



5'

3'

CCCTGGTGTTCATGCTAAGTTCGTTAGTCCCTTAATTTAATCTTTCATCATTACCAGAGTAATTAACATACCTCACTATGGA
GGGACCACAAAAAGTACGATTCAAGCAATCAGGGAATTAATTAGAAAAGTAGTAATGGTCTCATTAAATTGTATGGAGTGATACCT

85

SORL1

SORL1-201

GGCTTGAAAAGAACCACCACTTCAGCAAATTCACAAATGAGCAGATAATATTCAAATATTTCCCTCACAAAGAGCTGTTATTGA
CCGAACTTTTCTTGGTGGTGAAGTCGTTAAGGTTGTTTACTCGTCTATTATAAGTTTATAAAGGGAGTGTTCTCGACAATAACT

170

SORL1

SORL1-201

TGAGGGCGTGGGTTAGTAGGGTTTGAGTGATTGCTCTTGAGGGGCTGGAGTGCCTACTTTTGTAAATAAATATTTCTGAAGATAAT
ACTCCCGCACCCAATCATCCCAAACCTCACTAACGAGAACTCCCGACCTCACGGATGAAAACATTATTTATAAAGACTTCTATTA

255

SORL1

SORL1-201

TCAGCAAGGGACAAAAACAGTTTGTAAAGCCATCTAAACTGGCAGGAAAGCTATTTTCTTCTACTGGAAGATAGAACAGGGA
AGTCGTTCCCTGTTTTGTCAAACAAATTCGGTAGATTTGACCGTCTTTTCGATAAAAGAGAAGATGACCTTCTATCTTGTCCCT

340

SORL1

SORL1-201

ACGAAGTGGAGAAATCTCATTCCATTGTGGGCCACCTCCTATGTAAAAGAGAGAAAAAAGGCATGGAATAGGAGGCAGGGAT
TGCTTCACCTCTTTAGAGTAAGGTAACACCCGGTGGAGGATACATTTTCTCTTTTTTTTTCCGTACCTTATCCTCCGTCCCTA

425

SORL1

SORL1-201

ATACCAGGAAAGAAAAAGATGCTTTTACAGGACTAATGGGGGCGTAATATCTTTGCAAAGATGAGGTAATCTGGGCATCTGGAA
TATGGTCCTTTCTTTTCTACGAAAGTGTCTGATTACCCCGGCATTATAGAAACGTTTCTACTCCATTAGACCCGTAGACCTT

510

SORL1

SORL1-201

GGATTTTTTAAATGCAAGAATTTTTCTTCTTTACAATTACTATGAAAACACACATTCCTTGGCCAGGACCAGCCAAGAATTCCA
CCTAAAAAATTTACGTTCTTAAAAAGAAGGAAATGTTAATGATACTTTTGTGTGTAAGGAACCGGTCTGGTCGGTTCTTAAGGT

595

SORL1

SORL1-201

TTCTTTTCCAGGTTAAGCATTGCGCGCTGGAATGCCGCATGCTGCTCTGAACATAATCCTAAAAACGTAATTTCTGGATTCAGG
AAGGAAAAGGTCCAATTCGTAACGCGCGACCTTACGGCGTACGACGAGACTTGTATTAGGATTTTGTGCATAAAGACCTAAGTCC

680

SORL1

SORL1-201

TTCTACTTTATGGGTATTAGTTTCTTAGAGGAAAAAAGCCAGAGTGACAGAATGAGGTTTATAGATGCTGGAGAGAGATGTG
AAGATGAAATACCCATAATCAAAGAATCTCCTTTTTTTTTCGGGTCTCACTGTCTTACTCCAAATATCTACGACCTCTCTTACAC

765

SORL1

SORL1-201

GGGCAAAAGCCTTGCTGCTGCAAATGTAGCTTTTCATGTCCCTATACCTTAGCTGGCCCCCTCCCTGGGAATGACAGCGGGAAGGT
CCCGTTTTTCGGAACGACGACGTTTACATCGAAAAGTACAGGGATATGGAATCGACCGGGGGAGGGACCCCTTACTGTGCGCCCTTCCA

850

SORL1

SORL1-201

TTCTTGACAACCAAAAGGGGAGGTAGGTTACCATGTGATGGTAACATAGATACTTCTAAAGTGACCTGGAACCAAAAGGAAAAAGA
AAGGAACTGTTGGTTTTCCCTCCATCCAATGGTACACTACCATTGTATCTATGAAGATTTCACTGGACCTTGGTTTTCTTTTTCT

935

SORL1

SORL1-201

AGGAAAACCTTACCTTATTAATAAATTGTAGGTAGATTTATTTTTTGGATGCATTATCTATATTACAGCTTTTATAAAGAAGGTGAGT
TCCTTTTGAATGGAATAATTTTAACATCCATCTAAATAAAAAAAGTACGTAATAGATATAATGTGCAAAAATATTTCTTCCACTCA

1020

SORL1

SORL1-201

GGTACATGTTAAGTCACTGAGTGTATGGAATCAGGAAGTGGGCAGGAATGGCTAACCCAGGCATGCAGCAAAAAGAATTCCGATTT
CCATGTACAATTCAGTGACTCACATACTTAGTCCTTACCCGTCCTTACCGATTGGGTCCGTACGTCGTTTTCTTAAGGCTAAA

1105

SORL1

SORL1-201

GCATCTTGGTCCCATATGCAACACACTGTCAAGATGCACACTTTAGACACAGATGCTGGTGTGCTGCTTGTGTCCACTCCTGGGG
CGTAGAACCAAGGGTATACGTTGTGTGACAGTTCTACGTGTGAAATCTGTGTCTACGACCACACGACGAACACAGGTGAGGACCCC

1190

SORL1

SORL1-201

AAGAATCTGGATGTTTCCCAAGCCGTTCCCTAAGTGGACAAGACAGTGTACTGGGTCTTCTATTTCCAGTTGTCTGACATTAGG
TTCTTAGACCTACAAAGGGTTCGGCAAGGGATTACCTGTTCTGTGCATGACCCAGAAGGATAAAGGTCAACAGACTGTAATCC

1275

SORL1

SORL1-201

TAAGTATCTTCAGCACTCAGGACCTTCATTTCTACATCTTAAAAATCATCCACGGTAGCGTCTGTATCATAACAGGCAGCACAGT
ATTCATAGAAGTCGTGAGTCTGGAAGTAAAGATGTAGAATTTTGTAGAGGTGCCATCGCAGACATAGTATTGTCCGTCGTGTCA

1360

SORL1

SORL1-201

GTAGTGGTTAAAGCATAGACTCTGGATCCAGAGTGCCTGGGTTCCAATCTTGGTTCTGCCACTTGCTAGTTGTGTGACCTTGGGT
CATCACCAATTTTCGTATCTGAGACCTAGGTCTCACGGACCAAGGTTAGAACCAAGACGGTGAACGATCAACACACTGGAACCCA

1445

SORL1

SORL1-201

GAGTTACTTAACCTCTCTGGTCTCAGTTTTCTCATTTGTAAAAATTTGGTTAACAAGAGTTCTACCATCAGGCAGTTGTTGTGGGT
CTCAATGAATTGGAGAGACCAGAGTCAAAAGAGTAAACATTTTAAACCAATTGTTCTCAAGATGGTAGTCCGTCAACAACACCCA

1530

SORL1

SORL1-201

CTTAAACAATACCCGATACGTAGTAAGCACATTATACACAATATGTACACAATTTATATTTGTTGAGTAGAAACAGAATTTTTGT
GAATTTGTTATGGGCTATGCATCATTTCGTGTAATATGTGTTATACATGTGTTAAATATAAAACAACCTCATCTTTGTCTTAAAAACA

1615

SORL1

SORL1-201

GGTGATTATGTTGTGGAACATTTTGTAAATAGCCAAGAACAATGCATTATTAGTATTATTTTGGAGATCTAAGAGGTTTCATAGA
CCACTAATACAACACCTTGTAAAAACATTTATCGGTTCTTGTTTACGTAATAATCATAATAAAACCTCTAGATTCTCCAAGTATCT

1700

SORL1

SORL1-201

ATTGCCATATGGTGTGTGAACAATATGAATAAGTGAGCAAATTGATTAGAGAGCTTAGTTACAAAGCTTCAGTGACTAATGGTC
TAACGGTATACCACAACACTTGTATACTTATTTCACTCGTTTAACTAATCTCTCGAATCAATGTTTCGAAGTCACTGATTACCAG

1785

SORL1

SORL1-201

TCTCGTCAACAAGATGATGATGCTGTGGTGATACAGTCACTGAGGAGGGAGAACAGGGCGATTGGTGTAAATTAGGTTGGCAAGT
AGAGCAGTTGTTCTACTACTACGACACCACTATGTCAGTGCCTCCTCCCTCTTGTCCCGCTAACCACATTAATCCAACCGTTCA

1870

SORL1

SORL1-201

GTGACTTGAAGACTGGCAGGCTTAGCCAGAAAGTATGGTTGTTGAAGCATGCATATTGGGAGATTTAGAATAAAGAAAAACATAA
CACTGAACTTCTGACCGTCCGAATCGGGTCTTCATACCAACAACCTTCGTACGTATAACCCTCTAAATCTTATTTCTTTTTGTATT

1955

SORL1

SORL1-201

CAAGTAAAAACACTTGCAGATGAAGAAACAGATTTCACTGGAGTTTAAAGTAACTTGCCTGAGGCAGAAATGTGATTCCATTACACAC
GTTCAATTTTGTGAACGTCTACTTCTTTGTCTAAGTGACCTCAAATTCATTGAACGGACTCCGTCTTTACACTAAGGTAATGTGTG

2040

SORL1

SORL1-201

CTCCTGAGTCTTGATTTCTGTGCTCTTCACTTGGTCCACACCACATGCCAATGAATTTGAGGTTTGTGTATGAGAAACAAATAGG
GAGGACTCAGAACTAAAGACACGAGAAGTGAACCAGGTGTGGTGTACGGTTACTTAAACTCCAAACACATACTCTTTGTTTATCC

2125

SORL1

SORL1-201

TCAGATGTGCTAGGACCTCTTCAGCATCCCCTGGGTCCAACCTCCCACGTGTCTTGTGTGTCTGGCAGAAGAGAACGAGTTTCATT
AGTCTACACGATCCTGGAGAAGTTCGTAGGGGACCCAGGTTGGAGGGTGCACAGAACACACAGACCGTCTTCTCTTGTCTCAAGTAA

