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(54) **Titre : MARQUEURS GENETIQUES POUR PREVOIR LA REPONSE A L'ACETATE DE GLATIRAMERE**
(54) **Title: GENETIC MARKERS PREDICTIVE OF RESPONSE TO GLATIRAMER ACETATE**

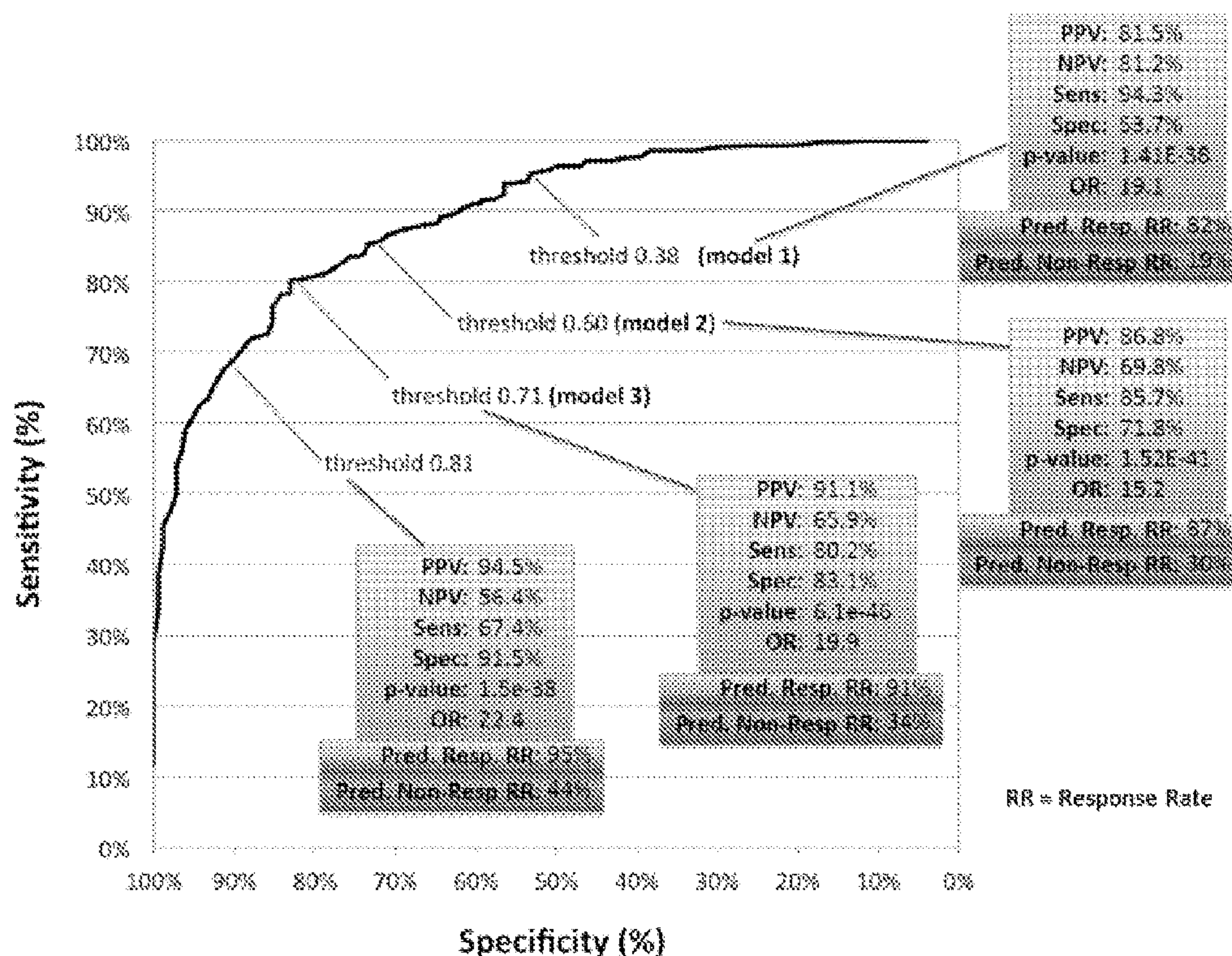


Figure 1

(57) **Abrégé/Abstract:**

The present invention provides a method for treating a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis with a pharmaceutical composition comprising glatiramer acetate and a pharmaceutically acceptable carrier, comprising the steps of: (i) determining a genotype corresponding to the nucleotide polymorphisms consisting of: Group 1, of the subject at a location location of one or more single (SNPs) selected from the group.



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(54) Title: GENETIC MARKERS PREDICTIVE OF RESPONSE TO GLATIRAMER ACETATE

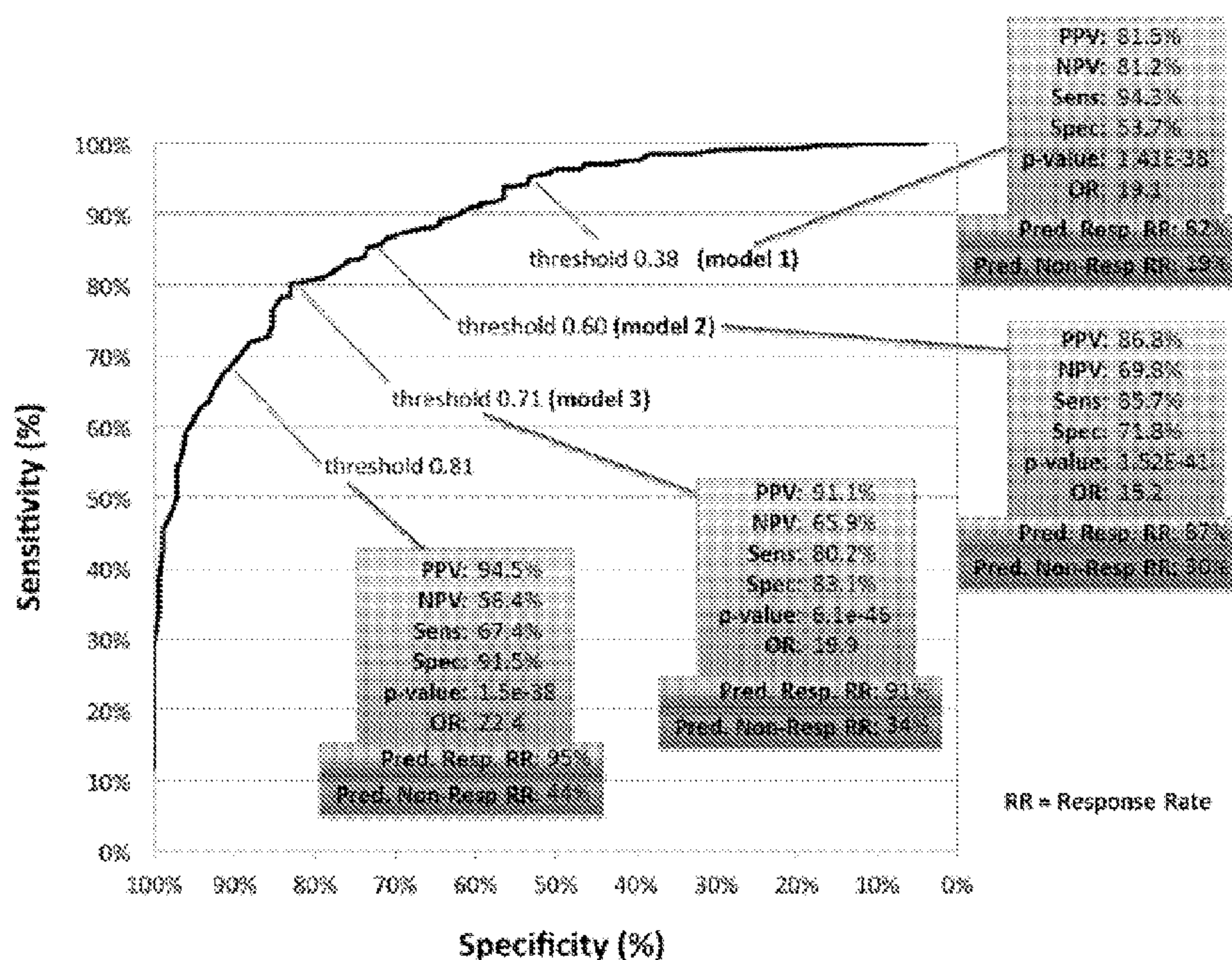


Figure 1

(57) Abstract: The present invention provides a method for treating a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis with a pharmaceutical composition comprising glatiramer acetate and a pharmaceutically acceptable carrier, comprising the steps of: (i) determining a genotype corresponding to the nucleotide polymorphisms consisting of: Group 1, of the subject at a location of one or more single (SNPs) selected from the group.

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GENETIC MARKERS PREDICTIVE OF RESPONSE TO GLATIRAMER ACETATE

This application claims the priority of U.S. Provisional Application No. 61/893,807, filed October 21, 2013, U.S. Provisional Application No. 62/048,127, filed September 9, 2014, and U.S. Provisional Application No. 62/048,641, filed September 10, 2014, the contents of which are hereby incorporated by reference.

Throughout this application various publications are referenced. The disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

BACKGROUND OF THE INVENTION*15 Multiple Sclerosis*

Multiple sclerosis (MS) is a chronic, debilitating autoimmune disease of the central nervous system (CNS) with either relapsing-remitting (RR) or progressive course leading to neurologic deterioration and disability. At time of initial diagnosis, RRMS is the most common form of the disease (1) which is characterized by unpredictable acute episodes of neurological dysfunction (relapses), followed by variable recovery and periods of clinical stability. The vast majority of RRMS patients eventually develop secondary progressive (SP) disease with or without superimposed relapses. Around 15% of patients develop a sustained deterioration of their neurological function from the beginning; this form is called primary progressive (PP) MS. Patients who have experienced a single clinical event (Clinically Isolated Syndrome or "CIS") and who show lesion dissemination on subsequent magnetic resonance imaging (MRI) scans according to McDonald's criteria, are also considered as having relapsing MS.(2)

With a prevalence that varies considerably around the world, MS is the most common cause of chronic neurological disability in young

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adults.(3,4) Anderson et al. estimated that there were about 350,000 physician-diagnosed patients with MS in the United States in 1990 (approx. 140 per 100,000 population).(5) It is estimated that about 2.5 million individuals are affected worldwide.(6) In general, there
5 has been a trend toward an increasing prevalence and incidence of MS worldwide, but the reasons for this trend are not fully understood.(5)

Current therapeutic approaches consist of i) symptomatic treatment
10 ii) treatment of acute relapses with corticosteroids and iii) treatment aimed to modify the course of the disease. Currently approved therapies target the inflammatory processes of the disease. Most of them are considered to act as immunomodulators but their mechanisms of action have not been completely elucidated.
15 Immunosuppressants or cytotoxic agents are also used in some patients after failure of conventional therapies. Several medications have been approved and clinically ascertained as efficacious for the treatment of RR-MS; including BETASERON®, AVONEX® and REBIF®, which are derivatives of the cytokine interferon
20 beta (IFNB), whose mechanism of action in MS is generally attributed to its immunomodulatory effects, antagonizing pro-inflammatory reactions and inducing suppressor cells.(7) Other approved drugs for the treatment of MS include Mitoxantrone and Natalizumab.

25 *Glatiramer Acetate*

Glatiramer acetate (GA) is the active substance in Copaxone®, a marketed product indicated for reduction of the frequency of relapses in patients with RRMS. Its effectiveness in reducing relapse rate and disability accumulation in RR-MS is comparable to
30 that of other available immunomodulating treatments.(8,9,10) Glatiramer acetate consists of the acetate salts of synthetic polypeptides containing four naturally occurring amino acids: L-glutamic acid, L-alanine, L-tyrosine and L-lysine. The average molecular weight of glatiramer acetate is between 5,000 and 9,000
35 Daltons. At a daily standard dose of 20 mg, GA is generally well

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tolerated, however response to the drug is variable. In various clinical trials, GA reduced relapse rates and progression of disability in patients with RR-MS. The therapeutic effect of GA is supported by the results of magnetic resonance imaging (MRI) findings from various clinical centers (11), however there are no validated predictive biomarkers of response to GA treatment.

A possible initial mode of action of GA is associated with binding to MHC molecules and consequent competition with various myelin antigens for their presentation to T cells.(12) A further aspect of its mode of action is the potent induction of T helper 2 (Th2) type cells that presumably can migrate to the brain and lead to in situ bystander suppression.(13) It has been shown that GA treatment in MS results in the induction of GA-specific T cells with predominant Th2 phenotype both in response to GA and cross-reactive myelin antigens.(13,14) Furthermore, the ability of GA-specific infiltrating cells to express anti-inflammatory cytokines such as IL-10 and transforming growth factor-beta (TGF- β) together with brain-derived neurotrophic factor (BDNF) seem to correlate with the therapeutic activity of GA in EAE.(15,16,17)

Clinical experience with GA consists of information obtained from completed and ongoing clinical trials and from post-marketing experience. The clinical program includes three double-blind, placebo-controlled studies in RRMS subjects treated with GA 20 mg/day.(18,19,20) A significant reduction in the number of relapses, compared with placebo, was seen. In the largest controlled study, the relapse rate was reduced by 32% from 1.98 under placebo to 1.34 under GA 20 mg. GA 20 mg has also demonstrated beneficial effects over placebo on MRI parameters relevant to RRMS. A significant effect in median cumulative number of Gd-enhancing lesions over 9 months of treatment (11 lesions in the 20 mg group compared to 17 lesions under placebo) was demonstrated.

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The clinical program with GA also includes one double-blind study in chronic-progressive MS subjects, (21) one double-blind placebo-controlled study in primary progressive patients, (22) one double-blind placebo-controlled study in CIS patients (23) and numerous
5 open-label and compassionate use studies, mostly in RRMS. The clinical use of GA has been extensively reviewed and published in the current literature (24,25,26,27).

U.S. Patent No. 7,855,176 discloses administering glatiramer acetate
10 to patients afflicted with relapsing-remitting multiple sclerosis (RRMS) by subcutaneous injection of 0.5 ml of an aqueous pharmaceutical solution which contains in solution 20 mg glatiramer acetate and 20 mg mannitol (34).

15 U.S. Patent Application Publication No. US 2011-0046065 A1 discloses administering glatiramer acetate to patients suffering from relapsing-remitting multiple sclerosis by three subcutaneous injections of a therapeutically effective dose of glatiramer acetate over a period of seven days with at least one day between every
20 subcutaneous injection (35).

Pharmacogenomics

Pharmacogenomics is the methodology which associates genetic variability with physiological responses to drug. Pharmacogenetics
25 is a subset of pharmacogenomics and is defined as "the study of variations in DNA sequence as related to drug response" (ICH E15; fda.gov/downloads/RegulatoryInformation/Guidances/ucm129296.pdf).

Pharmacogenetics focuses on genetic polymorphism in genes related to drug metabolism, drug mechanism of action, disease type, and side
30 effects. Pharmacogenetics is the cornerstone of Personalized Medicine which allows the development of more individualized drug therapies to obtain more effective and safe treatment.

Pharmacogenetics has become a core component of many drug

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development programs, being used to explain variability in drug response among subjects in clinical trials, to address unexpected emerging clinical issues, such as adverse events, to determine eligibility for a clinical trial (pre-screening) to optimize trial yield, to develop drug-linked diagnostic tests to identify patients who are more likely or less likely to benefit from treatment or who may be at risk of adverse events, to provide information in drug labels to guide physician treatment decisions, to better understand the mechanism of action or metabolism of new and existing drugs, and to provide better understanding of disease mechanisms.

Generally, Pharmacogenetics analyses are performed in either of two methodology approaches: Candidate genes research technique, and Genome Wide Association Study (GWAS). Candidate genes research technique is based on the detection of polymorphism in candidate genes pre-selected using the knowledge on the disease, the drug mode of action, toxicology or metabolism of drug. The Genome Wide Association Study (GWAS) enables the detection of more than 1 M (one million) polymorphisms across the genome. This approach is used when related genes are unknown. DNA arrays used for GWAS can be also analyzed per gene as in candidate gene approach.

Pharmacogenetic studies

Various pharmacogenetic studies were done in MS patients. For example, a Genome-Wide Association study by Byun et al. (36) focused on extreme clinical phenotypes in order to maximize the ability to detect genetic differences between responders and non-responders to interferon-beta. A multi-analytical approach detected significant associations between several SNPs and treatment response. Responders and Non-Responders had significantly different genotype frequencies for SNPs located in many genes, including *glypican 5*, *collagen type XXV $\alpha 1$* , *hyaluronan proteoglycan link protein*, *calpastatin*, and *neuronal PAS domain protein 3*. Other studies used pharmacogenetic analyses in order to characterize the genomic profile and gene expression profile of IFN responders and non-responders.

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Other pharmacogenetic studies analyzed the genetic background associated with response to Glatiramer Acetate. For examples, Fusco C et al (37) assessed a possible relationship between HLA alleles and response to GA (N=83 RRMS). DRB1*1501 allele frequency was increased in MS patients compared to healthy controls (10.8% vs 2.7%; $p = 0.001$). In DRB1*1501 carriers the response rate was 81.8% compared to 39.4% in non-carriers of DRB1*1501 and to 50 % in the whole study population. Grossman et al (38) genotyped HLA-DRB1*1501 and 61 SNPs within a total of 27 other candidate genes, on DNA from two clinical trial cohorts. The study revealed no association between HLA-DRB1*1501 and response to GA. The results of the study are disclosed in the international application published as WO2006/116602 (39).

Pharmacogenetics is the cornerstone of personalized medicine which allows the development of more individualized drug therapies to obtain more effective and safe treatment. Multiple Sclerosis is a complex disease with clinical heterogeneity. In patients afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis, the ability to determine the likelihood of treatment success would be an important tool improving the therapeutic management of the patients. As the therapeutic options for MS and CIS increase, the importance of being able to determine who will respond favorably to therapy and specifically to GA, has become of increasing significance.

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SUMMARY OF THE INVENTION**INDEPENDENT EMBODIMENTS**

The present invention provides a method for treating a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis with a pharmaceutical composition comprising glatiramer acetate and a pharmaceutically acceptable carrier, comprising the steps of:

- (i) determining a genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of: kgp10090631, kgp1009249, kgp10152733, kgp10224254, kgp10305127, kgp10351364, kgp10372946, kgp10404633, kgp10412303, kgp10523170, kgp1054273, kgp10558725, kgp10564659, kgp10591989, kgp10594414, kgp10619195, kgp10620244, kgp10632945, kgp10633631, kgp10679353, kgp10788130, kgp10826273, kgp10910719, kgp10922969, kgp10948564, kgp10967046, kgp10974833, kgp1098237, kgp11002881, kgp11010680, kgp11077373, kgp11141512, kgp11206453, kgp11210903, kgp1124492, kgp11281589, kgp11285862, kgp11328629, kgp11356379, kgp11407560, kgp11453406, kgp11467007, kgp11514107, kgp11543962, kgp11580695, kgp11627530, kgp11633966, kgp11686146, kgp11702474, kgp11711524, kgp11768533, kgp11804835, kgp11843177, kgp12008955, kgp12083934, kgp12182745, kgp12230354, kgp1224440, kgp12371757, kgp124162, kgp12426624, kgp12557319, kgp1285441, kgp13161760, kgp1355977, kgp1371881, kgp15390522, kgp1683448, kgp1688752, kgp1699628, kgp1753445, kgp1779254, kgp1786079, kgp18379774, kgp18432055, kgp18525257, kgp1912531, kgp19568724, kgp20163979, kgp2023214, kgp2045074, kgp20478926, kgp2092817, kgp21171930, kgp2245775, kgp2262166, kgp22778566, kgp22793211, kgp22811918, kgp22823022, kgp2282938, kgp2299675, kgp23298674, kgp2356388, kgp23672937, kgp23737989, kgp2388352, kgp2391411, kgp24131116, kgp24415534, kgp2446153, kgp2451249, kgp2465184, kgp24729706,

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 15 rs9913349, rs9931167 and rs9931211 (hereinafter Group 1),
 (ii) identifying the subject as a predicted responder to
 glatiramer acetate if the genotype of the subject contains
 one or more A alleles at the location of kgp10152733,
 kgp10224254, kgp10305127, kgp10351364, kgp10372946,
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 kgp1699628, kgp1753445, kgp1779254, kgp1786079, kgp18379774,
 kgp18525257, kgp20163979, kgp2023214, kgp20478926,
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 30 kgp26026546, kgp26533576, kgp27500525, kgp27571222,
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 kgp3276689, kgp337461, kgp345301, kgp355027, kgp355723,
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 35 kgp4418535, kgp4543470, kgp4573213, kgp4634875, kgp4755147,
 kgp4842590, kgp485316, kgp5068397, kgp5334779, kgp5483926,

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kgp5564995, kgp5869992, kgp5908616, kgp6032617, kgp6038357,
 kgp6076976, kgp6091119, kgp6127371, kgp61811, kgp6214351,
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 5 kgp7117398, kgp7178233, kgp7186699, kgp7506434, kgp759150,
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 kgp8036704, kgp8046214, kgp8106690, kgp8110667, kgp8178358,
 kgp8200264, kgp8372910, kgp841428, kgp8602316, kgp8615910,
 kgp8793915, kgp8796185, kgp8990121, kgp9018750, kgp9354462,
 10 kgp9368119, kgp9410843, kgp9450430, kgp9530088, kgp9627338,
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 20 rs2071472, rs2139612, rs2241883, rs2309760, rs241440,
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 25 rs423239, rs4254166, rs4356336, rs4584668, rs4780822,
 rs4782279, rs5024722, rs6032209, rs6110157, rs623011,
 rs6497396, rs6845927, rs6895094, rs6899068, rs7024953,
 rs7028906, rs7029123, rs7062312, rs7187976, rs7191155,
 rs720176, rs7228827, rs7496451, rs7563131, rs759458,
 30 rs7666442, rs7670525, rs7677801, rs7725112, rs7850,
 rs7862565, rs7948420, rs8035826, rs8053136, rs8055485,
 rs823829, rs9315047, rs9501224, rs9508832, rs950928,
 rs9597498, rs9670531, rs9671124, rs9817308, rs9834010,
 rs9876830 or rs9931211 (hereinafter Group 2),
 35 one or more C alleles at the location of kgp10910719,
 kgp11077373, kgp11453406, kgp12426624, kgp2045074,

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kgp22811918, kgp23298674, kgp2709692, kgp28687699,
 kgp3496814, kgp3669685, kgp3730395, kgp4056892, kgp4370912,
 kgp5053636, kgp5216209, kgp5292386, kgp6023196, kgp652534,
 kgp7059449, kgp7189498, kgp7521990, kgp7792268, kgp8303520,
 5 kgp9320791, kgp9795732, rs10201643, rs11022778, rs11136970,
 rs11147439, rs11691553, rs1579771, rs16901784, rs2136408,
 rs2325911, rs241443, rs2857104, rs3803277, rs3885907,
 rs4738738, rs4894701, rs502530, rs6032205, rs6687976,
 rs6718758, rs6835202, rs714342, rs7524868, rs7844274,
 10 rs9393727 or rs9671182 (hereinafter Group 3),
 one or more G alleles at the location of kgp10090631,
 kgp1009249, kgp10412303, kgp10523170, kgp1054273,
 kgp10558725, kgp10632945, kgp10679353, kgp10788130,
 kgp10826273, kgp10922969, kgp10948564, kgp10967046,
 15 kgp1098237, kgp11010680, kgp11141512, kgp11206453,
 kgp11210903, kgp1124492, kgp11281589, kgp11356379,
 kgp11467007, kgp11543962, kgp11580695, kgp11633966,
 kgp11686146, kgp11843177, kgp12008955, kgp12371757,
 kgp1285441, kgp13161760, kgp1355977, kgp15390522, kgp1683448,
 20 kgp1688752, kgp1912531, kgp19568724, kgp2092817, kgp2245775,
 kgp22793211, kgp22823022, kgp2282938, kgp2299675, kgp2356388,
 kgp23672937, kgp23737989, kgp2388352, kgp2391411,
 kgp24131116, kgp24415534, kgp2446153, kgp2451249,
 kgp24729706, kgp25543811, kgp25921291, kgp26271158,
 25 kgp2638591, kgp26528455, kgp2688306, kgp26995430, kgp270001,
 kgp2715873, kgp27640141, kgp2788291, kgp2923815, kgp29367521,
 kgp293787, kgp2959751, kgp297178, kgp3048169, kgp3182607,
 kgp3202939, kgp3267884, kgp3418770, kgp3450875, kgp3477351,
 kgp3598409, kgp3651767, kgp3854180, kgp3933330, kgp3984567,
 30 kgp4011779, kgp4096263, kgp4127859, kgp4155998, kgp4346717,
 kgp4420791, kgp4479467, kgp4524468, kgp4559907, kgp4705854,
 kgp4734301, kgp4812831, kgp487328, kgp4898179, kgp5002011,
 kgp5014707, kgp5017029, kgp512180, kgp5144181, kgp5159037,
 kgp5388938, kgp5409955, kgp5440506, kgp5441587, kgp55646,
 35 kgp5579170, kgp5680955, kgp6190988, kgp6539666, kgp6567154,
 kgp6599438, kgp6603796, kgp6737096, kgp6768546, kgp6835138,

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kgp6996560, kgp7063887, kgp7092772, kgp7121374, kgp7181058,
 kgp7331172, kgp7416024, kgp7481870, kgp767200, kgp7714238,
 kgp7747883, kgp8107491, kgp8169636, kgp8174785, kgp8183049,
 kgp8192546, kgp8335515, kgp8437961, kgp8440036, kgp85534,
 5 kgp8599417, kgp8767692, kgp8777935, kgp8817856, kgp8869954,
 kgp9071686, kgp9078300, kgp9354820, kgp9421884, kgp9551947,
 kgp9601362, kgp9627406, kgp9699754, kgp971582, kgp9854133,
 rs1079303, rs10841322, rs10954782, rs11002051, rs11029907,
 rs11083404, rs11085044, rs11192461, rs1157449, rs12494712,
 10 rs12943140, rs13002663, rs13419758, rs1380706, rs1387768,
 rs1410779, rs1508102, rs1532365, rs16886004, rs16895510,
 rs16927077, rs16930057, rs17224858, rs17238927, rs17329014,
 rs17638791, rs1886214, rs1894408, rs196295, rs196341,
 rs196343, rs1979992, rs1979993, rs2043136, rs2071470,
 15 rs2074037, rs2175121, rs241435, rs241447, rs241451, rs241452,
 rs241454, rs2598360, rs2621321, rs2621323, rs2816838,
 rs2839117, rs2857101, rs2934491, rs3135388, rs3218328,
 rs3799383, rs3815822, rs3818675, rs419132, rs4360791,
 rs4449139, rs4669694, rs4709792, rs4769060, rs4822644,
 20 rs484482, rs543122, rs6535882, rs6840089, rs7020402,
 rs7217872, rs7348267, rs7579987, rs7672014, rs7860748,
 rs7864679, rs7928078, rs8050872, rs858341, rs931570,
 rs9346979, rs9376361, rs9579566, rs9913349 or rs9931167
 (hereinafter Group 4), or

25 one or more T alleles at the location of kgp18432055,
 kgp279772, kgp3991733 or kgp7242489; and

(iii) administering the pharmaceutical composition comprising
 glatiramer acetate and a pharmaceutically acceptable carrier
 to the subject only if the subject is identified as a
 30 predicted responder to glatiramer acetate.

