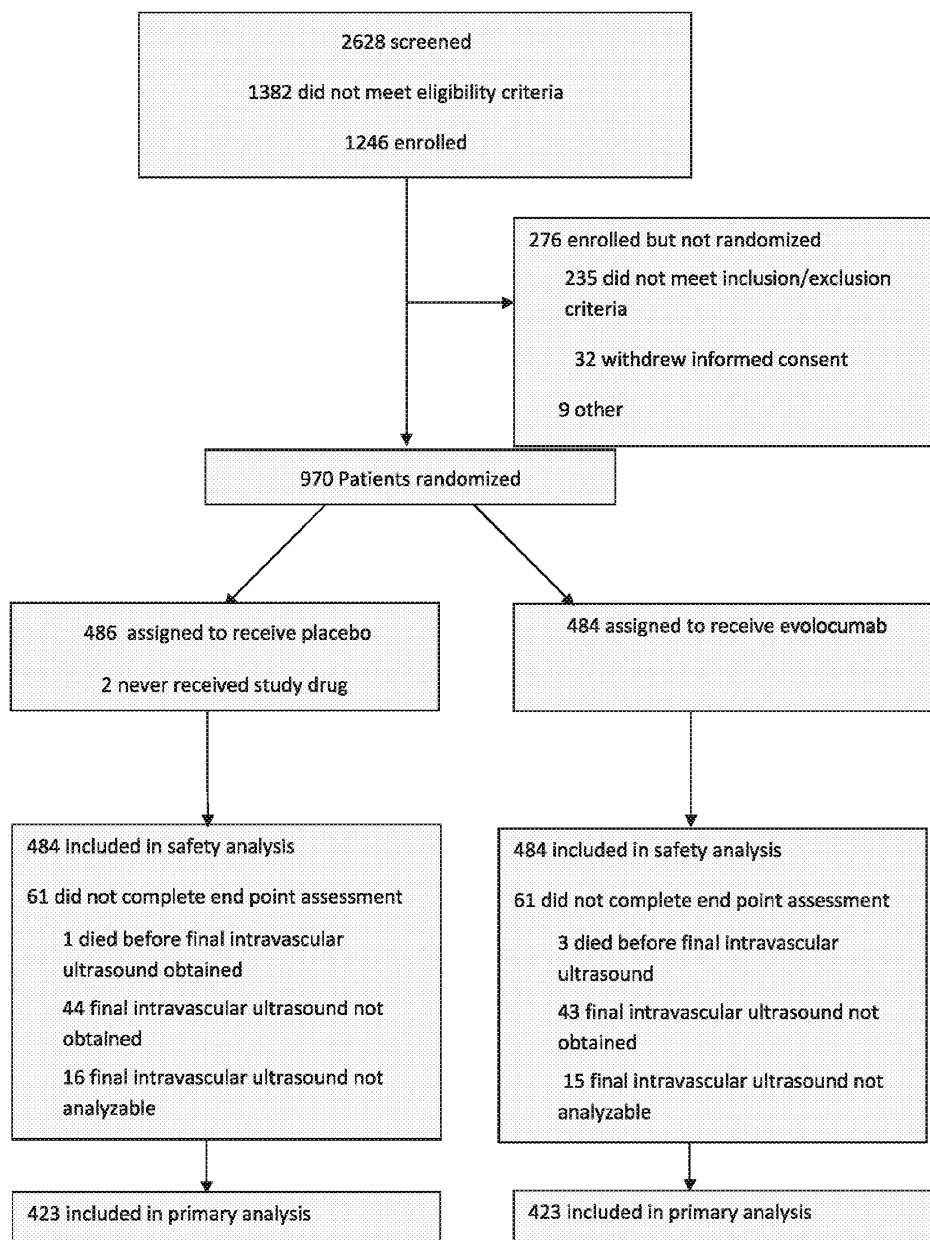


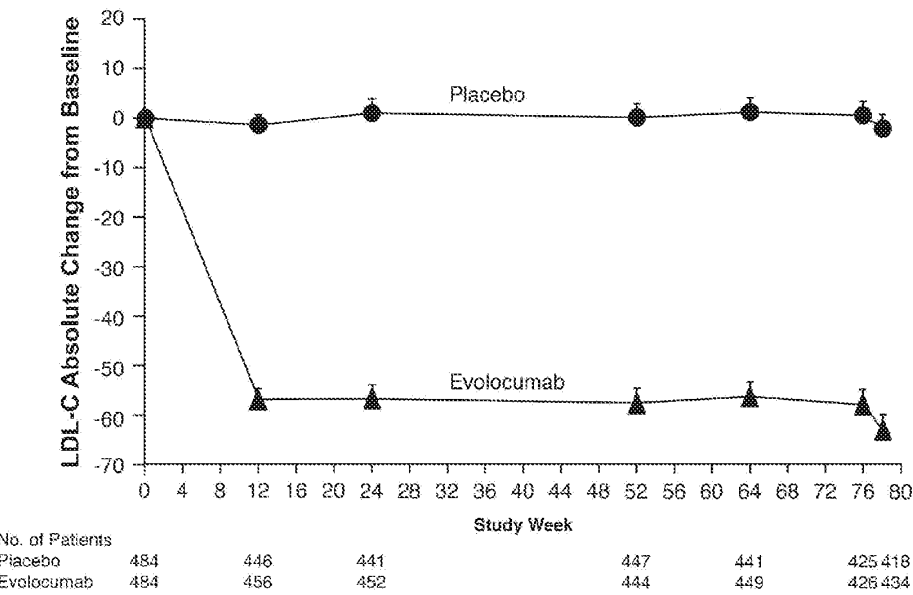
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FIG. 1 Flow of Patients Through the Trial



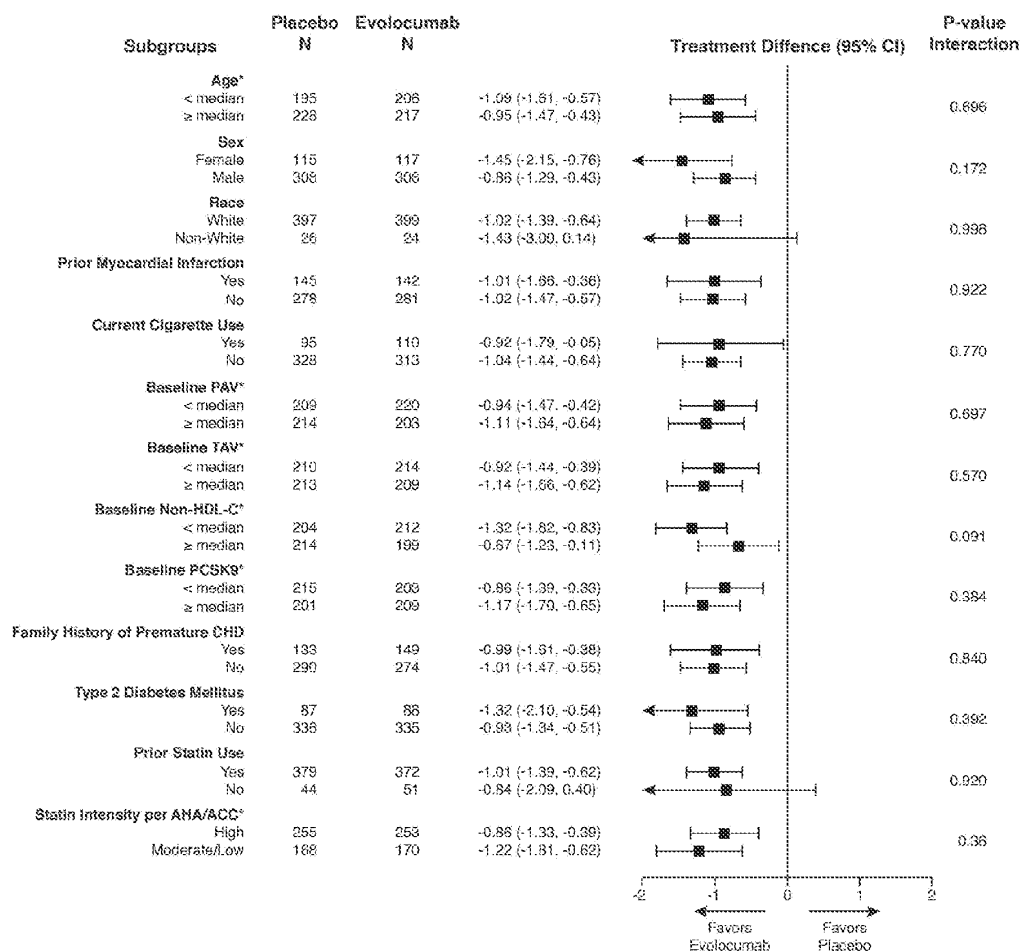
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FIG. 2



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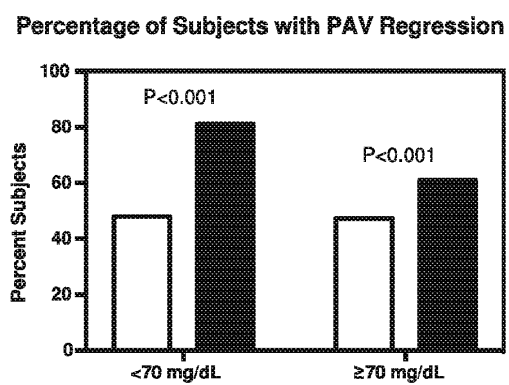
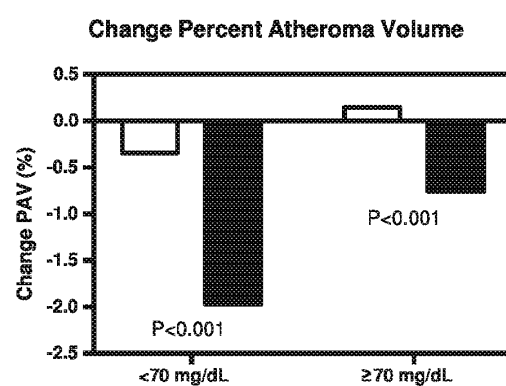
FIG. 3.



*Median values:
 Age: 60 years
 PAV: 36.68
 TAV: 175.08
 Non-HDL: 115
 PCSK9: 315

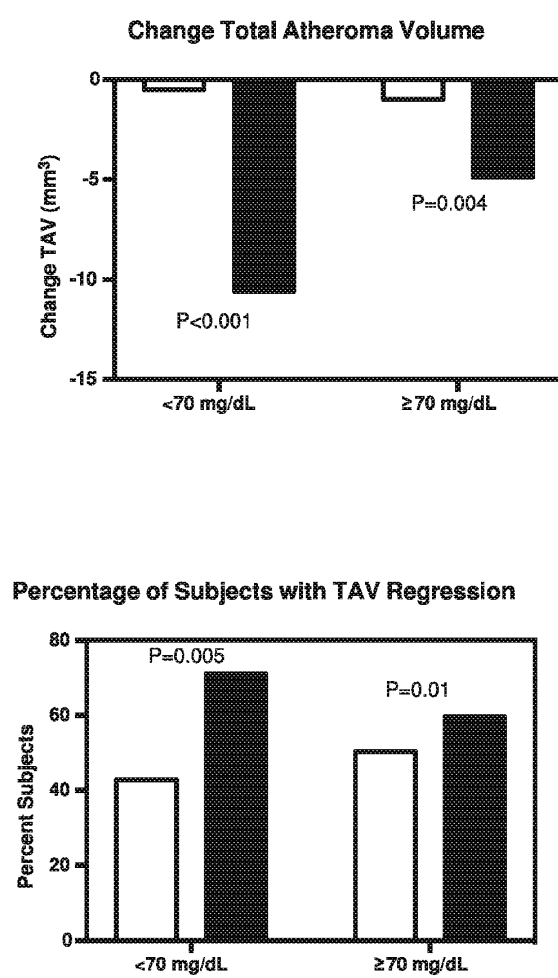
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FIG. 4A



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FIG. 4B



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FIG. 4C

Exploratory Subgroup: Baseline LDL-C <70 mg/dL

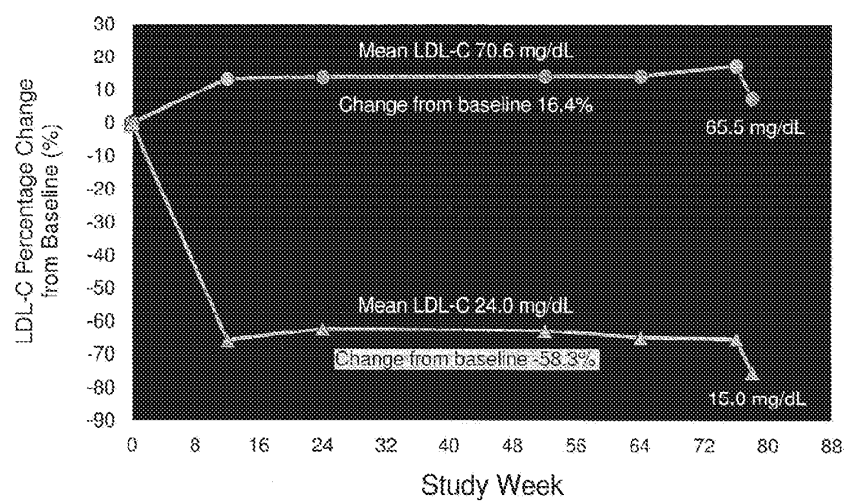
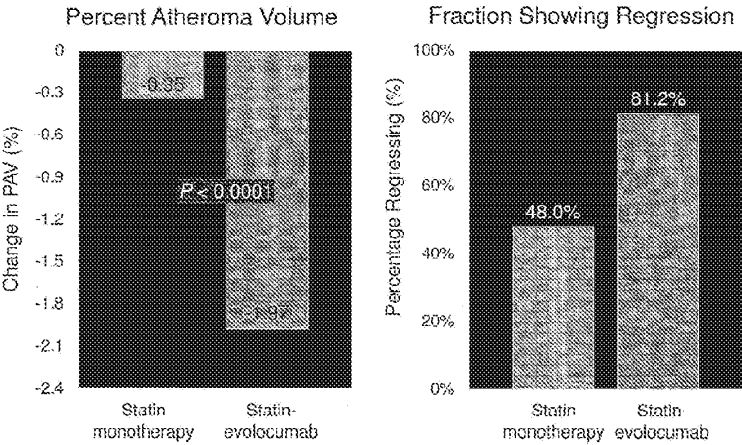


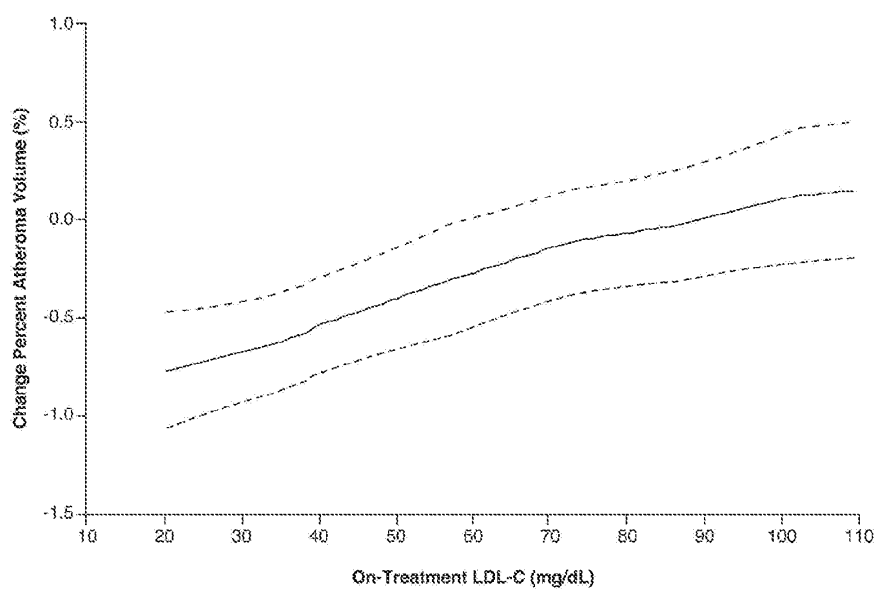
FIG. 4D

Exploratory Subgroup: Baseline LDL-C <70 mg/dL



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FIG. 5



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FIG. 6

alirocumab

Heavy chain

EVQLVESGGG LVQPGGSLRL SCAASGFTFN NYAMNWVRQA PGKGLDWVST 50
ISGSGGTTNY ADSVKGRFII SRDSSKHTLY LQMNSLRAED TAVYYCAKDS 100
NWGNFDLWGR GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS VFLPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPVY 350
TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPG 447 (SEQ ID NO: 4)

