGAGAAAAAAAAAGGCATGGAATAGGAGGCAGGGATATACCAGGAAAGAAAAAGATGCT
TAACACCCGGTGGAGGATACATTTTCTCTCTTTTTTTTTCCGTACCTTATCCTCCGTCCCTATATGGTCCTTTCTTTTTCTACGA

340

SORL1 >

SORL1-201 >

TTCACAGGACTAATGGGGGCGTAATATCTTTGCAAAGATGAGGTAATCTGGGCATCTGGAAGGATTTTTTAAATGCAAGAATTT
AAGTGTCTTGATTACCCCGGCATTATAGAAACGTTTCTACTCCATTAGACCCGTAGACCTTCTAAAAAATTTACGTTCTTAAA

425

SORL1 >

SORL1-201 >

TTCTTCCTTTACAATTACTATGAAAACACACATTCTTTGGCCAGGACCAGCCAAGAATTCCATTCTTTTTCCAGGTTAAGCATTG
AAGAAGGAAATGTTAATGATACTTTTGTGTGTAAGGAACCGGTCTGGTTCGTTCTTAAGGTAAGGAAAAGGTCCAATTCGTAAC

510

SORL1 >

SORL1-201 >

CGCGCTGGAATGCCGCATGCTGCTCTGAACATAATCCTAAAACACGTATTTCTGGATTCAAGTTCTACTTTATGGGTATTAGTTT
GCGCGACCTTACGGCGTACGACGAGACTTGTATTAGGATTTGTGCATAAAGACCTAAGTCCAAGATGAAATACCCATAATCAA

595

SORL1 >

SORL1-201 >

CTTAGAGGAAAAAAGCCAGAGTGACAGAATGAGGTTTATAGATGCTGGAGAGAGATGTGGGGCAAAAGCCTTGCTGCTGCAA
GAATCTCCTTTTTTTTCGGGTCTCACTGTCTTACTCCAAATATCTACGACCTCTCTCTACACCCCGTTTTTCGGAACGACGACGTT

680

SORL1 >

SORL1-201 >

ATGTAGCTTTCATGTCCCTATACCTTAGCTGGCCCCCTCCCTGGGAATGACAGCGGGAAAGGTTTCTTGACAACCAAAAAGGGGAG
TACATCGAAAGTACAGGGATATGGAATCGACCGGGGGAGGGACCTTACTGTGCGCCTTCCAAAGGAACTGTTGGTTTTCCCTC

765

SORL1 >

SORL1-201 >

GTAGGTTACCATGTGATGGTAACATAGATACTTCTAAAGTGACCTGGAACCAAAGGAAAAGAAGGAAAACCTTACCTTATTA
CATCCAATGGTACACTACCATTGTATCTATGAAGATTTCACTGGACCTTGGTTTTCTTTTTCTTCTTTTGAATGGAATAATTTTT

850

SORL1 >

SORL1-201 >

TTGTAGGTAGATTTATTTTTTGGATGCATTATCTATATTACAGCTTTTATAAAGAAGGTGAGTGGTACATGTTAAGTCACTGAGTG
AACATCCATCTAAATAAAAAAATACTACGTAATAGATATAATGTCGAAAAATTTTCTTCCACTCACCATGTACAATTCAGTGACTCAC

935

SORL1

SORL1-201

TATGGAATCAGGAAGTGGGCAGGAATGGCTAACCCAGGCATGCAGCAAAGAATTCCGATTTGCATCTTGGTCCCATATGCAACA
ATACCTTAGTCCTTACCCGTCCTTACCGATTGGGTCCGTACGTCGTTTTCTTAAGGCTAAACGTAGAACCAGGGGTATACGTTGT

1020

SORL1

SORL1-201

CACTGTCAAGATGCACACTTTAGACACAGATGCTGGTGTGCTGCTTGTGTCCACTCCTGGGGAAGAATCTGGATGTTTCCCAAGC
GTGACAGTTCTACGTGTGAAATCTGTGTCTACGACCACACGACGAACACAGGTGAGGACCCCTTCTTAGACCTACAAAGGGTTCG

1105

SORL1

SORL1-201

CGTTCCTAAGTGGACAAGACAGTGTACTGGGTCTTCCATTTCCAGTTGTCTGACATTAGGTAAGTATCTTCAGCACTCAGGAC
GCAAGGGATTACCTGTTCTGTACATGACCCAGAAGGATAAAGGTCAACAGACTGTAATCCATTCATAGAAGTCGTGAGTCCTG

1190

SORL1

SORL1-201

CTTCATTTCTACATCTTAAAAATCATCCACGGTAGCGTCTGTATCATAACAGGCAGCACAGTGTAGTGGTTAAAGCATAGACTCT
GAAGTAAAGATGTAGAATTTTTAGTAGGTGCCATCGCAGACATAGTATTGTCCGTCTGTGTCACATCACCAATTTTCGTATCTGAGA

1275

SORL1

SORL1-201

GGATCCAGAGTGCCTGGGTTCCAATCTTGGTTCTGCCACTTGTAGTTGTGTGACCTTGGGTGAGTTACTTAACCTCTCTGGTCT
CCTAGGTCTCACGGACCCAAGGTTAGAACCAAGACGGTGAACGATCAACACACTGGAACCCACTCAATGAATTGGAGAGACCAGA

1360

SORL1

SORL1-201

CAGTTTTCTCATTTGTAAAATTTGGTTAAACAAGAGTTCTACCATCAGGCAGTTGTTGTGGGTCTTAAACAATACCCGATACGTAG
GTCAAAAGAGTAAACATTTTAAACCAATTGTTCTCAAGATGGTAGTCCGTCAACAACACCCAGAATTTGTTATGGGCTATGCATC

1445

SORL1

SORL1-201

TAAGCACATTATACACAATATGTACACAATTTATATTTGTTGAGTAGAAACAGAATTTTTGTGGTGATTATGTTGTGGAACATTT
ATTCGTGTAATATGTGTTATACATGTGTTAAATATAAAACACTCATCTTTGTCTTAAAAACACCACTAATACAACACCTTGTA

1530

SORL1

SORL1-201

TGTAATAGCCAAGAACAATGCATTATTAGTATTATTTGGAGATCTAAGAGGTTTCATAGAATTGCCATATGGTGTGTTGTGAACA
ACATTTATCGGTTCTTGTGTTACGTAATAATCATAATAAAACCTCTAGATTCTCCAAGTATCTTAAACGGTATACCACAACACTTGT

1615

SORL1

SORL1-201

ATATGAATAAGTGAGCAAATTTGATTAGAGAGCTTAGTTACAAAGCTTCAGTGACTAATGGTCTCTCGTCAACAAGATGATGATGC
TATACTTATTCAGTCTGTTAACTAATCTCTCGAATCAATGTTTCGAAGTCACTGATTACCAGAGAGCAGTTGTTCTACTACTACG

1700

SORL1

SORL1-201

TGTGGTGATACAGTCACGTGAGGAGGGGAGAACAGGGCGATTGGTGTAAATTAGGTTGGCAAGTGTGACTTGAAGACTGGCAGGCTT
ACACCACTATGTCAAGTGCACCTCCTCCCTCTTGTCCCGCTAACCCACATTAATCCAACCGTTCACACTGAACTTCTGACCGTCCGAA

1785

SORL1

SORL1-201

AGCCCAGAAGTATGGTTGTTGAAGCATGCATATTGGGAGATTTAGAATAAAGAAAAACATAACAAGTAAACACTTGCAGATGAA
TCGGGTCTTCATACCAACAACCTTCGTACGTATAACCCTCTAAATCTTATTTCTTTTGTATTGTTTCAATTTGTGAACGTCTACTT

1870

SORL1

SORL1-201

GAAACAGATTCACCTGGAGTTTAAAGTAACTTGCCTGAGGCAGAAATGTGATTCCATTACACACCTCCTGAGTCTTGATTTCTGTGC
CTTTGTCTAAGTGACCTCAAATTCATTGAACGGACTCCGTCTTTACACTAAGGTAATGTGTGGAGGACTCAGAACTAAAGACACG

1955

SORL1

SORL1-201

TCTTCACTTGGTCCACACCACATGCCAATGAATTTGAGGTTTGTGTATGAGAAACAAATAGGTCAGATGTGCTAGGACCTCTTCA
AGAAGTGAACCAGGTGTGGTGTACGGTTACTTAAACTCCAACACATACTCTTTGTTTATCCAGTCTACACGATCCTGGAGAAGT

2040

SORL1

SORL1-201

GCATCCCCTGGGTCCAACCTCCCACGTGTCTTGTGTGTCTGGCAGAAGAGAACGAGTTCATTCTGTATGCTGTGAGGAAATCCAT
CGTAGGGGACCCAGGTTGGAGGGTGCACAGAACACACAGACCGTCTTCTCTTGCTCAAGTAAGACATACGACACTCCTTTAGGTA

2125

SORL1

SORL1-201

E N E F I L Y A V R K S I

ENSE00000991345

SORL1-201

CTACCGCTATGACCTGGCCTCGGGAGCCACCGAGCAGTTGCCTCTCACCGGGCTACGGGCAGCAGTGGCCCTGGACTTTGACTAT
GATGGCGATACTGGACCGGAGCCCTCGGTGGCTCGTCAACGGAGAGTGGCCCGATGCCCGTCGTCACCGGGACCTGAAACTGATA

2210

SORL1

SORL1-201

Y R Y D L A S G A T E Q L P L T G L R A A V A L D F D Y

ENSE00000991345

SORL1-201

GAGCACAACCTGTTTGTATTGGTCCGACCTGGCCTTGGACGTCATCCAGGTGAGTCAGCGCTTGGTCTGACTGTGGGAGCTGTGCA
CTCGTGTGACAAACATAAACCAGGCTGGACCGGAACCTGCAGTAGGTCCACTCAGTCGCGAACCAGACTGACACCCTCGACACGT

2295

SORL1

SORL1-201

E H N C L Y W S D L A L D V I Q

ENSE00000991345

SORL1-201

TCGTGACTGCCCTGTCTGATAAGCTGCATGCAGAATGGCCTATGGAAATGGGCAGTTAGAAGTTTGTAAAGTGTACTCATCTCA
AGCACTGACGGGACAGGACTATTCGACGTACGTCTTACCGGATACCTTTACCCGTC AATCTTCAAACATTCACAATGAGTAGAGT

