

5'

3'

GAAGATAGAACAGGGAACGAAAGTGGAGAAATCTCATTCCATTGTGGGGCCACCTCCTATGTAAAAGAGAGAAAAAAAAAAGGCATGG
CTTCTATCTTGTCCCTTGCTTACCTCTTTAGAGTAAGGTAACACCCGGTGGAGGATACATTTTCTCTCTTTTTTTTTTCCGTACC

85

SORL1

SORL1-201

AATAGGAGGCAGGGATATACCAGGAAAGAAAAAGATGCTTTTACAGGACTAATGGGGGCCGTAATATCTTTGCAAAGATGAGGTA
TTATCCTCCGTCCCTATATGGTCCCTTCTTTTTCTACGAAAGTGTCTTGATTACCCCCGGCATTATAGAAACGTTTCTACTCCAT

170

SORL1

SORL1-201

ATCTGGGCATCTGGAAGGATTTTTTAAATGCAAGAATTTTTCTTCTTTTACAATTACTATGAAAACACACATTCCTTGCCAGGA
TAGACCCGTAGACCTTCTAAAAAATTTACGTTCTTAAAAAGAAGGAAATGTTAATGATACTTTTGTGTGTAAGGAACCCGGTCCCT

255

SORL1

SORL1-201

CCAGCCAAGAATTCCATTCCCTTTTCCAGGTTAAGCATTGCGCGCTGGAATGCCGCATGCTGCTCTGAACATAATCCTAAAAACAG
GGTCGGTTCTTAAGGTAAGGAAAAAGGTCCAATTCGTAACGCGCGACCTTACGGCGTACGACGAGACTTGTATTAGGATTTTGTGC

340

SORL1

SORL1-201

TATTTCTGGATTCAGGTTCTACTTTATGGGTATTAGTTTCTTAGAGGAAAAAAAAAGCCCAGAGTGACAGAATGAGGTTTATAGAT
ATAAAGACCTAAGTCCAAGATGAAATACCCATAATCAAAGAATCTCCTTTTTTTTTCGGGTCTCACTGTCTTACTCCAAATATCTA

425

SORL1

SORL1-201

GCTGGAGAGAGATGTGGGGCAAAAGCCTTGCTGCTGCAAATGTAGCTTTTCATGTCCCTATACCTTAGCTGGCCCCCTCCCTG66A
CGACCTCTCTACACCCCGTTTTTCGGAACGACGACGTTTACATCGAAAAGTACAGGGATATGGAATCGACCGGGGGAGGGACCT

510

SORL1

SORL1-201

ATGACAGCGGGAAAGGTTTCCCTTGACAACCAAAAGGGGAGGTAGGTTACCATGTGATGGTAACATAGATACTTCTAAAGTGACCTG
TACTGTCGCCCTTCCAAAGGAACTGTTGGTTTTCCCTCCATCCAATGGTACACTACCATTGTATCTATGAAGATTTCACTGGAC

595

SORL1

SORL1-201

GAACCAAAGGAAAAAGAAGGAAAACTTACCTTATTAATAAATTGTAGGTAGATTTATTTTTTGGATGCATTATCTATATTACAGCTTT
CTTGGTTTCTTTTTCTTCTTTTTGAATGGAATAATTTTTAACATCCATCTAAATAAAAAACTACGTAATAGATATAATGTGCGAAA

680

SORL1

SORL1-201

TATAAAGAAGGTGAGTGGTACATGTTAAGTCACTGAGTGTATGGAATCAGGAAGTGGGCAGGAATGGCTAACCCAGGCATGCAGC
ATATTTCTTCCACTCACCATGTACAATTCAGTGACTCACATACCTTAGTCTTCCACCCGTCCTTACCGATTGGGTCCGTACGTCG

765

SORL1

SORL1-201

AAAAGAATTCCGATTTGCATCTTGGTCCCATATGCAACACACTGTCAAGATGCACACTTTAGACACAGATGCTGGTGTGCTGCTT
TTTTCTTAAGGCTAAACGTAGAACCAGGGTATACGTTGTGTGACAGTTCTACGTGTGAAATCTGTGTCTACGACCACACGACGAA

850

SORL1

SORL1-201

GTGTCCACTCCTGGGGAAGAATCTGGATGTTTCCCAAGCCGTTCCCTAAGTGGACAAGACAGTGTACTGGGTCTTCTATTTCCA
CACAGGTGAGGACCCCTTCTTAGACCTACAAAGGGTTCGGCAAGGGGATTACCTGTTCTGTACATGACCCAGAAGGATAAAGGT

935

SORL1

SORL1-201

GTTGTCTGACATTAGGTAAGTATCTTCAGCACTCAGGACCTTCATTTCTACATCTTAAAAATCATCCACGGTAGCGTCTGTATCA
CAACAGACTGTAATCCATTCATAGAAGTCGTGAGTCCTGGAAGTAAAGATGTAGAATTTTATAGTAGGTGCCATCGCAGACATAGT

1020

SORL1

SORL1-201

TAAACGGCAGCACAGTGTAGTGGTTAAAGCATAGACTCTGGATCCAGAGTGCCTGGGTTCCAATCTTGGTTCTGCCACTTGCTAG
ATTGTCCGTCGTGTCACATCACCAATTTTCGTATCTGAGACCTAGGTCTCACGGACCCAAGGTTAGAACCAAGACGGTGAACGATC

1105

SORL1

SORL1-201

TTGTGTGACCTTGGGTGAGTTACTTAACCTCTCTGGTCTCAGTTTTCTCATTTGTAAAATTTGGTTAACAAGAGTTCTACCATCA
AACCACTGGAACCCACTCAATGAATTGGAGAGACCAGAGTCAAAGAGTAAACATTTTAAACCAATTGTTCTCAAGATGGTAGT

1190

SORL1

SORL1-201

GGCAGTTGTTGTGGGTCTTAAACAATACCCGATACGTAGTAAGCACATTATACACAATATGTACACAATTTATATTTGTTGAGTA
CCGTCAACAACACCCAGAATTTGTTATGGGCTATGCATCATTTCGTGTAATATGTGTTATACATGTGTTAAATATAAACAACCTCAT

1275

SORL1

SORL1-201

GAAACAGAAATTTTGTGGTGATTATGTTGTGGAACATTTTGTAAATAGCCAAGAACAATGCATTATTAGTATTATTTTGGAGAT
CTTTGTCTTAAAAACACCCTAATACAACACCTTGTAACATTTATCGGTTCTTGTGTTACGTAATAATCATAATAAACCTCTA

1360

SORL1

SORL1-201

CTAAGAGGTTTCATAGAATTGCCATATGGTGTGGAACAATATGAATAAGTGAAGCAAAATGATTAGAGAGCTTAGTTACAAAGCT
GATTCTCCAAGTATCTTAACGGTATACCACAACACTTGTATACTTATTCACCTCGTTTAACTAATCTCTCGAATCAATGTTTCGA

1445

SORL1

SORL1-201

TCAGTGACTAATGGTCTCTCGTCAACAAGATGATGATGCTGTGGTGATACAGTCACGTGAGGAGGGAGAACAGGGCGATTGGTGT
AGTCACTGATTACCAGAGAGCAGTTGTTCTACTACTACGACACCACTATGTCAGTGCCTCCTCCCTCTTGTCCCCTAACCACA

1530

SORL1

SORL1-201

AATTAGGTTGGCAAGTGTGACTTGAAGACTGGCAGGCTTAGCCCAGAAGTATGGTTGTTGAAGCATGCATATTGGGAGATTTAGA
TTAATCCAACCGTTCACACTGAACTTCTGACCGTCCGAATCGGGTCTTCATACCAACAACCTTCGTACGTATAACCCTCTAAATCT

1615

SORL1

SORL1-201

ATAAAGAAAAACATAACAAGTAAACACTTGCAGATGAAGAAACAGATTCACTGGAGTTTAAAGTAACTTGCCTGAGGCAGAAATG
TATTTCTTTTTGTATTGTTTCAATTTGTGAACGTCTACTTCTTTGTCTAAGTGACCTCAAATTCATTGAACGGACTCCGTCTTTAC

1700

SORL1

SORL1-201

TGATTCCATTACACACCTCCTGAGTCTTGATTTCTGTGCTCTTCACTTGGTCCACACCACATGCCAATGAATTTGAGGTTTGTGT
ACTAAGGTAATGTGTGGAGGACTCAGAACTAAAGACACGAGAAGTGAACCAGGTGTGGTGTACGGTTACTTAAACTCCAAACACA

1785

SORL1

SORL1-201

ATGAGAAACAAATAGGTCAGATGTGCTAGGACCTCTTCAGCATCCCCTGGGTCCAACCTCCCACGTGTCTTGTGTGTCTGGCAGA
TACTCTTTGTTTATCCAGTCTACACGATCCTGGAGAAGTCGTAGGGGACCCAGGTTGGAGGGTGCACAGAACACACAGACCGTCT

1870

SORL1

SORL1-201

SORL1-201

AGAGAACGAGTTCATTCTGTATGCTGTGAGGAAATCCATCTACCGCTATGACCTGGCCTCGGGAGCCACCGAGCAGTTGCCTCTC
TCTCTTGCTCAAGTAAGACATACGACACTCCTTTAGGTAGATGGCGATACTGGACCGGAGCCCTCGGTGGCTCGTCAACGGAGAG

1955

SORL1

SORL1-201

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

ENSE00000991345

SORL1-201

ACGGGGCTACGGGCAGCAGTGGCCCTGGACTTTGACTATGAGCACAACCTGTTTGTATTGGTCCGACCTGGCCTTGGACGTCATCC
TGGCCCGATGCCCGTCTGTCACCGGGACCTGAAACTGATACTCGTGTGACAAACATAACCAGGCTGGACCGGAACCTGCAGTAGG

2040

SORL1

SORL1-201

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

ENSE00000991345

SORL1-201

AGGTGAGTCAGCGCTTGGTCTGACTGTGGGAGCTGTGCATCGTGACTGCCCTGTCCTGATAAGCTGCATGCAGAATGGCCTATGG
TCCACTCAGTCGCGAACCCAGACTGACACCCTCGACACGTAGCACTGACGGGACAGGACTATTTCGACGTACGTCTTACCGGATACC

