Human WNT Protein Alignments

```
gi|4885655|ref|NP_005421.1|1      MGLWALLPGW--------------------VSATLLLALAALPAALAANS 30
gi|4507927|ref|NP_003382.1|2      ------MNAPLG--------------------GIWLWLPLLLTWLTPEVN 24
gi|13518017|ref|NP_004176.2|2b    -------MLDGLGVV--------------AISIFGIQLKTEGSLRTAVPGIP 31
gi|13540477|ref|NP_110380.1|3     ------MEPH--------------------LLGLLLGLLLGGTRVLAGYP 24
gi|14916475|ref|NP_149122.1|3a    ------MAP---------------------LGYFL-LLCSLKQALGSYP 21
gi|17402922|ref|NP_110388.2|4     ------MSPRSCLR----------------------SLRLLVFAVFSAAA 22
gi|40806205|ref|NP_003383.2|5a    ------MKKSIGILSPGVALGMAGSAMSSKFFLVALAIFFSFAQVVIEAN 44
gi|14249180|ref|NP_116031.1|5b    -------------------------MPSLLLLFTAALLSSWAQLLTDAN 24
gi|16507239|ref|NP_006513.1|6     ----------------------------MLPPLPSRLGLLLLLLLCP 19
gi|17505191|ref|NP_004616.2|7a    ------MNRKARRC----------------LGHLFLSLG--MVYLRIGGF 26
gi|17505193|ref|NP_478679.1|7b    ------MHRNFRKW----------------IFYVFLCFG--VLYVKLGAL 26
gi|17505195|ref|NP_490645.1|8a    ------------------------------------------MGNLFMLWAA 10
gi|110735437|ref|NP_003384.2|8b   ---------------------------------------------MFLSKPS 7
gi|15082261|ref|NP_003386.1|9a    -------------------------MLDGSPLARWLAAAFGLTLLLAALR 25
gi|17017976|ref|NP_003387.1|9b    -------------------------MR--PPPALALAGLC----LLALPA 19
gi|16936520|ref|NP_079492.2|10a   ------MGSAHPRP-----------WLRLRPQPQPRPALWVLLFFLLLLA 33
gi|16936522|ref|NP_003385.2|10b   -------------------------MLEEPRPRPPPSGLAGLLFLALCS 24
gi|17017974|ref|NP_004617.2|11    ---------------------------------MRARPQVCEALLFALALQ 18
gi|17402916|ref|NP_476509.1|16    ------MDRAALLG----------------LARLCALWAALLVLFPYGAQ 28
gi|21357511|ref|NP_650272.1|D     ---------------------------------MIFAITFFMGIT------- 12

gi|4885655|ref|NP_005421.1|1      SGRWWG-------IVNVASSTNLLTDSKSLQLVLEPSLQLLSRKQRRLIR 73
gi|4507927|ref|NP_003382.1|2      SSWWY--------------MRATGGS-----SRVMCDNVPGLVSSQRQLCH 56
gi|13518017|ref|NP_004176.2|2b    TQSAFN--------KC---LQRYIGALG---ARVICDNIPGLVSRQRQLCQ 68
gi|13540477|ref|NP_110380.1|3     --IWWS-------LALGQQYTSLGS-----QPLLCGSIPGLVPKQLRFCR 60
gi|14916475|ref|NP_149122.1|3a    --IWWS-------LAVGPQYSSLGS-----QPILCASIPGLVPKQLRFCR 57
gi|17402922|ref|NP_110388.2|4     SNWLYL--------AK-----LSSVGSIS---EEETCEKLKGLIQRQVQMCK 58
gi|40806205|ref|NP_003383.2|5a    SWWSLG--------MNNPVQMSEVYIIG---AQPLCSQLAGLSQGQKKLCH 84
gi|14249180|ref|NP_116031.1|5b    SWWSLA-------LN-PVQRPEMFIIG---AQPVCSQLPGLSPGQRKLCQ 63
gi|16507239|ref|NP_006513.1|6     AHVGG-------------LWWAVGSPLVMDPTSICRKARRLAGRQAELCQ 56
gi|17505191|ref|NP_004616.2|7a    SSVVA--------------LGAS-----------IICNKIPGLAPRQRAICQ 53
gi|17505193|ref|NP_478679.1|7b    SSVVA--------------LGAN-----------IICNKIPGLAPRQRAICQ 53
gi|17505195|ref|NP_490645.1|8a    LGIC--------------------------CAAFSASAWSVNNFLITGPK 34
gi|110735437|ref|NP_003384.2|8b   VYICLF-----------------------TCVLQLSHSWSVNNFLMTGPK 34
gi|15082261|ref|NP_003386.1|9a    PSAAYFGLTGSEPLTILP--LTLEPEAAAQAHYKACDRLKLERKQRRMCR 73
gi|17017976|ref|NP_003387.1|9b    AAASYFGLTGREVLTPFPGLGTAAAPAQGGAHLKQCDLLKLSRRQKQLCR 69
gi|16936520|ref|NP_079492.2|10a   AAMPRS-------APNDILDLRLPPEPVLNANTVCLTLPGLSRRQMEVCV 76
gi|16936522|ref|NP_003385.2|10b   RALS-----------NEILGLKLPGEPPLTANTVCLTLSGLSKRQLGLCL 63
gi|17017974|ref|NP_004617.2|11    TGVCYG---------IKWLALSKTPSALALN-QTQHCKQLEGLVSAQVQLCR 60
gi|17402916|ref|NP_476509.1|16    GNWMW-------------LGIASFGVP----EKLGCANLP-LNSRQKELCK 61
gi|21357511|ref|NP_650272.1|D     -----------------------------STLAAVLEPMSYYQYTQFQ 31
```

FIG. 1

```
gi|4885655|ref|NP_005421.1|1          QNPGILHSVSGGLQSAVRECKWQFRNRRWNCPTAPG---------PHLFGK 115
gi|4507927|ref|NP_003382.1|2          RHPDVMRAISQGVAEWTAECQHQFRQHRWNCNTLDR----------DHSLFGR  99
gi|13518017|ref|NP_004176.2|2b        RYPDIMRSVGEGAREWIRECQHQFRHHRWNCTTLDR----------DHTVFGR 111
gi|13540477|ref|NP_110380.1|3         NYIEIMPSVAEGVKLGIQECQHQFRGRRWNCTTIDDS---------LAIFGP 103
gi|14916475|ref|NP_149122.1|3a        NYVEIMPSVAEGIKIGIQECQHQFRGRRWNCTTVHDS---------LAIFGP 100
gi|17402922|ref|NP_110388.2|4         RNLEVMDSVRRGAQLAIEECQYQFRNRRWNCSTLD----------SLFVFGK 100
gi|40806205|ref|NP_003383.2|5a        LYQDHMQYIGEGAKTGIKECQYQFRHRRWNCSTVD----------NTSVFGR 126
gi|14249180|ref|NP_116031.1|5b        LYQEHMAYIGEGAKTGIKECQHQFRQRRWNCSTAD----------NASVFGR 105
gi|16507239|ref|NP_006513.1|6         AEPEVVAELARGAPLGVRECQFQFRFRRWNCSSHS----------KAFGR 96
gi|17505191|ref|NP_004616.2|7a        SRPDAIIVIGEGSQMGLDECQFQFRNGRWNCS-----------ALGERTVFGK 95
gi|17505193|ref|NP_478679.1|7b        SRPDAIIVIGEGAQMGINECQYQFRFGRWNCS-----------ALGEKTVFGQ 95
gi|17505195|ref|NP_490645.1|8a        AYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQ---------LSTHN 76
gi|110735437|ref|NP_003384.2|8b       AYLIYSSSVAAGAQSGIEECKYQFAWDRWNCPERALQ---------LSSHG 76
gi|15082261|ref|NP_003386.1|9a        RDPGVAETLVEAVSMSALECQFQFRFERWNCTLEGRY-----------RAS 113
gi|17017976|ref|NP_003387.1|9b        REPGLAETLRDAAHLGLLECQFQFRHERWNCSLEG-------------RMG 107
gi|16936520|ref|NP_079492.2|10a       RHPDVAASAIQGIQIAIHECQHQFRDQRWNCSSLETR----NKIPYESP 121
gi|16936522|ref|NP_003385.2|10b       RNPDVTASALQGLHIAVHECQHQLRDQKWNCSALEGG-----GRLPHHSA 108
gi|17017974|ref|NP_004617.2|11        SNLELMHTVVHAAREVMKACRRAFADMRWNCSSIEL-----------APNYLL 102
gi|17402916|ref|NP_476509.1|16        RKPYLLPSIREGARLGIQECGSQFRHERWNCMITAAATTAPMGASPLFGY 111
gi|21357511|ref|NP_650272.1|D         APLSWEDITGKGLKQALDSCQQSFQWQRWNCPSQDFVQ-------KNSKP 74
                                                 .      :    ****
gi|4885655|ref|NP_005421.1|1          IVNRGCRETAFIFATTSAGVTHSVARSCSEGSIESCTCDYRRR---------- 158
gi|4507927|ref|NP_003382.1|2          VLLRSSRESAFVYAISSAGVVFAITRACSQGEVKSCSCDPKKM---------- 142
gi|13518017|ref|NP_004176.2|2b        VMLRSSREAAFVYAISSAGVVHAITRACSQGELSVCSCDPYTR---------- 154
gi|13540477|ref|NP_110380.1|3         VLDKATRESAFVHAIASAGVAFAVTRSCAEGTSTICGCDSHHK---------- 146
gi|14916475|ref|NP_149122.1|3a        VLDKATRESAFVHAIASAGVAFAVTRSCAEGTAAICGCSSRHQ---------- 143
gi|17402922|ref|NP_110388.2|4         VVTQGTREAAFVYAISSAGVAFAVTRACSSGELEKCGCDRTVH---------- 143
gi|40806205|ref|NP_003383.2|5a        VMQIGSRETAFTYAVSAAGVVNAMSRACREGELSTCGCS--RA---------- 167
gi|14249180|ref|NP_116031.1|5b        VMQIGSRETAFTHAVSAAGVVNAISRACREGELSTCGCS--RT---------- 146
gi|16507239|ref|NP_006513.1|6         ILQQDIRETAFVFATAAGASHAVTQACSMGELLQCGCQAPRG---------- 139
gi|17505191|ref|NP_004616.2|7a        ELKVGSREAAFTYAITAAGVAHAITAACTQGNLSDCGCDKEKQ---------- 138
gi|17505193|ref|NP_478679.1|7b        ELRVGSREAAFTYAATAAGVAHAVTAACSQGNLSNCGCDREKQ---------- 138
gi|17505195|ref|NP_490645.1|8a        RLRSATRETSFTHAISSAGVMYIITKNCSMGDFENCGCDGSNN---------- 119
gi|110735437|ref|NP_003384.2|8b       GLRSANRETAFVHATSSAGVMYTLTRNCSLGDFDNCGCDDSRN---------- 119
gi|15082261|ref|NP_003386.1|9a        LLKRGFKETAFLYAISSAGLTHALAKACSAGRMERCTCDEAPD---------- 156
gi|17017976|ref|NP_003387.1|9b        LLKRGFKETAFLYAVSSAALTHTLARACSAGRMERCTCDDSPG---------- 150
gi|16936520|ref|NP_079492.2|10a       IFSRGFRESAFAYAIAAAGVVHAVSNACALGKLKACGCDASRRGDEEAFR 171
gi|16936522|ref|NP_003385.2|10b       ILKRGFRESAFSFSMLAAGVMHAVATACSLGKLVSCGCGWKGSGEQDRLR 158
gi|17017974|ref|NP_004617.2|11        DLERGTRESAFVYALSAAAISHAIARACTSGDLPGCSCGPVPG---------- 145
gi|17402916|ref|NP_476509.1|16        ELSSGTKETAFTYAVMAAGLVHSVTRSCSAGNMTECSCDTTLQ---------- 154
gi|21357511|ref|NP_650272.1|D         EENSPNREDVYVAAISMAAIVHTLTKDCANGVIAGCGCTENALN---------- 118
                                         :*  :  ::  *.    ::  *  *   * *
```

FIG. 1 (Continued)

```
gi|4885655|ref|NP_005421.1|1      ----------------------------------GFG---GPDWHWGGCSDNIDFG 177
gi|4507927|ref|NP_003382.1|2      ----------------------------------GSAKDSKGIFDWGGCSDNIDYG 164
gi|13518017|ref|NP_004176.2|2b    ----------------------------------GRHHDQRGDFDWGGCSDNIHYG 176
gi|13540477|ref|NP_110380.1|3     ----------------------------------GPP---GEGWKWGGCSEDADFG 165
gi|14916475|ref|NP_149122.1|3a    ----------------------------------GSP---GKGWKWGGCSEDIEFG 162
gi|17402922|ref|NP_110388.2|4     ----------------------------------GVS---PQGFQWSGCSDNIAYG 162
gi|40806205|ref|NP_003383.2|5a    ----------------------------------ARPKDLPRDWLWGGCGDNIDYG 189
gi|14249180|ref|NP_116031.1|5b    ----------------------------------ARPKDLPRDWLWGGCGDNVEYG 168
gi|16507239|ref|NP_006513.1|6     ----------RAPPRPSGLP-GTPGP-PGPAGSPEGSAAWEWGGCGDDVDFG 179
gi|17505191|ref|NP_004616.2|7a    ----------------------------------GQYHRDEG-WKWGGCSADIRYG 159
gi|17505193|ref|NP_478679.1|7b    ----------------------------------GYYNQAEG-WTWGGCSADVRYG 159
gi|17505195|ref|NP_490645.1|8a    ----------------------------------GKTGGHGWIWGGCSDNVEFG 139
gi|110735437|ref|NP_003384.2|8b   ----------------------------------GQLGGQGWLWGGCSDNVGFG 139
gi|15082261|ref|NP_003386.1|9a    ----------------------------------LENREAWQWGGCGDNLKYS 175
gi|17017976|ref|NP_003387.1|9b    ----------------------------------LESRQAWQWGVCGDNLKYS 169
gi|16936520|ref|NP_079492.2|10a   RKLHRLQLDALQRGKGLSHGVPEHPALPTASPGLQDSWEWGGCSPDMGFG 221
gi|16936522|ref|NP_003385.2|10b   AKL---LQLQALSRGKSFPHSLFSPGPGSSPSPGPQDTWEWGGCNHDMDFG 206
gi|17017974|ref|NP_004617.2|11    ----------------------------EPPGPGNRWGGCADNLSYG 164
gi|17402916|ref|NP_476509.1|16    ----------------------------NGGSASEG-WHWGGCSDDVQYG 175
gi|21357511|ref|NP_650272.1|D     ----------------------------------VPCAHEPTKA 128
                                                                     *  :  .

gi|4885655|ref|NP_005421.1|1      RLFGREFVDSGEKGR----------DLRFLMNLHNNEAGRTTVFSEMRQECK 219
gi|4507927|ref|NP_003382.1|2      IKFARAFVDAKERKG----------KDARALMNLHNNRAGRKAVKRFLKQECK 207
gi|13518017|ref|NP_004176.2|2b    VRFAKAFVDAKEKRL----------KDARALMNLHNNECGRTAVRRFLKLECK 219
gi|13540477|ref|NP_110380.1|3     VLVSREFADARENRP----------DARSAMNKHNNEAGRTTILDHMHLKCK 207
gi|14916475|ref|NP_149122.1|3a    GMVSREFADARENRP----------DARSAMNRHNNEAGRQAIASHMHLKCK 204
gi|17402922|ref|NP_110388.2|4     VAFSQSFVDVRERSKGASS-----SRALMNLHNNEAGRKALLTHMRVECK 207
gi|40806205|ref|NP_003383.2|5a    YRFAKEFVDARERERIHAKGSYESARILMNLHNNEAGRRTVYNLADVACK 239
gi|14249180|ref|NP_116031.1|5b    YRFAKEFVDAREREKNFAKGSEEQGRVLMNLQNNEAGRRAVYKMADVACK 218
gi|16507239|ref|NP_006513.1|6     DEKSRLFMDARHKRG----------RGDIRALVQLHNNEAGRLAVRSHTRTECK 223
gi|17505191|ref|NP_004616.2|7a    IGFAKVFVDAREIKQNART----------LMNLHNNEAGRKILEENMKLECK 201
gi|17505193|ref|NP_478679.1|7b    IDFSRRFVDAREIKKNARR----------LMNLHNNEAGRKVLEDRMQLECK 201
gi|17505195|ref|NP_490645.1|8a    ERISKLFVDSLEKGK----------DARALMNLHNNRAGRLAVRATMKRTCK 181
gi|110735437|ref|NP_003384.2|8b   EAISKQFVDALETGQ----------DARAAMNLHNNEAGRKAVKGTMKRTCK 181
gi|15082261|ref|NP_003386.1|9a    SKFVKEFLG-RRSSKD----------LRARVDFHNNLVGVKVIKAGVETTCK 216
gi|17017976|ref|NP_003387.1|9b    TKFLSNFLGSKRGNKD----------LRARADAHNTHVGIKAVKSGLRTTCK 211
gi|16936520|ref|NP_079492.2|10a   ERFSKDFLDSREP----------HRDIHARMRLHNNRVGRQAVMENMRRKCK 263
gi|16936522|ref|NP_003385.2|10b   EKFSRDFLDSREA----------PRDIQARMRIHNNRVGRQVVTENLKEKCK 248
gi|17017974|ref|NP_004617.2|11    LLMGAKFSDAPMKVKKTGS-----QANKLMRLHNSEVGRQALRASLEMKCK 210
gi|17402916|ref|NP_476509.1|16    MWFSRKFLDFPIGNTTGKEN----KVLLAMNLHNNEAGRQAVAKLMSVDCR 222
gi|21357511|ref|NP_650272.1|D     LEQYEKHFGSGSGAIG----------HNRRVVGALLQRSLEQECR 163
                                              :*     :      *:
```

