```
Wnt-1       -------MGLWALLPGW----------------VSATLLLALAALPAALA 27
Wnt-2       ---------MNAPLG-------------------GIWLWLPLLLTWLTP 21
Wnt-2b      ---------MLDGLGVV-----------AISIFGIQLKTEGSLRTAVP 28
Wnt-3       ------------MEPH---------------LLGLLLGLLLGGTRVLA 21
Wnt-3a      ------------MAP-----------------LGYFL-LLCSLKQALG 18
Wnt-4       ------------MSPR---------------SCLRSLRLLVFAVFSAA 21
Wnt-5a      ---------MKKSIGILSPGVALGMAGSAMSSKFFLVALAIFFSFAQVVI 41
Wnt-5b      ------------------------------MPSLLLLFTAALLSSWAQLLT 21
Wnt-6       ------------------------------MLPPLPSRLGLLLLLL 16
Wnt-7a      ---------MNRKARRC---------------LGHLFLSLG--MVYLRI 23
Wnt-7b      ---------MHRNFRKW---------------IFYVFLCFG--VLYVKL 23
Wnt-8a      ----------------------------MGNLFMLWAALGIC---C 15
Wnt-8       ---------------------------------MFLSKPSVYICLFTC 15
Wnt-9a      ----------------------------MLDGSPLARWLAAAFGLTLLLA 22
Wnt-9b      ----------------------------MR--PPPALALAGLC----LLA 16
Wnt-10a     MGSAHPRP--------------------WLRLRPQPQPRPALWVLLFFLL 30
Wnt-10b     ----------------------------MLEEPRPRPPPSGLAGLLFLA 21
Wnt-11      ---------------------------------MRARPQVCEALLFAL 15
Wnt-16      ---------MDRAALLG---------------LARLCALWAALLVLFPY 25

Wnt-1       ANSSGRWWGIVNVASSTNLLTD-------SKSLQLVLEPSLQLLSRKQRR 70
Wnt-2       EVNSSWWY--------MRATGGS-----------SRVMCDNVPGLVSSQRQ 53
Wnt-2b      GIPTQSAFNKC---LQRYIGAL-------G---ARVICDNIPGLVSRQRQ 65
Wnt-3       GYP--IWWSLALGQQYTSLGS-----------QPLLCGSIPGLVPKQLR 57
Wnt-3a      SYP--IWWSLAVGPQYSSLGS-----------QPILCASIPGLVPKQLR 54
Wnt-4       ASN---WLYLAKLSSVGSISE-----------EETCEKLKGLIQRQVQ 55
Wnt-5a      EANSWWSLGMNNPVQMSEVYII-------G---AQPLCSQLAGLSQGQKK 81
Wnt-5b      DANSWWSLALN-PVQRPEMFII-------G---AQPVCSQLPGLSPGQRK 60
Wnt-6       LCPAHVGG------LWWAVGSP-------LVMDPTSICRKARRLAGRQAE 53
Wnt-7a      GGFSSVVA------LGAS-----------------IICNKIPGLAPRQRA 50
Wnt-7b      GALSSVVA------LGAN-----------------IICNKIPGLAPRQRA 50
Wnt-8a      AAFSASAWS-----------------------------------VNNFLIT 31
Wnt-8       VLQLSHSWS-----------------------------------VNNFLMT 31
Wnt-9a      ALRPSAAYFGLTGSEPLTILP--LTLEPEAAAQAHYKACDRLKLERKQRR 70
Wnt-9b      LPAAAASYFGLTGREVLTPFPGLGTAAAPAQGGAHLKQCDLLKLSRRQKQ 66
Wnt-10a     LLAAAMPRSAPNDILDLRLPPE-------PVLNANTVCLTLPGLSRRQME 73
Wnt-10b     LCSRALS----NEILGLKLPGE-------PPLTANTVCLTLSGLSKRQLG 60
Wnt-11      ALQTGVCYGIKWLALSKTPSAL-------ALN-QTQHCKQLEGLVSAQVQ 57
Wnt-16      GAQGNWMW------LGIASFGV-------P---EKLGCANLP-LNSRQKE 58

Wnt-1       LIRQNPGILHSVSGGLQSAVRECKWQFRNRRWNCP-------TAPG-PHL 112
Wnt-2       LCHRHPDVMRAISQGVAEWTAECQHQFRQHRWNCN-------TLDRDHSL 96
Wnt-2b      LCQRYPDIMRSVGEGAREWIRECQHQFRHHRWNCT-------TLDRDHTV 108
Wnt-3       FCRNYIEIMPSVAEGVKLGIQECQHQFRGRRWNCT-------TIDDSLAI 100
Wnt-3a      FCRNYVEIMPSVAEGIKIGIQECQHQFRGRRWNCT-------TVHDSLAI 97
Wnt-4       MCKRNLEVMDSVRRGAQLAIEECQYQFRNRRWNCS-------TLDS-LPV 97
Wnt-5a      LCHLYQDHMQYIGEGAKTGIKECQYQFRHRRWNCS-------TVD-NTSV 123
Wnt-5b      LCQLYQEHMAYIGEGAKTGIKECQHQFRQRRWNCS-------TAD-NASV 102
Wnt-6       LCQAEPEVVAELARGARLGVRECQFQFRFRRWNCS-----SHS-----KA 93
```

FIG. 1

```
Wnt-7a      ICQSRPDAIIVIGEGSQMGLDECQFQFRNGRWNCS---------ALGERTV 92
Wnt-7b      ICQSRPDAIIVIGEGAQMGINECQYQFRFGRWNCS---------ALGEKTV 92
Wnt-8a      GPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCP---------ENALQLS 73
Wnt-8       GPKAYLIYSSSVAAGAQSGIEECKYQFAWDRWNCP---------ERALQLS 73
Wnt-9a      MCRRDPGVAETLVEAVSMSALECQFQFRFERWNCT----------LEGRY 110
Wnt-9b      LCRREPGLAETLRDAAHLGLLECQFQFRHERWNCS----------LEG-- 104
Wnt-10a     VCVRHPDVAASAIQGIQIAIHECQHQFRDQRWNCS-----SLETRNKIPY 118
Wnt-10b     LCLRNPDVTASALQGLHIAVHECQHQLRDQRWNCS-----ALEGGGRLPH 105
Wnt-11      LCRSNLELMHTVVHAAREVMKACRRAFADMRWNCS---------SIELAPN 99
Wnt-16      LCKRKPYLLPSIREGARLGIQECGSQFRHERWNCMITAAATTAPMGASPL 108

Wnt-1       FGKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPG- 161
Wnt-2       FGRVLLRSSRESAFVYAISSAGVVFAITRACSQGEVKSCSCDPKKMGSAK 146
Wnt-2b      FGRVMLRSSREAAFVYAISSAGVVHAITRACSQGELSVCSCDPYTRGRHH 158
Wnt-3       FGPVLDKATRESAFVHAIASAGVAFAVTRSCAEGTSTICGCDSHHKGPP- 149
Wnt-3a      FGPVLDKATRESAFVHAIASAGVAFAVTRSCAEGTAAICGCSSRHQGSP- 146
Wnt-4       FGKVVTQGTREAAFVYAISSAGVAFAVTRACSSGELEKCGCDRTVHGVS- 146
Wnt-5a      FGRVMQIGSRETAFTYAVSAAGVVNAMSRACREGELSTCGCS--RAARPK 171
Wnt-5b      FGRVMQIGSRETAFTHAVSAAGVVNAISRACREGELSTCGCS--RTARPK 150
Wnt-6       FGRILQQDIRETAFVFAITAAGASHAVTQACSMGELLQCGCQAPRG---- 139
Wnt-7a      FGKELKVGSREAAFTYAIIAAGVAHAITAACTQGNLSDCGCDKEKQGQYH 142
Wnt-7b      FGQELRVGSREAAFTYAITAAGVAHAVTAACSQGNLSNCGCDREKQGYYN 142
Wnt-8a      THNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTG 123
Wnt-8       SHGGLRSANRETAFVHAISSAGVMYTLTRNCSLGDFDNCGCDDSRNGQLG 123
Wnt-9a      RASLLKRGFKETAFLYAISSAGLTHALAKACSAGRMERCTCDEAPDLENR 160
Wnt-9b      RMGLLKRGFKETAFLYAVSSAALTHTLARACSAGRMERCTCDDSPGLESR 154
Wnt-10a     ESPIFSRGFRESAFAYAIAAAGVVHAVSNACALGKLKACGCDASRRGDEE 168
Wnt-10b     HSAILKRGFRESAFSFSMLAAGVMHAVATACSLGKLVSCGCGWKGSGEQD 155
Wnt-11      YLLDLERGTRESAFVYALSAAAISHAIARACTSGDLPGCSCGPVPGEPP- 148
Wnt-16      FGYELSSGTKETAFIYAVMAAGLVHSVTRSCSAGNMTECSCDTTLQNGGS 158

Wnt-1       ----------------------------------------GPDWHWGGCSDNI 174
Wnt-2       D---------------------------------------SKGIFDWGGCSDNI 161
Wnt-2b      D---------------------------------------QRGDFDWGGCSDNI 173
Wnt-3       ----------------------------------------GEGWKWGGCSEDA 162
Wnt-3a      ----------------------------------------GKGWKWGGCSEDI 159
Wnt-4       ----------------------------------------PQGFQWSGCSDNI 159
Wnt-5a      D---------------------------------------LPRDWLWGGCGDNI 186
Wnt-5b      D---------------------------------------LPRDWLWGGCGDNV 165
Wnt-6       ------------RAPPRPSGLP-GTPGP-PGPAGSPEGSAAWEWGGCGDDV 176
Wnt-7a      R---------------------------------------DEG-WKWGGCSADI 156
Wnt-7b      Q---------------------------------------AEG-WKWGGCSADV 156
Wnt-8a      ----------------------------------------GHGWIWGGCSDNV 136
Wnt-8       ----------------------------------------GQGWLWGGCSDNV 136
Wnt-9a      E---------------------------------------AWQWGGCGDNL 172
Wnt-9b      Q---------------------------------------AWQWGVCGDNL 166
Wnt-10a     AFRRKLHRLQLDALQRGKGLSHGVPEHPALPTASPGLQDSWEWGGCSPDM 218
Wnt-10b     RLRAKL--LQLQALSRGKSFPHSLPSPGPGSSPSPGPQDTWEWGGCNHDM 203
Wnt-11      ----------------------------------------GPGNRWGGCADNL 161
Wnt-16      A---------------------------------------SEG-WHWGGCSDDV 172

Wnt-1       DFGRLFGREFVDSGEKGR--------DLRFLMNLHNNEAGRTTVFSEMRQ 216
```