Light chain

DIVMTQSPDS LAVSLGERAT INCKSSQSVL YRSNNRNFLG WYQQKPGQPP 50
NLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQYYTT 100
PYTFGQGTKI EIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNMFYPREA 150
KVQWKVDNAL QSGNSQESVT EQDSKDSTYS LSSTLTLSKA DYEKHKVYAC 200
EVTHQGLSP VTKSFNRGEC 220 (SEQ ID NO: 5)

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FIG. 7**bococizumab**

Heavy chain:

QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYMHWVRQA PGQGLEWMGE 50
ISPFGGRTNY NEKFCSRVTM TRDTSTSTVY MELSSLRSED TAVYYCARER 100
PLYASDLWGQ GTTVTVSSAS TKGPSVFPLA PCSRSTSEST AALGCLVKDY 150
FPEPVTWSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSNFGTQTYT 200
CNVDHKPSNT KVDKTVKRC CVECPPCPAP PVAGPSVFLF PPKPKDTLMI 250
SRTPEVTCVV VDVSHEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTFRVV 300
SVLTVVHQDW LNGKEYCKV SNKGLPSSIE KTISKTKGQP REPQVYTLPP 350
SREEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPMLDSGGS 400
FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK 444 (SEQ ID NO: 6)

Light chain:

DIQMTQSPSS LSASVGDRTV ITCRASQGIS SALAWYQQKP GKAPKLLIYS 50
ASYRYTGVPV RFGSGSGTD FTFITSLQP EDIATYYCQQ RYSLWRTFGQ 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC 214 (SEQ ID NO: 7)

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FIG 8

Seq ID No.	LINE	V	D	J	FR1	CDR1	FR2
8		Germline			QVQLVQSGAEVFRPGASVIVSCAS	GTFTSGIS	WYQAPGQGLENNG
9	20D10	VH1-18		JH4B			
10	26E10	VH1-18		JH4B			
11	21B12	VH1-18		JH4B			
12	23G1	VH1-18		JH4B			
13	26H5	VH1-18		JH4B			
14	27H3	VH1-18		JH4B			
15	31D1	VH1-18		JH4B			
16	27E7	VH1-18		JH4B			
17	30B9	VH1-18		JH4B			
18	19H9	VH1-18		JH4B			
19	17C2	VH1-18		JH4B			
20	25A7	VH1-18		JH4B			
21		Germline			QVQLVQSGAEVFRPGASVIVSCAS	GTFTSGIS	WYQAPGQGLENNG
22	3K6	VH1-18		JH4B			
23		Germline			EVQLVDSGGGVGGSGSLKLSAAS	QTFPSYWM	WYQAPGQGLENNV
24	3H6	VH3-7	D7-27	JH3A			
25		Germline			EVQLVDSGGGVGGSGSLKLSAAS	QTFPSYWM	WYQAPGQGLENNV
26	9C9	VH3-7	D7-27	JH3B			
27	1A12	VH3-7	D7-27	JH3B			
28		Germline			EVQLVDSGGGVGGSGSLKLSAAS	QTFPSYWM	WYQAPGQGLENNV
29	31H4	VH3-21	D3-3	JH3A			
30		Germline			EVQLVDSGGGVGGSGSLKLSAAS	QTFPSYWM	WYQAPGQGLENNV
31	13B5	VH3-23		JH4B			

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FIG. 9

Seq ID	LINE	V	D	J	F1	CD1	F2
70		Germline					
71	2325	VR3-33	D2-0	3840	EVQLVGGGVQPGHSLSCAS	QTFSSVMS	WVQAPKCLEVA
72	2504	VR3-23	D2-8	3848			
73		Germline			QVCLVSGGVQPGHSLSCAS	QTFSSVMS	WVQAPKCLEVA
74	30A4	VR3-33		3868			
75		Germline			QVCLVSGGVQPGHSLSCAS	QTFSSVMS	WVQAPKCLEVA
76	27A6	VR3-33	D6-6	3868			
77	28B12	VR3-33	D6-6	3868			
289	28B12v1	VR3-33	D6-6	3868			
78	28D6	VR3-33	D6-6	3868			
79	16F12	VR3-33	D6-6	3868			
80	22E2	VR3-33	D6-6	3868			
81	31B12	VR3-33	D6-6	3868			
290	31B12v1	VR3-33	D6-6	3868			
82		Germline			QVCLVSGGVQPGHSLSCAS	QTFSSVMS	WVQAPKCLEVA
83	31G11	VR3-33	D6-19	3868			
84		Germline			QVCLVSGGVQPGHSLSCAS	QTFSSVMS	WVQAPKCLEVA
85	3C4	VR4-31		3868			
86		Germline			QVCLVSGGVQPGHSLSCAS	QTFSSVMS	WVQAPKCLEVA
87	27E2	VR3-31	D3-3	3848			
88		Germline			QVCLVSGGVQPGHSLSCAS	QTFSSVMS	WVQAPKCLEVA
89	31A4	VR4-34	D6-6	3848			
90		Germline			QVCLVSGGVQPGHSLSCAS	QTFSSVMS	WVQAPKCLEVA
91	13H1	VR6-3		3848			

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FIG 10

Seq. ID No.	LINE	CDR2	FR3	CDR3	FR4
8		WISAVNGNTNYAQKIQG	KVTMTDTSTSTAMELSLASDDTAVYICAR	YGMGV	WGQGITVTVSS
9	20D10				
10	26E10				
11	21B12				
12	23G1				
13	26H5				
14	27H5				
15	31D1				
16	27E7				
17	30B9				
18	19H9				
19	17C2				
20	25A7				
21		WISAVNGNTNYAQKIQG	KVTMTDTSTSTAMELSLASDDTAVYICAR	GY DX	WGQGITVTVSS
22	3B6				
23		NINQSGSEYVYDGVAG	KFTTSPQNAKNSLYLQMSLSAEQDAVYICAR	NWG AFQV	WGQGITVTVSS
24	9H6			ES	
25		NINQSGSEYVYDGVAG	KFTTSPQNAKNSLYLQMSLSAEQDAVYICAR	NWG AFQV	WGQGITVTVSS
26	9C9			ES	
27	1A12			ES	
28		SISGSSYLYADSVAG	KFTTSPQNAKNSLYLQMSLSAEQDAVYICAR	DIDPGSTTADV	WGQGITVTVSS
29	31H4				
30		AISGSSSTLYADSVAG	KFTTSPQNAKNSLYLQMSLSAEQDAVYICAR	FOY	WGQGITVTVSS
31	13B5			EVTSF	

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FIG 11

Seq ID No.	LINE	CDR2	FR3	CDR3	FR4
32		AIGGGSTYADSVRG	RPTISDRNSKPTLVIGIHSLSRAEDTAVTYCAR	VIMQYA DY	WGQGLVTVSS
33	23B5	T-----DN-----		RF-----MD-----	
34	25G4	T-----N-----		RF-----RL-----	
35		VWYDGSNKYADSVRG	RPTISDRNSKPTLVIGIHSLSRAEDTAVTYCAR	YTHGMGV	WGQGLVTVSS
36	30R4	T-----D-----		ETGPKL-----	
37		VWYDGSNKYADSVRG	RPTISDRNSKPTLVIGIHSLSRAEDTAVTYCAR	IAA GMDV	WGQGLVTVSS
38	27A6	L-----S-----D-----		AIADLYTY-----	
39	28B12	L-----N-----		AIADLYTY-----	
40	28D6	L-----N-----		AIADLYTY-----	
41	16P12	L-----S-----D-----		AIADLYTY-----	
42	22E2	L-----N-----		AIADLYTY-----	
43	22E2v1	L-----N-----		AIADLYTY-----	
44	31B12	L-----N-----		PGGLAEPG-----	
45	31B12v1	L-----N-----		KQGL-----PG-----	
46		VWYDGSNKYADSVRG	RPTISDRNSKPTLVIGIHSLSRAEDTAVTYCAR	GIADVYVGMGV	WGQGLVTVSS
47	31G11	L-----N-----T-----Y-----			
48		YLYSGSTYNPGLKS	RVTISVDTSKNQPSKLSGVTAADTAVTYCAR	YVYGMGV	WGQGLVTVSS
49	3C4	L-----N-----	I-----	GGVTT-----A-----	
50		YLYSGSTYNPGLKS	RVTISVDTSKNQPSKLSGVTAADTAVTYCAR	EDIRNV IVDY	WGQGLVTVSS
51	27B2	L-----N-----		-----P-----	
52		YLYSGSTYNPGLKS	RVTISVDTSKNQPSKLSGVTAADTAVTYCAR	GGIV FIN	WGQGLVTVSS
53	31A4	L-----N-----D-----	-----K-----N-----	-----P-----	
54		RYLYSGKWNQYAVGVKS	RIITINDETSKNQPSKLSGVTAADTAVTYCAR	FDY	WGQGLVTVSS
55	13H1	L-----N-----K-----G-----		GGETAA-----	

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STRUCTURAL FORMULA

Heavy chain

EVQLVDSGAE	VKKPGASVKV	SKKASGYTLT	SGKISNVRQA	PGQGLRMGW	50
VSEFNGNTNY	AGKLGGRGTM	YTDPSITSTAI	NKLRSLRSD	TAVYTCARGY	100
GMDVWGQGT	VTSSASTNG	DSVTFSLAPCS	ESTSESTAAI	GGLVNDYFEE	150
PVTVSSNSGA	LTSGVHTFPA	VLOSAGLYSL	SNVTVNPSON	TGTQTTTNY	200
DHRTSNTKND	KIKERKOCVE	CFDCEAPFVA	GPSVFLPDK	PDYTLNISRT	250
PEVTCVVYDV	SHEDSEVDFN	KYYDGEVHN	ANTKPSSECF	NSTFRVGVYL	300
TVVHQWLNG	KKKRCFVSNE	GLPASLEKTI	SKTKGQPRRF	QVYTLFPGRE	350
ENTNKQVSLT	GLVKGFPFSD	IATWEESNGQ	FENNYKTTFE	MLSDGSPFL	400
YSELTVKKR	WQQGNVTSCS	VMHEALHNRV	TQKSLSLSPK	K	441

(SEQ ID NO: 56)

Light chain

ESALTQPAAY	SGSPGQSITI	SGTGTSSDWG	GINSVSWYQQ	RPGKAPKLM	50
YEVSNRPSGV	SNRPSGSKSG	NTASLTISGL	QASDEADYTC	NSYTSISMVF	100
GGTYKLTVLG	QPKAPSVTL	EPSPSEELQA	NKATLVCLIS	LFYFGAVTYA	150
WRADSEPVKA	GVETTFPSNQ	SNMRYAASK	LSLTPEQWKS	RRSYSCGVTH	200
RGSTVENTVA	FIEDG				212

(SEQ ID NO: 57)

Disulfide bridges

22-90	22-90	22-98	22-99	129-214	129-214
137-196	137-196	142-198	142-198	217-217	218-218
231-231	234-234	255-315	255-315	361-419	361-419

Glycosylation sites (N)

Asn-291 Asn-291

MOLECULAR FORMULA

 $C_{6242}H_{9648}N_{1358}O_{1296}S_{56}$

EVOLOCUMAB

FIG. 12

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Constant Domains

Human IgG2:

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVT
 VPSSNFGTQTYTCNVDHKPSNTKVDKTVKCCVECPPCPAPPVAGPSVFLFPPKPKOTLMISRTPEVTC
 VVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVLHGDWLNQKEYKCKVSNKGLF
 APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLD
 SDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTOKLSLSLSPGK (SEQ ID NO: 58)

Human IgG4:

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVT
 VPSSSLGKTQTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPPEFLGGPSVFLFPPKPKDITLMISHTPEVT
 CVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHGDWLNQKEYKCKVSNKGLI
 PSSIEKTISKAKGQPREPQVYTLPPSQEENTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL
 DSDGSFFLYSRLTVDKSRWQEGNVFCSSVMHEALHNHYTOKLSLSLSLGK (SEQ ID NO: 59)

Human lambda:

DPKAAPSVTLFPPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSY
 LSLTPEQWWSKRSYSYSCGVTHEGSTVEKTVAPTECS (SEQ ID NO: 60)

Human kappa:

TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQDESVTEQDSKDSITYSLSS
 TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 61)

FIG. 13

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QEDEDGDYEEELVLAIRSEEDGLAEAPEHGTTATEHRC AKDPWRLPGTYVVVLKEETHL
SQSERTARRLOAQAAARRGYLTKILHYFHQLLPQFLVKMSGDLLELAALKLPHVDYIEEDS
SVFAQSIPWNLERITPPRYRADEYQPPDGGSLVEVYLLDTSIQSDHREIEGRVMVTD FEN
VPEEDGTRFHRRQASKCD SHGTHLAGVVSGRDAQVARGASMRLRVLNCQGKGTVSGT
LIGLEFIRKSQVLVQPVGFLVVLLPLAGGYSRVLNAACQRLARAGVVLVTAAGNFRDDAC
LYSPASAPEVITVOATNAQDQPVTLGTLGTNFGRCVDLFAPGEDHIGASSDCSTCFVSQS
GTSQAAAHVAGIAAMMLSAEPFLTLAELRQRLIHFS AKDVINEAWFPEDQRVLTPNLVA
ALPPSTHGAGWQLPCRTVWSAHS GPTRMATAIARCAPDEELLSCSSPSRSGKRRGERME
AQGGKLV CRAHNAFGGEGVYAIARCCLLPQANCSVHTAPPAEASMGTRVHCHQQGHV
LTGCSHWEVEDLGTHKPPVLRPRGQPNQCVGHREASIHASCCHAPGLECKVKEHGIPA
PQGGQVTVACEEGWTLTGCSALPGTSHVLGAYAVDNTCVVRSRDVSTTGSTSEEAVTAV
AICCRSRHLAQASQELQ

SEQ ID NO:1

FIG. 14A

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```

          10      20      30      40      50
Query 1  atggggaacgtcaagctccaggggtccctggtagggcgctgcactgctgct SEQ ID NO:2
Frame1  M G T V S S R R S W W F L F L L L SEQ ID NO:3

          60      70      80      90     100
Query 1  gctgctgctgctgctgctgctgggtccaggggggcgcctgctggcagggggg
Frame1  L L L L L L G F A G A R A G A A E

          110     120     130     140     150
Query 1  agggagggcactacagggcggcgtggctggctgacgctggcctccagggagggc
Frame1  D G E Y E N L V L A L R G D E E E

          160     170     180     190     200
Query 1  ggctggggcgaagggacggcgagggggagggcggcgacggcgacgcttccggcgctg
Frame1  Q L A E A E E H G E Y A T E H R E

          210     220     230     240     250
Query 1  cggcaggggacggctggggggtggcggcgacggcgacggctggctggctggcggc
Frame1  A K D P W R L P G E Y V V V L R E

          260     270     280     290     300
Query 1  agggagcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggc
Frame1  E T K L E Q S E K T A P R L Q A

          310     320     330     340     350
Query 1  cggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggc
Frame1  Q A R K K G E L L L K L L E V S E G

          360     370     380     390     400
Query 1  cctctctctggcgttctggtgtaggggagggcggcggcggcggcggcggcggc
Frame1  L P P P P L V K R S G P L L S L A

          410     420     430     440     450
Query 1  ccttggcgttgcggcgtgctggcggcggcggcggcggcggcggcggcggcggc
Frame1  L K L P R V D Y L S S D S G V E

          460     470     480     490     500
Query 1  ggccggggcggcggcggcggcggcggcggcggcggcggcggcggcggcggc
Frame1  A G K I P N N L P D L T E F R K R