FIG. 1 (Continued)

```
gi|4885655|ref|NP_005421.1|1      CHG---MSGSCTVRTCWMRLPTLRAVGDVLRDRFDGASRVLYGNRGSNRA 266
gi|4507927|ref|NP_003382.1|2      CHG-----VSGSCTLRTCWLAMADFRKTGDYLWRKYNGAIQVVMN-------QD 249
gi|13518017|ref|NP_004176.2|2b    CHG---VSGSCTLRTCWRALSDFRKTGDYLRRRYDGAVQVMAT-------QD 261
gi|13540477|ref|NP_110380.1|3     CHG---LSGSCEVKTCWMAQPDFRAIGDFLKDKYDSASEMVVEK---HRE 251
gi|14916475|ref|NP_149122.1|3a    CHG---LSGSCEVKTCWWSQPDFRAIGDFLKDKYDSASEMVVEK---HRE 248
gi|17402922|ref|NP_110388.2|4     CHG---VSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR----VG 250
gi|40806205|ref|NP_003383.2|5a    CHG-----VSGSCSLKTCWLQLADFRKVGDALKEKYDSAAAMRLN-------SR 281
gi|14249180|ref|NP_116031.1|5b    CHG---VSGSCSLKTCWLQLAEFRKVGDRLKEKYDSAAAMRVT-------RK 260
gi|16507239|ref|NP_006513.1|6     CHG---LSGSCALRTCWQKLPFFREVGARLLERFHGASRVMGTN-------D 265
gi|17505191|ref|NP_004616.2|7a    CHG---VSGSCTTKTCWTTLPQFRELGYVLKDKYNE-AVHVEPVRASRNKR 248
gi|17505193|ref|NP_478679.1|7b    CHG---VSGSCTTKTCWTTLPKFREVGHLLKEKYNAAVQVEVVRASRLRQ 248
gi|17505195|ref|NP_490645.1|8a    CHG---ISGSCSIQTCWLQLAEFREMGDYLKAKYDQALKLEMDKRQLRAG 228
gi|110735437|ref|NP_003384.2|8b   CHG-----VSGSCTTQTCWLQLPEFREVGAHLKEKYHAALKVDLLQG-----AG 225
gi|15082261|ref|NP_003386.1|9a    CHG---VSGSCTVRTCWRQLAPFHEVGKHLKHKYETALKVGSTTNEAAGE 263
gi|17017976|ref|NP_003387.1|9b    CHG---VSGSCAVRTCWKQLSPFRETGQVLKLRYDSAVRVSSATNEALGR 258
gi|16936520|ref|NP_079492.2|10a   CHG----TSGSCQLKTCWQVTPEFRTVGALLRSRFHRATLIRPHNR-----N 306
gi|16936522|ref|NP_003385.2|10b   CHG---TSGSCQFKTCWRAAPEFRAVGAALRERLGRAIFTIDTHNR-----N 291
gi|17017974|ref|NP_004617.2|11    CHG---VSGSCSIRTCWKGLQELQDVAADLKTRYLSATKVVHRP-----MG 253
gi|17402916|ref|NP_476509.1|16    CHG-----VSGSCAVKTCWKTMSSFEKIGHLLKDKYENSIQISDKTKRKMRR 269
gi|21357511|ref|NP_650272.1|D     CKQPGAVQGECQEECVAVLKPFEAIAQDLLQMYDDAIQLEGAS------- 207
                                  *:      .*.*   .*      :.  .    *      :  :

gi|4885655|ref|NP_005421.1|1      SRAELLRLEPEDP----------AHKPPSPHDLVYFEKSPNFCTYSGRLGTAG 309
gi|4507927|ref|NP_003382.1|2      GTGFTVANER-------------FKKPTKNDLVYFENSPDYCIRDREAGSLG 288
gi|13518017|ref|NP_004176.2|2b    GANFTAARQG-------------YRRATRTDLVYFDNSPDYCVLDKAAGSLG 300
gi|13540477|ref|NP_110380.1|3     SRGWVETLRAKYS----------LFKPPTERDLVYYENSPNFCEPNPETGSFG 294
gi|14916475|ref|NP_149122.1|3a    SRGWVETLRPRYT----------YFKVPTERDLVYYEASPNFCEPNPETGSFG 291
gi|17402922|ref|NP_110388.2|4     SSRALVPRNAQ-------------FKPHTDEDLVYLEPSPDFCEQDMRSGVLG 290
gi|40806205|ref|NP_003383.2|5a    GK-LVQVNSR-------------FNSPTTQDLVYIDESPDYCVRNESTGSLG 319
gi|14249180|ref|NP_116031.1|5b    GR-LELVNSR-------------FTQPTPEDLVYVDPSPDYCLRNESTGSLG 298
gi|16507239|ref|NP_006513.1|6     GKALLPAVR--------------TLKPPGRADLLYAADSPDFCAPNRRTGSPG 304
gi|17505191|ref|NP_004616.2|7a    PTVTLKIKKPLS-----------YRKPMDTDLVYIEKSPNYCEEDPVTGSVG 288
gi|17505193|ref|NP_478679.1|7b    PTFLRTKQLRS-------------YQKPMETDLVYIEKSPNYCEEDAATGSVG 288
gi|17505195|ref|NP_490645.1|8a    NSAEGHWVPAEA-----------FLPSAEAELIFLEESPDYCTCNSSLGIYG 269
gi|110735437|ref|NP_003384.2|8b   NSAAGRGAIADT-----------FRSISTRELVHLEDSPDYCLENKTLGLLG 266
gi|15082261|ref|NP_003386.1|9a    AGAISPPRGRASGAGGS------DPLPRTPELVHLDDSPSFCLAGR--FSPG 307
gi|17017976|ref|NP_003387.1|9b    LELWAPAR-----QGSLTK-----GLAPRSGDLVYMEDSPSFCRPSK--YSPG 299
gi|16936520|ref|NP_079492.2|10a   GGQLEPGPAGAPSPAPGAPGPRRRASPADLVYFEKSPDFCEREPRLDSAG 356
gi|16936522|ref|NP_003385.2|10b   SGAFQPERLR--------------PRRLSG--ELVYFEKSPDFCERDPTMGSPG 328
gi|17017974|ref|NP_004617.2|11    TRKHLVPKDLD-------------IRPVKDSELVYLQSSPDFCMKNEKVGSHG 293
gi|17402916|ref|NP_476509.1|16    -----REKDQRK-------------IPIHKD-DLLYVNKSPNYCVEDKKLGIPG 304
gi|21357511|ref|NP_650272.1|D     SNLKIMWQN-----------------IPLDSLVFMQDSPNYCERDATGLWKG 242
                                                          .*:.   ** .:*       *
```

FIG. 1 (Continued)

```
gi|4885655|ref|NP_005421.1|1        TAGRACNSSSPA------LDGCELLC---CGRGHRTRTQRVTER----------CN 346
gi|4507927|ref|NP_003382.1|2        TAGRVCNLTSRG------MDSCEVMC---CGRGYDTSHVTRMTK----------CG 325
gi|13518017|ref|NP_004176.2|2b      TAGRVCSKTSKG------TDGCEIMC---CGRGYDTTRVTRVTQ----------CE 337
gi|13540477|ref|NP_110380.1|3       TRDRTCNVTSHG------IDGCDLLC---CGRGHNTRTEKRKEK----------CH 331
gi|14916475|ref|NP_149122.1|3a      TRDRTCNVSSHG------IDGCDLLC---CGRGHNARAERRREK----------CR 328
gi|17402922|ref|NP_110388.2|4       TRGRTCNKTSKA------IDGCELLC---CGRGFHTAQVELAER----------CS 327
gi|40806205|ref|NP_003383.2|5a      TQGRLCNKTSEG------MDGCELMC---CGRGYDQFKTVQTER----------CH 356
gi|14249180|ref|NP_116031.1|5b      TQGRLCNKTSEG------MDGCELMC---CGRGYNQFKSVQVER----------CH 335
gi|16507239|ref|NP_006513.1|6       TRGRACNSSAPD------LSGCDLLC---CGRGHRQESVQLEEN----------CL 341
gi|17505191|ref|NP_004616.2|7a      TQGRACNKTAPQ-----ASGCDLMC---CGRGYNTHQYARVWQ----------CN 325
gi|17505193|ref|NP_478679.1|7b      TQGRLCNRTSPG------ADGCDTMC---CGRGYNTHQYTKVWQ----------CN 325
gi|17505195|ref|NP_490645.1|8a      TEGRECLQNSHN------TSRWERRS---CGRLCTECGLQVEERKTEVISSCN 313
gi|110735437|ref|NP_003384.2|8b     TEGRECLRRGRA------LGRWERRS---CRRLCGDCGLAVEERRAETVSSCN 310
gi|15082261|ref|NP_003386.1|9a      TAGRRCHREK----------NCESIC---CGRGHNTQSRVVTRP----------CQ 340
gi|17017976|ref|NP_003387.1|9b      TAGRVCSREA----------SCSSLC---CGRGYDTQSRLVAFS----------CH 332
gi|16936520|ref|NP_079492.2|10a     TVGRLCNKSSAG------SDGCGSMC---CGRGHNILRQTRSER----------CH 393
gi|16936522|ref|NP_003385.2|10b     TRGRACNKTSRL------LDGCGSLC---CGRGHNVLRQTRVER----------CH 365
gi|17017974|ref|NP_004617.2|11      TQDRQCNKTSNG------SDSCDLMC---CGRGYNPYTDRVVER----------CH 330
gi|17402916|ref|NP_476509.1|16      TQGRECNRTSEG------ADGCNLLC---CGRGYNTHVVPHVER----------CE 341
gi|21357511|ref|NP_650272.1|D       TRGRQCSKDGSGSLEERLSCQQLCRVCGYRVRSQHVRTERR----------CN 285
                                     * .* *                .   *                    *

gi|4885655|ref|NP_005421.1|1        CTFHWCCHVSCRNCTHTRVLHECL---------------------- 370
gi|4507927|ref|NP_003382.1|2        CKFHWCCAVRCQDCLEALDVHTCKAPKNADWTTAT---------- 360
gi|13518017|ref|NP_004176.2|2b      CKFHWCCAVRCKECRNTVDVHTCKAPKKAEWLDQT---------- 372
gi|13540477|ref|NP_110380.1|3       CIFHWCCYVSCQECIRIYDVHTCK---------------------- 355
gi|14916475|ref|NP_149122.1|3a      CVFHWCCYVSCQECTRVYDVHTCK---------------------- 352
gi|17402922|ref|NP_110388.2|4       CKFHWCCFVKCRQCQRLVELHTCR---------------------- 351
gi|40806205|ref|NP_003383.2|5a      CKFHWCCYVKCKKCTEIVDQFVCK---------------------- 380
gi|14249180|ref|NP_116031.1|5b      CKFHWCCFVRCKKCTEIVDQYICK---------------------- 359
gi|16507239|ref|NP_006513.1|6       CRFHWCCVVQCHRCRVRKELSLCL---------------------- 365
gi|17505191|ref|NP_004616.2|7a      CKFHWCCYVKCNTCSERTEMYTCK---------------------- 349
gi|17505193|ref|NP_478679.1|7b      CKFHWCCFVKCNTCSERTEVFTCK---------------------- 349
gi|17505195|ref|NP_490645.1|8a      CKFQWCCTVKCDQCRHVVSKYYCARSP-----GSAQSLGKGSA 351
gi|110735437|ref|NP_003384.2|8b     CKFHWCCAVRCEQCRRRVTKYFCSRAERPRGGAAHKPGRKP- 351
gi|15082261|ref|NP_003386.1|9a      CQVRWCCYVECRQCTQREEVYTCKG--------------------- 365
gi|17017976|ref|NP_003387.1|9b      CQVQWCCYVECQQCVQEELVYTCKH--------------------- 357
gi|16936520|ref|NP_079492.2|10a     CRFHWCCFVVCEECRITEWVSVCK---------------------- 417
gi|16936522|ref|NP_003385.2|10b     CRFHWCCYVLCDECKVTEWVNVCK---------------------- 389
gi|17017974|ref|NP_004617.2|11      CKYHWCCYVTCRRCERTVERYVCK---------------------- 354
gi|17402916|ref|NP_476509.1|16      CKFIWCCYVRCRRCESMTDVHTCK---------------------- 365
gi|21357511|ref|NP_650272.1|D       CKLVWGFRLQCDVCVQLERQYSCY---------------------- 309
                                     *   *   : *  *        *
```

XXXX BOLD predicted signal sequence by SignalP 3.0

XXXX BOLD and Underlined text is the initial Wnt7a truncated Wnt7a peptide (235-349)

XXXX BOLD, underlined and italic is another example of a truncated Wnt7a peptide (264-349)