2125

SORL1

SORL1-201

Q

SORL1-201

AAATGGGCAGTTAGAAGTTTGTAAAGTGTACTCATCTCAGGGCTGACAGGTGAAAGTTTCCAGTCTTCTGTGTTAGTATTTTTCT
TTTACCCGTCAATCTTCAAACATTACAATGAGTAGAGTCCCGACTGTCCACTTTCAAAGGTCAGAAGACACAATCATAAAAAGA

2210

SORL1

SORL1-201

SORL1-201

TTCTCTGTCTTCATCTGTTTCATATAGGAAGGATAAAGAAAGCCCTAAATCCACAGACCTGCTTGAAAGTGAGGTCTTGCTTTTTCC
AAGAGACAGAAGTAGACAAGTATATCTTCTTCTTTTCGGGATTTAGGTGTCTGGACGAACTTTCACTCCAGAACGAAAAGG

2295

SORL1

SORL1-201

SORL1-201

TGCTGGGAAGGTGTTGGGACTAGTAATGTAGGATGATTAGTTGCCCCCTATTGTGCCAACTGCCTCTTGAGCATCTTTCTTCCC
ACGACCCCTTCCACAACCCTGATCATTACATCCTACTAATCAACGGGGGGATAACACGGTTGACGGAGAAGCTCGTAGAAAAGAAGGG

2380

SORL1

SORL1-201

SORL1-201

AAGCCATGATACAGTAACACTTGACTTACCCATAGCTCACATAATTATCCACTTCAGCTGTTCTGAACACAGGTAAGAACCAGGA
TTCGGTACTATGTCATTGTTGAACTGAATGGGTATCGAGTGTATTAATAGGTGAAGTCGACAAGACTTGTGTCCATTCTTGGTCTT

2465

SORL1

SORL1-201

SORL1-201

AGTAAGCATTAAAGAGCCCTGGACAGGCCAGGTGGATAGCCATACGCTCACACCCATGCATTTAAAGGAGAGCTCTTTGATCTTT
TCATTTCGTAATTTCTCGGGACCTGTCCGGTCCACCTATCGGTATGCGAGTGTGGGTACGTAAATTTCTCTCGAGAAACTAGAAA

2550

SORL1

SORL1-201

SORL1-201

ATTCATTGTCTACTTAATCCTTTTAGAAAAGCAATTCCAACAAATTTTTATCTAGATTCCAACCCAACAGAAATTTACAGTGCC
TAAGTAACAGATGAATTAGGAAAATCTTTTCGTTAAGGTTGTTTAAAAATAGATCTAAGGTTGGGTTGTCTTTAAAGTGTACGG

2635

SORL1

SORL1-201

SORL1-201

TGGGTATTTGAGGGGCTTGGGGTGGGGGATGGCGGTGATGCTGAATGGAGCTGTCCAACAATAGCACTTGATGGCTAAGAGCCTC
ACCCATAAACTCCCCGAACCCACCCCTACCGCCACTACGACTTACCTCGACAGGTTGTTATCGTGAAGTACCGATTCTCGGAG

2720

SORL1

SORL1-201

SORL1-201

ACAGGGAAGAAAGAGTATAAAGCAGACACAAGAAGTGAATGTAACAGCAGTCTGGTTTCACTTATTTTAAAGCAAACAGACT
TGTCCCTTCTTTCTCATATTTTCGTCTGTGTTCTTGACTTTACATTGTCGTCAGACCAAAGTGAATAAAATTTTCGTTTGTCTGA

2805

SORL1

SORL1-201

SORL1-201

CATACAATCTCAGTAATCTCTGACTTTATTATTGCCATACAGCATAATTTAGTAACCAGTGTTTCATAATGATAATGCAGAGTAAT
GTATGTTAGAGTCATTAGAGACTGAAATAATAACGGTATGTCGTATTAAATCATTGGTCACAAGTATTACTATTACGTCTCATTA

2890

SORL1

SORL1-201

SORL1-201

ATATATGATTAAATTTCTCTTTATTCTGCTTTAAAAAACAAAAATGTAGTATATTTTAGAAATGCTTTTCATGAAAACCTGGCTTCA
TATACTAATTTAAGAGAAATAAGACGAAATTTTTTGTTTTTTACATCATATAAAATCTTTACGAAAGTACTTTTTGGACCGAAGT

2975

SORL1

SORL1-201

SORL1-201

TGTGTCTGGAAAGTTTACTAACGTAAAACATCTCATCCCTTGCCAGTCTGCCAGTTGAATAAAGGGTTACCTTCATGGGACTG
ACACAGACCTTTCAAATGATTGCATTTTGTAGAGTAGGGAACGGTCAGGACGGTCAACTTATTTCCCAATGGGAAGTACCCTGAC

3060

SORL1

SORL1-201

SORL1-201

ACTTGGCAGGGGGTCGTTTGAACAGTTCCTAGCATTATTATTACTTTTTCTCTCTTAAGCGCCTCTGTTTGAATGGAAGCACAGG
TGAACCGTCCCCCAGCAAACCTGTCAAGGATCGTAAATAATAATGAAAAGAGAGAATTCGCGGAGACAAACTTACCTTCGTGTCC

3145

SORL1

SORL1-201

815 820
R L C L N G S T G
ENSE00000991346

SORL1-201

GCAAGAGGTGATCATCAATTTCTGGCCTGGAGACAGTAGAAGCTTTGGCTTTTGAACCCCTCAGCCAGCTGCTTTACTGGGTAGAT
CGTTCTCCACTAGTAGTTAAGACCGGACCTCTGTTCATCTTCGAAACCGAAAACCTTGGGGAGTCGGTCGACGAAATGACCCATCTA

3230

SORL1

SORL1-201

825 830 835 840 845 850
Q E V I I N S G L E T V E A L A F E P L S Q L L Y W V D
ENSE00000991346

SORL1-201

GCAGGCTTCAAAAAGATTGAGGTATGTGTATTTTCGTGCTGTTCTTAATTAAGGGAGCAGGCGGGGCACCTGGGCTTTGAGCCAC
CGTCCGAAGTTTTTCTAACTCCATACACATAAAAAGCACGACAAGAATTAATTCCTCGTCCGCCCCGTGGACCCGAAACTCGGTG

3315

SORL1

SORL1-201

855
A G F K K I E
ENSE00000991346

SORL1-201

ATTTGACACAGAGGCAAGGGCCAGTGTGTGTCAGATTACTCAGGAAATTTACTGCGAGTTTCCAGAGAATGGACCAGCTGAGCCTCT
TAAACTGTGTCTCCGTTCCCGGTCACACAGTCTAATGAGTCTTTAAATGACGCTCAAAGGTCTCTTACCTGGTCGACTCGGAGA

3400

SORL1

SORL1-201

SORL1-201

GGAGAGGAGAGAAAAGGGGGTAAGTACCTGTGAGTTGATCTTTTGGCTAGCAGAAGCTTAGCTAATAACAATAAATGGTAATATT
CCTCTCCTCTCTTTTCCCCATTTCATGGACACTCAACTAGAAAACCGATCGTCTTCGAATCGATTATTGTTATTTACCATTATAA

3485

SORL1

SORL1-201

SORL1-201

TTTATTTTATTTATATATGTACTTACTTATTTTATTTATATATTTTATTTTGTTTTATTTTACTACTTTTATTAAACATGATGGCA
AAATAAAATAAATATATACATGAATGAATAAAATAAATATATAATAAAAAACAAAAATAAAATGATGAAAAATAATTTGTACTACCGT

3570

SORL1

SORL1-201

SORL1-201

AAAAC TACAATCACTTTTGCATCAGCCTAATATCATGGTATTATTATAATGCTATAACAATAATCGTCTAGTATTATTTTATTTCG
TTTTGATGTTAGTGAAAAACGTAGTCGGATTATAGTACCATAATAATATTACGATATTGTTATTAGCAGATCATAATAAAATAAGC

3655

SORL1

SORL1-201

SORL1-201

ATTAGAGTGATAGCAACAATATCATCATCATCATCATTGCCACTGTTATTAATCCCCATTTCTCTGCAACTTAGCTACCTAG
TAATCTCACTATCGTTGTTATAGTAGTAGTAGTAGTAACGGTGACAATAATTAGGGGTAAAGAGACGTTGAATCGATGGATC

3740

SORL1

SORL1-201

SORL1-201

TAACTGTCCCACCTTATATACCCAAGGCAAGGATGATGAGTGACCTCTAAACTGCCAAATCTTTGTCTGGGGGAATGTAGTGTG
ATTGGACAGGGTGGAATATATGGGTTCCGTTCTACTACTCACTGGAGATTTGACGGTTTAGAAACAGACCCCTTACATCACAC

3825

SORL1

SORL1-201

SORL1-201

CTCAGCTCACTGCCTCAGCACCTCTTTATACTGACTCTGCATGGAGAGACGGCATGTGGGTGAAGTGGGAAGTGCAGTAGAAGCA
GAGTCGAGTGACGGAGTCGTGGAGAAATATGACTGAGACGTACCTCTCTGCCGTACACCCACTTCACCCCTTACGTCATCTTCGT

3910

SORL1

SORL1-201

SORL1-201

GGGAGATGCAGAGGGCTAAGAGGAGTTGCAAGACGAAAGACACAGACTCGAGAGATAGACCCAGATGTAGGCTTGACTCCACTAG
CCCTCTACGTCTCCCGATTCTCCTCAACGTTCTGCTTTCTGTGTCTGAGCTCTCTATCTGGGTCTACATCCGAACTGAGGTGATC

3995

SORL1

SORL1-201

SORL1-201

CTCAGCGACATGGGGCAAGGTGCTTATGCTTTCTAAACTTCAGTTGCTTCATGCGTTAGATGGAGATTCATATATTCGCACAACC
GAGTCGCTGTACCCCGTTCCACGAATACGAAAGATTTGAAGTCAACGAAGTACGCAATCTACCTCTAAGTATATAAGCGTGTGG

4080

SORL1

SORL1-201

SORL1-201

ATTTGACAGGGGTTCTCTGCATGATACATGTGGTTTAGGTTCTGATGATAAAGCAGTGGGCAGGACACACACGTTCTTGTTCAG
TAAACTGTCCCAAGAGACGTACTATGTACACCAAATCCAAGACTACTATTTTCGTCACCCGTCCTGTGTGTGCAAGAACAAGGTC