          510     520     530     540     550
Query 1  ggagggtggcggcggcggcggcggcggcggcggcggcggcggcggcggcggc
Frame1  K D K Y Q P P D G G D L V E V Y L

```

FIG. 14B1

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```
      560      570      580      590      600
Query: 1 tccctagacacacagcatcacagagtcacccacagggaaatccagggccaggtc
Frame: 1 L D T S I Q S S H R B I B G R V

      610      620      630      640      650
Query: 1 atggctcacagacctccagacatgagccacagggagagagggacccgctccs
Frame: 1 R V T S F E N V F E E D C I R F R

      660      670      680      690      700
Query: 1 cagacaggtccagccagtgctgagagagccatgcacccacccagggagggag
Frame: 1 R Q A S K C D S E S T H L A G V V

      710      720      730      740      750
Query: 1 ccagggccgggagtcggcgctggccagggatgcacacatggcgaggtcg
Frame: 1 S G E D A G V A K G A S M R S L

      760      770      780      790      800
Query: 1 cggctgctcaactgcaggggaaggggacgcttagggccacatctatagg
Frame: 1 S V L N C Q G K G T V S S I L I G

      810      820      830      840      850
Query: 1 ccggaggttatctcgggaaagagagatggtcacagctgaggggacatagg
Frame: 1 L S F I E K G Q L V Q P V S F L V

      860      870      880      890      900
Query: 1 cgtgagctggacatggacggggaggtacagagccgttcacacagggagcc
Frame: 1 V L L F L A G D Y S A V I N A A

      910      920      930      940      950
Query: 1 tgcacagcagctggagggggctgggctgctgctgctgctgctgctgctgctg
Frame: 1 C C H L K R A G V V L V T A A D N

      960      970      980      990     1000
Query: 1 cctcggagagagagctgctgctcctactcccccagctcagctcccgaggtac
Frame: 1 F R D D A C L Y E P A S A E E V I

     1010     1020     1030     1040     1050
Query: 1 tccagcttggggcacacatgcccagggccaggggagagccctggggact
Frame: 1 F V G A T N A Q D Q P V F L C T

      1060      1070      1080      1090      1100
Query: 1 ctggggacacactcggcgttggctggacatcttggccacagggaggg
Frame: 1 L G T N F C R C V C L P A R G E D
```

FIG. 14B2

[illegible]

FIG. 14B3

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```

      850      860      870      880      890      900
      -----
Query   : caatggacacaaacagggcaagtacacaggtgacagctcgaatggga
Frame1 : H C H Q Q D B V E T Q D S S H W E

      950      960      970      980      990      1000
      -----
Query   : agtggaggaactcaggaacacagagcggcgtgctgagggcagaaggtc
Frame1 : V E D L Q T H K F F V L E E A Q Q

      1050      1060      1070      1080      1090      1100
      -----
Query   : agcgcacacagctgctgaggaacagagagagagagctcgaatgggtg
Frame1 : F H Q C V G H B E A E I H A S C

      1150      1160      1170      1180      1190      1200
      -----
Query   : tggatggcagaagctgggaatggaagtcagaagcaggaatcagagc
Frame1 : C H A P D L E C H V K E H E I P A

      1250      1260      1270      1280      1290      1300
      -----
Query   : caatcagggcaggtgacgtggagctggagggaggtggacatggctg
Frame1 : F Q G G Q V T V A C D S B W T L T B

      1350      1360      1370      1380      1390      1400
      -----
Query   : gctggagcgaactcctgggaactcgaagctcctgggggctcagcgtc
Frame1 : C S A L P G T S K V L S A V A V

      1450      1460      1470      1480      1490      1500
      -----
Query   : gacacacggtgtatgctcagggagcgggacatcagcactacagggcag
Frame1 : D H E E V V S S B D V E T T E S T

      1550      1560      1570      1580      1590      1600
      -----
Query   : cagcgaagagcagctgacacagcttgcaatctgctgacggagcagc
Frame1 : S E E A V T A Y A I C C E D B H L