FIG. 1 (Continued)

```
Wnt-2       DYGIKFARAFVDAKERKG--------KDARALMNLHNNRAGRKAVKRFLKQ 204
Wnt-2b      HYGVRFAKAFVDAKEKRL--------KDARALMNLHNNRCGRTAVRRFLKL 216
Wnt-3       DFGVLVSREFADARENRP---------DARSAMNKHNNEAGRTTILDHMHL 204
Wnt-3a      EFGGMVSREFADARENRP---------DARSAMNRHNNEAGRQAIASHMHL 201
Wnt-4       AYGVAFSQSFVDVRERSKG------ASSSRALMNLHNNEAGRKAILTHMRV 204
Wnt-5a      DYGYRFAKEFVDARERERIHAKGSYESARILMNLHNNEAGRRTVYNLADV 236
Wnt-5b      EYGYRFAKEFVDARERERKNFAKGSEEQGRVLMNLQNNEAGRRAVYKMADV 215
Wnt-6       DFGDEKSRLFMDARHKRG-------RGDIRALVQLHNNEAGRLAVRSHTRT 220
Wnt-7a      RYGIGFAKVFVDAREIKQN---ART------LMNLHNNEAGRKILEENMKL 198
Wnt-7b      RYGIDFSRRFVDAREIKKN---ARR------LMNLHNNEAGRKVLEDRMQL 198
Wnt-8a      EFGERISKLFVDSLEKGKD---------ARALMNLHNNRAGRLAVRATMKR 178
Wnt-8       GFGEAISKQFVDALETGQD---------ARAAMNLHNNEAGRKAVKGTMKR 178
Wnt-9a      KYSSKFVKEFLG-RRSSKD---------LRARVDFHNNLVGVKVIKAGVET 213
Wnt-9b      KYSTKFLSNFLGSKRGNKD---------LRARADAHNTHVGIKAVKSGLRT 208
Wnt-10a     GFGERFSKDFLDSREP---------HRDIHARMRLHNNRVGRQAVMENMRR 260
Wnt-10b     DFGEKFSRDFLDSREA---------PRDIQARMRIHNNRVGRQVVTENLKR 245
Wnt-11      SYGLLMGAKFSDAPMKVKKTG-----SQANKLMRLHNSEVGRQALRASLEM 207
Wnt-16      QYGMWFSRKFLDFPIGNTT---GKENKVLLAMNLHNNEAGRQAVAKLMSV 219

Wnt-1       ECKCHGMSGSCTVRTCWMRLPTLRAVGDVLRDRFDGASRVLYGNRGSNRA 266
Wnt-2       ECKCHGVSGSCTLRTCWLAMADFRKTGDYLWRKYNGAIQVVMNQ---DGT 251
Wnt-2b      ECKCHGVSGSCTLRTCWRALSDFRRTGDYLRRRYDGAVQVMATQ---DGA 263
Wnt-3       KCKCHGLSGSCEVKTCWWAQPDFRAIGDFLKDKYDSASEMVVEK---HRE 251
Wnt-3a      KCKCHGLSGSCEVKTCWWSQPDFRAIGDFLKDKYDSASEMVVEK---HRE 248
Wnt-4       ECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR---VGS 251
Wnt-5a      ACKCHGVSGSCSLKTCWLQLADFRKVGDALKEKYDSAAAMRLNS---RGK 283
Wnt-5b      ACKCHGVSGSCSLKTCWLQLAEFRKVGDRLKEKYDSAAAMRVTR---KGR 262
Wnt-6       ECKCHGLSGSCALRTCWQKLPPFREVGARLLERFHGASRVMGTN---DGK 267
Wnt-7a      ECKCHGVSGSCTTKTCWTTLPQFRELGYVLKDKYNEAVHVEPVR---ASR 245
Wnt-7b      ECKCHGVSGSCTTKTCWTTLPKFREVGHLLKEKYNAAVQVEVVR---ASR 245
Wnt-8a      TCKCHGISGSCSIQTCWLQLAEFREMGDYLKAKYDQALKIEMDKRQ--LR 226
Wnt-8       TCKCHGVSGSCTTQTCWLQLPEFREVGAHLKEKYHAALKVDLLQG----- 223
Wnt-9a      TCKCHGVSGSCTVRTCWRQLAPFHEVGKHLKHKYETALKVGSTTNEAAGE 263
Wnt-9b      TCKCHGVSGSCAVRTCWKQLSPFRETGQVLKLRYDSAVKVSSATNEALGR 258
Wnt-10a     KCKCHGTSGSCQLKTCWQVTPEFRTVGALLRSRFHRATLIRPHNR--NGG 308
Wnt-10b     KCKCHGTSGSCQFKTCWRAAPEFRAVGAALRERLGRAIFIDTHNR--NSG 293
Wnt-11      KCKCHGVSGSCSIRTCWKGLQELQDVAADLKTRYLSATKVVHRP---MGT 254
Wnt-16      DCRCHGVSGSCAVKTCWKTMSSFEKIGHLLKDKYENSIQISDKT---KRK 266

Wnt-1       SRAELLR-----LEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTA 311
Wnt-2       GFTVAN-----------ERFKKPTKNDLVYFENSPDYCIRDREAGSLGTA 290
Wnt-2b      NFTAAR-----------QGYRRATRTDLVYFDNSPDYCVLDKAAGSLGTA 302
Wnt-3       SRGWVET-----LRAKYSLFKPPTERDLVYYENSPNFCEPNPETGSFGTR 296
Wnt-3a      SRGWVET-----LRPRYTYFKVPTERDLVYYEASPNFCEPNPETGSFGTR 293
Wnt-4       SR----A-----LVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTR 292
Wnt-5a      -LVQVN-----------SRFNSPTTQDLVYIDPSPDYCVRNESTGSLGTQ 321
Wnt-5b      -LELVN-----------SRFTQPTPEDLVYVDPSPDYCLRNESTGSLGTQ 300
Wnt-6       ALLPAVR----------TLKPPGRADLLYAADSPDFCAPNRRTGSPGTR 306
Wnt-7a      NKRPTFL-----KIKKPLSYRKPMDTDLVYIEKSPNYCEEDPVTGSVGTQ 290
Wnt-7b      LRQPTFL-----RIKQLRSYQKPMETDLVYIEKSPNYCEEDAATGSVGTQ 290
Wnt-8a      AGNSAEG-----HWVPAEAFLPSAEAELIFLEESPDYCTCNSSLGIYGTE 271
Wnt-8       AGNSAAG-----RGAIADTFRSISTRELVHLEDSPDYCLENKTLGLLGTE 268
```

