SEQ ID NO:1

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   1      atggggg ccgcacgcag cccgccgtcc gctgtcccgg ggcccctgct
  48  ggggctgctc ctgctgctcc tgggcgtgct ggccccgggt ggcgcctccc tgcgactcct
 108 ggaccaccgg gcgctggtct gctcccagcc ggggctaaac tgcacggtca agaatagtac
 168 ctgcctggat gacagctgga ttcaccctcg aaacctgacc ccctcctccc caaaggacct
 228 gcagatccag ctgcactttg cccacaccca acaaggagac ctgttccccg tggctcacat
 288 cgaatggaca ctgcagacag acgccagcat cctgtacctc gagggtgcag agttatctgt
 348 cctgcagctg aacaccaatg aacgtttgtg cgtcaggttt gagtttctgt ccaaactgag
 408 gcatcaccac aggcggtggc gttttacctt cagccacttt gtggttgacc ctgaccagga
 468 atatgaggtg accgttcacc acctgcccaa gcccatccct gatggggacc caaaccacca
 528 gtccaagaat ttccttgtgc ctgactgtga gcacgccagg atgaaggtaa ccacgccatg
 588 catgagctca ggcagcctgt gggaccccaa catcaccgtg gagaccctgg aggcccacca
 648 gctgcgtgtg agcttcaccc tgtggaacga atctacccat taccagatcc tgctgaccag
 708 ttttccgcac atggagaacc acagttgctt tgagcacatg caccacatac ctgcgcccag
 768 accagaagag ttccaccagc gatccaacgt cacactcact ctacgcaacc ttaaagggtg