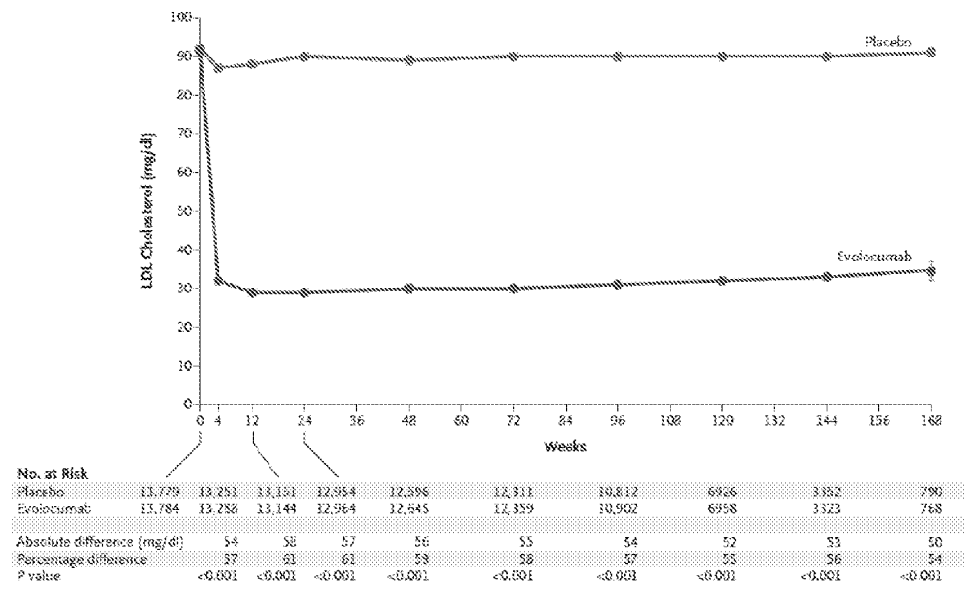
      1650      1660      1670      1680      1690      1700
      -----
Query   : tggcgcagggctcaccaggaatcag
Frame1 : A Q A S Q E L Q

```

FIG 14B4

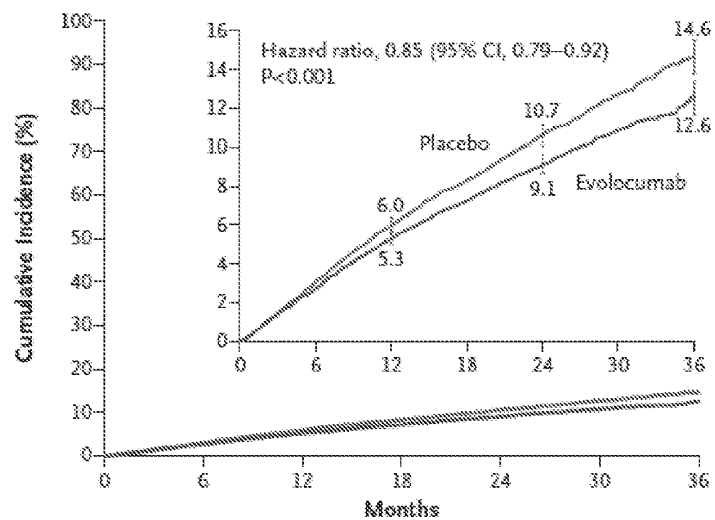
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FIG. 15

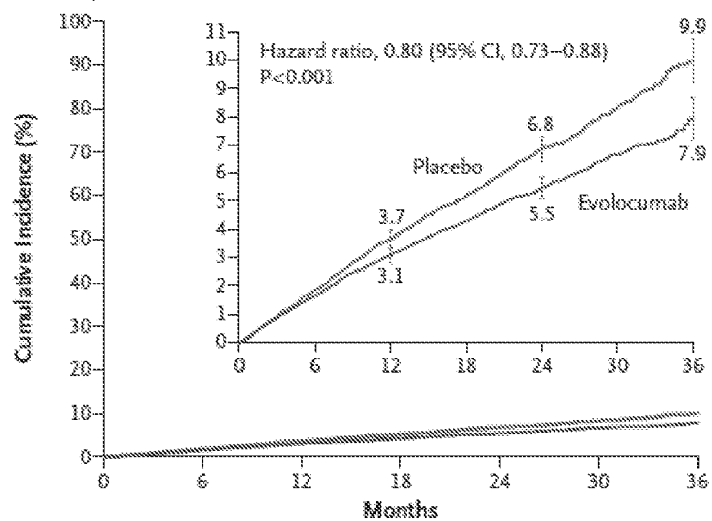


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Figure 16A and Figure 16 B

A Primary Efficacy End Point**No. at Risk**

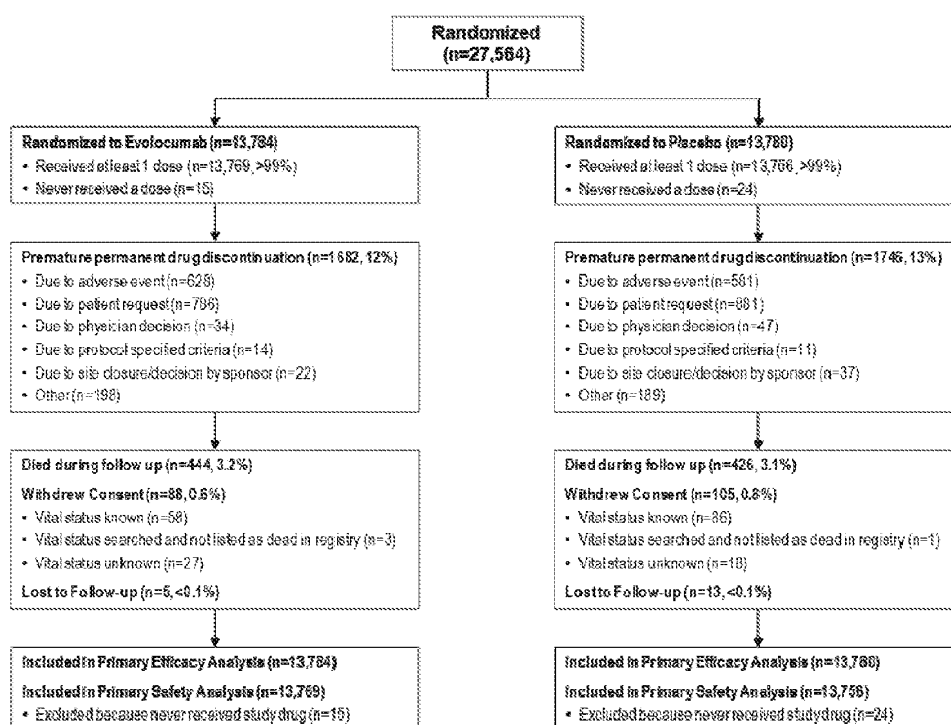
Placebo	13,780	13,278	12,825	11,871	7610	3690	686
Evolocumab	13,784	13,351	12,939	12,070	7771	3746	689

B Key Secondary Efficacy End Point**No. at Risk**

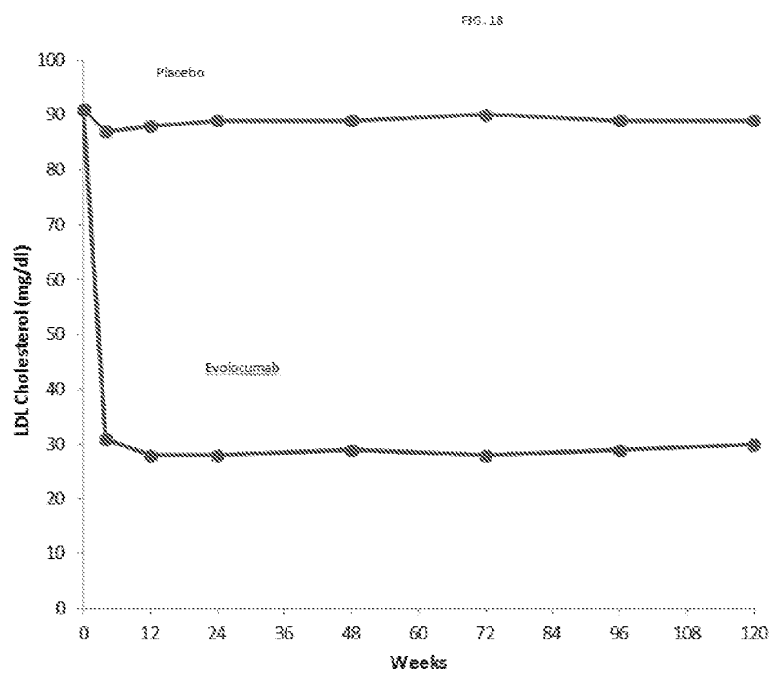
Placebo	13,780	13,449	13,142	12,288	7944	3893	731
Evolocumab	13,784	13,501	13,241	12,456	8094	3935	724

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FIG. 17



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FIG. 19

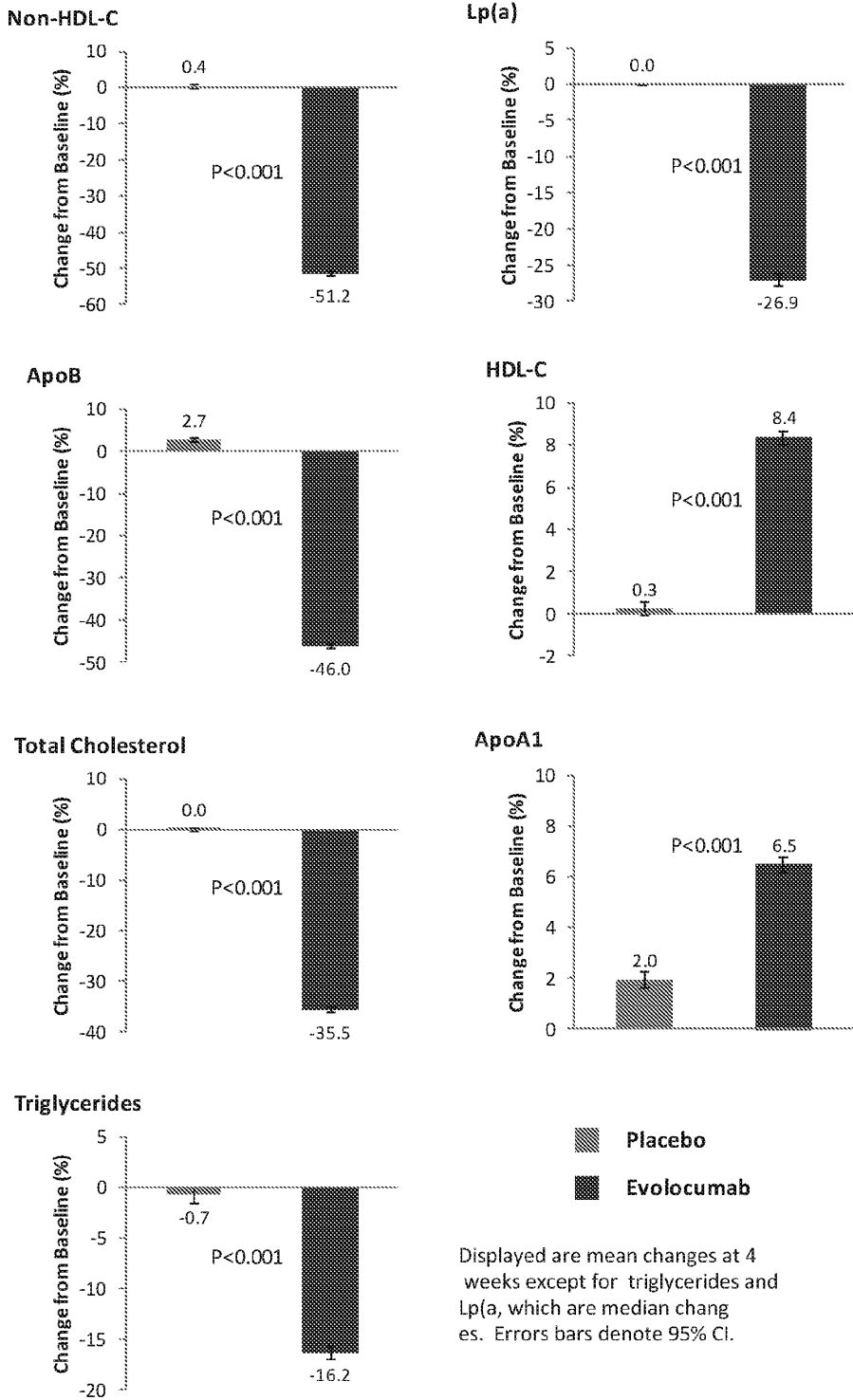
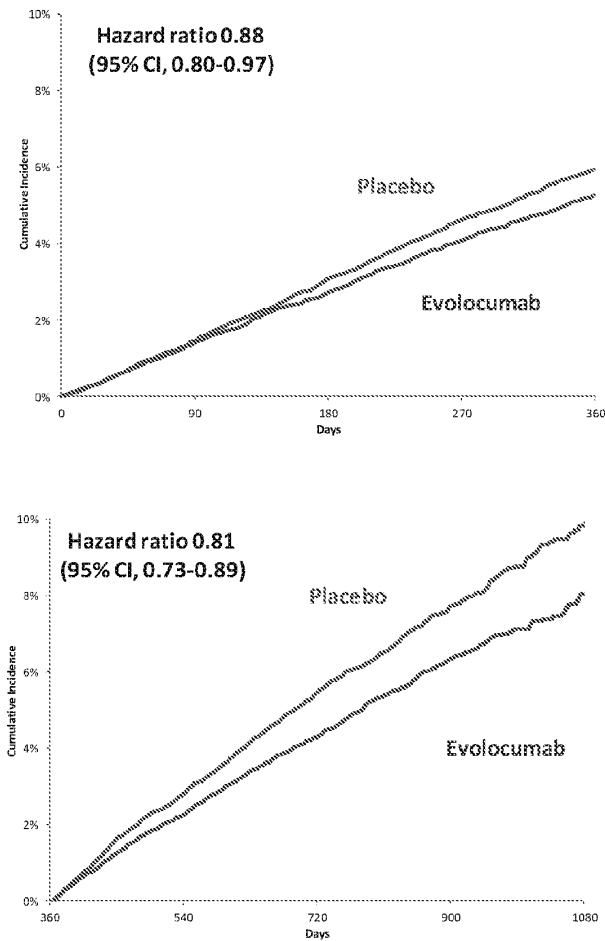


FIG. 20

A. Primary endpoint



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FIG. 21

B. Key Secondary endpoint