4165

SORL1

SORL1-201

SORL1-201

TAGAGCTTAGATTTTAGTGGAGGAAGCAAAATAATAAATCAGTTCTGTTGGTGGTACATGCTGCAAAGACTCTGAAGCAGTGCAG
ATCTCGAATCTAAAATCACCTCCTTCGTTTTATTATTTAGTCAAGACAACCACCATGTACGACGTTTCTGAGACTTCGTACCGTC

4250

SORL1

SORL1-201

SORL1-201

TGTGATTGCGCTTTTGGAGAGTGGGGCAACATTAGAATAGGCAGACAGAGCAGGCAACTTGAGGTTGATGTCTTAGCTGAGCCCT
ACACTAACGCGAAAACCTCTCACCCCGTTGTAATCTTATCCGTCTGTCTCGTCCGTTGAACTCCAACCTACAGAATCGACTCGGGA

4335

SORL1

SORL1-201

SORL1-201

GGCTGAGAAGAGGATGATCTTTTGTCCACCTCCTGGGGATGCTGATAGAAGTGAACCTGGCATCTACTGAATGCTGCCTCGGTGGT
CCGACTCTTCTCCTACTAGAAAACAGGTGGAGGACCCCTACGACTATCTTCACTTGACCGTAGATGACTTACGACGGAGCCACCA

4420

SORL1

SORL1-201

SORL1-201

TATGTTATTGCTCTTTCTCCTTTCTTTAATTGCGTGTGGTCAGCACTTGGCTAGGGGCTAAAAGAATGCAGGTGATGCACAAG
ATACAATAACGAGAAAAGAGAGGAAAAGAAATTAACGCACACCAGTCGTGAACCGATCCCCGATTTTCTTACGTCCACTACGTGTTTC

4505

SORL1

SORL1-201

SORL1-201

CACCCACCTTTTACAGGCTGTGGGGCGACCACTGCACAACCTCAAATACTGTTGGTGCAAAATGGTGTGATGAGCCAAGGTGC
GTGGGTGGAAAAGTGTCCGACACCCCGCTGGTGACGTGTTGAGTTTATGACAACCACGTTTTACCACAGTCTACTCGGTTCCACG

4590

SORL1

SORL1-201

SORL1-201

AGAGCTACTGATGCTTATTGGTCCAGGTGGGTCAGAAGAGTTAGGAAAGTAGGCAGGCCTGGCAGTGAGGTTTGAAGGAGAGTTA
TCTCGATGACTACGAATAACCAGGTCCACCCAGTCTTCTCAATCCTTTTCATCCGTCCGGACCGTCACTCCAAACTTCCTCTCAAT

4675

SORL1

SORL1-201

SORL1-201

TGCCTTGATTAGATTAAGCAGTGGGGCAGGTAGGCCCAGGATGGGATGTGGCAAGAGCAGACAGCAGTGAAGTCCGCATCAGGCTT
ACGGAACTAATCTAATTCGTACCCCGTCCATCCGGGTCTACCTACACCGTTCTCGTCTGTCTCACTCAGGCCTAGTCCGAA

4760

SORL1

SORL1-201

SORL1-201

GGAGAAGCAAGAGATGACCAGCCTGGCTGACGGGAAGGAGCAAGAATATGAGTCCCACCTGTGGACTCTTCATTGCAAGGCTGTG
CCTCTTCGTTCTCTACTGGTTCGGACCGACTGCCCTTCTCGTTCTTATACTCAGGGTGGACACCTGAGAAGTAACGTTCCGACAC

4845

SORL1

SORL1-201

SORL1-201

ACATTGAGAATTTGTTTTATGGGAGTGTGGAGTCATCGATTGCCTTGGAAACGTGGAGTGACACGGGATGGTGAAATAAGTAAATG
TGTAACCTCTTAAACAAAATACCCTCACACCTCAGTAGCTAACGGAACTTGCACCTCACTGTGCCCTACCACCTTATTTCATTTAC

4930

SORL1

SORL1-201

SORL1-201

CTCATTTGCTTATTTACTTATTTGAGTAATTTACTTATTGATACTGCTTTGTCCAGATCATCATGCCCTGGAAACTGGGGCTTAC
GAGTAAACGAATAAATGAATAAACTCATTAAATGAATAACTATGACGAAACAGGTCTAGTAGTACGGGACCTTTGACCCCGAATG

5015

SORL1

SORL1-201

SORL1-201

ATGGTTCTAGCTCCTCTTTTCAGACCACTTGAAAATTGTCCCATGAGTCAGAGGAAGGAACAGCGCATTGTGACTAGAAGTTGGGG
TACCAAGATCGAGGAGAAAAGTCTGGTGAACCTTTAACAGGGTACTCAGTCTCCTTCTTGTCTGCGTAACACTGATCTTCAACCCC

5100

SORL1

SORL1-201

SORL1-201

CAGGTTTCGCAGATGGGTCAGGTCAGGGAAATAGGCAGGCATGGAGGGGGCATGTCTGTAGCAGAAGCTGAGTAGCCATCTTTGG
GTCCAAAAGCGTCTACCCAGTCCAGTCCCTTTATCCGTCCGTACCTCCCCGTACAGACATCGTCTTCGACTCATCGGTAGAAAACC

5185

SORL1

SORL1-201

SORL1-201

CAATGGGGGTCTTTAAGGAGCTCCGATCCATCTCAGCCTCTTTTCCCCCTGTTTTTGTTCAGGTAGCTAATCCAGATGGCGACTTC
GTTACCCCCAGAAATTCCTCGAGGCTAGGTAGAGTCGGAGAAAAGGGGGACAAAACAGTCCATCGATTAGGTCTACCGCTGAAG

5270

SORL1

SORL1-201

SORL1-201

860 865
V A N P D G D F
ENSE00003463448

CGACTCACAATCGTCAATTCCTCTGTGCTTGATCGTCCCAGGGCTCTGGTCCTCGTGCCCAAGAGGGGGTAAGTGTGGCCCAAA
GCTGAGTGTTAGCAGTTAAGGAGACACGAACTAGCAGGGTCCCAGAGACCAGGAGCACGGGGTTCTCCCCATTACACAACGGGGTTT

5355

SORL1

SORL1-201

R L T I V N S S V L D R P R A L V L V P Q E G

ENSE00003463448

SORL1-201

AGGAAATCAGTCTTGCGTCCAATGCTACTACTAATAGATTCTCATGGAAACACAGACTGCGGGACAAAACTCTGTTTCTCATGAT
TCCTTTAGTCAGAACGCAGGTTACGATGTGATTATCTAAGAGTACCTTTGTGTCTGACGCCCTGTTTTTGAGACAAAGAGTACTA

5440

SORL1

SORL1-201

SORL1-201

GGTGGTTGAAATGGTCTATTAAGTGAAGTTTGAGACCACAGCTTAGTCATCGTGGTCAGGTAACCTCCGTTTCGCTTTTTGTTAG
CCACCAACTTTACCAGATAATTGACTCTTCAAACCTCTGGTGTGCAATCAGTAGCACCAGTCCATTGAGGCAAGCGAAAAACAATC

5525

SORL1

SORL1-201

SORL1-201

CCAGTGTGAGAGTCTCTTTAGGCATCCAGATGTCTTGCATCTGTGGGTTGTTTCTCTAGAAAAGTTGATGTTAAAAGAGAGCTTC
GGTCACAGTCTCAGAGAAATCCGTAGGTCTACAGAACGTAGACACCCAACAAGAGATCTTTTCAACTACAATTTTCTCTCGAAG

5610

SORL1

SORL1-201

SORL1-201

TGTAGACATAGACAGGCCTGCTTGGATATTGTGAGAACTTTCTCTTGAGTTTCATGCATGGTACAAAACATTTAATTCATTCCATC
ACATCTGTATCTGTCCGGACGAACCTATAACACTCTTGAAAGAGAAGTCAAAGTACGTACCATGTTTGTAAATTAAGTAAGGTAG

5695

SORL1

SORL1-201

SORL1-201

TTTCCCCTGCCTTCCCAGCATGTGTAGGTTTTCTTACGTACAATCAGTGTGCACTTGGGGAAGGCAAAGGTGCTTTTTATTAAGT
AAAGGGGACGGAAGGGTCGTACACATCCAAAAGAATGCATGTTAGTCACACGTGAACCCCTTCCGTTTCCACGAAAAATAATTGA

5780

SORL1

SORL1-201

SORL1-201

CATTAAGTGAAGGAAACATAATTAAGAGGGAAATTTCTGGATTTGACATTTCTGGCTTTTCTCTCTCGTAGCATTTATGATAGAGA
GTAATTGACTTCTTTGTATTAATTTCTCCCTTTAAGACCTAAACTGTAAGACCGAAAAGGAGAGAGCATCGTAAATACTATCTCT

5865

SORL1

SORL1-201

SORL1-201

ATTGGCACAATTTTTTCAAGGAAAATTCTAAGAGTAATGTATGTACTTGGTTGACAATATTTAGAGAGAACAGCACTTTATGAA
TAACCGTGTTAAAAAAGTTCCTTTTAAGATTCTCATTACATACATGAACCAACTGTTATAAATCTCTCTTGTCTGCGTAAATACTT

5950

SORL1

SORL1-201

SORL1-201

AAAAATTTGCATTCTTCCTTTTCATTCTTAACCCCTTACCCCTCACACTTCCTAGTGGTAATCATTGTTAATAATGTCTTGTGTAT
TTTTTAAACGTAAGAAGGAAAAGTAAGAATTGGGAAATGGGAGTGTGAAGGATCACCATTAGTAACAATTATTACAGAACACATA

6035

SORL1

SORL1-201

SORL1-201

PCR Forward

ATGCACGCCAAATAGGATTGTA

CTTTCATGATTGCTTTTACTTATGTACAAGTATTATCTTTAAAACACACACATATACACACACATGCACGCCAAATAGGATTGTA
GAAAGTACTAACGAAAATGAATACATGTTTCATAATAGAAATTTGTGTGTGTATATGTGTGTGTACGTGCGGTTTATCCTAACAT

6120

SORL1

SORL1-201

SORL1-201

PCR Forward

GTG

GTGTAGTTACTATTCTGTACCTTTTTAAACAAACTTAATATGTATTGAAAATAGTTCTGTGTGAGCATATATAGATTTTTAGGTT
CACATCAATGATAAGACATGGAAAAATTTGTTTGAATTATACATAACTTTTATCAAGACACACTCGTATATATCTAAAAATCCAA