FIG. 1 (Continued)

```
         .    .    .    1    .    .    .    .    2    .    .    .    .    3    .    .    .    .    4    .    .    .    .    5    .    .    .    .    6
AA       MNRKARRCLGHLFLSLGMVYLRIGGFSSVVALGASICNKIPGLAPEQRAICQSRPDAII
PROF sec      HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
Rel sec  971567666667776544432101035532345201110012454560987640542478
SUB sec  LL.HHHHHHHHHHHHH.....LL....L.....L.HHHHHHH..L...HH

         .    .    .    .    7    .    .    .    .    8    .    .    .    .    9    .    .    .    .   10    .    .    .    .   11    .    .    .    .   12
AA       VIGEGSQMGLIECQFQFRNGRMNCSALGERTVTGKELEVGSREAAFTYAILAAGVAHAIT
PROF sec HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
Rel sec  88866676608888876402333333444321110012252236868688643698887
SUB sec  HHHHHHHHHHHHHHHHH.....................L...HHHHHHHH..HHHHHH

         .    .    .    .   13    .    .    .    .   14    .    .    .    .   15    .    .    .    .   16    .    .    .    .   17    .    .    .    .   18
AA       AACTQGNLSDCGCDKERQGQYHRDECGWNWGGCSADIRYGIGFAKVFVDAKEIKQNAKTLM
PROF sec HHHH                HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
Rel sec  64202266321334545466666553531233211133356777764202311323677776
SUB sec  H....Lh.....L.L.LLLLLLLLL.....................HHHHHH.....HHHHH

         .    .    .    .   19    .    .    .    .   20    .    .    .    .   21    .    .    .    .   22    .    .    .    .   23    .    .    .    .   24
AA       NLHNWEAGRKILEEAMKLECKCHGVSGSCTTKTCWTTLPQFRELGYVLKDKYNEAVHVEP
PROF sec HHH  HHHHHHHHHH  EEEE  HHHHHHHHH  HHHHHHHHHHHHH  EEEEE
Rel sec  42022434668778630001311022320002456642100567878808753124325665
SUB sec  .....HHHHH.....................HHH.....HHHHHHHHHH.....EEEE

         .    .    .    .   25    .    .    .    .   26    .    .    .    .   27    .    .    .    .   28    .    .    .    .   29    .    .    .    .   30
AA       VRASRNKRPTFLKIKNPLSYNKAMDTDLVYIEKSPNYCEEDPVTGSVGTQGRACNNTAPQ
PROF sec E                   EEEE
Rel sec  10453444322235556455677656347751571101145565644545452114655666
SUB sec  ...L.....LLLL.LLLLLLLL..EEE.LL.....LLLLL...L.L....LLLLL

         .    .    .    .   31    .    .    .    .   32    .    .    .    .   33    .    .    .    .   34    .    .    .    .   35
AA       ASECDLMCGRGYNTHQYARVWQCNCKFHWCCYVRCNTCSERTEMYTCK
PROF sec      EEE    EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
Rel sec  5642010102331012356543100366677665100001211221107
SUB sec  LL.....EEEEE.....EEEEEEEE.....L
```

FIG. 2A

```
              ....,....1....,....2....,....3....,....4....,....5....,....6
AA            MAPLGYFLLLCSLKQALGSYPIWWSLAVGPQYSSLGSQPILCASIPGLVPKQLRFCRNYV
PROF sec        EEEEEEEEEEEEEE      EEEEEEE                 HHHHH     HHHHHHHHH
Rel sec       950333322222221013331222231024543456652010100135557888765043
SUB sec       LL.........................L...LLLL.........LLHHHHHHHH...

              ....,....7....,....8....,....9....,....10...,....11...,....12
AA            EIMPSVAEGIKIGIQECQHQFRGRRWNCTTVHDSLAIFGPVLDKATRESAFVHAIASAGV
PROF sec       HHHHHHHHHHHHHHHHHHHHHHH               HHH      HHHHHHHHHHHHH
Rel sec       036788877777689888876412233333444321001110025213678888875215
SUB sec       ..HHHHHHHHHHHHHHHHHHHH......................L...HHHHHHHHH..H

              ....,....13...,....14...,....15...,....16...,....17...,....18
AA            AFAVTRSCAEGTAAICGCSSRHQGSPGKGWKWGGCSEDIEFGGMVSREFADARENRPDAR
PROF sec      HHHHHHHHH                            HHHHHHHHHHHH   HHH    HH
Rel sec       888876420266310323556676766542223332221234777776421121031346
SUB sec       HHHHHH....LL......LLLLLLLLLL..............HHHHHH...........H

              ....,....19...,....20...,....21...,....22...,....23...,....24
AA            SAMNRHNNEAGRQAIASHMHLKCKCHGLSGSCEVKTCWWSQFDFRAIGDFLKDKYDSASE
PROF sec      HHHHH     HHHHHHHHHH    EEEE          HHHHHHHH   HHHHHHHHHHHH EE
Rel sec       776310224336788864000121101222100123454122157788888865224304
SUB sec       HHH........HHHHHH...................H.....HHHHHHHHHHH......

              ....,....25...,....26...,....27...,....28...,....29...,....30
AA            MVVEKHRESRGWVETLRPRYTYFKVPTERDLVYYEASPNFCEPNPETGSFGTRDRTCNVS
PROF sec      EEEE                              EEEE
Rel sec       675014554432222234555556676452577404611012466766445445201455
SUB sec       EEE...LL..........LLLLLLLLL.L.EEE...L......LLLLL..L..L....LL

              ....,....31...,....32...,....33...,....34...,....35.
AA            SHGIDGCDLLCCGRGHNARAERRREKCRCVFHWCCYVSCQECTRVYDVHTCK
PROF sec              EEEE     EEEEEEEEEEEEEEEEEEEEEEE    EEEEEEEE
Rel sec       4565543100002441013455553211256666776511210132222207
SUB sec       .LLLL...............EEEE....EEEEEEEEE.............L
```

FIG. 2B

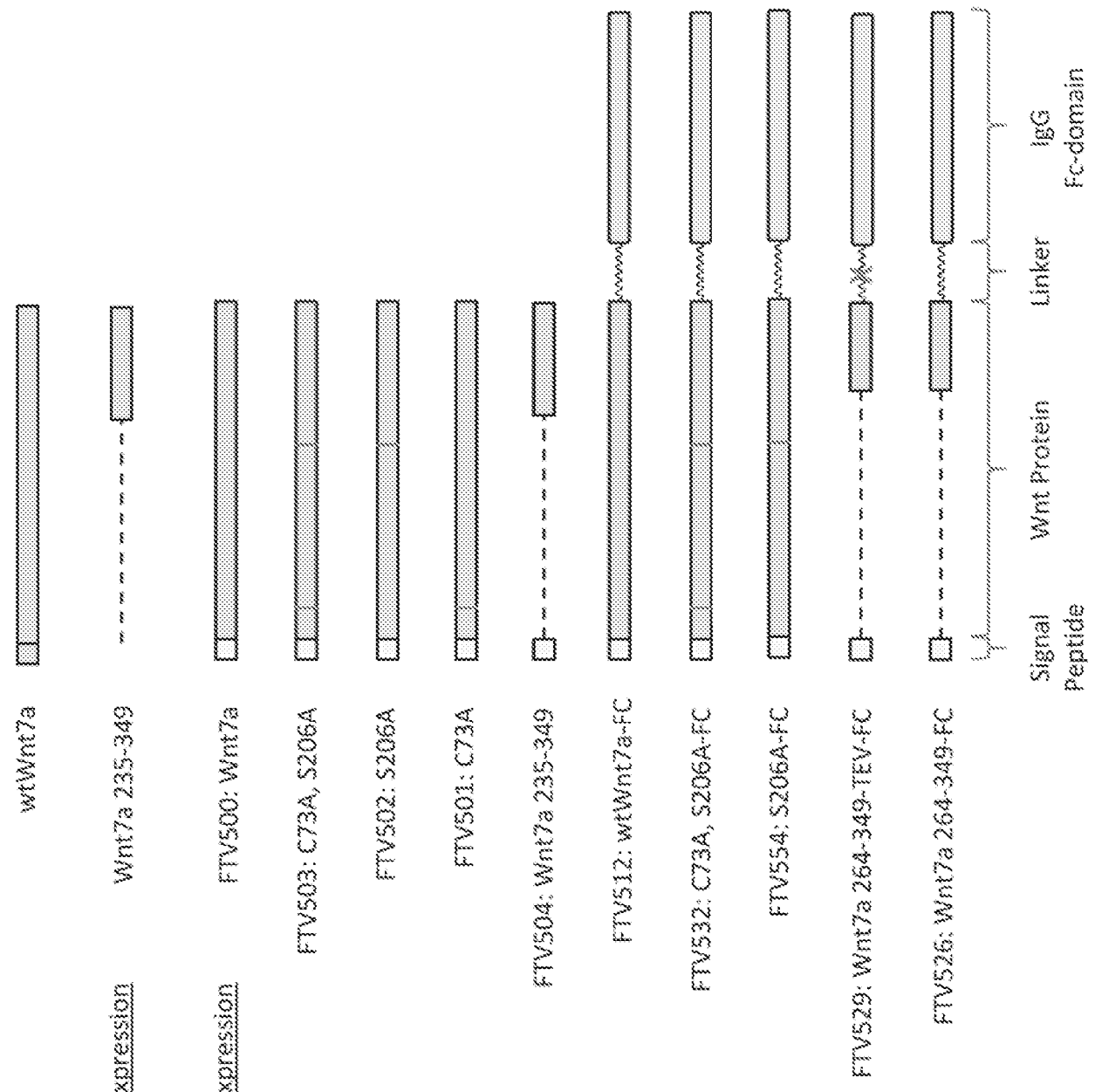

wtWnt7a
Bacterial Expression
Wnt7a 235-349
Mammalian Expression
FTV500: Wnt7a
FTV503: C73A, S206A
FTV502: S206A
FTV501: C73A
FTV504: Wnt7a 235-349
FTV512: wtWnt7a-FC
FTV532: C73A, S206A-FC
FTV554: S206A-FC
FTV529: Wnt7a 264-349-TEV-FC
FTV526: Wnt7a 264-349-FC
Signal Peptide
Wnt Protein
Linker
IgG Fc-domain

FIG. 3

WNT7A	Fusion	Expression mg/L
Wild-type		0.9
Wild-type	Fc	4.6
C73, S206A		1.7
C73, S206A	Fc	11.9
C73A, S206A		1.4
C73A, S206A	Fc	12.0
aa264-349	Fc	10.8