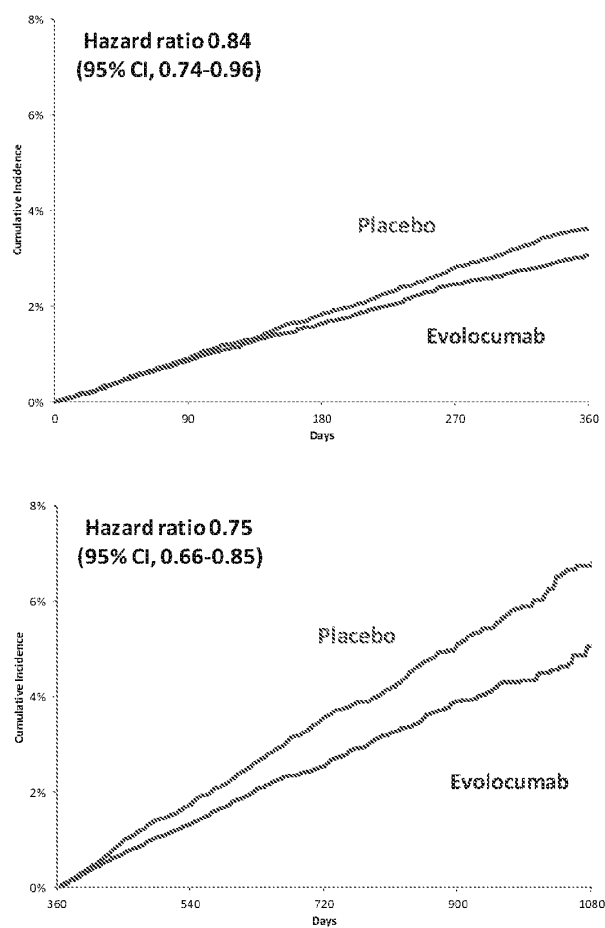
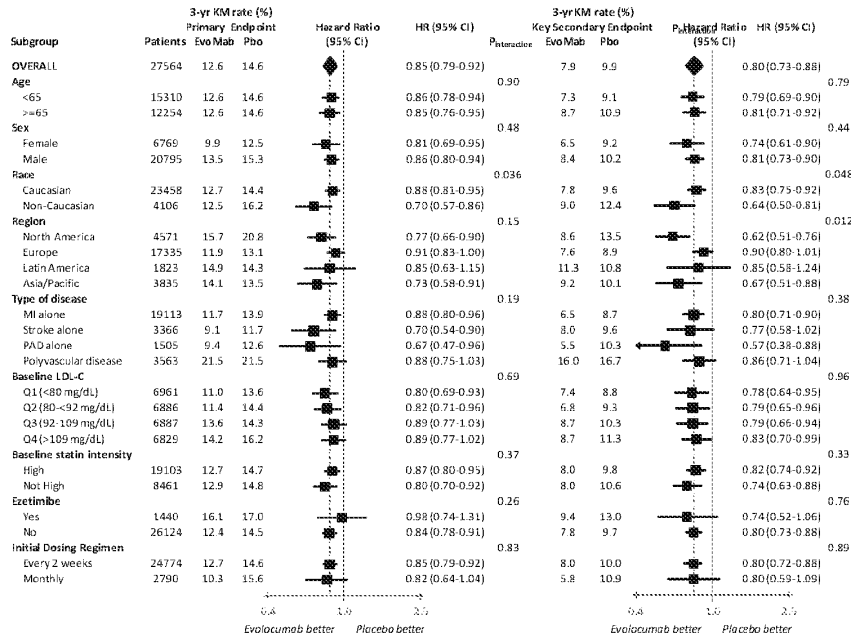
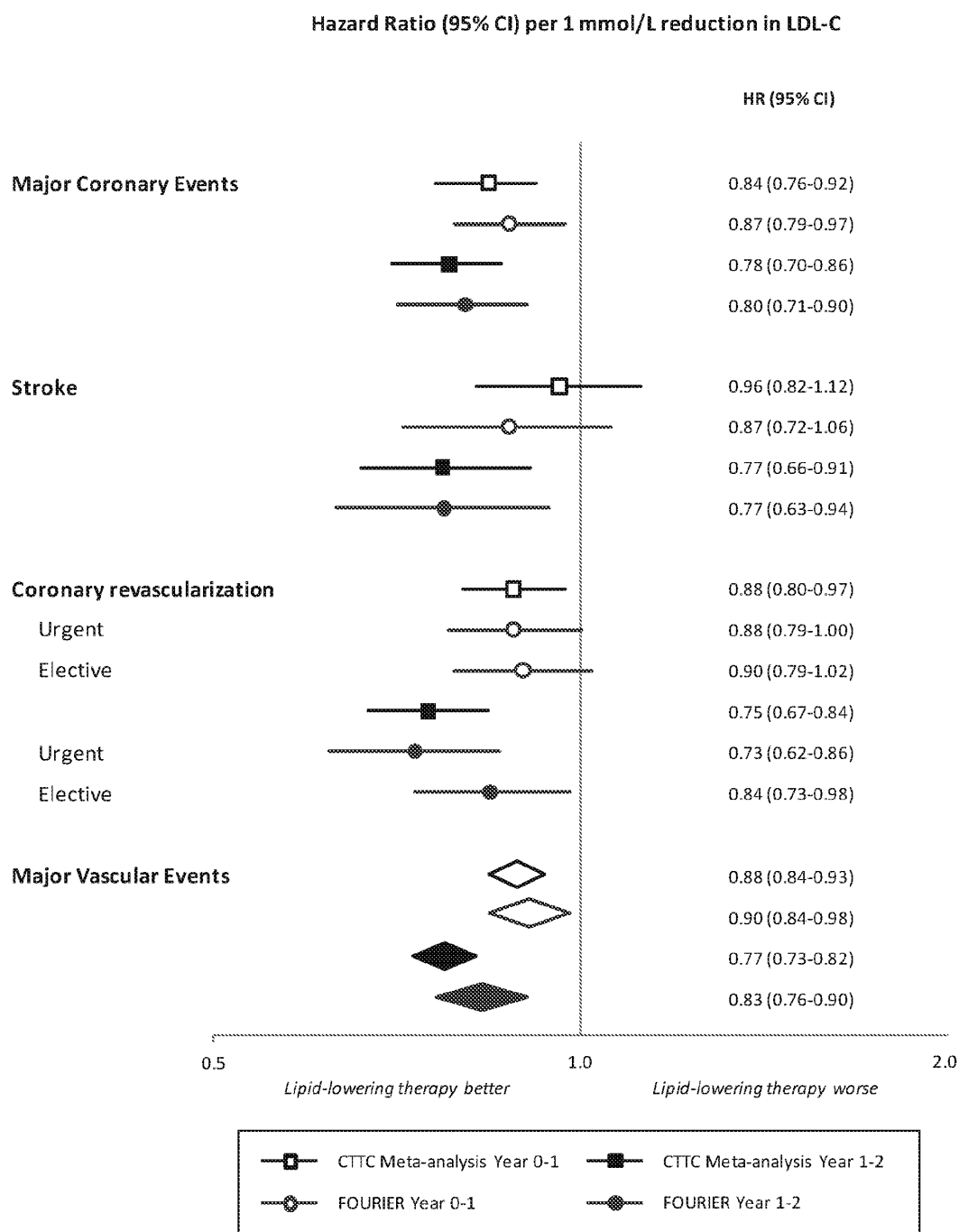


FIG. 22



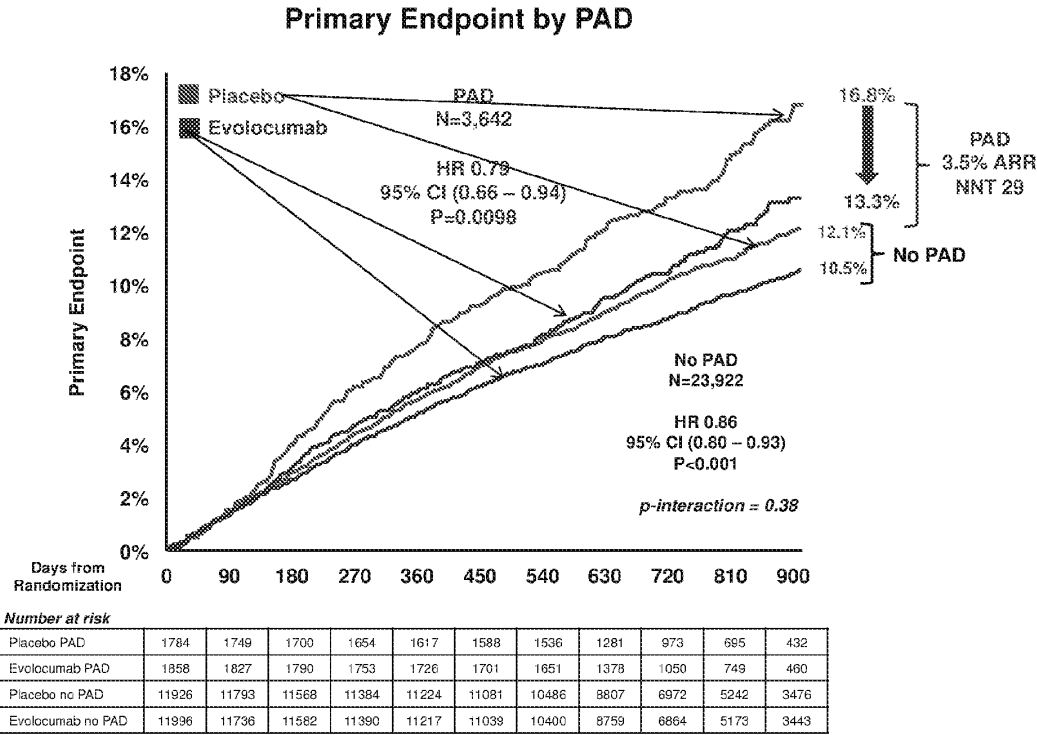
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FIG. 23



Data from Cholesterol Treatment Trialists Collaboration (CTTC) are from *Lancet* 2010;376:1670-81

FIG. 24A



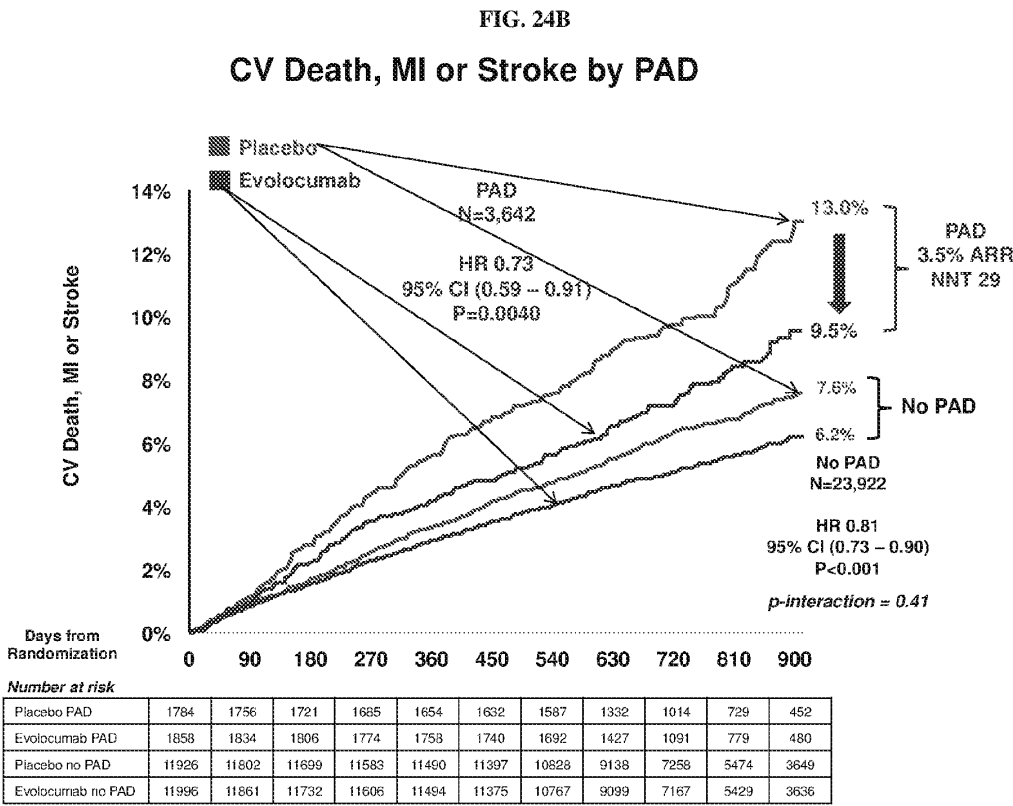


FIG. 25A
Major Adverse Limb Events – All Patients

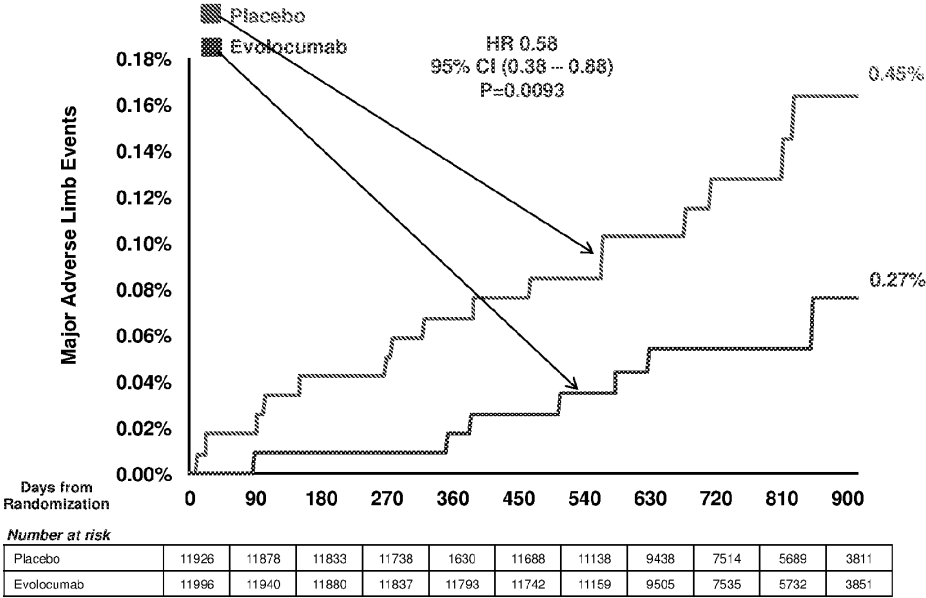
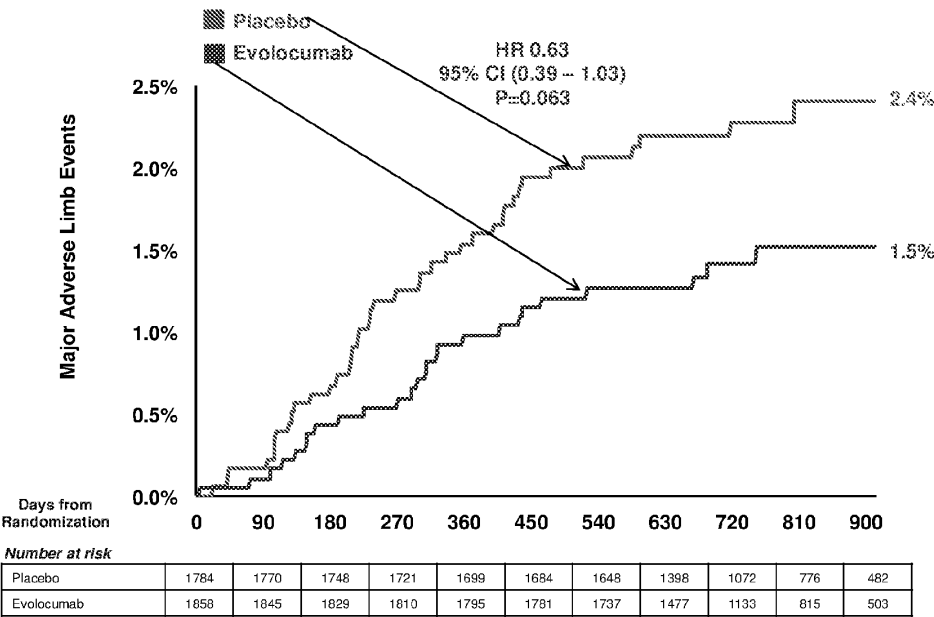
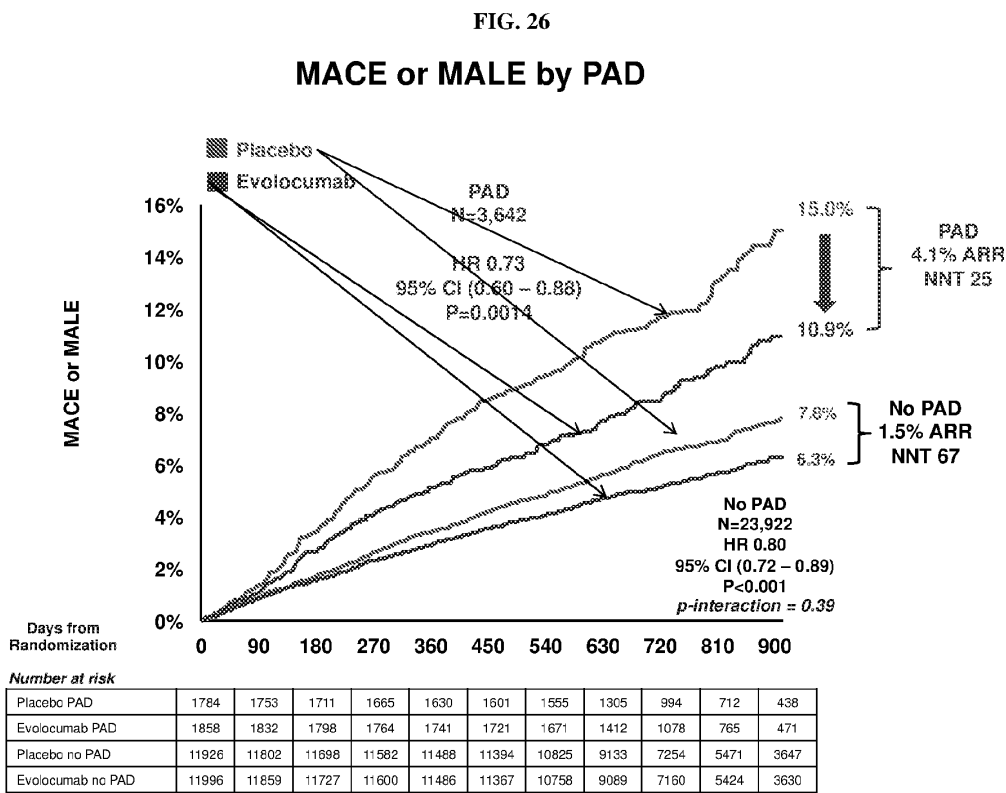


FIG. 25B

Major Adverse Limb Events – Patients with PAD

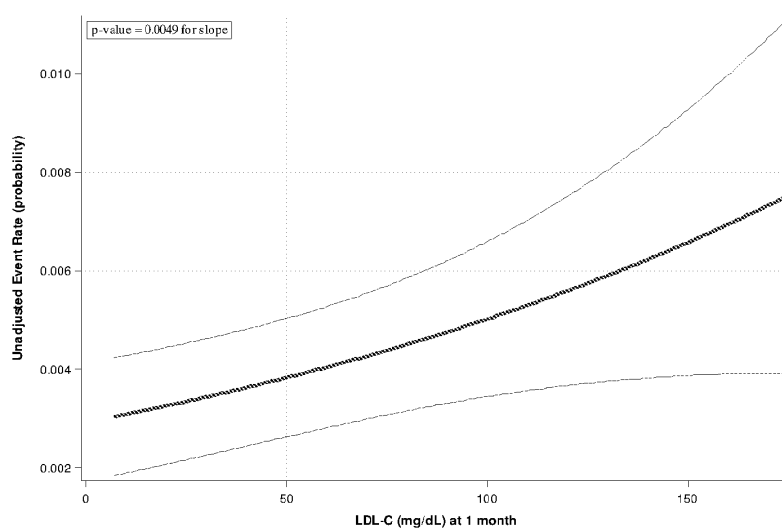


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FIG. 27
Achieved LDL-C and Major Adverse Limb Events



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FIG. 28

Cardiovascular Outcomes at 2.5 Yrs in Placebo Patients by Symptomatic PAD at Baseline

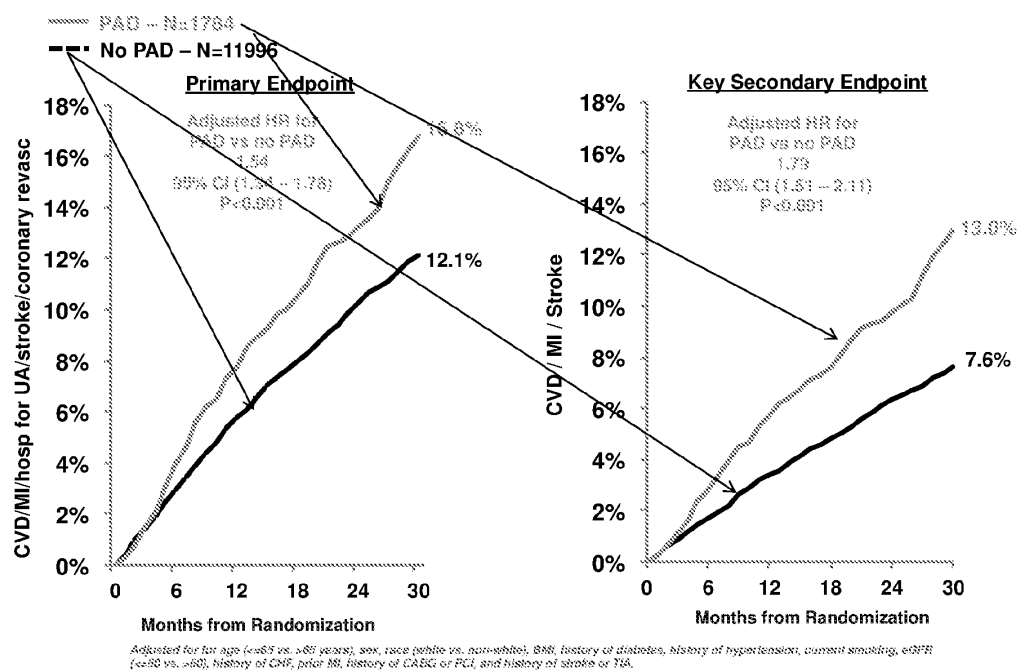


FIG. 29

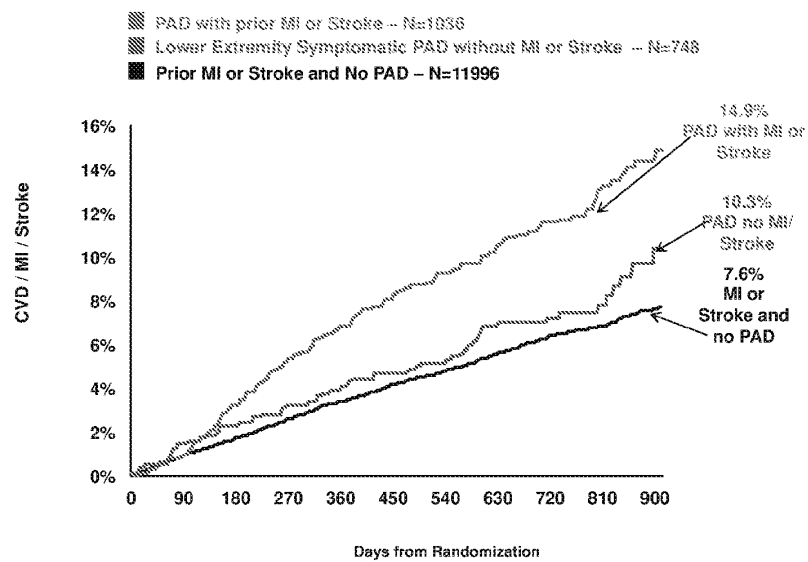
CV Death, MI or Stroke at 2.5 Years in Placebo Patients by Disease State

FIG. 30

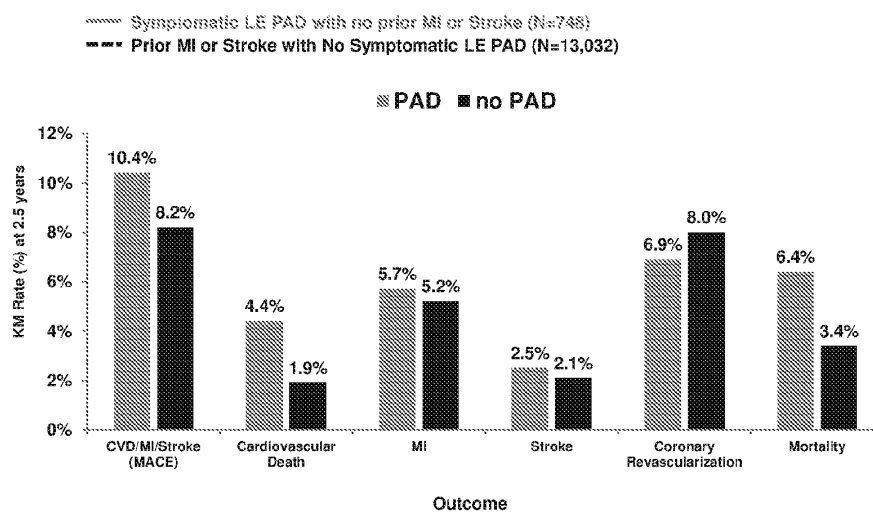
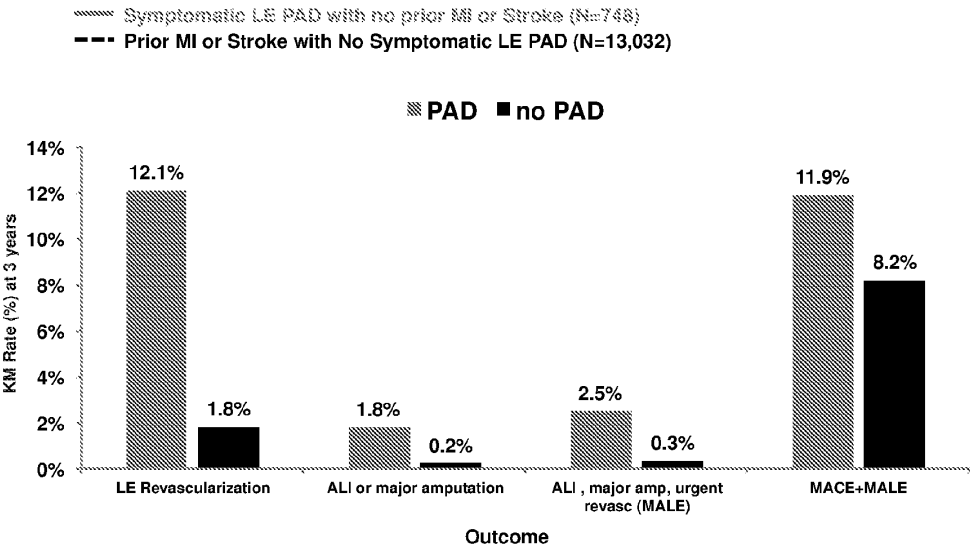