FIG. 1 (Continued)

```
Wnt-9a      AGAISPPRGR--ASGAGGSDPLPRTPELVHLDDSPSFCLAGR--FSPGTA 309
Wnt-9b      LELWAPAR-----QGSLTKGLAPRSGDLVYMEDSPSFCRPSK--YSPGTA 301
Wnt-10a     QLEPGPAGAPSPAPGAPGPRRRASPADLVYFEKSPDFCEREPRLDSAGTV 358
Wnt-10b     AFQPRLR----------PRRLSG--ELVYFEKSPDFCERDPTMGSPGTR 330
Wnt-11      RKHLVPK---------DLDIRPVKDSELVYLQSSPDFCMKNEKVGSHGTQ 295
Wnt-16      MRR---------REKDQRKIPIHKD-DLLYVNKSPNYCVEDKKLGIPGTQ 306

Wnt-1       GRACNSSSPALDGCELLCCGRGHRTRTQRVTER-------CNCTFHWCCH 354
Wnt-2       GRVCNLTSRGMDSCEVMCCGRGYDTSHVTRMTK-------CGCKFHWCCA 333
Wnt-2b      GRVCSKTSKGTDGCEIMCCGRGYDTTRVTRVTQ-------CECKFHWCCA 345
Wnt-3       DRTCNVTSHGIDGCDLLCCGRGHNTRTEKRKEK-------CHCIFHWCCY 339
Wnt-3a      DRTCNVSSHGIDGCDLLCCGRGHNARAERRREK-------CRCVFHWCCY 336
Wnt-4       GRTCNKTSKAIDGCELLCCGRGFHTAQVELAER-------CSCKFHWCCF 335
Wnt-5a      GRLCNKTSEGMDGCELMCCGRGYDQFKTVQTER-------CHCKFHWCCY 364
Wnt-5b      GRLCNKTSEGMDGCELMCCGRGYNQFKSVQVER-------CHCKFHWCCF 343
Wnt-6       GRACNSSAPDLSGCDLLCCGRGHRQESVQLEEN-------CLCRFHWCCV 349
Wnt-7a      GRACNKTAPQASGCDLMCCGRGYNTHQYARVWQ-------CNCKFHWCCY 333
Wnt-7b      GRLCNRTSPGADGCDTMCCGRGYNTHQYTKVWQ-------CNCKFHWCCF 333
Wnt-8a      GRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCT 321
Wnt-8       GRECLRRGRALGRWERRSCRRLCGDCGLAVEERRAETVSSCNCKFHWCCA 318
Wnt-9a      GRRCHREK----NCESICCGRGHNTQSRVVTRP-------CQCQVRWCCY 348
Wnt-9b      GRVCSREA----SCSSLCCGRGYDTQSRLVAFS-------CHCQVQWCCY 340
Wnt-10a     GRLCNKSSAGSDGCGSMCCGRGHNILRQTRSER-------CHCRFHWCCF 401
Wnt-10b     GRACNKTSRLLDGCGSLCCGRGHNVLRQTRVER-------CHCRFHWCCY 373
Wnt-11      DRQCNKTSNGSDSCDLMCCGRGYNPYTDRVVER-------CHCKYHWCCY 338
Wnt-16      GRECNRTSEGADGCNLLCCGRGYNTHVVRHVER-------CECKFIWCCY 349

Wnt-1       VSCRNCTHTRVLHECL---------------- 370
Wnt-2       VRCQDCLEALDVHTCKAPKNADWTTAT------- 360
Wnt-2b      VRCKECRNTVDVHTCKAPKKAEWLDQT------- 372
Wnt-3       VSCQECIRIYDVHTCK---------------- 355
Wnt-3a      VSCQECTRVYDVHTCK---------------- 352
Wnt-4       VKCRQCQRLVELHTCR---------------- 351
Wnt-5a      VKCKKCTEIVDQFVCK---------------- 380
Wnt-5b      VRCKKCTEIVDQYICK---------------- 359
Wnt-6       VQCHRCRVRKELSLCL---------------- 365
Wnt-7a      VKCNTCSERTEMYTCK---------------- 349
Wnt-7b      VKCNTCSERTEVFTCK---------------- 349
Wnt-8a      VKCDQCRHVVSKYYCARSP----GSAQSLGKGSA 351
Wnt-8       VRCEQCRRRVTKYFCSRAERPRGGAAHKPGRKP- 351
Wnt-9a      VECRQCTQREEVYTCKG---------------- 365
Wnt-9b      VECQQCVQEELVYTCKH---------------- 357
Wnt-10a     VVCEECRITEWVSVCK---------------- 417
Wnt-10b     VLCDECKVTEWVNVCK---------------- 389
Wnt-11      VTCRRCERTVERYVCK---------------- 354
Wnt-16      VRCRRCESMTDVHTCK---------------- 365
```

FIG. 1 (Continued)