 828 ctgtcgccac caagtgcaga tccagccctt cttcagcagc tgcctcaatg actgcctcag
 888 acactccgcg actgtttcct gcccagaaat gccagacact ccagaaccaa ttccggacta
 948 catgcccctg tgggtgtact ggttcatcac gggcatctcc atcctgctgg tgggctccgt
1008 catcctgctc atcgtctgca tgacctggag gctagctggg cctggaagtg aaaaatacag
1068 tgatgacacc aaatacaccg atggcctgcc tgcggctgac ctgatccccc caccgctgaa
1128 gcccaggaag gtctggatca tctactcagc cgaccacccc ctctacgtgg acgtggtcct
1188 gaaattcgcc cagttcctgc tcaccgcctg cggcacggaa gtggccctgg acctgctgga
1248 agagcaggcc atctcggagg caggagtcat gacctgggtg ggccgtcaga agcaggagat
1308 ggtggagagc aactctaaga tcatcgtcct gtgctcccgc ggcacgcgcg ccaagtggca
1368 ggcgctcctg ggccgggggg cgcctgtgcg gctgcgctgc gaccacggaa agcccgtggg
1428 ggacctgttc actgcagcca tgaacatgat cctcccggac ttcaagaggc cagcctgctt
1488 cggcacctac gtagtctgct acttcagcga ggtcagctgt gacggcgacg tccccgacct
1548 gttcggcgcg gcgccgcggt acccgctcat ggacaggttc gaggaggtgt acttccgcat
1608 ccaggacctg gagatgttcc agccgggccg catgcaccgc gtaggggagc tgtcgggggа
1668 caactacctg cggagcccgg gcggcaggca gctccgcgcc gccctggaca ggttccggga