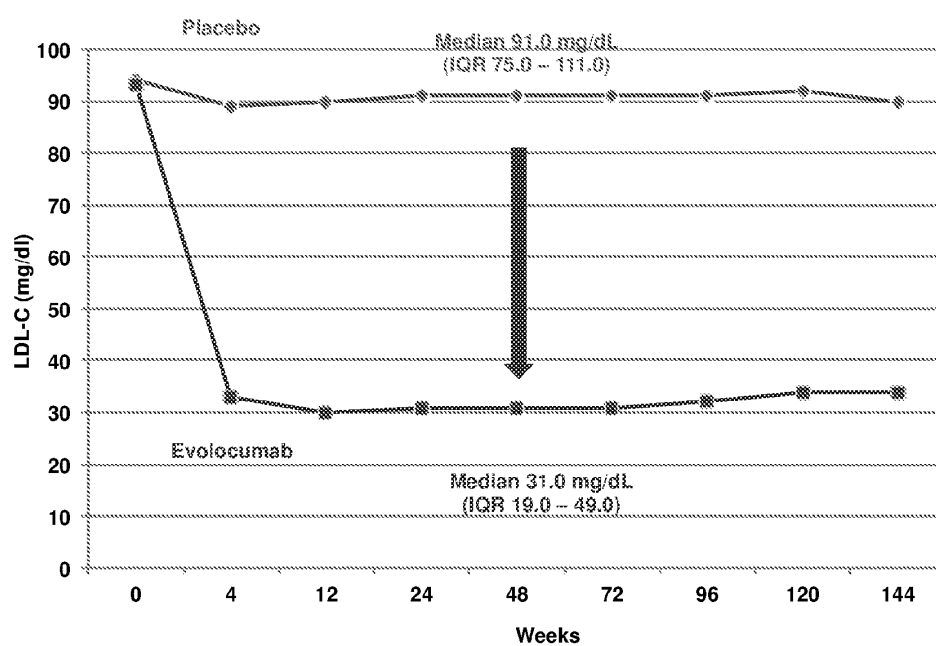
Cardiovascular Outcomes at 2.5 Yrs in Placebo Patients by Symptomatic PAD and no MI/Stroke at Baseline

FIG. 31
Limb Outcomes at 2.5 Yrs in Placebo Patients by
Symptomatic PAD and no MI or Stroke at Baseline



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FIG. 32

LDL Cholesterol by Treatment Group in Patients with Symptomatic Lower Extremity PAD

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FIG. 33A

Primary Endpoint in Patients with PAD and no MI or Stroke

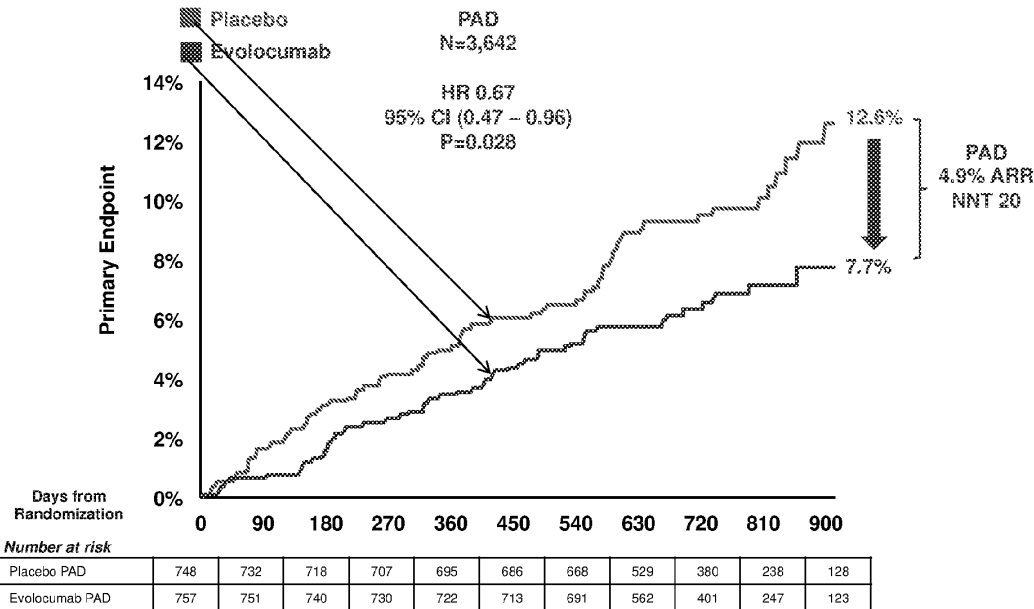


FIG. 33B

CV Death, MI or Stroke in Patients with PAD and no MI or Stroke

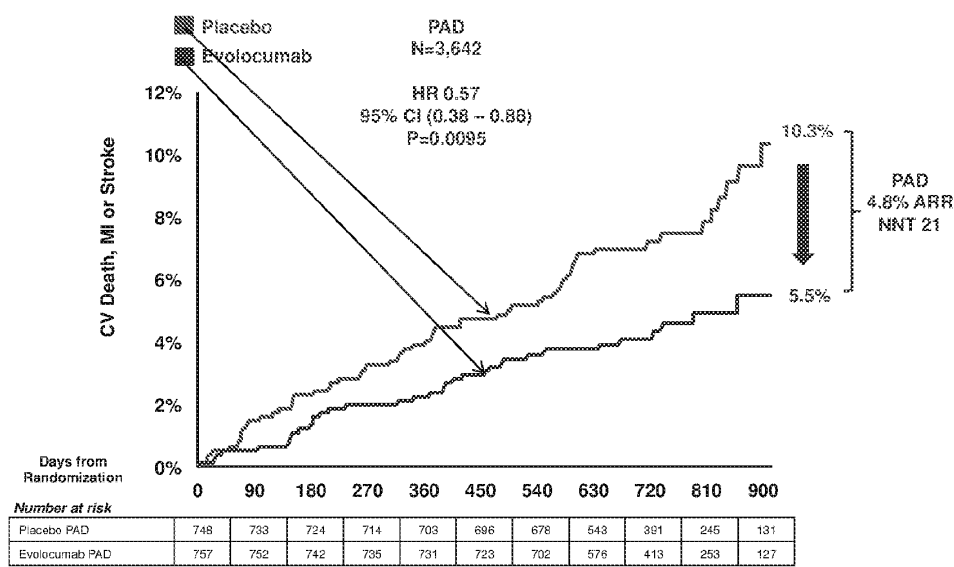


FIG. 33C

Major Adverse Limb Events – Patients with PAD and no MI or Stroke

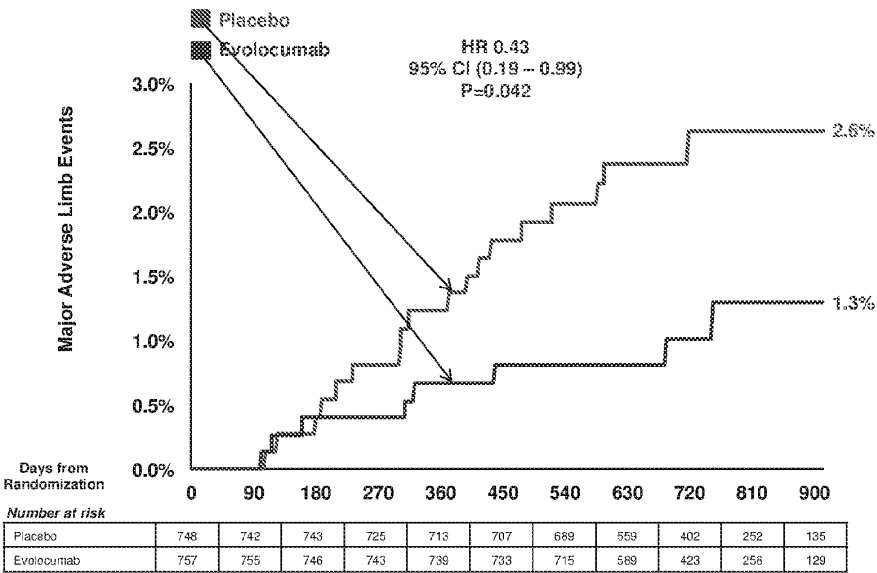
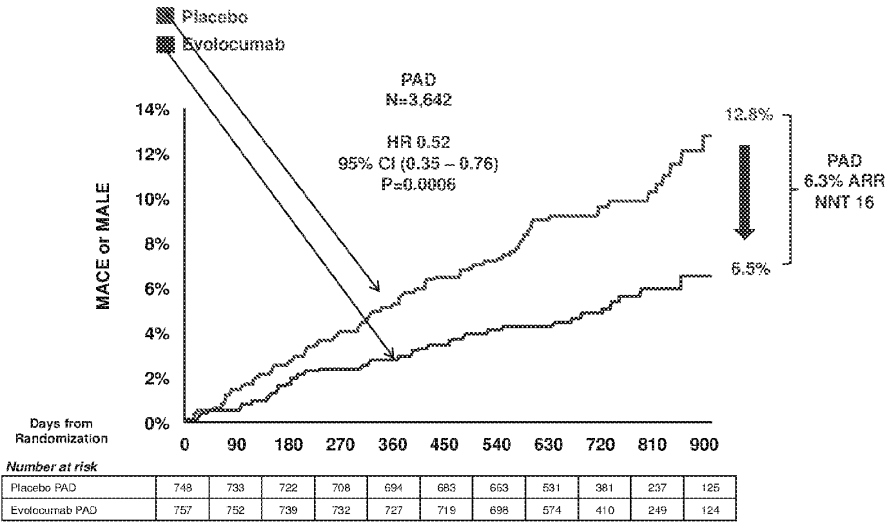


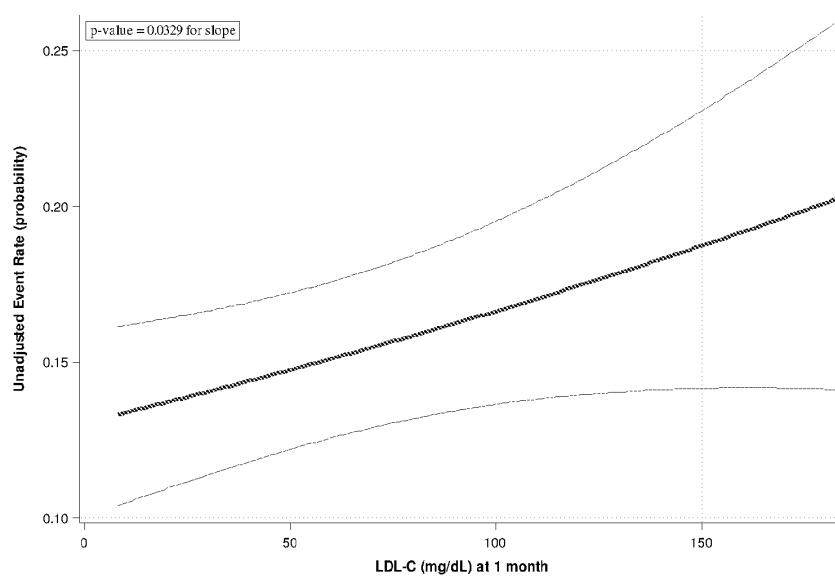
FIG. 34

MACE or MALE in Patients with PAD and no MI or Stroke



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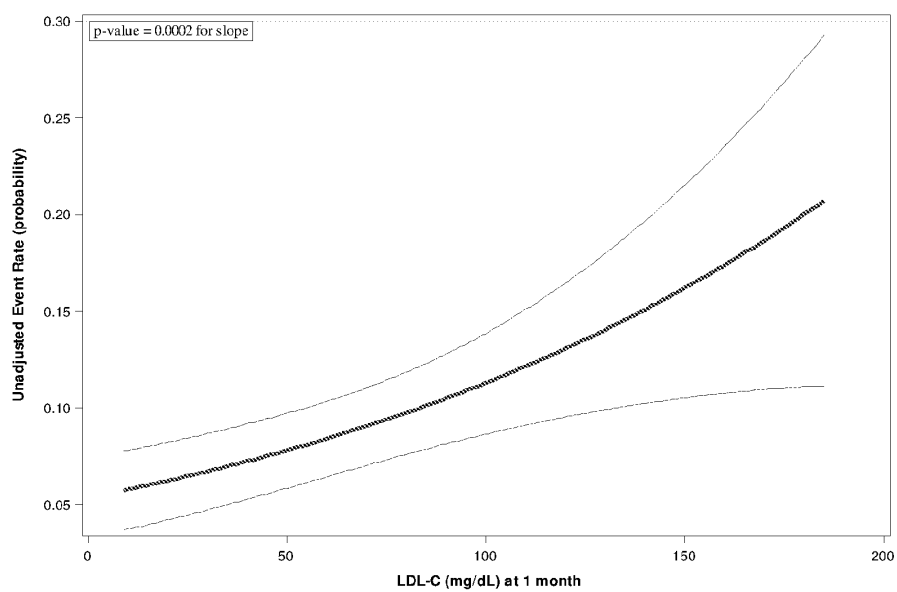
FIG. 35

Achieved LDL-C and MACE or MALE in Patients with PAD