The present invention also provides a method of identifying a human
 subject afflicted with multiple sclerosis or a single clinical
 attack consistent with multiple sclerosis as a predicted responder
 or as a predicted non-responder to glatiramer acetate, the method
 35 comprising determining the genotype of the subject at a location
 corresponding to the location of one or more single nucleotide

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polymorphisms (SNPs) selected from the group consisting of Group 1, and identifying the human subject as a predicted responder to glatiramer acetate if the genotype of the subject contains

one or more A alleles at the location of Group 2,

5 one or more C alleles at the location of Group 3,

one or more G alleles at the location of Group 4, or

one or more T alleles at the location of kgp18432055, kgp279772, kgp3991733 or kgp7242489,

10 or identifying the human subject as a predicted non-responder to glatiramer acetate if the genotype of the subject contains no A alleles at the location of Group 2,

no C alleles at the location of Group 3,

no G alleles at the location of Group 4, or

15 no T alleles at the location of kgp18432055, kgp279772, kgp3991733 or kgp7242489.

The present invention also provides a kit for identifying a human subject afflicted with multiple sclerosis or a single clinical
20 attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the kit comprising at least one probe specific for the location of a SNP selected from the group consisting of Group 1.

25 The present invention also provides a kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the kit comprising at least one pair of PCR primers designed to amplify a
30 DNA segment which includes the location of a SNP selected from the group consisting of Group 1.

The present invention also provides a kit for identifying a human subject afflicted with multiple sclerosis or a single clinical
35 attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the kit

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comprising a reagent for performing a method selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of mismatch (CCM), gene chip and
5 denaturing high performance liquid chromatography (DHPLC) for determining the genotype of the subject at a location corresponding to the location of at least one SNP selected from the group consisting of Group 1.

10 The present invention also provides a kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the kit comprising reagents for TaqMan Open Array assay designed for
15 determining the genotype of the subject at a location corresponding to the location of at least one SNP selected from the group consisting of Group 1.

The present invention also provides a kit for identifying a human subject afflicted with multiple sclerosis or a single clinical
20 attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the kit comprising

- a) at least one probe specific for a location corresponding to the location of at least one SNP;
- 25 b) at least one pair of PCR primers designed to amplify a DNA segment which includes a location corresponding to the location of at least one SNP;
- c) at least one pair of PCR primers designed to amplify a DNA segment which includes a location corresponding to the
30 location of at least one SNP and at least one probe specific for a location corresponding to the location of at least one SNP;
- d) a reagent for performing a method selected from the group consisting of restriction fragment length polymorphism (RFLP)
35 analysis, sequencing, single strand conformation polymorphism

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analysis (SSCP), chemical cleavage of mismatch (CCM), gene
chip and denaturing high performance liquid chromatography
(DHPLC) for determining the identity of at least one SNP; or
e) reagents for TaqMan Open Array assay designed for determining
5 the genotype at a location corresponding to the location of at
least one SNP,
wherein the at least one SNP is selected from the group
consisting of Group 1.

The present invention also provides a probe for identifying the
10 genotype of a location corresponding to the location of a SNP
selected from the group consisting of kgp10090631, kgp1009249,
kgp10148554, kgp10152733, kgp10215554, kgp10224254, kgp10305127,
kgp10351364, kgp10372946, kgp10404633, kgp10412303, kgp10523170,
kgp1054273, kgp10558725, kgp10564659, kgp10591989, kgp10594414,
15 kgp10619195, kgp10620244, kgp10632945, kgp10633631, kgp10679353,
kgp10762962, kgp10788130, kgp10826273, kgp10836214, kgp10910719,
kgp10922969, kgp10948564, kgp10967046, kgp10974833, kgp1098237,
kgp10989246, kgp11002881, kgp11010680, kgp11077373, kgp11141512,
kgp11206453, kgp11210903, kgp1124492, kgp11281589, kgp11285862,
20 kgp11285883, kgp11328629, kgp11356379, kgp11407560, kgp11453406,
kgp11467007, kgp11514107, kgp11543962, kgp11580695, kgp11604017,
kgp11627530, kgp11633966, kgp11686146, kgp11702474, kgp11711524,
kgp11755256, kgp11768533, kgp11804835, kgp11843177, kgp12008955,
kgp12083934, kgp1211163, kgp12182745, kgp12230354, kgp1224440,
25 kgp12253568, kgp12371757, kgp124162, kgp12426624, kgp12557319,
kgp12562255, kgp1285441, kgp13161760, kgp1355977, kgp1371881,
kgp1432800, kgp15390522, kgp1682126, kgp1683448, kgp1688752,
kgp1699628, kgp1753445, kgp1758575, kgp1779254, kgp1786079,
kgp18379774, kgp18432055, kgp18525257, kgp1912531, kgp19568724,
30 kgp20163979, kgp2023214, kgp2045074, kgp20478926, kgp2092817,
kgp21171930, kgp2176915, kgp2245775, kgp2262166, kgp22778566,
kgp22793211, kgp22811918, kgp22823022, kgp2282938, kgp22839559,
kgp2299675, kgp23298674, kgp2356388, kgp23672937, kgp23737989,
kgp2388352, kgp2391411, kgp24131116, kgp24415534, kgp2446153,
35 kgp2451249, kgp24521552, kgp2465184, kgp24729706, kgp24753470,

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	kgp25191871,	kgp25216186,	kgp25543811,	kgp25921291,	kgp25952891,
	kgp26026546,	kgp26271158,	kgp2638591,	kgp26528455,	kgp26533576,
	kgp2688306,	kgp26995430,	kgp270001,	kgp2709692,	kgp2715873,
	kgp27500525,	kgp27571222,	kgp27640141,	kgp2788291,	kgp279772,
5	kgp28532436,	kgp28586329,	kgp28687699,	kgp2877482,	kgp28817122,
	kgp2920925,	kgp2923815,	kgp29367521,	kgp293787,	kgp2958113,
	kgp2959751,	kgp297178,	kgp29794723,	kgp2993366,	kgp30282494,
	kgp3048169,	kgp304921,	kgp3182607,	kgp3188,	kgp3202939,
	kgp3205849,	kgp3218351,	kgp3267884,	kgp3276689,	kgp3287349,
	kgp337461,	kgp3418770,	kgp3420309,	kgp3450875,	kgp345301,
10	kgp3477351,	kgp3488270,	kgp3496814,	kgp355027,	kgp355723,
	kgp3593828,	kgp3598409,	kgp3598966,	kgp3624014,	kgp3651767,
	kgp3669685,	kgp3697615,	kgp3730395,	kgp3812034,	kgp3854180,
	kgp3933330,	kgp394638,	kgp3951463,	kgp3984567,	kgp3991733,
	kgp4011779,	kgp4037661,	kgp4056892,	kgp4096263,	kgp4127859,
15	kgp4137144,	kgp4155998,	kgp4162414,	kgp4223880,	kgp433351,
	kgp4346717,	kgp4370912,	kgp4418535,	kgp4420791,	kgp4456934,
	kgp4479467,	kgp4524468,	kgp4543470,	kgp4559907,	kgp4573213,
	kgp4575797,	kgp4591145,	kgp4634875,	kgp4705854,	kgp4734301,
	kgp4755147,	kgp4812831,	kgp4842590,	kgp485316,	kgp487328,
20	kgp4892427,	kgp4898179,	kgp4970670,	kgp4985243,	kgp5002011,
	kgp5014707,	kgp5017029,	kgp5053636,	kgp5068397,	kgp512180,
	kgp5144181,	kgp5159037,	kgp5216209,	kgp5252824,	kgp5292386,
	kgp5326762,	kgp5334779,	kgp5388938,	kgp5409955,	kgp541892,
	kgp5440506,	kgp5441587,	kgp5483926,	kgp55646,	kgp5564995,
25	kgp5579170,	kgp5680955,	kgp5691690,	kgp5747456,	kgp5869992,
	kgp5894351,	kgp5908616,	kgp5924341,	kgp5949515,	kgp6023196,
	kgp6032617,	kgp6038357,	kgp6042557,	kgp6076976,	kgp6081880,
	kgp6091119,	kgp6127371,	kgp61811,	kgp6190988,	kgp6194428,
	kgp6213972,	kgp6214351,	kgp6228750,	kgp6236949,	kgp625941,
30	kgp6301155,	kgp6429231,	kgp6469620,	kgp6505544,	kgp6507761,
	kgp652534,	kgp6539666,	kgp6567154,	kgp6599438,	kgp6603796,
	kgp6666134,	kgp6700691,	kgp6737096,	kgp6768546,	kgp6772915,
	kgp6828277,	kgp6835138,	kgp6889327,	kgp6959492,	kgp6990559,
	kgp6996560,	kgp7006201,	kgp7059449,	kgp7063887,	kgp7077322,
35	kgp7092772,	kgp7117398,	kgp7121374,	kgp7151153,	kgp7161038,
	kgp7178233,				

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kgp7181058, kgp7186699, kgp7189498, kgp7242489, kgp7331172,
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 25 rs11562998, rs11563025, rs1157449, rs11648129, rs11691553,
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 30 rs1397481, rs1410779, rs1474226, rs1478682, rs1508102, rs1508515,
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rs1894408, rs1905248, rs196295, rs196341, rs196343, rs197523,
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 rs4780822, rs4782279, rs4797764, rs4822644, rs484482, rs4894701,
 rs4978567, rs5024722, rs502530, rs528065, rs543122, rs6032205,
 rs6032209, rs6110157, rs623011, rs6459418, rs6497396, rs6535882,
 rs6577395, rs6687976, rs6718758, rs6811337, rs6835202, rs6840089,
 20 rs6845927, rs6895094, rs6899068, rs7020402, rs7024953, rs7028906,
 rs7029123, rs7062312, rs7119480, rs7123506, rs714342, rs7187976,
 rs7191155, rs720176, rs7217872, rs7228827, rs7231366, rs7348267,
 rs7496451, rs7524868, rs7563131, rs7579987, rs759458, rs7666442,
 rs7670525, rs7672014, rs7677801, rs7680970, rs7684006, rs7696391,
 25 rs7698655, rs7725112, rs7819949, rs7844274, rs7846783, rs7850,
 rs7860748, rs7862565, rs7864679, rs7928078, rs7948420, rs7949751,
 rs7961005, rs8000689, rs8018807, rs8035826, rs8050872, rs8053136,
 rs8055485, rs823829, rs858341, rs9315047, rs931570, rs9346979,
 rs9376361, rs9393727, rs9501224, rs9508832, rs950928, rs9579566,
 30 rs9597498, rs961090, rs9670531, rs9671124, rs9671182, rs967616,
 rs9817308, rs9834010, rs9876830, rs9913349, rs9931167, rs9931211,
 rs9948620 and rs9953274 (hereinafter Group 5).

The present invention also provides glatiramer acetate or a
 pharmaceutical composition comprising glatiramer acetate for use in
 35 treating a human subject afflicted with multiple sclerosis or a

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single clinical attack consistent with multiple sclerosis which human subject is identified as a predicted responder to glatiramer acetate by:

5 a) determining a genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of: Group 1, and

b) identifying the subject as a predicted responder to glatiramer acetate if the genotype of the subject contains
10 one or more A alleles at the location of Group 2,
one or more C alleles at the location of Group 3,
one or more G alleles at the location of Group 4, or
one or more T alleles at the location of kgp18432055,
kgp279772, kgp3991733 or kgp7242489.

15 The present invention also provides a method of determining the genotype of a human subject comprising identifying whether the genotype of a human subject contains

one or more A alleles at the location of Group 2,
one or more C alleles at the location of Group 3,
20 one or more G alleles at the location of Group 4, or
one or more T alleles at the location of kgp18432055,
kgp279772, kgp3991733 or kgp7242489.

The present invention also provides a method of identifying a human subject afflicted with multiple sclerosis or a single clinical
25 attack consistent with multiple sclerosis who is predicted to have a slower course of disease progression, comprising the steps of:

(i) determining a genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group
30 consisting of: kgp10148554, kgp10215554, kgp10762962,
kgp10836214, kgp10989246, kgp11285883, kgp11604017,
kgp11755256, kgp1211163, kgp12253568, kgp12562255,
kgp1432800, kgp1682126, kgp1758575, kgp2176915,
kgp22839559, kgp24521552, kgp2877482, kgp2920925,
35 kgp2993366, kgp3188, kgp3287349, kgp3420309, kgp3488270,

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kgp3598966, kgp3624014, kgp3697615, kgp394638,
 kgp4037661, kgp4137144, kgp433351, kgp4456934,
 kgp4575797, kgp4591145, kgp4892427, kgp4970670,
 kgp4985243, kgp5252824, kgp5326762, kgp541892,
 5 kgp5691690, kgp5747456, kgp5894351, kgp5924341,
 kgp5949515, kgp6042557, kgp6081880, kgp6194428,
 kgp6213972, kgp625941, kgp6301155, kgp6429231,
 kgp6828277, kgp6889327, kgp6990559, kgp7006201,
 kgp7151153, kgp7161038, kgp7653470, kgp7778345,
 10 kgp7932108, kgp8145845, kgp8644305, kgp8847137,
 kgp9143704, kgp9409440, kgp956070, kgp9909702,
 kgp9927782, rs10038844, rs1026894, rs10495115,
 rs11562998, rs11563025, rs11750747, rs11947777,
 rs12043743, rs12233980, rs12341716, rs12472695,
 15 rs12881439, rs13168893, rs13386874, rs1357718, rs1393037,
 rs1393040, rs1397481, rs1474226, rs1508515, rs1534647,
 rs16846161, rs1715441, rs17187123, rs17245674,
 rs17419416, rs1793174, rs1883448, rs1905248, rs209568,
 rs2354380, rs2618065, rs263247, rs2662, rs28993969,
 20 rs34647183, rs35615951, rs3768769, rs3847233, rs3858034,
 rs3858035, rs3858036, rs3858038, rs3894712, rs4740708,
 rs4797764, rs4978567, rs528065, rs6459418, rs6577395,
 rs6811337, rs7119480, rs7123506, rs7231366, rs7680970,
 rs7684006, rs7696391, rs7698655, rs7819949, rs7846783,
 25 rs7949751, rs7961005, rs8000689, rs8018807, rs961090,
 rs967616, rs9948620 and rs9953274 (hereinafter Group 6),
 and
 (ii) identifying the subject as predicted to have a slower
 course of disease progression if the genotype of the
 30 subject contains
 one or more A alleles at the location of kgp10762962,
 kgp11285883, kgp11604017, kgp1211163, kgp12253568,
 kgp12562255, kgp2176915, kgp24521552, kgp2877482,
 kgp2993366, kgp3188, kgp3624014, kgp394638, kgp4037661,
 35 kgp433351, kgp4456934, kgp4575797, kgp4591145,
 kgp4892427, kgp4970670, kgp4985243, kgp5252824,

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kgp5326762, kgp541892, kgp5747456, kgp5894351,
 kgp6042557, kgp6081880, kgp6194428, kgp6429231,
 kgp7006201, kgp7151153, kgp7161038, kgp7653470,
 kgp8145845, kgp8644305, kgp9143704, kgp9409440,
 5 kgp9909702, kgp9927782, rs10038844, rs10495115,
 rs11750747, rs12341716, rs12881439, rs13168893,
 rs1393040, rs1474226, rs1534647, rs1715441, rs17187123,
 rs17245674, rs17419416, rs1793174, rs1883448, rs1905248,
 rs263247, rs34647183, rs35615951, rs3847233, rs3858038,
 10 rs4740708, rs528065, rs6459418, rs6577395, rs6811337,
 rs7680970, rs7684006, rs7698655, rs7961005, rs8018807,
 rs9948620 or rs9953274 (hereinafter Group 7),
 one or more C alleles at the location of kgp10836214,
 kgp1432800, kgp22839559, kgp6301155, kgp6828277,
 15 rs2354380, rs2662, rs3858035, rs3894712, rs4797764 or
 rs7696391 (hereinafter Group 8),
 one or more G alleles at the location of kgp10148554,
 kgp10215554, kgp10989246, kgp11755256, kgp1682126,
 kgp1758575, kgp2920925, kgp3287349, kgp3420309,
 20 kgp3488270, kgp3598966, kgp3697615, kgp4137144,
 kgp5691690, kgp5924341, kgp5949515, kgp6213972,
 kgp625941, kgp6889327, kgp6990559, kgp7778345,
 kgp7932108, kgp8847137, kgp956070, rs1026894, rs11562998,
 rs11563025, rs11947777, rs12233980, rs12472695,
 25 rs13386874, rs1357718, rs1393037, rs1397481, rs1508515,
 rs16846161, rs209568, rs2618065, rs28993969, rs3768769,
 rs3858034, rs3858036, rs4978567, rs7119480, rs7123506,
 rs7231366, rs7819949, rs7846783, rs7949751, rs8000689,
 rs961090 or rs967616 (hereinafter Group 9), or
 30 one or more T alleles at the location of rs12043743.

The present invention also provides a kit for identifying a human
 subject afflicted with multiple sclerosis or a single clinical
 attack consistent with multiple sclerosis who is predicted to have a
 slower course of disease progression, the kit comprising

35 a) at least one probe specific for a location corresponding to
 the location of at least one SNP;

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- b) at least one pair of PCR primers designed to amplify a DNA segment which includes a location corresponding to the location of at least one SNP;
- 5 c) at least one pair of PCR primers designed to amplify a DNA segment which includes a location corresponding to the location of at least one SNP and at least one probe specific for a location corresponding to the location of at least one SNP;
- 10 d) a reagent for performing a method selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of mismatch (CCM), gene chip and denaturing high performance liquid chromatography (DHPLC) for determining the identity of at least one SNP; or
- 15 e) reagents for TaqMan Open Array assay designed for determining the genotype at a location corresponding to the location of at least one SNP,
- wherein the at least one SNP is selected from the group consisting of Group 6.

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BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. Figure 1 shows Receiver Operating Characteristics for optimization of test threshold.

Figure 2. Figure 2 shows Response Rate of Predicted Responders (green line) and Response Rate of Predicted Non-Responders (red line) by predictive test threshold.

Figure 3. Figure 3 shows overall percent of Predicted Responders by predictive test threshold.

Figure 4. Figure 4 shows chi square P-values (-Log P-value) of different test thresholds in the ability of the test to differentiate between cases and controls. A threshold of 0.71 demonstrated the most significant p-value.

Figure 5. Figure 5 shows overall Response to glatiramer acetate as Predicted by Model (model 3, threshold 0.71) for Predicted Responders (left panel) and Predicted Non-Responders (right panel).

Figure 6. Figure 6 shows GALA and FORTE patients were stratified by clearly defined response. High Response: improved ARR (ARR change $<(-1)$, during study versus prior 2 years). Low Response: no change or worsening of ARR (ARR change ≥ 0 , during study versus previous 2 years).

Figure 7. Figure 7 shows predictive model building for GALA and FORTE cohorts.

Figure 8. Figure 8 shows the algorithm and calculation of values for all genotyped patients of the Gala and FORTE cohorts, based on the predictive model (11 SNPs and 2 clinical variables).

Figure 9. Figure 9 shows the algorithm and calculation of values for all genotyped patients of the Gala and FORTE cohorts, based on the 11 SNPs in the predictive model, without including the clinical variables, and using a threshold at ~30% of the population classified as "predicted responders".

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DETAILED DESCRIPTION OF THE INVENTION

Embodiments of the Invention

The present invention provides a method for treating a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis with a pharmaceutical composition comprising glatiramer acetate and a pharmaceutically acceptable carrier, comprising the steps of:

- (i) determining a genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of: Group 1,
- (ii) identifying the subject as a predicted responder to glatiramer acetate if the genotype of the subject contains one or more A alleles at the location of Group 2,
one or more C alleles at the location of Group 3,
one or more G alleles at the location of Group 4, or
one or more T alleles at the location of kgp18432055, kgp279772, kgp3991733 or kgp7242489; and
- (iii) administering the pharmaceutical composition comprising glatiramer acetate and a pharmaceutically acceptable carrier to the subject only if the subject is identified as a predicted responder to glatiramer acetate.

In some embodiments step (i) further comprises determining a genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of: rs10988087, rs1573706, rs17575455, rs2487896, rs3135391, rs6097801 and rs947603, and wherein step (ii) further comprises identifying the subject as a predicted responder to glatiramer acetate if the genotype of the subject contains one or more A alleles at the location of rs10988087, one or more C alleles at the location of rs17575455, or one or more G alleles at the location of rs1573706, rs2487896, rs3135391, rs6097801 or rs947603.

In some embodiments administering the pharmaceutical composition comprising glatiramer acetate and a pharmaceutically acceptable

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carrier comprises administering to the human subject three subcutaneous injections of the pharmaceutical composition over a period of seven days with at least one day between every subcutaneous injection.