2380

SORL1

SORL1-201

SORL1-201

GGGCTGACAGGTGAAAAGTTTCCAGTCTTCTGTGTTAGTATTTTTCTTTCTCTGTCTTCATCTGTTTCATATAGGAAGGATAAAGAA

CCCGACTGTCCACTTTCAAAGGTCAGAAGACACAATCATAAAAAGAAAGAGACAGAAGTAGACAAGTATATCCTTCTCTATTTCTT

2465

SORL1

SORL1-201

SORL1-201

AGCCCTAAATCCACAGACCTGCTTGAAAGTGAGGTCTTGCTTTTCTGCTGGGAAGGTGTTGGGACTAGTAATGTAGGATGATTA

TCGGGATTTAGGTGTCTGGACGAACCTTCACTCCAGAACGAAAAGGACGACCCTTCCACAACCCTGATCATTACATCCTACTAAT

2550

SORL1

SORL1-201

SORL1-201

GTTGCCCCCTATTGTGCCAACTGCCTCTTGAGCATCTTTCTTCCCAAGCCATGATACAGTAACACTTGACTTACCCATAGCTCA

CAACGGGGGGATAACACGGTTGACGGAGAAGCTCGTAGAAAGAAGGGTTTCGGTACTATGTCATTGTGAACTGAATGGGTATCGAGT

2635

SORL1

SORL1-201

SORL1-201

CATAATTATCCACTTCAGCTGTTCTGAACACAGGTAAGAACCAGGAAGTAAGCATTAAAGAGCCCTGGACAGGCCAGGTGGATAG

GTATTAATAGGTGAAGTCGACAAGACTTGTGTCCATTCTTGGTCTTTCATTTCGTAATTTCTCGGGACCTGTCCGGTCCACCTATC

2720

SORL1

SORL1-201

SORL1-201

CCATACGCTCACACCCATGCATTTAAAGGAGAGCTCTTTGATCTTTATTTCATTGTCTACTTAATCCTTTTAGAAAAGCAATTCCA

GGTATGCGAGTGTGGGTACGTAATTTCTCTCGAGAAACTAGAAATAAGTAACAGATGAATTAGGAAAATCTTTTCGTTAAGGT

2805

SORL1

SORL1-201

SORL1-201

ACAAATTTTATCTAGATTCCAACCCAACAGAAATTTACAGTGCCTGGGTATTTGAGGGGCTTGGGGTGGGGGATGGCGGTGAT

TGTTTAAAAATAGATCTAAGGTTGGGTGTCTTTAAAGTGTACGGACCCATAAACTCCCCGAACCCACCCCTACCGCCACTA

2890

SORL1

SORL1-201

SORL1-201

GCTGAATGGAGCTGTCCAACAATAGCACTTGATGGCTAAGAGCCTCACAGGGAAGAAAGAGTATAAAAGCAGACACAAGAACTGA

CGACTTACCTCGACAGGTTGTTATCGTGAACCTACCGATTCTCGGAGTGTCCCTTCTTTCTCATATTTTCGTCTGTGTTCTTGACT

2975

SORL1

SORL1-201

SORL1-201

AATGTAACAGCAGTCTGGTTTTCACTTATTTTTAAAAGCAAACAGACTCATACAATCTCAGTAATCTCTGACTTTATTATTGCCATA
TTACATTGTCGTCAGACCAAAGTGAATAAAAATTTTCGTTTGTCTGAGTATGTTAGAGTCATTAGAGACTGAAATAATAACGGTAT

3060

SORL1

SORL1-201

SORL1-201

CAGCATAATTTAGTAACCAGTGTTCATAATGATAATGCAGAGTAATATATATGATTAAATTCTCTTTATTCTGCTTTAAAAACA
GTCGTATTAAATCATTGGTCACAAGTATTACTATTACGTCTCATTATATATACTAATTTAAGAGAAATAAGACGAAATTTTTTGT

3145

SORL1

SORL1-201

SORL1-201

AAAATGTAGTATATTTTAGAAATGCTTTCATGAAAACCTGGCTTCATGTGTCTGGAAAGTTTACTAACGTAAAACATCTCATCCC
TTTTACATCATATAAAATCTTTACGAAAGTACTTTTGGACCGAAGTACACAGACCTTTCAAATGATTGCATTTTGTAGAGTAGGG

3230

SORL1

SORL1-201

SORL1-201

TTGCCAGTCCTGCCAGTTGAATAAAGGGTTACCCCTTCATGGGACTGACTTGGCAGGGGGTCGTTTGAACAGTTCCTAGCATTAT
AACGGTCAGGACGGTCAACTTATTTCCAATGGGAAGTACCCTGACTGAACCGTCCCCCAGCAAACCTTGTCAAGGATCGTAAATA

3315

SORL1

SORL1-201

SORL1-201

TATTACTTTTCTCTCTTAAGCGCCTCTGTTTGAATGGAAGCACAGGGCAAGAGGTGATCATCAATTCTGGCCTGGAGACAGTAGA
ATAATGAAAAGAGAGAATTCGCGGAGACAAACTTACCTTCGTGTCCCGTTCTCCACTAGTAGTTAAGACCGGACCTCTGTCACT

3400

SORL1

SORL1-201

R L C L N G S T G Q E V I I N S G L E T V E
ENSE00000991346

SORL1-201

AGCTTTGGCTTTTGAACCCCTCAGCCAGCTGCTTTACTGGGTAGATGCAGGCTTCAAAAAGATTGAGGTATGTGTATTTTCGTGC
TCGAAACCGAAAACCTTGGGGAGTCGGTCGACGAAATGACCCATCTACGTCCGAAGTTTTTCTAACTCCATACACATAAAAGCACG

3485

SORL1

SORL1-201

A L A F E P L S Q L L Y W V D A G F K K I E
ENSE00000991346

SORL1-201

TGTTCTTAATTAAGGGAGCAGGCGGGGCACCTGGGCTTTGAGCCACATTTGACACAGAGGCAAGGGCCAGTGTGTTCAGATTACTC
ACAAGAATTAATTCCTCGTCCGCCCGTGGACCCGAAACTCGGTGTAAACTGTGTCTCCGTTCCCGGTCACACAGTCTAATGAG

3570

SORL1

SORL1-201

SORL1-201

AGGAAATTTACTGCGAGTTTCCAGAGAATGGACCAGCTGAGCCTCTGGAGAGGAGAGAAAAGGGGGTAAGTACCTGTGAGTTGAT
TCCTTTAAATGACGCTCAAAGGTCTCTTACCTGGTCGACTCGGAGACCTCTCCTCTCTTTTCCCCCATTTCATGGACACTCAACTA

3655

SORL1

SORL1-201

SORL1-201

CTTTTGGCTAGCAGAAGCTTAGCTAATAACAATAAATGGTAATATTTTTATTTTATTTATATATGTACTTACTTATTTTATTTAT
GAAAACCGATCGTCTTCGAATCGATTATTGTTATTTACCATTATAAAAAATAAAATAAATATATACATGAATGAATAAAAAATAAATA

3740

SORL1

SORL1-201

SORL1-201

ATATTATTTTTGTTTTATTTTACTACTTTTTATTAACATGATGGCAAAAACACAATCACTTTTGCATCAGCCTAATATCATGGT
TATAATAAAAAACAAAATAAAATGATGAAAATAATTTGTAACCGTTTTTGATGTTAGTGAAAACGTAGTCGGATTATAGTACCA

3825

SORL1

SORL1-201

SORL1-201

ATTATTATAATGCTATAACAATAATCGTCTAGTATTATTTTATTCGATTAGAGTGATAGCAACAATATCATCATCATCATCA
TAATAATATTACGATATTGTTATTAGCAGATCATAATAAAAAAAGCTAATCTCACTATCGTTGTTATAGTAGTAGTAGTAGT

3910

SORL1

SORL1-201

SORL1-201

TTGCCACTGTTATTAATCCCATTCTCTGCAACTTAGCTACCTAGTAACCTGTCCCACCTTATATACCCAAGGCAAGGATGATG
AACGGTGACAATAATTAGGGGTAAAGAGACGTTGAATCGATGGATCATTGGACAGGGTGGAATATATGGGTTCCGTTCTACTAC

3995

SORL1

SORL1-201

SORL1-201

AGTGACCTCTAAACTGCCAAATCTTTGCTGGGGGAATGTAGTGTGCTCAGCTCACTGCCTCAGCACCTCTTTATACTGACTCTG
TCACTGGAGATTTGACGGTTTAGAAACAGACCCCTTACATCACACGAGTCGAGTGACGGAGTCGTGGAGAAATATGACTGAGAC

4080

SORL1

SORL1-201

SORL1-201

CATGGAGAGACGGCATGTGGGTGAAGTGGGAAGTGCAGTAGAAGCAGGGAGATGCAGAGGGCTAAGAGGAGTTGCAAGACGAAAG
GTACCTCTCTGCCGTACACCCACTTCACCCCTCACGTCACTTCGTCCTCTACGTCTCCCGATTCTCCTCAACGTTCTGCTTTC

4165

SORL1

SORL1-201

SORL1-201

ACACAGACTCGAGAGATAGACCCAGATGTAGGCTTGACTCCACTAGCTCAGCGACATGGGGCAAGGTGCTTATGCTTTCTAAACT
TGTGTCTGAGCTCTCTATCTGGGTCTACATCCGAACTGAGGTGATCGAGTCGCTGTACCCCGTTCCACGAATACGAAAGATTTGA

4250

SORL1

SORL1-201

SORL1-201

TCAGTTGCTTCATGCGTTAGATGGAGATTCATATATTCGCACAACCATTTGACAGGGGTTCTCTGCATGATACATGTGGTTTAGG
AGTCAACGAAGTACGCAATCTACCTCTAAGTATATAAGCGTGTGGTAAACTGTCCCAAGAGACGTACTATGTACACCAAATCC