Wnt-7A Alignment

```
          10         20         30         40         50         60         70         80
  ---------+---------+---------+---------+---------+---------+---------+---------+
  1 MNRKARRCLGHLFLSLGMVYLRIGGFSSVVALGASIICNKIPGLAPRQRAICQSRPDAIIVIGEGSQMGLDECQFQFRNG Wnt7A_Human
  1 MTRKARRCLGHLFLSLGIVYLRIGGFSSVVALGASIICNKIPGLAPRQRAICQSRPDAIIVIGEGSQMGLDECQFQFRNG Wnt7A_Mouse
  1 MTRKARRCLGHLFLSLGIVYLRIGDFSSVVALGASIICNKIPGLAPRQRAICQSRPDAIIVIGEGSQMGLDECQFQFRNG Wnt7A_Rat
  1 MNRKTRRWIFHIFLSLGIVYIKIGGFSSVVALGASIICNKIPGLAPRQRAICQSRPDAIIVIGEGSQMGINECQFQFRNG Wnt7A_Chicken
  1 MSRKTRRWIFHIFLCLGIIYLKIGGFSSVVALGASIICNKIPGLAPRQRTICQSRPDAIIVIGEGAQMGINECQFQFKNG Wnt7A_Zebrafish
  1 MNRKARRCLGHLFLSLGLVYLRIGGFSSVVALGASIICNKIPGLAPRQRAICQSRPDAIIVIGEGSQMGLDECQFQFRNG Wnt7A_Pig
  1 MNRKARRCLGHLFLSLGMVYLRIGGFSSVVALGASIICNKIPGLAPRQRAICQSRPDAIIVIGEGSQMGLDECQFQFRNG Wnt7A_Cow

          90        100        110        120        130        140        150        160
  ---------+---------+---------+---------+---------+---------+---------+---------+
 81 RWNCSALGERTVFGKELKVGSREAAFTYAIIAAGVAHAITAACTQGNLSDCGCDKEKQGQYHRDEGWKWGGCSADIRYGI Wnt7A_Human
 81 RWNCSALGERTVFGKELKVGSREAAFTYAIIAAGVAHAITAACTQGNLSDCGCDKEKQGQYHRDEGWKWGGCSADIRYGI Wnt7A_Mouse
 81 RWNCSALGERTVFGKELKVGSREAAFTYAIIAAGVAHAITAACTQGNLSDCGCDKEKQGQYHRDEGWKWGGCSADIRYGI Wnt7A_Rat
 81 RWNCSALGERTVFGKELKVGSREAAFTYAIIAAGVAHAITAACTQGNLSDCGCDKEKQGQYHKEEGWKWGGCSADIRYGI Wnt7A_Chicken
 81 RWNCSALGERTVFGKELKVGSKEAAFTYAIIAAGVAHAITAACTQGTLSGCGCDKEKQGFYNQEEGWKWGGCSADIRYGL Wnt7A_Zebrafish
 81 RWNCSALGERTVFGKELKVGSREAAFTYAIIAAGVAHAITAACTQGNLSDCGCDKEKQGQYHRDEGWKWGGCSADIRYGI Wnt7A_Pig
 81 RWNCSALGERTVFGKELKVGSREAAFTYAIIAAGVAHAITAACTQGNLSDCGCDKEKQGQYHRDEGWKWGGCSADIRYGI Wnt7A_Cow

          170        180        190        200        210        220        230        240
  ---------+---------+---------+---------+---------+---------+---------+---------+
161 GFAKVFVDAREIKQNARTLMNLHNNEAGRKILEENMKLECKCHGVSGSCTTKTCWTTLPQFRELGYVLKDKYNEAVHVEP Wnt7A_Human
161 GFAKVFVDAREIKQNARTLMNLHNNEAGRKILEENMKLECKCHGVSGSCTTKTCWTTLPQFRELGYVLKDKYNEAVHVEP Wnt7A_Mouse
161 GFAKVFVDAREIKQNARTLMNLHNNEAGRKILEENMKLECKCHGVSGSCTTKTCWTTLPQFRELGYVLKDKYNEAVHVEP Wnt7A_Rat
161 GFAKVFVDAREIKQNARTLMNLHNNEAGRKILEENMKLECKCHGVSGSCTTKTCWTTLPKFRELGYILKDKYNEAVQVEP Wnt7A_Chicken
161 SFSKVFLDAREIKQNARTLMNLHNNEVGRKILEKNMRLECKCHGVSGSCTTKTCWTTLPKFRQLGYILKERYNHAVHVEP Wnt7A_Zebrafish
161 GFAKVFVDAREIKQNARTLMNLHNNEAGRKILEENMKLECKCHGVSGSCTTKTCWTTLPQFRELGYVLKDKYNEAVHVEP Wnt7A_Pig
161 GFAKVFVDAREIKQNARTLMNLHNNEAGRKILEENMKLECKCHGVSGSCTTKTCWTTLPQFRELGYVLKDKYNEAVHVEP Wnt7A_Cow

          250        260        270        280        290        300        310        320
  ---------+---------+---------+---------+---------+---------+---------+---------+
241 VRASRNKRPTFLKIKKPLSYRKPMDTDLVYIEKSPNYCEEDPVTGSVGTQGRACNKTAPQASGCDLMCCGRGYNTHQYAR Wnt7A_Human
241 VRASRNKRPTFLKIKKPLSYRKPMDTDLVYIEKSPNYCEEDPVTGSVGTQGRACNKTAPQASGCDLMCCGRGYNTHQYAR Wnt7A_Mouse
241 VRASRNKRPTFLKIKKPLSYRKPMDTDLVYIEKSPNYCEEDPVTGSVGTQGRACNKTAPQASGCDLMCCGRGYNTHQYAR Wnt7A_Rat
241 VRASRNKRPTFLKIKKPLSYRKPMDTDLVYIEKSPNYCEEDPVTGSVGTQGRMCNKTAQQSNGCDLMCCGRGYNTHQYSR Wnt7A_Chicken
241 VRASRNKRPAFLKVKKPYSYRKPMDTDLVYIEKSPNYCEADPVTGSMGTQGRICNKTAQHTNGCDLMCCGRGYNTHQYSR Wnt7A_Zebrafish
241 VRASRNKRPTFLKIKKPLSYRKPMDTDLVYIEKSPNYCEEDPVTGSVGTQGRACNKTAPQASGCDLMCCGRGYNTHQYAR Wnt7A_Pig
241 VRASRNKRPAFLKIKKPLSYRKPMDTELVYIEKSPSYCEEDPATGSVGTQGRACNKTAPQASGCDLMCCGRGYNTHQYAR Wnt7A_Cow

          330        340
  ---------+---------+----------
321 VWQCNCKFHWCCYVKCNTCSERTEMYTCK                                                    Wnt7A_Human
321 VWQCNCKFHWCCYVKCNTCSERTEMYTCK                                                    Wnt7A_Mouse
321 VWQCNCKFHWCCYVKCNTCSERTEMYTCK                                                    Wnt7A_Rat
321 VWQCNCKFHWCCYVKCNTCSERTEVYTCK                                                    Wnt7A_Chicken
321 VWQCNCKFLWCCYVKCNTCSERTEVYTCK                                                    Wnt7A_Zebrafish
321 VWQCNCKFHWCCYVKCNTCSERTEVYTCK                                                    Wnt7A_Pig
321 VWQCNCKFHWCCYVKCNTCSERTEVYTCK                                                    Wnt7A_Cow
```

FIG. 2

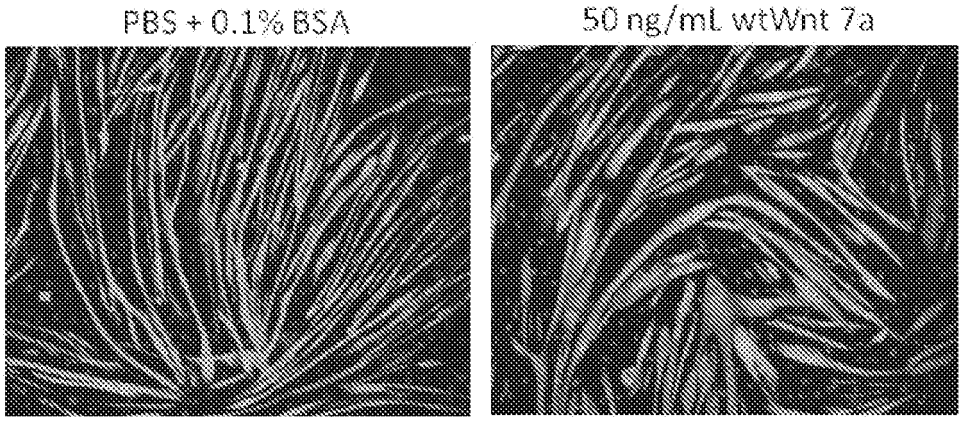

PBS + 0.1% BSA
50 ng/mL wtWnt 7a

FIG. 3A

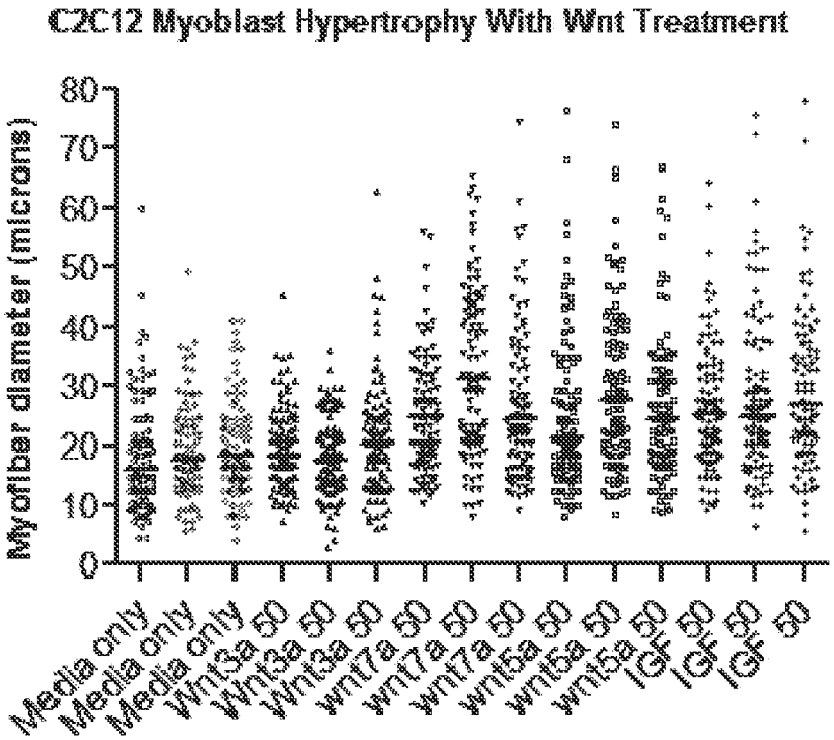

C2C12 Myoblast Hypertrophy With Wnt Treatment
Myofiber diameter (microns)
0
10
20
30
40
50
60
70
80
Media only
Media only
Media only
Wnt3a 50
Wnt3a 50
Wnt3a 50
wnt7a 50
wnt7a 50
wnt7a 50
wnt5a 50
wnt5a 50
wnt5a 50
IGF 50
IGF 50
IGF 50