5 In some embodiments the pharmaceutical composition is a unit dose of a 1 ml aqueous solution comprising 40 mg of glatiramer acetate.

In some embodiments the pharmaceutical composition is a unit dose of a 1 ml aqueous solution comprising 20 mg of glatiramer acetate.

10 In some embodiments the pharmaceutical composition is a unit dose of a 0.5 ml aqueous solution comprising 20 mg of glatiramer acetate.

In some embodiments the pharmaceutical composition comprising glatiramer acetate and a pharmaceutically acceptable carrier is administered as a monotherapy.

15 In some embodiments the pharmaceutical composition comprising glatiramer acetate and a pharmaceutically acceptable carrier is administered in combination with at least one other multiple sclerosis drug.

The present invention also provides a method of identifying a human subject afflicted with multiple sclerosis or a single clinical
20 attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the method comprising determining the genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of Group 1,
25 and

identifying the human subject as a predicted responder to glatiramer acetate if the genotype of the subject contains

one or more A alleles at the location of Group 2,
one or more C alleles at the location of Group 3,
30 one or more G alleles at the location of Group 4, or
one or more T alleles at the location of kgp18432055, kgp279772, kgp3991733 or kgp7242489,

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or identifying the human subject as a predicted non-responder to glatiramer acetate if the genotype of the subject contains no A alleles at the location of Group 2, no C alleles at the location of Group 3, 5 no G alleles at the location of Group 4, or no T alleles at the location of kgp18432055, kgp279772, kgp3991733 or kgp7242489.

10 In some embodiments the methods further comprise determining a genotype of the subject at a location corresponding to the location of one or more SNPs selected from the group consisting of: rs10988087, rs1573706, rs17575455, rs2487896, rs3135391, rs6097801 and rs947603, and identifying the human subject as a predicted responder to glatiramer acetate if the genotype of the subject 15 contains one or more A alleles at the location of rs10988087, one or more C alleles at the location of rs17575455, or one or more G alleles at the location of rs1573706, rs2487896, rs3135391, rs6097801 or rs947603, or identifying the human subject as a predicted non-responder to glatiramer acetate if the genotype of the 20 subject contains no A alleles at the location of rs10988087, no C alleles at the location of rs17575455, or no G alleles at the location of rs1573706, rs2487896, rs3135391, rs6097801 or rs947603. In some embodiments the genotype is determined from a nucleic acid-containing sample that has been obtained from the subject.

25 In some embodiments determining the genotype comprises using a method selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of mismatch (CCM), denaturing high performance liquid chromatography 30 (DHPLC), Polymerase Chain Reaction (PCR) and an array, or a combination thereof.

In some embodiment, applying the algorithm depicted in Figure 8 or in Figure 9 to identify the subject as a predicted responder or as a predicted non-responder to glatiramer acetate.

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In some embodiments the genotype is determined using at least one pair of PCR primers and at least one probe.

In some embodiments the array is selected from the group consisting of a gene chip, and a TaqMan Open Array.

- 5 In some embodiments the gene chip is selected from the group consisting of a DNA array, a DNA microarray, a DNA chip, and a whole genome genotyping array.

In some embodiments the array is a TaqMan Open Array.

- 10 In some embodiments the gene chip is a whole genome genotyping array.

In some embodiments determining the genotype of the subject at the location corresponding to the location of the said one or more SNPs comprises:

- 15 (i) obtaining DNA from a sample that has been obtained from the subject;
- (ii) optionally amplifying the DNA; and
- 20 (iii) subjecting the DNA or the amplified DNA to a method selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of mismatch (CCM), denaturing high performance liquid chromatography (DHPLC), Polymerase Chain Reaction (PCR) and an array, or a combination thereof, for determining the identity the one or more SNPs.

- 25 In some embodiments the array comprises a plurality of probes suitable for determining the identity of the one or more SNPs.

In some embodiments the array is a gene chip.

In some embodiments the gene chip is a whole genome genotyping array.

- 30 In some embodiments the human subject is a naïve patient.

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In some embodiments the human subject has been previously administered glatiramer acetate.

In some embodiments the human subject has been previously administered a multiple sclerosis drug other than glatiramer
5 acetate.

In some embodiments the genotype is determined at locations corresponding to the locations of 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16 or more single nucleotide polymorphisms (SNPs).

In some embodiments the one or more SNPs is selected from the group
10 consisting of kgp24415534, kgp6214351, kgp6599438, kgp7747883, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408 and rs759458 (hereinafter Group 10).

In some embodiments the one or more SNPs is selected from the group
15 consisting of kgp24415534, kgp6214351, kgp6599438, kgp7747883, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, and rs759458.

In some embodiments the one or more SNPs is selected from the group
20 consisting of kgp24415534, kgp6214351, kgp6599438, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, and rs759458.

In some embodiments, if rs3135391 is the at least one SNP selected, then selecting at least one SNP other than rs3135391.

In some embodiments the one or more SNPs comprise 2, 3, 4, 5, 6, 7, 8, 9 or 10 of the SNPs selected from the group consisting of Group
25 10.

In some embodiments the one or more SNPs further comprise rs3135391.

In some embodiments the one or more SNPs comprise 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 of the SNPs selected from the group consisting of kgp24415534, kgp6214351, kgp6599438, kgp7747883, kgp8110667,

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kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391 and rs759458.

In some embodiments the one or more single nucleotide polymorphisms (SNPs) further comprise 2, 3, 4, 5, 6, 7, 8, 9 or 10 of the SNPs
5 selected from the group consisting of kgp24415534, kgp6214351, kgp6599438, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391 and rs759458.

In some embodiments the genotype of the subject at the location
corresponding to the location of one or more of the SNPs is
10 determined indirectly by determining the genotype of the subject at a location corresponding to the location of at least one SNP that is in linkage disequilibrium with the one or more SNPs.

In some embodiments the genotype of the subject at the location
corresponding to the location of the one or more SNPs is determined
15 by indirect genotyping.

In some embodiments the indirect genotyping allows identification of the genotype of the subject at the location corresponding to the location of the one or more SNPs with a probability of at least 85%.

In some embodiments the indirect genotyping allows identification of
20 the genotype of the subject at the location corresponding to the location of the one or more SNPs with a probability of at least 90%.

In some embodiments the indirect genotyping allows identification of the genotype of the subject at the location corresponding to the location of the one or more SNPs with a probability of at least 99%.

25 In some embodiments the methods further comprise the step of determining the log number of relapses in the last two years for the human subject.

In some embodiments the methods further comprise the step of
determining the baseline Expanded Disability Status Scale (EDSS)
30 score for the human subject.

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In some embodiments the methods further comprise determining the genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of: Group 6, and

- 5 identifying the human subject as a predicted responder to glatiramer acetate if the genotype of the subject contains
- one or more A alleles at the location of Group 7,
 - one or more C alleles at the location of Group 8,
 - one or more G alleles at the location of Group 9, or
 - 10 one or more T alleles at the location of rs12043743.

The present invention also provides a kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the kit

15 comprising at least one probe specific for the location of a SNP selected from the group consisting of Group 1.

The present invention also provides a kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder

20 or as a predicted non-responder to glatiramer acetate, the kit comprising at least one pair of PCR primers designed to amplify a DNA segment which includes the location of a SNP selected from the group consisting of Group 1.

The present invention also provides a kit for identifying a human

25 subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the kit comprising a reagent for performing a method selected from the group consisting of restriction fragment length polymorphism (RFLP)

30 analysis, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of mismatch (CCM), gene chip and denaturing high performance liquid chromatography (DHPLC) for determining the genotype of the subject at a location corresponding

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to the location of at least one SNP selected from the group consisting of Group 1.

In some embodiments the gene chip is a whole genome genotyping array.

5 In some embodiments the kit comprises

(i) at least one pair of PCR primers designed to amplify a DNA segment which includes the location a SNP selected from the group consisting of Group 1, and

10 (ii) at least one probe specific for the location of a SNP selected from the group consisting of Group 1.

The present invention also provides a kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the kit
15 comprising reagents for TaqMan Open Array assay designed for determining the genotype of the subject at a location corresponding to the location of at least one SNP selected from the group consisting of Group 1.

In some embodiments the kit further comprises instructions for use
20 of the kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate.

In some embodiments the one or more single nucleotide polymorphisms
25 (SNPs) are selected from the group consisting of Group 10.

In some embodiments the one or more single nucleotide polymorphisms (SNPs) comprise 2, 3, 4, 5, 6, 7, 8, 9 or 10 of the SNPs selected from the group consisting of Group 10.

In some embodiments the one or more SNPs further comprise rs3135391.

30 The present invention also provides a kit for identifying a human subject afflicted with multiple sclerosis or a single clinical

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attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the kit comprising

- 5 a) at least one probe specific for a location corresponding to the location of at least one SNP;
- b) at least one pair of PCR primers designed to amplify a DNA segment which includes a location corresponding to the location of at least one SNP;
- 10 c) at least one pair of PCR primers designed to amplify a DNA segment which includes a location corresponding to the location of at least one SNP and at least one probe specific for a location corresponding to the location of at least one SNP;
- 15 d) a reagent for performing a method selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of mismatch (CCM), gene chip and denaturing high performance liquid chromatography (DHPLC) for determining the identity of at least one SNP; or
- 20 e) reagents for TaqMan Open Array assay designed for determining the genotype at a location corresponding to the location of at least one SNP,

wherein the at least one SNP is selected from the group consisting of Group 1.

- 25 In some embodiments the at least one single nucleotide polymorphisms (SNPs) are selected from the group consisting of Group 10,

preferably wherein the kit further comprises instructions for use of the kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate.

In some embodiments the at least one single nucleotide polymorphisms (SNPs) comprise 2, 3, 4, 5, 6, 7, 8, 9 or 10 of the SNPs selected from the group consisting of Group 10.

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In some embodiments the at least one single nucleotide polymorphisms (SNPs) further comprise rs3135391.

In some embodiments the genotype of the subject at the location corresponding to the location of one or more of the SNPs is
5 determined by indirect genotyping,

In some embodiments the genotype of the subject at the location corresponding to the location of one or more of the SNPs is determined indirectly by determining the genotype of the subject at a location corresponding to the location of at least one SNP that is
10 in linkage disequilibrium with the one or more SNPs.

In some embodiments the kit comprises

- a) at least one probe specific for a location corresponding to the location of at least one SNP;
- b) at least one pair of PCR primers designed to amplify a DNA
15 segment which includes a location corresponding to the location of at least one SNP;
- c) at least one pair of PCR primers designed to amplify a DNA segment which includes a location corresponding to the location of at least one SNP and at least one probe specific for a location corresponding to the location of at least one
20 SNP;
- d) a reagent for performing a method selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of mismatch (CCM), gene
25 chip and denaturing high performance liquid chromatography (DHPLC) for determining the identity of at least one SNP; or
- e) reagents for TaqMan Open Array assay designed for determining the genotype at a location corresponding to the location of at
30 least one SNP,

wherein the at least one SNP is in linkage disequilibrium with the one or more SNPs.

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In some embodiments determining the genotype of the subject at a location corresponding to the location of at least one SNP that is in linkage disequilibrium with the one or more SNPs allows identification of the genotype of the subject at the location
5 corresponding to the location of the one or more SNPs with a probability of at least 85%.

In some embodiments determining the genotype of the subject at a location corresponding to the location of at least one SNP that is in linkage disequilibrium with the one or more SNPs allows
10 identification of the genotype of the subject at the location corresponding to the location of the one or more SNPs with a probability of at least 90%.

In some embodiments determining the genotype of the subject at a location corresponding to the location of at least one SNP that is
15 in linkage disequilibrium with the one or more SNPs allows identification of the genotype of the subject at the location corresponding to the location of the one or more SNPs with a probability of at least 99%.

The present invention also provides a probe for identifying the
20 genotype of a location corresponding to the location of a SNP selected from the group consisting of Group 5.

The present invention also provides a probe for identifying the genotype of a location corresponding to the location of a SNP selected from the group consisting of kgp24415534, kgp6214351,
25 kgp6599438, kgp7747883, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, and rs759458.

In some embodiments the SNP is in linkage disequilibrium with the one or more SNPs.

30 The present invention also provides glatiramer acetate or a pharmaceutical composition comprising glatiramer acetate for use in treating a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis which

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human subject is identified as a predicted responder to glatiramer acetate by:

- a) determining a genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of:
5 Group 1, and
- b) identifying the subject as a predicted responder to glatiramer acetate if the genotype of the subject contains
10 one or more A alleles at the location of Group 2,
 one or more C alleles at the location of Group 3,
 one or more G alleles at the location of Group 4, or
 one or more T alleles at the location of kgp18432055,
 kgp279772, kgp3991733 or kgp7242489.

15 In some embodiments the genotype of the subject at the location corresponding to the location of one or more of the SNPs is determined indirectly by determining the genotype of the subject at a location corresponding to the location of at least one SNP that is in linkage disequilibrium with the one or more SNPs.

20 The present invention also provides a method of determining the genotype of a human subject comprising identifying whether the genotype of a human subject contains

- one or more A alleles at the location of Group 2,
- one or more C alleles at the location of Group 3,
- one or more G alleles at the location of Group 4, or
- 25 one or more T alleles at the location of kgp18432055,
 kgp279772, kgp3991733 or kgp7242489.

In some embodiments identifying whether the genotype of a human subject contains

- 30 one or more A alleles at the location of Group 2,
- one or more C alleles at the location of Group 3,
- one or more G alleles at the location of Group 4, or
- one or more T alleles at the location of kgp18432055,
kgp279772, kgp3991733 or kgp7242489 is determined indirectly
by determining the genotype of the subject at a location

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corresponding to the location of at least one SNP that is in linkage disequilibrium with the one or more SNPs.

The present invention also provides a method of determining the genotype of a human subject comprising identifying the genotype of a human subject at the location of kgp6214351, kgp6599438, kgp7747883, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, or rs759458.

The present invention also provides a method of identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis who is predicted to have a slower course of disease progression, comprising the steps of:

- (i) determining a genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of: Group 6, and
- (ii) identifying the subject as predicted to have a slower course of disease progression if the genotype of the subject contains
 - one or more A alleles at the location of Group 7,
 - one or more C alleles at the location of Group 8,
 - one or more G alleles at the location of Group 9, or
 - one or more T alleles at the location of rs12043743.

In some embodiments the genotype of the subject at the location corresponding to the location of one or more of the SNPs is determined indirectly by determining the genotype of the subject at a location corresponding to the location of at least one SNP that is in linkage disequilibrium with the one or more SNPs.

The present invention also provides a kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis who is predicted to have a slower course of disease progression, the kit comprising

- a) at least one probe specific for a location corresponding to the location of at least one SNP;

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- b) at least one pair of PCR primers designed to amplify a DNA segment which includes a location corresponding to the location of at least one SNP;
- c) at least one pair of PCR primers designed to amplify a DNA segment which includes a location corresponding to the location of at least one SNP and at least one probe specific for a location corresponding to the location of at least one SNP;
- d) a reagent for performing a method selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of mismatch (CCM), gene chip and denaturing high performance liquid chromatography (DHPLC) for determining the identity of at least one SNP; or
- e) reagents for TaqMan Open Array assay designed for determining the genotype at a location corresponding to the location of at least one SNP,
- wherein the at least one SNP is selected from the group consisting of Group 6.

For the foregoing embodiments, each embodiment disclosed herein is contemplated as being applicable to each of the other disclosed embodiments. Thus, all combinations of the various elements described herein are within the scope of the invention.

Definitions

As used herein, a genetic marker refers to a DNA sequence that has a known location on a chromosome. Several non-limiting examples of classes of genetic markers include SNP (single nucleotide polymorphism), STR (short tandem repeat), and SFP (single feature polymorphism). VNTR (variable number tandem repeat), microsatellite polymorphism, insertions and deletions. The genetic markers associated with the invention are SNPs. As used herein a SNP or "single nucleotide polymorphism" refers to a specific site in the genome where there is a difference in DNA base between individuals. In some embodiments the SNP is located in a coding region of a gene.

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In other embodiments the SNP is located in a noncoding region of a gene. In still other embodiments the SNP is located in an intergenic region.

Several non-limiting examples of databases from which information on
5 SNPs or genes that are associated with human disease can be
retrieved include: NCBI resources, The SNP Consortium LTD, NCBI
dbSNP database, International HapMap Project, 1000 Genomes Project,
Glovar Variation Browser, SNPStats, PharmGKB, GEN-Snip, and SNPedia.

SNPs are identified herein using the rs identifier numbers in
10 accordance with the NCBI dbSNP database, which is publically
available at: ncbi.nlm.nih.gov/projects/SNP/ or using the kgp
identifier numbers, which were created by Illumina. Genotype at the
kgp SNPs can be obtained by using the Illumina genotyping arrays. In
addition, SNPs can be identified by the specific location on the
15 chromosome indicated for the specific SNP.

Additional information about identifying SNPs can be obtained from
the NCBI database SNP FAQ archive located at
ncbi.nlm.nih.gov/books/NBK3848/ or from literature available on the
Illumina website located at
20 illumina.com/applications/genotyping/literature.ilmn.

In some embodiments, SNPs in linkage disequilibrium with the SNPs
associated with the invention are useful for obtaining similar
results. As used herein, linkage disequilibrium refers to the non-
random association of SNPs at one loci. Techniques for the
25 measurement of linkage disequilibrium are known in the art. As two
SNPs are in linkage disequilibrium if they are inherited together,
the information they provide is correlated to a certain extent. SNPs
in linkage disequilibrium with the SNPs included in the models can
be obtained from databases such as HapMap or other related
30 databases, from experimental setups run in laboratories or from
computer-aided in-silico experiments. Determining the genotype of a
subject at a position of SNP as specified herein, e.g. as specified
by NCBI dbSNP rs identifier, may comprise "direct genotyping", e.g.
by determining the identity of the nucleotide of each allele at the
35 locus of SNP, and/or "indirect genotyping", defined herein as

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evaluating/determining the identity of an allele at one or more loci that are in linkage disequilibrium with the SNP in question, allowing one to infer the identity of the allele at the locus of SNP in question with a substantial degree of confidence. In some cases, indirect genotyping may comprise determining the identity of each allele at one or more loci that are in sufficiently high linkage disequilibrium with the SNP in question so as to allow one to infer the identity of each allele at the locus of SNP in question with a probability of at least 85%, at least 90% or at least 99% certainty.

10 A genotype at a position of SNP (genotype "at a" SNP) may be represented by a single letter which corresponds to the identity of the nucleotide at the SNP, where A represents adenine, T represents thymine, C represents cytosine, and G represents guanine. The identity of two alleles at a single SNP may be represented by a two letter combination of A, T, C, and G, where the first letter of the two letter combination represents one allele and the second letter represents the second allele, and where A represents adenine, T represents thymine, C represents cytosine, and G represents guanine. Thus, a two allele genotype at a SNP can be represented as, for example, AA, AT, AG, AC, TT, TG, TC, GG, GC, or CC. It is understood that AT, AG, AC, TG, TC, and GC are equivalent to TA, GA, CA, GT, CT, and CG, respectively.

The SNPs of the invention can be used as predictive indicators of the response to GA in subjects afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis. Aspects of the invention relate to determining the presence of SNPs through obtaining a patient DNA sample and evaluating the patient sample for the presence of one or more SNPs, or for a certain set of SNPs. It should be appreciated that a patient DNA sample can be extracted, and a SNP can be detected in the sample, through any means known to one of ordinary skill in art. Some non-limiting examples of known techniques include detection via restriction fragment length polymorphism (RFLP) analysis, arrays including but not limited to planar microarrays or bead arrays, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of

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mismatch (CCM), Polymerase chain reaction (PCR) and denaturing high performance liquid chromatography (DHPLC).

In some embodiments, the genotyping array is a whole genome genotyping array. In some embodiments, the Whole-genome genotyping
5 arrays as defined here are arrays that contain hundreds of thousands to millions of genetic sequences (which may also be named "probes"). In some embodiments, Whole-genome genotyping arrays contain 500,000 probes or more. In some embodiments, Whole-genome genotyping arrays contain 1 million probes or more. In some embodiments, Whole-genome
10 genotyping arrays contain 5 million probes or more.

In some embodiments, a SNP is detected through PCR amplification and sequencing of the DNA region comprising the SNP. In some embodiments SNPs are detected using arrays, exemplified by gene chip, including but not limited to DNA arrays or microarrays, DNA chips, and whole
15 genome genotyping arrays, all of which may be for example planar arrays or bead arrays, or a TaqMan open Array. Arrays/Microarrays for detection of genetic polymorphisms, changes or mutations (in general, genetic variations) such as a SNP in a DNA sequence, may comprise a solid surface, typically glass, on which a high number of
20 genetic sequences are deposited (the probes), complementary to the genetic variations to be studied. Using standard robotic printers to apply probes to the array a high density of individual probe features can be obtained, for example probe densities of 600 features per cm² or more can be typically achieved. The positioning
25 of probes on an array is precisely controlled by the printing device (robot, inkjet printer, photolithographic mask etc) and probes are aligned in a grid. The organization of probes on the array facilitates the subsequent identification of specific probe-target interactions. Additionally it is common, but not necessary, to
30 divide the array features into smaller sectors, also grid-shaped, that are subsequently referred to as sub-arrays. Sub-arrays typically comprise 32 individual probe features although lower (e.g. 16) or higher (e.g. 64 or more) features can comprise each sub-array. In some arrays the probes are connected to beads instead of

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the solid support. Such arrays are called "bead arrays" or "bead
CHIPs".

In some embodiments, detection of genetic variation such as the
presence of a SNP involves hybridization to sequences which
5 specifically recognize the normal and the mutant allele in a
fragment of DNA derived from a test sample. Typically, the fragment
has been amplified, e.g. by using the polymerase chain reaction
(PCR), and labeled e.g. with a fluorescent molecule. A laser can be
used to detect bound labeled fragments on the chip and thus an
10 individual who is homozygous for the normal allele can be
specifically distinguished from heterozygous individuals (in the
case of autosomal dominant conditions then these individuals are
referred to as carriers) or those who are homozygous for the mutant
allele. In some embodiments, the amplification reaction and/or
15 extension reaction is carried out on the microarray or bead itself.
For differential hybridization based methods there are a number of
methods for analyzing hybridization data for genotyping: Increase in
hybridization level: The hybridization levels of probes
complementary to the normal and mutant alleles are compared.
20 Decrease in hybridization level: Differences in the sequence between
a control sample and a test sample can be identified by a decrease
in the hybridization level of the totally complementary
oligonucleotides with a reference sequence. A loss approximating
100% is produced in mutant homozygous individuals while there is
25 only an approximately 50% loss in heterozygotes. In Microarrays for
examining all the bases of a sequence of "n" nucleotides
("oligonucleotide") of length in both strands, a minimum of "2n"
oligonucleotides that overlap with the previous oligonucleotide in
all the sequence except in the nucleotide are necessary. Typically
30 the size of the oligonucleotides is about 25 nucleotides. However it
should be appreciated that the oligonucleotide can be any length
that is appropriate as would be understood by one of ordinary skill
in the art. The increased number of oligonucleotides used to
reconstruct the sequence reduces errors derived from fluctuation of
35 the hybridization level.

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However, the exact change in sequence cannot be identified with this method; in some embodiments this method is combined with sequencing to identify the mutation. Where amplification or extension is carried out on the microarray or bead itself, three methods are presented by way of example: In the Minisequencing strategy, a mutation specific primer is fixed on the slide and after an extension reaction with fluorescent dideoxynucleotides, the image of the Microarray is captured with a scanner. In the Primer extension strategy, two oligonucleotides are designed for detection of the wild type and mutant sequences respectively. The extension reaction is subsequently carried out with one fluorescently labeled nucleotide and the remaining nucleotides unlabelled. In either case the starting material can be either an RNA sample or a DNA product amplified by PCR. In the Tag arrays strategy, an extension reaction is carried out in solution with specific primers, which carry a determined 5' sequence or "tag". The use of Microarrays with oligonucleotides complementary to these sequences or "tags" allows the capture of the resultant products of the extension. Examples of this include the high density Microarray "Flex-flex" (Affymetrix). In the Illumina 1M Duo BeadChip array (illumina.com/products/human1m_duo_dna_analysis_beadchip_kits.ilmn), SNP genotypes are generated from fluorescent intensities using the manufacturer's default cluster settings.