4335

SORL1

SORL1-201

SORL1-201

TTCTGATGATAAAGCAGTGGGCAGGACACACACGTTCTTGTTCCAGTAGAGCTTAGATTTTTAGTGGAGGAAGCAAAATAATAAAT
AAGACTACTATTTTCGTCACCCGTCCTGTGTGTGCAAGAACAAGGTCATCTCGAATCTAAAATCACCTCCTTCGTTTTATTATTTA

4420

SORL1

SORL1-201

SORL1-201

CAGTTCTGTTGGTGGTACATGCTGCAAAGACTCTGAAGCAGTGCAGTGTGATTGCGCTTTTGGAGAGTGGGGCAACATTAGAATA
GTCAAGACAACCACCATGTACGACGTTTCTGAGACTTCGTCACGTCACACTAACGCGAAAACCTCTCACCCCGTTGTAATCTTAT

4505

SORL1

SORL1-201

SORL1-201

GGCAGACAGAGCAGGCAACTTGAGGTTGATGTCTTAGCTGAGCCCTGGCTGAGAAGAGGATGATCTTTTGTCCACCTCCTGGGGA
CCGTCTGTCTCGTCCGTTGAACTCCAACCTACAGAATCGACTCGGGACCGACTCTTCTCCTACTAGAAAACAGGTGGAGGACCCCT

4590

SORL1

SORL1-201

SORL1-201

TGCTGATAGAAGTGAAGTGGCATCTACTGAATGCTGCCTCGGTGGTTATGTTATTGCTCTTTCTCTCCTTTCTTTAATTGCGTGT
ACGACTATCTTCACTTGACCGTAGATGACTTACGACGGAGCCACCAATACAATAACGAGAAAAGAGAGGAAAAGAAATTAACGCACA

4675

SORL1

SORL1-201

SORL1-201

GGTCAGCACTTGGCTAGGGGCTAAAAGAATGCAGGTGATGCACAAGCACCCACCTTTTTCACAGGCTGTGGGGCGACCACTGCACA
CCAGTCGTGAACCGATCCCGATTTTCTTACGTCCACTACGTGTTTCGTGGGTGGAAAAGTGTCCGACACCCCGCTGGTGACGTGT

4760

SORL1

SORL1-201

SORL1-201

ACTCAAATACTGTTGGTGCAAAATGGTGTGTCAGATGAGCCAAGGTGTCAGAGCTACTGATGCTTATTGGTCCAGGTGGGTCAGAAGA
TGAGTTTATGACAACCACGTTTTTACCACAGTCTACTCGGTTCCACGTCTCGATGACTACGAATAACCAGGTCCACCCAGTCTTCT

4845

SORL1

SORL1-201

SORL1-201

GTTAGGAAAGTAGGCAGGCCTGGCAGTGAGGTTTGAAGGAGAGTTATGCCTTGATTAGATTAAGCAGTGGGGCAGGTAGGCCAG
CAATCCTTTCATCCGTCCGGACCGTCACTCCAAACTTCTCTCAATACGGAACCTAATCTAATTCGTCACCCCGTCCATCCGGGTC

4930

SORL1

SORL1-201

SORL1-201

GATGGGATGTGGCAAGAGCAGACAGCAGTGAGTCCGCATCAGGCTTGAGAGAAGCAAGAGATGACCAGCCTGGCTGACGGGAAGGA
CTACCCTACACCGTTCTCGTCTGTCGTCACTCAGGCGTAGTCCGAACCTCTTCGTTCTCTACTGGTCGGACCGACTGCCCTTCT

5015

SORL1

SORL1-201

SORL1-201

GCAAGAATATGAGTCCCACCTGTGGACTCTTCATTGCAAGGCTGTGACATTGAGAATTTGTTTTATGGGAGTGTGGAGTCATCGA
CGTTCTTATACTCAGGGTGGACACCTGAGAAGTAACGTTCCGACACTGTAACCTTTAAACAAAATACCCTCACACCTCAGTAGCT

5100

SORL1

SORL1-201

SORL1-201

TTGCCTTGGAAACGTGGAGTGACACGGGATGGTGAAATAAGTAAATGCTCATTTGCTTATTTACTTATTTGAGTAATTTACTTATT
AACGGAACTTGCACCTCACTGTGCCCTACCACTTTATTCAATTTACGAGTAAACGAATAAATGAATAAACTCATTAAATGAATAA

5185

SORL1

SORL1-201

SORL1-201

GATACTGCTTTGTCCAGATCATCATGCCCTGGAAACTGGGGCTTACATGGTTCTAGCTCCTCTTTCAGACCACTTGAAAATTGTC
CTATGACGAAACAGGTCTAGTAGTACGGGACCTTTGACCCCGAATGTACCAAGATCGAGGAGAAAAGTCTGGTGAACCTTTTAACAG

5270

SORL1

SORL1-201

SORL1-201

CCATGAGTCAGAGGAAGGAACAGCGCATTGTGACTAGAAGTTGGGGCAGGTTTCGCAGATGGGTCAGGTCAGGGAAATAGGCAGG
GGTACTCAGTCTCCTTCTTGTGCGGTAACACTGATCTTCAACCCCGTCAAAGCGTCTACCCAGTCCAGTCCCTTTATCCGTCC

5355

SORL1

SORL1-201

SORL1-201

CATGGAGGGGGCATGTCTGTAGCAGAAAGCTGAGTAGCCATCTTTGGCAATGGGGGTCTTTAAGGAGCTCCGATCCATCTCAGCCT
GTACCTCCCCCGTACAGACATCGTCTTCGACTCATCGGTAGAAACCGTTACCCCCAGAAATTCCTCGAGGCTAGGTAGAGTCGGA

5440

SORL1

SORL1-201

SORL1-201

CTTTTCCCCCTGTTTTTGTGTCAGGTAGCTAATCCAGATGGCGACTTCCGACTCACAATCGTCAATTCCTCTGTGCTTGATCGTCCC
GAAAAGGGGGGACAAAAACAGTCCATCGATTAGGTCTACCGCTGAAGGCTGAGTGTTAGCAGTTAAGGAGACACGAACTAGCAGGG

5525

SORL1

SORL1-201

V A N P D G D F R L T I V N S S V L D R P

ENSE00003463448

SORL1-201

AGGGCTCTGGTCTCTCGTGCCCCAAGAGGGGGTAAGTGTGCCCCAAAAGGAAATCAGTCTTGCGTCCAATGCTACACTAATAGATT
TCCCGAGACCAGGAGCACGGGGTTCTCCCATTCACAACGGGGTTTTCTTTAGTCAGAACGCAGGTTACGATGTGATTATCTAA

5610

SORL1

SORL1-201

R A L V L V P Q E G

ENSE00003463448

SORL1-201

CTCATGGAAACACAGACTGCGGGACAAAACTCTGTTTCTCATGATGGTGGTTGAAATGGTCTATTAAGTGAAGTTTGAAGACC
GAGTACCTTTGTGTCTGACGCCCTGTTTTTGAAGACAAAGAGTACTACCACCAACTTTACCAGATAATTGACTCTTCAAACCTCTGG

5695

SORL1

SORL1-201

SORL1-201

ACAGCTTAGTCATCGTGGTCAGGTAACCTCCGTTTCGCTTTTTGTTAGCCAGTGTGAGAGTCTCTTTAGGCATCCAGATGTCTTGCA
TGTCGAATCAGTAGCACCAGTCCATTGAGGCAAGCGAAAAACAATCGGTCACAGTCTCAGAGAAATCCGTAGGTCTACAGAACGT

5780

SORL1

SORL1-201

SORL1-201

TCTGTGGGTTGTTTCTCTAGAAAAAGTTGATGTTAAAAGAGAGCTTCTGTAGACATAGACAGGCCTGCTTGGATATTGTGAGAACT
AGACACCCAACAAGAGATCTTTTCAAACATAAATTTCTCTCGAAGACATCTGTATCTGTCCGGACGAACCTATAAACTCTTGA

5865

SORL1

SORL1-201

SORL1-201

TTCTCTTGAGTTTCATGCATGGTACAAACATTTAATTCATTCCATCTTTCCCTGCTTCCCAGCATGTGTAGGTTTTCTTACGT
AAGAGAACTCAAAGTACGTACCATGTTTGTAAATTAAGTAAGGTAGAAAAGGGGACGGAAGGGTCTGACACATCCAAAAGAATGCA

5950

SORL1

SORL1-201

SORL1-201

ACAATCAGTGTGCACTTGGGGAAGGCAAAGGTGCTTTTTATTAACCTCATTAACCTGAAGGAAACATAATTAAGAGGGAAATTTCTGG
TGTTAGTCACACGTGAACCCCTTCCGTTTTCCACGAAAAATAATTGAGTAATTGACTTCCTTTGTATTAATTCTCCCTTTAAGACC

6035

SORL1

SORL1-201

SORL1-201

ATTTGACATTCTGGCTTTTCTCTCTCGTAGCATTATGATAGAGAATTGGCACAATTTTTTTCAAGGAAAATTCTAAGAGTAAT
TAAACTGTAAGACCGAAAAGGAGAGAGCATCGTAAATACTATCTCTTAACCGTGTTAAAAAAAAGTTCCCTTTAAGATTCTCATTA

6120

SORL1

SORL1-201

SORL1-201

GTATGTACTIONGGTTGACAATATTTAGAGAGAACAGCACTTTATGAAAAAATTTGCATTCTTCCTTTTTCATTCTTAACCCCTTTAC
CATACATGAACCAACTGTTATAAATCTCTCTTGTGCGTGAATACTTTTTTAAACGTAAGAAGGAAAAGTAAGAATTGGGAAATG

6205

SORL1

SORL1-201

SORL1-201

CCTCACACTTCCTAGTGGTAATCATTGTTAATAATGTCTTGTGTATCTTTCATGATTGCTTTTACTTATGTACAAGTATTATCTT
GGAGTGTGAAGGATCACCATTAGTAACAATTATTACAGAACACATAGAAAGTACTAACGAAAATGAATACATGTTTCATAATAGAA

6290

SORL1

SORL1-201

SORL1-201

PCR Forward
ATGCACGCCAAATAGGATTGTAGTG

TAAAAACACACACATATACACACACATGCACGCCAAATAGGATTGTAGTGTAGTTACTATTCTGTACCTTTTAAACAAACTTAAT
ATTTTGTGTGTGTATATGTGTGTGTACGTGCGGTTTATCCTAACATCACATCAATGATAAGACATGGAAAAATTTGTTTGAATTA