FIG. 4

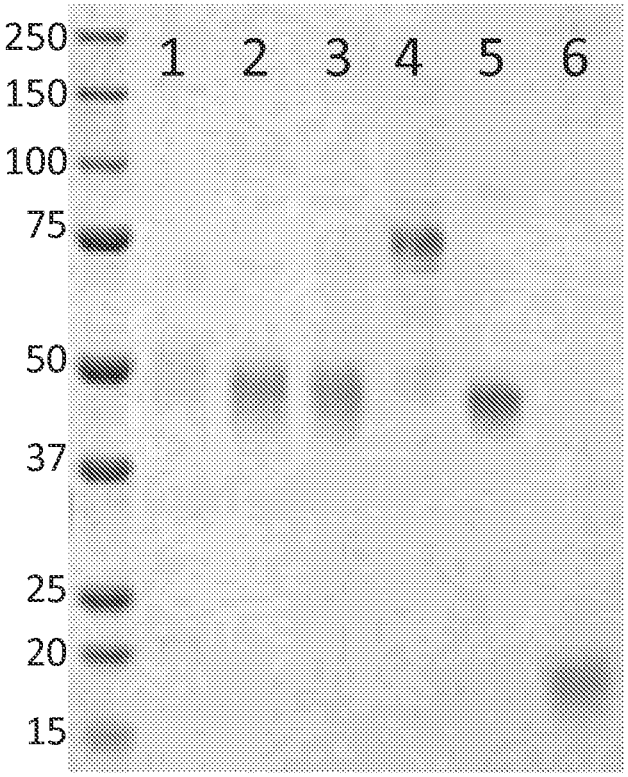


FIG. 5

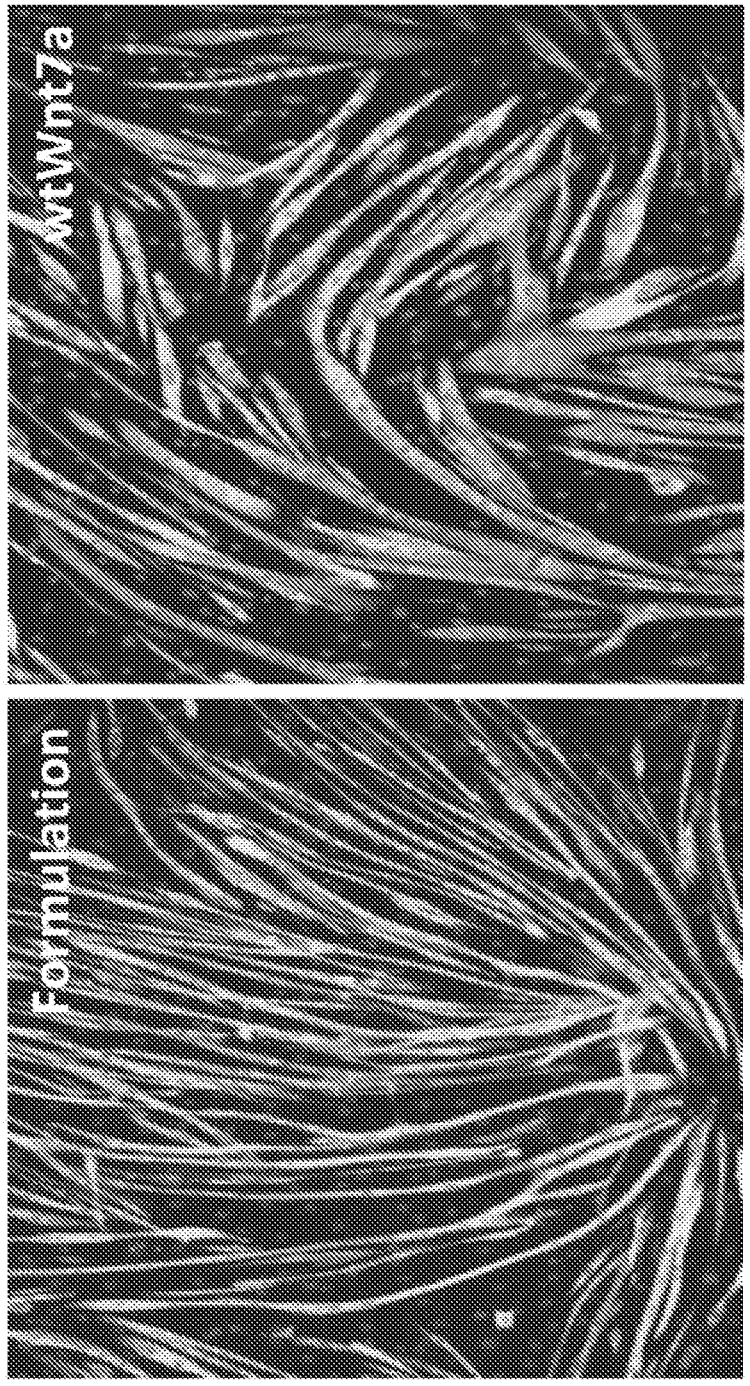


FIG. 6

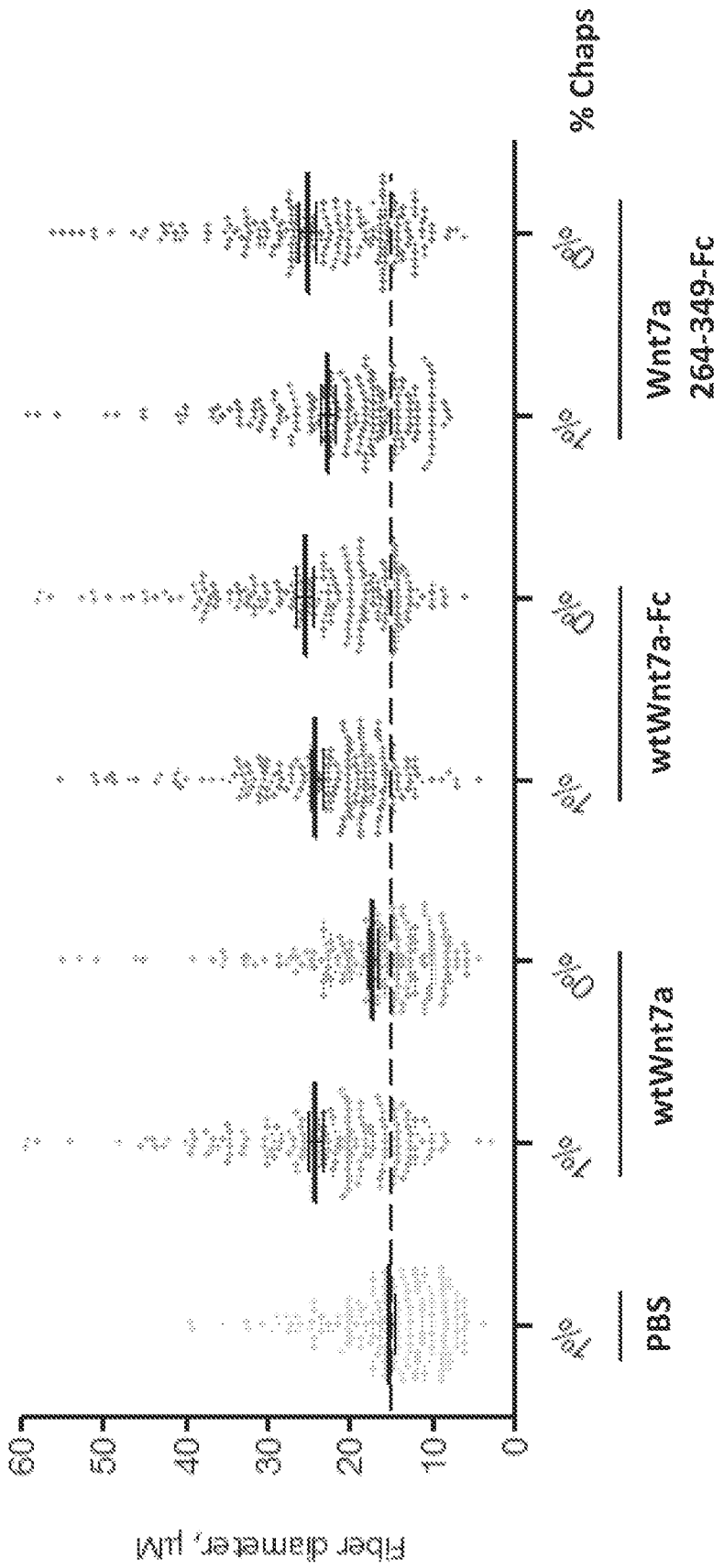

fiber diameter, μM
60
50
40
30
20
10
0
PBS
wtWnt7a
wtWnt7a-Fc
Wnt7a
264-349-Fc
% Chaps
0%
1%

FIG. 7

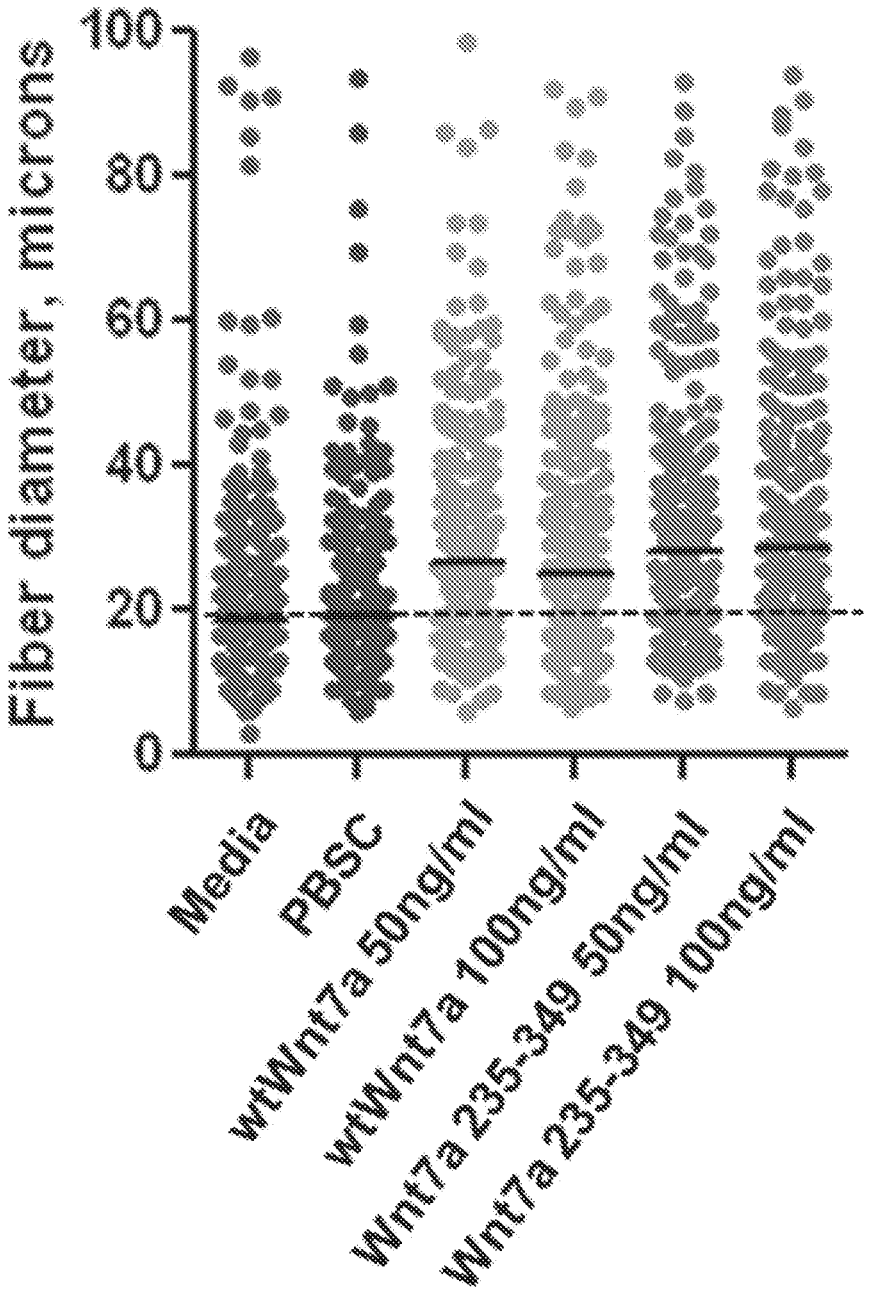

Fiber diameter, microns
100
80
60
40
20
0
Media
PBSC
wtWnt7a 50ng/ml
wtWnt7a 100ng/ml
Wnt7a 235-349 50ng/ml
Wnt7a 235-349 100ng/ml

FIG. 8A

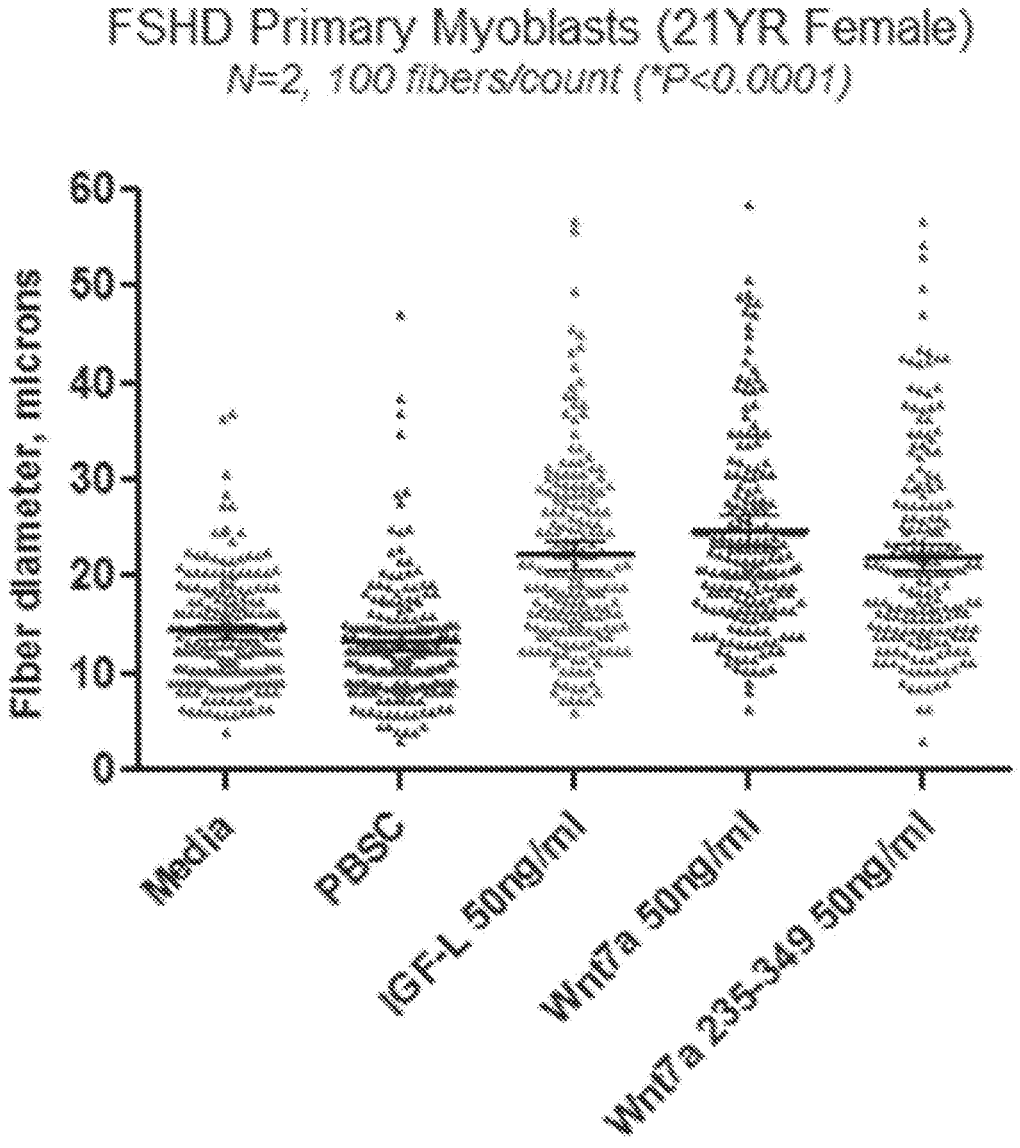

FSHD Primary Myoblasts (21YR Female)
N=2, 100 fibers/count (*P<0.0001)
Fiber diameter, microns
0
10
20
30
40
50
60
Media
PBSC
IGF-L 50ng/ml
Wnt7a 50ng/ml
Wnt7a 235-349 50ng/ml

FIG. 8B

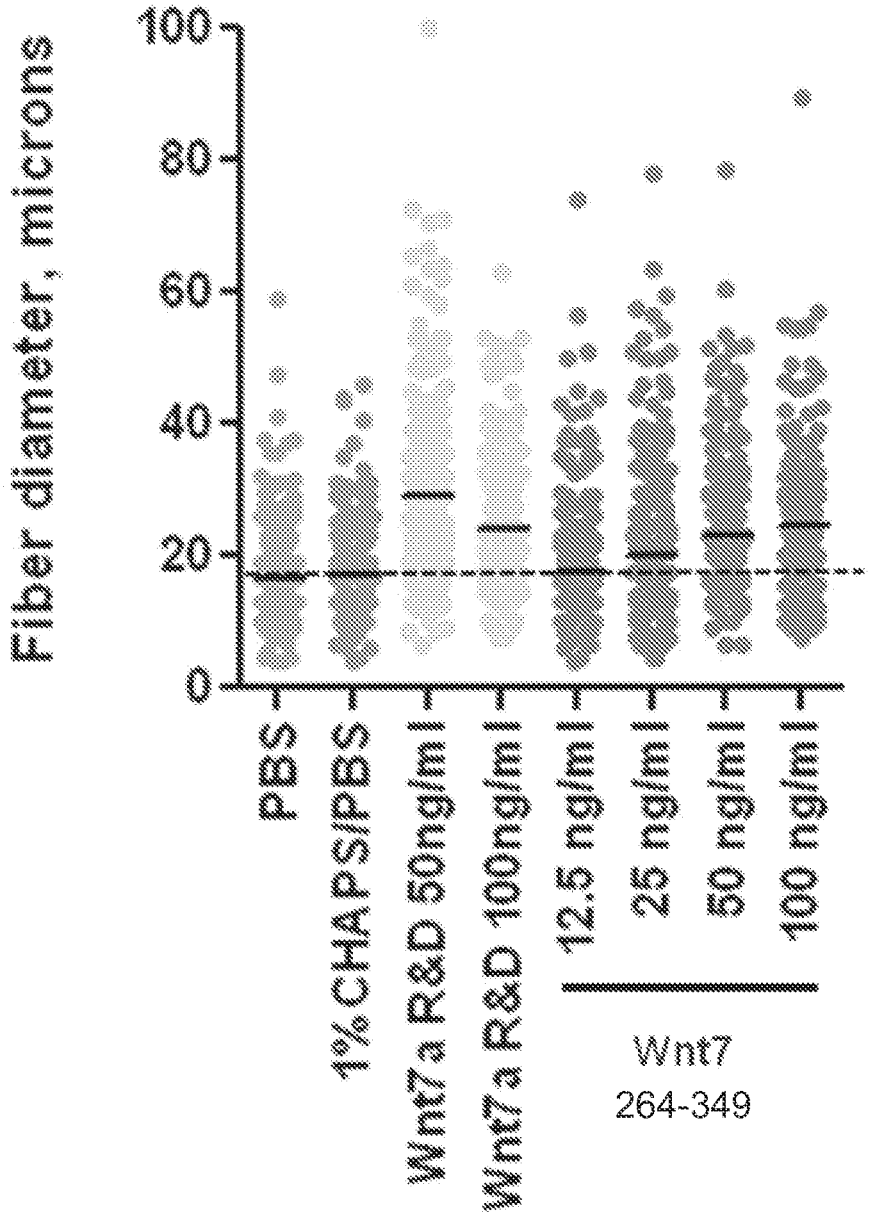

Fiber diameter, microns
100
80
60
40
20
0
PBS
1% CHAPS/PBS
Wnt7a R&D 50ng/ml
Wnt7a R&D 100ng/ml
12.5 ng/ml
25 ng/ml
50 ng/ml
100 ng/ml
Wnt7
264-349