2210

SORL1

SORL1-201

E N E F I
ENSE0000991345
SORL1-201

CTGTATGCTGTGAGGAAATCCATCTACCGCTATGACCTGGCCTCGGGAGCCACCGAGCAGTTGCCTCTACCGGGCTACGGGCAG
GACATACGACACTCCTTTAGGTAGATGGCGATACTGGACCGGAGCCCTCGGTGGCTCGTCAACGGAGAGTGGCCCCGATGCCCGTC

2295

SORL1

SORL1-201

L Y A V R K S I Y R Y D L A S G A T E Q L P L T G L R A
ENSE0000991345
SORL1-201

CAGTGGCCCTGGACTTTGACTATGAGCACAACCTGTTTGTATTGGTCCGACCTGGCCTTGGACGTCATCCAGGTGAGTCAGCGCTT
GTCACCGGGACCTGAAACTGATACTCGTGTGACAAACATAACCAGGCTGGACCGGAACCTGCAGTAGGTCCACTCAGTCGCGAA

2380

SORL1

SORL1-201

A V A L D F D Y E H N C L Y W S D L A L D V I Q
ENSE0000991345
SORL1-201

GGTCTGACTGTGGGAGCTGTGCATCGTGACTGCCCTGTCCTGATAAGCTGCATGCAGAATGGCCTATGGAAATGGGCAGTTAGAA
CCAGACTGACACCCTCGACACGTAGCACTGACGGGACAGGACTATTTCGACGTACGTCTTACCGGATACCTTTACCCGTC AATCTT

2465

SORL1

SORL1-201

SORL1-201

GTTTGTAAGTGTTACTCATCTCAGGGCTGACAGGTGAAAGTTTTCCAGTCTTCTGTGTTAGTATTTTTCTTTCTCTGTCTTCATCT
CAAACATTCACAATGAGTAGAGTCCCGACTGTCCACTTTCAAAGGTCAGAAGACACAATCATAAAAAAGAAAAGAGACAGAAGTAGA

2550

SORL1

SORL1-201

SORL1-201

GTTTCATATAGGAAGGATAAAGAAAGCCCTAAATCCACAGACCTGCTTGAAAGTGAGGTCTTGCTTTTTCTGCTGGGAAGGTGTTG
CAAGTATATCCTTCTATTTCTTTTCGGGATTTAGGTGTCTGGACGAACTTTCACTCCAGAACGAAAAGGACGACCTTCCACAAC

2635

SORL1

SORL1-201

SORL1-201

GGACTAGTAATGTAGGATGATTAGTTGCCCCCTATTGTGCCAACTGCCTCTTGAGCATCTTTCTTCCCAAGCCATGATACAGTA
CCTGATCATTACATCCTACTAATCAACGGGGGATAACACGGTTGACGGAGA AACTCGTAGAAAGAAGGGTTCGGTACTATGTCAT

2720

SORL1

SORL1-201

SORL1-201

ACACTTGACTTACCCATAGCTCACATAATTATCCACTTCAGCTGTTCTGAACACAGGTAAGAACCAGGAAGTAAGCATTAAAGAG
TGTGAACTGAATGGGTATCGAGTGTATTAATAGGTGAAGTCGACAAGACTTGTGTCCATTCTTGGTCCTTCATTTCGTAATTTCTC

2805

SORL1

SORL1-201

SORL1-201

CCCTGGACAGGCCAGGTGGATAGCCATACGCTCACACCCATGCATTTAAAGGAGAGCTCTTTGATCTTTATTTCATTGTCTACTTA
GGGACCTGTCCGGTCCACCTATCGGTATGCGAGTGTGGGTACGTAAATTTCTCTCGAGAAACTAGAAAATAAGTAACAGATGAAT

2890

SORL1

SORL1-201

SORL1-201

ATCCTTTTAGAAAAGCAATTCCAACAAATTTTTATCTAGATTCCAACCCAACAGAAATTTACAGTGCCTGGGTATTTGAGGGGC
TAGGAAAATCTTTTCGTTAAGGTTGTTTAAAAATAGATCTAAGGTTGGGTTGTCTTTAAAGTGTACGGACCCATAAACTCCCCG

2975

SORL1

SORL1-201

SORL1-201

TTGGGGTGGGGGATGGCGGTGATGCTGAATGGAGCTGTCCAACAATAGCACTTGATGGCTAAGAGCCTCACAGGGAAGAAAGAGT
AACCCACCCCTACCGCCACTACGACTTACCTCGACAGGTTGTTATCGTGAACCTACCGATTCTCGGAGTGTCCCTTCTTTCTCA

3060

SORL1

SORL1-201

SORL1-201

ATAAAGCAGACACAAGAAGCTGAAATGTAACAGCAGTCTGGTTTCACTTATTTTAAAAGCAAACAGACTCATACAATCTCAGTAA
TATTTTCGTCTGTGTTCTTGACTTTACATTGTCGTCAGACCAAAGTGAATAAAATTTTCGTTTGTCTGAGTATGTTAGAGTCATT

3145

SORL1

SORL1-201

SORL1-201

TCTCTGACTTTTATTATTGCCATACAGCATAATTTAGTAACCAAGTGTTCATAATGATAATGCAGAGTAATATATATGATTAAATTC
AGAGACTGAAATAATAACGGTATGTCGTATTAATCATTGGTCACAAGTATTACTATTACGTCTCATTATATATACTAATTTAAG

3230

SORL1

SORL1-201

SORL1-201

TCTTTATTCTGCTTTAAAAAACAAAAATGTAGTATATTTTAGAAATGCTTTTCATGAAAACCTGGCTTCATGTGTCTGGAAAAGTTT
AGAAATAAGACGAAATTTTTGTTTTTACATCATATAAAATCTTTACGAAAGTACTTTTTGGACCGAAGTACACAGACCTTTCAA

3315

SORL1

SORL1-201

SORL1-201

ACTAACGTAAAACATCTCATCCCTTGCCAGTCTGCCAGTTGAATAAAGGGTTACCCCTTCATGGGACTGACTTGGCAGGGGGTTCG
TGATTGCATTTTGTAGAGTAGGGAACGGTCAGGACGGTCAACTTATTTCCCAATGGGAAGTACCCTGACTGAACCGTCCCCCAGC

3400

SORL1

SORL1-201

SORL1-201

TTTGAACAGTTCCTAGCATTATTATTACTTTTTCTCTTTAAGCGCCTCTGTTTGAATGGAAGCACAGGGCAAGAGGTGATCATC
AAACTTGTCAAGGATCGTAAATAATAATGAAAAGAGAGAATTCGCGGAGACAAACTTACCTTCGTGTCCCGTTCTCCACTAGTAG

3485

SORL1

SORL1-201

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

SORL1-201

AATTCTGGCCTGGAGACAGTAGAAGCTTTGGCTTTTGAACCCCTCAGCCAGCTGCTTTACTGGGTAGATGCAGGCTTCAAAAAGA
TTAAGACCGGACCTCTGTCACTTTCGAAACCGAAAACCTTGGGGAGTCGGTGCAGCAAATGACCCATCTACGTCCGAAGTTTTTCT

3570

SORL1

SORL1-201

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

SORL1-201

TTGAGGTATGTGTATTTTCGTGCTGTTCTTAATTAAGGGAGCAGGCGGGGCACCTGGGCTTTGAGCCACATTTGACACAGAGGGCA
AACTCCATACACATAAAAAGCACGACAAGAATTAATTCCTCGTCCGCCCGTGAGACCCGAAACTCGGTGTAAACTGTGTCTCCGT

3655

SORL1

SORL1-201

I E
ENSE...

SORL1-201

AGGGCCAGTGTGTCAGATTACTCAGGAAATTTACTGCGAGTTTTCCAGAGAATGGACCAGCTGAGCCTCTGGAGAGGAGAGAAAAG
TCCCGGTCACACAGTCTAATGAGTCCTTTAAATGACGCTCAAAGGTCTCTTACCTGGTCGACTCGGAGACCTCTCCTCTCTTTTC

3740

SORL1

SORL1-201

SORL1-201

GGGGTAAGTACCTGTGAGTTGATCTTTTGGCTAGCAGAAGCTTAGCTAATAACAATAAATGGTAATATTTTTATTTATTTATAT
CCCCATTCATGGACACTCAACTAGAAAACCGATCGTCTTCGAATCGATTATTGTTATTTACCATTATAAAAAATAAAATAAATATA

3825

SORL1

SORL1-201

SORL1-201

ATGTACTIONTATTTTATTTATATATTATTTTTGTTTTATTTTACTACTTTTTATTAACATGATGGCAAAAACACTACAATCACTT
TACATGAATGAATAAAATAAATATATAATAAAAAACAAAATAAAATGATGAAAATAATTTGTACTIONTATTTTATTTGTTAGTGAA

3910

SORL1

SORL1-201

SORL1-201

TTGCATCAGCCTAATATCATGGTATTATTATAATGCTATAACAATAATCGTCTAGTATTATTTTATTCGATTAGAGTGATAGCAA
AACGTAGTCGGATTATAGTACCATAATAATATTACGATATTGTTATTAGCAGATCATAATAAAATAAGCTAATCTCACTATCGTT

3995

SORL1

SORL1-201

SORL1-201

CAATATCATCATCATCATCATTGCCACTGTTATTAATCCCCATTTCTCTGCAACTTAGCTACCTAGTAACCTGTCCACCTT
GTTATAGTAGTAGTAGTAGTAGTAACGGTGACAATAATTAGGGGTAAAGAGACGTTGAATCGATGGATCATTGGACAGGGTGGAA

4080

SORL1

SORL1-201

SORL1-201

ATATACCAAGGCAAGGATGATGAGTGACCTCTAAACTGCCAAATCTTTGTCTGGGGGAATGTAGTGTGCTCAGCTCACTGCCTC
TATATGGGTTCCGTTCTACTACTCACTGGAGATTTGACGGTTTAGAAACAGACCCCTTACATCACACGAGTCGAGTGACGGAG

4165

SORL1

SORL1-201

SORL1-201

AGCACCTCTTTATACTGACTCTGCATGGAGAGACGGCATGTGGGTGAAAGTGGGAAGTGCAGTAGAAGCAGGGGAGATGCAGAGGGC
TCGTGGAGAAATATGACTGAGACGTACCTCTCTGCCGTACACCCACTTCACCCCTTCACGTCATCTTCGTCCCTCTACGTCTCCCG