6375

SORL1

SORL1-201

SORL1-201

ATGTATTGAAAATAGTTCTGTGTGAGCATATATAGATTTTTAGGTTTTACAGTATTCTATTATATGTACCATAATGTGTCACTTC
TACATAACTTTTATCAAGACACACTCGTATATATCTAAAAATCCAAAGTGTGCATAAGATAATATACATGGTATTACACAGTGAAG

6460

SORL1

SORL1-201

SORL1-201

CTCTGCTGATTAACATTTAGTTTTAATATACATACATACATTTCTTTGTATATTATCTTTGCATAATTTGATTTTATCTATAGA
GAGACGACTAATTGTAAATCAAATTATATGTATGTATATGTAAGAAACATATAATAGAAACGTATTAACCTAAAATAGATATCT

6545

SORL1

SORL1-201

SORL1-201

TAAATTCTAGTAAAGGAATTTCCAGGTGAAGGAATTTAAGTAGTTTCAGGTGTTGTCATTACATATTGTTATAATAATGCTGAAA
ATTTAAGATCATTTCCTTAAAGGTCCACTTCCTTAAATTCATCAAAGTCCACAACAGTAATGTATAACAATATTATTACGACTTT

6630

SORL1

SORL1-201

SORL1-201

TAACCAGCCGGATCATTTCGAAAGGAGTTTCTGACCTTTTCTGGAGTAGTATTTGAGCTCCCATTTTCTCTAGTATTGATGAGGTAT
ATTGGTTCGGCCTAGTAAGCTTTTCTCAAAGACTGGAAAAAGACCTCATCATAAACTCGAGGGTAAAGAGATCATAACTACTCCATA

6715

SORL1

SORL1-201

SORL1-201

Sanger Sequencing

CGGAGCAATATGGAT

GTGTTCTGTCCCCATTTTCGCTAGGGTGATGTTCTGGACAGACTGGGGAGACCTGAAGCCTGGGATTTATCGGAGCAATATGGAT
CACAAGACAGGGGTAAAAGCGATCCCACTACAAGACCTGTCTGACCCCTCTGGACTTCGGACCCCTAAATAGCCTCGTTATACCTA

6800

SORL1

SORL1-201

890 895 900 905
V M F W T D W G D L K P G I Y R S N M D

ENSE00003546837

SORL1-201

Sanger Sequencing

GGTTC

GGTTCTGCTGCCTATCACCTGGTGTCTGAGGATGTGAAGTGGCCCAATGGCATCTCTGTGGACGACCAGTGGATTTACTGGACGG
CCAAGACGACGGATAGTGGACCACAGACTCCTACACTTCACCGGGTTACCGTAGAGACACCTGCTGGTACCTAAATGACCTGCC

6885

SORL1

SORL1-201

910 915 920 925 930 935
G S A A Y H L V S E D V K W P N G I S V D D Q W I Y W T

ENSE00003546837

SORL1-201

Donor Template WT -> SNV

C

Donor Template WT -> SNV

gRNA Protospacer

ATAGAGCGGATCACGTTTCAG

ATGCCTACCTGGAGTGCATAGAGCGGATCACGTTTCAGTGGCCAGCAGCGCTCTGTTCATTCTGGACAACCTCCCGCACCCCTATGC
TACGGATGGACCTCACGTATCTCGCCTAGTCAAGTCAACCGGTCGTCGCGAGACAGTAAGACCTGTTGGAGGGCGTGGGGGATACG

6970

SORL1

SORL1-201

D A Y L E C I E R I T F S G Q Q R S V I L D N L P H P Y A

ENSE0003546837

SORL1-201

Donor Template WT -> SNV

Protospacer Sequence

PAM

SNV

TACGGATGGACCTCACGTATCTCGCCTAGTCAAGTCAACCGGTCGTCGCGAGACAGTAAGACCTGTTGGAGGGCGTGGGGGATACG

Donor Template WT -> SNV

CATTGCTGTCTTTAAGGTGAGTCCATTTGTTGCTGCCGGACA6TCTGCTAGAGCGGGTGAGGAGCATATGAGATCAGGAGCCTGC
GTAACGACAGAAATTCACCTCAGGTAAACAACGACGGCCTGTCTAGACGATCTCGCCCACTCCTCGTATACTCTAGTCCTCGGACG

7055

SORL1

SORL1-201

I A V F K 970

ENSE0003546837

SORL1-201

Donor Template WT -> SNV

GTAACGACAGAAAT

Donor Template WT -> SNV

ATCCCTGGGCTTTGCAGAGAAGCTGTTTAACTTCTTAAAGGTTGCCTTTTTTCCAAATTTGAGATAACTTATTTTCAGCCTATGG
TAGGGACCCGAAACGTCTCTTCGACAAATTGAAGAATTTCCAACGGAAAAAAGGTTTTAACTCTATTGAATAAAAAGTCGGATACC

7140

SORL1

SORL1-201

SORL1-201

AGGGATGCCAGGCAGAGGCGCCAAGGGTCCAGGCTCCCTGCTGTTTCACATTTCAAAAAGGTTAAAAGTGAAGGCTCTTCCCATGA
TCCCTACGGTCCGTCTCCGCGGTTCCCAGGTCCGAGGGGACGACAAGTGTAAAGTTTTCCAATTTTCACTTCCGAGAAGGGTACT

7225

SORL1

SORL1-201

SORL1-201

ACATTCCCAGTTTGGCCCTCAGTGTCAAGTAGCCTCATTTTCAGGGTGGTGTCTTCATTTTTTGTGCGCTTTGCTCACTTTATTCTC
TGTAAGGGTCAAACGGGGAGTCAAGTTCATCGGAGTAAAGTCCCACCACAGAAGTAAAAAACACGCGAAACGAGTGAAATAAGAG

7310

SORL1

SORL1-201

SORL1-201

TGATGACTTCCGGTGAGCTCTGCACCACCTATAGTGCCTTGCAGTTCTTTTTTCGACTCTGGAGAGCAACATGGCTCTTCCCAACT
ACTACTGAAGGCCACTCGAGACGTGGTGGATATCACGGAACGTCAAGAAAAAGCTGAGACCTCTCGTTGTACCGAGAAGGGTTGA

7395

SORL1

SORL1-201

SORL1-201

CTGAGACCTCTCGTTGTACCGAGAA

PCR Reverse

CTGGGAAACAGATTTCAAACCTGAGGGGGTTGGGTTTGTGTCATAAACTTGAATGCTTATCAGATAGTTTCTTTTGGGCAGTTTCT
GACCCTTTGTCTAAAGTTTACTCCCCAACCCAAACACAGTATTTGAACTTACGAATAGTCTATCAAAGAAAAACCCGTCAAAGA

7480

SORL1

SORL1-201

SORL1-201

TCTGTGGGGTTATATGGTGAGGTTTGGATAAAATTGCTGTCTTTGCATTTAAGTAGAATCTTGATCAGGCTAGTCATTTCAGCCA
AGACACCCCAATATACCACTCCAAACCTATTTTAACGACAGGAAACGTAATTCATCTTAGAACTAGTCCGATCAGTAAGTCGGT

7565

SORL1

SORL1-201

SORL1-201

ATAAATGTTAGTTGTCTCTCGCTGGGGGAACTCTTACCCTTAGAGAGAACCAGAATAAAGAACGAAAGAGCTGGACTAATGGGC
TATTTACAATCAACAGAGGACGGACCCCTTGAGAATGGGAATCTCTCTTGGTCTTATTTCTTGCTTTCTCGACCTGATTACCCG

7650

SORL1

SORL1-201

SORL1-201

AAAGGTTTTCTTTTAGAATGAAATCTACTGGGATGACTGGTCACAGCTCAGCATATTCGAGCTTCCAAATACAGTGGGTCCCA
TTTCCAAAAGAAAAATCTTACTTTAGATGACCCTACTGACCAGTGTGCGAGTCGTATAAGGCTCGAAGGTTTATGTCACCCAGGGT

7735

SORL1

SORL1-201

N E I Y W D D W S Q L S I F R A S K Y S G S Q

ENSE00000532819

SORL1-201

GATGGAGATTCTGGCAAACAGCTCACGGGGCTCATGGACATGAAGATTTTCTACAAGGGGAAGAACACTGGTAAGCCAGAGTCT
CTACCTCTAAGACCGTTTGGTTCGAGTGCCCGAGTACCTGTACTTCTAAAAGATGTTCCCTTCTTGTGACCATTTCGGTCTCAGA

7820

SORL1

SORL1-201

M E I L A N Q L T G L M D M K I F Y K G K N T

ENSE00000532819

SORL1-201

CTTCTTTTGTCTCTGTAGAGTTGATCTCAAGAAAGGGGCTGCGTGTGGCCAATCTCTGCTCAGAGTAGGAGCTGGCAGCCTGCAT
GAAGAAAACAGAGACATCTCAACTAGAGTTCTTTCCCGACGCACACCGGTTAGAGACGAGTCTCATCCTCGACCGTCCGGACGTA

7905

SORL1

SORL1-201

SORL1-201

CTTTGTTGTCACGACAACATGCACATTATTTAATTTCTTCTAATGACATCTTAATTTCTTTTCTAATGATACACAAACAGCTGG
GAAACAACAGTGCTGTTGTACGTGTAATAAATTAAGAAGGATTACTGTAGAATTAAGAAAAGATTACTATGTGTTTGTGCGACC

7990

SORL1

SORL1-201

SORL1-201

AAGACAGCATGCTTTTGCCTGCCTAGAGTGTGGTGCTTGGTGGGTAATTACACCCTCCTCCTGCCCTTGGCCCCTGACTGATTG
TTCTGTCGTACGAAAACGGACGGATCTCACAACCACGAACCACCCATTAATGTGGGAGGAGGACGGGAACCGGGGACTGACTAAC

8075

SORL1

SORL1-201

SORL1-201

GTGGCGCGGCTTCTGTTGCAGCTGGGAGAGTCCCTAACATGTGCTTAATCCCTGTTTGGCATGCTTGCAGGAAGAGACTCTGTGCT
CACCGCGCCGAAGACAACGTCGACCCTCTCAGGATTGTACACGAATTAGGGACAAACCGTACGAACGTCCTTCTCTGAGACACGA