In some aspects of the invention measurement of clinical variables comprises part of the prediction model predicting response to GA along with the genetic variables. Some non-limiting examples are age of the patient (in years), gender of patient, clinical manifestations, MRI parameter, country, ancestry, and years of exposure to treatment) "Clinical manifestations" include but are not limited to EDSS score such as baseline EDSS score, log of number of relapses in last 2 Years and relapse rate. "MRI parameters" include but are not limited to the volume and/or number of T1 enhancing lesions and/or T2 enhancing lesions; exemplified by baseline volume of T2 lesion, number of Gd-T1 lesions at baseline. In certain aspect of the invention, the clinical variables taken into account are as measured at the time of the decision about the treatment suitable

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for the patient, or measured at a time point determined by the physician, researcher or other professional involved in the decision.

The identification of a patient as a responder or as a non-responder to GA based on the presence of at least one SNP from tables 2-32 and 34-44, a set of SNPs from tables 2-32 and 34-44, or the combination of a SNP or a set of SNPs from tables 2-32 and 34-44 with one or more clinical variables described above, may be used for predicting response to GA.

Also within the scope of the invention are kits and instructions for their use. In some embodiments kits associated with the invention are kits for identifying one or more SNPs within a patient sample. In some embodiments a kit may contain primers for amplifying a specific genetic locus. In some embodiments, a kit may contain a probe for hybridizing to a specific SNP. The kit of the invention can include reagents for conducting each of the following assays including but not limited to restriction fragment length polymorphism (RFLP) analysis, arrays including but not limited to planar microarrays or bead arrays, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of mismatch (CCM), and denaturing high performance liquid chromatography (DHPLC), PCR amplification and sequencing of the DNA region comprising the SNP. A kit of the invention can include a description of use of the contents of the kit for participation in any biological or chemical mechanism disclosed herein. A kit can include instructions for use of the kit components alone or in combination with other methods or compositions for assisting in screening or diagnosing a sample and/or determining whether a subject is a responder or a non-responder to GA.

30 Forms of Multiple Sclerosis:

There are five distinct disease stages and/or types of MS:

- 1) benign multiple sclerosis;
- 2) relapsing-remitting multiple sclerosis (RRMS);
- 3) secondary progressive multiple sclerosis (SPMS);

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4) progressive relapsing multiple sclerosis (PRMS); and

5) primary progressive multiple sclerosis (PPMS).

Benign multiple sclerosis is a retrospective diagnosis which is characterized by 1-2 exacerbations with complete recovery, no
5 lasting disability and no disease progression for 10-15 years after the initial onset. Benign multiple sclerosis may, however, progress into other forms of multiple sclerosis.

Patients suffering from RRMS experience sporadic exacerbations or relapses, as well as periods of remission. Lesions and evidence of
10 axonal loss may or may not be visible on MRI for patients with RRMS. SPMS may evolve from RRMS. Patients afflicted with SPMS have relapses, a diminishing degree of recovery during remissions, less frequent remissions and more pronounced neurological deficits than RRMS patients. Enlarged ventricles, which are markers for atrophy of
15 the corpus callosum, midline center and spinal cord, are visible on MRI of patients with SPMS.

PPMS is characterized by a steady progression of increasing neurological deficits without distinct attacks or remissions. Cerebral lesions, diffuse spinal cord damage and evidence of axonal
20 loss are evident on the MRI of patients with PPMS. PPMS has periods of acute exacerbations while proceeding along a course of increasing neurological deficits without remissions. Lesions are evident on MRI of patients suffering from PRMS.(28)

A clinically isolated syndrome (CIS) is a single monosymptomatic
25 attack compatible with MS, such as optic neuritis, brain stem symptoms, and partial myelitis. Patients with CIS that experience a second clinical attack are generally considered to have clinically definite multiple sclerosis (CDMS). Over 80 percent of patients with a CIS and MRI lesions go on to develop MS, while approximately 20
30 percent have a self-limited process.(29,30) Patients who experience a single clinical attack consistent with MS may have at least one lesion consistent with multiple sclerosis prior to the development of clinically definite multiple sclerosis.

Multiple sclerosis may present with optic neuritis, blurring of
35 vision, diplopia, involuntary rapid eye movement, blindness, loss of

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balance, tremors, ataxia, vertigo, clumsiness of a limb, lack of co-ordination, weakness of one or more extremity, altered muscle tone, muscle stiffness, spasms, tingling, paraesthesia, burning sensations, muscle pains, facial pain, trigeminal neuralgia, stabbing sharp pains, burning tingling pain, slowing of speech, slurring of words, changes in rhythm of speech, dysphagia, fatigue, bladder problems (including urgency, frequency, incomplete emptying and incontinence), bowel problems (including constipation and loss of bowel control), impotence, diminished sexual arousal, loss of sensation, sensitivity to heat, loss of short term memory, loss of concentration, or loss of judgment or reasoning.

Relapsing Form of Multiple Sclerosis:

The term relapsing MS includes:

- 1) patients with RRMS;
- 2) patients with SPMS and superimposed relapses; and
- 3) patients with CIS who show lesion dissemination on subsequent MRI scans according to McDonald's criteria.

As used herein, relapsing forms of multiple sclerosis include: Relapsing-remitting multiple sclerosis (RRMS), characterized by unpredictable acute episodes of neurological dysfunction (relapses), followed by variable recovery and periods of clinical stability;

Secondary Progressive MS (SPMS), wherein patients having RRMS develop sustained deterioration with or without relapses superimposed; and

Primary progressive-relapsing multiple sclerosis (PPRMS) or progressive-relapsing multiple sclerosis (PRMS), an uncommon form wherein patients developing a progressive deterioration from the beginning can also develop relapses later on.

Kurtzke Expanded Disability Status Scale (EDSS):

The Kurtzke Expanded Disability Status Scale (EDSS) is a method of quantifying disability in multiple sclerosis. The EDSS replaced the previous Disability Status Scales which used to bunch people with MS in the lower brackets. The EDSS quantifies disability in eight Functional Systems (FS) and allows neurologists to assign a

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Functional System Score (FSS) in each of these. The Functional Systems are: pyramidal, cerebellar, brainstem, sensory, bowel and bladder, visual & cerebral (according to mult-sclerosis.org/expandeddisabilitystatusscale).

5

Clinical Relapse:

A clinical relapse, which may also be used herein as "relapse," "confirmed relapse," or "clinically defined relapse," is defined as the appearance of one or more new neurological abnormalities or the
10 reappearance of one or more previously observed neurological abnormalities.

This change in clinical state must last at least 48 hours and be immediately preceded by a relatively stable or improving neurological state of at least 30 days. This criterion is different
15 from the clinical definition of exacerbation "at least 24 hours duration of symptoms," (31) as detailed in the section "relapse evaluation."

An event is counted as a relapse only when the subject's symptoms are accompanied by observed objective neurological changes,
20 consistent with:

a) an increase of at least 0.5 in the EDSS score or one grade in the score of two or more of the seven FS (32); or,

b) two grades in the score of one of FS as compared to the previous evaluation.

25 The subject must not be undergoing any acute metabolic changes such as fever or other medical abnormality. A change in bowel/bladder function or in cognitive function must not be entirely responsible for the changes in EDSS or FS scores.

30 As used herein, a "multiple sclerosis drug" is a drug or an agent intended to treat clinically defined MS, CIS, any form of neurodegenerative or demyelinating diseases, or symptoms of any of the above mentioned diseases. "Multiple sclerosis drugs" may include but are not limited to antibodies, immunosuppressants, anti-inflammatory agents, immunomodulators, cytokines, cytotoxic agents

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and steroids and may include approved drugs, drugs in clinical trial, or alternative treatments, intended to treat clinically defined MS, CIS or any form of neurodegenerative or demyelinating diseases. "Multiple sclerosis drugs" include but are not limited to
5 Interferon and its derivatives (including BETASERON®, AVONEX® and REBIF®), Mitoxantrone and Natalizumab. Agents approved or in-trial for the treatment of other autoimmune diseases, but used in a MS or CIS patient to treat MS or CIS are also defined as multiple sclerosis drugs.

10 As used herein, a "naïve patient" is a subject that has not been treated with any multiple sclerosis drugs as defined in the former paragraph.

The administration of glatiramer acetate may be oral, nasal, pulmonary, parenteral, intravenous, intra-articular, transdermal,
15 intradermal, subcutaneous, topical, intramuscular, rectal, intrathecal, intraocular, buccal or by gavage.

As used herein, "GALA" is a phase 3 clinical trial entitled "A Study in Subjects With Relapsing-Relmitting Multiple Sclerosis (RRMS) to Assess the Efficacy, Safety and Tolerability of Glatiramer Acetate
20 (GA) Injection 40 mg Administered Three Times a Week Compared to Placebo (GALA)." The GALA trial has the ClinicalTrials.gov Identifier NCT01067521, and additional information about the trial can be found at clinicaltrials.gov/ct2/show/NCT01067521.

As used herein, "FORTE" is a phase 3 clinical trial entitled
25 "Clinical Trial Comparing Treatment of Relapsing-Relmitting Multiple Sclerosis (RR-MS) With Two Doses of Glatiramer Acetate (GA)." The FORTE trial has the ClinicalTrials.gov Identifier NCT00337779 and additional information, including study results can be found at clinicaltrials.gov/ct2/show/NCT00337779.

30 As used herein, "about" with regard to a stated number encompasses a range of +10 percent to -10 percent of the stated value. By way of example, about 100 mg/kg therefore includes the range 90-100 mg/kg and therefore also includes 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 018, 109 and 110 mg/kg.

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Accordingly, about 100 mg/kg includes, in an embodiment, 100 mg/kg.

It is understood that where a parameter range is provided, all integers within that range, tenths thereof, and hundredths thereof, are also provided by the invention. For example, "0.2-5 mg/kg" is a disclosure of 0.2 mg/kg, 0.21 mg/kg, 0.22 mg/kg, 0.23 mg/kg etc. up to 0.3 mg/kg, 0.31 mg/kg, 0.32 mg/kg, 0.33 mg/kg etc. up to 0.4 mg/kg, 0.5 mg/kg, 0.6 mg/kg etc. up to 5.0 mg/kg.

All combinations of the various elements described herein are within the scope of the invention.

This invention will be better understood by reference to the Experimental Details which follow, but those skilled in the art will readily appreciate that the specific experiments detailed are only illustrative of the invention as described more fully in the claims which follow thereafter.

Experimental Details

Description of the Study

Copaxone® (Glatiramer acetate) is a leading drug for the treatment of MS that is marketed by TEVA. Glatiramer acetate significantly improves patient outcomes, but glatiramer acetate treatment is not equally effective in all patients. Individual differences between patients, including inherited genetic factors, can account for significant differences in individual responses to medications. A consequence of this diversity is that no single medication is effective in all patients. Clinical and genetic factors are predictive of patient response to glatiramer acetate.

In the following Examples, predictive genetic factors of glatiramer acetate treatment response are identified and a diagnostic model is demonstrated to help guide MS drug therapy to significantly improve patient outcomes.

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Examples**Example 1 Patient Populations**

Response definitions were received from patients from two large glatiramer acetate clinical trial cohorts (GALA, FORTE) and patients were categorized as responder, non-responder, extreme-responder, or extreme non-responder according to the criteria set forth in Table 1.

Table 1. Definition of Glatiramer Acetate Responders and Non-Responders and population representation in GALA and FORTE cohorts.

		Number of samples (% of cohort)		
		GALA	FORTE	GALA placebo
Responders	Responders: Change in Annual Relapse Rate (ARR) from previous 2 years < -1	200 (26%)	221 (36%)	97 (25%)
	Extreme Responders: Change in ARR from previous 2 years < -1 and new T2 Lesions = 0 and Relapse Free	66 (8.5%)	95 (16%)	23 (6%)
Non-Responders	Non-Responders: Change in ARR from previous 2 years ≥ 0	123 (16%)	68 (11%)	101 (26%)
	Extreme Non-Responders: Change in ARR from previous 2 years ≥ 0 and new T2 Lesions ≥ 1	79 (10%)	38 (6%)	73 (19%)

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Example 2 Patient Genotyping

DNA samples from categorized patients were subject to quality control analysis followed by genotyping with the Illumina OMNI-5M genome wide array. This array tests 4,301,331 variants with a median marker
5 spacing of 360 bp. The array includes 84,004 non-synonymous SNPs including 43,904 variants in the MHC region. Over 800 patients were genotyped.

Genotyping Quality Control

10 An Illumina-derived algorithm of SNP cluster definitions (*i.e.*, the specific parameters used to determine specific genotypes of each SNP) was used to determine the 4,301,331 genotypes for each of the genotyped samples. For genotyping QC, SNPs were evaluated as either pass, fail, or the SNP cluster calling definitions were revised and the SNP was re-evaluated as pass or fail.

15 Evaluation of SNPs with poor cluster separation values (*i.e.*, the location of SNP calling clusters were very close together) identified 126 SNPs for which SNP clustering was manually corrected. Evaluation of SNPs that were not in Hardy-Weinburg equilibrium identified 1,000 SNPs for which SNP clustering was manually
20 corrected. Evaluation of SNPs with low GC scores (GC score: an Illumina-developed score of overall SNP performance) identified 10,000 SNPs for which SNP clustering was manually corrected. Evaluation of SNPs with low GC scores also identified 160,000 SNPs for which SNP clustering was revised using Illumina GenomeStudio
25 software to re-define SNP cluster calling definitions. A total of 524 SNPs were scored as "failed" and removed from further analyses due to poor SNP clustering that could not be manually corrected.

In addition, SNPs with low call rates (*i.e.*, a low number of genotype calls were generated from a particular SNP test) were
30 scored as "fail" and removed from further analyses. Applying a "call rate" threshold of >85% to the 4,301,331 SNPs tested (*i.e.*, for each SNP, the % of samples for which a genotype was called) resulted in "fails" for 4,384 SNPs, yielding a total of 4,296,423 SNPs available for subsequent analyses (99.89% of variants tested).

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Finally, samples with call rates less than 94% (*i.e.*, samples for which less than 94% of the genotyped SNPs produced genotype calls) were removed. This resulted in the removal of 31 samples with call rates of 49-93%, and resulted in a final cohort of 776 samples for subsequent analyses. Notably, of these 31 excluded samples, 18 (58%) had very low (<1 ng/ul) DNA concentrations and 12 of the other 13 excluded samples had low DNA quality (OD 260/280 ratio <1.8 or >2.0), or low DNA volumes.

For the final 776 samples, the overall median sample genotype call rate was 99.88% (min. 94.26%, max. 99.96%) indicative of high quality genotype data for these samples.

Example 3 Overview of Genetic Analysis

Genotype data was merged with selected clinical data (Responder/Non-Responder status, country, age, gender, ancestry, log of number of relapses in last 2 Years, baseline EDSS score, baseline volume of T2 lesion, number of Gd-T1 lesions at baseline, and years of exposure to treatment). Association and regression analyses were conducted using SVS7 software.

Analyses were conducted using standard association analyses and regression analyses. To maximize the statistical power for high priority variants, the analyses began with focused list of candidate variants (35), then expanded to a larger number of variants in 30 genes, then expanded to variants in 180 candidate genes, and finally expanded to the entire genome-wide analysis.

For each stage of association analyses, results were calculated to identify genetic associations using three genetic models:

1. Allelic Model (chi-square, chi-square -10LogP, fisher exact, fisher exact -10LogP, values for fisher and chi-square with Bonferoni correction, Odds Ratios and Confidence Bounds, Regression P-value, Regression -log10 P, Call Rate (Cases), Call Rate (Controls), Minor Allele Frequency, Allele Freq. (Cases), Allele Freq. (Controls), Major Allele Frequency, Allele Freq. (Cases), Allele Freq. (Controls), Genotype Counts for cases and controls,

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Missing Genotype Counts, Allele Counts for cases and controls).

2. Additive Model (Cochrane-Armitage Trend Test P-value, Exact for
of Cochrane Armitage Trend Test, $-\log_{10}$ P-values, Correlation/Trend
test P-value, Correlation/Trend $-\log_{10}$ P, Call Rate, Call Rate
5 (Cases), Call Rate (Controls), Minor Allele Frequency, Allele Freq.
(Cases), Allele Freq. (Controls)).

3. Genotypic Model (chi-square, chi-square $-\log_{10}$ P, fisher exact,
fisher exact $-\log_{10}$ P, values for fisher and chi-square with
Bonferoni correction, Odds Ratios and Confidence Bounds, Regression
10 P-value, Regression $-\log_{10}$ P, Call Rate (Cases), Call Rate
(Controls), Minor Allele Frequency, Allele Freq. (Cases), Allele
Freq. (Controls), Major Allele Frequency, Allele Freq. (Cases),
Allele Freq. (Controls), Genotype Counts for cases and controls,
Missing Genotype Counts, Allele Counts for Cases and controls).

15 For each stage of regression analyses, results were calculated to
identify genetic associations using an additive genetic model.

Example 4 Stages of Analysis

Stage 1. Discovery Cohort (n = 318: 198 R vs. 120 NR) - In the first
stage of analysis, the discovery cohort (GALA) was analyzed to
20 identify variants associated with good response vs. poor response.

Stage 2. Replication Cohort (n = 262: 201 R vs. 61 NR) - In the
second stage of each analysis, variants selected in the discovery
cohort were analyzed to identify replicating associations in the
FORTE replication cohort associated with good response vs. poor
25 response.

Stage 3. Combined Cohorts (n = 580: 399 R vs. 111 NR) - In the third
stage of the analysis, the combined GALA and FORTE cohorts were
analyzed.

Stage 4. Placebo Cohort (n = 196: 95 R vs. 101 NR) In the fourth
30 stage of the analysis, the placebo cohort (GALA placebo) was
analyzed to identify variants associated with placebo response/non-
response. These results will be used to confirm whether
significantly associated variants are specific to glatiramer acetate

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drug response versus disease severity.

An overview of these analyses is presented in Table A. For each stage a step-wise analysis was performed in order to maximize study power.

5

Table A: Overview of the analyses used to identify genetic markers predictive of response to glatiramer acetate.

	<u>Discovery Cohort</u>	<u>Replication Cohort</u>	<u>Combined Cohorts for Comparative Parameters</u>
Step 1	Candidate SNPs (35) - Additive, Allelic, Genotypic, Regression Candidate SNPs, Extreme - Additive, Allelic, Genotypic, Regression	Candidate SNPs (35) - Additive, Allelic, Genotypic, Regression Candidate SNPs, Extreme - Additive, Allelic, Genotypic, Regression	Candidate SNPs (35) - Additive, Allelic, Genotypic, Regression Candidate SNPs, Extreme - Additive, Allelic, Genotypic, Regression
Step 2	Candidate Genes (30) - Additive, Allelic, Genotypic, Regression Candidate Genes, Extreme - Additive, Allelic, Genotypic, Regression	Candidate Genes (30) - Additive, Allelic, Genotypic, Regression Candidate Genes, Extreme - Additive, Allelic, Genotypic, Regression	Candidate Genes (30) - Additive, Allelic, Genotypic, Regression Candidate Genes, Extreme - Additive, Allelic, Genotypic, Regression
Step 3	Candidate Genes (180) - Additive, Allelic, Genotypic, Regression Candidate Genes, Extreme - Additive, Allelic, Genotypic, Regression	Candidate Genes (180) - Additive, Allelic, Genotypic, Regression Candidate Genes, Extreme - Additive, Allelic, Genotypic, Regression	Candidate Genes (180) - Additive, Allelic, Genotypic, Regression Candidate Genes, Extreme - Additive, Allelic, Genotypic, Regression
Step 4	Genome-wide - Additive, Allelic, Genotypic, Regression + Corrected for ancestry + Corrected for clinical covariates + Corrected for top SNP Genome-wide, Extreme - Additive, Allelic, Genotypic, Regression + Corrected for clinical covariates + Corrected for top SNP	Genome-wide - Additive, Allelic, Genotypic, Regression + Corrected for ancestry + Corrected for clinical covariates + Corrected for top SNP Genome-wide, Extreme - Additive, Allelic, Genotypic, Regression + Corrected for clinical covariates + Corrected for top SNP	Genome-wide - Additive, Allelic, Genotypic, Regression + Corrected for ancestry + Corrected for clinical covariates + Corrected for top SNP Genome-wide, Extreme - Additive, Allelic, Genotypic, Regression + Corrected for clinical covariates + Corrected for top SNP

Example 5 Analysis Part 1 - Analysis of Candidate Variants

10 The initial analysis was limited to 35 genetic variants identified in high priority genes. Power (80%) with Bonferroni statistical correction for multiple testing to identify significant genetic associations with an odds ratio >3, for variants with an allele frequency greater than 10%. (Or rare alleles (2.5%) with an odds ratio >7).

15

Results for Standard Response Definition, Candidate Variants Selected a priori for Additive, Allelic and Genotypic models are presented in tables 2-4, respectively.