4250

SORL1

SORL1-201

SORL1-201

TAAGAGGAGTTGCAAGACGAAAGACACAGACTCGAGAGATAGACCCAGATGTAGGCTTGACTCCACTAGCTCAGCGACATGGGGC
ATTCTCCTCAACGTTCTGCTTTCTGTGTCTGAGCTCTCTATCTGGGTCTACATCCGAACTGAGGTGATCGAGTCGCTGTACCCCG

4335

SORL1

SORL1-201

SORL1-201

AAGGTGCTTATGCTTTCTAAACTTCAGTTGCTTCATGCGTTAGATGGAGATTCATATATTCGCACAACCATTTGACAGGGGTTCT
TTCCACGAATACGAAAGATTTGAAGTCAACGAAGTACGCAATCTACCTCTAAGTATATAAGCGTGTGGTAAACTGTCCCCAAGA

4420

SORL1

SORL1-201

SORL1-201

CTGCATGATACATGTGGTTTAGGTTCTGATGATAAAGCAGTGGGCAGGACACACACGTTCTTGTTCCAGTAGAGCTTAGATTTTA
GACGTACTATGTACACCAAATCCAAGACTACTATTTTCGTACCCCGTCTGTGTGTGCAAGAACAAGGTCATCTCGAATCTAAAAT

4505

SORL1

SORL1-201

SORL1-201

GTGGAGGAAGCAAAATAATAAATCAGTTCTGTTGGTGGTACATGCTGCAAAGACTCTGAAGCAGTGCAGTGTGATTGCGCTTTTG
CACCTCCTTCGTTTTATTATTTAGTCAAGACAACCACCATGTACGACGTTTCTGAGACTTTCGTACGTCACACTAACCGGAAAAAC

4590

SORL1

SORL1-201

SORL1-201

GAGAGTGGGGCAACATTAGAATAGGCAGACAGAGCAGGCAACTTGAGGTTGATGTCTTAGCTGAGCCCTGGCTGAGAAGAGGATG
CTCTCACCCCGTTGTAATCTTATCCGTCTGTCTCGTCCGTTGAACTCCAACACTACAGAATCGACTCGGGACCGACTCTTCTCCTAC

4675

SORL1

SORL1-201

SORL1-201

ATCTTTTGTCCACCTCCTGGGGATGCTGATAGAAGTGAACCTGGCATCTACTGAATGCTGCCTCGGTGGTTATGTTATTGCTCTTT
TAGAAAACAGGTGGAGGACCCCTACGACTATCTTCACTTGACCGTAGATGACTTACGACGGAGCCACCAATACAATAACGAGAAA

4760

SORL1

SORL1-201

SORL1-201

CTCTCCTTTCTTTAATTGCGTGTGGTCAGCACTTGGCTAGGGGGCTAAAAAGAATGCAGGTGATGCACAAGCACCCACCTTTTCACA
GAGAGGAAAAGAAATTAACGCACACCAGTCGTGAACCGATCCCCGATTTTCTTACGTCCACTACGTGTTTCGTGGGTGGAAAAGTGT

4845

SORL1

SORL1-201

SORL1-201

GGCTGTGGGGCGACCACTGCACAACCTCAAATACTGTTGGTGCAAATGGTGTGAGATGAGCCAAGGTGCAGAGCTACTGATGCTT
CCGACACCCCGCTGGTGACGTGTTGAGTTTATGACAACCACGTTTTACCACAGTCTACTCGGTTCCACGTCTCGATGACTACGAA

4930

SORL1

SORL1-201

SORL1-201

ATTGGTCCAGGTGGGTCAGAAGAGTTAGGAAAGTAGGCAGGCCCTGGCAGTGAGGTTTGAAGGAGAGTTATGCCTTGATTAGATTA
TAACCAGGTCCACCCAGTCTTCTCAATCCTTTCATCCGTCCGGACCGTCACTCCAAACTTCTCTCAATACGGAACCTAATCTAAT

5015

SORL1

SORL1-201

SORL1-201

AGCAGTGGGGCAGGTAGGCCCAGGATGGGATGTGGCAAGAGCAGACAGCAGTGAGTCCGCATCAGGCTTGGAGAAGCAAGAGATG
TCGTACCCCGTCCATCCGGGTCCCTACCCTACACCGTTCTCGTCTGTCTCACTCAGGCCTAGTCCGAACCTCTTCGTTCTCTAC

5100

SORL1

SORL1-201

SORL1-201

ACCAGCCTGGCTGACGGGAAGGAGCAAGAATATGAGTCCCACCTGTGGACTCTTCATTGCAAGGCTGTGACATTGAGAATTTGTT
TGGTCGGACCGACTGCCCTTCTCGTTCTTATACTCAGGGTGGACACCTGAGAAGTAACGTTCCGACACTGTAACCTTTAAACAA

5185

SORL1

SORL1-201

SORL1-201

TTATGGGAGTGTGGAGTCATCGATTGCCTTGGAACGTGGAGTGACACGGGATGGTGAATAAGTAAATGCTCATTGCTTATTTA
AATACCCTCACACCTCAGTAGCTAACGGAACCTTGACCTCACTGTGCCCTACCACTTTATTCAATTTACGAGTAAACGAATAAAT

5270

SORL1

SORL1-201

SORL1-201

CTTATTTGAGTAATTTACTTATTGATACTGCTTTGTCCAGATCATCATGCCCTGGAAACTGGGGCTTACATGGTTCTAGCTCCTC
GAATAAACTCATTAAATGAATAACTATGACGAAACAGGTCTAGTAGTACGGGACCTTTGACCCCGAATGTACCAAGATCGAGGAG

5355

SORL1

SORL1-201

SORL1-201

TTTCAGACCACTTGAAAATTGTCCCATGAGTCAGAGGAAGGAACAGCGCATTGTGACTAGAAAGTTGGGGCAGGTTTCGCAGATGG
AAAGTCTGGTGAACCTTTTAACAGGGTACTCAGTCTCCTTCTTGTGCGGTAACACTGATCTTCAACCCCGTCCAAAGCGTCTACC

5440

SORL1

SORL1-201

SORL1-201

GTCAGGTCAGGGAAATAGGCAGGCATGGAGGGGGCATGTCTGTAGCAGAAGCTGAGTAGCCATCTTTGGCAATGGGGGTCTTTAA
CAGTCCAGTCCCTTTATCCGTCCGTACCTCCCCGTACAGACATCGTCTTCGACTCATCGGTAGAAACCGTTACCCCCAGAAATT

5525

SORL1

SORL1-201

SORL1-201

GGAGCTCCGATCCATCTCAGCCTCTTTTCCCCCTGTTTTTGTGAGGTAGCTAATCCAGATGGCGACTTCCGACTCACAATCGTCA
CCTCGAGGCTAGGTAGAGTCGGAGAAAAGGGGGACAAAACAGTCCATCGATTAGGTCTACCGCTGAAGGCTGAGTGTTAGCAGT

5610

SORL1

SORL1-201

V A N P D G D F R L T I V
ENSE00003463448

SORL1-201

ATTCTCTGTGCTTGATCGTCCCAGGGCTCTGGTCCTCGTGCCCCAAGAGGGGTAAGTGTGGCCCCAAAAGGAAATCAGTCTTGC
TAAGGAGACACGAACTAGCAGGGTCCCGAGACCAGGAGCACGGGGTTCTCCCCATTCACAACGGGGTTTTCTTTAGTCAGAACG

5695

SORL1

SORL1-201

N S S V L D R P R A L V L V P Q E G
ENSE00003463448

SORL1-201

GTCCAATGCTACACTAATAGATTCTCATGGAAACACAGACTGCGGGACAAAACTCTGTTTCTCATGATGGTGGTTGAAATGGTC
CAGGTTACGATGTGATTATCTAAGAGTACCTTTGTGTCTGACGCCCTGTTTTTGGAGACAAAGAGTACTACCACCAACTTTACCAG

5780

SORL1

SORL1-201

SORL1-201

TATTAAGTGAAGTTTGGAGACCACAGCTTAGTCATCGTGGTCAGGTAAGTCCGTTTCGCTTTTTGTTAGCCAGTGTGAGAGTCTC
ATAATTGACTCTTCAAACCTCTGGTGTGGAATCAGTAGCACCAGTCCATTGAGGCAAGCGAAAAACAATCGGTACAGTCTCAGAG

5865

SORL1

SORL1-201

SORL1-201

TTTAGGCATCCAGATGTCTTGCATCTGTGGGTTGTTTCTCTAGAAAAGTTGATGTTAAAAGAGAGCTTCTGTAGACATAGACAGG
AAATCCGTAGGTCTACAGAACGTAGACACCCAACAAGAGATCTTTTCAAACATAATTTTCTCTCGAAGACATCTGTATCTGTCC

5950

SORL1

SORL1-201

SORL1-201

CCTGCTTGGATATTGTGAGAAGCTTTCTCTTGAGTTTCATGCATGGTACAAACATTTAATTCATTCCATCTTTCCCCTGCCTTCCC
GGACGAACCTATAACACTCTTGAAAGAGAAGCTCAAAGTACGTACCATGTTTGTAAATTAAGTAAGGTAGAAAGGGGACGGAAGGG

6035

SORL1

SORL1-201

SORL1-201

AGCATGTGTAGGTTTTCTTACGTACAATCAGTGTGCACTTGGGGAAGGCAAAGGTGCTTTTTTATTAAGTCAATTAAGTGAAGGAAA
TCGTACACATCCAAAAGAATGCATGTTAGTCACACGTGAACCCCTTCCGTTTCCACGAAAAATAATTGAGTAATTGACTTCCTTT

6120

SORL1

SORL1-201

SORL1-201

CATAATTAAGAGGGAAATTCTGGATTTGACATTCTGGCTTTTCTCTCTCGTAGCATTTATGATAGAGAATTGGCACAATTTTTT
GTATTAATTCTCCCTTTAAGACCTAAACTGTAAGACCGAAAAGGAGAGAGCATCGTAAATACTATCTCTTAACCGTGTAAAAAA

6205

SORL1

SORL1-201

SORL1-201

TCAAGGAAAATTCTAAGAGTAATGTATGTACTTGGTTGACAATATTTAGAGAGAACAGCACTTTATGAAAAAATTTGCATTCTT
AGTTCCTTTAAGATTCTCATTACATACATGAACCAACTGTTATAAATCTCTTGTGCGTAAATACTTTTTTTAAACGTAAGAA