1728 ctggcaggtc cgctgtcccg actggttcga atgtgagaac ctctactcag cagatgacca
1788 ggatgccccg tccctggacg aagaggtgtt tgaggagcca ctgctgcctc cgggaaccgg
1848 catcgtgaag cgggcgcccc tggtgcgcga gcctggctcc caggcctgcc tggccataga
1908 cccgctggtc ggggaggaag gaggagcagc agtggcaaag ctggaacctc acctgcagcc
1968 ccggggtcag ccagcgccgc agcccctcca caccctggtg ctcgccgcag aggagggggc
2028 cctggtggcc gcggtggagc ctgggcccct ggctgacggt gccgcagtcc ggctggcact
2088 ggcgggggag ggcgaggcct gcccgctgct gggcagcccg ggcgctgggc gaaatagcgt
2148 cctcttcctc cccgtggacc ccgaggactc gccccttggc agcagcaccc ccatggcgtc
2208 tcctgacctc cttccagagg acgtgaggga gcacctcgaa ggcttgatgc tctcgctctt
2268 cgagcagagt ctgagctgcc aggcccaggg gggctgcagt agacccgcca tggtcctcac
2328 agacccacac acgccctacg aggaggagca gcggcagtca gtgcagtctg accagggcta
2388 catctccagg agctccccgc agccccccga gggactcacg gaaatggagg aagaggagga
2448 agaggagcag gacccaggga agccggccct gccactctct cccgaggacc tggagagcct
2508 gaggagcctc cagcggcagc tgcttttccg ccagctgcag aagaactcgg gctgggacac
2568 gatggggtca gagtcagagg ggcccagtgc atga
```

Figure 1A

SEQ ID NO:2