Table 2. Additive Model, Candidate Variants (Gala, Forte, and Combined cohorts)

GALA					FORTE					COMBINED				
Source	Name	Ch	Gene		Armitage Odds Ratio (Resp.)	Allele Freq. (Non-Resp.)	P-value	Armitage Odds Ratio (Resp.)	Allele Freq. (Non-Resp.)	Armitage Odds Ratio (Resp.)	Allele Freq. (Non-Resp.)	P-value	Armitage Odds Ratio (Resp.)	Allele Freq. (Non-Resp.)
Top Priority	Tchelet GWAS	rs3135391	6	HLA-DRB1	0.040	17%	0.040	0.66	24%	0.049	23%	0.014	0.70	27%
Top Priority	Tchelet GWAS	rs3135388	6	HLA-DRB1	0.047	17%	0.049	0.64	23%	0.049	23%	0.017	0.70	27%
Top Priority	Tchelet GWAS	rs947603	10	CEP55	0.054	26%	0.16	1.48	19%	0.16	23%	0.027	1.42	18%
Top Priority	Tsareva 2011	rs1800629	6	TNF	0.088	12%	0.65	0.68	17%	0.65	12%	0.09	0.75	16%
Top Priority	Tchelet GWAS	rs4344916	2	AC083939.1	0.32	34%	0.46	1.20	30%	0.46	34%	0.70	1.05	33%
Top Priority	Tchelet GWAS	rs10950359	7	AC074389.1	0.32	29%	0.40	0.85	33%	0.40	25%	0.51	0.91	29%
Top Priority	Tchelet GWAS	rs12256889	10	CYP26C1	0.33	31%	0.064	0.84	35%	0.064	33%	0.77	1.04	31%
Top Priority	Comi	rs974060	7	TAC1	0.34	32%	0.78	1.18	28%	0.78	27%	0.67	1.06	28%
Top Priority	Tchelet GWAS	rs17771939	8	AC016885.1	0.36	29%	0.0032	1.18	26%	0.0032	28%	0.35	0.88	31%
Top Priority	Tsareva 2011	rs6897932	5	IL7Ra	0.39	20%	0.63	0.84	23%	0.63	24%	0.44	0.89	24%
Top Priority	Tchelet GWAS	rs11599624	10	P11-655H13	0.39	15%	0.50	1.23	13%	0.50	11%	0.43	1.17	12%
Top Priority	Comi	rs1558896	7	TAC1	0.40	34%	0.85	1.15	30%	0.85	29%	0.73	1.05	30%
Top Priority	Tchelet GWAS	rs11617134	13	P11-629E24	0.41	5%	0.95	0.76	7%	0.95	7%	0.64	0.89	7%
Top Priority	Tchelet GWAS	rs17575455	2	AC078940.2	0.41	33%	0.0062	0.87	36%	0.0062	31%	0.019	0.73	39%
Top Priority	Grossman 2007	rs946685	1	IL12RB2	0.43	17%	0.22	1.19	15%	0.22	18%	0.17	1.28	14%
Top Priority	Tchelet GWAS	rs4343256	15	CRTC3	0.47	8%	0.71	1.27	6%	0.71	7%	0.72	1.09	7%
Top Priority	Tchelet GWAS	rs6097801	20	CYP24A1	0.47	11%	0.27	0.84	13%	0.27	14%	0.29	0.83	15%
Top Priority	Tchelet GWAS	rs1007328	15	AC012409.1	0.50	48%	0.050	0.89	51%	0.050	47%	0.08	0.80	53%
Top Priority	Tsareva 2011	rs231775	2	CTLA4	0.51	42%	0.59	1.12	39%	0.59	40%	0.46	1.10	41%
Top Priority	Tchelet GWAS	rs9944913	18	NOL4	0.52	10%	0.054	0.84	12%	0.054	9%	0.08	0.71	9%
Top Priority	Tchelet GWAS	rs1573706	20	PTPRT	0.55	17%	0.15	0.88	19%	0.15	17%	0.19	0.80	20%
Top Priority	Grossman 2007	rs1415148	1	CTSS	0.56	39%	0.38	0.90	41%	0.38	41%	0.88	1.02	40%
Top Priority	Tchelet GWAS	rs2487896	10	HPSE2	0.57	14%	0.0006	0.88	16%	0.0006	12%	0.013	0.65	19%
Top Priority	Tchelet GWAS	rs10931091	2	AC074182.1	0.58	11%	0.53	1.17	9%	0.53	7%	0.88	0.97	9%
Top Priority	Comi	rs269976	18	SLC14A2	0.59	8%	0.22	1.18	7%	0.22	8%	0.26	1.32	6%
Top Priority	Grossman 2007	rs2275235	1	CTSS	0.62	34%	0.25	0.91	35%	0.25	37%	0.66	1.06	34%
Top Priority	Tchelet GWAS	rs4369324	10	P11-655H13	0.64	25%	0.25	1.10	23%	0.25	20%	0.49	1.11	22%
Top Priority	Tchelet GWAS	rs4148871	6	TAP2	0.69	21%	0.37	0.93	22%	0.37	23%	0.79	1.04	21%
Top Priority	Grossman 2007	rs2001791	3	CD86	0.74	14%	0.036	1.08	13%	0.036	13%	0.36	0.85	14%
Top Priority	Tchelet GWAS	rs10988087	9	SET	0.77	4%	0.0062	0.89	4%	0.0062	4%	0.065	0.61	7%
Top Priority	Grossman 2007	rs1129055	3	CD86	0.83	26%	0.40	1.04	25%	0.40	30%	0.97	0.99	28%
Top Priority	Tchelet GWAS	rs10853605	18	MEX3C	0.91	43%	0.34	1.02	43%	0.34	44%	0.49	1.09	44%
Top Priority	Comi	rs4890535	18	SLC14A2	0.94	9%	0.46	1.02	9%	0.46	9%	0.66	1.10	9%
Top Priority	Tchelet GWAS	rs2177073	18	DTNA	0.95	11%	0.033	1.02	11%	0.033	10%	0.21	0.79	13%
Top Priority	Tchelet GWAS	rs2521644	7	NPY	0.97	43%	0.64	0.99	43%	0.64	47%	0.67	1.06	44%

Table 3. Allelic Model, Candidate Variants (Gala, Forte, and Combined cohorts)

		GALA										FORTE										COMBINED											
		Odds Ratio					Fisher's					Odds Ratio					Fisher's					Odds Ratio					Fisher's						
		Ratio		Allele		Freq.		(Non-Resp.)		Allele		Freq.		(Non-Resp.)		Ratio		Allele		Freq.		(Non-Resp.)		Ratio		Allele		Freq.		(Non-Resp.)			
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
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		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
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		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
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		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
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		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
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		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
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		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P	
		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele	
		Fisher's		Exact P		Allele		Fisher's		Exact P		Allele		Fisher's		Exact P		Fisher's		Exact P		Allele		F									

Table 4. Genotypic Model, Candidate Variants (Gala, Forte, and Combined cohorts)

GALA				FORTE				COMBINED										
Source	Name	Ch	Gene	Fisher's Exact P	Allele Freq.	Allele Freq. (Non- Resp.)	Fisher's Exact P	Allele Freq.	Allele Freq. (Non- Resp.)	Fisher's Exact P	Allele Freq.	Allele Freq. (Non- Resp.)	DD (Contr ols)	DD (Contr ols)	dd (Contr ols)			
Top Priority	Comi rs1558896	7	TAC1	0.0043	34%	30%	0.36	29%	30%	0.0029	31%	30%	53	11	142	87	203	83
Top Priority	Comi rs974060	7	TAC1	0.040	32%	28%	0.60	27%	29%	0.042	30%	28%	46	11	145	81	208	89
	Previous GWAS rs947603	10	CEP55	0.055	26%	19%	0.43	23%	16%	0.050	24%	18%	22	8	148	50	228	123
	Previous GWAS rs10853605	18	MEX3C	0.11	43%	43%	0.54	44%	39%	0.31	44%	41%	79	27	190	96	130	58
Top Priority	Tchelet GWAS rs3135391	6	HLA-DRB1	0.11	17%	24%	0.0093	23%	32%	0.014	20%	27%	20	10	122	77	257	94
Top Priority	Tsareva 2011 rs1800629	6	TNF	0.13	12%	17%	0.33	12%	14%	0.19	12%	16%	10	6	77	46	310	129
Top Priority	Tchelet GWAS rs3135388	6	HLA-DRB1	0.14	17%	24%	0.0093	23%	32%	0.018	20%	27%	20	10	122	76	257	94
	Previous GWAS rs10950359	7	AC074389.1	0.15	29%	33%	0.54	25%	21%	0.18	27%	29%	39	14	138	77	222	90
	Grossman 2007 rs2001791	3	CD86	0.19	14%	13%	0.052	13%	21%	0.56	14%	16%	11	5	87	47	301	129
	Previous GWAS rs6097801	20	CYP24A1	0.20	11%	13%	0.19	14%	18%	0.042	13%	15%	14	3	72	48	313	130
	Previous GWAS rs10931091	2	AC074182.1	0.26	11%	9%	0.64	7%	9%	0.54	9%	9%	3	3	65	27	331	150
	Previous GWAS rs1007328	15	AC012409.1	0.29	48%	51%	0.10	47%	57%	0.20	48%	53%	88	48	204	96	107	37
	Previous GWAS rs17575455	2	AC078940.2	0.30	33%	36%	0.018	31%	44%	0.055	32%	39%	42	26	170	89	186	66
Top Priority	Comi rs4890535	18	SLC14A2	0.33	9%	9%	0.91	9%	7%	0.37	9%	9%	5	4	65	23	329	154
	Previous GWAS rs1573706	20	PTPRT	0.37	17%	19%	0.33	17%	22%	0.24	17%	20%	7	7	120	58	272	116
	Previous GWAS rs12256889	10	CYP26C1	0.41	31%	35%	0.021	33%	25%	0.75	32%	31%	39	19	178	75	182	87
Top Priority	Grossman 2007 rs1415148	1	CTSS	0.42	39%	41%	0.60	41%	36%	0.99	40%	39%	60	27	195	88	142	66
	Previous GWAS rs4344916	2	AC083939.1	0.51	34%	30%	0.67	34%	33%	0.49	34%	33%	52	18	167	83	179	80
Top Priority	Grossman 2007 rs2275235	1	CTSS	0.54	34%	35%	0.37	37%	31%	0.90	35%	34%	47	19	187	85	164	77
Top Priority	Comi rs269976	18	SLC14A2	0.55	8%	7%	0.47	8%	5%	0.25	8%	6%	3	2	60	19	336	160
	Previous GWAS rs11617134	13	RP11-629E24.2	0.57	5%	7%	0.90	7%	7%	0.82	6%	7%	3	1	41	22	355	158
Top Priority	Grossman 2007 rs946685	1	IL12RB2	0.65	17%	15%	0.47	18%	13%	0.40	18%	14%	10	2	119	48	268	131
Top Priority	Tchelet GWAS rs17771939	8	AC016885.1	0.67	29%	26%	0.0095	28%	43%	0.44	29%	31%	35	22	159	70	205	89
Top Priority	Tsareva 2011 rs6897932	5	IL7Ra	0.68	20%	23%	0.39	24%	26%	0.62	22%	24%	21	13	135	62	242	106
Top Priority	Tchelet GWAS rs4148871	6	TAP2	0.69	21%	22%	0.73	23%	19%	0.66	22%	21%	18	10	137	56	244	115
	Previous GWAS rs2487896	10	HPSE2	0.71	14%	16%	0.0019	12%	25%	0.049	13%	19%	6	6	92	55	301	119
	Previous GWAS rs11599624	10	RP11-655H13.1	0.72	15%	13%	0.44	11%	9%	0.69	13%	12%	7	3	92	36	300	142
	Previous GWAS rs2177073	18	DTNA	0.77	11%	11%	0.053	10%	17%	0.23	11%	13%	4	5	77	38	317	138
	Grossman 2007 rs1129055	3	CD86	0.78	26%	25%	0.61	30%	34%	0.67	28%	28%	33	12	158	78	208	91
Top Priority	Tsareva 2011 rs231775	2	CTLA4	0.81	42%	39%	0.32	40%	37%	0.77	41%	38%	68	28	189	83	142	70
	Previous GWAS rs10988087	9	SET	0.83	4%	4%	0.015	4%	11%	0.15	4%	7%	1	1	31	22	367	156
	Previous GWAS rs4343256	15	CRTC3	0.84	8%	6%	0.69	7%	8%	0.93	8%	7%	1	0	58	25	340	155
Top Priority	Tchelet GWAS rs9944913	18	NOL4	0.84	10%	12%	0.073	9%	15%	0.14	9%	13%	2	3	71	40	326	138
	Previous GWAS rs4369324	10	RP11-655H13.2	0.86	25%	23%	0.29	20%	15%	0.82	22%	20%	23	9	132	56	244	116
Top Priority	Tchelet GWAS rs2521644	7	NPY	1.00	43%	43%	0.83	47%	44%	0.76	45%	44%	83	33	193	92	123	56

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In some embodiments genetic markers presented in Tables 2, 3 and 4 are identified as predictive of response to glatiramer acetate if the p-value for the GALA cohort is less than about 0.12, less than about 0.08, less than about 0.05, less than about 0.01 or less than
5 about 0.005.

In some embodiments genetic markers presented in Tables 2, 3 and 4 are identified as predictive of response to glatiramer acetate if the p-value for the FORTE cohort is less than about 0.12, less than about 0.08, less than about 0.05, less than about 0.01, less than
10 about 0.005 or less than about 0.001.

In some embodiments genetic markers presented in Tables 2, 3 and 4 are identified as predictive of response to glatiramer acetate if the p-value for the Combined cohort is less than about 0.12, less than about 0.08, less than about 0.05, less than about 0.01, less
15 than about 0.005 or less than about 0.001.

Example 6 Analysis Part 2 - Analysis of Candidate Genes (30)

The second analysis was limited to a selected set of genetic variants in 30 priority candidate genes (4,012 variants). Power (80%) to identify significant genetic associations with an odds
20 ratio >4, for variants with an allele frequency greater than 10%. (Or rare alleles (5%) with an odds ratio >6).

Results for Standard Response Definition, Top 30 Candidate Genes Selected a priori for Additive, Allelic and Genotypic models are presented in tables 5-7, respectively.

25 In some embodiments genetic markers presented in Tables 5, 6 and 7 are identified as predictive of response to glatiramer acetate if the p-value for the GALA cohort is less than about 0.05, less than about 0.01 or less than about 0.005.

In some embodiments genetic markers presented in Tables 5, 6 and 7
30 are identified as predictive of response to glatiramer acetate if the p-value for the FORTE cohort is less than about 0.10, less than about 0.05, less than about 0.01, less than about 0.005 or less than about 0.001.

[illegible]

Table 5b. Additive Model, Analysis of Candidate Genes (30) – replicated p<0.05 (Gala, Forte, and Combined cohorts)

GALA										FORTE										COMBINED									
Name	Ch	Gene	Armitage P-value	Odds Ratio	Allele Freq. (Resp.)	Allele Freq. (Non-Resp.)	Armitage P-value	Odds Ratio	Allele Freq. (Resp.)	Allele Freq. (Non-Resp.)	Armitage P-value	Odds Ratio	Allele Freq. (Resp.)	Allele Freq. (Non-Resp.)	Armitage P-value	Odds Ratio	Allele Freq. (Resp.)	Allele Freq. (Non-Resp.)	Armitage P-value	Odds Ratio	DD (Case/ols)	DD (Contr/ols)	Dd (Case/ols)	Dd (Contr/ols)	dd (Case/ols)	dd (Contr/ols)			
rs1894407	6	HLA-DOB/TAP2	0.002	1.77	42%	30%	0.02	1.72	40%	29%	0.00011	1.73	41%	30%	0.00011	1.73	41%	30%	0.00011	1.73	57	16	213	75	128	90			
rs1894406	6	HLA-DOB/TAP2	0.003	1.74	40%	29%	0.02	1.76	36%	25%	0.00027	1.68	38%	27%	0.00027	1.68	38%	27%	0.00027	1.68	51	13	202	73	146	95			
rs1894408	6	HLA-DOB/TAP2	0.003	1.72	42%	31%	0.01	1.82	41%	28%	0.00010	1.73	41%	30%	0.00010	1.73	41%	30%	0.00010	1.73	58	16	211	74	127	89			
rs2857103	6	TAP2	0.006	1.70	37%	27%	0.00	2.04	36%	22%	0.00011	1.78	36%	25%	0.00011	1.78	36%	25%	0.00011	1.78	39	11	211	69	149	100			
kgp10224254	6	HLA-DOB	0.006	1.63	42%	32%	0.04	1.58	39%	29%	0.00115	1.56	40%	31%	0.00115	1.56	40%	31%	0.00115	1.56	59	18	205	75	135	88			
rs241451	6	TAP2	0.006	1.69	37%	27%	0.01	1.86	35%	23%	0.00026	1.72	36%	26%	0.00026	1.72	36%	26%	0.00026	1.72	39	12	207	68	150	100			
rs9501224	6	TAP2	0.007	1.69	37%	27%	0.00	2.04	36%	22%	0.00013	1.77	36%	25%	0.00013	1.77	36%	25%	0.00013	1.77	39	11	211	70	149	100			
rs2071469	6	HLA-DOB	0.007	1.62	43%	32%	0.04	1.58	39%	29%	0.00140	1.55	41%	31%	0.00140	1.55	41%	31%	0.00140	1.55	59	18	205	76	134	87			
rs241443	6	TAP2	0.011	1.63	37%	27%	0.01	2.01	35%	22%	0.00030	1.71	36%	25%	0.00030	1.71	36%	25%	0.00030	1.71	40	11	202	69	152	99			
rs2621323	6	HLA-DOB/TAP2	0.019	1.56	37%	29%	0.00	2.07	36%	22%	0.00033	1.69	37%	26%	0.00033	1.69	37%	26%	0.00033	1.69	43	12	207	71	149	97			
rs241456	6	TAP2	0.021	1.55	31%	23%	0.01	2.00	30%	18%	0.00086	1.66	31%	21%	0.00086	1.66	31%	21%	0.00086	1.66	32	9	180	59	187	113			
rs2621321	6	HLA-DOB/TAP2	0.024	1.54	32%	23%	0.01	2.05	30%	18%	0.00090	1.66	31%	22%	0.00090	1.66	31%	22%	0.00090	1.66	31	9	183	60	184	112			
rs2857104	6	TAP2	0.024	1.54	32%	23%	0.01	2.03	30%	18%	0.00099	1.65	31%	22%	0.00099	1.65	31%	22%	0.00099	1.65	31	9	183	60	185	112			
rs2857101	6	TAP2	0.025	1.53	31%	23%	0.01	2.00	30%	18%	0.00115	1.64	30%	21%	0.00115	1.64	30%	21%	0.00115	1.64	31	9	181	59	187	112			
rs241446	6	TAP2	0.025	1.53	31%	23%	0.01	1.96	30%	18%	0.00126	1.63	30%	21%	0.00126	1.63	30%	21%	0.00126	1.63	32	9	176	59	188	113			
rs241454	6	TAP2	0.026	1.53	31%	23%	0.01	2.02	30%	18%	0.00102	1.65	31%	22%	0.00102	1.65	31%	22%	0.00102	1.65	32	9	180	60	185	112			
kgp974569	6	TAP2	0.028	1.52	31%	23%	0.01	2.02	30%	18%	0.00112	1.64	31%	22%	0.00112	1.64	31%	22%	0.00112	1.64	32	9	180	60	186	112			
rs241447	6	TAP2	0.028	1.52	31%	23%	0.01	2.01	30%	18%	0.00111	1.64	31%	22%	0.00111	1.64	31%	22%	0.00111	1.64	32	9	180	60	184	111			
rs241444	6	TAP2	0.028	1.52	31%	23%	0.01	2.00	30%	18%	0.00122	1.63	31%	22%	0.00122	1.63	31%	22%	0.00122	1.63	32	9	180	60	187	112			
rs2071472	6	HLA-DOB	0.029	1.49	35%	27%	0.02	1.79	33%	22%	0.00221	1.56	34%	25%	0.00221	1.56	34%	25%	0.00221	1.56	40	12	191	67	168	102			
rs2071470	6	HLA-DOB	0.029	1.49	35%	27%	0.02	1.79	33%	22%	0.00221	1.56	34%	25%	0.00221	1.56	34%	25%	0.00221	1.56	40	12	191	67	168	102			
rs241449	6	TAP2	0.033	1.50	31%	23%	0.01	1.99	30%	18%	0.00135	1.63	30%	21%	0.00135	1.63	30%	21%	0.00135	1.63	32	9	175	58	188	112			
rs241452	6	TAP2	0.033	1.50	31%	24%	0.01	2.01	30%	18%	0.00142	1.62	31%	22%	0.00142	1.62	31%	22%	0.00142	1.62	32	9	179	60	186	111			
rs241453	6	TAP2	0.034	1.50	31%	23%	0.01	2.02	30%	18%	0.00131	1.63	31%	22%	0.00131	1.63	31%	22%	0.00131	1.63	32	9	179	60	187	112			
rs241440	6	TAP2	0.034	1.50	31%	23%	0.01	1.96	30%	18%	0.00179	1.61	30%	22%	0.00179	1.61	30%	22%	0.00179	1.61	32	9	177	60	189	112			
kgp8036704	6	TAP2	0.035	1.50	31%	23%	0.01	2.02	30%	18%	0.00155	1.63	30%	22%	0.00155	1.63	30%	22%	0.00155	1.63	29	9	183	60	186	112			
kgp7747883	18	MBP	0.036	0.70	35%	43%	0.01	0.57	33%	45%	0.00086	0.64	34%	44%	0.00086	0.64	34%	44%	0.00086	0.64	43	33	181	92	174	56			
rs241445	6	TAP2	0.036	1.49	31%	24%	0.01	2.00	30%	18%	0.00156	1.62	31%	22%	0.00156	1.62	31%	22%	0.00156	1.62	32	9	179	60	187	111			
P1_M_061510	6	TAP2	0.037	1.49	31%	23%	0.01	2.02	30%	18%	0.00141	1.62	30%	22%	0.00141	1.62	30%	22%	0.00141	1.62	32	9	178	60	187	112			
rs241442	6	TAP2	0.039	1.48	31%	24%	0.01	2.02	30%	18%	0.00156	1.62	31%	22%	0.00156	1.62	31%	22%	0.00156	1.62	32	9	179	60	187	111			
kgp2388352	6	TAP2	0.042	1.47	31%	24%	0.01	2.02	30%	18%	0.00146	1.62	31%	22%	0.00146	1.62	31%	22%	0.00146	1.62	34	10	173	57	185	111			
kgp25543811	18	MBP	0.048	0.15	0%	2%	0.01	0.10	0%	2%	0.00229	0.12	0%	2%	0.00229	0.12	0%	2%	0.00229	0.12	0	0	2	7	397	173			
kgp4346717	18	MBP	0.049	0.15	0%	2%	0.01	?	0%	2%	0.00174	0.07	0%	2%	0.00174	0.07	0%	2%	0.00174	0.07	0	0	1	6	398	175			
kgp3182607	6	PSMB9	0.049	0.15	0%	2%	0.02	0.23	1%	4%	0.00685	0.24	1%	2%	0.00685	0.24	1%	2%	0.00685	0.24	0	0	5	9	394	172			
rs241435	6	TAP2	0.049	0.15	0%	2%	0.02	0.23	1%	4%	0.00685	0.24	1%	2%	0.00685	0.24	1%	2%	0.00685	0.24	0	0	5	9	394	172			
kgp26271158	6	PSMB9	0.049	0.15	0%	2%	0.04	0.29	1%	4%	0.01475	0.29	1%	2%	0.01475	0.29	1%	2%	0.01475	0.29	0	0	6	9	393	172			

Table 6. Allelic Model, Analysis of Candidate Genes (30) (Gala, Forte, and Combined cohorts)