6290

SORL1

SORL1-201

SORL1-201

CCTTTTCATTCTTAACCCTTTACCCTCACACTTCCTAGTGGTAATCATTGTTAATAATGTCTTGTGTATCTTTCATGATTGCTTT
GGAAAAGTAAGAATTGGGAAATGGGAGTGTGAAGGATCACCATTAGTAACAATTATTACAGAACACATAGAAAAGTACTAACGAAA

6375

SORL1

SORL1-201

SORL1-201

PCR Forward

ATGCACGCCAAATAGGATTGTAGTG

TACTTATGTACAAGTATTATCTTTAAAACACACACATATACACACACATGCACGCCAAATAGGATTGTAGTGTAGTTACTATTCT
ATGAATACATGTTTCATAATAGAAAATTTGTGTGTGTATATGTGTGTGTACGTGCGGTTTATCCTAACATCACATCAATGATAAGA

6460

SORL1

SORL1-201

SORL1-201

GTACCTTTTTAAACAAACTTAATATGTATTGAAAATAGTTCTGTGTGAGCATATATAGATTTTTAGGTTTTCACAGTATTCTATTA
CATGGAAAATTTGTTTGAATTATACATAACTTTTATCAAGACACACTCGTATATATCTAAAAATCCAAAGTGTGATAAGATAAT

6545

SORL1

SORL1-201

SORL1-201

TATGTACCATAATGTGTCACCTTCCTCTGCTGATTAACATTTAGTTTAAATATACATACATATACATTTCTTTGTATATTATCTTTG
ATACATGGTATTACACAGTGAAGGAGACGACTAATTGTAATCAAATTATATGTATGTATATGTAAAGAAACATATAATAGAAAC

6630

SORL1

SORL1-201

SORL1-201

CATAATTTGATTTTATCTATAGATAAATTCTAGTAAAGGAATTTCCAGGTGAAGGAATTTAAGTAGTTTCAGGTGTTGTCATTAC
GTATTAAGTAAAATAGATATCTATTTAAGATCATTTTCCTTAAAGGTCCACTTCCTTAAATTCATCAAAGTCCACAACAGTAATG

6715

SORL1

SORL1-201

SORL1-201

ATATTGTTATAATAATGCTGAAATAACCAGCCGGATCATTGCAAAGGAGTTTCTGACCTTTTCTGGAGTAGTATTTGAGCTCCCA
TATAACAATATTATTACGACTTTATTGGTCGGCCTAGTAAGCTTTCTCAAAGACTGGAAAAGACCTCATCATAAACTCGAGGGT

6800

SORL1

SORL1-201

SORL1-201

TTTCTCTAGTATTGATGAGGTATGTGTTCTGTCCCATTTTCGCTAGGGTGATGTTCTGGACAGACTGGGGAGACCTGAAGCCTG
AAAGAGATCATAACTACTCCATACACAAGACAGGGGTAAAAGCGATCCCCTACAAGACCTGTCTGACCCCTCTGGACTTCGGAC

6885

SORL1

SORL1-201

SORL1-201

890 895 900
V M F W T D W G D L K P
ENSE00003546837

Sanger Sequencing

CGGAGCAATATGGATGGTTC

GGATTTATCGGAGCAATATGGATGGTTCCTGCTGCCTATCACCTGGTGTCTGAGGATGTGAAGTGGCCCAATGGCATCTCTGTGGA
CCTAAATAGCCTCGTTATACCTACCAAGACGACGGATAGTGGACCACAGACTCCTACACTTCACCGGGTTACCGTAGAGACACCT

6970

SORL1

SORL1-201

SORL1-201

905 910 915 920 925
G I Y R S N M D G S A A Y H L V S E D V K W P N G I S V D
ENSE00003546837

gRNA Protospacer
ATAGAGCGGATCA TGTTCAG

CGACCAGTGGATTTACTGGACGGATGCCTACCTGGAGTGCATAGAGCGGATCA CGTTCAGTGGCCAGCAGCGCTCTGTCAATTCTG
GCTGGTACCTAAATGACCTGCCTACGGATGGACCTCACGTATCTCGCCTAGT GCAAGTCACCGGTCGTTCGCGAGACAGTAAGAC

7055

SORL1

SORL1-201

930 D Q W I Y W T D A Y L E C I E R I T F S G Q Q R S V I L 955

ENSE00003546837

SORL1-201

Donor Template SNV -> REV

Protospacer Sequence

PAM

SNV

CTACGGATGGACCTCACGTATCTCGCCTAGT GCAAGTCACCGGTCGTTCGCGAGACAGTAAGAC

Donor Template SNV -> REV

GACAACCTCCCGCACCCCTATGCCATTGCTGTCTTTAAGGTGAGTCCATTTGTTGCTGCCGGACAGTCTGCTAGAGCGGGTGAGG
CTGTTGGAGGGCGTGGGGATACGGTAACGACAGAAATTCACCTCAGGTAACAACGACGGCCTGTCAGACGATCTCGCCCACTCC

7140

SORL1

SORL1-201

960 D N L P H P Y A I A V F K 970

ENSE00003546837

SORL1-201

Donor Template SNV -> REV

CTGTTGGAGGGCGTGGGGATACGGTAACGACAGAAAT

Donor Template SNV -> REV

AGCATATGAGATCAGGAGCCTGCATCCCTGGGCTTTGCAGAGAAGCTGTTTAACTTCTTAAAGGTTGCCTTTTTCCAAATTTGA
TCGTATACTCTAGTCCTCGGACGTAGGGACCCGAAACGTCTCTTCGACAAATTGAAGAATTTCCAACGGAAAAAGGTTTAACT

7225

SORL1

SORL1-201

SORL1-201

GATAACTTATTTTCAGCCTATGGAGGGATGCCAGGCAGAGGGCGCAAGGGTCCAGGCTCCCCTGCTGTTACATTTCAAAAAGGTT
CTATTGAATAAAAAGTCGGATACCTCCCTACGGTCCGTCTCCGCGGTTCCAGGTTCCGAGGGGACGACAAGTGTAAGTTTTTCCAA

7310

SORL1

SORL1-201

SORL1-201

AAAAGTGAAGGCTCTTCCCATGAACATTCCCAGTTTTGCCCTCAGTGTCAAGTACCTCATTTCAAGGGTGGTGTCTTCATTTTTTG
TTTTCACTTCCGAGAAGGGTACTTGTAAGGGTCAAACGGGGAGTCACAGTCATCGGAGTAAAGTCCCACCACAGAAGTAAAAAAC

7395

SORL1

SORL1-201

SORL1-201

TGCGCTTTGCTCACTTTATTCTCTGATGACTTCCGGTGAGCTCTGCACCACCTATAGTGCCTTGCAGTTCTTTTTTCGACTCTGGA
ACGC GAAACGAGTGAAATAAGAGACTACTGAAGGCCACTCGAGACGTGGTGGATATCACGGAACGTCAAGAAAAAGCTGAGACCT

7480

SORL1

SORL1-201

SORL1-201

CTGAGACCT
PCR Reverse

GAGCAACATGGCTCTTCCCAACTCTGGGAAACAGATTTCAAACCTGAGGGGGTTGGGTTTGTGTCATAAACTTGAATGCTTATCAG
CTCGTTGTACCGAGAAGGGTTGAGACCCTTTGTCTAAAGTTTACTCCCAACCCAAACACAGTATTTGAACTTACGAATAGTC

7565

SORL1

SORL1-201

SORL1-201

CTCGTTGTACCGAGAA

PCR Reverse

ATAGTTTCTTTTGGGCAGTTTCTTCTGTGGGGTTATATGGTGAGGTTTGGATAAAATTGCTGTCTTTGCATTTAAGTAGAATCT
TATCAAAGAAAACCCGTCAAAGAAGACACCCCAATATACCACTCCAAACCTATTTTAACGACAGGAAACGTAAATTCATCTTAGA

7650

SORL1

SORL1-201

SORL1-201

TGATCAGGCTAGTCATTCAGCCAATAAATGTTAGTTGTCTCCTGCCTGGGGGAACTCTTACCCTTAGAGAGAACCAGAATAAAGA
ACTAGTCCGATCAGTAAGTCGGTTATTTACAATCAACAGAGGACGGACCCCTTGAGAATGGGAATCTCTCTTGGTCTTATTTCT

7735

SORL1

SORL1-201

SORL1-201

ACGAAAGAGCTGGACTAATGGGCAAAGGTTTTCTTTTGAATGAAATCTACTGGGATGACTGGTCACAGCTCAGCATATTCCGA
TGCTTTCTCGACCTGATTACCCGTTTCCAAAAGAAAAATCTTACTTTAGATGACCCTACTGACCAGTGTGCGAGTCGTATAAGGCT

7820

SORL1

SORL1-201

N E I Y W D D W S Q L S I F R
ENSE00000532819

SORL1-201

GCTTCCAAATACAGTGGGTCCCAGATGGAGATTCTGGCAAACCAGCTCACGGGGCTCATGGACATGAAGATTTTCTACAAGGGGA
CGAAGGTTTATGTCACCCAGGGTCTACCTCTAAGACCGTTTGGTCGAGTGCCCCGAGTACCTGTACTTCTAAAAGATGTTCCCT

7905

SORL1

SORL1-201

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

ENSE00000532819

SORL1-201

AGAACACTGGTAAGCCAGAGTCTCTTTTGTCTCTGTAGAGTTGATCTCAAGAAAGGGGCTGCGTGTGGCCAATCTCTGCTCA
TCTTGTGACCATTTCGGTCTCAGAGAAGAAAAACAGAGACATCTCAACTAGAGTTCTTTCCCGACGCACACCCGGTTAGAGACGAGT

7990

SORL1

SORL1-201

1015
K N T
ENSE00000...

SORL1-201

GAGTAGGAGCTGGCAGCCTGCATCTTTGTTGTCACGACAACATGCACATTATTTAATTTCTTCCTAATGACATCTTAATTTCTTT
CTCATCCTCGACCCTCGGACGTAGAAACAACAGTGCTGTTGTACGTGTAATAAATTAAGAAGGATTACTGTAGAATTAAGAAA

8075

SORL1

SORL1-201

SORL1-201

TCTAATGATACACAAACAGCTGGAAGACAGCATGCTTTTGCCTGCCTAGAGTGTTGGTGCTTGGTGGGTAATTACACCCTCCTCC
AGATTACTATGTGTTTGTGCGACCTTCTGTCTGACGAAAACGGACGGATCTCACAACCACGAACCACCCATTAATGTGGGAGGAGG