FIG. 8C

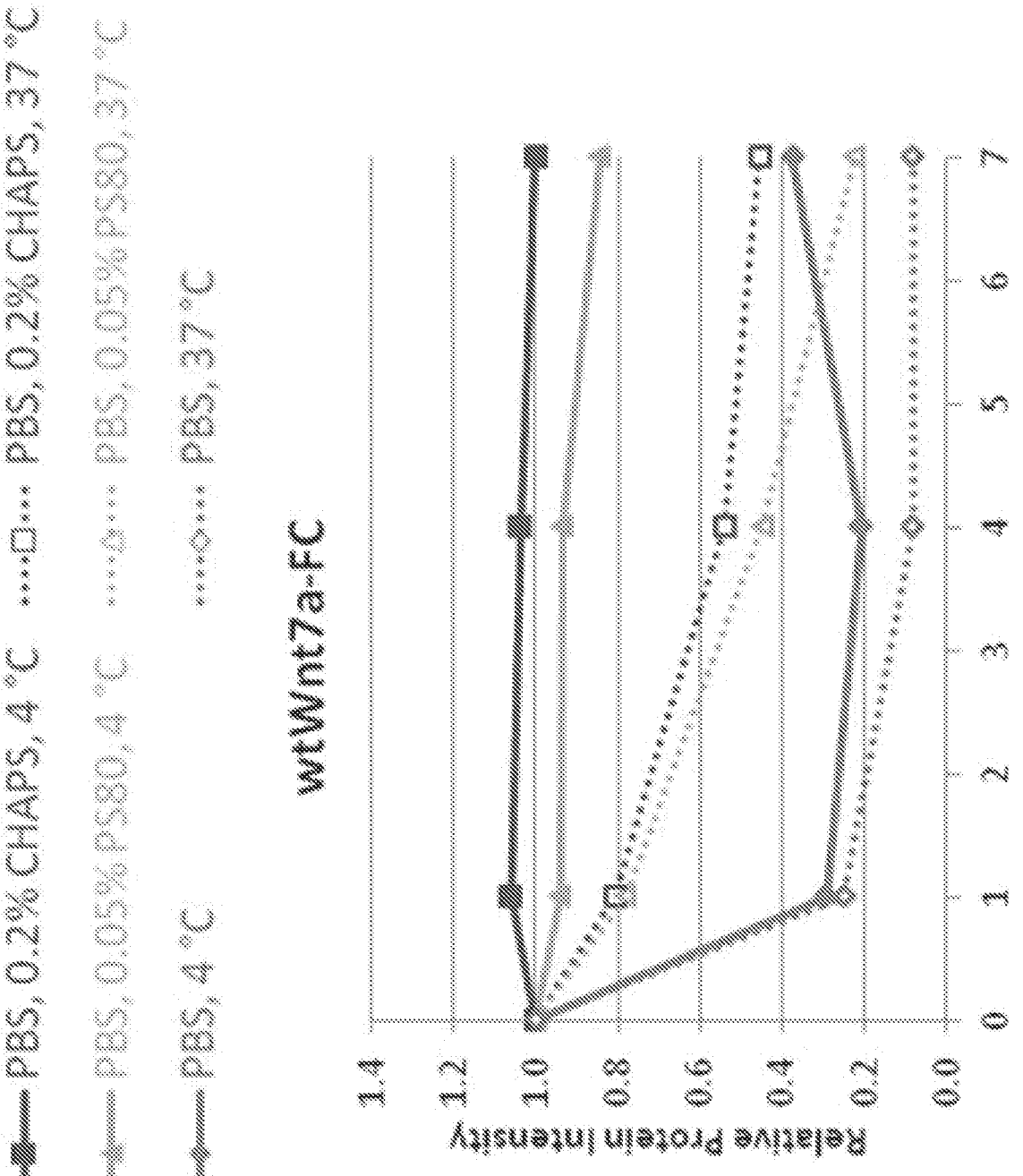

PBS, 0.2% CHAPS, 4 °C
PBS, 0.2% CHAPS, 37 °C
PBS, 0.05% PS80, 4 °C
PBS, 0.05% PS80, 37 °C
PBS, 4 °C
PBS, 37 °C
wtWnt7a-FC
Relative Protein Intensity
Incubation time (d)
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
0
1
2
3
4
5
6
7

FIG. 9A

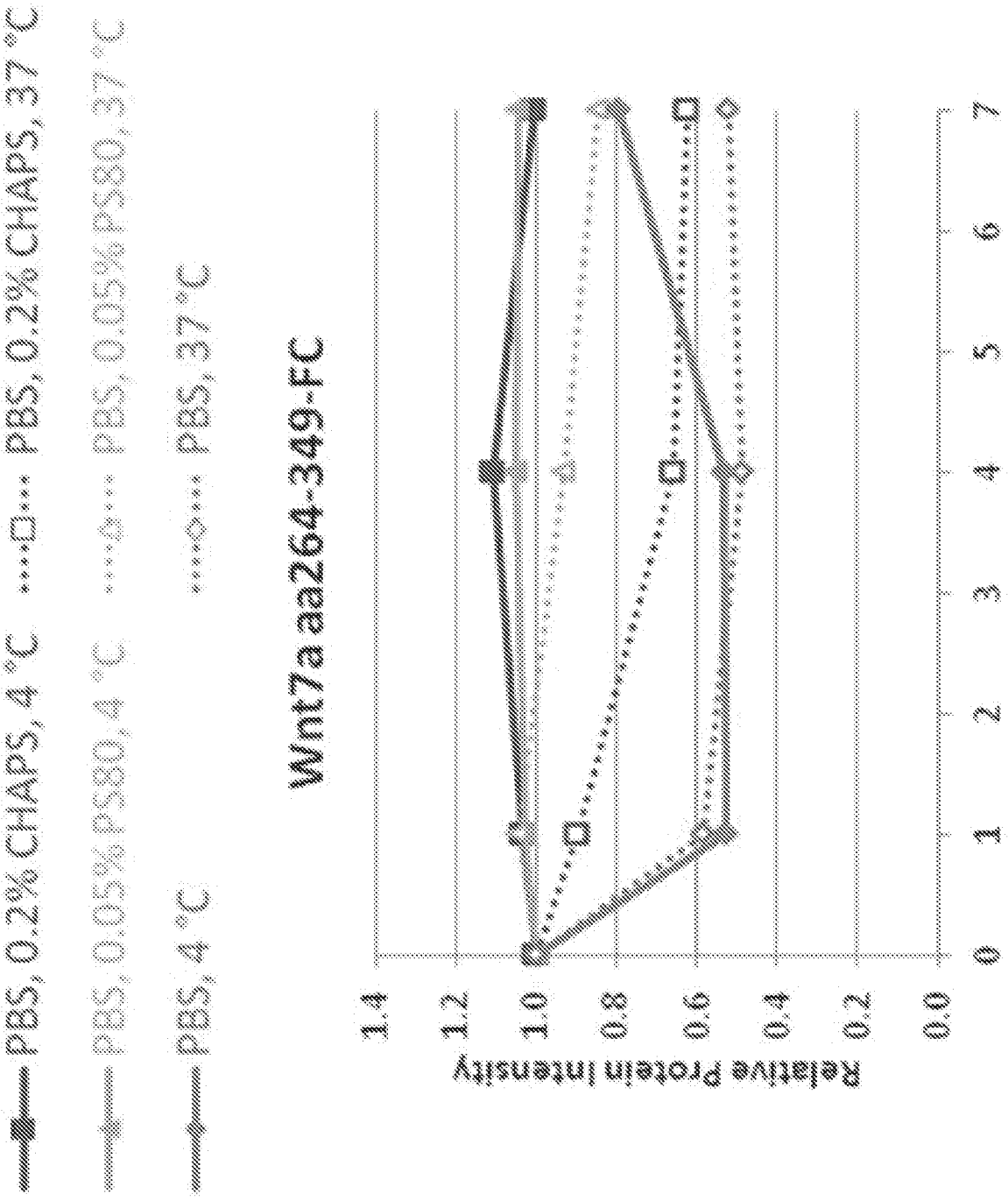

PBS, 0.2% CHAPS, 4 °C
PBS, 0.2% CHAPS, 37 °C
PBS, 0.05% PS80, 4 °C
PBS, 0.05% PS80, 37 °C
PBS, 4 °C
PBS, 37 °C
Wnt7a aa264-349-FC
Relative Protein Intensity
Incubation time (d)
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
0
1
2
3
4
5
6
7

FIG. 9B

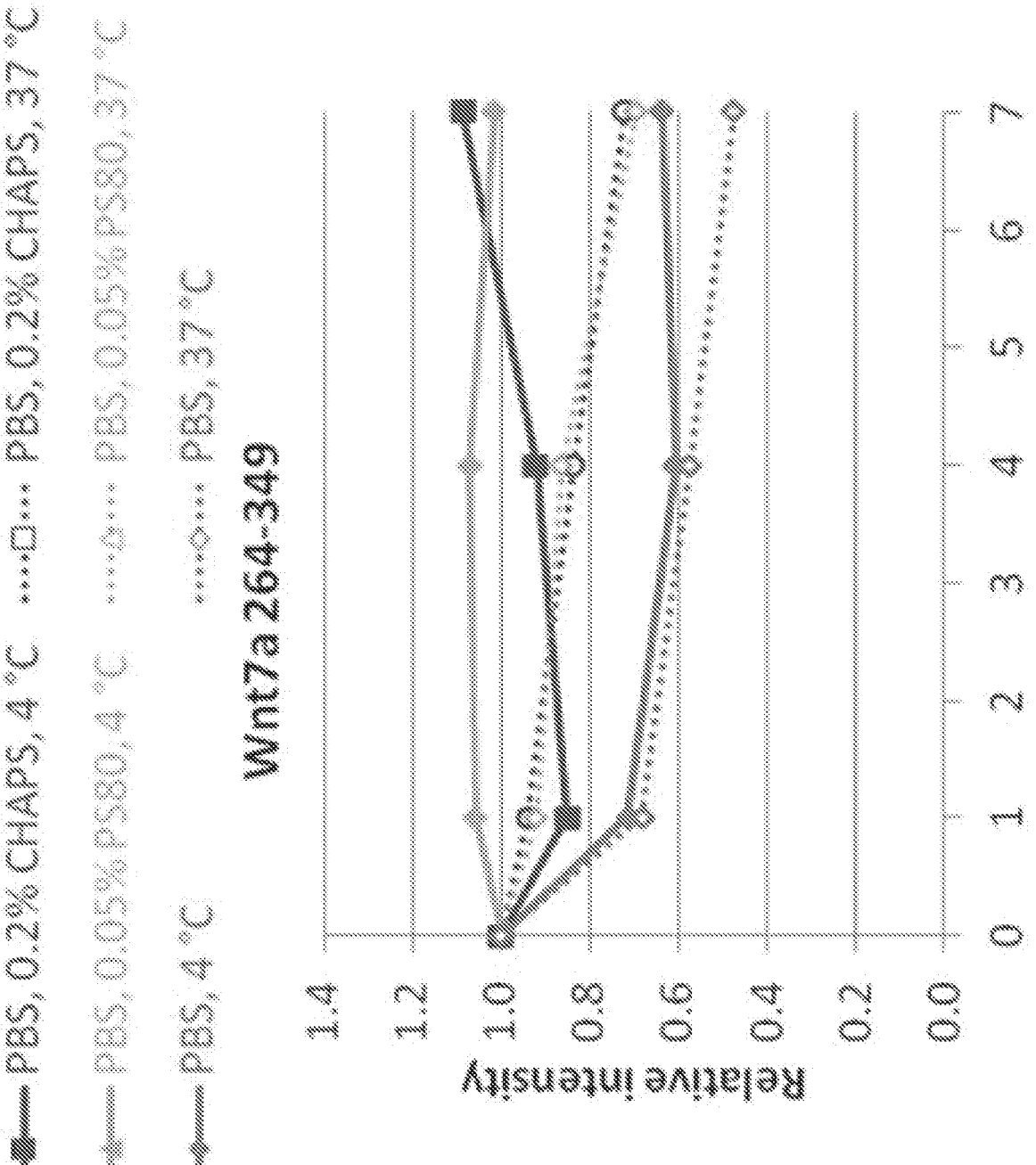

PBS, 0.2% CHAPS, 4 °C
PBS, 0.05% PS80, 4 °C
PBS, 4 °C
PBS, 0.2% CHAPS, 37 °C
PBS, 0.05% PS80, 37 °C
PBS, 37 °C
Wnt7a 264-349
Relative intensity
Incubation time (d)
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
0
1
2
3
4
5
6
7

FIG. 9C

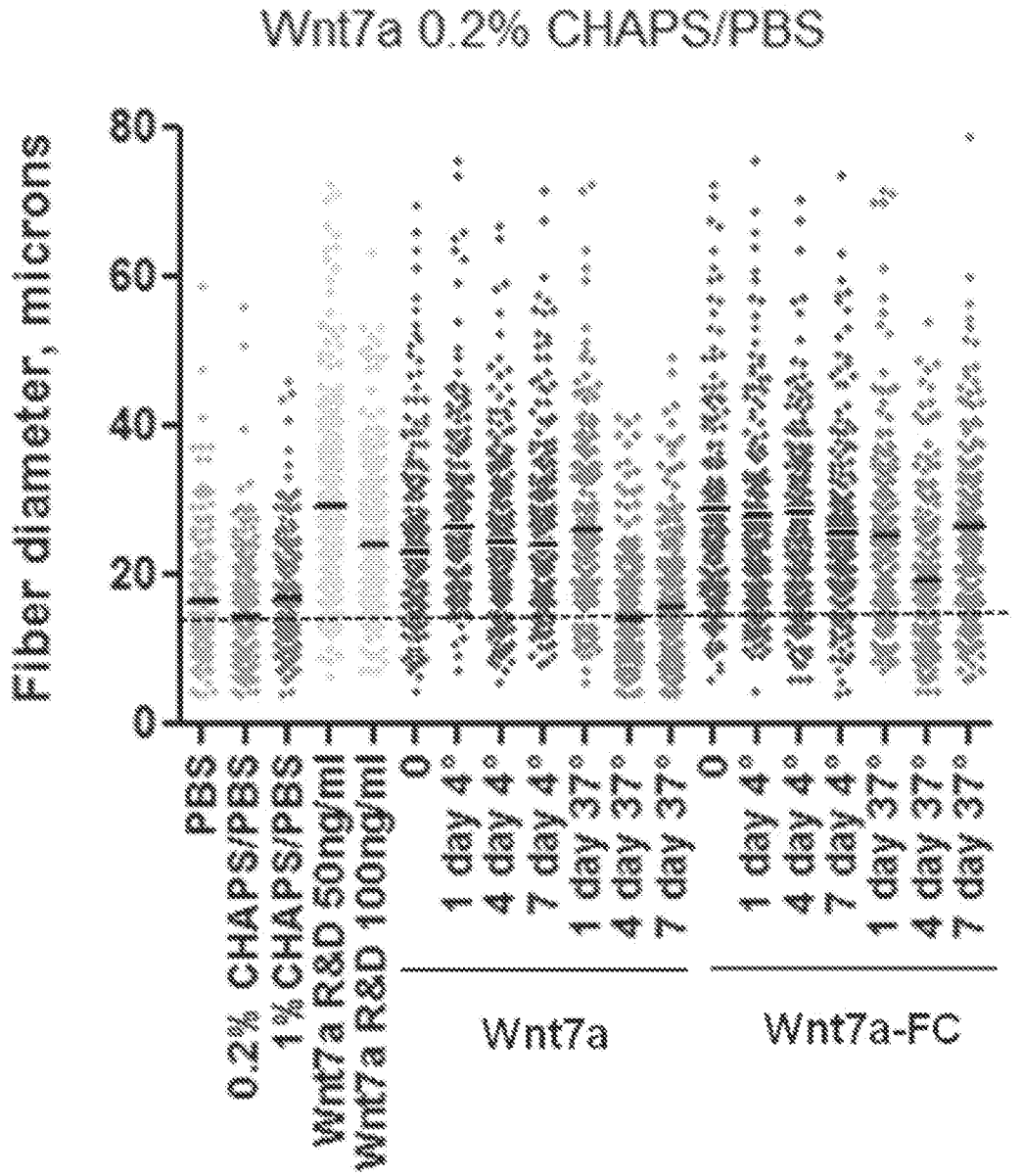

Wnt7a 0.2% CHAPS/PBS
Fiber diameter, microns
0
20
40
60
80
PBS
0.2% CHAPS/PBS
1% CHAPS/PBS
Wnt7a R&D 50ng/ml
Wnt7a R&D 100ng/ml
0
1 day 4°
4 day 4°
7 day 4°
1 day 37°
4 day 37°
7 day 37°
0
1 day 4°
4 day 4°
7 day 4°
1 day 37°
4 day 37°
7 day 37°
Wnt7a
Wnt7a-FC