GALA										FORTE										COMBINED									
Gene Locations																													
Name	Ch	Gene(s)	Mutation (s)	Fisher's Exact P	Odds Ratio (Minor Allele)	Allele Freq. (Cases)	Allele Freq. (Controls)	Fisher's Exact P	Odds Ratio (Minor Allele)	Allele Freq. (Cases)	Allele Freq. (Controls)	Fisher's Exact P	Odds Ratio (Minor Allele)	Allele Freq. (Cases)	Allele Freq. (Controls)	Fisher's Exact P	Odds Ratio (Minor Allele)	Allele Freq. (Cases)	Allele Freq. (Controls)	DD (s)	DD (ols)	Dd (s)	Dd (ols)	dd (s)	dd (ols)	Contr (Case)	Contr (Case)	Contr (Case)	Contr (Case)
kgp11795	6	?	?	0.003	2.10	20%	11%	0.248	1.49	16%	11%	0.0022	1.80	18%	11%	0.0022	1.80	18%	11%	16	3	111	33	271	144				
kgp51108	17	CCL5	Silent	0.003	0.00	0%	3%	1.000	?	0%	0%	0.0046	0.07	0%	2%	0.0046	0.07	0%	2%	0	0	1	6	398	175				
rs1894407	6	?	?	0.003	1.68	42%	30%	0.0247	1.67	40%	29%	0.0002	1.66	41%	30%	0.0002	1.66	41%	30%	57	16	213	75	128	90				
kgp89008	6	?	?	0.003	2.00	20%	11%	0.248	1.47	16%	11%	0.0033	1.73	18%	11%	0.0033	1.73	18%	11%	16	3	112	35	270	143				
kgp64748	6	TNF	Silent	0.003	2.00	20%	11%	0.307	1.44	16%	12%	0.0042	1.72	18%	11%	0.0042	1.72	18%	11%	16	3	112	35	270	142				
rs1894406	6	?	?	0.004	1.66	40%	29%	0.0212	1.73	36%	25%	0.0004	1.63	38%	27%	0.0004	1.63	38%	27%	51	13	202	73	146	95				
rs909253	6	LTA,LTA	Silent,Sile	0.004	0.59	25%	36%	0.816	0.95	27%	28%	0.0112	0.70	26%	33%	0.0112	0.70	26%	33%	30	19	146	83	220	79				
rs1894408	6	?	?	0.005	1.64	42%	31%	0.0105	1.78	41%	28%	0.0002	1.67	41%	30%	0.0002	1.67	41%	30%	58	16	211	74	127	89				
kgp93199	3	CCR5,CCR5	Silent,Sile	0.005	1.60	48%	37%	0.895	1.06	45%	43%	0.0182	1.36	47%	39%	0.0182	1.36	47%	39%	84	30	203	82	110	69				
kgp92969	3	?	?	0.005	1.66	37%	26%	0.514	1.16	35%	31%	0.0086	1.44	36%	28%	0.0086	1.44	36%	28%	53	16	178	68	167	96				
kgp41867	6	LTA,LTA	Missense	0.005	0.60	25%	36%	0.816	0.94	27%	28%	0.0136	0.71	26%	33%	0.0136	0.71	26%	33%	30	19	147	82	222	80				
kgp71788	18	SLC14A2	Silent	0.006	0.21	1%	5%	0.471	3.07	3%	1%	0.13	0.52	2%	3%	0.13	0.52	2%	3%	1	1	12	10	384	169				
kgp92969	10	?	?	0.006	0.21	1%	5%	0.267	2.53	4%	2%	0.34	0.70	3%	4%	0.34	0.70	3%	4%	0	0	20	13	376	168				
kgp12106	18	MBP,MBP	Silent,Sile	0.006	0.50	9%	16%	0.089	0.54	7%	12%	0.0004	0.49	8%	15%	0.0004	0.49	8%	15%	4	7	54	39	334	132				
kgp61377	3	CCR5,CCR5	Silent,Sile	0.007	1.58	48%	37%	0.917	1.04	45%	41%	0.0255	1.34	47%	40%	0.0255	1.34	47%	40%	85	30	201	83	111	68				
kgp10224	6	?	?	0.007	1.59	42%	32%	0.053	1.56	39%	29%	0.0013	1.54	40%	31%	0.0013	1.54	40%	31%	59	18	205	75	135	88				
kgp58541	18	NOL4,NOL4,f	Silent,Sile	0.008	0.15	1%	3%	1.000	1.33	3%	2%	0.28	0.61	2%	3%	0.28	0.61	2%	3%	0	0	15	11	383	170				
kgp10991	3	CCR5,CCR5	Silent,Sile	0.008	1.58	48%	37%	0.755	1.07	45%	43%	0.0208	1.35	47%	39%	0.0208	1.35	47%	39%	85	30	194	81	110	68				
kgp93942	18	MBP,MBP	Silent,Sile	0.009	?	3%	0%	0.725	0.81	2%	2%	0.10	2.92	2%	1%	0.10	2.92	2%	1%	1	0	17	3	379	177				
kgp12268	3	?	?	0.009	0.24	1%	5%	0.487	0.60	2%	3%	0.0075	0.36	2%	4%	0.0075	0.36	2%	4%	0	0	13	16	386	165				
kgp26488	6	TAP1	Silent	0.009	0.24	1%	5%	1.000	1.83	1%	1%	0.0235	0.38	1%	4%	0.0235	0.38	1%	4%	0	0	11	13	388	168				
kgp51629	3	CCR5,CCR5	Silent,Sile	0.009	1.60	37%	27%	0.385	1.24	35%	30%	0.0087	1.45	36%	28%	0.0087	1.45	36%	28%	54	17	177	67	166	97				
kgp52492	3	CCR5,CCR5	Silent,Sile	0.009	1.61	37%	27%	0.384	1.22	35%	30%	0.0087	1.44	36%	28%	0.0087	1.44	36%	28%	54	17	177	67	167	97				
kgp72120	3	CCR5,CCR5	Silent,Sile	0.009	1.61	37%	27%	0.384	1.22	35%	30%	0.0087	1.44	36%	28%	0.0087	1.44	36%	28%	54	17	177	67	167	97				
kgp42098	3	?	?	0.009	1.61	37%	27%	0.584	1.14	35%	32%	0.0153	1.40	36%	28%	0.0153	1.40	36%	28%	53	17	178	68	167	95				
rs2071469	6	HLA-DOB	Silent	0.009	1.57	43%	32%	0.053	1.56	39%	29%	0.0017	1.52	41%	31%	0.0017	1.52	41%	31%	59	18	205	76	134	87				
rs241451	6	TAP2,TAP2	Silent,Sile	0.011	1.58	37%	27%	0.0144	1.80	35%	23%	0.0004	1.64	36%	26%	0.0004	1.64	36%	26%	39	12	207	68	150	100				
rs2857103	6	TAP2	Silent	0.011	1.59	37%	27%	0.0057	1.94	36%	22%	0.0003	1.68	36%	25%	0.0003	1.68	36%	25%	39	11	211	69	149	100				
kgp10626	18	NOL4,NOL4,f	Silent,Sile	0.011	1.73	24%	15%	0.793	1.11	20%	18%	0.0326	1.43	22%	16%	0.0326	1.43	22%	16%	17	9	140	41	242	131				
rs9501224	6	TAP2	Silent	0.012	1.57	37%	27%	0.0057	1.94	36%	22%	0.0003	1.67	36%	25%	0.0003	1.67	36%	25%	39	11	211	70	149	100				
kgp44902	6	?	?	0.013	0.29	2%	5%	1.000	1.83	1%	1%	0.0291	0.41	2%	4%	0.0291	0.41	2%	4%	0	0	12	13	387	168				
kgp58475	4	IL15,IL15,IL1,f	Silent,Sile	0.014	0.10	0%	3%	1.000	1.53	1%	1%	0.13	0.39	1%	2%	0.13	0.39	1%	2%	0	0	6	7	390	174				
kgp35097	18	NOL4,NOL4,f	Silent,Sile	0.014	0.39	3%	8%	0.127	3.14	5%	2%	0.23	0.70	4%	6%	0.23	0.70	4%	6%	1	1	31	19	367	161				
rs3733904	5	ERAP2,ERAP2	Silent,Sile	0.016	1.61	30%	21%	0.176	1.45	24%	18%	0.0102	1.49	27%	20%	0.0102	1.49	27%	20%	37	4	141	64	221	113				
kgp28530	18	SLC14A2	Silent	0.016	?	2%	0%	1.000	1.22	2%	2%	0.08	3.92	2%	1%	0.08	3.92	2%	1%	0	0	17	2	382	179				

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Table 7b. Genotypic Model, Analysis of Candidate Genes (30) - replicated p<0.05 (Gala, Forte, and Combined cohorts)

GALA			FORTE			COMBINED											
Columns	Ch	Positio	Fisher's Exact	Allele Freq. (Case)	Allele Freq. (Controls)	Fisher's Exact	Allele Freq. (Case)	Allele Freq. (Controls)	Fisher's Exact	Allele Freq. (Case)	Allele Freq. (Controls)	DD (Case)	DD (Control Is)	Dd (Case)	Dd (Control Is)	dd (Case)	dd (Control Is)
rs1894407	6	32787036	0.001	0.42	0.30	0.045	0.40	0.29	0.0002	0.41	0.30	57	16	213	75	128	90
rs2857103	6	32791299	0.004	0.37	0.27	0.017	0.36	0.22	0.0002	0.36	0.25	39	11	211	69	149	100
rs1894408	6	32786833	0.001	0.42	0.31	0.026	0.41	0.28	0.0002	0.41	0.30	58	16	211	74	127	89
rs9501224	6	32792910	0.005	0.37	0.27	0.017	0.36	0.22	0.0003	0.36	0.25	39	11	211	70	149	100
rs241451	6	32796480	0.004	0.37	0.27	0.043	0.35	0.23	0.0004	0.36	0.26	39	12	207	68	150	100
rs241443	6	32797115	0.012	0.37	0.27	0.021	0.35	0.22	0.0008	0.36	0.25	40	11	202	69	152	99
rs2621323	6	32788707	0.013	0.37	0.29	0.012	0.36	0.22	0.0009	0.37	0.26	43	12	207	71	149	97
rs1894406	6	32787056	0.003	0.40	0.29	0.040	0.36	0.25	0.0010	0.38	0.27	51	13	202	73	146	95
rs2621321	6	32789480	0.032	0.32	0.23	0.029	0.30	0.18	0.0023	0.31	0.22	31	9	183	60	184	112
rs241456	6	32795965	0.029	0.31	0.23	0.035	0.30	0.18	0.0023	0.31	0.21	32	9	180	59	187	113
rs2857104	6	32790167	0.032	0.32	0.23	0.031	0.30	0.18	0.0025	0.31	0.22	31	9	183	60	185	112
rs2857101	6	32794676	0.032	0.31	0.23	0.034	0.30	0.18	0.0029	0.30	0.21	31	9	181	59	187	112
rs241454	6	32796144	0.037	0.31	0.23	0.029	0.30	0.18	0.0029	0.31	0.22	32	9	180	60	185	112
kgp974569	6	32796057	0.043	0.31	0.23	0.029	0.30	0.18	0.0032	0.31	0.22	32	9	180	60	186	112
rs241447	6	32796751	0.043	0.31	0.23	0.035	0.30	0.18	0.0032	0.31	0.22	32	9	180	60	184	111
rs241444	6	32797109	0.043	0.31	0.23	0.035	0.30	0.18	0.0034	0.31	0.22	32	9	180	60	187	112
kgp8036704	6	32796521	0.042	0.31	0.23	0.038	0.30	0.18	0.0034	0.30	0.22	29	9	183	60	186	112
kgp2388352	6	32797297	0.037	0.31	0.24	0.025	0.30	0.18	0.0036	0.31	0.22	34	10	173	57	185	111
rs241446	6	32796967	0.036	0.31	0.23	0.040	0.30	0.18	0.0037	0.30	0.21	32	9	176	59	188	113
rs241449	6	32796653	0.047	0.31	0.23	0.037	0.30	0.18	0.0038	0.30	0.21	32	9	175	58	188	112
rs241452	6	32796346	0.047	0.31	0.24	0.034	0.30	0.18	0.0040	0.31	0.22	32	9	179	60	186	111

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In some embodiments genetic markers presented in Tables 5, 6 and 7 are identified as predictive of response to glatiramer acetate if the p-value for the Combined cohort is less than about 0.05, less than about 0.01, less than about 0.005, less than about 0.001, less than about 0.0005 or less than about 10^{-4} .

Example 7 Analysis Part 3 - Analysis of Candidate Genes (180)

The third analysis was limited to a selected set of genetic variants in 180 priority candidate genes (25,461 variants).

Results for Standard Response Definition, 180 Candidate Genes Selected a priori for Additive, Allelic and Genotypic models are presented in tables 8-10, respectively.

In some embodiments genetic markers presented in Tables 8, 9 and 10 are identified as predictive of response to glatiramer acetate if the p-value for the GALA cohort is less than about 0.05, less than about 0.01, less than about 0.005, less than about 0.001, less than about 0.0005 or less than about 10^{-4} .

In some embodiments genetic markers presented in Tables 8, 9 and 10 are identified as predictive of response to glatiramer acetate if the p-value for the FORTE cohort is less than about 0.05, less than about 0.01 or less than about 0.005.

In some embodiments genetic markers presented in Tables 8, 9 and 10 are identified as predictive of response to glatiramer acetate if the p-value for the Combined cohort is less than about 0.05, less than about 0.01, less than about 0.005, less than about 0.001, less than about 0.0005 or less than about 10^{-4} .

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Table 8. Additive Model, Analysis of Candidate Genes (180) (Gala, Forte, and Combined cohorts)

Name	Ch	Positio	Gene(s)	Mutati	Gene	GALA		FORTE		Combined		DD		Dd		dd	
						Armitage	Regression	Armitage	Regression	Armitage	Regression	DD	(Controls	DD	(Controls	dd	(Controls
						p	Odd's Ratio	p	Odd's Ratio	p	Odd's Ratio	(Cases)	%	(Cases)	%	(Cases)	%
rs1894407	6	32787036	?	?	?	0.001752	1.6	0.018124	1.7	0.000106	1.7	57	16	213	75	128	90
rs1894406	6	32787056	?	?	?	0.002628	1.7	0.017319	1.8	0.000266	1.7	51	13	202	73	146	95
rs1894408	6	32786833	?	?	?	0.003022	1.7	0.0093	1.8	9.82E-05	1.7	58	16	211	74	127	89
kgp6599438	20	40848626	PTFR1,PTF	Silent,Site	INTRON	0.003702	0.2	0.015514	0.3	0.000248	0.3	0	0	11	18	386	163
kgp293787	20	40905098	PTFR1,PTF	Silent,Site	INTRON	0.004862	0.2	0.021866	0.4	0.002548	0.4	0	2	15	15	384	164
rs2857103	6	32791299	TAP2	Silent	INTRON	0.005722	1.7	0.004127	2.0	0.000113	1.8	39	11	211	69	149	100
kgp10224254	6	32785904	?	?	?	0.005947	1.6	0.04442	1.6	0.001151	1.6	59	18	205	75	135	88
rs241451	6	32796480	TAP2,TAP	Silent,Site	INTRON	0.006256	1.7	0.011254	1.9	0.000258	1.7	39	12	207	68	150	100
rs9501224	6	32792910	TAP2	Silent	INTRON	0.006526	1.7	0.004127	2.0	0.000132	1.8	39	11	211	70	149	100
rs2071469	6	32784783	HLA-DOB	Silent	UTR	0.00676	1.6	0.04442	1.6	0.001396	1.6	59	18	205	76	134	87
rs10162089	13	31316738	ALOX5AP	Silent,Site	INTRON	0.007794	1.6	0.031551	1.6	0.001396	1.5	96	24	190	88	110	67
rs241443	6	32797115	TAP2,TAP	Silent,Site	INTRON,E	0.010544	1.6	0.005279	2.0	0.000302	1.7	40	11	202	69	152	99
rs3218328	22	37524008	IL2RB	Silent	UTR	0.010948	0.2	0.013938	0.1	0.000296	0.1	0	0	3	10	395	169
kgp5334779	6	32628420	HLA-DQB1	Silent,Site	INTRON	0.016802	1.5	0.027424	1.7	0.001874	1.6	50	10	199	83	148	87
kgp10632945	20	4682507	?	?	?	0.018738	0.6	0.034771	0.6	0.001254	0.6	10	11	118	70	270	100
rs2621323	6	32788707	?	?	?	0.018977	1.6	0.003089	2.1	0.000333	1.7	43	12	207	71	149	97
rs1410779	9	5083173	JAK2	Silent	INTRON	0.019287	0.6	0.012868	0.5	0.001732	0.6	8	10	112	66	277	105
kgp4479467	6	32629331	HLA-DQB1	Silent,Site	INTRON	0.020268	1.5	0.015944	1.8	0.00125	1.6	54	11	195	82	147	88
rs241456	6	32795965	TAP2,TAP	Silent,Site	INTRON	0.021233	1.6	0.008542	2.0	0.000863	1.7	32	9	180	59	187	113
rs2621321	6	32789480	?	?	?	0.02375	1.5	0.007193	2.0	0.0009	1.7	31	9	183	60	184	112
rs2857104	6	32790167	TAP2	Silent	INTRON	0.02375	1.5	0.007888	2.0	0.000987	1.7	31	9	183	60	185	112
rs2857101	6	32794676	TAP2,TAP	Silent,Site	INTRON	0.024806	1.5	0.009327	2.0	0.001148	1.6	31	9	181	59	187	112
rs241446	6	32796967	TAP2,TAP	Silent,Site	INTRON,E	0.024864	1.5	0.01086	2.0	0.001258	1.6	32	9	176	59	188	113
kgp4898179	6	32629347	HLA-DQB1	Silent,Site	INTRON	0.025265	1.5	0.018682	1.8	0.001906	1.6	54	11	195	83	148	87
rs241454	6	32796144	TAP2,TAP	Silent,Site	INTRON	0.025652	1.5	0.007804	2.0	0.001019	1.6	32	9	180	60	185	112
kgp9699754	10	79358319	KONM1A1	Silent,Site	INTRON	0.026989	?	0.041077	?	0.001744	~Infinity	0	0	21	0	377	179
kgp974569	6	32796057	TAP2,TAP	Silent,Site	INTRON	0.02648	1.5	0.007804	2.0	0.001117	1.6	32	9	180	60	186	112
rs241447	6	32796751	TAP2,TAP	Silent,Mi	INTRON,E	0.02848	1.5	0.008343	2.0	0.001108	1.6	32	9	180	60	184	111
rs241444	6	32797109	TAP2,TAP	Silent,Site	INTRON,E	0.02848	1.5	0.008542	2.0	0.001222	1.6	32	9	180	60	187	112

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Name	Ch	Positio	% Mutati	(s)	p	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio	Armitage	% Odds Ratio

Table 9. Allelic Model, Analysis of Candidate Genes (180) (Gala, Forte, and Combined cohorts)

GALA										FORTE				COMBINED													
Gene										Odds Ratio				Odds Ratio				Odds Ratio									
Locations										Fisher's (Minor Allele %)				Fisher's (Minor Allele %)				Fisher's (Minor Allele %)									
Mutati										Exact				Exact				Exact									
Gene(s)										Allele %				Allele %				Allele %									
Positio										Ratio				Ratio				Ratio									
Allele										Case %				Case %				Case %									
Frequency										Frequency				Frequency				Frequency									
DD										DD				DD				DD									
dd										dd				dd				dd									
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Name	Chromos	Gene	Locations	Gene(s)	Mutatio	(s)	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	Fisher's	Ratio	Odds	F

Table 10. Genotypic Model, Analysis of Candidate Genes (180) (Gala, Forte, and Combined cohorts)

			GALA												FORTE												COMBINED											
Columns	Ch	Positic	Exact	DD	DD	Dd	Dd	dd	dd	Fisher's	DD	DD	DD	DD	Dd	Dd	dd	dd	Fisher's	DD	DD	DD	DD	Dd	Dd	dd	dd											
				(Cases	(Contr	(Cases	(Contr	(Cases	(Contr	Exact	(Cases	(Contr	(Cases	(Contr	(Cases	(Contr	(Cases	(Contr	Exact	(Cases	(Contr	(Cases	(Contr	(Cases	(Contr	(Cases	(Contr											
rs1894407	6	32787036	0.0006	26	13	114	46	58	61	0.0447	31	3	99	29	70	29	0.0002	57	16	0.0002	57	16	213	75	128	90												
rs1894408	6	32786833	0.0011	26	13	113	46	58	59	0.0258	32	3	98	28	69	30	0.0002	58	16	0.0002	58	16	211	74	127	89												
rs1894406	6	32787056	0.0031	25	11	109	47	64	62	0.0398	26	2	93	26	82	33	0.0010	51	13	0.0010	51	13	202	73	146	95												
rs2857103	6	32791299	0.0038	17	9	112	46	69	64	0.0171	22	2	99	23	80	36	0.0002	39	11	0.0002	39	11	211	69	149	100												
rs241451	6	32796480	0.0045	17	9	110	46	70	65	0.0429	22	3	97	22	80	35	0.0004	39	12	0.0004	39	12	207	68	150	100												
rs9501224	6	32792910	0.0047	17	9	112	47	69	64	0.0171	22	2	99	23	80	36	0.0003	39	11	0.0003	39	11	211	70	149	100												
kgp6599438	20	40843626	0.0054	0	0	4	11	193	109	0.0235	0	0	7	7	193	54	0.0007	0	0	0.0007	0	0	11	18	386	163												
rs241443	6	32797115	0.0115	18	9	107	47	70	63	0.0208	22	2	95	22	82	36	0.0008	40	11	0.0008	40	11	202	69	152	99												
kgp293787	20	40905098	0.0124	0	1	2	7	196	112	0.0340	0	1	13	8	188	52	0.0059	0	2	0.0059	0	2	15	15	384	164												
rs2621323	6	32788707	0.0134	18	10	111	48	69	61	0.0122	25	2	96	23	80	36	0.0009	43	12	0.0009	43	12	207	71	149	97												
rs3218328	22	37524008	0.0153	0	0	2	7	196	111	0.0409	0	0	1	3	199	58	0.0008	0	0	0.0008	0	0	3	10	395	169												
kgp9699754	10	79358319	0.0275	0	0	8	0	190	118	0.0430	0	0	13	0	187	61	0.0005	0	0	0.0005	0	0	21	0	377	179												
rs241456	6	32795965	0.0287	16	8	92	39	90	73	0.0346	16	1	88	20	97	40	0.0023	32	9	0.0023	32	9	180	59	187	113												
rs2621321	6	32789480	0.0321	16	8	93	40	89	72	0.0291	15	1	90	20	95	40	0.0023	31	9	0.0023	31	9	183	60	184	112												
rs2857104	6	32790167	0.0321	16	8	93	40	89	72	0.0309	15	1	90	20	96	40	0.0025	31	9	0.0025	31	9	183	60	185	112												
rs2857101	6	32794676	0.0321	16	8	92	39	90	72	0.0340	15	1	89	20	97	40	0.0029	31	9	0.0029	31	9	181	59	187	112												
rs241446	6	32796967	0.0364	16	8	90	39	90	73	0.0399	16	1	86	20	98	40	0.0037	32	9	0.0037	32	9	176	59	188	113												
kgp2388352	6	32797297	0.0367	16	9	88	37	89	71	0.0254	18	1	85	20	96	40	0.0036	34	10	0.0036	34	10	173	57	185	111												
rs241454	6	32796144	0.0374	16	8	92	40	89	72	0.0291	16	1	88	20	96	40	0.0029	32	9	0.0029	32	9	180	60	185	112												
kgp11976832	2	29990267	0.0410	2	2	21	4	174	114	0.0394	1	0	21	1	176	60	0.0019	3	2	0.0019	3	2	42	5	350	174												
kgp8036704	6	32796521	0.0422	15	8	92	40	90	72	0.0377	14	1	91	20	96	40	0.0034	29	9	0.0034	29	9	183	60	186	112												
kgp974569	6	32796057	0.0427	16	8	92	40	90	72	0.0291	16	1	88	20	96	40	0.0032	32	9	0.0032	32	9	180	60	186	112												
rs241447	6	32796751	0.0427	16	8	92	40	90	72	0.0347	16	1	88	20	94	39	0.0032	32	9	0.0032	32	9	180	60	184	111												
rs241444	6	32797109	0.0427	16	8	92	40	90	72	0.0346	16	1	88	20	97	40	0.0034	32	9	0.0034	32	9	180	60	187	112												
kgp4470107	7	18205779	0.0446	30	8	63	48	105	64	0.0063	26	5	75	37	100	19	0.0048	56	13	0.0048	56	13	138	85	205	83												
rs241452	6	32796346	0.0469	16	8	92	40	90	71	0.0337	16	1	87	20	96	40	0.0040	32	9	0.0040	32	9	179	60	186	111												
rs241449	6	32796653	0.0472	16	8	88	38	91	72	0.0365	16	1	87	20	97	40	0.0038	32	9	0.0038	32	9	175	58	188	112												
kgp4934352	20	15669073	0.0476	2	5	40	33	155	82	0.0099	1	3	51	8	148	50	0.0160	3	8	0.0160	3	8	91	41	303	132												

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Example 8 Analysis Part 4 - Genome Wide Analysis

A full genome-wide analysis was then conducted (4 M variants). Power (80%) with Bonferroni statistical correction to identify significant genetic associations with an odds ratio >7 , for variants with an allele frequency greater than 10%. (Or rare alleles (5%) with an odds ratio >11). Approximately 4,200 variants were selected for analysis in stage 2 (replication) ($P < 0.001$).

Replication Cohort ($n = 262$: 201 R vs. 61 NR) - In the second stage of analysis, variants selected in the discovery cohort were analyzed to identify replicating associations in the FORTE replication cohort associated with good response vs. poor response. Based upon an analysis of an estimated 4,200 variants, there is statistical power (80%) with Bonferroni correction to identify significant genetic associations with an odds ratio >6.5 , for variants with an allele frequency greater than 5%.

Combined Cohorts ($n = 580$: 399 R vs. 111 NR) - In the third stage of the analysis, the combined GALA and FORTE cohorts were analyzed identify variants associated with response/non-response using a full genome-wide analysis (4 M variants).

Results for Standard Response Definition, Genome Wide Analysis for Additive, Allelic and Genotypic models are presented in tables 11-13, respectively.

In some embodiments genetic markers presented in Tables 11, 12 and 13 are identified as predictive of response to glatiramer acetate if the p-value for the GALA cohort is less than about 0.001, less than about 0.0005, less than about 10^{-4} or less than about $5 * 10^{-5}$.

In some embodiments genetic markers presented in Tables 11, 12 and 13 are identified as predictive of response to glatiramer acetate if the p-value for the FORTE cohort is less than about 0.05, less than about 0.01, less than about 0.005, less than about 0.001 or less than about 0.0005.