8160

SORL1

SORL1-201

SORL1-201

TGCCCTTGGCCCTGACTGATTGGTGGCGCGGCTTCTGTTGCAGCTGGGAGAGTCCTAACATGTGCTTAATCCCTGTTTGGCATG
ACGGGAACC GGGGACTGACTAACCACCGCGCCGAAGACAACGTCGACCCTCTCAGGATTGTACACGAATTAGGGACAAACCGTAC

8245

SORL1

SORL1-201

SORL1-201

CTTGCAGGAAGAGACTCTGTGCTGGGTGCTCAGATAGTTGTTGCTTCCCTGACAGGGCCTCTTGCTTGTCTCTGGTTGCCAGAT
GAACGTCCTTCTCTGAGACACGACCCACGAGTCTATCAACAACGAAGGACTGTCCCGGAGAACGAACAAGAGACCAACGGGTCTA

8330

SORL1

SORL1-201

SORL1-201

GACCTATTGCTCATTGACCGTACCTACCTCTGCTGGAATGGCACTGTGTAGTTAGGTGTTGTTTTAATTAACTTTTCCACCATG
CTGGATAACGAGTAACTGGCATGGATGGAGACGACCTTACCGTGACACATCAATCCACAACAAAATTAATTGAAAAGGGTGGTAC

8415

SORL1

SORL1-201

SORL1-201

AAACCCTAAACCCCATGAAGAAAAGAGATGGTCTTTTTTATTCCCGATAGTTTTACCAGTGTCTAGCACTTTGTAGGTGCTCAAT
TTTGGGATTTGGGGTACTTCTTTCTCTACCAGAAAAAATAAGGGGCTATCAAAATGGTCACAGATCGTGAACATCCACGAGTTA

8500

SORL1

SORL1-201

SORL1-201

TCATATTTGTTGAAAAGAATAAGGGATGAAAAGGGAGGGGAAGAATTGCAGTGGGTGCAGACAGTAGCTGTCTTAGAGATCTACTG
AGTATAAACAACTTTCTTATTCCCTACTTTTCCCTCCCTTCTTAACGTCACCCACGCTCTGTGCATCGACAGAATCTCTAGATGAC

8585

SORL1

SORL1-201

SORL1-201

GGTGAGGCTTCAAGAACTGCTATGAGGCTTTGACCTGCTAGTCCTGGAGTCTGAGACTATTCAGTGGAAAGCCTTTATCATTTC
CCACTCCGAAGTTCTTGACGATACTCCGAAACTGGACGATCAGGACCTCAGACTCTGATAAGTCACCTTTCGGAAATAGTAAAGT

8670

SORL1

SORL1-201

SORL1-201

TGACTGCTCTTTGATTTTGCTTATCTCCCAGCCATACTATTGATTCTAGAGGAGAAAGATCAGAGGATTACCAGGAAGAATAGTC
ACTGACGAGAACTAAAACGAATAGAGGGTCGGTATGATAACTAAGATCTCCTCTTTCTAGTCTCCTAATGGTCTTCTTATCAG

8755

SORL1

SORL1-201

SORL1-201

CCTTTAAGAATTTCCCTCTTTATCTCAGCAGGATTAATGGCATCCTGGGTTTGCTGATTCTCCTTTATTGACAAACTGCTAAGT
GGAAATCTTAAAGGGAGAAATAGAGTCGTCCTAATTTACCGTAGGACCCAAACGACTAAGAGGAAATAACTGTTTGACGATTCA

8840

SORL1

SORL1-201

SORL1-201

TTTCTGTTCTTAACCTGGAATGTTGATATTGTTTTATGGTTCTTGGCTGACCCTATACTAGGAGAAAATTGACAGGGGAAATAATA
AAAGACAAGAATTGACCTTACAACCTATAACAAAATACCAAGAACC GACTGGGATATGATCCTCTTTTAACCTGTCCCTTTATTAT

8925

SORL1

SORL1-201

SORL1-201

CTGTTATAGATATCATTGTTATCCTCTTGGGATTGTGAAGATAGCATGAGAACACCCTGGGAAAACCTATAAAGTGCTTACAAAT
GACAATATCTATAGTAACAATAGGAGAACCCTAACACTTCTATCGTACTCTTGTGGGACCCTTTTGATATTTACAGAAATGTTTA

9010

SORL1

SORL1-201

SORL1-201

GTAAGACGATATTATTTGTTATGTCTTCAACCTGACCTGTGAGGTAGGGAAGGCTGGTATTATGATCCATGGTTTATAGATTAG
CATTCTGCTATAATAACAATACAGAAGTGGTGACTGGACACTCCATCCCTTCCGACCATAATACTAGGTACCAAATATCTAATC

9095

SORL1

SORL1-201

SORL1-201

GGAATTAATCTCAGATATGAATTAGCTTTCCCAAATATCCTCACTAGTTTAGGGGCTGGCCTTTTGTGCAATTCTGCCGCTA
CCTTAATTTAGAGTCTATACTTAATCGAAAGGGTTTTATAGGAGTGATCAAATCCCCGACCGGAAAAACAACGTTAAGACGGCGAT

9180

SORL1

SORL1-201

SORL1-201

AATGGAGAAGTCACATTCTTTCTTAGAGGAGGCACCTGTTTTAGAATCAGGAGAGTTGAAGGAATCTTGCTTCTCAGCTCCAGTG
TTACCTCTTCAGTGTAAGAAAGAATCTCCTCCGTGGACAAAATCTTAGTCCTCTCAACTTCCTTAGAACGAAGAGTCGAGGTCAC

9265

SORL1

SORL1-201

SORL1-201

ACTGAAATCTTCAGACCTTTGTTTAATGGAGGACATCCACCCCTACTGATCTGACTTGCTAGCTAGCAGAGTGGATTTTTAGTAT
TGACTTTAGAAGTCTGGAAACAAATTACCTCCTGTAGGTGGGGATGACTAGACTGAACGATCGATCGTCTCACCTAAAAATCATA

9350

SORL1

SORL1-201

SORL1-201

TTCTCCAAGTGGATTTTTAGCATTCTCCATGTTACCACTTAGTCCAGAAGAGTGGGTCTTCATTTTTACAAGTGCTTGTATGCA
AAGAGGTTACCTAAAAATCGTAAAGAGGTACAATGGTGAATCAGGTCTTCTCACCCAGAAGTAAAAATGTTACGGAACATACGT

9435

SORL1

SORL1-201

SORL1-201

TGTGCTTGTGTTGATTTGCACACAGGAGCTTCTGAAACACTGTGTGCAGATGAAGCCAGTGGCTACCCGGTCACAACCTTACTTCCC
ACACGAACAAACTAAACGTGTGTCTCGAAGACTTTGTGACACACGTCTACTTCGGTCCACCGATGGGCCAGTGTTGAATGAAGGG

9520

SORL1

SORL1-201

SORL1-201

AGTCTTGACTGTCCACTTCATCCCAAGAACTTGGGCACAGCTGACATGCAGTCACACCTGTGACTGAGGAGCAGTGCGGGAGGAG
TCAGAACTGACAGGTGAAGTAGGGTTCTTGAACCCGTGTCGACTGTACGTGAGTGTGGACACTGACTCCTCGTCACGCCCTCCTC

9605

SORL1

SORL1-201

SORL1-201

AGAGTTTGTGGTCTCAGCACATGCAAACGTGGTGTCTTGGTGCCAGTCAGACAGGTCTGCAATCCTCACCTTAGGTGTAGTTTCC
TCTCAAACACCAGAGTCGTGTACGTTTGCACCACAGAACCACGGTCAGTCTGTCCAGACGTTAGGAGTGAATCCACATCAAAGG

9690

SORL1

SORL1-201

SORL1-201

CTTTCATGCCTCAAAGAGTCATCTTTCATTTAAGTTAGCCAGAGTCATTTTGGGGCCCAGAGTGAGGTCTGGATAGATGACAGGCT
GAAAGTACGGAGTTTCTCAGTAGAAGTAAATTCAATCGGTCTCAGTAAAACCCCGGGTCTCACTCCAGACCTATCTACTGTCCGA

9775

SORL1

SORL1-201

SORL1-201

GGTTTAAAAGGGAGATATGTATTAGCAGGGCATAGTGGCACATGCCTGTAGTCTCAGCTCCTCAGGAGGCGGAGGTGGGAGCATC
CCAAATTTTCCCTCTATACATAATCGTCCCGTATCACCGTGTACGGACATCAGAGTCGAGGAGTCCTCCGCCTCCACCCTCGTAG

9860

SORL1

SORL1-201

SORL1-201

ACCTGAGCTCGGGAGGTTGAGGCTGCAGTTAGCCAAGGTCGTGCTGCTGCACTCCATCCTGGGTGACAGAGTGAGACCCTGTCAC
TGGACTCGAGCCCTCCAACCTCCGACGTCAATCGGTTCCAGCACGACGACGTGAGGTAGGACCCACTGTCTCACTCTGGGACAGTG

9945

SORL1

SORL1-201

SORL1-201

CGAAAAAAAAAAAAAAAAAGGCTGGGGGAGATCTGTGTTGGTGAGTAGAACACAGACCTGGACCTGTGCATGGGCGGCTGTGACT
GCTTTTTTTTTTTTTTTTTTCCGACCCCTCTAGACACAACCACTCATCTTGTGTCTGGACCTGGACACGTACCCGCCGACACTGA

10,030

SORL1

SORL1-201

SORL1-201

GTCCCTTTGGCCATGGCCAGTTGTCGCCTCTCTGCTCCTTTCTGTTTGCCTTTGGGATTTTCTCTTGCTGTCTTTGGTTGTGAG
CAGGGAAACCGGTACCGGTCAACAGCGGAGAGACGAGGAAAGACAAACGGAAACCCTAAAAGAGAACGACAGGAAACCAACTC

10,115

SORL1

SORL1-201

SORL1-201

CAGGATACTTCCAGGAGACCTACTGCCTCCAAACACAGGGCTGGAGAAAGACGTTTTTGTCTTTCTCTGCAGCCCAGTTTGGGTC
GTCCTATGAAGGTCCTCTGGATGACGGAGGTTTGTGTCCCGACCTCTTTCTGCAAAAACAGAAAGAGACGTCGGGTCAAACCCAG

10,200

SORL1

SORL1-201

SORL1-201

AAATCAAAGCTTTTGCAGTGGTGTCTGGCTGTCAGCACTGTCTATGAGCACTCCGCACCTCTTGGCCTTGAACCTTGTGTTGCTCTA
TTTAGTTTCGAAAACGTCACCACAGACCGACAGTCGTGACAGATACTCGTGAGGCGTGGAGAACCAGAACTTGAACAAACGAGAT