FIG. 3B

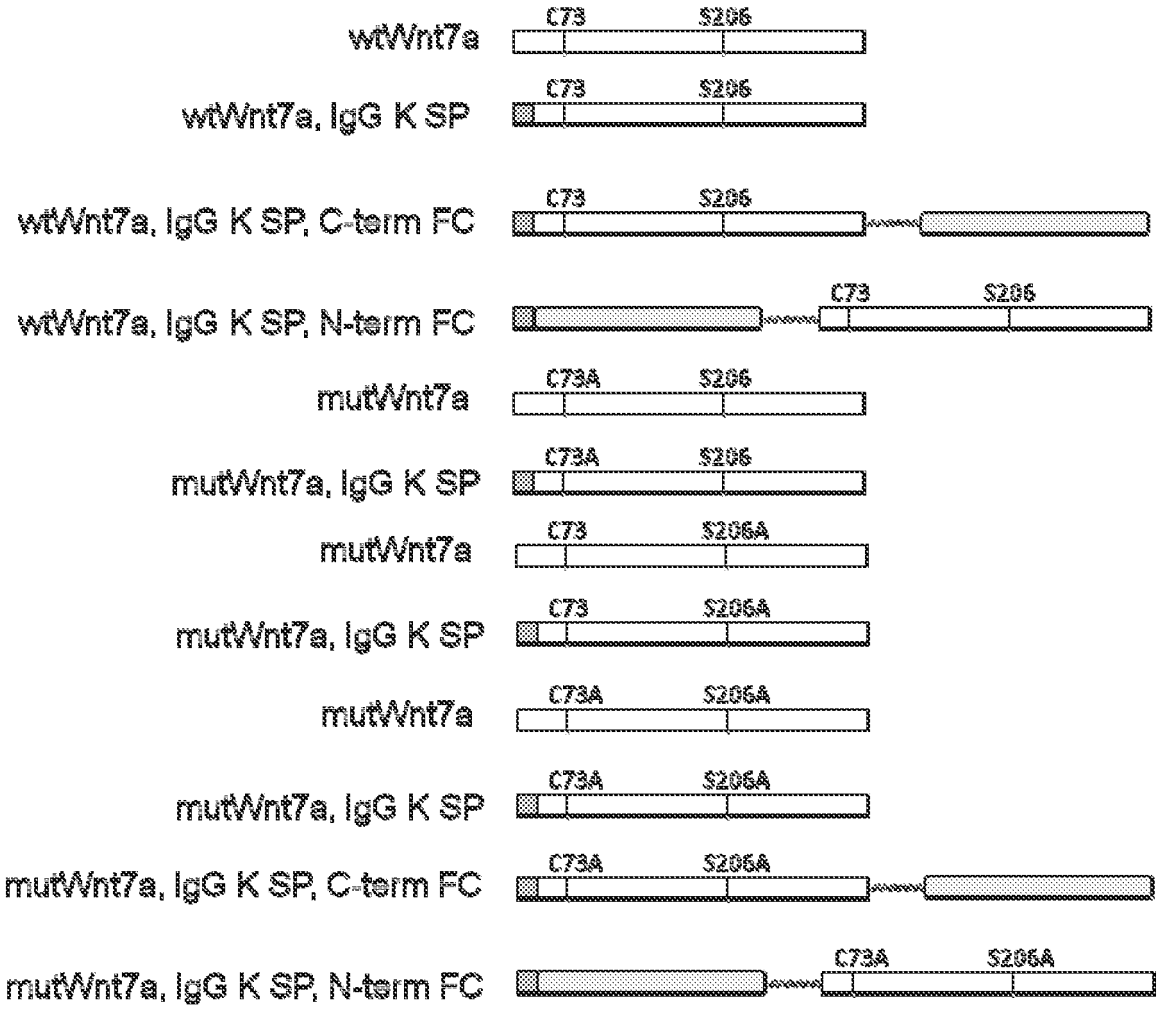

wtWnt7a
C73
S206
wtWnt7a, IgG K SP
C73
S206
wtWnt7a, IgG K SP, C-term FC
C73
S206
wtWnt7a, IgG K SP, N-term FC
C73
S206
mutWnt7a
C73A
S206
mutWnt7a, IgG K SP
C73A
S206
mutWnt7a
C73
S206A
mutWnt7a, IgG K SP
C73
S206A
mutWnt7a
C73A
S206A
mutWnt7a, IgG K SP
C73A
S206A
mutWnt7a, IgG K SP, C-term FC
C73A
S206A
mutWnt7a, IgG K SP, N-term FC
C73A
S206A