FIG. 10A

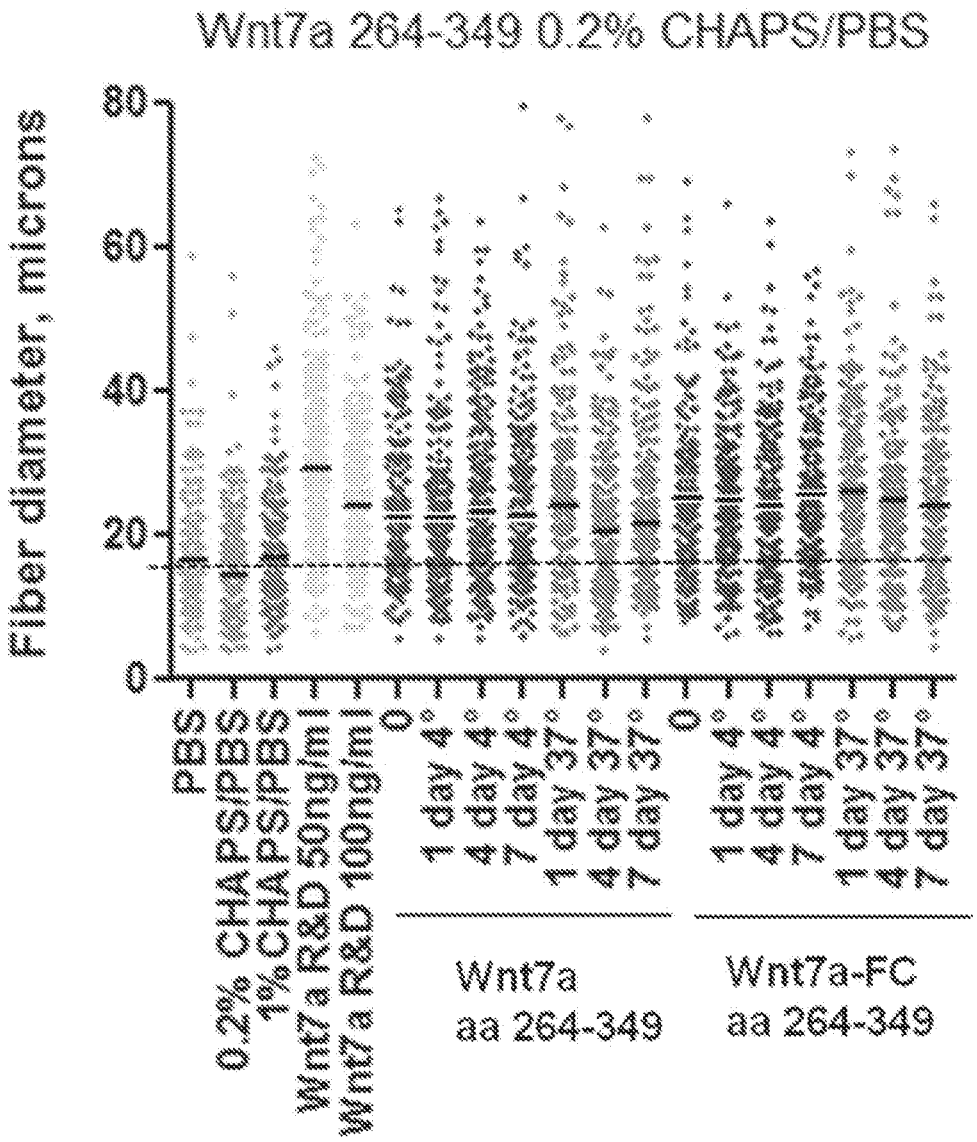

Wnt7a 264-349 0.2% CHAPS/PBS
Fiber diameter, microns
0
20
40
60
80
PBS
0.2% CHAPS/PBS
1% CHAPS/PBS
Wnt7a R&D 50ng/ml
Wnt7a R&D 100ng/ml
0
1 day 4°
4 day 4°
7 day 4°
1 day 37°
4 day 37°
7 day 37°
0
1 day 4°
4 day 4°
7 day 4°
1 day 37°
4 day 37°
7 day 37°
Wnt7a
aa 264-349
Wnt7a-FC
aa 264-349

FIG. 10B

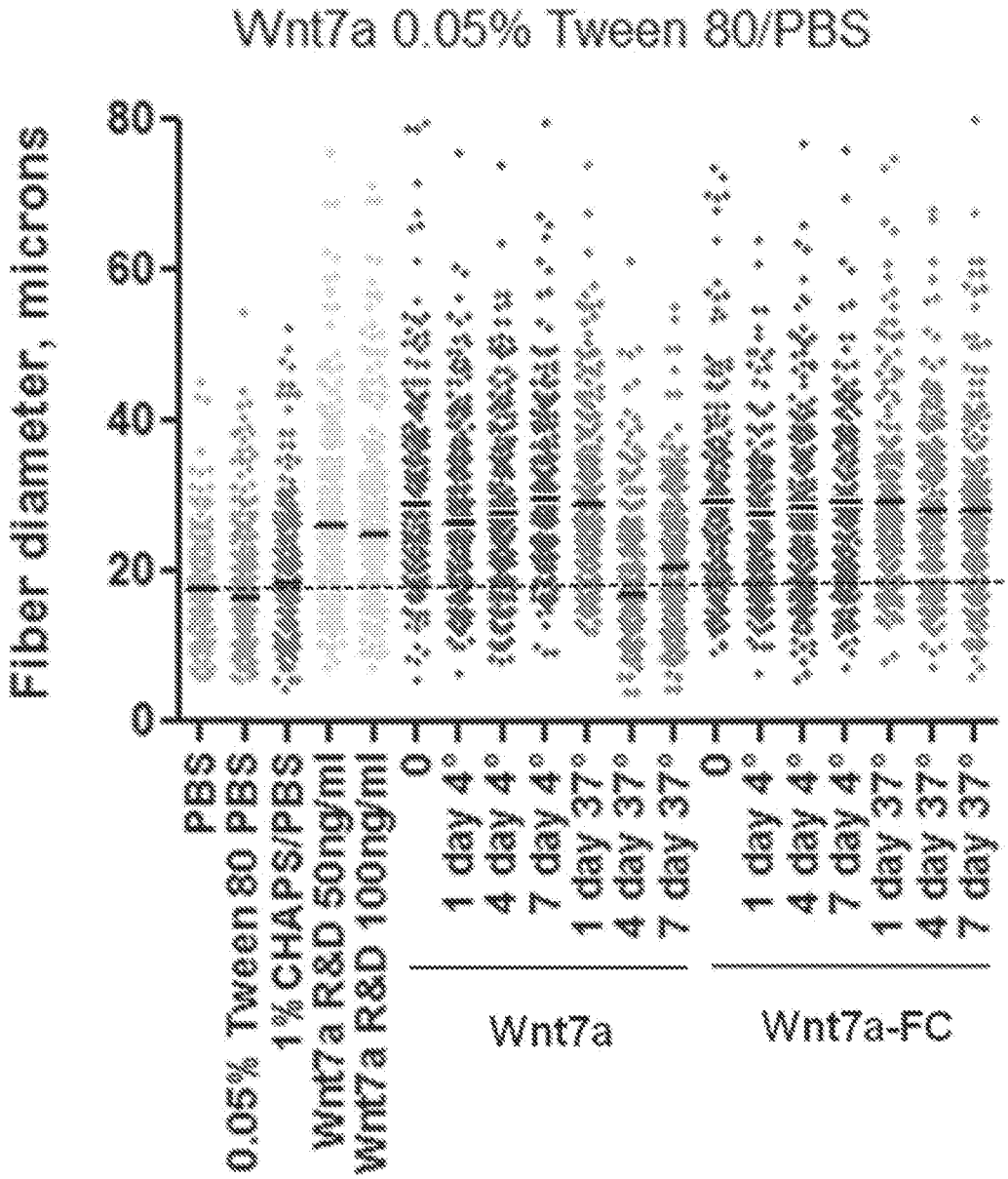

Wnt7a 0.05% Tween 80/PBS
Fiber diameter, microns
0
20
40
60
80
PBS
0.05% Tween 80 PBS
1% CHAPS/PBS
Wnt7a R&D 50ng/ml
Wnt7a R&D 100ng/ml
0
1 day 4°
4 day 4°
7 day 4°
1 day 37°
4 day 37°
7 day 37°
0
1 day 4°
4 day 4°
7 day 4°
1 day 37°
4 day 37°
7 day 37°
Wnt7a
Wnt7a-FC

FIG. 11A

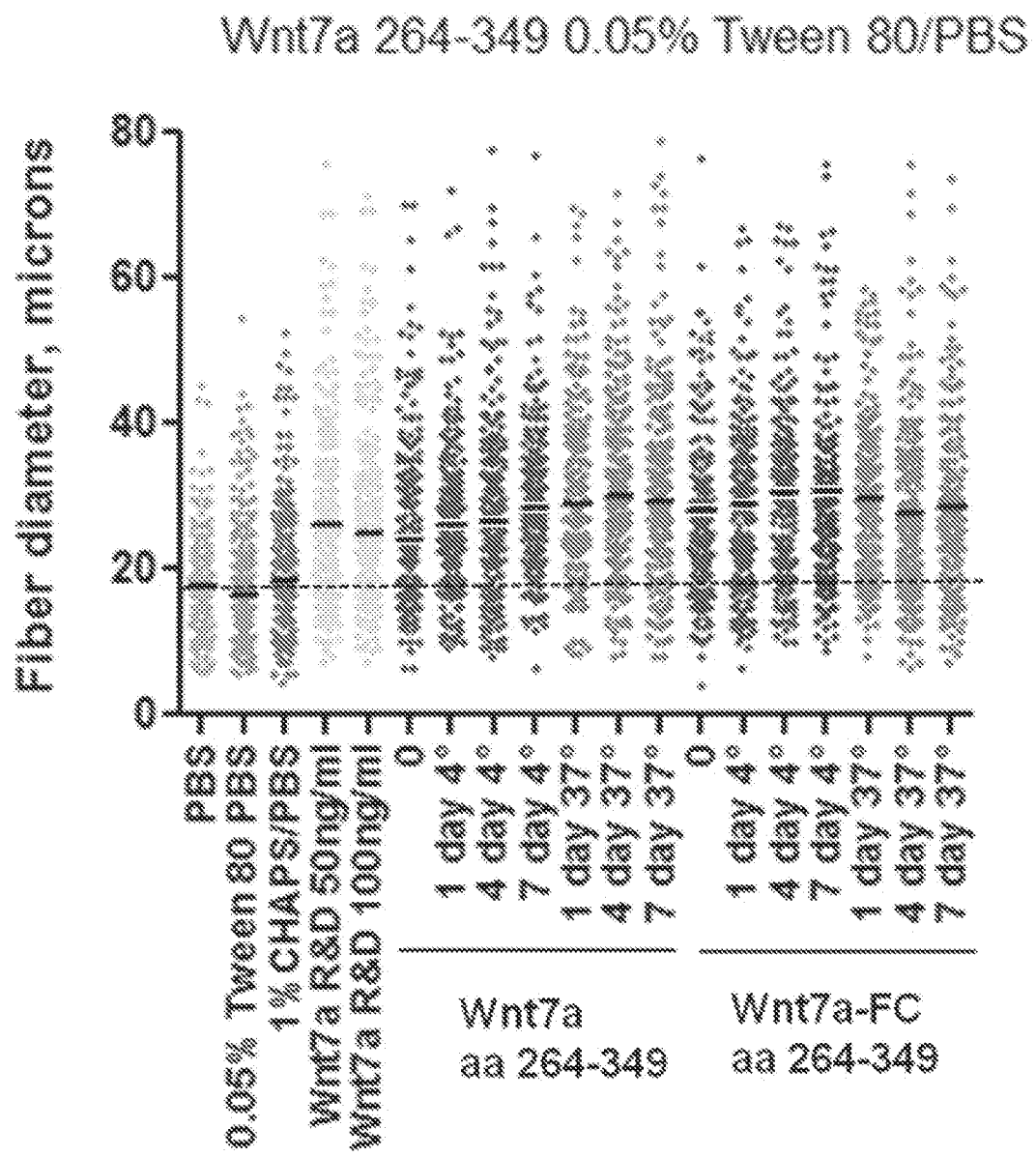

Wnt7a 264-349 0.05% Tween 80/PBS
Fiber diameter, microns
0
20
40
60
80
PBS
0.05% Tween 80 PBS
1% CHAPS/PBS
Wnt7a R&D 50mg/ml
Wnt7a R&D 100mg/ml
0
1 day 4°
4 day 4°
7 day 4°
1 day 37°
4 day 37°
7 day 37°
0
1 day 4°
4 day 4°
7 day 4°
1 day 37°
4 day 37°
7 day 37°
Wnt7a
aa 264-349
Wnt7a-FC
aa 264-349

FIG. 11B

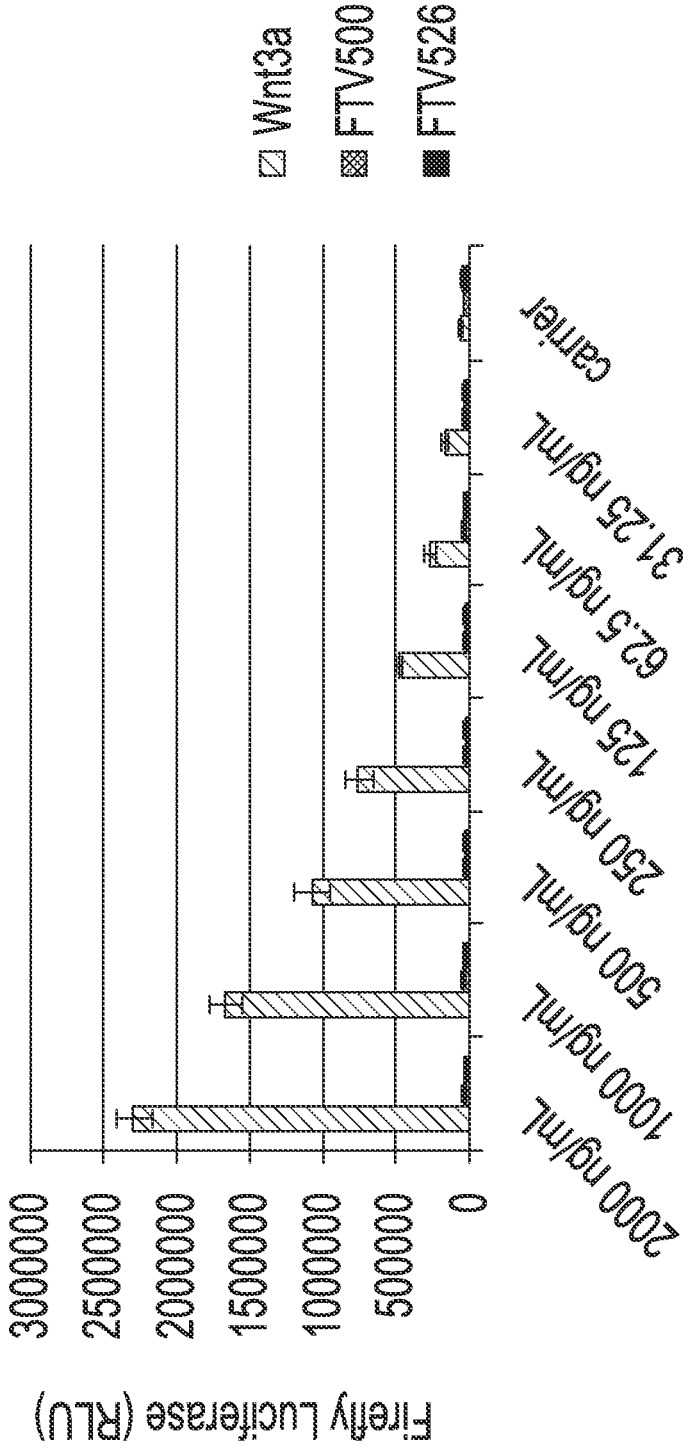

A549 (lung)
Firefly Luciferase (RLU)
3000000
2500000
2000000
1500000
1000000
500000
0
Wnt3a
FTV500
FTV526
2000 ng/mL
1000 ng/mL
500 ng/mL
250 ng/mL
125 ng/mL
62.5 ng/mL
31.25 ng/mL
carrier