10,285

SORL1

SORL1-201

SORL1-201

ACCTGCTTGCTTTTTTGGACACTGATAGGACACTTGCTTTTTTGGACATTGTATTACAGATCCACGGTGTGTGTTGGATCTAGC
TGGACGAACGAAAAAACCTGTGACTATCCTGTGAACGAAAAAACCTGTAACATAATGTCTAGGTGCCACACACAACCTAGATCG

10,370

SORL1

SORL1-201

SORL1-201

ACTTGGAGAAATGCTAAAAATCCACTCTGCTAGCTAGCAAGTCAGATCAGTAGGGGTGGATGTCCTCCATCAAGCAAGGGCCTGA
TGAACCTCTTTACGATTTTTAGGTGAGACGATCGATCGTTTCAGTCTAGTCATCCCCACCTACAGGAGGTAGTTTCGTTCCCGGACT

10,455

SORL1

SORL1-201

SORL1-201

ATATTTTCAGTCACTGGAGCTGAGAAGCAAGATTCCTTCAACTCTCCTTATTTTTAAACAGGTGACTCCTCTAAGAAAGAATGTGA
TATAAAGTCAGTGACCTCGACTCTTCGTTCTAAGGAAGTTGAGAGGAATAAAATTTGTCCACTGAGGAGATTCTTTCTTACACT

10,540

SORL1

SORL1-201

SORL1-201

CTCCTGTCCATCTTTATTATTTTTGTTGTCTCCTCCTAACACATTCGGGACTTTCTACAGTAGTCTCCTGCTTATTTGCCATTTT
GAGGACAGGTAGAAATAATAAAAAACAACAGAGGAGGATTGTGTAAGCCCTGAAAGATGTCATCAGAGGACGAATAAACGGTAAAA

10,625

SORL1

SORL1-201

SORL1-201

GCTTTCTGTGATTTTCAGCTACCTGCGGTCAACCACTGTCCAAAAATATATATGGAAGATTCCAGAAATAACAATGTATAAGATT
CGAAAGACACTAAAGTCGATGGACGCCAGTTGGTGACAGGTTTTTATATATACCTTCTAAGGTCTTTATTTGTTACATATTCTAA

10,710

SORL1

SORL1-201

SORL1-201

TAAATTGCTTGCTGTTCTGAATAGTGTGATGAAATCTTGTACTGTCTCCTCCCTGTCCCACCTGGGATGTGAATCCTCCCTTTGT
ATTTAACGAACGACAAGACTTATCACACTACTTTAGAACATGACAGAGGAGGGACAGGGTGGACCCTACACTTAGGAGGGAAACA

10,795

SORL1

SORL1-201

SORL1-201

CCAGCGTCTCATGCTGTTGATGCTGCCGGCTCATTAGTCCCTTTAGGAGCCGGCTGGGTTATCAGGGTGTCAAAGTACTGCAGTT
GGTCGCAGAGTACGACAACCTACGACGGCCGAGTAATCAGGGAAATCCTCGGCCGACCCAATAGTCCCACAGTTTCATGACGTCAA

10,880

SORL1

SORL1-201

SORL1-201

CTTGTACGCAAGGAACCCCTTATTTTTACTTTCATGATGACCCTACACCTCAAGAGTAGTGATTCCAGTAATTTGGATATGCCAAAGG
GAACATGCGTTCCCTTGGGAATAAAATGAAGTACTACTGGGATGTGGAGTTCTCATCACTAAGGTCATTAAACCTATACGGTTTTCC

10,965

SORL1

SORL1-201

SORL1-201

GAGGTTGTAAAGTGCTTCCTTTAGGGAAAGGGTGAAAGTTCTAGACTTAATAAGGGAGGAAAAAATCTTACACCGAGTTTGCT
CTCCAACATTTACGAAGGAAATCCCTTTCCCACTTTCAAGATCTGAATTATCCCTCCTTTTTTTTAGAATGTGGCTCAAACGA

11,050

SORL1

SORL1-201

SORL1-201

AAGATCTGCTGTAAGAACGAACCTTCTATCTCTGAAATTGTAAAGAAAGAAAAAGAAATTCATGCACAGTATAGGTTTGGTCCTA
TTCTAGACGACATTCTTGCTTGGAAAGATAGAGACTTTAACATTTCTTTCTTTTTCTTTAAGTACGTGTCATATCCAAACCAGGAT

11,135

SORL1

SORL1-201

SORL1-201

TCTGCAGTTTCAGGTGTCAGCTAGGGGTCTTGGAAATTGGGGGTTTTTGGAAATAAGAGGGGACTACTATATTAACCAAGTGTTAAAT
AGACGTCAAAGTCCACAGTCGATCCCCAGAACCTTAACCCCCAAAACCTTATTCTCCCCTGATGATATAATTGGTTCACAATTTA

11,220

SORL1

SORL1-201

SORL1-201

AATAATAATTGATAGTAACTACATGTATTGAGGGGTTGCTGTGTTATAAGTACCACAGTAATGTGCTTTGTGGGCTTGATAACC
TTATTATTAACATATCATTGATGTACATAACTCCCCAACGACACAATATTCATGGTGTCATTACACGAAACACCCGAACATATTGG

11,305

SORL1

SORL1-201

SORL1-201

TCACCTTCGTCTTCCCAAAGACTTCTATATGTACTATCAATATTTCCATTTTATAGGTGAGAATATGAAAGTCTGGTTTAGTAACT
AGTGAAGCAGAAGGGTTTCTGAAGATATACATGATAGTTATAAAGGTAAAATATCCACTCTTATACTTTTCAGACCAAATCATTGA

11,390

SORL1

SORL1-201

SORL1-201

TGTGTAGGTCACACTTTTAGTAAGTGGTAAGAATTTGCACTGTGGCCCGTTGACTTCAAAGCCTGAACTTCGATAAAACCACCCG
ACACATCCAGTGTGAAAATCATTACCATTTCTTAAACGTGACACCGGGCAACTGAAGTTTCGGACTTGAAGCTATTTTGGTGGGC

11,475

SORL1

SORL1-201

SORL1-201

GCTCTGCTCCCTCTGTCATGTGTTGCTAGAAATAGCAGTGCCTGGTAGTATGACAGCAGTTTCAGAAGTACTGTTCTAGATTTTGA
CGAGACGAGGGAGACAGTACACAACGATCTTATCGTACACGGGACCATCATACTGTCGTCAAGTCTTCATGACAAGATCTAAAAC

11,560

SORL1

SORL1-201

SORL1-201

TTGATGATGGTTCATAATAAAAAATGTTGTTTCAGTTGCAACATTTATCAATTTGAAATATTTGGTCCTTTATAGCTAGCTGGTTTT
AACTACTACCAAGTATTATTTTTACAACAAGTCAACGTTGTAATAGTTAAACTTTATAAACAGGAAATATCGATCGACCAAAA

11,645

SORL1

SORL1-201

SORL1-201

TATTTTTTATTTGTTTAGTTTTTGGAGACAGAGTCTCGTTCTGTTACCCCGGCTGGAGTGCAGTGATGTGATCTTGGCTCACTG
ATAAAAAATAAACAAATCAAAAAACCTCTGTCTCAGAGCAAGACAATGGGGCCGACCTCACGTCACTACACTAGAACCGAGTGAC

11,730

SORL1

SORL1-201

SORL1-201

CAACCTCTGCCTCCTGGGTTCAAGCAATTCTCATGCCTCAGCCTCCTAAGTAGCTGGGACTAAAGGCATGTGCCACCATGCCTGG
GTTGGAGACGGAGGACCCAAGTTCGTTAAGAGTACGGAGTCGGAGGATTCATCGACCCTGATTTCCGTACACGGTGGTACGGACC

11,815

SORL1

SORL1-201

SORL1-201

CTAATTTTTTGTATTTTAGTAGAGATTGGGTTTCACCATGTTGCCAGGCTGGTCTTGAACCTCTGAGCTCAGGCAATCTGCACG
GATTAATAAACATAAAATCATCTCTAACCCAAAGTGGTACAACGGGTCCGACCAGAACTTGAGGACTCGAGTCCGTTAGACGTGC

11,900

SORL1

SORL1-201

SORL1-201

CCCCGGCCTCCCAAAGTGCTAGGATTTACAGGTGTGAGCCACTGTGTCTGGCCACTAGCTGGTTTTTAAATGGTATAACTGGAAT
GGGGCCGGAGGGTTTTACGATCCTAAATGTCCACACTCGGTGACACAGACCGGTGATCGACCAAAAATTTACCATATTGACCTTA

11,985

SORL1

SORL1-201

SORL1-201

TTATTCTTTGTAAAGTGTGTTTTTCTTTAAAGAGGTTACTTTACAAGATTGTTGATGTATTTCAGTTGCTCCTGCGATGGCTCTT
AATAAGAAACATTTACACAAAAAAGAAATTTCTCCAATGAAATGTTCTAACAACCTACATAAGTCAACGAGGACGCTACCGAGAA

12,070

SORL1

SORL1-201

SORL1-201

GGAGCTTTGGAATTCTTTTGCAGTTTTTGAATTCTCCTTTAGAGCCTGCAGTAAGTATGTGCTTTTAAGTATCTATAATGAGGGC
CCTCGAAACCTTAAGAAAACGTCAAAACCTTAAGAGGAAATCTCGGACGTCATTTCATACACGAAAATTCATAGATATTACTCCCG

12,155

SORL1

SORL1-201

SORL1-201

ACATATTTATTATTTGAGGTAGATTTGATTTTGATAATTGCCAAGTGTATAGATACTTGAGATGATGACATTTTTGGCTCCTAAA
TGTATAAATAATAAACTCCATCTAAACTAAAACCTTAACGGTTCACATATCTATGAACTCTACTACTGTAAAAACCGAGGATTT

12,240

SORL1

SORL1-201

SORL1-201

GTATTCCTGGAGGAATTTTCCAAACAGGAAATGTGAAAATGTTCTGAACATGCCCAGTGAAGACATCACGGGGCTATGTGTTTGA
CATAAGGACCTCCTTAAAAGGTTTGTCTTTACACTTTTACAAGACTTGTACGGGTCACCTCTGTAGTGCCCCGATACACAACT