Table 11. Additive Model, Genome Wide Analysis, p-value sorted by GALA cohort (Gala, Forte, and Combined cohorts)

GALA										FORTE										COMBINED									
Gene		Locations		Gene(s)		Position		Mutati		Regre		Allele		Regres		Allele		Regressi		Allele		Allele							
										ssion	Armitage	Odds	Case	Freq.	Freq.	ssion	Armitage	Odds	Case	Freq.	Freq.	on Odds	Case	Freq.	Contro	Case	Cont	Case	Cont
Name	Cl	Cl	Position	Gene(s)	Mutati	(s)	P	Armitage	Ratio	P	Armitage	Odds	Case	Freq.	P	Armitage	Ratio	P	Armitage	Odds	Case	Freq.	Contro	Case	Cont	Case	Cont	Case	Cont
kgp541056	1	65738507	DNAIC6	Silent		INTRON	2.75E-05	0.44	0.18	0.33	3.24E-02	1.79	0.26	0.16		4.67E-02	0.75	0.22	0.27	15	15	146	69	238	97				
rs9817308	3	124182136	KALRN,KA	Silent,Sile		INTRON	2.85E-05	0.49	0.41	0.58	2.64E-02	0.62	0.45	0.57		5.18E-06	0.55	0.43	0.57	71	55	199	96	127	29				
rs1749972	1	65736258	DNAIC6	Silent		INTRON	3.00E-05	0.44	0.19	0.33	3.93E-02	1.76	0.26	0.17		4.33E-02	0.74	0.22	0.28	15	15	146	68	237	95				
kgp24415534	2	174156875	?	?		?	3.40E-05	0.05	0.00	0.05	1.10E-02	0.14	0.00	0.03		3.98E-07	0.08	0.00	0.04	0	0	3	16	396	165				
kgp10594414	1	216039833	USH2A	Silent		INTRON	3.57E-05	0.05	0.00	0.05	1.25E-02	0.24	0.01	0.05		2.44E-06	0.14	0.01	0.05	0	0	6	18	391	163				
rs10841337	12	19897179	?	?		?	4.26E-05	0.47	0.22	0.37	4.27E-02	0.64	0.27	0.36		1.56E-05	0.55	0.24	0.36	22	24	147	84	227	73				
rs543122	3	124164156	KALRN,KA	Silent,Sile		INTRON	4.73E-05	0.50	0.41	0.57	1.39E-02	0.59	0.44	0.57		3.17E-06	0.54	0.42	0.57	70	54	195	97	131	29				
kgp4705854	12	19907696	?	?		?	5.01E-05	0.51	0.30	0.47	2.87E-02	0.63	0.33	0.43		4.80E-06	0.55	0.31	0.46	41	38	169	89	189	54				
kgp8192546	12	19903173	?	?		?	6.52E-05	0.47	0.21	0.36	2.64E-02	0.62	0.26	0.36		1.29E-05	0.55	0.24	0.36	21	23	146	84	232	74				
kgp12008955	2	73759636	ALMS1	Silent		INTRON	9.26E-05	?	0.00	0.04	3.65E-04	0.12	0.01	0.06		3.98E-07	0.08	0.00	0.04	0	0	3	16	396	165				
kgp5564995	6	26414060	BTN3A1,B	Silent,Sile		UTR,EXON	1.56E-04	3.35	0.15	0.06	3.98E-02	2.30	0.14	0.07		2.28E-05	2.88	0.14	0.06	1	0	109	21	274	151				
kgp1699628	6	18032535	?	?		?	1.73E-04	0.51	0.44	0.58	2.99E-02	0.63	0.47	0.58		2.72E-05	0.57	0.45	0.58	72	62	218	85	109	32				
kgp1009249	12	19838534	?	?		?	1.74E-04	0.48	0.18	0.31	1.03E-02	0.54	0.21	0.32		9.55E-06	0.51	0.20	0.31	10	16	136	80	253	84				
rs9579566	13	30980265	?	?		?	2.08E-04	0.23	0.02	0.08	9.90E-03	0.30	0.02	0.07		4.19E-06	0.26	0.02	0.08	0	1	18	27	381	153				
kgp26026546	13	79972606	RBM26	Silent		INTRON	2.20E-04	?	0.00	0.03	4.46E-04	0.06	0.00	0.04		4.46E-07	0.03	0.00	0.04	0	0	1	13	397	167				
rs17577980	6	32359821	HCG23	Silent		INTRON	2.33E-04	2.36	0.23	0.11	5.31E-03	2.94	0.16	0.07		1.66E-05	2.36	0.20	0.09	13	5	130	23	255	150				
kgp9288015	6	28194629	ZNF193,Zf	Silent,Sile		INTRON	2.71E-04	0.48	0.14	0.26	3.92E-02	0.61	0.22	0.30		1.76E-04	0.57	0.18	0.28	13	11	117	78	267	92				
kgp10619195	4	99417717	TSPAN5	Silent		INTRON	2.87E-04	0.29	0.04	0.10	3.30E-02	0.46	0.05	0.10		3.54E-05	0.36	0.04	0.10	0	2	32	33	366	146				
kgp6022882	6	28197186	ZNF193,Zf	Silent,Sile		INTRON	3.03E-04	0.48	0.14	0.26	3.95E-02	0.61	0.22	0.30		1.99E-04	0.57	0.18	0.28	13	11	118	78	267	92				
rs1579771	3	15727882	C3orf55,C	Silent,Sile		INTRON	3.35E-04	2.02	0.38	0.25	1.64E-02	1.81	0.36	0.25		1.96E-05	1.91	0.37	0.25	39	9	213	71	146	101				
kgp8474976	6	32407906	HLA-DRA	Silent		INTRON	3.66E-04	2.72	0.17	0.08	4.16E-02	2.35	0.12	0.06		1.64E-04	2.39	0.15	0.07	3	0	111	26	285	155				
kgp6127371	4	153856357	?	?		?	3.69E-04	0.18	0.01	0.06	9.38E-03	0.28	0.02	0.07		1.23E-05	0.23	0.02	0.06	0	0	13	23	384	157				
kgp11210903	22	30898906	SEC14L4,S	Silent,Sile		INTRON	3.70E-04	0.10	0.01	0.05	4.98E-02	0.19	0.00	0.02		1.48E-05	0.12	0.01	0.04	0	0	4	14	395	167				
kgp5869992	12	49219569	CACNB3,C	Silent,Sile		INTRON	3.71E-04	0.57	0.39	0.54	2.00E-02	0.62	0.38	0.50		1.13E-05	0.58	0.38	0.53	60	58	184	74	152	48				
rs6535882	4	153848128	?	?		?	3.83E-04	0.18	0.01	0.06	9.06E-03	0.27	0.02	0.07		1.24E-05	0.23	0.02	0.06	0	0	13	23	386	158				
kgp6700691	4	153849531	?	?		?	3.83E-04	0.18	0.01	0.06	9.06E-03	0.27	0.02	0.07		1.24E-05	0.23	0.02	0.06	0	0	13	23	386	158				
kgp2356388	16	19771577	IQCK	Silent		INTRON	3.88E-04	0.43	0.12	0.22	1.94E-03	0.45	0.14	0.26		5.78E-06	0.46	0.13	0.23	4	5	98	75	297	101				
kgp3933330	7	28583709	CREB5,CRI	Silent,Sile		INTRON	4.00E-04	2.42	0.20	0.09	3.21E-02	2.15	0.16	0.08		6.67E-05	2.26	0.18	0.09	15	1	111	29	271	151				
kgp4559907	6	133255252	?	?		?	4.08E-04	0.56	0.31	0.45	3.11E-02	0.63	0.35	0.46		6.02E-05	0.60	0.33	0.46	46	37	171	91	180	53				
rs10456405	6	32212867	?	?		?	4.24E-04	1.94	0.33	0.19	4.00E-02	1.80	0.22	0.13		2.89E-04	1.75	0.27	0.17	35	11	144	38	212	129				
kgp4127859	6	324344481	?	?		?	4.49E-04	2.42	0.20	0.10	1.43E-02	2.53	0.16	0.07		5.43E-05	2.32	0.18	0.09	8	0	127	33	263	148				
rs11022778	11	13390860	ARNTL,AR	Silent,Sile		INTRON	4.49E-04	1.96	0.34	0.20	4.87E-02	1.58	0.37	0.27		2.37E-05	1.86	0.35	0.23	52	5	176	72	171	104				
rs1508102	11	116379889	?	?		?	4.99E-04	0.34	0.04	0.12	4.52E-02	0.50	0.06	0.11		9.87E-05	0.42	0.05	0.12	0	4	41	34	357	143				
kgp4223880	2	10584122	ODC1	Silent		INTRON	4.99E-04	0.06	0.00	0.04	3.23E-02	0.22	0.01	0.03		4.19E-05	0.13	0.01	0.04	0	0	4	13	394	167				
kgp9627338	17	90155	RP34L,R	Silent,Sile		INTRON	5.01E-04	0.47	0.10	0.21	3.13E-03	0.43	0.11	0.20		3.52E-06	0.45	0.10	0.21	6	7	71	61	320	113				
kgp2446153	5	152980439	GRIA1,GRI	Silent,Sile		INTRON	5.31E-04	0.06	0.00	0.04	3.17E-02	0.22	0.01	0.03		4.35E-05	0.13	0.01	0.04	0	0	4	13	395	168				
kgp1786079	7	144701118	?	?		?	5.35E-04	0.48	0.11	0.21	9.86E-03	0.49	0.13	0.22		2.09E-05	0.49	0.12	0.22	4	11	86	56	308	114				
rs19191155	16	19800213	IQCK	Missense		EXON	5.38E-04	0.44	0.12	0.22	1.93E-03	0.45	0.14	0.26		7.89E-06	0.46	0.13	0.23	4	5	97	74	295	101				
rs9931167	16	19792598	IQCK	Silent		INTRON	5.38E-04	0.44	0.12	0.22	1.94E-03	0.45	0.14	0.26		8.07E-06	0.46	0.13	0.23	4	5	98	74	297	101				
rs3829539	16	19722366	C16orf88	Silent		INTRON	5.38E-04	0.44	0.12	0.22	2.10E-03	0.45	0.15	0.26		8.80E-06	0.47	0.13	0.23	4	5	98	74	296	101				
kgp1584138	9	124827130	TTL11,Tf	Silent,Sile		INTRON	0.000545	0.24	0.02	0.08	3.99E-02	0.45	0.03	0.08		1.47E-04	0.35	0.03	0.08	1	1	20	26	378	154				

Table 11b. Additive Model, Genome Wide Analysis, p-value sorted by Combined cohort (Gala, Forte, and Combined cohorts)

GALA										FORTE										COMBINED									
Gene					Regre ssion					Allele					Regre ssion					Allele									
Locations					Armitage Odds					Allele Freq.					Armitage Odds					Allele Freq.									
Name	Cl	Position	Gene(s)	Mutatio. (s)	P	Ratio	Case	Contro. (s)	Allele	Ratio	Case	Contro. (s)	Allele	Armitage	Ratio	Case	Contro. (s)	Allele	Armitage	Ratio	Case	Contro. (s)	Allele						
kgp24415534	2	174156875	?	?	3.40E-05	0.05	0.00	0.05	1.10E-02	0.14	0.00	0.03	3.98E-07	0.08	0.00	0.04	0	0	3	16	396	165							
kgp12008955	2	73759636	ALMS1	Silent	9.26E-05	?	0.00	0.04	3.65E-04	0.12	0.01	0.06	3.98E-07	0.08	0.00	0.04	0	0	3	16	396	165							
kgp26026546	13	79972606	RBM26	Silent	2.20E-04	?	0.00	0.03	4.46E-04	0.06	0.00	0.04	4.46E-07	0.03	0.00	0.04	0	0	1	13	397	167							
rs16886004	7	78021500	MAG12	Silent	2.28E-03	2.15	0.20	0.11	3.25E-05	5.56	0.20	0.05	9.81E-07	2.79	0.20	0.09	6	2	147	28	246	149							
kgp25952891	13	80027089	?	?	5.58E-04	?	0.00	0.03	4.30E-04	0.06	0.00	0.04	1.41E-06	0.04	0.00	0.03	0	0	1	12	398	168							
kgp3450875	16	57268931	RSPRY1	Silent	6.63E-03	0.19	0.01	0.04	1.51E-05	0.07	0.00	0.07	1.99E-06	0.12	0.01	0.05	0	0	5	17	394	164							
rs10251797	7	78025427	MAG12	Silent	3.18E-03	2.07	0.20	0.11	4.05E-05	5.49	0.19	0.05	2.21E-06	2.67	0.20	0.09	6	2	145	29	248	150							
kgp2299675	20	16933074	?	?	4.43E-03	0.26	0.02	0.05	4.23E-05	0.13	0.01	0.08	2.28E-06	0.19	0.01	0.06	0	0	11	23	388	158							
kgp10594414	1	216039833	USH2A	Silent	3.57E-05	0.05	0.00	0.05	1.25E-02	0.34	0.01	0.05	2.44E-06	0.14	0.01	0.05	0	0	6	18	391	163							
kgp1688752	21	43016736	?	?	8.83E-04	0.34	0.05	0.11	1.48E-03	0.33	0.03	0.13	2.53E-06	0.33	0.04	0.11	1	2	30	37	368	142							
kgp12230354	5	27037978	CDH9	Silent	3.70E-03	0.21	0.01	0.05	3.31E-05	0.14	0.02	0.09	2.74E-06	0.19	0.01	0.06	0	0	10	22	386	159							
rs543122	3	124164156	KALRN, KA	Silent,Sile	4.73E-05	0.50	0.41	0.57	1.39E-02	0.59	0.44	0.57	3.17E-06	0.54	0.42	0.57	70	54	195	97	131	29							
kgp6236949	2	60301030	?	?	6.37E-04	0.56	0.31	0.44	7.57E-03	0.55	0.26	0.39	3.26E-06	0.54	0.28	0.42	30	34	166	85	203	62							
kgp9627338	17	90155	RPH3AL, R	Silent,Sile	5.01E-04	0.47	0.10	0.21	3.13E-03	0.43	0.11	0.20	3.52E-06	0.45	0.10	0.21	6	7	71	61	320	113							
kgp11141512	20	35283733	NDRG3, N	Silent,Sile	3.33E-03	0.30	0.02	0.07	3.65E-04	0.12	0.01	0.06	4.12E-06	0.21	0.01	0.06	0	1	11	21	388	158							
rs9579566	13	30980265	?	?	2.08E-04	0.23	0.02	0.08	9.90E-03	0.30	0.02	0.07	4.19E-06	0.26	0.02	0.08	0	1	18	27	381	153							
rs2816838	10	52714759	?	?	1.94E-03	0.51	0.14	0.23	1.80E-03	0.42	0.11	0.22	4.79E-06	0.46	0.13	0.23	4	8	92	67	303	106							
kgp4705854	12	19907696	?	?	5.01E-05	0.51	0.30	0.47	2.87E-02	0.63	0.33	0.43	4.80E-06	0.55	0.31	0.46	41	38	169	89	189	54							
rs9817308	3	124182136	KALRN, KA	Silent,Sile	2.85E-05	0.49	0.41	0.58	2.64E-02	0.62	0.45	0.57	5.18E-06	0.55	0.43	0.57	71	55	199	96	127	29							
kgp8817856	6	32744440	?	?	6.02E-04	0.53	0.36	0.49	3.73E-04	0.46	0.12	0.60	5.33E-06	0.53	0.39	0.53	50	44	208	103	135	34							
kgp6214351	11	75546691	UVRAG	Silent	3.98E-03	0.42	0.05	0.11	2.65E-04	0.26	0.04	0.13	5.51E-06	0.35	0.05	0.12	0	2	37	39	361	140							
kgp2356388	16	19771577	IQCK	Silent	3.88E-04	0.43	0.12	0.22	1.94E-03	0.45	0.14	0.26	5.78E-06	0.46	0.13	0.23	4	5	98	75	297	101							
kgp7416024	9	21453902	?	?	2.14E-03	0.13	0.01	0.04	3.81E-04	0.12	0.01	0.06	6.06E-06	0.13	0.01	0.04	0	0	5	16	393	165							
rs6718758	2	60328802	?	?	5.70E-03	0.63	0.33	0.45	5.96E-04	0.47	0.28	0.44	6.08E-06	0.55	0.31	0.44	35	38	175	85	189	58							
rs7579987	2	60307009	?	?	6.99E-03	0.64	0.36	0.47	3.91E-04	0.45	0.31	0.48	6.43E-06	0.55	0.33	0.47	40	41	184	87	175	52							
rs7217872	17	88988	RPH3AL, R	Silent,Sile	1.03E-03	0.49	0.11	0.20	2.42E-03	0.42	0.11	0.21	7.50E-06	0.47	0.11	0.21	6	7	74	61	319	113							
rs13394010	2	60302746	?	?	7.74E-03	0.64	0.35	0.46	3.91E-04	0.45	0.31	0.48	7.81E-06	0.56	0.33	0.47	39	41	185	86	175	53							
rs7191155	16	19800213	IQCK	Missense	5.38E-04	0.44	0.12	0.22	1.93E-03	0.45	0.14	0.26	7.89E-06	0.46	0.13	0.23	4	5	97	74	295	101							
rs9931167	16	19792598	IQCK	Silent	5.38E-04	0.44	0.12	0.22	1.94E-03	0.45	0.14	0.26	8.07E-06	0.46	0.13	0.23	4	5	98	74	297	101							
rs11691553	2	60303554	?	?	8.54E-03	0.65	0.35	0.46	3.72E-04	0.45	0.31	0.48	8.19E-06	0.56	0.33	0.47	39	41	183	86	174	53							
rs11648129	16	19820694	IQCK	Silent	6.54E-04	0.45	0.12	0.22	1.64E-03	0.44	0.14	0.26	8.23E-06	0.47	0.13	0.23	4	5	97	74	297	102							
kgp25216186	1	23758427	ASAP3,AS	Silent,Sile	1.32E-03	0.07	0.00	0.03	2.45E-03	0.07	0.00	0.03	8.36E-06	0.07	0.00	0.03	0	0	2	12	397	169							
kgp29794723	10	18397332	?	?	4.77E-03	0.31	0.02	0.07	3.54E-04	0.18	0.02	0.08	8.64E-06	0.25	0.02	0.07	0	0	16	26	382	155							
rs3829539	16	19722366	C16orf88	Silent	5.38E-04	0.44	0.12	0.22	2.10E-03	0.45	0.15	0.26	8.80E-06	0.47	0.13	0.23	4	5	98	74	296	101							
rs6895094	5	141037277	ARAP3	Silent	6.58E-04	0.56	0.38	0.52	1.19E-02	0.60	0.35	0.48	9.24E-06	0.57	0.37	0.51	56	46	181	92	161	43							
kgp1009249	12	19838534	?	?	1.74E-04	0.48	0.18	0.31	1.03E-02	0.54	0.21	0.32	9.55E-06	0.51	0.20	0.31	10	16	136	80	253	84							
rs10203396	2	60305110	?	?	8.67E-03	0.65	0.36	0.46	4.43E-04	0.46	0.31	0.48	9.72E-06	0.56	0.33	0.47	39	41	186	87	173	53							
kgp3854180	16	19721806	C16orf88	Silent	6.54E-04	0.45	0.12	0.22	1.94E-03	0.45	0.14	0.26	1.00E-05	0.47	0.13	0.23	4	5	98	74	297	102							
rs6497396	16	19735697	IQCK	Silent	1.30E-03	0.48	0.13	0.23	7.65E-04	0.43	0.16	0.29	1.02E-05	0.48	0.14	0.25	6	6	102	77	290	98							
rs8055485	16	19750051	IQCK	Silent	6.54E-04	0.45	0.12	0.22	2.10E-03	0.45	0.15	0.26	1.09E-05	0.47	0.13	0.23	4	5	98	74	296	102							
rs9931211	16	19813605	IQCK	Silent	6.54E-04	0.45	0.12	0.22	2.10E-03	0.45	0.15	0.26	1.09E-05	0.47	0.13	0.23	4	5	98	74	296	102							

SUBSTITUTE SHEET (RULE 26)

Table 12b. Allelic Model, Genome Wide Analysis, p-value sorted by Combined cohort (Gala, Forte, and Combined cohorts)

GALA										FORTE										Combined												
Gene Locations					Fisher's (Minor Odds Ratio)					Fisher's (Minor Odds Ratio)					Fisher's (Minor Odds Ratio)					Fisher's (Minor Odds Ratio)												
Name	Chr	Positio	Gene(s)	Mutati	(s)	Exact P	Odds Ratio	Fisher's (Exact P)	Odds Ratio	Exact P	Odds Ratio	Fisher's (Exact P)	Odds Ratio	Exact P	Odds Ratio	Fisher's (Exact P)	Odds Ratio	Exact P	Odds Ratio	Exact P	Odds Ratio	Exact P	Odds Ratio	Exact P	Odds Ratio	Exact P	Odds Ratio	Exact P	Odds Ratio	Exact P	Odds Ratio	
kgp20478926	8	21050249	?	?		1.80E-04	0.23	5.60E-04	0.25	6.56E-07	0.26	5	15	14	8	377	156															
rs16886004	7	78021500	MAGI2	Silent	INTRON,E	3.92E-03	2.01	3.71E-05	4.80	1.41E-06	2.53	6	2	147	28	246	149															
kgp26026546	13	79972606	RBM26	Silent	INTRON	3.66E-04	0.00	3.19E-03	0.06	2.24E-06	0.03	0	0	1	13	397	167															
kgp24415534	2	1.74E+08	?	?		6.03E-05	0.05	2.85E-02	0.15	2.28E-06	0.08	0	0	3	16	396	165															
kgp12008955	2	73759636	ALMS1	Silent	INTRON	1.41E-04	0.00	2.03E-03	0.12	2.28E-06	0.08	0	0	3	16	396	165															
kgp12125601	5	1.52E+08	?	?		2.80E-03	1.77	3.73E-03	1.92	2.86E-06	1.95	136	35	35	17	219	122															
rs10251797	7	78025427	MAGI2	Silent	INTRON,E	4.27E-03	1.97	5.87E-05	4.05	3.32E-06	2.44	6	2	145	29	248	150															
kgp22793211	X	92601576	?	?		3.96E-04	0.55	3.25E-03	0.54	3.81E-06	0.55	93	65	126	65	177	50															
kgp6236949	2	60301030	?	?		6.28E-04	0.56	1.19E-02	0.56	4.07E-06	0.54	30	34	166	85	203	62															
rs543122	3	1.24E+08	KALRN, KA	Silent,Sile	INTRON	7.67E-05	0.51	1.70E-02	0.60	4.37E-06	0.55	70	54	195	97	131	29															
kgp24743841	1	63899572	ALG6	Silent	INTRON	9.49E-04	2.85	6.85E-03	2.70	4.63E-06	2.88	48	8	20	4	326	165															
kgp4705854	12	19907696	?	?		4.32E-05	0.50	3.06E-02	0.63	4.85E-06	0.45	41	38	169	89	189	54															
kgp9627338	17	90155	RPH3AL,R	Silent,Sile	INTRON	4.17E-04	0.44	5.38E-03	0.46	5.09E-06	0.45	6	7	71	61	320	113															
kgp1688752	21	43016736	?	?		2.14E-03	0.38	1.85E-03	0.23	5.78E-06	0.33	1	2	30	37	368	142															
kgp5869992	12	49219569	CACNB3,C	Silent,Sile	INTRON	2.02E-04	0.54	2.03E-02	0.61	6.60E-06	0.56	60	58	184	74	152	48															
rs17577980	6	32359821	HCG23	Silent	INTRON	1.11E-04	2.50	6.83E-03	2.75	6.67E-06	2.39	13	5	130	23	255	150															
kgp25952891	13	80027089	?	?		9.94E-04	0.00	3.13E-03	0.06	6.71E-06	0.04	0	0	1	12	398	168															
kgp8110667	22	32716792	?	?		4.71E-03	?	6.16E-03	?	7.05E-06	?	1	0	30	0	367	181															
kgp11210241	3	38537237	?	?		2.62E-03	?	1.03E-02	?	7.12E-06	?	1	0	30	0	368	181															
rs17687961	22	32716927	?	?		4.71E-03	?	6.20E-03	?	7.12E-06	?	1	0	30	0	368	181															
rs12013377	X	92620062	?	?		1.35E-03	0.59	2.51E-03	0.53	7.90E-06	0.56	97	66	129	66	173	49															
rs7579987	2	60307009	?	?		7.27E-03	0.63	7.35E-04	0.49	7.90E-06	0.56	40	41	184	87	175	52															
rs6718758	2	60328802	?	?		5.30E-03	0.62	1.23E-03	0.49	8.06E-06	0.55	35	38	175	85	189	58															
rs9817308	3	1.24E+08	KALRN, KA	Silent,Sile	INTRON	3.87E-05	0.50	3.01E-02	0.63	8.10E-06	0.56	71	55	199	96	127	29															
kgp22804809	X	92585610	?	?		1.10E-02	1.54	5.12E-05	1.39	8.38E-06	1.79	139	38	132	59	127	84															
rs6895094	5	1.41E+08	ARAP3	Silent	INTRON	9.49E-04	0.57	1.07E-02	0.53	8.54E-06	0.56	56	46	181	92	161	43															
kgp3450875	16	57268931	RSPRY1	Silent	INTRON	1.25E-02	0.20	2.10E-04	0.07	9.56E-06	0.13	0	0	5	17	394	164															
rs11691553	2	60303554	?	?		9.11E-03	0.64	7.16E-04	0.48	1.02E-05	0.56	39	41	183	86	174	53															
rs13394010	2	60302746	?	?		7.30E-03	0.64	7.35E-04	0.49	1.04E-05	0.56	39	41	185	86	175	53															
rs2139612	X	92614918	?	?		1.79E-03	0.59	3.37E-03	0.54	1.04E-05	0.57	96	65	129	67	173	49															
kgp11328629	10	1.21E+08	?	?		3.11E-03	2.49	1.97E-03	3.81	1.10E-05	2.86	6	0	97	19	295	162															
kgp10594414	1	2.16E+08	USH2A	Silent	INTRON	6.25E-05	0.05	2.37E-02	0.24	1.11E-05	0.15	0	0	6	18	391	163															
kgp11141512	20	35283733	NDRG3,N	Silent,Sile	INTRON	4.28E-03	0.29	2.03E-03	0.12	1.19E-05	0.20	0	1	11	21	388	158															
rs2816838	10	52714759	?	?		3.47E-03	0.53	3.94E-03	0.44	1.23E-05	0.48	4	8	92	67	303	106															
kgp2299675	20	16933074	?	?		7.25E-03	0.27	3.48E-04	0.14	1.24E-05	0.21	0	0	11	23	388	158															
rs6618396	X	89549121	?	?		5.45E-04	0.41	4.87E-02	0.46	1.30E-05	0.39	8	13	32	25	357	143															
rs7217872	17	88988	RPH3AL,R	Silent,Sile	INTRON	9.84E-04	0.46	5.73E-03	0.45	1.39E-05	0.46	6	7	74	61	319	113															
rs9579566	13	30980265	?	?		2.52E-04	0.23	2.24E-02	0.32	1.45E-05	0.26	0	1	18	27	381	153															
rs10203396	2	60305110	?	?		9.47E-03	0.64	1.05E-03	0.49	1.46E-05	0.57	39	41	186	87	173	53															
rs13419758	2	60302920	?	?		9.47E-03	0.64	1.07E-03	0.49	1.48E-05	0.57	40	41	185	87	174	53															
kgp22730987	X	68448739	?	?		1.75E-04	2.65	4.14E-02	2.06	1.50E-05	2.39	30	3	79	24	280	153															
kgp9320791	2	60309952	?	?		9.47E-03	0.64	1.09E-03	0.50	1.52E-05	0.57	39	41	187	87	172	53															
kgp2784875	10	1.25E+08	?	?		1.55E-04	2.07	4.05E-02	1.64	1.52E-05	1.90	94	20	90	40	174	100															
kgp6507761	7	319681	?	?		8.80E-03	0.64	1.70E-03	0.51	1.53E-05	0.57	78	61	185	83	135	37															
kgp6214351	11	75546691	UVRAG	Silent	INTRON	4.74E-03	0.42	1.08E-03	0.28	1.60E-05	0.36	0	2	37	39	361	140															
kgp12230354	5	27037978	CDH9	Silent	INTRON	5.97E-03	0.21	2.69E-04	0.15	1.65E-05	0.20	0	0	10	22	386	159															