8160

SORL1

SORL1-201

SORL1-201

GGGTGCTCAGATAGTTGTTGCTTCCTGACAGGGCCTCTTGCTTGTCTCTGGTTGCCAGATGACCTATTGCTCATTGACCGTAC
CCCACGAGTCTATCAACAACGAAGGACTGTCCC GGAGAACGAACAAGAGACCAACGGGTCTACTGGATAACGAGTAACTGGCATG

8245

SORL1

SORL1-201

SORL1-201

CTACCTCTGCTGGAATGGCACTGTGTAGTTAGGTGTTGTTTTAATTAACCTTTCCACCATGAAACCCTAAACCCCATGAAGAAA
GATGGAGACGACCTTACCGTGACACATCAATCCACAACAAAATTAATTGAAAAGGGTGGTACTTTGGGATTTGGGGTACTTCTTT

8330

SORL1

SORL1-201

SORL1-201

GAGATGGTCTTTTTTATTCCCGATAGTTTTACCAGTGTCTAGCACTTTGTAGGTGCTCAATTCATATTTGTTGAAAGAATAAGG
CTCTACCAGAAAAAATAAGGGGCTATCAAAATGGTCACAGATCGTGAAACATCCACGAGTTAAGTATAAACAACCTTTCTTATTCC

8415

SORL1

SORL1-201

SORL1-201

GATGAAAAGGGAGGGGAAGAATTGCAGTGGGTGCAGACAGTAGCTGTCTTAGAGATCTACTGGGTGAGGCTTCAAGAACTGCTAT
CTACTTTTCCCTCCCCTTCTTAACGTCACCCACGTCTGTCTATCGACAGAATCTCTAGATGACCCACTCCGAAGTTCTTGACGATA

8500

SORL1

SORL1-201

SORL1-201

GAGGCTTTGACCTGCTAGTCCTGGAGTCTGAGACTATTCAGTGGAAAGCCTTTATCATTTCATGACTGCTCTTTGATTTTGCTTA
CTCCGAAACTGGACGATCAGGACCTCAGACTCTGATAAGTCACCTTTCGGAAATAGTAAAGTACTGACGAGAAACTAAAACGAAT

8585

SORL1

SORL1-201

SORL1-201

TCTCCAGCCATACTATTGATTCTAGAGGAGAAAGATCAGAGGATTACCAGGAAGAATAGTCCCTTTAAGAATTTCCCTCTTTAT
AGAGGGTCGGTATGATAACTAAGATCTCCTCTTTCTAGTCTCCTAATGGTCCTTCTTATCAGGGAAATTCCTAAAGGGAGAAATA

8670

SORL1

SORL1-201

SORL1-201

CTCAGCAGGATTAATGGCATCCTGGGTTTGCTGATTCTCCTTTATTGACAAACTGCTAAGTTTTCTGTTCTTAACTGGAATGTT
GAGTCGTCCCTAATTTACCGTAGGACCCAAACGACTAAGAGGAAATAACTGTTTGACGATTCAAAGACAAGAATTGACCTTACAA

8755

SORL1

SORL1-201

SORL1-201

GATATTGTTTTATGGTTCTTGGCTGACCCTATACTAGGAGAAAATTGACAGGGGAAATAATACTGTTATAGATATCATTGTTATC
CTATAACAAAATACCAAGAACCGACTGGGATATGATCCTCTTTAACTGTCCCTTTATTATGACAATATCTATAGTAACAATAG

8840

SORL1

SORL1-201

SORL1-201

CTCTTGGGATTGTGAAGATAGCATGAGAACACCCTGGGAAAACCTATAAAGTGTCTTACAAATGTAAGACGATATTATTTGTTATG
GAGAACCTTAACACTTCTATCGTACTCTTGTGGGACCCTTTTGATATTTACAGAAATGTTTACATTCTGCTATAATAACAATAC

8925

SORL1

SORL1-201

SORL1-201

TCTTCACCACTGACCTGTGAGGTAGGGAAGGCTGGTATTATGATCCATGGTTTATAGATTAGGGAATTAATCTCAGATATGAAT
AGAAGTGGTGACTGGACACTCCATCCCTTCCGACCATAATACTAGGTACCAAATATCTAATCCCTTAATTTAGAGTCTATACTTA

9010

SORL1

SORL1-201

SORL1-201

TAGCTTTCCAAAATATCCTCACTAGTTTAGGGGCTGGCCTTTTGTGCAATTCTGCCGCTAAATGGAGAAGTCACATTCTTTCT
ATCGAAAGGGTTTTATAGGAGTGATCAAATCCCGACCGGAAAACAACGTTAAGACGGCGATTTACCTCTTCAGTGTAAAGAAAGA

9095

SORL1

SORL1-201

SORL1-201

TAGAGGAGGCACCTGTTTTAGAATCAGGAGAGTTGAAGGAATCTTGCTTCTCAGCTCCAGTGACTGAAATCTTCAGACCTTTGTT
ATCTCCTCCGTGGACAAAATCTTAGTCCTCTCAACTTCCTTAGAACGAAGAGTTCGAGGTCACTGACTTTAGAAGTCTGGAAACAA

9180

SORL1

SORL1-201

SORL1-201

TAATGGAGGACATCCACCCCTACTGATCTGACTTGCTAGCTAGCAGAGTGGATTTTTAGTATTTCTCCAAGTGGATTTTTAGCAT
ATTACCTCCTGTAGGTGGGGATGACTAGACTGAACGATCGATCGTCTCACCTAAAAATCATAAAGAGGTTACCTAAAAATCGTA

9265

SORL1

SORL1-201

SORL1-201

TTCTCCATGTTACCACTTAGTCCAGAAGAGTGGGTCTTCATTTTTACAAGTGCTTGTATGCATGTGCTTGTGTTGATTTGCACACA
AAGAGGTACAATGGTGAATCAGGTCTTCTCACCCAGAAGTAAAAATGTTACGAACATACGTACACGAACAACTAAACGTGTGT

9350

SORL1

SORL1-201

SORL1-201

GGAGCTTCTGAAACACTGTGTGCAGATGAAGCCAGTGGCTACCCGGTCACAACCTTACTTCCCAGTCTTGACTGTCCACTTCATCC
CCTCGAAGACTTTGTGACACACGTCTACTTCGGTCACCGATGGGCCAGTGTGTAATGAAGGGTCAGAAGTACAGGTGAAGTAGG

9435

SORL1

SORL1-201

SORL1-201

CAAGAAGTGGGCACAGCTGACATGCAGTCACACCTGTGACTGAGGAGCAGTGCGGGAGGAGAGATTTGTGGTCTCAGCACATG
GTTCTTGAACCCGTGTGCGACTGTACGTCAAGTGTGGACACTGACTCCTCGTCACGCCCTCCTCTCTCAAACACCAGAGTCTGTGTAC

9520

SORL1

SORL1-201

SORL1-201

CAAACGTGGTGTCTTGGTGCCAGTCAGACAGGTCTGCAATCCTCACCTTAGGTGTAGTTTCCCTTTCATGCCTCAAAGAGTCATC
GTTTGCACCACAGAACCACGGTCAAGTCTGTCCAGACGTTAGGAGTGGAAATCCACATCAAAGGGAAAGTACGGAGTTTCTCAGTAG

9605

SORL1

SORL1-201

SORL1-201

TTCATTTAAGTTAGCCAGAGTCATTTTTGGGGCCCAGAGTGGAGTCTGGATAGATGACAGGCTGGTTTTAAAGGGAGATATGTATT
AAGTAAATTC AATCGGTCTCAGTAAAACCCCGGGTCTCACTCCAGACCTATCTACTGTCCGACCAAATTTTCCCTCTATACATAA

9690

SORL1

SORL1-201

SORL1-201

AGCAGGGGCATAGTGGCACATGCCTGTAGTCTCAGCTCCTCAGGAGGCGGAGGTGGGAGCATCACCTGAGCTCGGGAGGTTGAGGC
TCGTCCCCTATCACCGTGTACGGACATCAGAGTCGAGGAGTCTCCGCCTCCACCCTCGTAGTGGACTCGAGCCCTCCAACCTCCG

9775

SORL1

SORL1-201

SORL1-201

TGCAGTTAGCCAAGGTCGTGCTGCTGCACTCCATCCTGGGTGACAGAGTGAGACCCTGTCACCGAAAAAAAAAAAAAAAAAAGGCT
ACGTCAATCGGTTCCAGCACGACGACGTGAGGTAGGACCCACTGTCTCACTCTGGGACAGTGGCTTTTTTTTTTTTTTTTTTCCGA

9860

SORL1

SORL1-201

SORL1-201

GGGGGAGATCTGTGTTGGTGAGTAGAACACAGACCTGGACCTGTGCATGGGCGGCTGTGACTGTCCCTTTGGCCATGGCCAGTTG
CCCCCTCTAGACACAACCACTCATCTTGTGTCTGGACCTGGACACGTACCCGCGGACACTGACAGGGAAACCGGTACCGGTCAAC

9945

SORL1

SORL1-201

SORL1-201

TCGCCTCTCTGCTCCTTTCTGTTTGCCTTTGGGATTTTCTCTTGCTGTCTTTGGTTGTGAGCAGGATACTTCCAGGAGACCTAC
AGCGGAGAGACGAGGAAAGACAAACGGAAACCTAAAAGAGAACGACAGGAAACCAACTCGTCCTATGAAGGTCTCTGGATG

10,030

SORL1

SORL1-201

SORL1-201

TGCCTCCAAACACAGGGCTGGAGAAAGACGTTTTGTCTTTCTCTGCAGCCAGTTTGGGTCAAATCAAAGCTTTTGCAGTGGTG
ACGGAGGTTTGTGTCCCGACCTCTTTCTGCAAAAACAGAAAGAGACGTGCGGTCAAACCCAGTTTAGTTTCGAAAACGTCAACCAC