12,325

SORL1

SORL1-201

SORL1-201

TCTTCTAAGGGAATGTCTTTGAAGATGATTGTCCACTCTTCACATTGAGATAACGGTTTTTCATATTGCCTGGTCCACTCAAGACA
AGAAGATTCCCTTACAGAACTTCTACTAACAGGTGAGAAGTGTAACTCTATTGCCAAAAGTATAACGGACCAGGTGAGTTCTGT

12,410

SORL1

SORL1-201

SORL1-201

ATTGTCATCCTGTATAAAGGGTCTGTGGCTGTGGTAGAACTGCCATCATAGGAGTTGGTGAATTACCCTTCCATCTTCTTCCAGC
TAACAGTAGGACATATTTCCAGACACCGACACCATCTTGACGGTAGTATCCTCAACCACCTAATGGGAAGGTAGAAGAAGGTCG

12,495

SORL1

SORL1-201

SORL1-201

TTCTCTCTGATGCAGCTCTCCCATTTTCCATTCTCTGGCTTCAGACTAGCCTAGACATTCTGCCCCTGCCTACCTCTTAGGATC
AAGAGAGACTACGTGAGAGGGTAAAAGGTAAGAGACCGAAGTCTGATCGGATCTGTAAGGACGGGGACGGATGGAGAATCCTAG

12,580

SORL1

SORL1-201

SORL1-201

AGTGACTTGGTTAGCTTGTTTTGCAGTTTTGCCCTGGTTACTGCCTCAGAGTACAGTTTTCATACATTTCTGCCTAGATCAGCCTC
TCACTGAACCAATCGAACAAAACGTCAAACGGGGACCAATGACGGAGTCTCATGTCAAAGTATGTAAGACGGATCTAGTCGGAG

12,665

SORL1

SORL1-201

SORL1-201

CTGAAATATGATACCCCATTTTGGAGTTCTCTACTCTTAGCTCTTCTTGCTTGTGTTTGGATAGGAATATTTGCTCTGCATATGAAAA
GACTTTTATACTATGGGGTAAAACTCAAGAGATGAGAATCGAGAAGAACGAACAAACCTATCCTTATAAACGAGACGTATACTTTT

12,750

SORL1

SORL1-201

SORL1-201

GGTTAGTGAAATGATTTTACAGACATGATCCCTGTGAAAAAATCATCCTGTAATAGAGTAGTTTTTTTTTATTTGTTTCGTTTTGT
CCAATCACTTTACTAAAATGTCTGTACTAGGGACACTTTTTTTAGTAGGACATTATCTCATCAAAAAAATAAACAAGCAAAAA

12,835

SORL1

SORL1-201

SORL1-201

TTGTTTGTGTTGTTTTGAGACAGGCTCTGGCTCTGTTACCCAGGCTGGAGTGCAGTGGCGCCATCTCAGCTAACTGCAGCCTCTG
AACAAACAAACAAAACTCTGTCCGAGACCGAGACAATGGGTCCGACCTCACGTCACCGCGGTAGAGTCGATTGACGTCGGAGAC

12,920

SORL1

SORL1-201

SORL1-201

TCTCCTGGGCTTAAGCAATCTTCCCACTTCAGCCTCTGAAGTGGCTGGGATCACAGATGTGTACCCGGCTAATTTTGCTTATTTT
AGAGGACCCGAATTCGTTAGAAGGGTGAAGTCGGAGACTTCACCGACCTAGTGTCTACACATGGGCCGATTAAAACGAATAAAA

13,005

SORL1

SORL1-201

SORL1-201

TTTTTTGTGGAGGCGGTCTTCACTATGTTGCTCAGGGTGGTCTCGAACTCCTGGGCTCGAGTGATCCTCCACCTCGGCCTCCCA
AAAAAACACCTCCGCCAGAAGTGATACAACGAGTCCCACCAGAGCTTGAGGACCCGAGCTCACTAGGAGGGTGGAGCCGGAGGGT

13,090

SORL1

SORL1-201

SORL1-201

AACTGCTGGGATTACAGATGTGAGCCACTGCACCCAGCCGGTAATAGAGTATTTTAAAAATAACATCATATTCCATTATTGTTTCAG
TTGACGACCCTAATGTCTACACTCGGTGACGTGGGTGGGCCATTATCTCATAAAATTTTATTGTAGTATAAGGTAATAACAAGTC

13,175

SORL1

SORL1-201

SORL1-201

GATCTTGGAACATTGAGTGATATATTGTTCTTTGAATACAAAACACATGTTCCACATCCTTGTGTTGAGTTGTTTCTCATGAGTG
CTAGAACCTTGTAACCTCACTATATAACAAGAACTTATGTTTTGTGTACAAGGGTGTAGGAACAACTCAACAAAGAGTACTCAC

13,260

SORL1

SORL1-201

SORL1-201

GTGGCTCTATGTCAATTCTGCATTCCCTCTTGTAGCCAGTGGCCTGTACCTTTGAACTAAAGGAGCCATCTGTGCCCACTAATGG
CACCGAGATACAGTTAAGACGTAAGGGGAGAACATCGGTCACCGGACATGGAACTTGATTTCTCGGTAGACACGGGTGATTACC

13,345

SORL1

SORL1-201

SORL1-201

ATCAGAGTGAAGGGATGTCTGGGACTTCTGCTCTAGTCAGCTGGTTAGTCTGCTATGGTAATTAAGCTGTTATGATTGATTATTT
TAGTCTCACTTCCCTACAGACCCTGAAGACGAGATCAGTCGACCAATCAGACGATACCATTAATTCGACAATACTAATAATAA

13,430

SORL1

SORL1-201

SORL1-201

ACTGAACCTTTTGGACTGTTTCATCATGTGGACTTCCCTTCCCTCTGGAGGTGTATGTTTTCTCTCTATTTACTGAATCTTTTGGG
TGACTTGGAAAACCTGACAAAAGTAGTACACCTGAAGGGGAAGGAGACCTCCACATACAAAAGAGAGATAAATGACTTAGAAAACCT

13,515

SORL1

SORL1-201

SORL1-201

ATGTTTCATCATATGAACCTCCCTTCCCTCTGGATGTGTGTGTTTTCTCTTTGGTAATACCTCTTACTCTTTTCCTTGGCATCATA
TACAAAGTAGTATACTTGGAGGGAAGGAGACCTACACACACAAAAGAGAAAACCATTTATGGAGAATGAGAAAAGGAACCGTAGTAT

13,600

SORL1

SORL1-201

SORL1-201

ATAACGTTGTTGCCATAGCATTGTGATTTTTATTTTTATTTGTAATGTAAATTAACCAATGATGTGCCACACACCCAAAAGCTAC
TATTGCAACAACGGTATCGTAACACTAAAAATAAAAAATAAACATTACATTTAATTGGTTACTACACGGGTGTGTGGGTTTTCGATG

13,685

SORL1

SORL1-201

SORL1-201

TGCGTATATTATCCATATCGACACTGATTATCATTGAACTTCGTCTAACCTGTAGGCCAGGATAGGCATGGCTTAGATGAAT
ACGCATATAATAGGTATAGCTGTGACTAATAGTAAGTACTTGAAGCAGATTGGACATCCGGTCCTATCCGTACCGAATCTACTTA

13,770

SORL1

SORL1-201

SORL1-201

GCTTGGCTGGGTGGCAACAGATGATTTGGATATGGTGCTGAAGTGTGGGAGGGCATCTCTGTCCATGACATAGCACGAATGAAGA
CGAACCGACCCACCGTTGTCTACTAAACCTATACCACGACTTCACACCCTCCCGTAGAGACAGGTACTGTATCGTGCTTACTTCT

13,855

SORL1

SORL1-201

SORL1-201

ATTAGCAATTGAGTTTTATCTAAGTTTTATGTTTCATTTTTCCCATTTTCATGATTAATAATTGCAGTCAAAAAGAAAAAACATGA
TAATCGTTAACTCAAAAATAGATTCAAAAATACAAGTAAAAAGGGTAAAAAGTACTAATTATTAACGTCAGTTTTCTTTTTTGTACT

13,940

SORL1

SORL1-201

SORL1-201

TTTCATAGTTTCTGTGACCCCATAGTTGTATCATGTTTCAGATTGTTATAAAATGGTTTATGCATCTTCTTACCTGCCATCCCCG
AAAGTATCAAAGACACTGGGGTATCAACATAGTACAAAAGTCTAACAATATTTTACCAAATACGTAGAAGAATGGACGGTAGGGGC

14,025

SORL1

SORL1-201

SORL1-201

GAACGATGTAGGGGATAGGATGGCACTTTTGCCATCCTCGTTTCATCCACAAAGGCTCCTTCTCAAGAGTGCAGTGGTGGATTTTA
CTTGCTACATCCCCTATCCTACCGTGAAAACGGTAGGAGCAAGTAGGTGTTTCCGAGGAAGAGTTCTCACGTCACCACCTAAAAT

14,110

SORL1

SORL1-201

SORL1-201

CGAACTCTCTCCGGTGCTGCCTTTAGTAAGCTGAACCAGAGAAAAGATTGGCAGGAGTGGGCTAGATCAGCATGAACTAGTCCTT
GCTTGAGAGAGGCCACGACGGAAATCATTGACTTGGTCTCTTTTCTAACCGTCTCACCCGATCTAGTCGTACTTGTATCAGGAA

14,195

SORL1

SORL1-201

SORL1-201

ACCTGAACACATTGCACAGCAGTGGCTGATGAGTACTGTGGTTGGCTCCTCCTTTAGCTCTTGAGGGGCACTCTGGCACAAAGGA
TGGACTTGTGTAACGTGTGTCGTCACCGACTACTCATGACACCAACCAGGAGGAAATCGAGAACTCCCCGTGAGACCGTGTTCCT

14,280

SORL1

SORL1-201

SORL1-201

ATTGAGAAGGGGAGGCCTGGATTTTTGTCTGGGCCACCATTAAACCAGGTGTATGTTCTAATTAAGGCCTTTGGGGCCCTAAGG
TAACTCTTCCCCTCCGGACCTAAAAACAGGACCCGGGTGGTAATTGGTCCACATACAAGATTAATTCCGGAAACCCCGGGATTCC

14,365

SORL1

SORL1-201

SORL1-201

AGCAGAAACCCACTCAAGCTAGCTCAAGTGAATGGTTTTATGGAATGAATAAAGGAGCCCAAAGATGAAAGTCTAGGAGAGCCTC
TCGTCTTTGGGTGAGTTCGATCGAGTTCACCTACCAAAAATACCTTACTTATTTCTCGGGTTTCTACTTTCAGATCCTCTCGGAG