FIG. 4

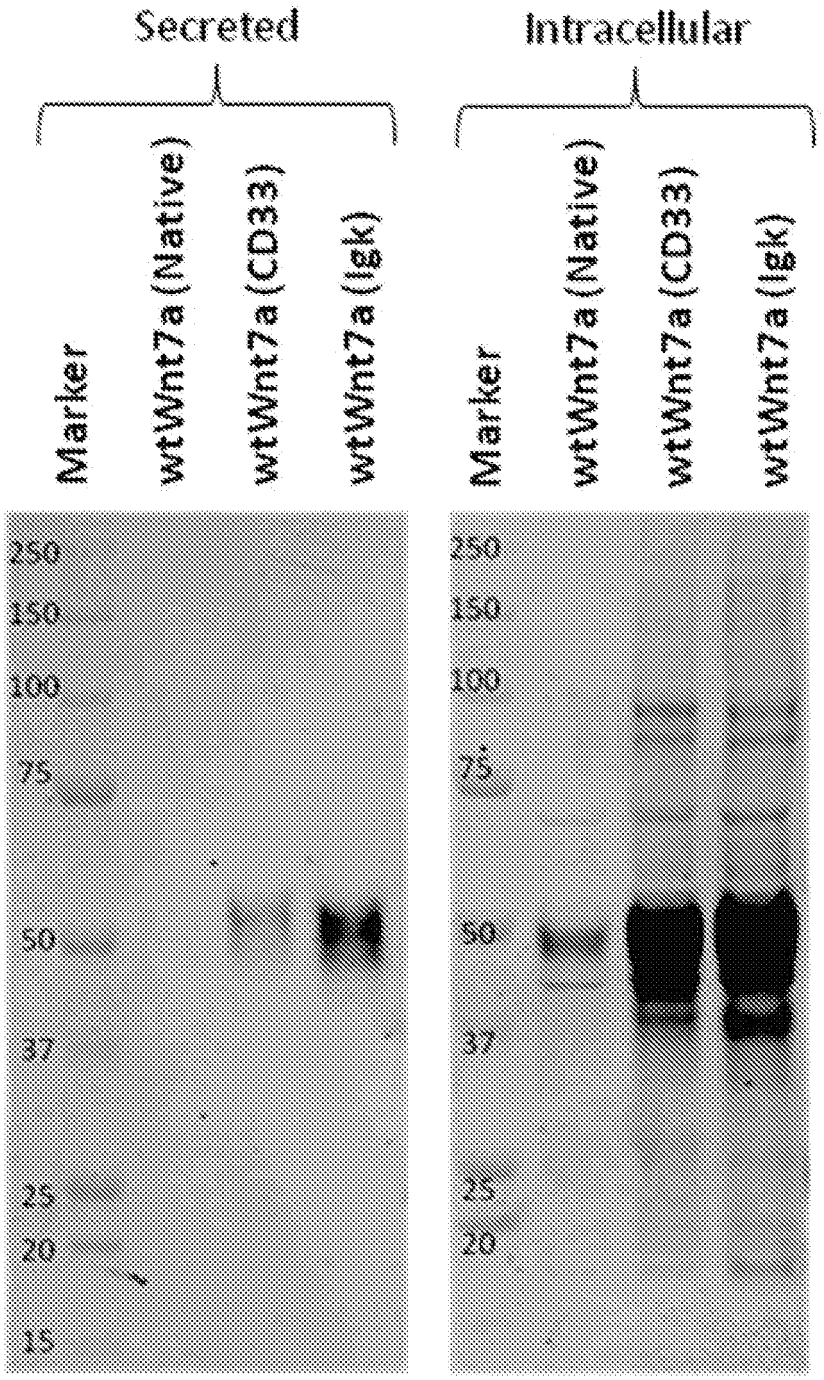

Secreted
Intracellular
Marker
wtWnt7a (Native)
wtWnt7a (CD33)
wtWnt7a (Igk)
Marker
wtWnt7a (Native)
wtWnt7a (CD33)
wtWnt7a (Igk)
250
150
100
75
50
37
25
20
15
250
150
100
75
50
37
25
20

FIG. 5

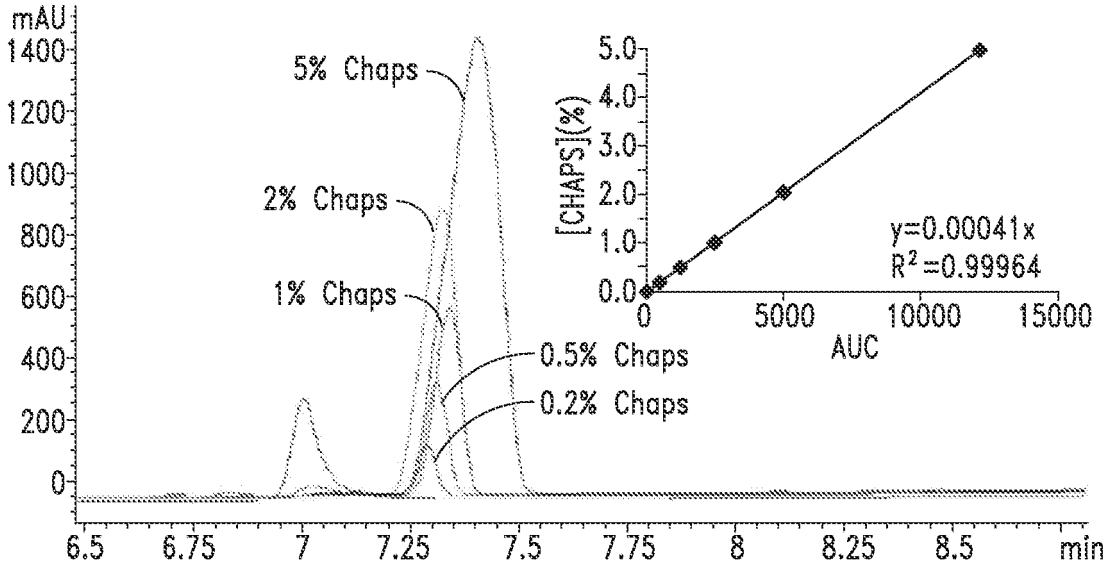

mAU
1400
1200
1000
800
600
400
200
0
5% Chaps
2% Chaps
1% Chaps
0.5% Chaps
0.2% Chaps
[CHAPS](%)
5.0
4.0
3.0
2.0
1.0
0.0
0
5000
10000
15000
AUC
y=0.00041x
R²=0.99964
6.5
6.75
7
7.25
7.5
7.75
8
8.25
8.5
min

FIG. 6A

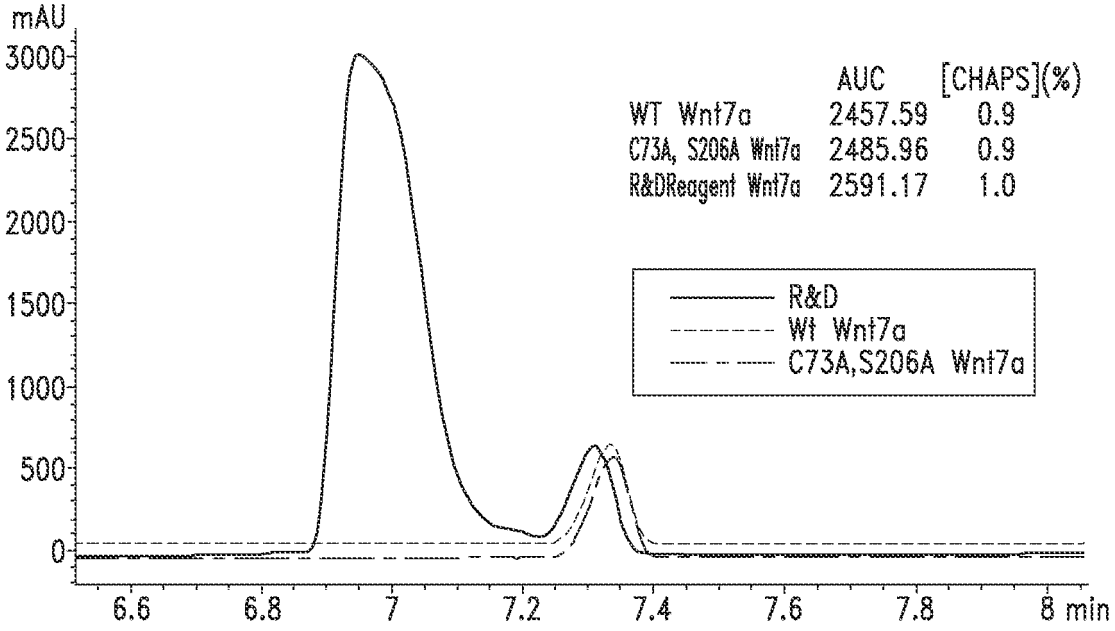
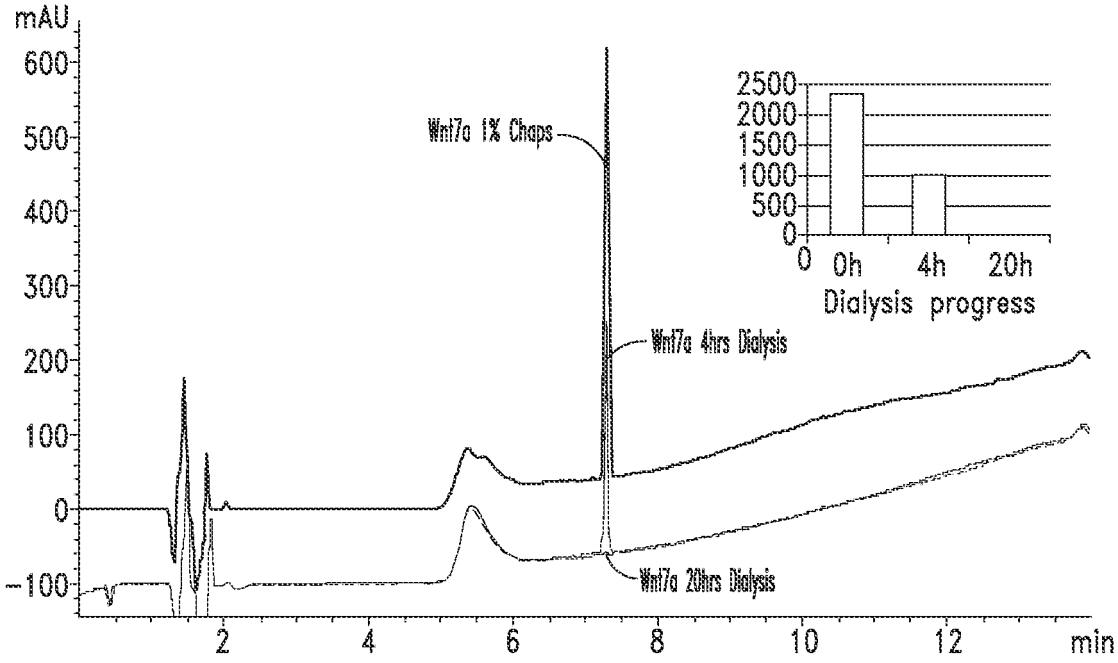

mAU
3000
2500
2000
1500
1000
500
0
AUC [CHAPS](%)
WT Wnt7a 2457.59 0.9
C73A, S206A Wnt7a 2485.96 0.9
R&DReagent Wnt7a 2591.17 1.0
R&D
Wt Wnt7a
C73A,S206A Wnt7a
6.6
6.8
7
7.2
7.4
7.6
7.8
8 min