10,115

SORL1

SORL1-201

SORL1-201

TCTGGCTGTCAGCACTGTCTATGAGCACTCCGCACCTCTTGGCCTTGAACCTGTTTGTCTAACCTGCTTGCTTTTTTTGGACAC
AGACCGACAGTCGTGACAGATACTCGTGAGGCGTGGAGAACCGGAACCTTGAACAAACGAGATTGGACGAACGAAAAAAAAACCTGTG

10,200

SORL1

SORL1-201

SORL1-201

TGATAGGACACTTGCTTTTTTGGACATTGTATTACAGATCCACGGTGTGTGTTGGATCTAGCACTTGGAGAAATGCTAAAAATCC
ACTATCCTGTGAACGAAAAACCTGTAACATAATGTCTAGGTGCCACACACAACCTAGATCGTGAACCTCTTTACGATTTTTAGG

10,285

SORL1

SORL1-201

SORL1-201

ACTCTGCTAGCTAGCAAGTCAGATCAGTAGGGGTGGATGTCCTCCATCAAGCAAGGGCCTGAATATTTTCAGTCACTGGAGCTGAG
TGAGACGATCGATCGTTTCAGTCTAGTCATCCCCACCTACAGGAGGTAGTTTCGTTCCCGGACTTATAAAGTCAGTGACCTCGACTC

10,370

SORL1

SORL1-201

SORL1-201

AAGCAAGATTCCTTCAACTCTCCTTATTTTAAAACAGGTGACTCCTCTAAGAAAGAATGTGACTCCTGTCCATCTTTATTATTTT
TTCGTTCTAAGGAAGTTGAGAGGAATAAAATTTTGTCCACTGAGGAGATTCTTTCTTACACTGAGGACAGGTAGAAATAATAAAA

10,455

SORL1

SORL1-201

SORL1-201

TGTTGTCTCCTCCTAACACATTCGGGACTTTCTACAGTAGTCTCCTGCTTATTTGCCATTTTGCTTTCTGTGATTTTCAGCTACCT
ACAACAGAGGAGGATTGTGTAAGCCCTGAAAGATGTCATCAGAGGACGAATAAACGGTAAAACGAAAGACACTAAAGTCGATGGA

10,540

SORL1

SORL1-201

SORL1-201

GCGGTCAACCACTGTCCAAAAATATATATGGAAGATTCCAGAAATAAACAATGTATAAGATTTAAATTGCTTGCTGTTCTGAATA
CGCCAGTTGGTGACAGGTTTTTATATATACCTTCTAAGGTCTTTATTTGTTACATATTCTAAATTTAACGAACGACAAGACTTAT

10,625

SORL1

SORL1-201

SORL1-201

GTGTGATGAAATCTTGACTGTCTCCTCCCTGTCCACCTGGGATGTGAATCCTCCCTTTGTCCAGCGTCTCATGCTGTTGATGC
CACACTACTTTAGAACATGACAGAGGAGGGACAGGGTGGACCCTACACTTAGGAGGGAAACAGGTCGCAGAGTACGACAACCTACG

10,710

SORL1

SORL1-201

SORL1-201

TGCCGGCTCATTAGTCCCTTTAGGAGCCGGCTGGGTTATCAGGGTGTCAAAGTACTGCAGTTCTTGTACGCAAGGAACCCTTATT
ACGGCCGAGTAATCAGGGAAATCCTCGGCCGACCCAATAGTCCACAGTTTCATGACGTCAAGAACATGCGTTCCTTGGAATAA

10,795

SORL1

SORL1-201

SORL1-201

TTACTTCATGATGACCCTACACCTCAAGAGTAGTGATTCCAGTAATTTGGATATGCCAAAGGGAGGTTGTAAAGTGCTTCCTTTA
AATGAAGTACTACTGGGATGTGGAGTTCTCATCACTAAGGTCAATTAACCTATACGGTTTCCCTCCAACATTTACGAAGGAAAT

10,880

SORL1

SORL1-201

SORL1-201

GGGAAAGGGTGAAAGTTCTAGACTTAATAAGGGAGGAAAAAAAAATCTTACACCGAGTTTGGCTAAGATCTGCTGTAAGAACGAACC
CCCTTTCCCACTTTCAAGATCTGAATTATTCCTCCTTTTTTTTGAAGTGTGGCTCAAACGATTCTAGACGACATTCTTGCTTGG

10,965

SORL1

SORL1-201

SORL1-201

TTCTATCTCTGAAATTGTAAAGAAAGAAAAAGAAATTCATGCACAGTATAGGTTTGGTCCTATCTGCAGTTTCAGGTGTCAGCTA
AAGATAGAGACTTTAACATTTCTTTCTTTTCTTTAAGTACGTGTCATATCCAAACCAGGATAGACGTCAAAGTCCACAGTCGAT

11,050

SORL1

SORL1-201

SORL1-201

GGGGTCTTGGAAATTGGGGGTTTTGGAATAAGAGGGGACTACTATATTAACCAAGTGTTAAATAATAAATTGATAGTAACTACA
CCCCAGAACCTTAACCCCAAAACCTTATTCTCCCCTGATGATATAATTGGTTCACAATTTATTATTATTAACATATCATTGATGT

11,135

SORL1

SORL1-201

SORL1-201

TGTATTGAGGGGTTGCTGTGTTATAAGTACCACAGTAATGTGCTTTGTGGGCTTGTATAACCTCACTTCGTCTTCCCAAAGACTT
ACATAACTCCCAACGACACAATATTCATGGTGTCAATTACACGAAACACCCGAACATATTGGAGTGAAGCAGAAGGGTTTCTGAA

11,220

SORL1

SORL1-201

SORL1-201

CTATATGTAATCAATATTTCCATTTTATAGGTGAGAATATGAAAGTCTGGTTTAGTAACTTGTGTAGGTCACACTTTTAGTAA
GATATACATGATAGTTATAAAGGTAAAATATCCACTCTTATACTTTTCAGACCAAATCATTGAACACATCCAGTGTGAAAATCATT

11,305

SORL1

SORL1-201

SORL1-201

GTGGTAAGAATTTGCACTGTGGCCCGTTGACTTCAAAGCCTGAACTTCGATAAAACCACCCGGCTCTGCTCCCTCTGTCATGTGT
CACCATTCTTAAACGTGACACCGGGCAACTGAAGTTTCGGACTTGAAGCTATTTTGGTGGGCGGAGACGAGGGAGACAGTACACA

11,390

SORL1

SORL1-201

SORL1-201

TGCTAGAATAGCAGTGCCCTGGTAGTATGACAGCAGTTCAGAAGTACTGTTCTAGATTTTGATTGATGATGGTTCATAATAAAAA
ACGATCTTATCGTCACGGGACCATCATACTGTCGTCAAGTCTTCATGACAAGATCTAAAACCTAACTACTACCAAGTATTATTTTT

11,475

SORL1

SORL1-201

SORL1-201

TGTTGTTTCAGTTGCAACATTTATCAATTTGAAATATTTGGTCCCTTTATAGCTAGCTGGTTTTTATTTTTTATTTGTTTAGTTTTT
ACAACAAGTCAACGTTGTAATAAGTTAAACTTTATAAACCGAGGAAATATCGATCGACCAAAAAATAAAAAATAAACAAATCAAAAA

11,560

SORL1

SORL1-201

SORL1-201

TGGAGACAGAGTCTCGTTCTGTTACCCCGGCTGGAGTGCAGTGATGTGATCTTGGCTCACTGCAACCTCTGCCTCCTGGGTTCAA
ACCTCTGTCTCAGAGCAAGACAATGGGGCCGACCTCACGTCACTACACTAGAACCAGGTGACGTTGGAGACGGAGGACCCAAGTT

11,645

SORL1

SORL1-201

SORL1-201

GCAATTTCTCATGCCTCAGCCTCCTAAGTAGCTGGGACTAAAGGCATGTGCCACCATGCCTGGCTAATTTTTTGTATTTTAGTAGA
CGTTAAGAGTACGGAGTCGGAGGATTCATCGACCCTGATTTCCGTACACGGTGGTACGGACCGATTAAAAACATAAAATCATCT

11,730

SORL1

SORL1-201

SORL1-201

GATTGGGTTTCACCATGTTGCCAGGCTGGTCTTGAACCTCTGAGCTCAGGCAATCTGCACGCCCGGCCTCCCAAAGTGCTAGG
CTAACCCAAAGTGGTACAACGGGTCCGACCAGAACTTGAGGACTCGAGTCCGTTAGACGTGCGGGGCCGGAGGGTTTTACGATCC

11,815

SORL1

SORL1-201

SORL1-201

ATTTACAGGTGTGAGCCACTGTGTCTGGCCACTAGCTGGTTTTTAAATGGTATAACTGGAATTTATTCTTTGTAAAGTGTGTTTT
TAAATGTCCACACTCGGTGACACAGACCGGTGATCGACCAAAAAATTTACCATATTGACCTTAAATAAGAAACATTTACACAAAA

11,900

SORL1

SORL1-201

SORL1-201

TTCTTTAAAGAGGTTACTTTACAAGATTGTTGATGTATTCAGTTGCTCCTGCGATGGCTCTTGGAGCTTTGGAATTTCTTTTGCAG
AAGAAATTTCTCCAATGAAATGTTCTAACAACACTACATAAGTCAACGAGGACGCTACCGAGAACCTCGAAACCTTAAGAAAACGTC

11,985

SORL1

SORL1-201

SORL1-201

TTTTGGAATTTCTCCTTTAGAGCCTGCAGTAAGTATGTGCTTTTAAAGTATCTATAATGAGGGCACATATTTATTATTTGAGGTAGA
AAAACCTTAAGAGGAAATCTCGGACGTCATTCATACACGAAAATTCATAGATATTACTCCCGTGTATAAATAATAAACTCCATCT

12,070

SORL1

SORL1-201

SORL1-201

TTTGATTTTGGATAATTGCCAAGTGTATAGATACTTGAGATGATGACATTTTTGGCTCCTAAAAGTATTCCTGGAGGAATTTTCCAA
AAACTAAAACATATTAACGGTTCACATATCTATGAACTCTACTACTGTAAAAACCGAGGATTTTCATAAGGACCTCCTTAAAAGGTT