6205

SORL1

SORL1-201

SORL1-201

TCACAGTATTCTATTATATGTACCATAATGTGTCACCTTCTCTGCTGATTAACATTTAGTTTAAATATACATACATATACATTTCT
AGTGTACATAAGATAATATACATGGTATTACACAGTGAAGGAGACGACTAATTGTAAATCAAATTATATGTATGTATATGTAAAGA

6290

SORL1

SORL1-201

SORL1-201

TTGTATATTATCTTTGCATAATTTGATTTTATCTATAGATAAATCTAGTAAAGGAATTTCCAGGTGAAGGAATTTAAGTAGTTT
AACATATAATAGAAACGTATTAAACTAAAATAGATATCTATTTAAGATCATTTCCTTAAAGGTCCACTTCCTTAAATTCATCAA

6375

SORL1

SORL1-201

SORL1-201

CAGGTGTTGTCATTACATATTGTTATAATAATGCTGAAATAACCAGCCGGATCATTTCGAAAGGAGTTTCTGACCTTTTCTGGAGT
GTCCACAACAGTAATGTATAACAATATTATTACGACTTTATTGGTCGGCCTAGTAAGCTTTCTCAAAGACTGGAAAAGACCTCA

6460

SORL1

SORL1-201

SORL1-201

AGTATTTGAGCTCCCATTTCTCTAGTATTGATGAGGTATGTGTTCTGTCCCCATTTTCGCTAGGGTGTATGTTCTGGACAGACTGG
TCATAAACTCGAGGGTAAAGAGATCATAACTACTCCATACACAAGACAGGGGTAAAAGCGATCCCCTACAAGACCTGTCTGACC

6545

SORL1

SORL1-201

890 895
V M F W T D W
ENSE00003546837

SORL1-201

Sanger Sequencing

CGGAGCAATATGGATGGTTC

GGAGACCTGAAGCCTGGGATTTATCGGAGCAATATGGATGGTTCCTGCTGCCTATCACCTGGTGTCTGAGGATGTGAAGTGGCCCA
CCTCTGGACTTCGGACCCTAAATAGCCTCGTTATACCTACCAAGACGACGGATAGTGGACCACAGACTCCTACACTTCACCGGGT

6630

SORL1

SORL1-201

900 905 910 915 920
G D L K P G I Y R S N M D G S A A Y H L V S E D V K W P

ENSE00003546837

SORL1-201

gRNA Protospacer

ATAGAGCGGATCACGTTTCAG

ATGGCATCTCTGTGGACGACCAGTGGATTTACTGGACGGATGCCTACCTGGAGTGCATAGAGCGGATCACGTTTCAGTGGCCAGCA
TACCGTAGAGACACCTGCTGGTCACCTAAATGACCTGCCTACGGATGGACCTCACGTATCTCGCCTAGTCAAGTCACCGGTCGT

6715

SORL1

SORL1-201

925 930 935 940 945 950
N G I S V D D Q W I Y W T D A Y L E C I E R I T F S G Q Q

ENSE00003546837

SORL1-201

Donor Template WT -> SNV

Protospacer Sequence

PAM

SNV

CTACGGATGGACCTCACGTATCTCGCCTAGTCAAGTCACCGGTCGT

Donor Template WT -> SNV

GCGCTCTGTCAATTCTGGACAACCTCCCGCACCCCTATGCCATTGCTGTCTTTAAGGTGAGTCCATTTGTTGCTGCCGGACAGTCT
C CGCGAGACAGTAAGACCTGTTGGAGGGCGTGGGGATACGGTAACGACAGAAATTCACCTCAGGTAAACAACGACGGCCTGTCAGA

6800

SORL1

SORL1-201

955 960 965 970
R S V I L D N L P H P Y A I A V F K

ENSE00003546837

SORL1-201

Donor Template WT -> SNV

CGCGAGACAGTAAGACCTGTTGGAGGGCGTGGGGATACGGTAACGACAGAAAT

Donor Template WT -> SNV

GCTAGAGCGGGTGAAGGAGCATATGAGATCAGGAGCCTGCATCCCTGGGCTTTGCAGAGAAGCTGTTTAACTTCTTAAAGGTTGCC
CGATCTCGCCCCACTCCTCGTATACTCTAGTCTCGGACGTAGGGACCCGAAACGTCTCTTCGACAAATTTGAAGAATTTCCAACGG

6885

SORL1

SORL1-201

SORL1-201

TTTTTCCAAATTTGAGATAACTTATTTTTCAGCCTATGGAGGGATGCCAGGCAGAGGGCGCCAAGGGTCCAGGCTCCCCTGCTGTT
AAAAAAGGTTTAAACTCTATTGAATAAAAAGTCGGATACCTCCCTACGGTCCGTCTCCGCGGTTCCAGGTCCGAGGGGACGACAA

6970

SORL1

SORL1-201

SORL1-201

CACATTTCAAAGGTTAAAAGTGAAGGCTCTTCCCATGAACATTCCCAGTTTGCCCCTCAGTGTGTCAGTAGCCTCATTTCAGGGTG
GTGTAAAAGTTTTCCAATTTTCACTTCCGAGAAGGGTACTTGTAAAGGGTCAAACGGGGAGTCACAGTCATCGGAGTAAAAGTCCCAC

7055

SORL1

SORL1-201

SORL1-201

GTGTCTTCATTTTTTGTGCGCTTTGCTCACTTTATTCTCTGATGACTTCCGGTGAGCTCTGCACCACCTATAGTGCCTTGCAGTT
CACAGAAGTAAAAACACGCGAAACGAGTGAAATAAGAGACTACTGAAGGCCACTCGAGACGTGGTGGATATCACGGAACGTCAA

7140

SORL1

SORL1-201

SORL1-201

CTTTTTCGACTCTGGAGAGCAACATGGCTCTTCCCAACTCTGGGAAACAGATTTCAAACCTGAGGGGGTTGGGTTTGTGTCATAAA
GAAAAAGCTGAGACCTCTCGTTGTACCGAGAAGGGTTGAGACCTTTGTCTAAAGTTTGACTCCCCCAACCCAAACACAGTATTT

7225

SORL1

SORL1-201

SORL1-201

CTGAGACCTCTCGTTGTACCGAGAA
PCR Reverse

CTTGAATGCTTATCAGATAGTTTCTTTGGGCAGTTTCTTCTGTGGGGTTATATGGTGAGGTTTGGATAAAAATTGCTGTCCTTTG
GAACCTACGAATAGTCTATCAAAGAAAACCCGTCAAAGAAGACACCCCAATATACCACTCCAAACCTATTTTAAACGACAGGAAAC

7310

SORL1

SORL1-201

SORL1-201

CATTTAAGTAGAATCTTGATCAGGCTAGTCATTTCAGCCAATAAATGTTAGTTGTCTCCTGCCTGGGGGAACCTTTACCCCTTAGAG
GTAAATTCATCTTAGAACTAGTCCGATCAGTAAGTCGGTTATTTACAATCAACAGAGGACGGACCCCTTGAAGTGGGAATCTC

7395

SORL1

SORL1-201

SORL1-201

AGAACCAGAATAAAGAACGAAAGAGCTGGACTAATGGGCAAAGGTTTTCTTTTTAGAATGAAATCTACTGGGATGACTGGTCACA
TCTTGGTCTTATTTCTTGTCTTCTCGACCTGATTACCCGTTTCCAAAAGAAAAATCTTACTTTAGATGACCCTACTGACCAGTGT

7480

SORL1

SORL1-201

SORL1-201

N E I Y W D D W S Q
ENSE00000532819

GCTCAGCATATTCCGAGCTTCCAAATACAGTGGGTCCCAGATGGAGATTCTGGCAAACCAGCTCACGGGGCTCATGGACATGAAG
CGAGTCGTATAAGGCTCGAAGGTTTATGTACCCAGGGTCTACCTCTAAGACCGTTTTGGTCGAGTGCCCCGAGTACCTGTACTTC

7565

SORL1

SORL1-201

985 990 995 1000 1005
L S I F R A S K Y S G S Q M E I L A N Q L T G L M D M K

ENSE00000532819

SORL1-201

ATTTTCTACAAGGGGAAGAACACTGGTAAGCCAGAGTCTCTTTTGTCTCTGTAGAGTTGATCTCAAGAAAGGGGCTGCGTGT
TAAAAGATGTTCCCTTCTTGTGACCATTCGGTCTCAGAGAAGAAAACAGAGACATCTCAACTAGAGTTCTTTCCCGACGCACA

7650

SORL1

SORL1-201

1010 1015
I F Y K G K N T

ENSE00000532819

SORL1-201

GGCCAATCTCTGCTCAGAGTAGGAGCTGGCAGCCTGCATCTTTGTTGTACGACAACATGCACATTATTTAATTTCTTCCTAATG
CCGGTTAGAGACGAGTCTCATCCTCGACCGTCCGGACGTAGAAAACAACAGTGCTGTTGTACGTGTAATAAATTAAGAAGGATTAC

7735

SORL1

SORL1-201

SORL1-201

ACATCTTAATTTCTTTTCTAATGATACACAAACAGCTGGAAGACAGCATGCTTTTGCCTGCCTAGAGTGTGGTGCTTGGTGGGT
TGTAGAATTAAGAAAAGATTACTATGTGTTTGTGACCTTCTGTGTCGACGAAAACGGACGGATCTCACAACCACGAACCACCCA

7820

SORL1

SORL1-201

SORL1-201

AATTACACCCTCCTCCTGCCCTTGGCCCCTGACTGATTGGTGGCGCGGCTTCTGTTGCAGCTGGGAGAGTCCTAACATGTGCTTA
TTAATGTGGGAGGAGGACGGGAACCGGGGACTGACTAACCACCGCGCCGAAGACAACGTCGACCCTCTCAGGATTGTACACGAAT

7905

SORL1

SORL1-201

SORL1-201

ATCCCTGTTTGGCATGCTTGCAGGAAGAGACTCTGTGCTGGGTGCTCAGATAGTTGTTGCTTCCCTGACAGGGCCTCTTGCTTGT
TAGGGACAAACCGTACGAACGTCCTTCTCTGAGACACGACCCACGAGTCTATCAACAACGAAGGACTGTCCCGGAGAACGAACAA

7990

SORL1

SORL1-201

SORL1-201

CTCTGGTTGCCAGATGACCTATTGCTCATTGACCGTACCTACCTCTGCTGGAATGGCACTGTGTAGTTAGGTGTTGTTTTAATT
GAGACCAACGGGTCTACTGGATAACGAGTAACTGGCATGGATGGAGACGACCTTACCGTGACACATCAATCCACAACAAAATTAA