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FIG. 36

Achieved LDL-C and MACE or MALE in Patients with PAD and no MI or Stroke



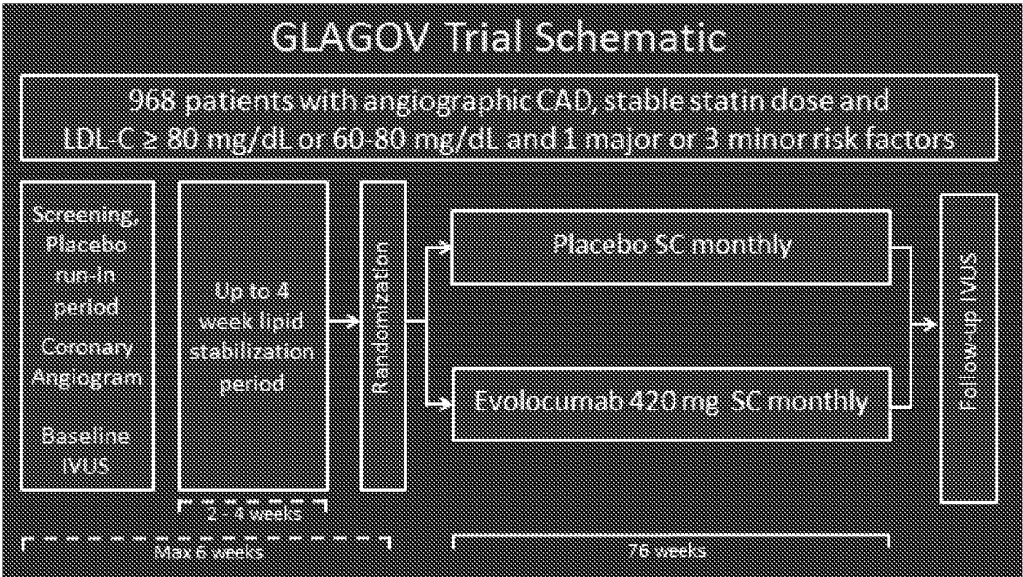


FIG. 37

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GLAGOV secondary analysis

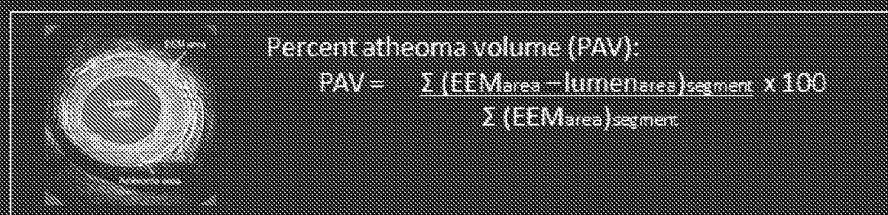


FIG. 38

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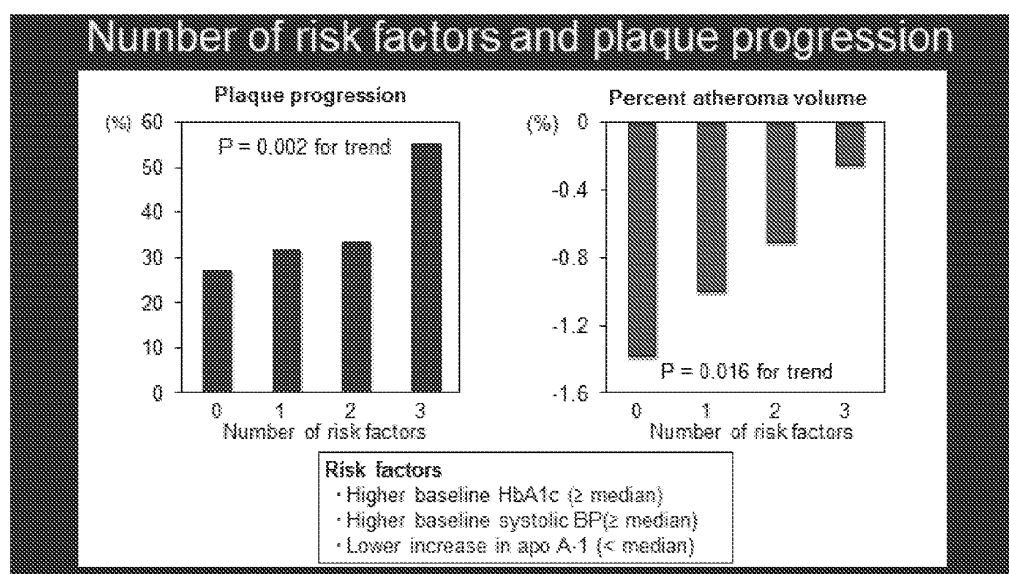


FIG. 39

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Trial Design

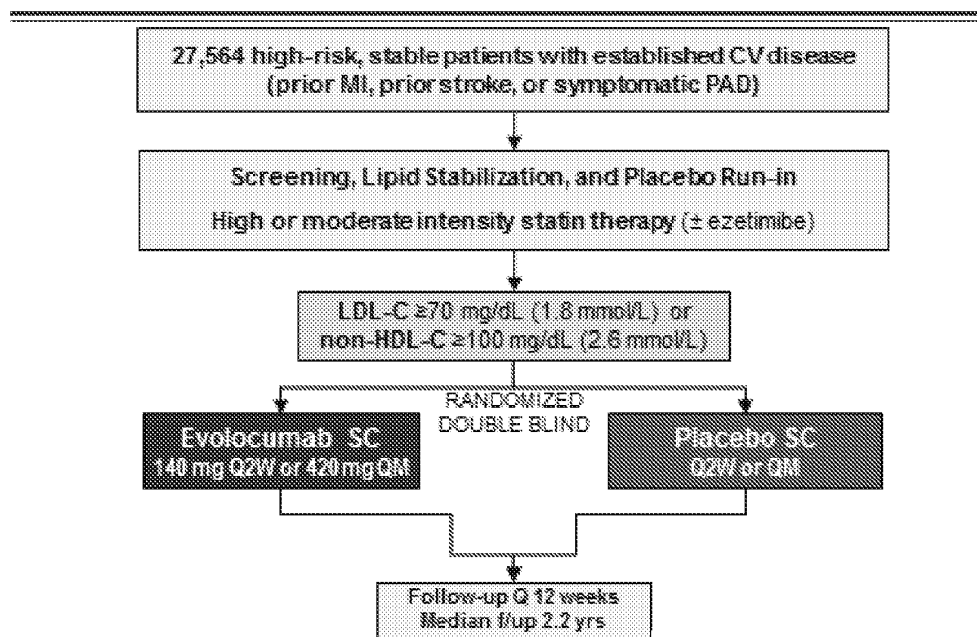


FIG. 40

Primary Results

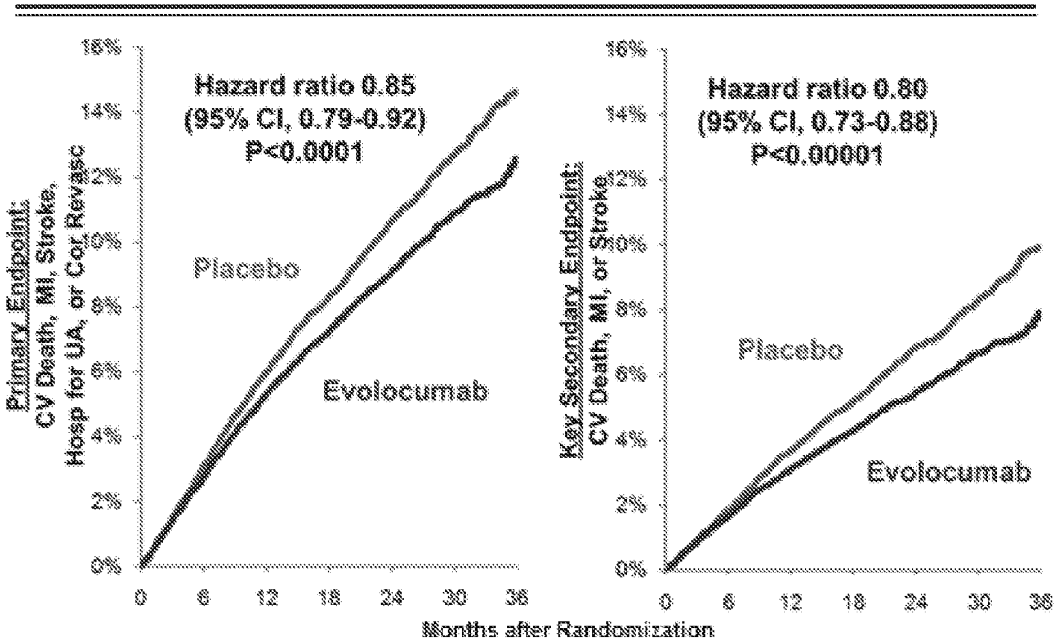


FIG. 41

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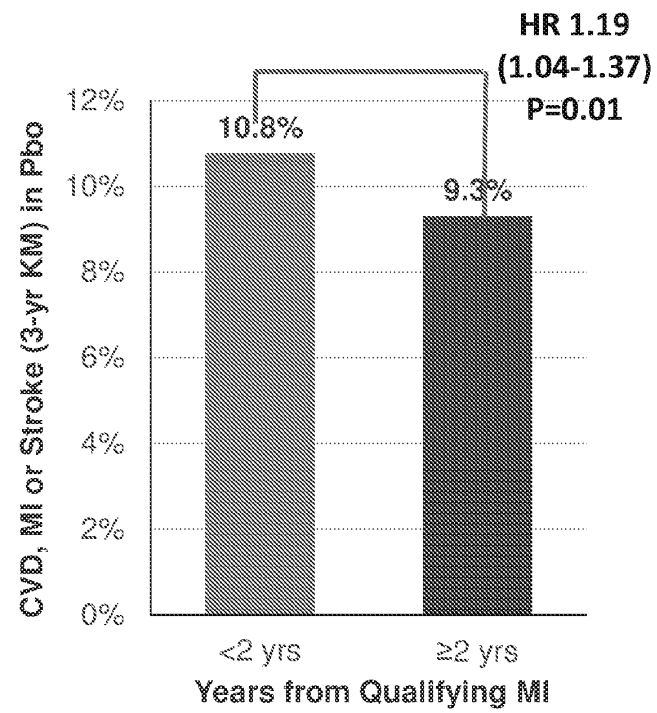


FIG. 42 .

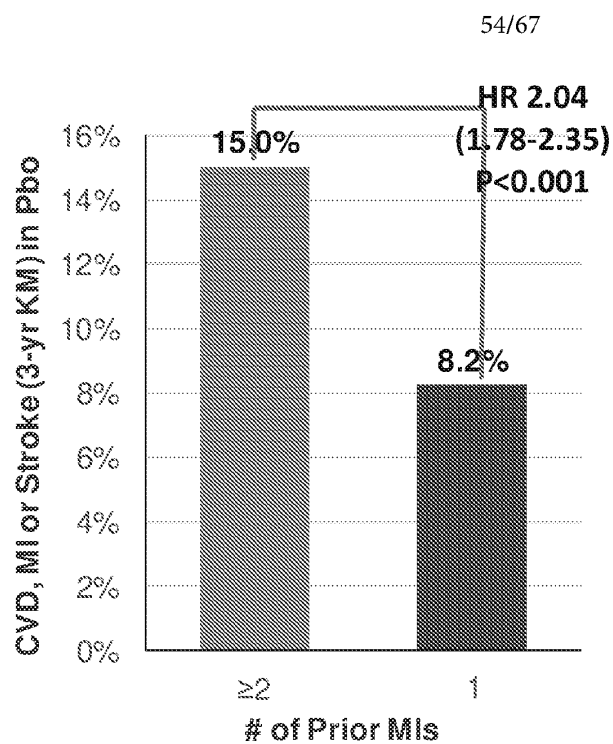


FIG. 43

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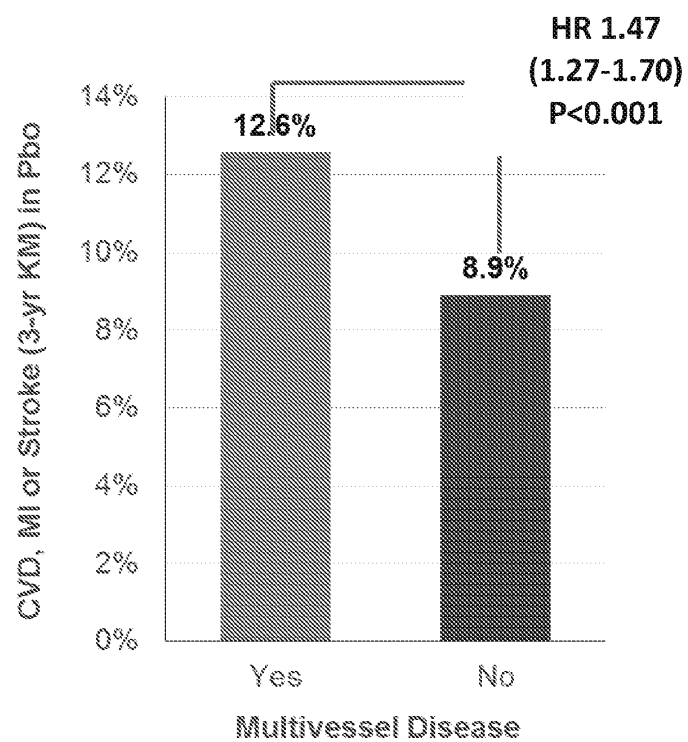


FIG. 44

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Benefit of EvoMab Based on Time from Prior MI

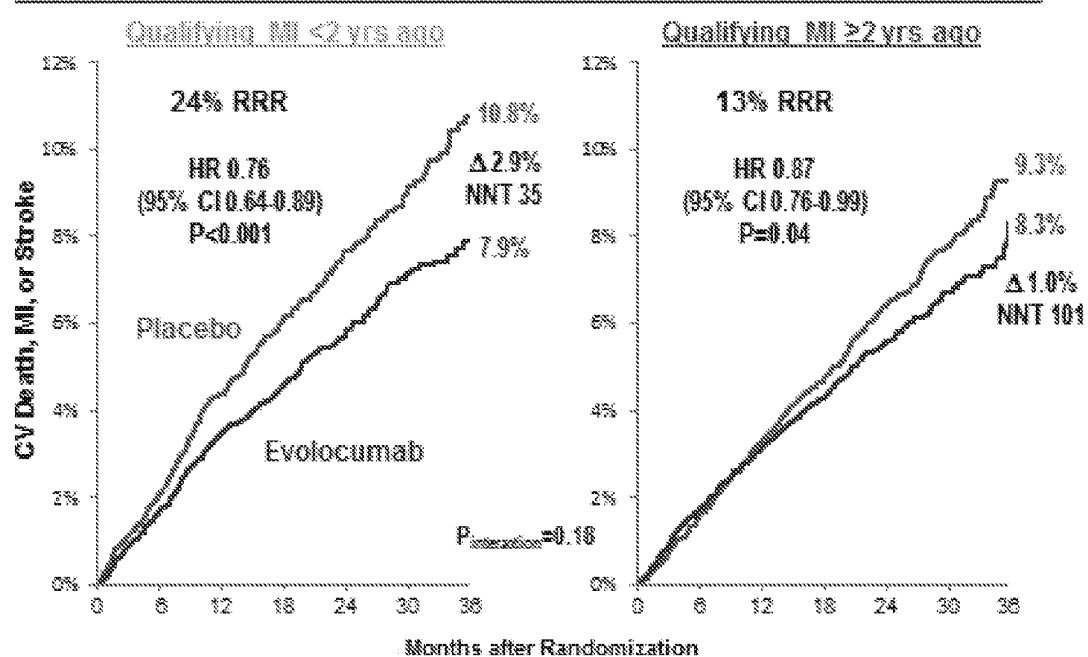


FIG. 45

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Benefit of EvoMab Based on # of Prior MIs

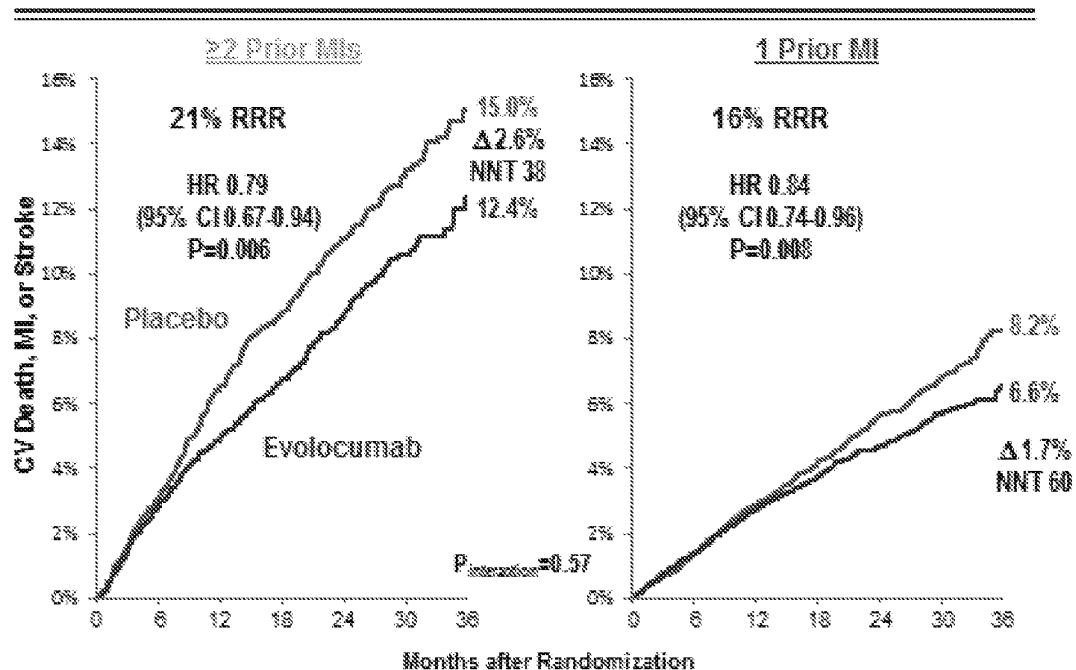


FIG. 46