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1       MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNC
51      TVKNSTCLDDSWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTL
101     QTDASILYLEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFV
151     VDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSG
201     SLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH
251     HIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT
301     VSCPEMPDTPEPIPDYMPLWVYWFITGISILLVGSVILLIVCMTWRLAGP
351     GSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYSADHPLYVDVVLKFAQ
401     FLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIVLCSRG
451     TRAKWQALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPACFGTYV
501     VCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPGRMHRV
551     GELSGDNYLRSPGGRQLRAALDRFRDWQVRCPDWFECENLYSADDQDAPS
601     LDEEVFEEPLLPPGTGIVKRAPLVREPGSQACLAIDPLVGEEGGAAVAKL
651     EPHLQPRGQPAPQPLHTLVLAAEEGALVAAVEPGPLADGAAVRLALAGEG
701     EACPLLGSPGAGRNSVLFLPVDPEDSPLGSSTPMASPDLLPEDVREHLEG
751     LMLSLFEQSLSCQAQGGCSRPAMVLTDPHTPYEEEQRQSVQSDQGYISRS
801     SPQPPEGLTEMEEEEEEEQDPGKPALPLSPEDLESLRSLQRQLLFRQLQK
851     NSGWDTMGSESEGPSA
```

Figure 1B

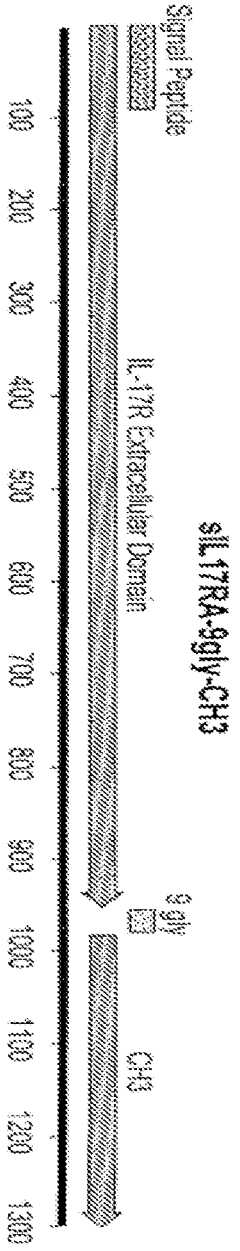

sIL17RA-9gly-CH3
Signal Peptide
IL-17R Extracellular Domain
9 gly
CH3
100
200
300
400
500
600
700
800
900
1000
1100
1200
1300

Figure 2

SEQ ID NO:3

```
1     ATGGGGGCCGCACGCAGCCCGCCGTCCGCTGTCCCGGGGCCCCTGCTGGGGCTGCTCCTG
61    CTGCTCCTGGGCGTGCTGGCCCCGGGTGGCGCCTCCCTGCGACTCCTGGACCACCGGGCG
121   CTGGTCTGCTCCCAGCCGGGGCTAAACTGCACGGTCAAGAATAGTACCTGCCTGGATGAC
181   AGCTGGATTCACCCTCGAAACCTGACCCCCTCCTCCCCAAAGGACCTGCAGATCCAGCTG
241   CACTTTGCCCACACCCAACAAGGAGACCTGTTCCCCGTGGCTCACATCGAATGGACACTG
301   CAGACAGACGCCAGCATCCTGTACCTCGAGGGTGCAGAGTTATCTGTCCTGCAGCTGAAC
361   ACCAATGAACGTTTGTGCGTCAGGTTTGAGTTTCTGTCCAAACTGAGGCATCACCACAGG
421   CGGTGGCGTTTTACCTTCAGCCACTTTGTGGTTGACCCTGACCAGGAATATGAGGTGACC
481   GTTCACCACCTGCCCAAGCCCATCCCTGATGGGGACCCAAACCACCAGTCCAAGAATTTC
541   CTTGTGCCTGACTGTGAGCACGCCAGGATGAAGGTAACCACGCCATGCATGAGCTCAGGC
601   AGCCTGTGGGACCCCAACATCACCGTGGAGACCCTGGAGGCCCACCAGCTGCGTGTGAGC