8075

SORL1

SORL1-201

SORL1-201

AACTTTTCCCACCATGAAACCCCTAAACCCCATGAAGAAAAGAGATGGTCTTTTTTATTCCCCGATAGTTTTACCAGTGTCTAGCAC
TTGAAAAGGGTGGTACTTTGGGATTTGGGGTACTTCTTTCTCTACCAGAAAAAATAAGGGGGCTATCAAAATGGTCACAGATCGTG

8160

SORL1

SORL1-201

SORL1-201

TTTGTAGGTGCTCAATTCATATTTGTTGAAAGAATAAGGGATGAAAAGGGAGGGGAAGAATTGCAGTGGGTGCAGACAGTAGCTG
AAACATCCACGAGTTAAGTATAAAACAACCTTCTTATTCCCTACTTTTCCCTCCCCTTCTTAACGTCACCCACGTCTGTTCATCGAC

8245

SORL1

SORL1-201

SORL1-201

TCTTAGAGATCTACTGGGTGAGGCTTCAAGAAGTCTATGAGGCTTTGACCTGCTAGTCCTGGAGTCTGAGACTATTCAGTGGAA
AGAATCTCTAGATGACCCACTCCGAAGTCTTGACGATACTCCGAAACTGGACGATCAGGACCTCAGACTCTGATAAGTCACTT

8330

SORL1

SORL1-201

SORL1-201

AGCCTTTATCATTTCATGACTGCTCTTTGATTTTGCTTATCTCCCAGCCATACTATTGATTCTAGAGGAGAAAAGATCAGAGGATT
TCGGAAATAGTAAAGTACTGACGAGAACTAAAACGAATAGAGGGTCGGTATGATAACTAAGATCTCCTCTTTCTAGTCTCCTAA

8415

SORL1

SORL1-201

SORL1-201

ACCAGGAAGAATAGTCCCTTTAAGAATTTCCCTCTTTATCTCAGCAGGATTAATGGCATCCTGGGTTTGCTGATTCTCCTTTAT
TGGTCTTTCTTATCAGGGAAATTTCTTAAAGGGGAGAAATAGAGTCGTCTTAATTTACCGTAGGACCCAAACGACTAAGAGGAAATA

8500

SORL1

SORL1-201

SORL1-201

TGACAAACTGCTAAGTTTTCTGTTCTTAACTGGAATGTTGATATTGTTTTATGGTTCTTGGCTGACCCTATACTAGGAGAAAATT
ACTGTTTGACGATTCAAAAAGACAAGAATTGACCTTACAACATAACAAAATACCAAGAACCGACTGGGATATGATCCTCTTTTAA

8585

SORL1

SORL1-201

SORL1-201

GACAGGGGAAATAATACTGTTATAGATATCATTGTTATCCTCTTGGGATTGTGAAGATAGCATGAGAACACCCTGGGAAAACCTAT
CTGTCCCCTTTATTATGACAATATCTATAGTAACAATAGGAGAACCCTAACACTTCTATCGTACTCTTGTGGGACCCTTTTGATA

8670

SORL1

SORL1-201

SORL1-201

AAAGTGTCTTACAAATGTAAGACGATATTATTTGTTATGTCTTCCACCTGACCTGTGAGGTAGGGAAAGGCTGGTATTATGATCC
TTTCACAGAATGTTTACATTCTGCTATAATAAACAATACAGAAGTGGTGACTGGACACTCCATCCCTTCCGACCATAATACTAGG

8755

SORL1

SORL1-201

SORL1-201

ATGGTTTATAGATTAGGGAATTAATCTCAGATATGAATTAGCTTTCCCAAATATCCTCACTAGTTTAGGGGCTGGCCTTTTGT
TACCAAATATCTAATCCCTTAATTTAGAGTCTATACTTAATCGAAAGGGTTTTATAGGAGTGATCAAATCCCCGACCGGAAAAACA

8840

SORL1

SORL1-201

SORL1-201

TGCAATTCTGCCGCTAAATGGAGAAGTCACATTCTTTCTTAGAGGAGGCACCTGTTTTAGAATCAGGAGAGTTGAAGGAATCTTG
ACGTTAAGACGGCGATTTACCTCTTCAGTGTAAGAAAGAATCTCCTCCGTGGACAAAATCTTAGTCTCTCAACTTCCTTAGAAC

8925

SORL1

SORL1-201

SORL1-201

CTTCTCAGCTCCAGTGACTGAAATCTTCAGACCTTTGTTTAATGGAGGACATCCACCCCTACTGATCTGACTTGCTAGCTAGCAG
GAAGAGTCGAGGTCAGTACTGACTTTAGAAGTCTGGAAACAAATTACCTCCTGTAGGTGGGGATGACTAGACTGAACGATCGATCGTC

9010

SORL1

SORL1-201

SORL1-201

AGTGGATTTTTAGTATTTCTCCAAGTGGATTTTTAGCATTTCTCCATGTTACCACTTAGTCCAGAAGAGTGGGTCTTCATTTTTA
TCACCTAAAAATCATAAAGAGGTTACCTAAAAATCGTAAAGAGGTACAATGGTGAATCAGGTCTTCTCACCCAGAAGTAAAAAT

9095

SORL1

SORL1-201

SORL1-201

CAAGTGCTTGTATGCATGTGCTTGTGTTTGAATTTGCACACAGGAGCTTCTGAAACACTGTGTGCAGATGAAGCCAGTGGCTACCCGG
GTTACGAAACATACGTACACGAACAACTAAACGTGTGCTCGAAGACTTTGTGACACACGTCTACTTCGGTCAACGATGGGCC

9180

SORL1

SORL1-201

SORL1-201

TCACAACCTTACTTCCCAGTCTTGACTGTCCACTTCATCCCAAGAACTTGGGCACAGCTGACATGCAGTCACACCTGTGACTGAGG
AGTGTTGAATGAAGGGTCAGAAGTGAAGTAGGGTTCTTGAACCCGTGTCGACTGTACGTCAAGTGTGGACACTGACTCC

9265

SORL1

SORL1-201

SORL1-201

AGCAGTGC GGGAGGAGAGAGTTTGTGGTCTCAGCACATGCAAACGTGGTGTCTTGGTGCCAGTCAGACAGGTCTGCAATCCTCAC
TCGT CACGCCCTCTCTCTCAAACACCAGAGTCGTGTACGTTTGCACCACAGAACCACGGTCAGTCTGTCCAGACGTTAGGAGTG

9350

SORL1

SORL1-201

SORL1-201

CTTAGGTGTAGTTTCCCTTTTCATGCCTCAAAGAGTCATCTTCAATTTAAGTTAGCCAGAGTCATTTTGGGGCCCAGAGTGAGGTCT
GAATCCACATCAAAGGGAAAGTACGGAGTTTCTCAGTAGAAGTAAATTC AATCGGTCTCAGTAAAACCCCGGGTCTCACTCCAGA

9435

SORL1

SORL1-201

SORL1-201

GGATAGATGACAGGCTGGTTTTAAAAGGGAGATATGTATTAGCAGGGCATAGTGGCACATGCCTGTAGTCTCAGCTCCTCAGGAGG
CCTATCTACTGTCCGACCAAATTTTCCCTCTATACATAATCGTCCCGTATCACCGTGTACGGACATCAGAGTCGAGGAGTCTCTCC

9520

SORL1

SORL1-201

SORL1-201

CGGAGGTGGGAGCATCACCTGAGCTCGGGAGGTTGAGGCTGCAGTTAGCCAAGGTCGTGCTGCTGCACTCCATCCTGGGTGACAG
GCCTCCACCCTCGTAGTGGACTCGAGCCCTCCAAC TCCGACGTCAATCGGTTCCAGCACGACGACGTGAGGTAGGACCCACTGTC

9605

SORL1

SORL1-201

SORL1-201

AGTGAGACCCTGTCACCGAAAAAAGGGCTGGGGGAGATCTGTGTTGGTGAGTAGAACACAGACCTGGACCTGTGC
TCACTCTGGGACAGTGGCTTTTTTTTTTTTTTTTTTCCGACCCCTCTAGACACAACCACTCATCTTGTGTCTGGACCTGGACACG

9690

SORL1

SORL1-201

SORL1-201

ATGGGCGGCTGTGACTGTCCCTTTGGCCATGGCCAGTTGTCGCCTCTCTGCTCCTTTCTGTTTGCCTTTGGGATTTTCTCTTGCT
TACCCGCGGACACTGACAGGGAAACCGGTACCGGTCAACAGCGGAGAGACGAGGAAAGACAAACGGAAACCTAAAAGAGAACGA

9775

SORL1

SORL1-201

SORL1-201

GTCCTTTGGTTGTGAGCAGGATACTTCCAGGAGACCTACTGCCTCAAACACAGGGCTGGAGAAAGACGTTTTTGTCTTTCTCTG
CAGGAAACCAACACTCGTCCTATGAAGGTCTCTGGATGACGGAGGTTTGTGTCCCGACCTCTTTCTGCAAAAACAGAAAGAGAC

9860

SORL1

SORL1-201

SORL1-201

CAGCCCAGTTTGGGTCAAATCAAAGCTTTTGCAGTGGTGTCTGGCTGTGACACTGTCTATGAGCACTCCGCACCTCTTGGCCTT
GTCGGGTCAAACCCAGTTTAGTTTCGAAAACGTCACCACAGACCGACAGTCGTGACAGATACTCGTGAGGCGTGGAGAACC GGAA

9945

SORL1

SORL1-201

SORL1-201

GAACTTGTTTGGCTCTAACCTGCTTGCTTTTTTGGACACTGATAGGACACTTGCTTTTTTGGACATTGTATTACAGATCCACGGT
CTTGAACAAACGAGATTGGACGAACGAAAAAACCTGTGACTATCCTGTGAACGAAAAAACCTGTAACATAATGTCTAGGTGCCA

10,030

SORL1

SORL1-201

SORL1-201

GTGTGTTGGATCTAGCACTTGGAGAAATGCTAAAAATCCACTCTGCTAGCTAGCAAGTCAGATCAGTAGGGGTGGATGTCCTCCA
CACACAACCTAGATCGTGAACCTCTTTACGATTTTTAGGTGAGACGATCGATCGTTTCAGTCTAGTCATCCCCACCTACAGGAGGT