FIG. 6B


mAU
600
500
400
300
200
100
0
−100
2
4
6
8
10
12
min
Wnt7a 1% Chaps
Wnt7a 4hrs Dialysis
Wnt7a 20hrs Dialysis
2500
2000
1500
1000
500
0
0
0h
4h
20h
Dialysis progress

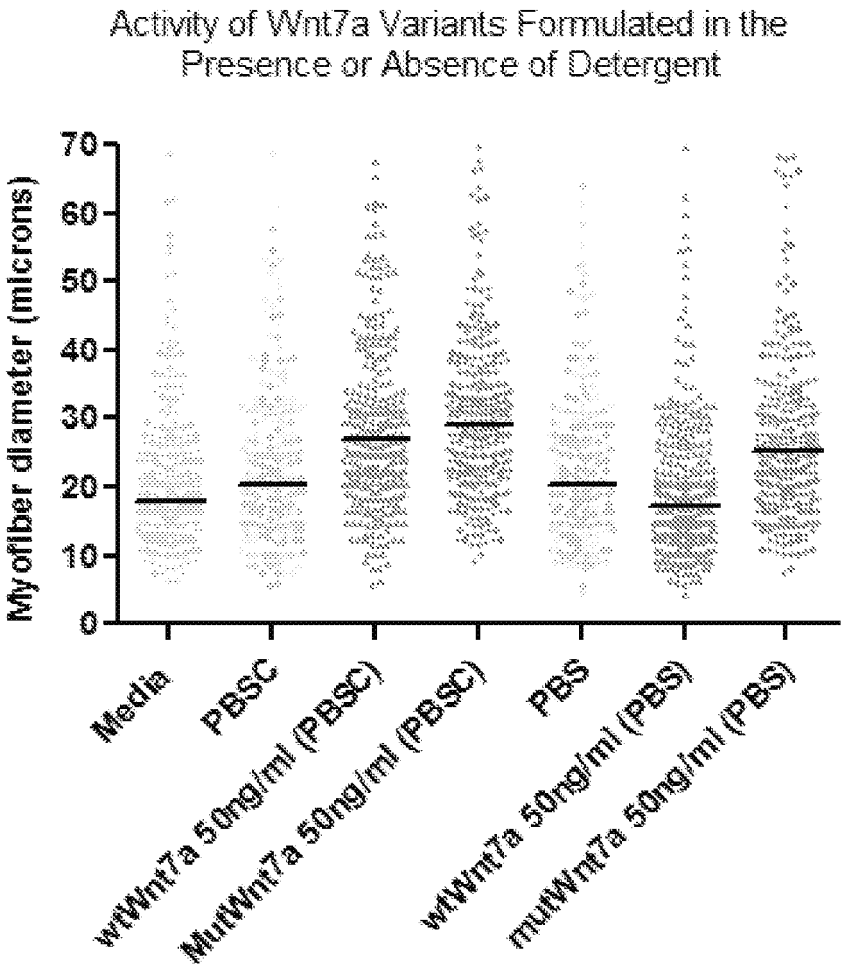

Activity of Wnt7a Variants Formulated in the Presence or Absence of Detergent
Myofiber diameter (microns)
0
10
20
30
40
50
60
70
Media
PBSC
wtWnt7a 50ng/ml (PBSC)
MutWnt7a 50ng/ml (PBSC)
PBS
wtWnt7a 50ng/ml (PBS)
mutWnt7a 50ng/ml (PBS)

FIG. 7

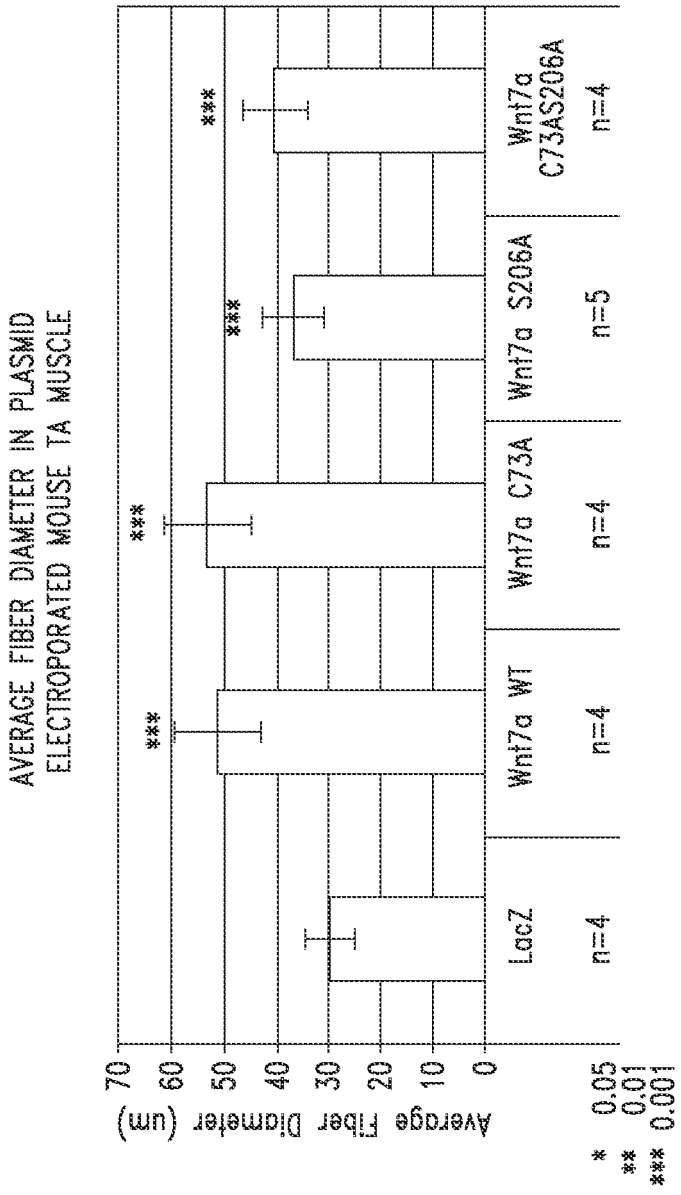

AVERAGE FIBER DIAMETER IN PLASMID
ELECTROPORATED MOUSE TA MUSCLE
Average Fiber Diameter (um)
70
60
50
40
30
20
10
0
***
***
***
LacZ
n=4
Wnt7a WT
n=4
Wnt7a C73A
n=4
Wnt7a S206A
n=5
Wnt7a C73AS206A
n=4
Electroporated Gene
* 0.05
** 0.01
*** 0.001