661   TTCACCCTGTGGAACGAATCTACCCATTACCAGATCCTGCTGACCAGTTTTCCGCACATG
721   GAGAACCACAGTTGCTTTGAGCACATGCACCACATACCTGCGCCCAGACCAGAAGAGTTC
781   CACCAGCGATCCAACGTCACACTCACTCTACGCAACCTTAAAGGGTGCTGTCGCCACCAA
841   GTGCAGATCCAGCCCTTCTTCAGCAGCTGCCTCAATGACTGCCTCAGACACTCCGCGACT
901   GTTTCCTGCCCAGAAATGCCAGACACTCCAGAACCAATTCCGGACTACATGACCGGTGGA
961   GGTGGAGGTGGAGGTGGAGGTCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC
1021  CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
1081  AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG
1141  CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG
1201  AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC
1261  CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAG
```

Figure 3A

SEQ ID NO:4

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1     MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNC
51    TVKNSTCLDDSWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTL
101   QTDASILYLEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFV
151   VDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSG
201   SLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH
251   HIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT
301   VSCPEMPDTPEPIPDYMTGGGGGGGGGQPREPQVYTLPPSRDELTKNQVS
351   LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
401   SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
```

Figure 3B

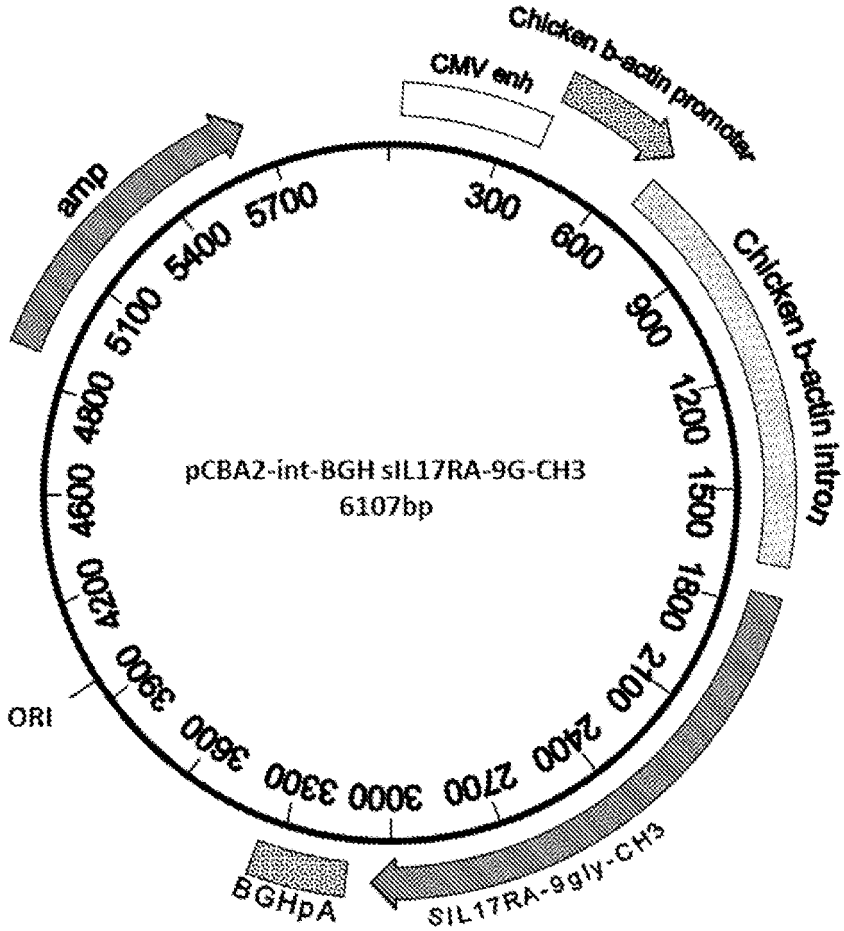

Chicken b-actin promoter
CMV enh
amp
Chicken b-actin intron
pCBA2-int-BGH sIL17RA-9G-CH3
6107bp
ORI
BGHpA
SIL17RA-9gly-CH3
300
600
900
1200
1500
1800
2100
2400
2700
3000
3300
3600
3900
4200
4600
4800
5100
5400
5700

Figure 4

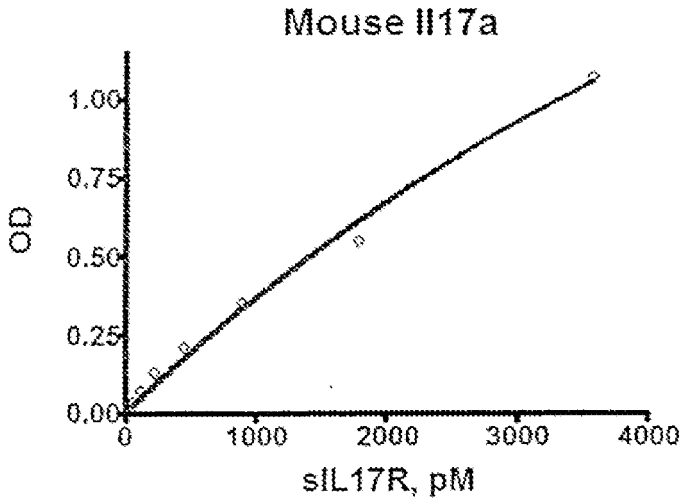


Figure 5A

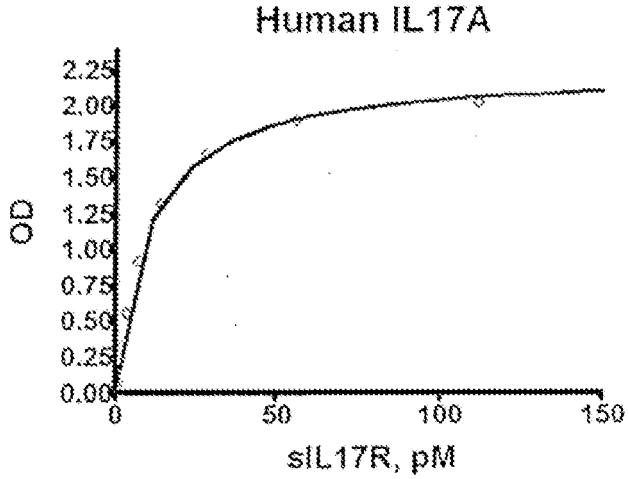


Figure 5B

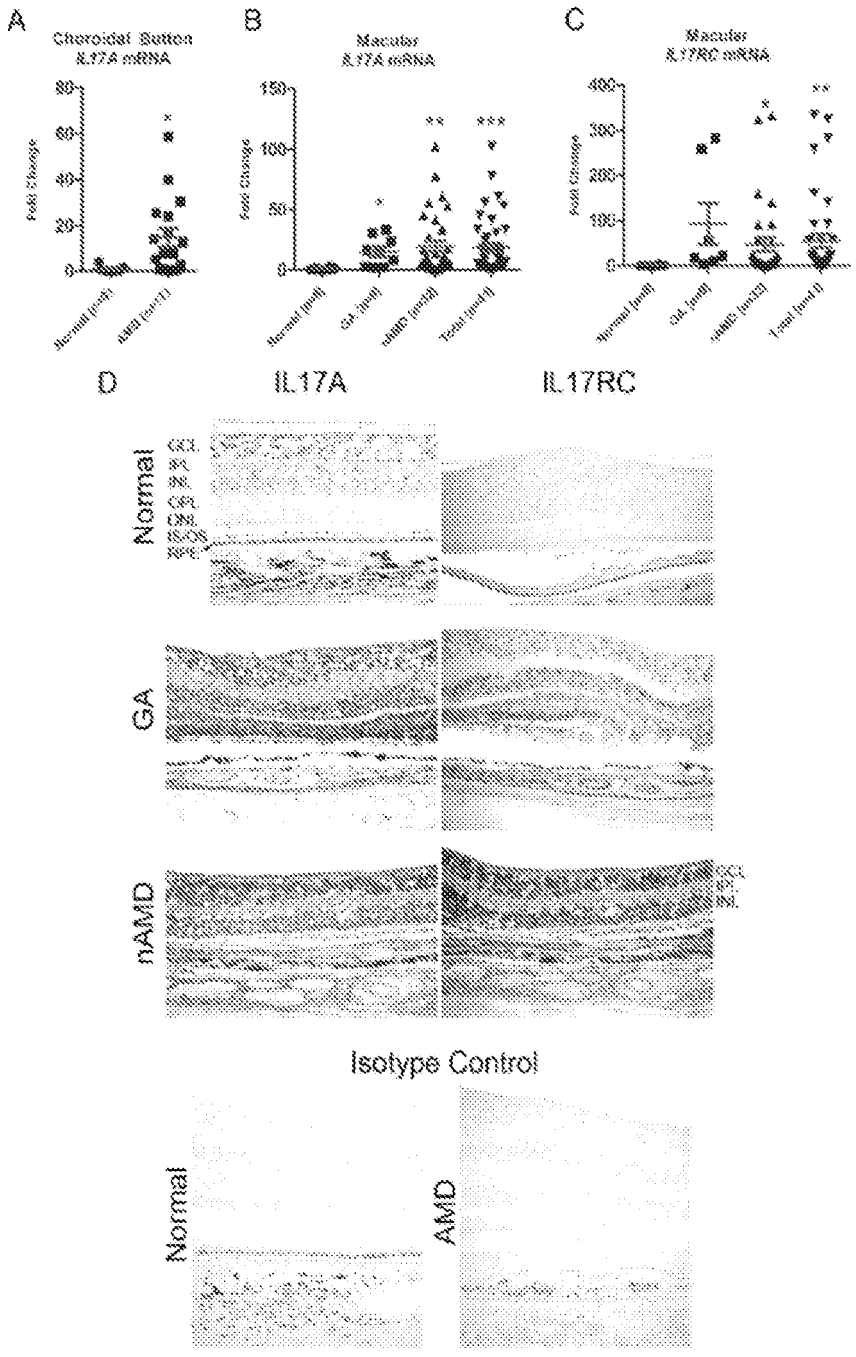

A
Choroidal Button
IL17A mRNA
B
Macular
IL17A mRNA
C
Macular
IL17RC mRNA
D
IL17A
IL17RC
Normal
GA
nAMD
Isotype Control
Normal
AMD

Figure 6

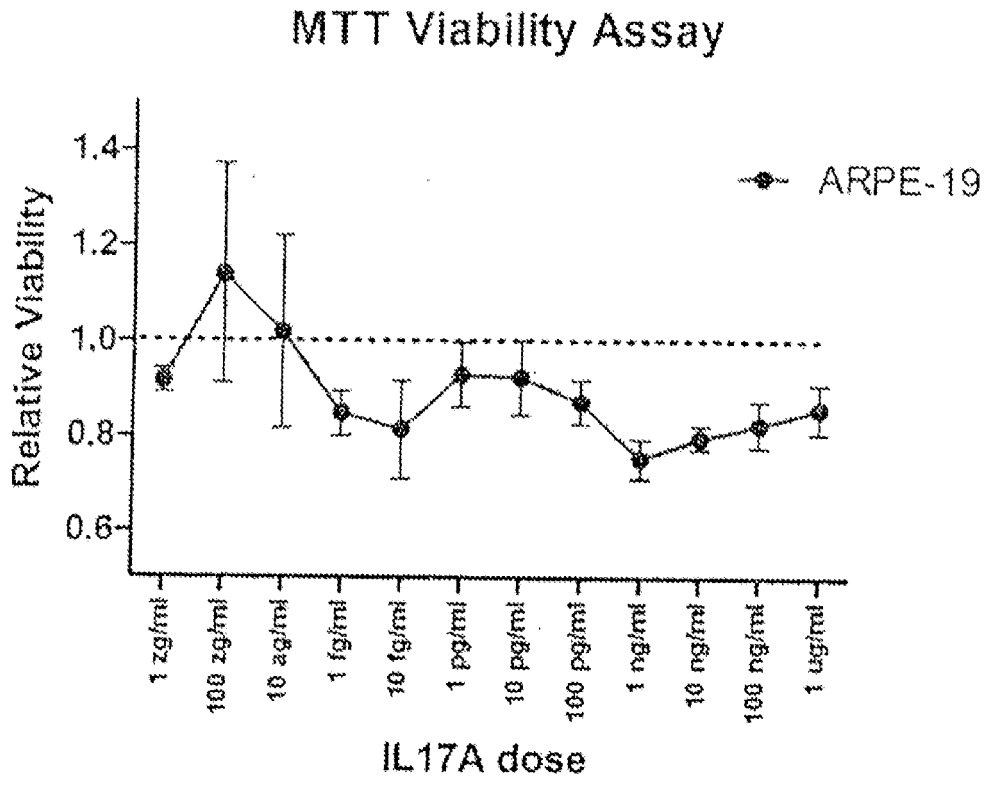

MTT Viability Assay
ARPE-19
Relative Viability
1.4
1.2
1.0
0.8
0.6
1 zg/ml
100 zg/ml
10 ag/ml
1 fg/ml
10 fg/ml
1 pg/ml
10 pg/ml
100 pg/ml
1 ng/ml
10 ng/ml
100 ng/ml
1 ug/ml