10,115

SORL1

SORL1-201

SORL1-201

TCAAGCAAGGGCCTGAATATTTTCAGTCACTGGAGCTGAGAAGCAAGATTCCTTCAACTCTCCTTATTTTTAAACAGGTGACTCCT
AGTTCGTTCCCGGACTTATAAAGTCAGTGACCTCGACTCTTCGTTCTAAGGAAGTTGAGAGGAATAAAATTTTGTCCACTGAGGA

10,200

SORL1

SORL1-201

SORL1-201

CTAAGAAAGAATGTGACTCCTGTCCATCTTTATTATTTTTGTTGTCTCCTCCTAACACATTCGGGACTTTCTACAGTAGTCTCCT
GATTCTTTCTTACACTGAGGACAGGTAGAAATAATAAAAAACAACAGAGGAGGATTGTGTAAGCCCTGAAAGATGTCATCAGAGGA

10,285

SORL1

SORL1-201

SORL1-201

GCTTATTTGCCATTTTGGCTTTCTGTGATTTTCAGCTACCTGCGGTCAACCACTGTCCAAAAATATATATGGAAGATTCAGAAATA
CGAATAAACGGTAAACGAAAGACACTAAAGTCGATGGACGCCAGTTGGTGACAGGTTTTTATATATACCTTCTAAGGTCTTTAT

10,370

SORL1

SORL1-201

SORL1-201

AACAATGTATAAGATTTAAATTGCTTGCTGTTCTGAATAGTGTGATGAAATCTTGTACTGTCTCCTCCCTGTCCACCTGGGATG
TTGTTACATATTCTAAATTTAACGAACGACAAGACTTATCACACTACTTTAGAACATGACAGAGGAGGGACAGGGTGGACCCTAC

10,455

SORL1

SORL1-201

SORL1-201

TGAATCCTCCCTTTGTCCAGCGTCTCATGCTGTTGATGCTGCCGGCTCATTAGTCCCTTTAGGAGCCGGCTGGGTTATCAGGGTG
ACTTAGGAGGGAAACAGGTCGCAGAGTACGACAACCTACGACGGCCGAGTAATCAGGGAAATCCTCGGCCGACCCAATAGTCCCAC

10,540

SORL1

SORL1-201

SORL1-201

TCAAAGTACTGCAGTTCTTGTACGCAAGGAACCCCTTATTTTACTTTCATGATGACCCTACACCTCAAGAGTAGTGATTCCAGTAAT
AGTTTCATGACGTCAAGAACATGCGTTCCTTGGGAATAAAATGAAGTACTACTGGGATGTGGAGTTCTCATCACTAAGGTCATTA

10,625

SORL1

SORL1-201

SORL1-201

TTGGATATGCCAAAGGGAGGTTGTAAAGTGCTTCCCTTTAGGGAAAGGGTGAAAGTTCTAGACTTAATAAGGGAGGAAAAAAATC
AACCTATACGGTTTCCCTCCAACATTTACGAAGGAAATCCCTTTCCCACTTTCAAGATCTGAATTATTCCCTCCTTTTTTTTTAG

10,710

SORL1

SORL1-201

SORL1-201

TTACACCGAGTTTGCTAAGATCTGCTGTAAGAACGAACCTTCTATCTCTGAAATTGTAAAGAAAGAAAAAGAAATTCATGCACAG
AATGTGGCTCAAACGATTCTAGACGACATTCTTGCTTGAAGATAGAGACTTTAACATTTCTTTCTTTTTCTTTAAGTACGTGTC

10,795

SORL1

SORL1-201

SORL1-201

TATAGGTTTGGTCCTATCTGCAGTTTCAGGTGTCAGCTAGGGGTCTTGAATTGGGGGTTTTGGAATAAGAGGGGACTACTATAT
ATATCCAAACCAGGATAGACGTCAAAGTCCACAGTCGATCCCCAGAACCTTAACCCCCAAAACCTTATTCTCCCCTGATGATATA

10,880

SORL1

SORL1-201

SORL1-201

TAACCAAGTGTTAAATAATAAATTGATAGTAACTACATGTATTGAGGGGTTGCTGTGTTATAAGTACCACAGTAATGTGCTTT
ATTGGTTCACAATTTATTATTAACTATCATTGATGTACATAACTCCCCAACGACACAATATTCATGGTGTGTCATTACACGAAA

10,965

SORL1

SORL1-201

SORL1-201

GTGGGCTTGTATAACCTCACTTCGTCTTCCCAAAGACTTCTATATGTAATATCAATATTTCCATTTTATAGGTGAGAATATGAAA
CACCCGAACATATTGGAGTGAAGCAGAAGGGTTTCTGAAGATATACATGATAGTTATAAAGGTAATAATCCACTCTTATACTTT

11,050

SORL1

SORL1-201

SORL1-201

GTCTGGTTTAGTAACTTGTGTAGGTCACACTTTTAGTAAAGTGGTAAGAATTTGCACTGTGGCCCGTTGACTTCAAAGCCTGAACT
CAGACCAAATCATTGAACACATCCAGTGTGAAAATCATTACCATTCTTAAACGTGACACCGGGCAACTGAAGTTTCGGACTTGA

11,135

SORL1

SORL1-201

SORL1-201

TCGATAAAACCACCCGGCTCTGCTCCCTCTGTCATGTGTTGCTAGAAATAGCAGTGCCCTGGTAGTATGACAGCAGTTCAGAAGTA
AGCTATTTTGGTGGGCCGAGACGAGGGAGACAGTACACAACGATCTTATCGTCACGGGACCATCATACTGTCGTCGAAGTCTTCAT

11,220

SORL1

SORL1-201

SORL1-201

CTGTTCTAGATTTTGATTGATGATGGTTCATAATAAAAAATGTTGTTTCAGTTGCAACATTTATCAATTTGAAATATTTGGTCCTTT
GACAAGATCTAAAACCTAACTACTACCAAGTATTATTTTTACAACAAGTCAACGTTGTAATAGTTAACTTTATAAACCCAGGAAA

11,305

SORL1

SORL1-201

SORL1-201

ATAGCTAGCTGGTTTTTATTTTTTATTTGTTTAGTTTTTTGGAGACAGAGTCTCGTTCTGTTACCCCGGCTGGAGTGCAGTGATG
TATCGATCGACCAAAAATAAAAAATAAACAAATCAAAAAACCTCTGTCTCAGAGCAAGACAATGGGGCCGACCTCACGTCACTAC

11,390

SORL1

SORL1-201

SORL1-201

TGATCTTGGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGCAATTCTCATGCCTCAGCCTCCTAAGTAGCTGGGACTAAAGGCAT
ACTAGAACCAGTGACGTTGGAGACGGAGGACCCAAGTTCGTTAAGAGTACGGAGTCGGAGGATTCATCGACCCTGATTTCCGTA

11,475

SORL1

SORL1-201

SORL1-201

GTGCCACCATGCCTGGCTAATTTTTGTATTTTAGTAGAGATTGGGTTTCACCATGTTGCCAGGCTGGTCTTGAACCTCCTGAGC
CACGGTGGTACGGACCGATTAAAAAACATAAAATCATCTCTAACCCAAAGTGGTACAACGGGTCCGACCAGAACTTGAGGACTCG

11,560

SORL1

SORL1-201

SORL1-201

TCAGGCAATCTGCACGCCCCGGCCTCCCAAAGTGCTAGGATTTACAGGTGTGAGCCACTGTGTCTGGCCACTAGCTGGTTTTTAA
AGTCCGTTAGACGTGCGGGGCCGGAGGGTTTCACGATCCTAAATGTCCACACTCGGTGACACAGACCGGTGATCGACCAAAAATT

11,645

SORL1

SORL1-201

SORL1-201

ATGGTATAACTGGAATTTATTCTTTGTAAAGTGTGTTTTTTCTTTAAAGAGGTTACTTTACAAGATTGTTGATGTATTTCAGTTGC
TACCATATTGACCTTAAATAAGAAACATTTTACACACAAAAAAGAAATTTCTCCAATGAAATGTTCTAACAACCTACATAAGTCAACG

11,730

SORL1

SORL1-201

SORL1-201

TCCTGCGATGGCTCTTGGAGCTTTGGAATTTCTTTTGCAGTTTTGGAATTTCTCCTTTAGAGCCTGCAGTAAGTATGTGCTTTTAAAG
AGGACGCTACCGAGAACCCTCGAAACCTTAAGAAAAACGTCAAAACCTTAAGAGGAAATCTCGGACGTCATTCATACACGAAAATTC

11,815

SORL1

SORL1-201

SORL1-201

TATCTATAATGAGGGCACATATTTATTATTTGAGGTAGATTTGATTTTGGATAATTGCCAAGTGTATAGATACTTGAGATGATGAC
ATAGATATTACTCCCGTGTATAAATAATAAACTCCATCTAAACTAAAACCTTAACGGTTCACATATCTATGAACTCTACTACTG

11,900

SORL1

SORL1-201

SORL1-201

ATTTTTGGCTCCTAAAGTATTCCTGGAGGAATTTTCCAAACAGGAAATGTGAAAATGTTCTGAACATGCCCAGTGAAGACATCAC
TAAAAACCGAGGATTTTATAAGGACCTCCTTAAAAGGTTTGTCTTTTACACTTTTACAAGACTTGACGGGTCACCTTCTGTAGTG

11,985

SORL1

SORL1-201

SORL1-201

GGGGCTATGTGTTTGATCTTCTAAGGGAATGTCTTTGAAGATGATTGTCCACTCTTCACATTGAGATAACGGTTTTTCATATTGCC
CCCCGATACACAACTAGAAGATTCCCTTACAGAACTTCTACTAACAGGTGAGAAGTGTAACTCTATTGCCAAAAGTATAACGG

12,070

SORL1

SORL1-201

SORL1-201

TGGTCCACTCAAGACAATTGTCATCCTGTATAAAGGGTCTGTGGCTGTGGTAGAACTGCCATCATAGGAGTTGGTGAATTACCCT
ACCAGGTGAGTTCTGTAAACAGTAGGACATATTTCCAGACACCGACACCATCTTGACGGTAGTATCCTCAACCACTTAATGGGA

12,155

SORL1

SORL1-201

SORL1-201

TCCATCTTCTTCCAGCTTCTCTCTGATGCAGCTCTCCATTTTCCATTCTCTGGCTTCAGACTAGCCTAGACATTCTGCCCCTG
AGGTAGAAGAAGGTGAAGAGAGACTACGTCGAGAGGGTAAAAGGTAAGAGACCGAAGTCTGATCGGATCTGTAAGGACGGGGAC