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Benefit of EvoMab Based on Time from Prior MI

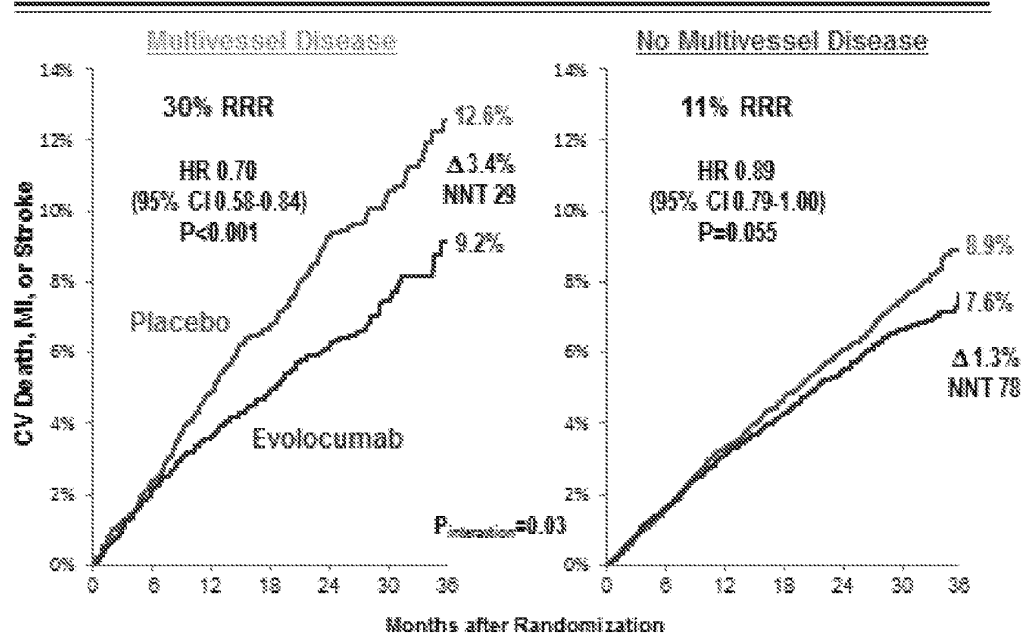


FIG. 47

Benefit of EvoMab Based on # of High-Risk MI Features

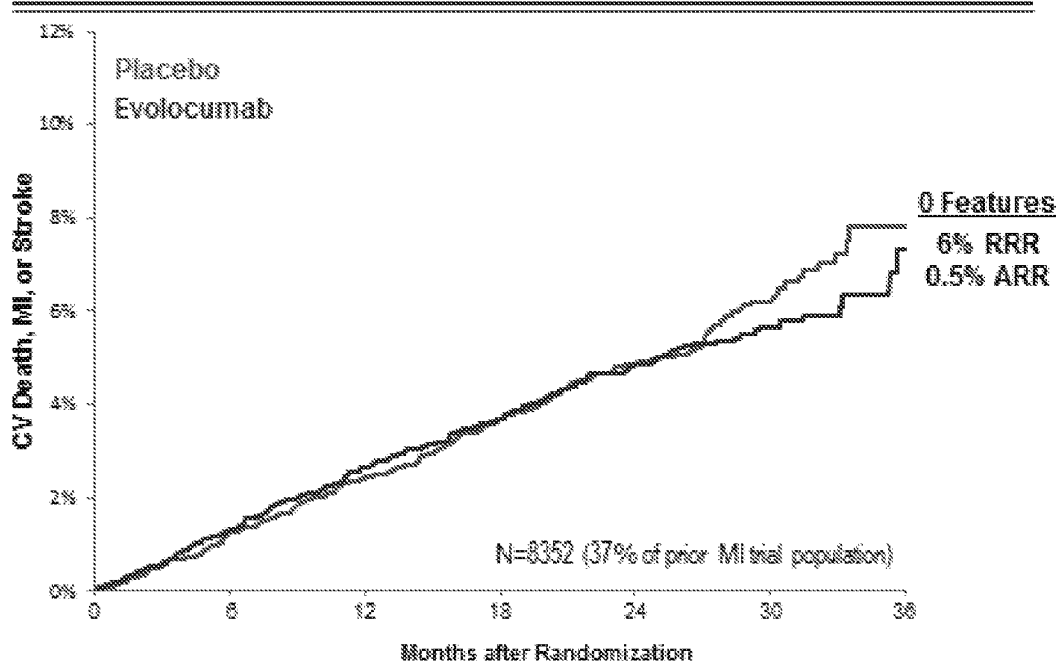


FIG. 48

Benefit of EvoMab Based on # of High-Risk MI Features

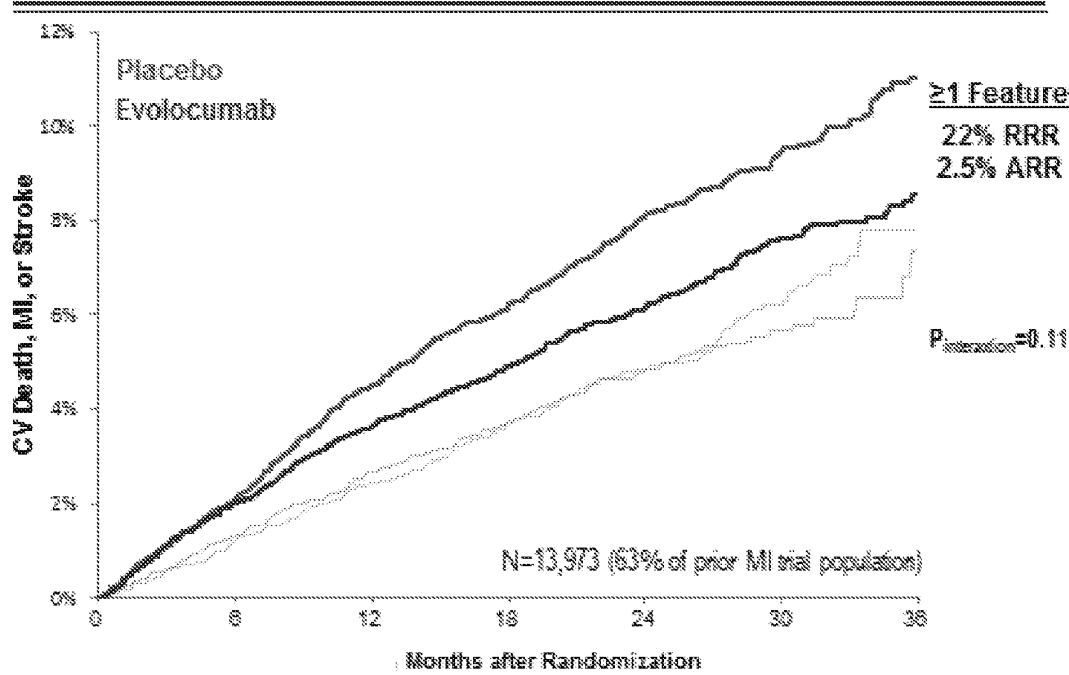


FIG. 49

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Landmark Analyses in Pts w/ a High-Risk MI Feature

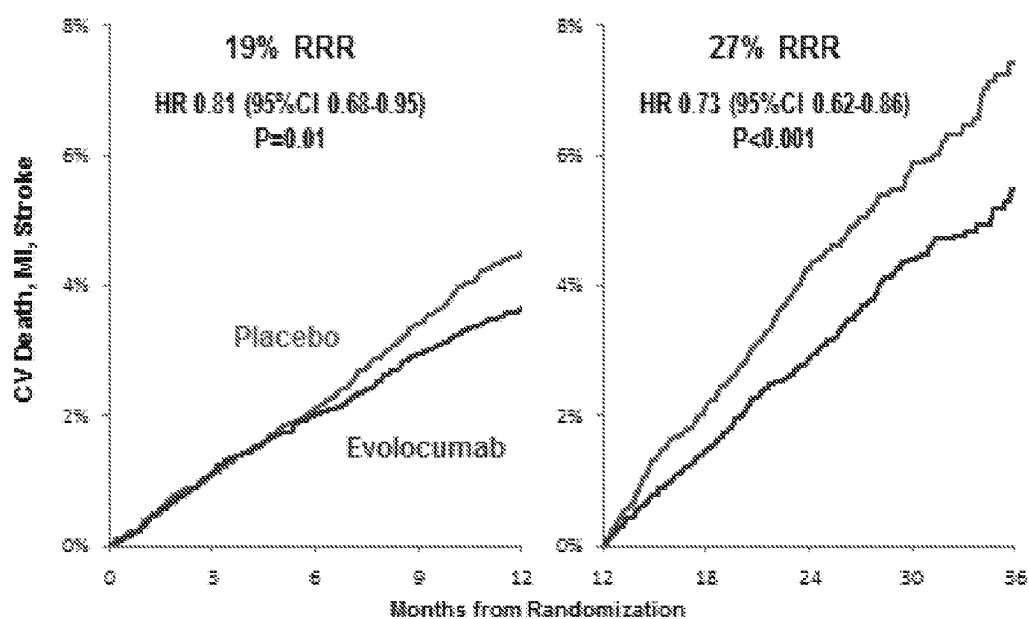


FIG. 50

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Landmark Analyses in Pts w/ a High-Risk MI Feature

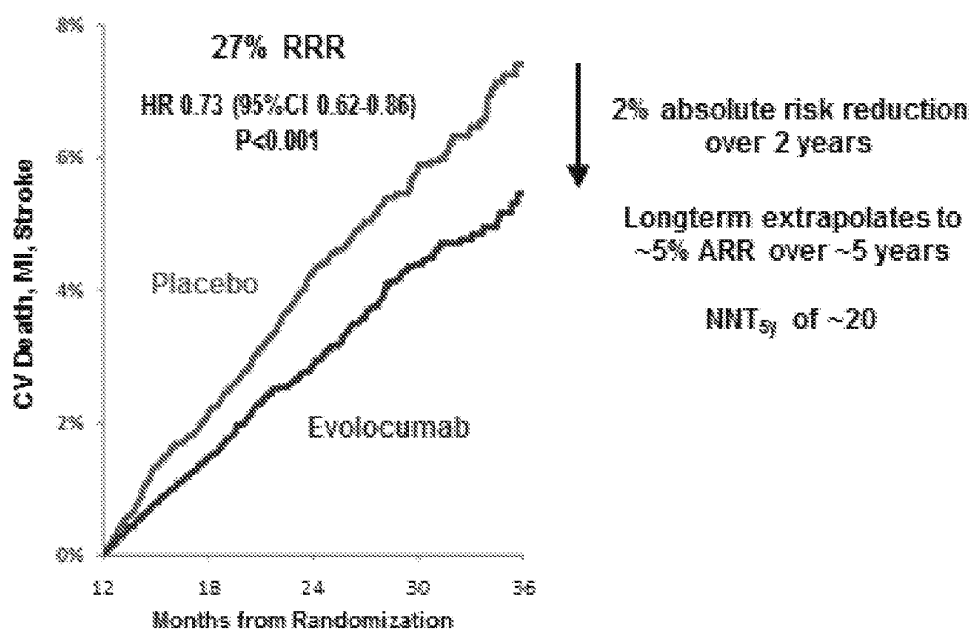


FIG. 51

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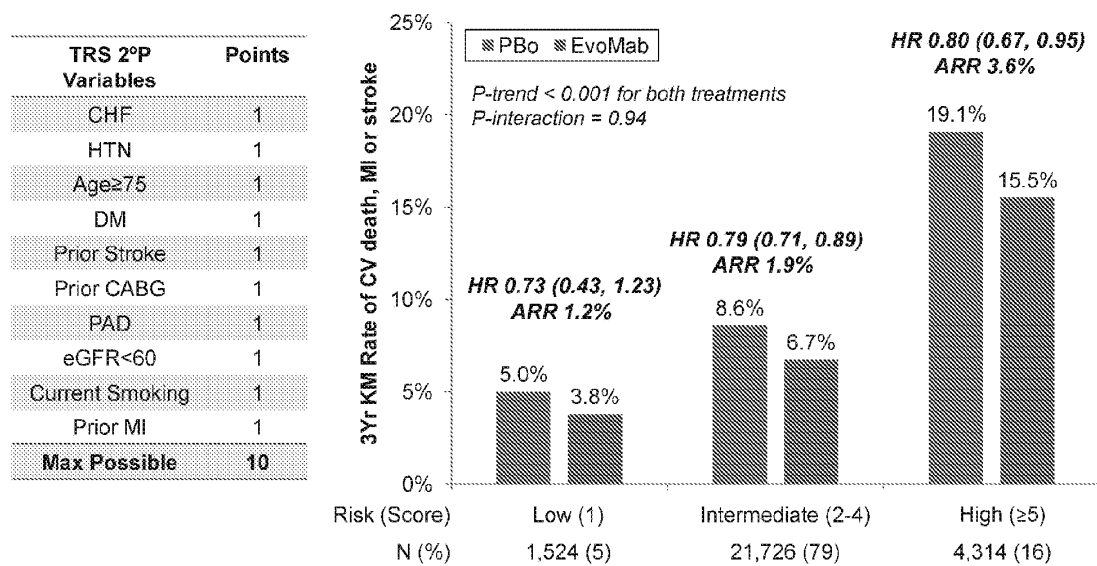


FIG. 52

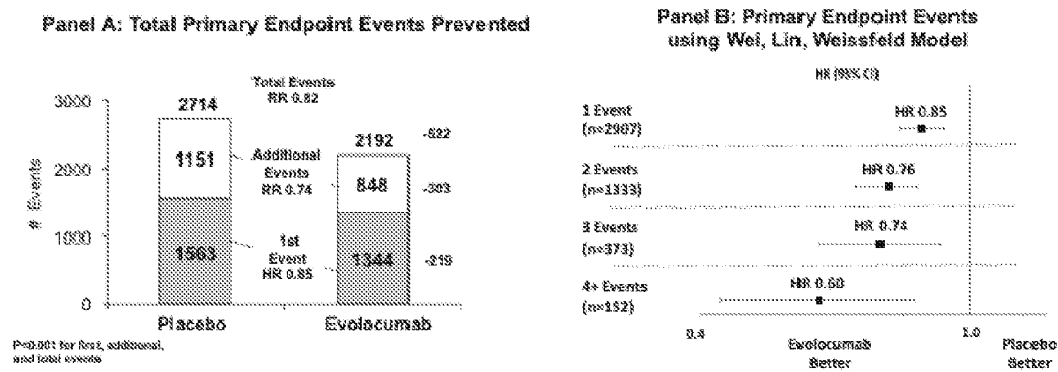


FIG. 53

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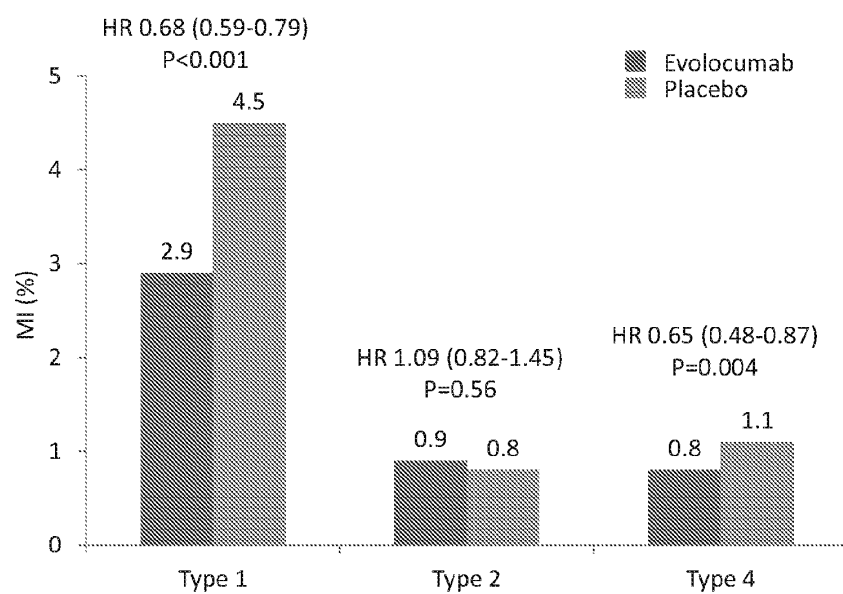


FIG. 54A

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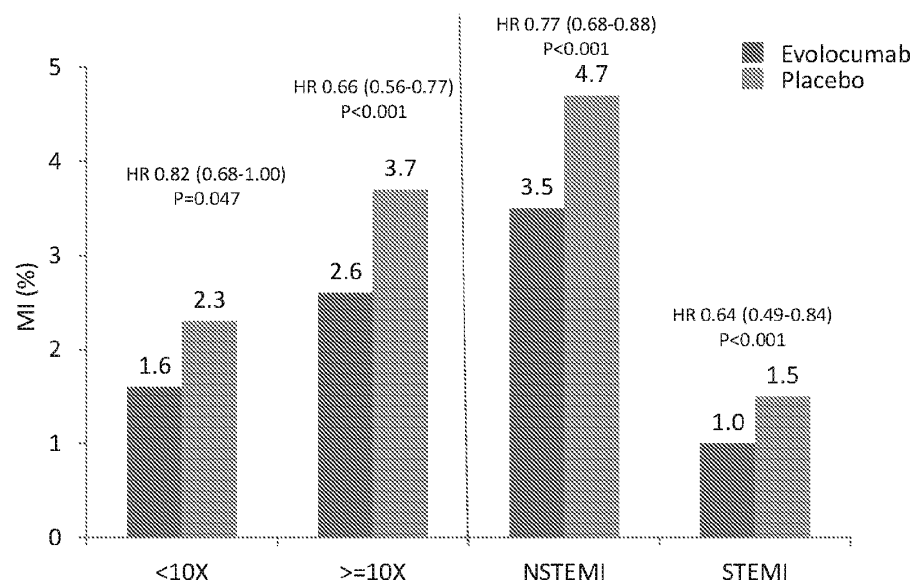


FIG. 54B

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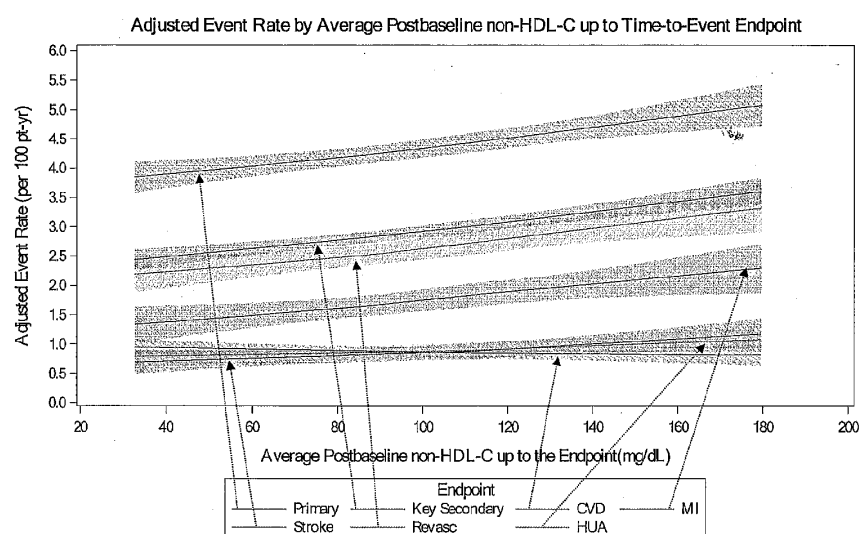


FIG. 55