IL17A dose

Figure 7

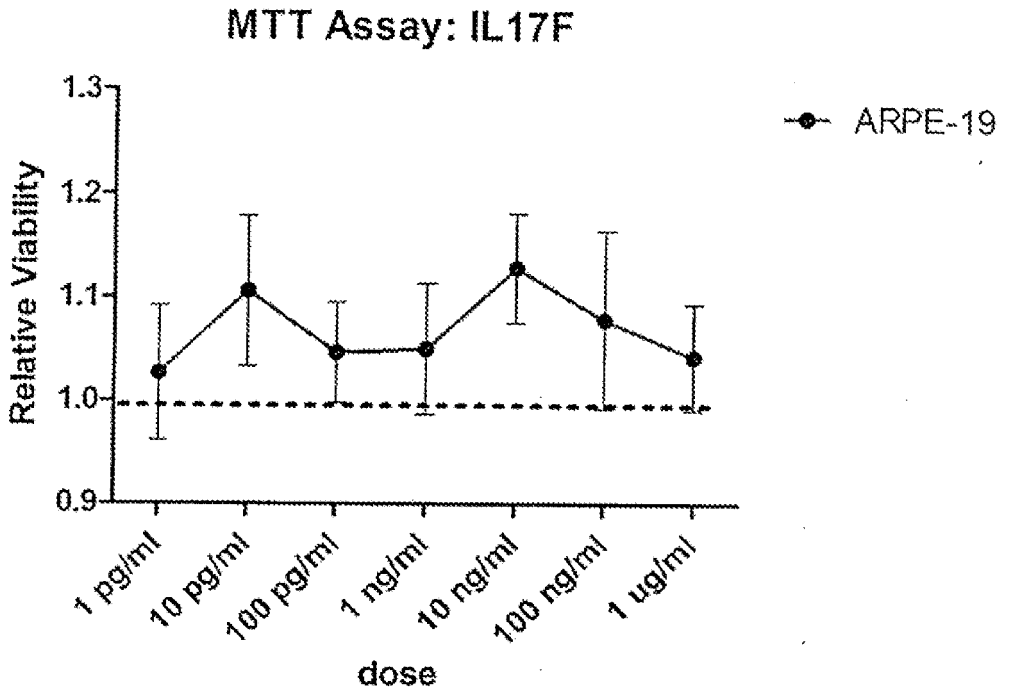

MTT Assay: IL17F
ARPE-19
Relative Viability
1.3
1.2
1.1
1.0
0.9
1 pg/ml
10 pg/ml
100 pg/ml
1 ng/ml
10 ng/ml
100 ng/ml
1 ug/ml
dose

Figure 8

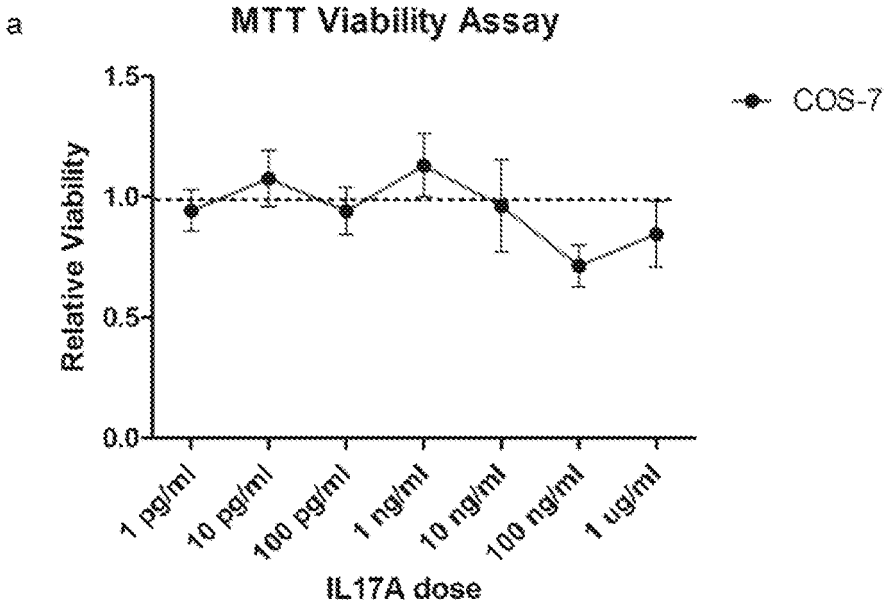


Figure 9A

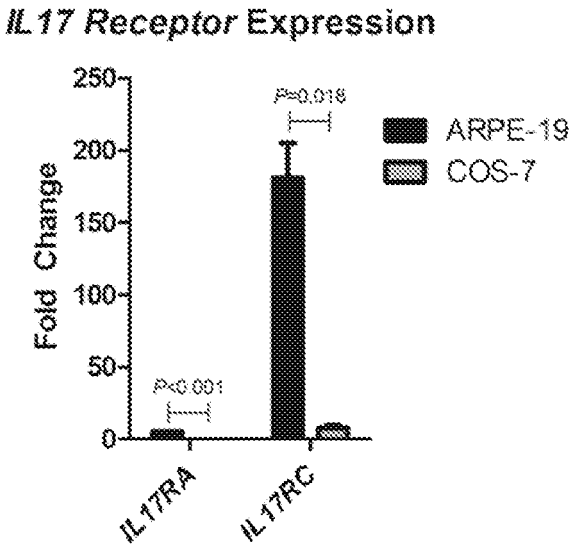


Figure 9B

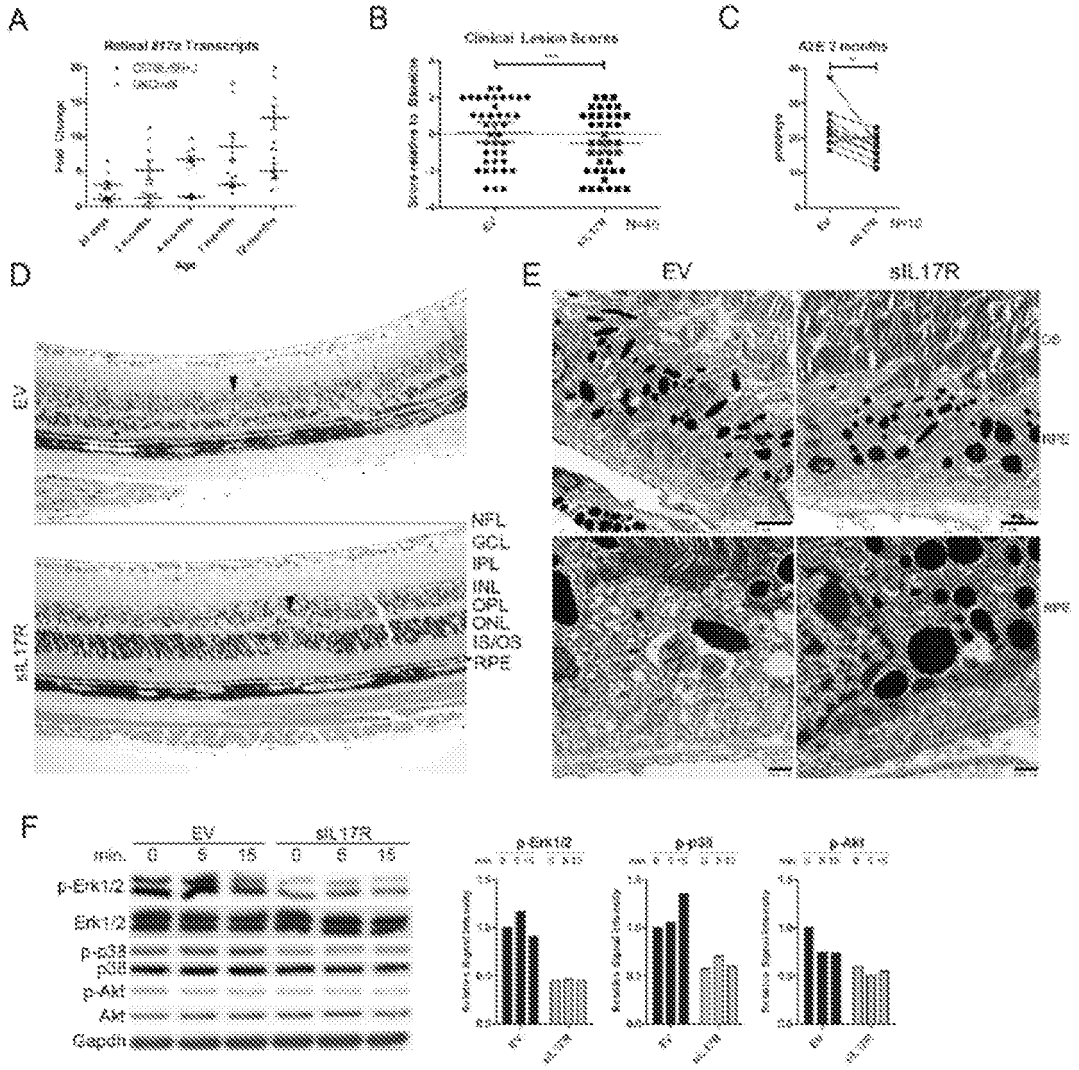

A
B
C
D
E
EV
sIL17R
NFL
GCL
IPL
INL
OPL
ONL
IS/OS
RPE
F
p-Erk1/2
Erk1/2
p-p38
p38
p-Akt
Akt
Gapdh

Figure 10

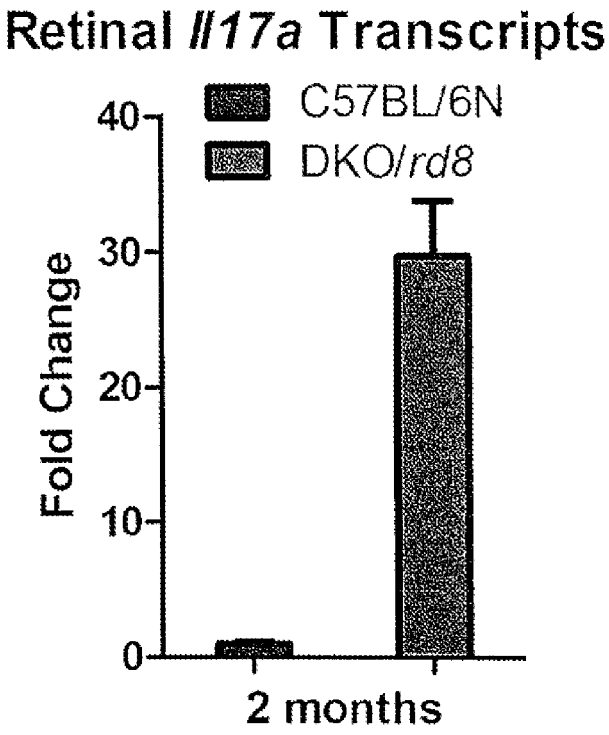

Retinal Il17a Transcripts
C57BL/6N
DKO/rd8
Fold Change
40
30
20
10
0
2 months

Figure 11

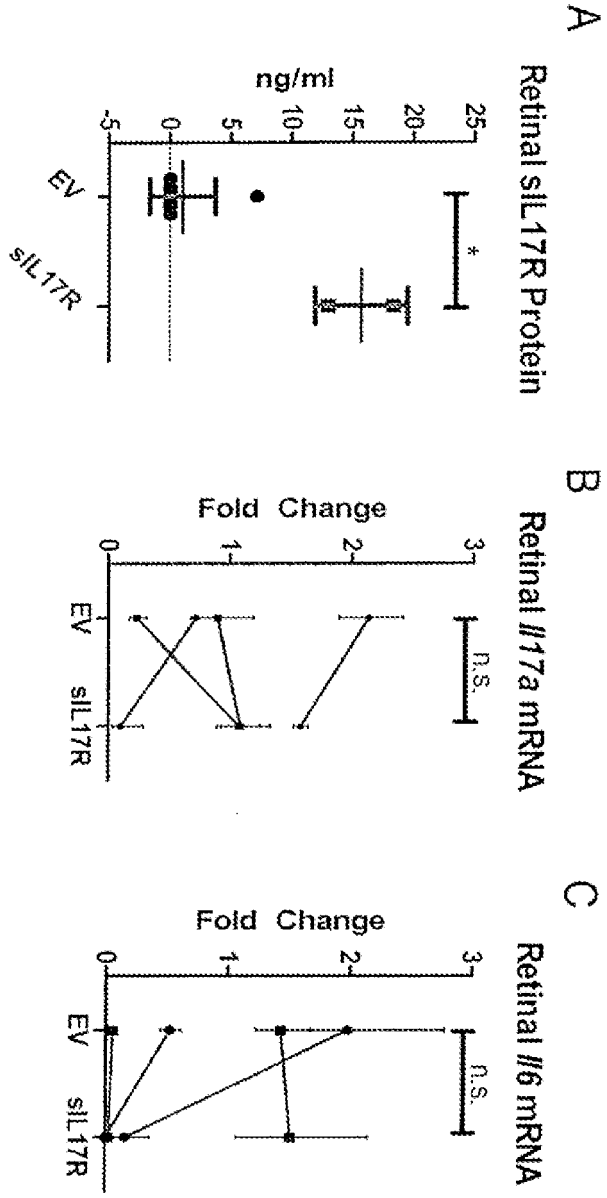

A
Retinal sIL17R Protein
ng/ml
-5
0
5
10
15
20
25
EV
sIL17R
*
B
Retinal Il17a mRNA
Fold Change
0
1
2
3
EV
sIL17R
n.s.
C
Retinal Il6 mRNA
Fold Change
0
1
2
3
EV
sIL17R
n.s.

Figure 12

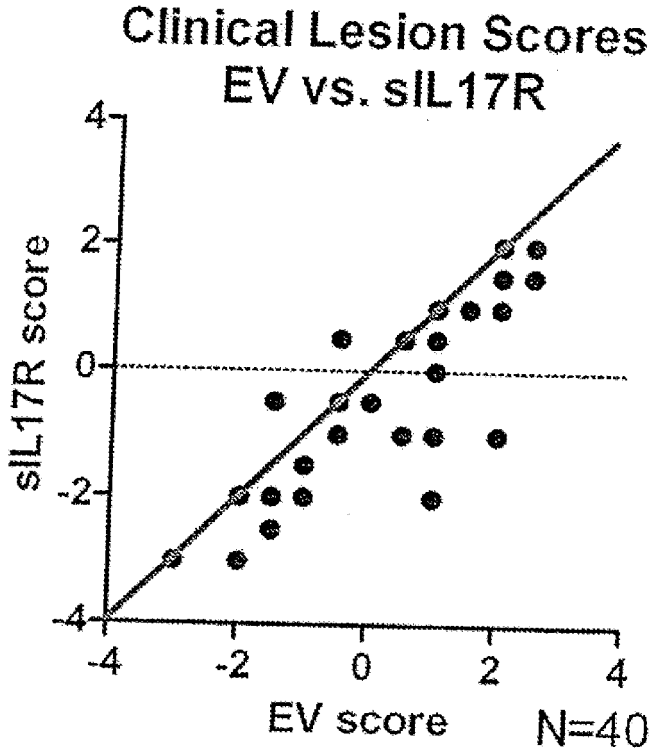

Clinical Lesion Scores
EV vs. sIL17R
sIL17R score
EV score
N=40
4
2
0
-2
-4
-4
-2
0
2
4

Figure 13

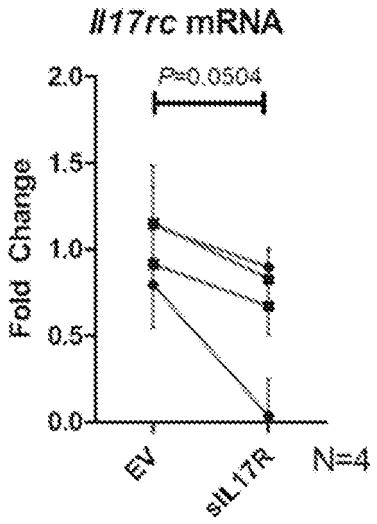


Figure 14A

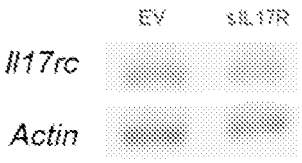


Figure 14B