12,240

SORL1

SORL1-201

SORL1-201

CCTACCTCTTAGGATCAGTGACTTGGTTAGCTTGTGTTTGCAGTTTGCCTTGGTTACTGCCTCAGAGTACAGTTTCATACATTTTC
GGATGGAGAATCCTAGTCACTGAAACCAATCGAACAAAACGTCAAACGGGGACCAATGACGGAGTCTCATGTCAAAGTATGTAAAG

12,325

SORL1

SORL1-201

SORL1-201

TGCCTAGATCAGCCTCCTGAAATATGATACCCCATTTTTGAGTTCTCTACTCTTAGCTCTTCTTGCTTGTGTTGGATAGGAATATTT
ACGGATCTAGTCGGAGGACTTTATACTATGGGGTAAAACCTCAAGAGATGAGAATCGAGAAGAACGAACAAAACCTATCCTTATAAA

12,410

SORL1

SORL1-201

SORL1-201

GCTCTGCATATGAAAAGGTTAGTGAAATGATTTTACAGACATGATCCCTGTGAAAAAATCATCCTGTAATAGAGTAGTTTTTTTT
CGAGACGTATACTTTTCCAATCACTTTACTAAAATGTCTGTACTAGGGACACTTTTTTTAGTAGGACATTATCTCATCAAAAAAA

12,495

SORL1

SORL1-201

SORL1-201

TATTTGTTTCGTTTTGTTTGTGTTTGTGTTTTGAGACAGGCTCTGGCTCTGTTACCCAGGCTGGAGTGCAGTGGCGCCATCTCAG
ATAAACAAGCAAAACAAACAAACAAACAAAACCTCTGTCCGAGACCGAGACAATGGGTCCGACCTCACGTCACCGCGGTAGAGTC

12,580

SORL1

SORL1-201

SORL1-201

CTAACTGCAGCCTCTGTCTCCTGGGCTTAAGCAATCTTCCCACTTCAGCCTCTGAAGTGGCTGGGATCACAGATGTGTACCCGGC
GATTGACGTCCGGAGACAGAGGACCCGAATTCGTTAGAAGGGTGAAGTCCGGAGACTTCACCGACCTAGTGTCTACACATGGGCCG

12,665

SORL1

SORL1-201

SORL1-201

TAATTTTGCTTATTTTTTTTTTGTGGAGGCGGTCTTCACTATGTTGCTCAGGGTGGTCTCGAACTCCTGGGCTCGAGTGATCCTC
ATTAAAACGAATAAAAAAAAAAACACCTCCGCCAGAAGTGATACAACGAGTCCCACCAGAGCTTGAGGACCCGAGCTCACTAGGAG

12,750

SORL1

SORL1-201

SORL1-201

CCACCTCGGCCTCCCAAACCTGCTGGGATTACAGATGTGAGCCACTGCACCCAGCCGGTAATAGAGTATTTTTAAAATAACATCATA
GGTGGAGCCGGAGGGTTTGACGACCCTAATGTCTACACTCGGTGACGTGGGTCCGCCATTATCTCATAAAATTTTATTGTAGTAT

12,835

SORL1

SORL1-201

SORL1-201

TTCCATTATTGTTTCAGGATCTTGGAACATTGAGTGATATATTGTTCTTTGAATACAAAAACACATGTTCCACATCCTTGTGTTGAG
AAGGTAATAACAAGTCTTAGAACCTTGTAACCTCACTATATAACAAGAACTTATGTTTTGTGTACAAGGGTGTAGGAACAACTC

12,920

SORL1

SORL1-201

SORL1-201

TTGTTTCTCATGAGTGGTGGCTCTATGTCAATTCTGCATTCCCTCTTGTAGCCAGTGGCCTGTACCTTTGAACTAAAGGAGCCAT
AACAAAGAGTACTCACCACCGAGATACAGTTAAGACGTAAGGGAGAACATCGGTCACCGGACATGGAAACTTGATTTCTCGGTA

13,005

SORL1

SORL1-201

SORL1-201

CTGTGCCCACTAATGGATCAGAGTGAAGGGATGTCTGGGACTTCTGCTCTAGTCAGCTGGTTAGTCTGCTATGGTAATTAAGCTG
GACACGGGTGATTACCTAGTCTCACTTCCCTACAGACCCTGAAGACGAGATCAGTCGACCAATCAGACGATACCATTAATTTCGAC

13,090

SORL1

SORL1-201

SORL1-201

TTATGATTGATTATTTACTGAACCTTTTGGACTGTTTCATCATGTGGACTTCCCTTCCCTCTGGAGGTGTATGTTTTCTCTCTATT
AATACTAACTAATAAATGACTTGGAAAACCTGACAAAGTAGTACACCTGAAGGGAAGGAGACCTCCACATACAAAAGAGAGATAA

13,175

SORL1

SORL1-201

SORL1-201

TACTGAATCTTTTGGAAATGTTTCATCATATGAACCTCCCTTCCCTCTGGATGTGTGTGTTTTCTCTTTGGTAATACCTCTTACTCT
ATGACTTAGAAAACCTTACAAAGTAGTATACTTGGAGGGAAGGAGACCTACACACACAAAAGAGAAACCATTATGGAGAATGAGA

13,260

SORL1

SORL1-201

SORL1-201

TTTCCTTGGCATCATAATAACGTTGTTGCCATAGCATTGTGATTTTTATTTTTATTTGTAATGTAAATTAACCAATGATGTGCC
AAAGGAACCGTAGTATTATTGCAACAACGGTATCGTAACACTAAAAATAAAAAATAAACATTACATTTAATTGGTTACTACACGGG

13,345

SORL1

SORL1-201

SORL1-201

ACACACCCAAAGCTACTGCGTATATTATCCATATCGACACTGATTATCATTTCATGAACTTCGTCTAACCTGTAGGCCAGGATAGG
TGTGTGGGTTTCGATGACGCATATAATAGGTATAGCTGTGACTAATAGTAAGTACTTGAAGCAGATTGGACATCCGGTCCTATCC

13,430

SORL1

SORL1-201

SORL1-201

CATGGCTTAGATGAATGCTTGGCTGGGTGGCAACAGATGATTTGGATATGGTGCTGAAGTGTGGGAGGGGCATCTCTGTCCATGAC
GTACCGAATCTACTTACGAACCGACCCACCGTTGTCTACTAAACCTATACCACGACTTCACACCCTCCCCTAGAGACAGGTA

13,515

SORL1

SORL1-201

SORL1-201

ATAGCACGAATGAAGAATTAGCAATTGAGTTTTATCTAAGTTTTTATGTTTCATTTTTCCCATTTTTCATGATTAATAATTGCAGTC
TATCGTGCTTACTTCTTAATCGTTAACTCAAAAATAGATTCAAAAATACAAGTAAAAAGGGTAAAAAGTACTAATTATTAACGTCAG

13,600

SORL1

SORL1-201

SORL1-201

AAAAGAAAAACATGATTTTCATAGTTTTCTGTGACCCCATAGTTGTATCATGTTTCAGATTGTTATAAAATGGTTTTATGCATCTTC
TTTTCTTTTTGTACTAAAGTATCAAAGACACTGGGGTATCAACATAGTACAAAGTCTAACAATATTTTACCAAATACGTAGAAG

13,685

SORL1

SORL1-201

SORL1-201

TTACCTGCCATCCCCGGAACGATGTAGGGGATAGGATGGCACTTTTGCCATCCTCGTTCATCCACAAAGGCTCCTTCTCAAGAGT
AATGGACGGTAGGGGCCCTTGCTACATCCCCTATCCTACCGTGAAAACGGTAGGAGCAAGTAGGTGTTTCCGAGGAAGAGTTCTCA

13,770

SORL1

SORL1-201

SORL1-201

GCAGTGGTGGATTTTACGAACCTCTCCGGTGCTGCCTTTAGTAAGCTGAACCAGAGAAAAGATTGGCAGGAGTGGGCTAGATCA
CGTCACCACCTAAAATGCTTGAGAGAGGGCCACGACGGAAATCATTGACTTGGTCTCTTTTCTAACCGTCTCACCCGATCTAGT

13,855

SORL1

SORL1-201

SORL1-201

GCATGAACTAGTCCTTACCTGAACACATTGCACAGCAGTGGCTGATGAGTACTGTGGTTGGCTCCTCCTTTAGCTCTTGAGGGGC
CGTACTTGATCAGGAATGGACTTGTGTAACGTGTCGTCACCGACTACTCATGACACCAACCGAGGAGGAAATCGAGAACTCCCCG

13,940

SORL1

SORL1-201

SORL1-201

ACTCTGGCACAAAGGAATTGAGAAGGGGAGGCCTGGATTTTTGTCCTGGGCCACCATTAAACCAGGTGTATGTTCTAATTAAGGC
TGAGACCGTGTTTCTTAACCTTCCCCTCCGGACCTAAAACAGGACCCGGGTGGTAATTGGTCCACATACAAGATTAATTCCG

14,025

SORL1

SORL1-201

SORL1-201

CTTTGGGGCCCTAAGGAGCAGAAACCCACTCAAGCTAGCTCAAGTGAATGGTTTTATGGAATGAATAAAGGAGCCCAAAGATGAA
GAAACCCCGGGATTCTCGTCTTTGGGTGAGTTCGATCGAGTTCACCTACCAAAAATACCTTACTTATTTCTCGGGTTTTCTACTT

14,110

SORL1

SORL1-201

SORL1-201

AGTCTAGGAGAGCCTCATGGGGACTGGAGCTGTTCTTTCTCTTTCCCTCTCATTAGGCCTCTTCTCTCTGTAAGCCTCTTTCTTT
TCAGATCCTCTCGGAGTACCCCTGACCTCGACAAGAAAAGAGAAAAGGGAGAGTAATCCGGAGAAGAGAGACATTCGGAGAAAAGAAA

14,195

SORL1

SORL1-201

SORL1-201

TTAAAAAAAAAATTATTCGGAATTTTGAAGGCAATGTTCAACTATATTATAGCCACTAGTGTTGTAATTGAGAAGTCCAAAGACA
AATTTTTTTTTTAATAAGCCTTAAAACCTCCGTTACAAGTTGATATAATATCGGTGATCACAACATTAACCTCTTCAGGTTTTCTGT