14,450

SORL1

SORL1-201

SORL1-201

ATGGGGACTGGAGCTGTTCTTTCTCTTTCCCTCTCATTAGGCCTCTTCTCTCTGTAAGCCTCTTTCTTTTAAAAAAAAAATTAT
TACCCCTGACCTCGACAAGAAAAGAGAAAAGGGAGAGTAATCCGGAGAAGAGAGACATTCGGAGAAAAGAAAAATTTTTTTTTTAATA

14,535

SORL1

SORL1-201

SORL1-201

TCGGAATTTTGAAGGCAATGTTCAACTATATTATAGCCACTAGTGTTGTAATTGAGAAGTCCAAAGACATTCTGGTTCTTTTTTA
AGCCTTAAAACTTCCGTTACAAGTTGATATAATATCGGTGATCACAACATTAACTCTTCAGGTTTCTGTAAGACCAAGAAAAAAT

14,620

SORL1

SORL1-201

SORL1-201

AATTAAAAAAAAAAATTTTTTAAAGGGATAGGATCTTGCTATATTGCCAGGCTGGATTTCGAGCTACCAGGCTCAAGTGATCCT
TTAATTTTTTTTTTAAAAAAAAATCCCTATCCTAGAACGATATAACGGGTCCGACCTAAGCTCGATGGTCCGAGTTCAGTAGGA

14,705

SORL1

SORL1-201

SORL1-201

CCTGCCTCAGCCTCCTGAGTAGCTGGGGCTACAGGTGCGTGCTGCCATGCCTGGCCTCCTTAAGTCTCTTTTAGTCTCCTGACGG
GGACGGAGTCGGAGGACTCATCGACCCCGATGTCCACGCACGACGGTACGGACCGGAGGAATTCAGAGAAAATCAGAGGACTGCC

14,790

SORL1

SORL1-201

SORL1-201

TCTGCAGACTGAGCTTATCTGCATACCCAGAGTTTTGACTTCCACACGGTTTTGGCTTGCCATGTGCCACTTCAACACCCATGCT
AGACGTCTGACTCGAATAGACGTATGGGTCTCAAACTGAAGGTGTGCCAAAACCGAACGGTACACGGTGAAGTTGTGGGTACGA

14,875

SORL1

SORL1-201

SORL1-201

CTGTGACCCTTTCCCTGGCTCCAGCTCCTTGGTTGCTTTCTTGTCTTTTCAAGTGACCCAATTACAAATTTCCAGGAGGAACCCTGC
GACTGTTGGGAAAAGGGACCGAGGTCGAGGAACCAACGAAAAGAACAGAAAAGTCACTGGGTTAATGTTTAAGGGTCTCCTTGGGACG

14,960

SORL1

SORL1-201

SORL1-201

TGCCTGGCTTGGCTCTGGGGCAGTCTGATCTGGCTGAAGACAGGATGCAAGTCACTGGTTATACTGAGCAGAAGTTTTTCAGCACA
ACGGACCGAACCGAGACCCCGTCAGACTAGACCGACTTCTGTCTACGTTTCAAGTCACTGACCAATATGACTCGTCTTCAAAAGTCGTGT

15,045

SORL1

SORL1-201

SORL1-201

GTAGGCGCCCCAAAGCTTGCCACTTGACCCCTTGAGAGCTTCTCGCTGTCTCTTCCGTAAGACGAGGAGGTTGCAAGTGGGTCTCCT
CATCCGCGGGGTTTCGAACGGTGAACCTGGGAACCTCTCGAAGAGCGACAGGAAAAGGCATTCTGCTCCTCCAACGTCACCCAGAGGA

15,130

SORL1

SORL1-201

SORL1-201

TCTTGTATTTCAGTACCTCCCTCATGGTGTGTATTAACCTACCTGCTGCTGTTTTGTCTTCCCTCCAGGAAGCAATGCCTGTGTGCC
AGAACATAAGTCATGGAGGGAGTACCACACATAATTGGATGGACGACGACAAAACAGAAGGGAGGTCCTTCGTTACGGACACACGG

15,215

SORL1

SORL1-201

1020
G S N A C V P
ENSE00003533392

SORL1-201

CAGGCCATGCAGCCTGCTGTGCCTGCCCAAGGCCAACAAACAGTAGAAGCTGCAGGTGTCCAGAGGATGTGTCCAGCAGTGTGCTT
GTCCGGTACGTCGGACGACACGGACGGGTTCCGGTTGTTGTTCATCTTCGACGTCCACAGGTCTCTTACACAGGTCGTCACACGAA

15,300

SORL1

SORL1-201

1025 1030 1035 1040 1045 1050
R P C S L L C L P K A N S R S C R C P E D V S S S V L

ENSE00003533392

SORL1-201

CCATCAGGGGACCTGATGTGTGACTGCCCTCAGGGCTATCAGCTCAAGAACAATACCTGTGTCAAACAAGGTACTTCCCTTTTTTC
GGTAGTCCCCTGGACTACACACTGACGGGAGTCCCGATAGTCGAGTCTTGTATTGGACACAGTTTGTTCATGAAGGGAAAAAG

15,385

SORL1

SORL1-201

1055 1060 1065 1070
P S G D L M C D C P Q G Y L K N N T C V K Q G T S L F

ENSE00003533392

SORL1-201

TTTTTGCCTGTCATCCTCCTTCTTTGTTTCTGCTCCCCGCCAGGGGAGGGAGGGATAGCTCTCTGTTTCTAACCTTTTTCGT
AAAAAACGGACAGTAGGAGGAAGGAAACAAAGGACGAGGGGCGGTCCCCTCCCTCCCTATCGAGAGACAAAGGATTGGAAAAGCA

15,470

SORL1

SORL1-201

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

GTTATTGGAAAAAGTCCAAGGTA AAAATCAAACCTACCAGATACTCATAAGAATACTGGTTTGGGTTCTAAGTCTCGGTAAGGGT
CAATAACCTTTTTCAGGTTCCATTTTTAGTTTGGATGGTCTATGAGTATTCTTATGACCAAACCAAGATTTCAGGACCATTCCCA

15,555

SORL1

SORL1-201

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

CAAAGAGGCCCTTCAGTCTCACTCAGAACAGGCCTATGCTGTACCTTTCTAAGTAGTAGCTGTGGTTTTTGGTTTTTCATGTCAGA
GTTTCTCCGGGAAGTCAGGAGTGAGTCTTGTCCGGATACGACATGGAAGATTTCATCATCGACACCAAAAACCAAAGTACAGTCT

15,640

SORL1

SORL1-201

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

TGGCACAGGCTTTCTTCAGGGTCTC 3'
-----|-----|-----|-----|
ACCGTGTCCGAAAGAAGTCCCAGAG 5'

15,665



Feature	Location	Size		Type
✓ SORL1	1 .. 15,665	15,665 bp	→	gene
/note	= gene ENSG00000137642 Protein coding			
SORL1-AS1	1 .. 15,665	15,665 bp	←	gene
/note	= gene ENSG00000246790 lncRNA			
✓ SORL1-201	1 .. 15,665	15,665 bp	→	prim_transcript
/note	= primary transcript ENST00000260197			
SORL1-AS1-201	1 .. 15,665	15,665 bp	←	prim_transcript
/note	= primary transcript ENST00000501964 lncRNA			
SORL1-AS1-202	1 .. 15,665	15,665 bp	←	prim_transcript
/note	= primary transcript ENST00000529160 lncRNA			
✓ SORL1-201	2194 .. 15,370	13,177 bp	→	CDS
▶ 6 segments = 957 bp				
/codon_start	= 1			
/note	= coding sequence ENSP00000260197			
/translation	= ENEFILYAVRKSIIYRYDLASGATEQLPLTGLRAAVALDFDYEHNCLYWSDLALDVIQ,,RLCLNGSTGQVEIINSGLTVEALAFEP LSQLLYWVDA GFKKIE,,VANPDGDFRLTIVNSSVLDLDRPRALVLPQEG,,VMFWTDWGD LKPGIYRSNMDGSAAYHLVSEDVKWPNGISVDDQWIYWTDAYLEC IERITFSGQQRSVILDNLPHPYAIAVFK,,NEIYWDDWSQLSIFRASKYSGSQMEILANQLTGLMDMKIFYKGKNT,,GSNACVPRPCSL LCLPKAN NSGRCPEYSSYLSQDLMCDCPQGYQLKNNTCVKQ 18 amino acids = 2.1 kDa			
SORL1-208	3299 .. 7094	3796 bp	→	prim_transcript
/note	= primary transcript ENST00000529445 Retained intron			
SORL1-203	5272 .. 7030	1759 bp	→	prim_transcript
/note	= primary transcript ENST00000524873 Retained intron			
✓ Donor Template SNV -> REV	6993 .. 7093	101 bp	⇌	misc_feature
✓ Protospacer Sequence	7011 .. 7030	20 bp	⇌	misc_feature
✓ SNV	7024 .. 7024	1 bp	⇌	misc_feature
/note	= REV = C SNV = T			
✓ PAM	7031 .. 7033	3 bp	⇌	misc_feature
SORL1-204	14,982 .. 15,665	684 bp	→	prim_transcript
/note	= primary transcript ENST00000525532			
SORL1-204	15,316 .. 15,370	55 bp	→	CDS
/note	= coding sequence ENSP00000434634			
/translation	= MCDPCPQGYQLKNNTCVKQ 18 amino acids = 2.1 kDa			

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = ATGCACGCCAAATAGGATTGTAGTG 44% GC / 7730.1 Da	25-mer	6423 .. 6447	60°C	Jan 11, 2023
✓ Sanger Sequencing /sequence = CGGAGCAATATGGATGGTTC 50% GC / 6197.1 Da	20-mer	6894 .. 6913	56°C	Jan 11, 2023
✓ Donor Template SNV -> REV /sequence = TAAAGACAGCAATGGCATAGGGGTGCGGGAGGTTGTCCAGAATGACAGAGCGCTGCTGGCCACTGAACGTGATCCGCTCTATGCACTC 50% GC / 7642.0 Da	100-mer	6993 .. 7092	80°C	Jan 11, 2023
✓ gRNA Protospacer /sequence = ATAGAGCGGATCATGTTCAG 45% GC / 6181.1 Da	20-mer	7011 .. 7023	39°C	Jan 11, 2023
✓ PCR Reverse /sequence = AAGAGCCATGTTGCTCTCCAGAGTC 52% GC / 7642.0 Da	25-mer	7472 .. 7496	62°C	Jan 11, 2023