FIG. 12A

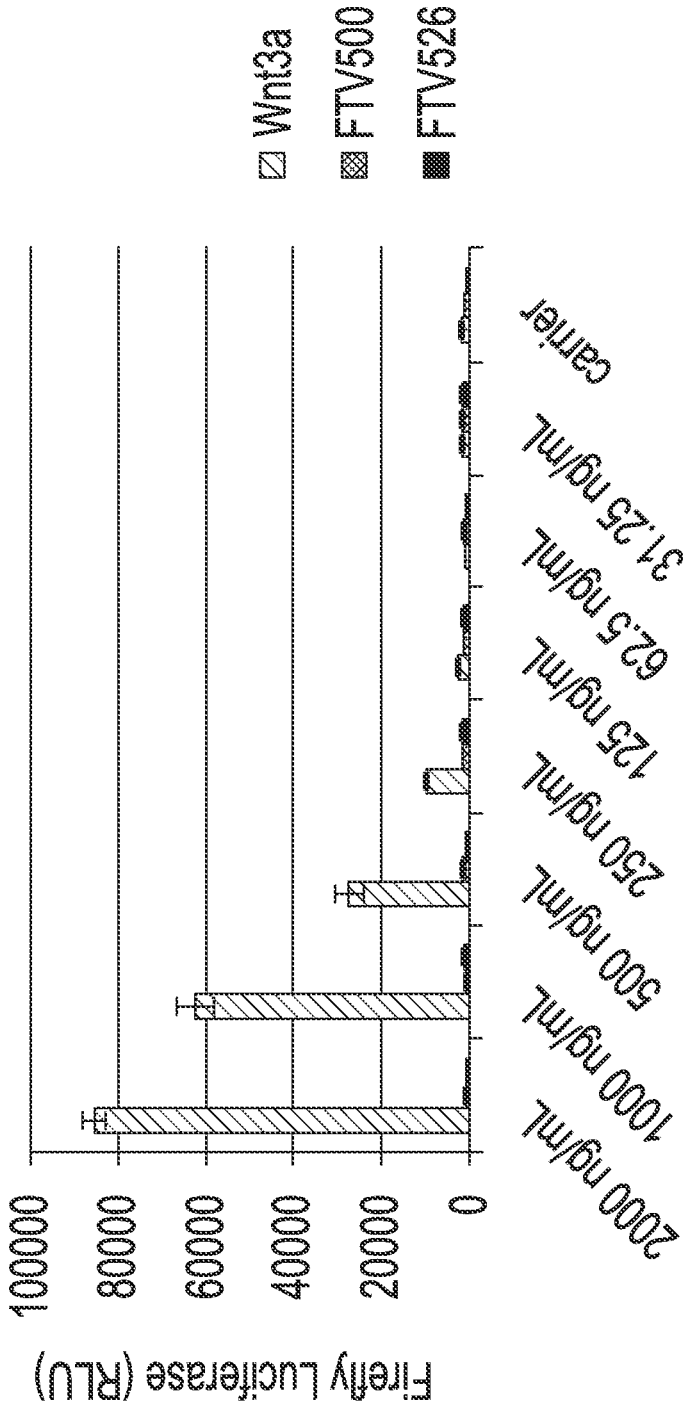

KG-1a (myeloblast)
Firefly Luciferase (RLU)
100000
80000
60000
40000
20000
0
Wnt3a
FTV500
FTV526
2000 ng/mL
1000 ng/mL
500 ng/mL
250 ng/mL
125 ng/mL
62.5 ng/mL
31.25 ng/mL
carrier

FIG. 12B

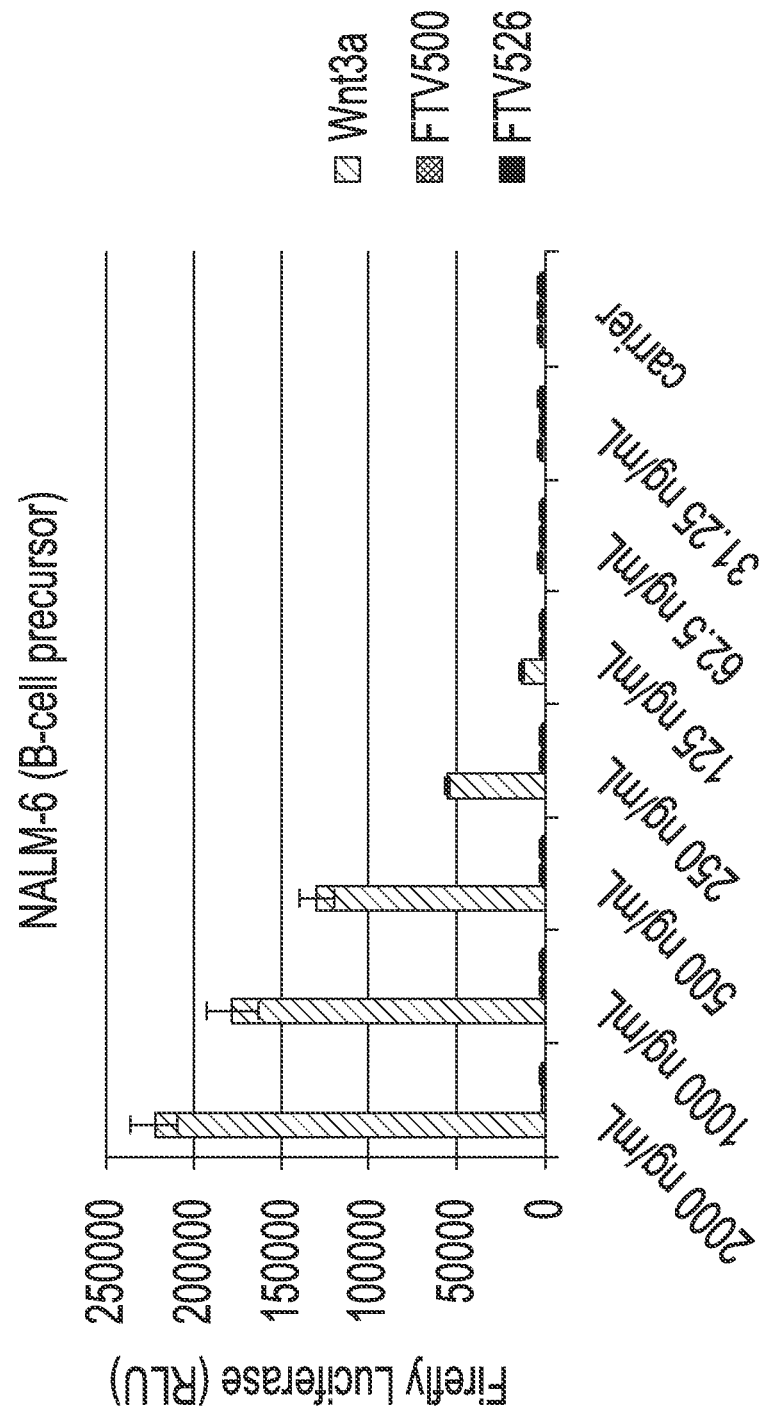

NALM-6 (B-cell precursor)
Firefly Luciferase (RLU)
250000
200000
150000
100000
50000
0
Wnt3a
FTV500
FTV526
2000 ng/mL
1000 ng/mL
500 ng/mL
250 ng/mL
125 ng/mL
62.5 ng/mL
31.25 ng/mL
carrier

FIG. 12C

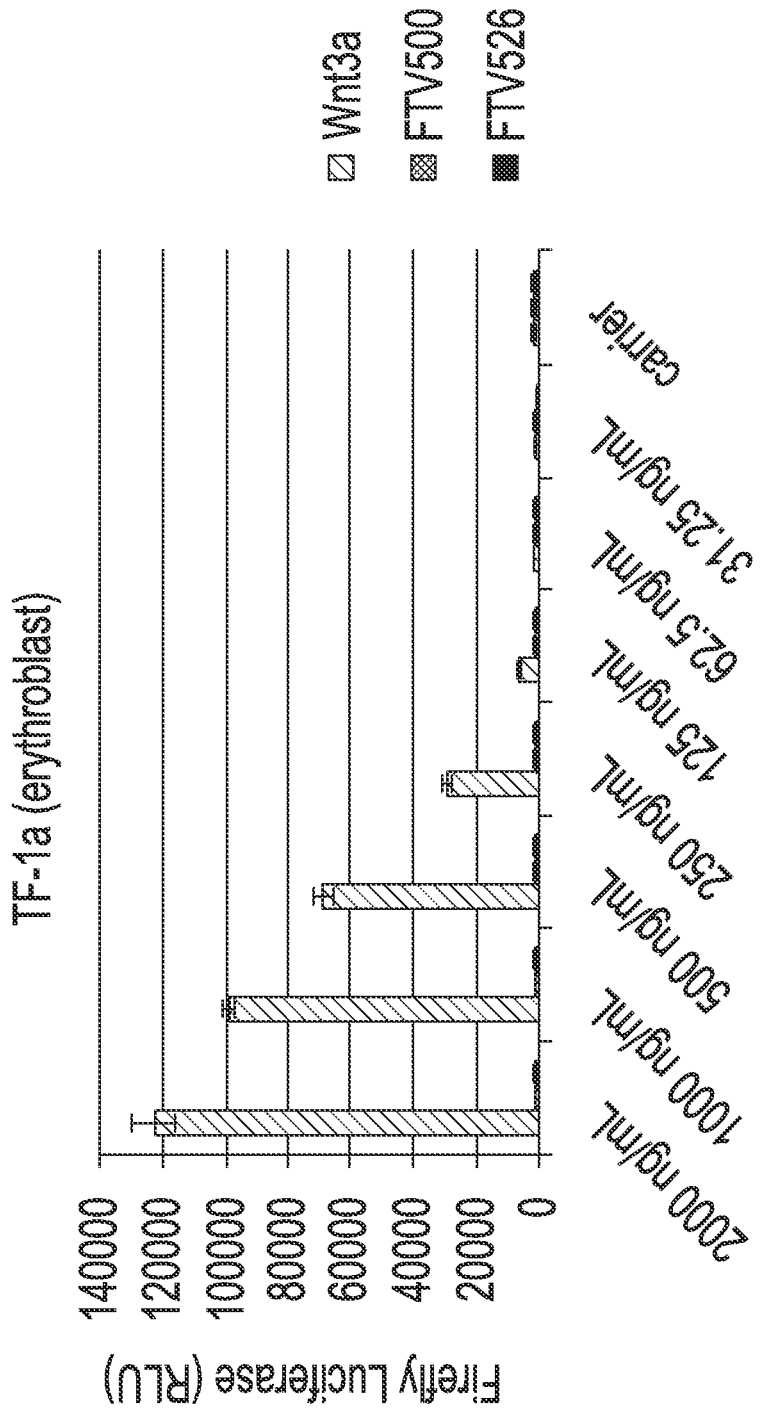

TF-1a (erythroblast)
Firefly Luciferase (RLU)
140000
120000
100000
80000
60000
40000
20000
0
Wnt3a
FTV500
FTV526
2000 ng/mL
1000 ng/mL
500 ng/mL
250 ng/mL
125 ng/mL
62.5 ng/mL
31.25 ng/mL
carrier