14,280

SORL1

SORL1-201

SORL1-201

TTCTGGTTCCTTTTTTAAATTAATAAAAAAAAAAATTTTTTTTAAAGGGATAGGATCTTGCTATATTGCCCAGGCTGGATTCGAGCTACC
AAGACCAAGAAAAAATTTAATTTTTTTTTTTTAAAAAAAAATTCCCTATCCTAGAACGATATAACGGGTCCGACCTAAGCTCGATGG

14,365

SORL1

SORL1-201

SORL1-201

AGGCTCAAGTGATCCTCCTGCCTCAGCCTCCTGAGTAGCTGGGGCTACAGGTGCGTGCTGCCATGCCTGGCCTCCTTAAGTCTCT
TCCGAGTTCCTAGGAGGACGGAGTTCGGAGGACTCATCGACCCCGATGTCCACGCACGACGGTACGGACCGGAGGAATTCAGAGA

14,450

SORL1

SORL1-201

SORL1-201

TTTAGTCTCCTGACGGTCTGCAGACTGAGCTTATCTGCATACCCAGAGTTTTGACTTCCACACGGTTTTTGGCTTGCCATGTGCCA
AAATCAGAGGACTGCCAGACGTCTGACTCGAATAGACGTATGGGTCTCAAAACTGAAGGTGTGCCAAAACCGAACGGTACACGGT

14,535

SORL1

SORL1-201

SORL1-201

CTTCAACACCCATGCTCTGTGACCCTTTCCCTGGCTCCAGCTCCTTGGTTGCTTTCTTGTCTTTTCAGTGACCCAATTACAAATTC
GAAGTTGTGGGTACGAGACACTGGGAAAAGGGACCGAGGTCGAGGAACCAACGAAAGAACAGAAAGTCACTGGGTTAATGTTTAAG

14,620

SORL1

SORL1-201

SORL1-201

CCAGGAGGAACCTGCTGCCTGGCTTGGCTCTGGGGCAGTCTGATCTGGCTGAAGACAGGATGCAAGTCACTGGTTATACTGAGC
GGTCTCCTTGGGACGACGGACCGAACCGAGACCCCGTCAGACTAGACCGACTTCTGTCTACGTTTCAGTGACCAATATGACTCG

14,705

SORL1

SORL1-201

SORL1-201

AGAAGTTTTTCAGCACAGTAGGGCGCCCCAAAGCTTGCCACTTGACCCTTGAGAGCTTCTCGCTGTCCTTTCCGTAAGACGAGGAGG
TCTTCAAAAAGTCGTGTCATCCGCGGGGTTTGAACGGTGAAGTGGGAAGTCTCGAAGAGCGACAGGAAAGGCATTCTGCTCCTCC

14,790

SORL1

SORL1-201

SORL1-201

TTGCAGTGGGTCTCCTTCTTGTATTTCAGTACCTCCCTCATGGTGTGTATTAACCTACCTGCTGCTGTTTGTCTTCCCTCCAGGAA
AACGTCACCCAGAGGAAGAACAATAAGTCATGGAGGGAGTACCACACATAATTGGATGGACGACGACAAACAGAAGGGAGGTCTT

14,875

SORL1

SORL1-201

SORL1-201

G

GCAATGCCTGTGTGCCAGGCCATGCAGCCTGCTGTGCCTGCCAAGGCCAACACAGTAGAAGCTGCAGGTGTCCAGAGGATGT
CGTTACGGACACACGGGTCCGGTACGTCGGACGACACGGACGGGTTCCGGTTGTTGTCATCTTCGACGTCCACAGGTCTCCTACA

14,960

SORL1

SORL1-201

SORL1-201

S N A C V P R P C S L L C L P K A N N S R S C R C P E D V

ENSE00003533392

GTCCAGCAGTGTGCTTCCATCAGGGGACCTGATGTGTGACTGCCCTCAGGGCTATCAGCTCAAGAACAATACCTGTGTCAAACAA
CAGGTCGTACACGAAGGTAGTCCCCTGGACTACACACTGACGGGAGTCCCGATAGTCGAGTTCTTGTATGGACACAGTTTGT

15,045

SORL1

SORL1-201

SORL1-201

S S S V L P S G D L M C D C P Q G Y Q L K N N T C V K Q

ENSE00003533392

GGTACTTCCCTTTTTCTTTTTGCTGTGCATCCTCCTTCTTTGTTTCTGCTCCCCGCCAGGGGAGGGAGGGATAGCTCTCTGT
CCATGAAGGGAAAAAGAAAAACGGACAGTAGGAGGAAGGAAACAAAGGACGAGGGGCGGTCCCCTCCCTCCCTATCGAGAGACA

15,130

SORL1

SORL1-201

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

SORL1-201

TTCCTAACCTTTTTCGTGTATTGGAAAAAGTCCAAGGTAAAAATCAAACCTACCAGATACTCATAAGAATACTGGTTTGGGTTCT
AAGGATTGGAAAAAGCACAATAACCTTTTTTCAGGTTCCATTTTAGTTGGATGGTCTATGAGTATTCTTATGACCAAACCCAAGA

15,215

SORL1

SORL1-201


F P N L F V L L E K V Q G K N Q T Y Q I L I R I L V W V L
(in frame with SORL1-201)

AAGTCCTGGTAAGGGTCAAAGAGGGCCCTTCAGTCCTCACTCAGAACAGGCCTATGCTGTACCTTTCTAAGTAGTAGCTGTGGTTT
TTCAGGACCATTCCCAGTTTCTCCGGGAAGTCAGGAGTGAGTCTTGTCCGGATACGACATGGAAAGATTCATCATCGACACCAAAA

15,300

SORL1

SORL1-201

S P G K G Q R G P S V L T Q N R P M L Y L S K 
----- (in frame with SORL1-201) ----->

TTGGTTTTCATGTCAGATGGCACAGGCTTTCTTCAGGGTCTCCCTTTTTATTCTTTTGCTTCTTCCTCTCCTCACCCATCCCTCAC
AACCAAAGTACAGTCTACCGTGTCCGAAAGAAGTCCCAGAGGGAAAAATAAGAAAACGAAGAAGGAGAGGAGTGGGTAGGGAGTG

15,385

SORL1

SORL1-201

ATCCAGGTTTCTTACCTGCTCCTG 3'
-----| 15,409
TAGGTCCAAAGAATGGACGAGGAC 5'

SORL1

SORL1-201

Feature	Location	Size		Type
✓ SORL1	1 .. 15,409	15,409 bp	■ →	gene
/note	= gene ENSG00000137642 Protein coding			
SORL1-AS1	1 .. 15,409	15,409 bp	■ ←	gene
/note	= gene ENSG00000246790 lncRNA			
✓ SORL1-201	1 .. 15,409	15,409 bp	■ →	prim_transcript
/note	= primary transcript ENST00000260197			
SORL1-AS1-201	1 .. 15,409	15,409 bp	■ ←	prim_transcript
/note	= primary transcript ENST00000501964 lncRNA			
SORL1-AS1-202	1 .. 15,409	15,409 bp	■ ←	prim_transcript
/note	= primary transcript ENST00000529160 lncRNA			
✓ SORL1-201	1870 .. 15,046	13,177 bp	■ →	CDS
▶ 6 segments = 957 bp				
/codon_start	= 1			
/note	= coding sequence ENSP00000260197			
/translation	= ENEFILYAVRKSIIYRYDLASGATEQLPLTGLRAAVALDFDYEHNCLYWSDALADV IQ,,RLCLNGSTGGQVEVIINSGLETVEALAFEP LSQLLYWVDA GFKKIE,,VANPDGDFRLTIVNSSVLD RPRALVLPQEG,,VMFWTDWGD LKPGIYRSNMDGSAAYHLVSE DVKWPNGISVDDQWIYWTDAYLEC IERITFSGQQRSVILDNLPHPYAIAVFK,,NEIYWDDWSQLSIFRASKYSGSQMEILANQLTGLMDMKIFYKGKNT,,GSNACVPRPCSL LCLPKAN NSGRCPEYSSYLSQDLMCD CPQGYQLKNNTCVKQ 18 amino acids = 2.1 kDa			
SORL1-208	2975 .. 6770	3796 bp	■ →	prim_transcript
/note	= primary transcript ENST00000529445 Retained intron			
SORL1-203	4948 .. 6706	1759 bp	■ →	prim_transcript
/note	= primary transcript ENST00000524873 Retained intron			
✓ Donor Template WT -> SNV	6669 .. 6768	100 bp	■ ⇌	misc_feature
✓ Protospacer Sequence	6687 .. 6706	20 bp	■ ⇌	misc_feature
✓ SNV	6700 .. 6700	1 bp	■ ⇌	misc_feature
/note	= WT = C SNV = T			
✓ PAM	6707 .. 6709	3 bp	■ ⇌	misc_feature
SORL1-204	14,658 .. 15,409	752 bp	■ →	prim_transcript
/note	= primary transcript ENST00000525532			
SORL1-204	14,992 .. 15,046	55 bp	■ →	CDS
/note	= coding sequence ENSP00000434634			
/translation	= MCD CPQGYQLKNNTCVKQ 18 amino acids = 2.1 kDa			

Primer	Length	Binding Sites	T _m	Date Added
✓ PCR Forward /sequence = ATGCACGCCAAATAGGATTGTAGTG 44% GC / 7730.1 Da	25-mer	6099 .. 6123	60°C	Jan 11, 2023
✓ Sanger Sequencing /sequence = CGGAGCAATATGGATGGTTC 50% GC / 6197.1 Da	20-mer	6570 .. 6589	56°C	Jan 11, 2023
✓ Donor Template WT -> SNV /sequence = TAAAGACAGCAATGGCATAGGGGTGCGGGAGGTTGTCCAGAATGACAGAGCGCTGCTGGCCACTGAACATGATCCGCTCTATGCACTC 55% GC / 6717.1 Da	100-mer	6669 .. 6768	79°C	Jan 11, 2023
✓ gRNA Protospacer /sequence = ATAGAGCGGATCACGTTTCAG 50% GC / 6166.1 Da	20-mer	6687 .. 6706	57°C	Jan 11, 2023
✓ PCR Reverse /sequence = AAGAGCCATGTTGCTCTCCAGAGTC 52% GC / 7642.0 Da	25-mer	7148 .. 7172	62°C	Jan 11, 2023