FIG. 8

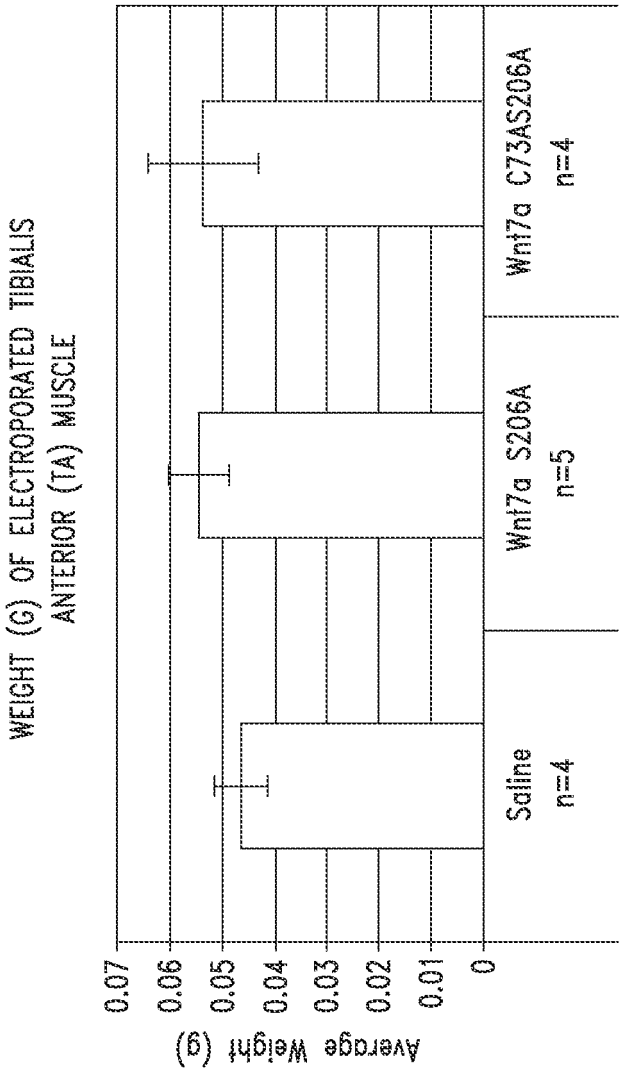

WEIGHT (G) OF ELECTROPORATED TIBIALIS ANTERIOR (TA) MUSCLE
Average Weight (g)
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0
Saline n=4
Wnt7a S206A n=5
Wnt7a C73AS206A n=4
Electroporated Gene

FIG. 9

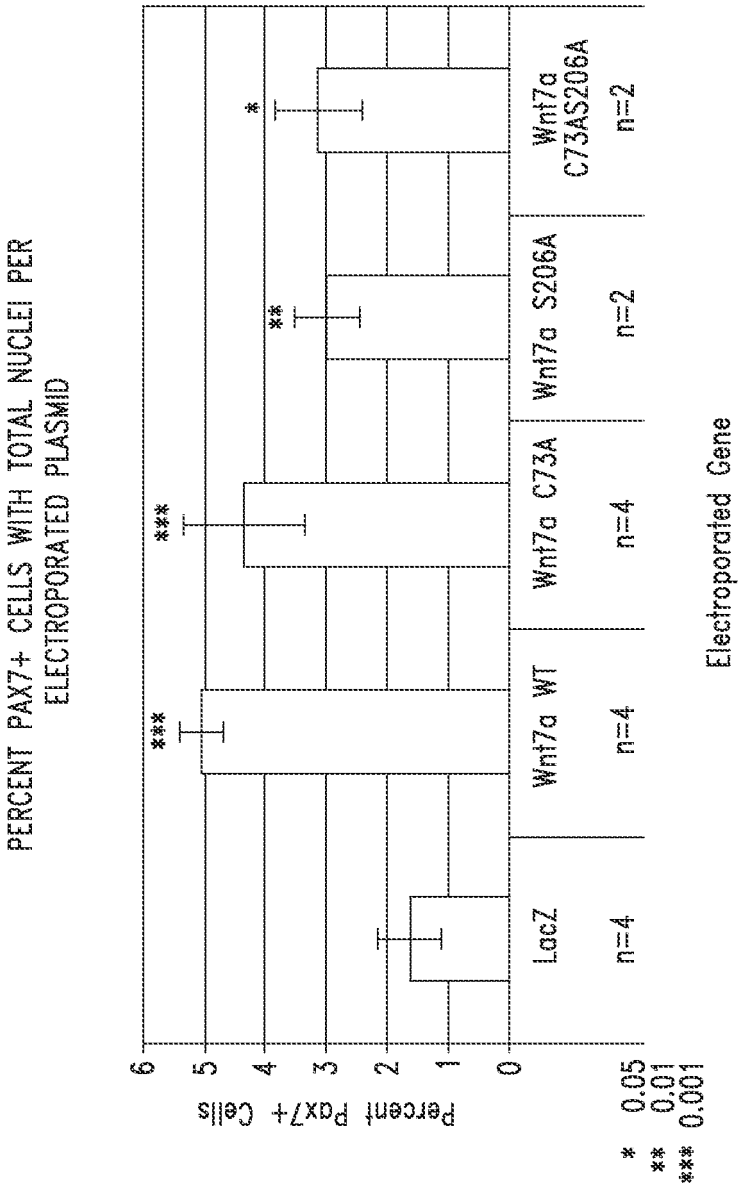

PERCENT PAX7+ CELLS WITH TOTAL NUCLEI PER ELECTROPORATED PLASMID
Percent Pax7+ Cells
0
1
2
3
4
5
6
***
***
**
*
LacZ
n=4
Wnt7a WT
n=4
Wnt7a C73A
n=4
Wnt7a S206A
n=2
Wnt7a C73AS206A
n=2
Electroporated Gene
* 0.05
** 0.01
*** 0.001

FIG. 10

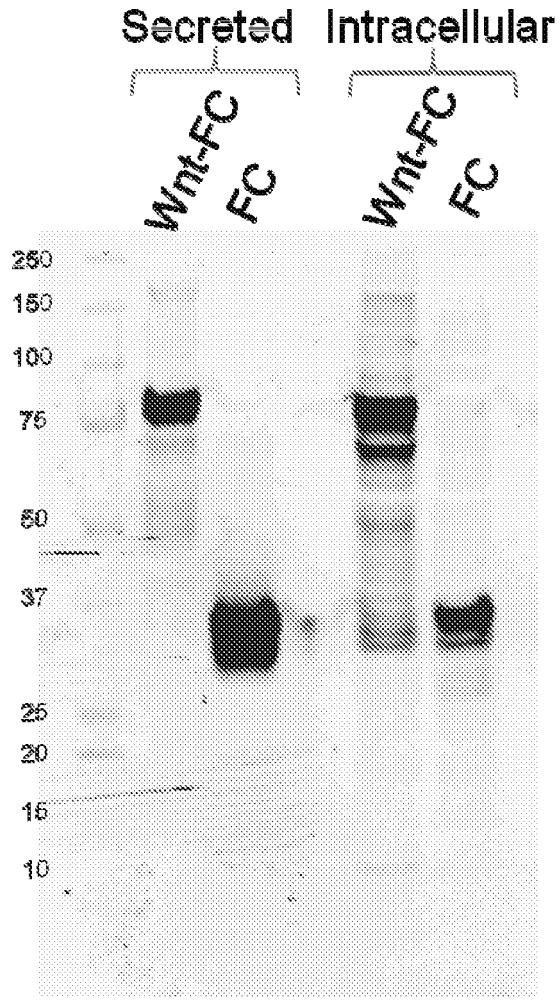

Secreted
Intracellular
Wnt-FC
FC
Wnt-FC
FC
250
150
100
75
50
37
25
20
15
10

FIG. 11A

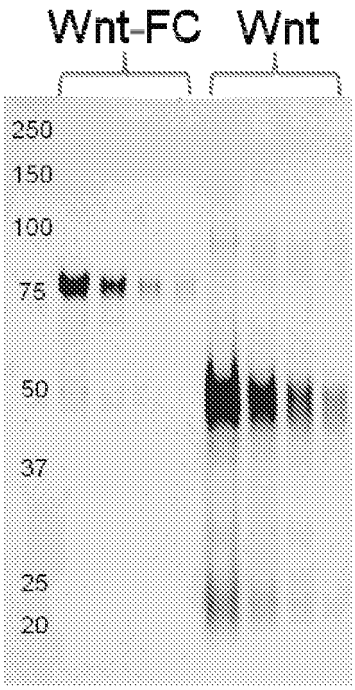


FIG. 11B