12,155

SORL1

SORL1-201

SORL1-201

ACAGGAAATGTGAAAATGTTCTGAACATGCCCAGTGAAGACATCACGGGGCTATGTGTTTGGATCTTCTAAGGGAATGTCTTTGAA
TGTCCCTTTACACTTTTACAAGACTTGTACGGGTCACTTCTGTAGTGCCCCGATACACAAACTAGAAGATTCCCTTACAGAAACTT

12,240

SORL1

SORL1-201

SORL1-201

GATGATTGTCCACTCTTTCACATTGAGATAACGGTTTTTCATATTGCCTGGTCCACTCAAGACAATTGTCATCCTGTATAAAGGGTC
CTACTAACAGGTGAGAAGTGTAACTCTATTGCCAAAAGTATAACGGACCAGGTGAGTTCTGTAAACAGTAGGACATATTTCCCAG

12,325

SORL1

SORL1-201

SORL1-201

TGTGGCTGTGGTAGAACTGCCATCATAGGAGTTGGTGAATTACCCTTCCATCTTCTTCCAGCTTCTCTCTGATGCAGCTCTCCCA
ACACCGACACCATCTTGACGGTAGTATCCTCAACCACTTAATGGGAAGGTAGAAGAAGGTGCAAGAGAGACTACGTCGAGAGGGT

12,410

SORL1

SORL1-201

SORL1-201

TTTTCCATTCTCTGGCTTCAGACTAGCCTAGACATTCTGCCCCTGCCTACCTCTTAGGATCAGTGACTTGGTTAGCTTGTGTTTG
AAAAGGTAAGAGACCGAAGTCTGATCGGATCTGTAAGGACGGGGACGGATGGAGAATCCTAGTCACTGAACCAATCGAACAAAAC

12,495

SORL1

SORL1-201

SORL1-201

CAGTTTGCCCCTGGTTACTGCCTCAGAGTACAGTTTTCATACATTTCTGCCTAGATCAGCCTCCTGAAATATGATACCCCATTTTG
GTCAAACGGGGACCAATGACGGAGTCTCATGTCAAAGTATGTAAAGACGGATCTAGTCGGAGGACTTTATACTATGGGGTAAAAC

12,580

SORL1

SORL1-201

SORL1-201

AGTTCTCTACTCTTAGCTCTTCTTGCTTGTGGATAGGAATATTTGCTCTGCATATGAAAAGGTTAGTGAAATGATTTTACAGA
TCAAGAGATGAGAATCGAGAAGAACGAACAAACCTATCCTTATAAACGAGACGTATACTTTTCCAATCACTTTACTAAAATGTCT

12,665

SORL1

SORL1-201

SORL1-201

CATGATCCCTGTGAAAAAAAAATCATCCTGTAATAGAGTAGTTTTTTTTTATTTTGTTCGTTTTGTTTGTGTTTGTGTTTGTGAGACAG
GTACTAGGGACACTTTTTTTTAGTAGGACATTATCTCATCAAAAAAAAAATAACAAGCAAAACAAACAAACAAACAAACAAACTCTGTGC

12,750

SORL1

SORL1-201

SORL1-201

GCTCTGGCTCTGTTACCCAGGCTGGAGTGCAGTGGCGCCATCTCAGCTAACTGCAGCCTCTGTCTCCTGGGCTTAAGCAATCTTC
CGAGACCGAGACAATGGGTCCGACCTCACGTCAACCGCGGTAGAGTCGATTGACGTGCGGAGACAGAGGACCCGAATTCGTTAGAAG

12,835

SORL1

SORL1-201

SORL1-201

CCACTTCAGCCTCTGAAGTGGCTGGGATCACAGATGTGTACCCGGCTAATTTTGTCTTATTTTTTTTTTGTGGAGGCGGTCTTCAC
GGTGAAGTCGGAGACTTCACCGACCCTAGTGTCTACACATGGGCGGATTAACGAATAAAAAAAAAAACACCTCCGCCAGAAGTG

12,920

SORL1

SORL1-201

SORL1-201

TATGTTGCTCAGGGTGGTCTCGAACTCCTGGGCTCGAGTGATCCTCCACCTCGGCCTCCCAAACCTGCTGGGATTACAGATGTGA
ATACAACGAGTCCCACCAGAGCTTGAGGACCCGAGCTCACTAGGAGGGTGGAGCCGGAGGGTTTGACGACCCTAATGTCTACACT

13,005

SORL1

SORL1-201

SORL1-201

GCCACTGCACCCAGCCGGTAATAGAGTATTTTAAAAATAACATCATATTCATTATTGTTTCAGGATCTTGGAACATTGAGTGATAT
CGGTGACGTGGGTCCGCCATTATCTCATAAAATTTTATTGTTAGTATAAGGTAATAACAAGTCCTAGAACCTTGTAACCTCACTATA

13,090

SORL1

SORL1-201

SORL1-201

ATTGTTCTTTGAATACAAAACACATGTTCCACATCCTTGTGTTGAGTTGTTTCTCATGAGTGGTGGCTCTATGTCAATTCTGCAT
TAACAAGAACTTATGTTTTGTGTACAAGGGTGTAGGAACAAACTCAACAAAGAGTACTCACCACCGAGATACAGTTAAGACGTA

13,175

SORL1

SORL1-201

SORL1-201

TCCCTCTTGTAGCCAGTGGCCTGTACCTTTGAACTAAAGGAGCCATCTGTGCCCACTAATGGATCAGAGTGAAGGGATGTCTGGG
AGGGAGAACATCGGTCAACCGACATGGAACTTGATTTCTCGGTAGACACGGGTGATTACCTAGTCTCACTTCCCTACAGACCC

13,260

SORL1

SORL1-201

SORL1-201

ACTTCTGCTCTAGTCAGCTGGTTAGTCTGCTATGGTAATTAAGCTGTTATGATTGATTATTTACTGAACCTTTTGGACTGTTTCA
TGAAGACGAGATCAGTCGACCAATCAGACGATACCATTAATTCGACAATACTAACTAATAAATGACTTGGAAAACCTGACAAAAGT

13,345

SORL1

SORL1-201

SORL1-201

TCATGTGGACTTCCCTTCCTCTGGAGGTGTATGTTTTCTCTCTATTTACTGAATCTTTTGGAAATGTTTCATCATATGAACCTCCC
AGTACACCTGAAGGGAAGGAGACCTCCACATACAAAAGAGAGATAAATGACTTAGAAAACCTTACAAAAGTAGTATACTTGGAGGG

13,430

SORL1

SORL1-201

SORL1-201

TTCCTCTGGATGTGTGTGTTTTCTCTTTGGTAATACCTCTTACTCTTTTTCTTGGCATCATAATAACGTTGTTGCCATAGCATTG
AAGGAGACCTACACACACAAAAGAGAAAACCATTTATGGAGAATGAGAAAAGGAACCGTAGTATTATTGCAACAACGGTATCGTAAC

13,515

SORL1

SORL1-201

SORL1-201

TGATTTTTATTTTTATTTGTAATGTAAATTAACCAATGATGTGCCACACACCCAAAGCTACTGCGTATATTATCCATATCGACA
ACTAAAATAAAAATAAACATTACATTTAATTGGTTACTACACGGGTGTGTGGGTTTCGATGACGCATATAATAGGTATAGCTGT

13,600

SORL1

SORL1-201

SORL1-201

CTGATTATCATTTCATGAACCTTCGTCTAACCTGTAGGCCAGGATAGGCATGGCTTAGATGAATGCTTGGCTGGGTGGCAACAGATG
GACTAATAGTAAGTACTTGAAGCAGATTGGACATCCGGTCTATCCGTACCGAATCTACTTACGAACCGACCCACCGTTGTCTAC

13,685

SORL1

SORL1-201

SORL1-201

ATTTGGATATGGTGCTGAAGTGTGGGAGGGCATCTCTGTCCATGACATAGCACGAATGAAGAATTAGCAATTGAGTTTTATCTAA
TAAACCTATACCACGACTTCACACCCTCCCGTAGAGACAGGTAAGTATCGTGCTTACTTCTTAATCGTTAACTCAAAAATAGATT

13,770

SORL1

SORL1-201

SORL1-201

GTTTTATGTTTCATTTTTCCCATTTTCATGATTAATAATTGCAGTCAAAAGAAAAACATGATTTTCATAGTTTCTGTGACCCCAT
CAAAAATACAAGTAAAAGGGTAAAAGTACTAATTATTAACGTCAGTTTTCTTTTTGTACTAAAGTATCAAAGACACTGGGGTA

13,855

SORL1

SORL1-201

SORL1-201

AGTTGTATCATGTTTCAGATTGTTATAAAAATGGTTTATGCATCTTCTTACCTGCCATCCCCGGAACGATGTAGGGGATAGGATGG
TCAACATAGTACAAAAGTCTAACAAATATTTTACCAAATACGTAGAAGAATGGACGGTAGGGGGCCTTGCTACATCCCCTATCCTACC

13,940

SORL1

SORL1-201

SORL1-201

CACTTTTGGCATCCTCGTTCATCCACAAAGGCTCCTTCTCAAGAGTGCAGTGGTGGATTTTACGAACTCTCTCCGGTGCTGCCTT
GTGAAAACGGTAGGAGCAAGTAGGTGTTTCCGAGGAAGAGTTCTCACGTACCACCTAAAATGCTTGAGAGAGGGCCACGACGGAA

14,025

SORL1

SORL1-201

SORL1-201

TAGTAAGCTGAACCAGAGAAAAGATTGGCAGGAGTGGGCTAGATCAGCATGAACTAGTCCTTACCTGAACACATTGCACAGCAGT
ATCATTGACTTGGTCTCTTTTCTAACCGTCTCACCCGATCTAGTCGTAAGTATGATCAGGAATGGACTTGTGTAACGTGTCGTC

14,110

SORL1

SORL1-201

SORL1-201

GGCTGATGAGTACTGTGGTTGGCTCCTCCTTTAGCTCTTGAGGGGCACTCTGGCACAAGGAATTGAGAAGGGGAGGCCTGGATT
CCGACTACTCATGACACCAACCGAGGAGGAAATCGAGAACTCCCCGTGAGACCGTGTTTCTTAACCTTTCCCCTCCGGACCTAA