FIG. 12D

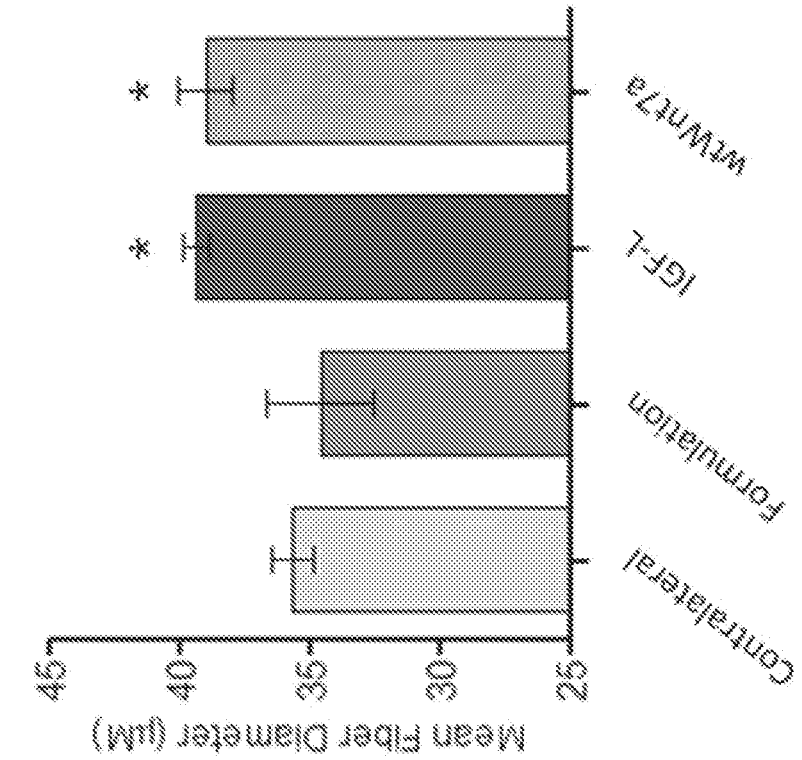


FIG. 13B

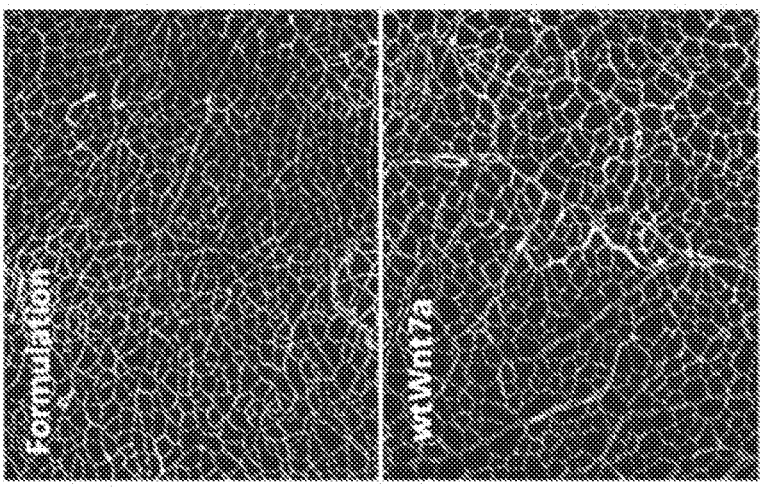


FIG. 13A

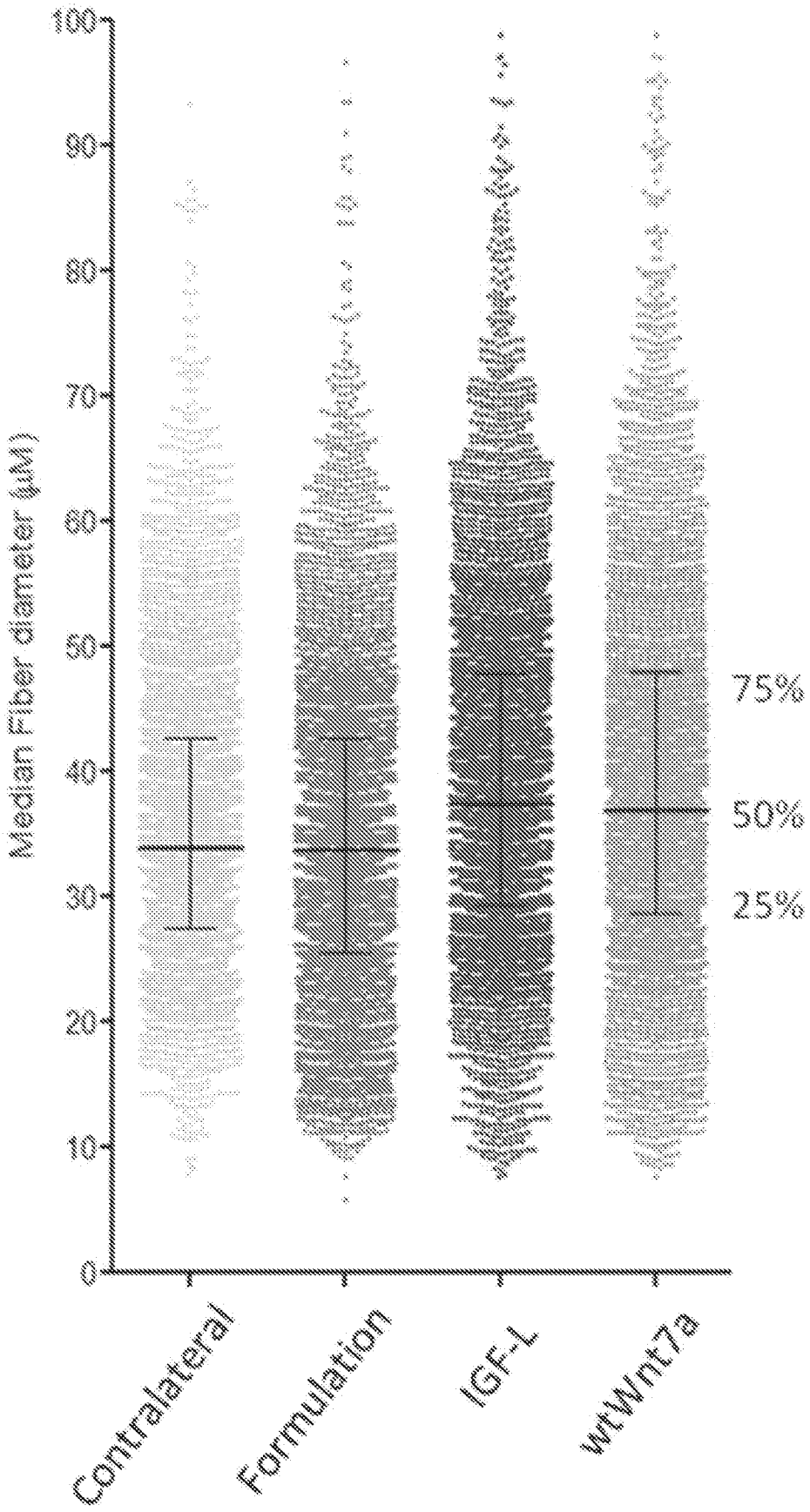

Median Fiber diameter (μM)
100
90
80
70
60
50
40
30
20
10
0
75%
50%
25%
Contralateral
Formulation
IGF-L
wtWnt7a

FIG. 13C

	Contralateral	Formulation	IGF-1	wtWnt7a
N (WT Mice)	7	6	6	5
Median	36.03	35.91	39.93	38.28
25% Percentile	33.35	31.69	38.14	37.07
75% Percentile	38.09	38.36	40.35	41.43
Mean	35.74 ± 2.09	34.65 ± 4.98	39.44 ± 1.23	39.05 ± 2.32
P value *	0.9974	0.6151	0.0007	0.0332
Hypertrophy (%) *	100	N/A	110.4	109.3

FIG. 13D

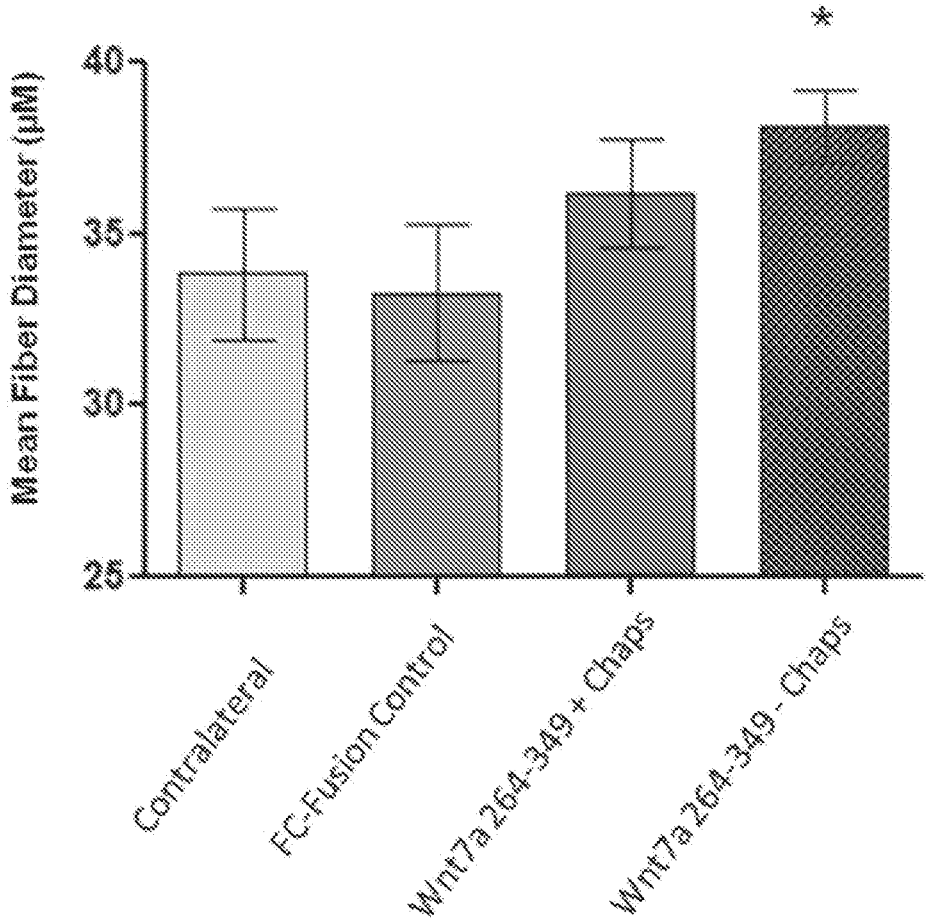


FIG. 14A

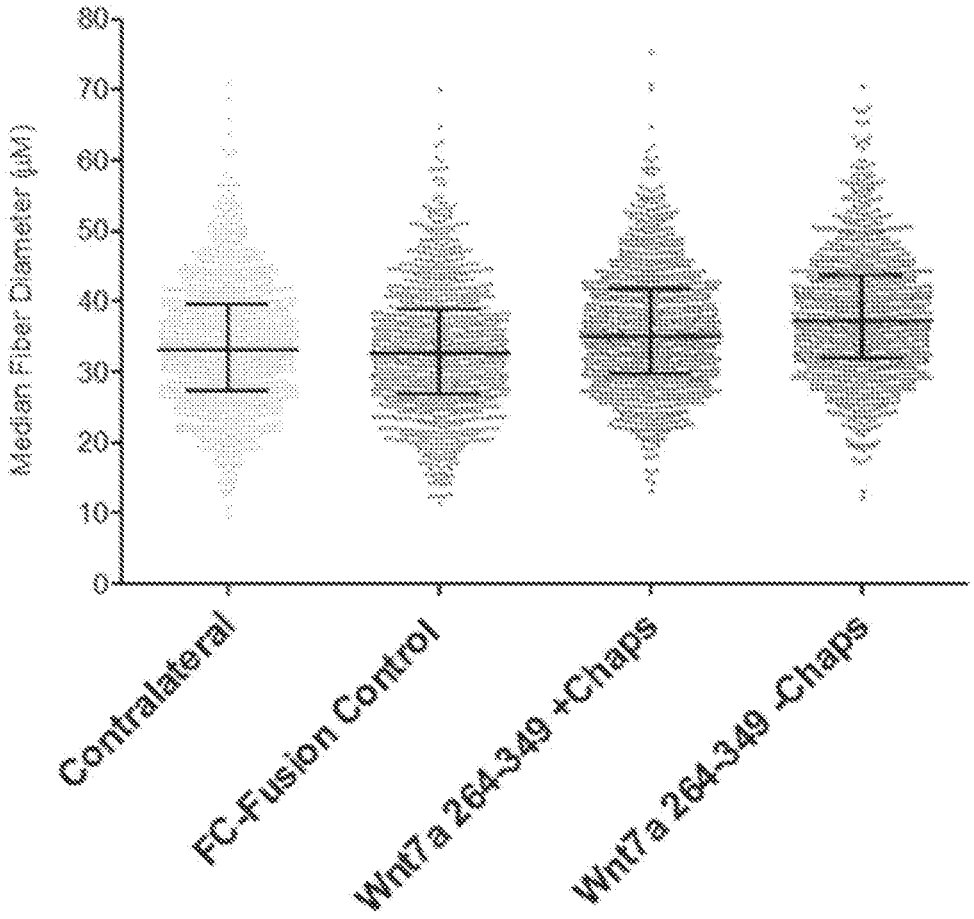


FIG. 14B

	FC-Control	264-349-FC (+Chaps)	264-349-FC (-Chaps)
N (MOX Mice)	4	4	4
Mean	33.28 ± 3.96	36.16 ± 3.15	38.13 ± 2.11
P Value *	0.9996	0.1648	0.0193
N (Diameter values)	4004	4004	4004
25% Percentile	18.52	23.94	25.31
Median	30.93	33.94	35.35
75% Percentile	43.83	45.37	48.59

FIG. 14C

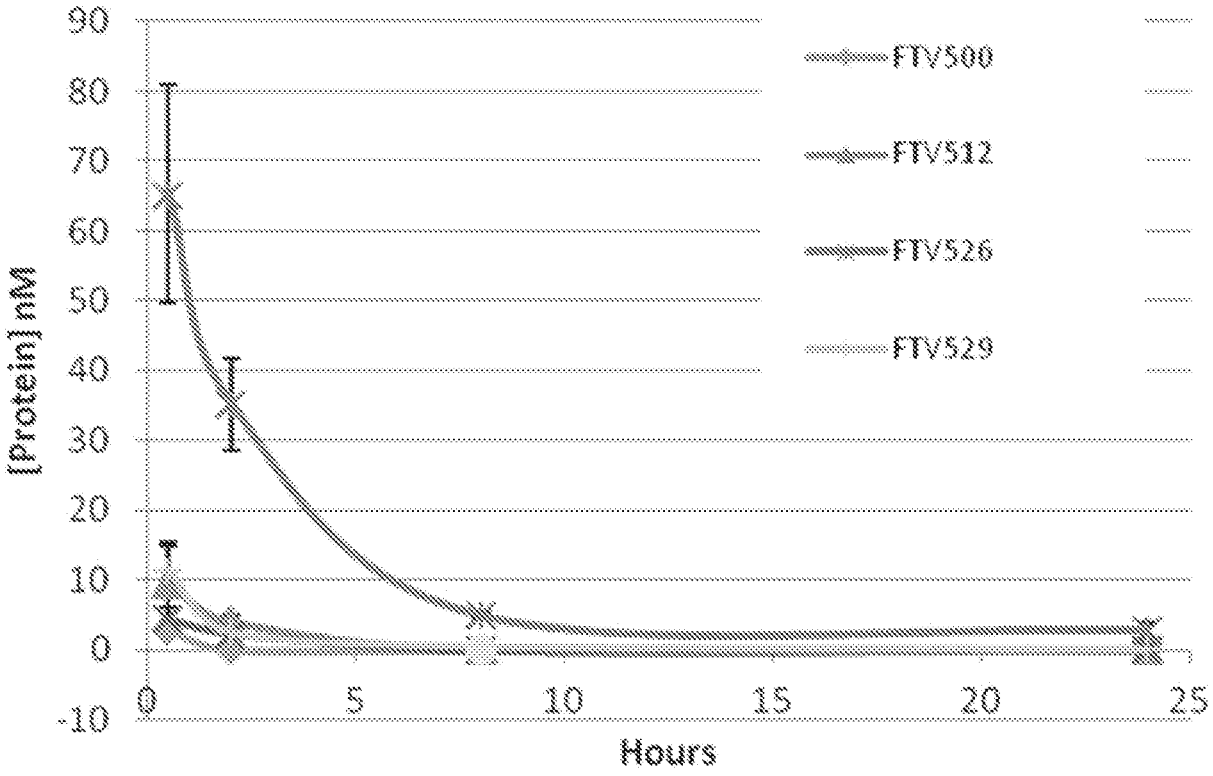


FIG. 15A

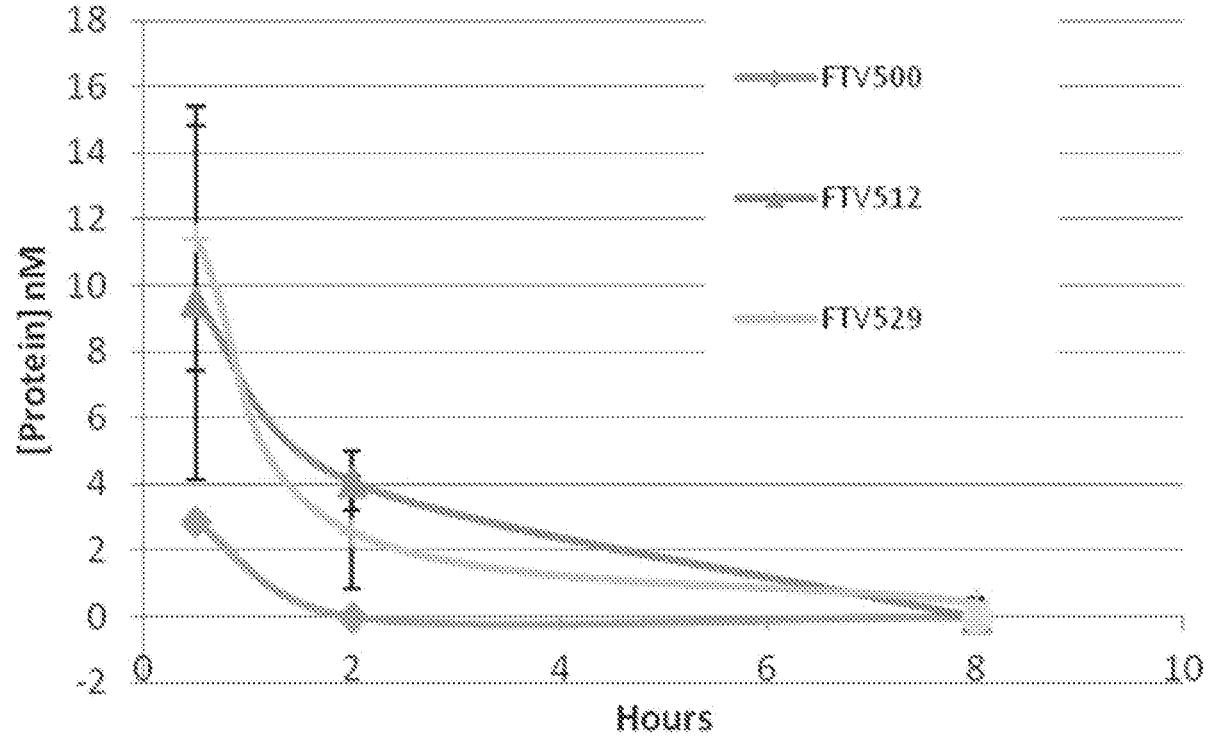


FIG. 15B