14,195

SORL1

SORL1-201

SORL1-201

TTTGTCTGGGGCCACCATTAACCAGGTGTATGTTCTAATTAAGGCCTTTGGGGCCCTAAGGAGCAGAAACCCACTCAAGCTAGC
AAACAGGACCCGGGTGGTAATTGGTCCACATACAAGATTAATTCGGAAACCCCGGGATTCTCGTCTTTGGGTGAGTTTCGATCG

14,280

SORL1

SORL1-201

SORL1-201

TCAAGTGAATGGTTTTATGGAATGAATAAAGGAGCCCAAAGATGAAAGTCTAGGAGAGCCTCATGGGGACTGGAGCTGTTCTTTC
AGTTCACTTACCAAAATACCTTACTTATTTCTCGGGTTTCTACTTTCAGATCCTCTCGGAGTACCCCTGACCTCGACAAGAAAAG

14,365

SORL1

SORL1-201

SORL1-201

TCTTTCCCTCTCATTAGGCCTCTTCTCTCTGTAAGCCTCTTTCTTTTTAAAAAAAAAATTATTCGGAATTTTGAAGGCAATGTTTC
AGAAAGGGAGAGTAATCCGGAGAAGAGAGACATTCCGAGAAAGAAAAATTTTTTTTTTAATAAGCCTTAAAACCTCCGTTACAAG

14,450

SORL1

SORL1-201

SORL1-201

AACTATATTATAGCCACTAGTGTGTAATTGAGAAGTCCAAAGACATTCTGGTTCTTTTTTAAATTAATAAAAAAAAAAATTTTTTTTT
TTGATATAATATCGGTGATCACAAACATTAACCTCTTCAGGTTTCTGTAAGACCAAGAAAAATTTAATTTTTTTTTTTTAAAAAAA

14,535

SORL1

SORL1-201

SORL1-201

AAGGGATAGGATCTTGCTATATTGCCCAGGCTGGATTTCGAGCTACCAGGCTCAAGTGATCCTCCTGCCTCAGCCTCCTGAGTAGC
TTCCCTATCCTAGAACGATATAACGGGTCCGACCTAAGCTCGATGGTCCGAGTTCACTAGGAGGACGGAGTCGGAGGACTCATCG

14,620

SORL1

SORL1-201

SORL1-201

TGGGGCTACAGGTGCGTGCTGCCATGCCTGGCCTCCTTAAGTCTCTTTTAGTCTCCTGACGGTCTGCAGACTGAGCTTATCTGCA
ACCCCGATGTCCACGCACGACGGTACGGACCGGAGGAATTCAGAGAAAATCAGAGGACTGCCAGACGTCTGACTCGAATAGACGT

14,705

SORL1

SORL1-201

SORL1-201

TACCCAGAGTTTTGACTTCCACACGGTTTTGGCTTGCCATGTGCCACTTCAACACCCATGCTCTGTGACCCTTTCCCTGGCTCCA
ATGGGTCTCAAACTGAAGGTGTGCCAAAACCGAACGGTACACGGTGAAGTTGTGGGTACGAGACACTGGGAAAGGGACCGAGGT

14,790

SORL1

SORL1-201

SORL1-201

GCTCCTTGTTGCTTTCTTGTCTTTCAAGTGACCCAATTACAAATTCAGGAGGAACCTGCTGCCTGGCTTGGCTCTGGGGCAG
CGAGGAACCAACGAAAGAACAGAAAAGTCACTGGGTTAATGTTTAAGGGTCTCCTTGGGACGACGGACCGAACCGAGACCCCGTC

14,875

SORL1

SORL1-201

SORL1-201

TCTGATCTGGCTGAAGACAGGATGCAAGTCACTGGTTATACTGAGCAGAAGTTTTTCAGCACAGTAGGCGCCCCAAAGCTTGCCAC
AGACTAGACCGACTTCTGTCTACGTTCAAGTGACCAATATGACTCGTCTTCAAAAAGTCGTGTCATCCGCGGGGTTTCGAACGGTG

14,960

SORL1

SORL1-201

SORL1-201

TTGACCCTTGAGAGCTTCTCGCTGTCCTTTCCGTAAGACGAGGAGGTTGCAGTGGGTCTCCTTCTTGTATTTCAGTACCTCCCTCA
AACTGGGAACCTCTCGAAGAGCGACAGGAAAGGCATTCTGCTCCTCCAACGTCACCCAGAGGAAGAACAATAAGTCATGGAGGGAGT

15,045

SORL1

SORL1-201

SORL1-201

TGGTGTGTATTAACCTACCTGCTGCTGTTTGTCTTCCCTCCAGGAAGCAATGCCTGTGTGCCCAGGCCATGCAGCCTGCTGTGCC
ACACACATAATTGGATGGACGACGACAAACAGAAGGGAGGTCTTTCGTTACGGACACACGGGTCCGGTACGTCGGACGACACGG

15,130

SORL1

SORL1-201

1020 1025 1030
G S N A C V P R P C S L L C

ENSE00003533392

SORL1-201

TGCCCAAGGCCAACAAACAGTAGAAGCTGCAGGTGTCCAGAGGATGTGTCCAGCAGTGTGCTTCCATCAGGGGACCTGATGTGTGA
ACGGGTTCCGGTTGTTGTCATCTTCGACGTCCACAGGTCTCCTACACAGGTCGTCACACGAAGGTAGTCCCCTGGACTACACACT

15,215

SORL1

SORL1-201

1035 1040 1045 1050 1055
L P K A N N S R S C R C P E D V S S S V L P S G D L M C D

ENSE00003533392

SORL1-201

CTGCCCTCAGGGCTATCAGCTCAAGAACAATACCTGTGTCAAACAAGGTA CTTCCCTTTTTCTTTTTTGCCTGTCATCCTCCTTC
GACGGGAGTCCCGATAGTCGAGTTCTTGTATGGACACAGTTTGTTCATGAAGGGAAAAAGAAAAACGGACAGTAGGAGGAAG

15,300

SORL1

SORL1-201

1060 1065 1070
C P Q G Y Q L K N N T C V K Q G T S L F L F C L S S S F

ENSE00003533392

SORL1-201

(in frame with SORL1-201)

CTTTGTTTCCTGCTCCCCGCCAGGGGAGGGAGGGATAGCTCTCTGTTTCCTA
GAAACAAAGGACGAGGGGCGGTCCCTCCCTCCCTATCGAGAGACAAAGGAT

3'

15,352

5'

SORL1

SORL1-201

L C F L L P A R G G R D S S L F P
(in frame with SORL1-201)

Feature	Location	Size		Type
✓ SORL1	1 .. 15,352	15,352 bp	→	gene
/note	= gene ENSG00000137642 Protein coding			
SORL1-AS1	1 .. 15,352	15,352 bp	←	gene
/note	= gene ENSG00000246790 lncRNA			
✓ SORL1-201	1 .. 15,352	15,352 bp	→	prim_transcript
/note	= primary transcript ENST00000260197			
SORL1-AS1-201	1 .. 15,352	15,352 bp	←	prim_transcript
/note	= primary transcript ENST00000501964 lncRNA			
SORL1-AS1-202	1 .. 15,352	15,352 bp	←	prim_transcript
/note	= primary transcript ENST00000529160 lncRNA			
✓ SORL1-201	2086 .. 15,262	13,177 bp	→	CDS
▶ 6 segments = 957 bp				
/codon_start	= 1			
/note	= coding sequence ENSP00000260197			
/translation	= ENEFILYAVRKSIIYRYDLASGATEQLPLTGLRAAVALDFDYEHNCLYWSDLALDVIQ,,RLCLNGSTGQVEVIINSGLETVEALAFEP LSQLLYWVDA GFKKIE,,VANPDGDFRLTIVNSSVLD RPRALVLPQEG,,VMFWTDWGD LKPGIYRSNMDGSAAYHLVSE DVKWPNGISVDDQWIYWTDAYLEC IERITFSGQQRSVILDNLPHPYAIAVFK,,NEIYWDDWSQLSIFRASKYSGSQMEILANQLTGLMDMKIFYKGKNT,,GSNACVPRPCSL LCLPKAN NSGRCPEYSSYLSQDLMCD CPQGYQLKNNTCVKQ 18 amino acids = 2.1 kDa			
SORL1-208	3191 .. 6986	3796 bp	→	prim_transcript
/note	= primary transcript ENST00000529445 Retained intron			
SORL1-203	5164 .. 6922	1759 bp	→	prim_transcript
/note	= primary transcript ENST00000524873 Retained intron			
✓ Donor Template WT -> SNV	6885 .. 6984	100 bp	⇌	misc_feature
✓ Protospacer Sequence	6903 .. 6922	20 bp	⇌	misc_feature
✓ SNV	6916 .. 6916	1 bp	⇌	misc_feature
/note	= WT = C SNV = T			
✓ PAM	6923 .. 6925	3 bp	⇌	misc_feature
SORL1-204	14,874 .. 15,352	479 bp	→	prim_transcript
/note	= primary transcript ENST00000525532			
SORL1-204	15,208 .. 15,262	55 bp	→	CDS
/note	= coding sequence ENSP00000434634			
/translation	= MCD CPQGYQLKNNTCVKQ 18 amino acids = 2.1 kDa			

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = ATGCACGCCAAATAGGATTGTAGTG 44% GC / 7730.1 Da	25-mer	6315 .. 6339	60°C	Jan 11, 2023
✓ Sanger Sequencing /sequence = CGGAGCAATATGGATGGTTC 50% GC / 6197.1 Da	20-mer	6786 .. 6805	56°C	Jan 11, 2023
✓ Donor Template WT -> SNV /sequence = TAAAGACAGCAATGGCATAGGGGTGCGGGAGGTTGTCCAGAATGACAGAGCGCTGCTGGCCACTGAACATGATCCGCTCTATGCACTC 55% GC / 6717.1 Da	100-mer	6885 .. 6984	79°C	Jan 11, 2023
✓ gRNA Protospacer /sequence = ATAGAGCGGATCACGTTTCAG 50% GC / 6166.1 Da	20-mer	6903 .. 6922	57°C	Jan 11, 2023
✓ PCR Reverse /sequence = AAGAGCCATGTTGCTCTCCAGAGTC 52% GC / 7642.0 Da	25-mer	7364 .. 7388	62°C	Jan 11, 2023