Table 13. Genotypic Model, Genome Wide Analysis, p-value sorted by GALA cohort (Gala, Forte, and Combined cohorts)

GALA										FORTE										COMBINED										
Gene Locations										Fisher's										Fisher's										
Name	Chr	Positio	Gene(s)	Mutatio	(s)	DD	DD	Dd	dd	Exact P	(s)	Cont	Case	Cont	Case	Cont	Case	Cont	Case	Exact P	(s)	Cont	Case	Cont	Case	Cont	Case	Cont	Case	
rs1325607	1	65751060	DNAJC6	Silent	INTRON	3.2E-05	3	13	64	52	131	55	2.4E-02	10	2	85	15	105	44	3.8E-02	13	15	149	67	236	99				
kgp12418f	14	95359055	?	?	?	3.4E-05	2	7	60	14	136	98	1.4E-02	3	1	43	24	155	36	4.1E-02	5	8	103	38	291	134				
kgp96625f	7	76454387	?	?	?	3.6E-05	32	3	88	44	77	67	7.3E-03	29	5	85	40	80	16	1.6E-03	57	8	173	84	166	83				
kgp43802f	14	80642167	?	?	?	3.9E-05	22	12	64	69	111	39	4.2E-02	20	1	76	31	103	29	5.0E-05	42	13	140	100	213	68				
kgp24415f	2	1.74E+08	?	?	?	5.1E-05	0	0	1	12	197	108	2.8E-02	0	0	2	4	199	57	1.9E-06	0	0	3	16	396	165				
kgp10594f	1	2.16E+08	USH2A	Silent	INTRON	5.3E-05	0	0	1	12	196	108	2.2E-02	0	0	5	6	195	55	8.9E-06	0	0	6	18	391	163				
kgp54472f	3	1.92E+08	FGF12	Silent	INTRON	6.7E-05	2	0	49	9	147	111	3.6E-02	2	3	43	7	156	51	5.1E-05	4	3	92	16	303	162				
rs2906681	7	21777119	DNAH11	Silent	INTRON	7.5E-05	27	35	110	39	61	46	2.7E-02	17	13	104	29	80	19	5.0E-06	44	48	214	68	141	65				
rs1757798	6	32359821	HCG23	Silent	INTRON	9.4E-05	11	4	68	17	118	97	1.6E-03	2	1	62	6	137	53	9.1E-07	13	5	130	23	255	150				
rs9275653	6	32685865	?	?	?	1.0E-04	13	28	99	47	86	44	3.7E-02	31	14	97	35	73	13	6.2E-04	44	42	196	82	159	56				
kgp42459f	3	1.73E+08	?	?	?	1.2E-04	43	6	97	68	58	46	3.2E-02	37	4	105	42	56	15	9.7E-06	80	10	202	110	114	61				
kgp12008f	2	73759636	ALMS1	Silent	INTRON	1.3E-04	0	0	0	9	198	111	1.8E-03	0	0	3	7	198	54	1.9E-06	0	0	3	16	396	165				
kgp76468f	2	73234432	SFXN5	Silent	INTRON	1.5E-04	2	0	49	10	146	110	2.5E-02	0	1	38	5	162	55	6.7E-05	2	1	87	15	308	165				
rs6471541	8	96528845	LOC10061	Silent,Sile	INTRON,E	1.5E-04	11	3	50	57	137	59	4.6E-02	13	2	68	12	119	47	4.9E-02	24	5	118	69	256	106				
rs9817308	3	1.24E+08	KALRN,KA	Silent,Sile	INTRON	1.5E-04	30	38	100	61	67	20	4.8E-02	41	17	99	35	60	9	2.2E-05	71	55	199	96	127	29				
kgp94700f	2	33764717	RASGRP3	Silent,Sile	INTRON	2.1E-04	14	2	88	33	96	85	2.4E-02	7	6	79	13	114	40	8.2E-04	21	8	167	48	210	125				
rs543122	3	1.24E+08	KALRN,KA	Silent,Sile	INTRON	2.3E-04	31	37	99	62	68	20	2.2E-02	39	17	96	35	63	9	1.1E-05	70	54	195	97	131	29				
kgp20932f	14	83364889	?	?	?	2.6E-04	30	21	101	34	67	64	2.3E-02	37	4	97	40	67	17	3.4E-02	67	25	198	74	134	81				
kgp36695f	2	34593996	?	?	?	2.7E-04	8	5	40	49	150	66	2.4E-02	9	2	46	25	143	34	1.2E-05	17	7	86	74	293	100				
rs1112437	2	34594367	?	?	?	3.3E-04	7	4	39	48	152	68	3.1E-02	8	1	45	24	146	36	2.2E-05	15	5	84	72	298	104				
kgp26026f	13	79972606	RBM26	Silent	INTRON	3.4E-04	0	0	0	8	198	111	3.0E-03	0	0	1	3	199	56	1.9E-06	0	0	1	13	397	167				
kgp93561f	5	15539360	FBXL7	Silent	INTRON	3.5E-04	3	6	66	18	129	96	1.2E-02	1	4	59	13	141	43	2.1E-05	4	10	125	31	270	139				
kgp15936f	2	33760276	RASGRP3	Silent,Sile	INTRON	4.1E-04	14	2	89	35	95	83	4.6E-02	7	6	76	16	116	39	3.8E-03	21	8	167	51	211	122				
rs2005154	9	36856828	PAX5	Silent	INTRON	4.6E-04	0	8	42	30	155	82	3.6E-02	0	2	45	9	155	50	2.0E-05	0	10	87	39	310	132				
kgp10859f	2	33756408	RASGRP3	Silent,Sile	INTRON	4.6E-04	14	2	87	34	97	84	1.2E-02	9	6	76	15	115	40	2.4E-03	19	8	165	49	212	124				
kgp59033f	14	95352842	?	?	?	4.7E-04	1	5	45	11	152	104	2.5E-02	0	0	32	18	169	43	1.9E-02	1	5	77	29	321	147				
kgp44879f	9	36861331	PAX5	Silent	INTRON	5.0E-04	0	8	44	31	154	81	1.5E-02	0	2	46	8	155	51	2.2E-05	0	10	90	39	309	132				
rs6520233	X	1.16E+08	?	?	?	5.2E-04	8	6	15	27	175	87	2.6E-02	7	5	30	16	164	40	1.7E-04	15	11	45	43	339	127				
rs9579566	13	30980265	?	?	?	5.3E-04	0	1	8	18	190	101	2.0E-02	0	0	10	9	161	52	2.0E-05	0	1	18	27	381	153				
rs1894407	6	32787036	?	?	?	5.6E-04	26	13	114	46	58	61	4.5E-02	31	1	69	29	70	29	2.4E-04	57	16	213	75	128	90				
kgp59671f	14	52506177	NID2	Silent	INTRON	5.7E-04	24	34	105	58	68	26	2.2E-02	36	10	91	39	74	12	4.7E-04	60	44	196	97	142	38				
kgp61273f	4	1.54E+08	?	?	?	5.8E-04	0	0	5	15	192	104	1.5E-02	0	0	8	8	192	53	4.6E-05	0	0	13	23	384	157				
kgp10092f	12	19838534	?	?	?	5.9E-04	4	11	63	51	131	57	2.9E-02	6	5	73	29	122	27	4.1E-05	10	16	136	80	253	84				
rs6535882	4	1.54E+08	?	?	?	6.0E-04	0	0	5	15	193	105	1.5E-02	0	0	8	8	193	53	4.7E-05	0	0	13	23	386	158				
kgp67006f	4	1.54E+08	?	?	?	6.0E-04	0	0	5	15	193	105	1.5E-02	0	0	8	8	193	53	4.7E-05	0	0	13	23	386	158				
kgp39191f	6	32379506	?	?	?	6.1E-04	11	4	69	20	117	95	1.2E-02	2	1	58	7	138	52	3.5E-05	13	5	127	27	255	147				
kgp10619f	4	99417717	TSPAN5	Silent	INTRON	6.3E-04	0	0	14	25	184	95	3.4E-02	0	2	18	8	182	51	1.4E-04	0	2	32	33	366	146				
kgp39333f	7	28583709	CREB5,CRI	Silent,Sile	INTRON	6.3E-04	12	0	54	21	131	99	3.0E-02	3	1	57	8	140	52	2.2E-04	15	1	111	29	271	151				
kgp45244f	22	32724532	?	?	?	6.4E-04	16	4	84	32	91	82	2.6E-02	31	4	81	13	107	42	8.7E-05	27	8	165	45	198	124				
kgp10372f	10	1.34E+08	JAKMIP3	Silent	INTRON	7.2E-04	0	0	20	1	178	119	2.1E-02	0	0	22	1	179	60	1.3E-05	0	0	42	2	357	179				
kgp50683f	16	19756348	IQCK	Silent	INTRON	8.7E-04	6	5	53	55	139	59	2.8E-03	4	7	73	27	123	27	7.3E-05	10	12	126	82	262	86				
rs924742	8	68464647	CPA6	Silent	INTRON	9.0E-04	23	17	108	40	67	63	4.1E-02	20	8	109	22	72	31	3.0E-05	43	25	217	62	139	94				
kgp27000f	16	19750275	IQCK	Silent	INTRON	9.2E-04	3	2	46	50	149	67	5.0E-03	3	4	56	26	142	31	4.8E-05	6	6	102	76	291	98				

Table 13b. Genotypic Model, Genome Wide Analysis, p-value sorted by Combined cohort (Gala, Forte, and Combined cohorts)

GALA										FORTE										COMBINED										
Gene		Locations		Mutati	Gene(s)	Positio	Fisher's		Case		Cont		Fisher's		Case		Cont		Fisher's		Case		Cont		Fisher's		Case		Cont	
Name	Chr	Chr	(s)				Exact	DD	DD	DD	DD	DD	DD	DD	DD	DD	DD	DD	DD	DD	DD	DD	DD	DD	DD	DD	DD	DD	DD	DD
rs1688600	7	78021500	MAGI2	Silent	INTRON,E	1.2E-03	3	2	73	22	122	94	3.0E-05	3	0	74	6	124	55	2.8E-07	6	2	147	28	246	149				
rs1025179	7	78025427	MAGI2	Silent	INTRON,E	3.5E-03	4	2	71	23	123	95	5.2E-05	2	0	74	6	125	55	8.5E-07	6	2	145	29	248	150				
rs1757798	6	32359821	HCG23	Silent	INTRON	9.4E-05	11	4	68	17	118	97	1.6E-03	2	1	62	6	137	53	9.1E-07	13	5	130	23	255	150				
rs1532365	12	49204421	?	?	?	1.3E-03	25	35	91	46	82	38	1.6E-03	18	17	97	22	84	22	1.1E-06	43	52	188	68	166	60				
kgp24415	2	1.74E+08	?	?	?	5.1E-05	0	0	1	12	197	108	2.8E-02	0	0	2	4	199	57	1.9E-06	0	0	3	16	396	165				
kgp12008	2	73759636	ALMS1	Silent	INTRON	1.3E-04	0	0	0	9	198	111	1.8E-03	0	0	3	7	198	54	1.9E-06	0	0	3	16	396	165				
kgp26026	13	79972606	RBM26	Silent	INTRON	3.4E-04	0	0	0	8	198	111	3.0E-03	0	0	1	5	199	56	1.9E-06	0	0	1	13	397	167				
rs931570	12	49195124	?	?	?	2.4E-03	25	34	91	48	82	38	1.7E-03	18	17	96	22	85	22	2.6E-06	43	51	187	70	167	60				
rs2453478	12	49202743	?	?	?	1.4E-03	25	35	91	47	82	38	4.1E-03	20	17	95	22	83	22	3.4E-06	45	52	186	69	165	60				
rs2906681	7	21777119	DNAH11	Silent	INTRON	7.5E-05	27	35	110	39	61	46	2.7E-02	17	13	104	29	80	19	5.0E-06	44	48	214	68	141	65				
kgp60113	8	57710655	?	?	?	1.4E-03	23	33	105	48	70	39	1.6E-03	30	22	106	21	64	18	5.7E-06	53	55	211	69	134	57				
kgp25952	13	80027089	?	?	?	9.4E-04	0	0	0	7	198	112	3.0E-03	0	0	1	5	200	56	5.9E-06	0	0	1	12	398	168				
kgp34508	16	57268931	RSPRY1	Silent	INTRON	1.2E-02	0	0	3	9	195	111	1.8E-04	0	0	2	8	199	53	7.8E-06	0	0	5	17	394	164				
rs9941015	16	81999495	?	?	?	2.0E-03	0	3	23	4	175	113	1.6E-03	0	3	17	1	183	57	7.9E-06	0	6	40	5	358	170				
rs7615587	3	18816847	?	?	?	3.2E-03	47	18	88	77	63	25	3.0E-03	52	9	87	42	60	10	8.5E-06	99	27	175	119	123	35				
rs4143493	6	51829939	PKHD1,PK	Silent,Sile	INTRON	1.2E-02	0	0	31	7	167	113	6.9E-04	0	0	41	2	160	99	8.5E-06	0	0	72	9	327	172				
kgp10594	1	2.16E+08	USH2A	Silent	INTRON	5.3E-05	0	0	1	12	196	108	2.2E-02	0	0	5	6	195	55	8.9E-06	0	0	6	18	391	163				
rs1495901	18	34235737	FHOD3	Silent	INTRON	3.1E-02	12	12	82	33	104	75	2.0E-04	12	12	103	16	86	33	9.0E-06	24	24	185	49	190	108				
kgp229967	20	16933074	?	?	?	6.4E-03	0	0	6	13	192	107	2.8E-04	0	0	5	10	196	51	9.1E-06	0	0	11	23	388	158				
rs2325911	6	1.25E+08	NKAIN2,N	Silent,Sile	INTRON	2.7E-03	4	0	40	43	154	77	2.5E-04	5	3	37	26	158	32	9.1E-06	9	3	77	69	312	109				
kgp42459	3	1.73E+08	?	?	?	1.2E-04	43	6	97	68	58	46	3.2E-02	37	4	105	42	56	15	9.7E-06	80	10	202	110	114	61				
rs4370047	3	18808580	?	?	?	2.6E-03	46	18	87	77	64	25	3.8E-03	49	9	88	42	62	10	9.7E-06	95	27	175	119	126	35				
rs9816291	3	18814426	?	?	?	2.7E-03	47	18	87	77	63	25	3.9E-03	51	9	88	42	60	10	9.7E-06	98	27	175	119	123	35				
kgp16887	21	43016736	?	?	?	1.4E-03	0	0	18	27	180	93	6.6E-03	1	2	12	10	188	49	1.0E-05	1	2	30	37	368	142				
rs543122	3	1.24E+08	KALRN,KA	Silent,Sile	INTRON	2.3E-04	31	37	99	62	68	20	2.2E-02	39	17	96	35	63	9	1.1E-05	70	54	195	97	131	29				
kgp36695	2	34593996	?	?	?	2.7E-04	8	5	40	49	150	66	2.4E-02	9	2	46	25	143	34	1.2E-05	17	7	86	74	293	100				
kgp12230	5	27037978	CDH9	Silent	INTRON	5.4E-03	0	0	4	11	193	109	2.0E-04	0	0	6	11	193	50	1.2E-05	0	0	10	22	386	159				
kgp10372	10	1.34E+08	JAKMIP3	Silent	INTRON	7.2E-04	0	0	20	1	178	119	2.1E-02	0	0	22	1	179	60	1.3E-05	0	0	42	2	357	179				
rs1049879	6	51829707	PKHD1,PK	Silent,Sile	INTRON	1.2E-02	0	0	31	7	167	113	1.1E-03	0	0	40	2	161	59	1.3E-05	0	0	71	9	328	172				
kgp50536	2	2.05E+08	?	?	?	1.3E-02	0	0	8	14	188	106	5.7E-05	1	0	9	14	190	47	1.4E-05	1	0	17	28	378	153				
kgp96273	17	90155	RP3AL,R	Silent,Sile	INTRON	1.4E-03	4	6	33	38	160	76	5.7E-03	2	1	38	23	160	37	1.5E-05	6	7	71	61	320	113				
kgp58699	12	49219569	CACNB3,C	Silent,Sile	INTRON	1.4E-03	33	39	88	51	77	29	1.1E-02	27	19	96	23	75	19	1.5E-05	60	58	184	74	152	48				
kgp62369	2	60301030	?	?	?	2.5E-03	18	25	85	56	95	39	2.5E-02	12	9	81	29	108	23	1.7E-05	30	34	166	85	203	62				
kgp59767	22	32675303	?	?	?	8.1E-03	0	0	11	0	187	120	9.0E-03	0	0	18	0	181	61	1.7E-05	0	0	29	0	368	181				
kgp11210	3	38537237	?	?	?	2.4E-03	0	0	13	0	185	120	1.9E-02	1	0	17	0	183	61	1.8E-05	1	0	30	0	368	181				
rs1768796	22	32716927	?	?	?	4.4E-03	0	0	12	0	186	120	1.6E-02	1	0	18	0	182	61	1.8E-05	1	0	30	0	368	181				
kgp81106	22	32716792	?	?	?	4.4E-03	0	0	12	0	186	120	1.1E-02	1	0	18	0	181	61	1.8E-05	1	0	30	0	367	181				
rs1102277	11	13390860	ARNTL,AR	Silent,Sile	INTRON	1.5E-03	24	4	85	41	89	75	1.4E-02	28	1	91	41	82	29	1.9E-05	52	5	176	72	171	104				
rs2005154	9	36856828	PAX5	Silent	INTRON	4.6E-04	0	8	42	30	155	82	3.6E-02	0	2	45	9	155	50	2.0E-05	0	10	87	39	310	132				
kgp11141	20	35283733	NDRG3,N	Silent,Sile	INTRON	7.3E-03	0	1	8	14	190	104	1.8E-03	0	0	3	7	198	54	2.0E-05	0	1	11	21	388	158				

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In some embodiments genetic markers presented in Tables 11, 12 and 13 are identified as predictive of response to glatiramer acetate if the p-value for the Combined cohort is less than about 0.05, less than about 0.01, less than about 0.005, less than about 0.001, or
5 less than about 0.0005, less than about 10^{-4} , less than about $5 * 10^{-5}$, less than about 10^{-5} , less than about $5 * 10^{-6}$, less than about 10^{-6} or less than about $5 * 10^{-7}$.

In the fourth stage of the analysis, the placebo cohort (n = 196: 95 R vs. 101 NR) (GALA placebo) was analyzed to identify variants
10 associated with placebo response/non-response. These results will be used to confirm whether significantly associated variants are specific to glatiramer acetate drug response versus disease severity.

Overlap with Placebo Cohort Results:

15 An analysis to investigate whether any of the highly associated variants ($P < 0.0001$) from the combined cohorts in the additive association analysis showed a similar significant association in the placebo cohort was conducted. This analysis identified two
overlapping associations with the placebo associations, which
20 include the 132nd top associated variant in the combined cohorts (variant kpg5144181) and the 242nd top associated variant in the combined cohort (kpg7063887).

Results for Standard Response Definition, Placebo Cohort Results for Additive, Allelic and Genotypic models are presented in tables 14-
25 16, respectively.

Table 14. Additive Model, Genome Wide Placebo Cohort Analysis

GALA PLACEBO cohort															
Name	Chr	Position	Gene(s)	Mutation	Gene Locations (s)	P	Armitage Regression Odds Ratio	Allele Freq. (Cases)	Allele Freq. (Controls)	DD (Case s)	DD (Cont rols)	Dd (Case s)	Dd (Cont rols)	dd (Case s)	dd (Cont rols)
rs12472695	2	65804266	?	?	?	2.31E-05	0.38	31%	51%	10	21	39	62	46	18
kgp3188	2	65804244	?	?	?	2.99E-05	0.39	36%	56%	13	25	41	63	40	13
kgp5747456	2	23932556	?	?	?	3.24E-05	Infinity	8%	0%	0	0	15	0	80	101
rs11562998	2	51814215	?	?	?	3.41E-05	6.52	14%	2%	2	0	23	5	70	96
rs11563025	2	51864372	?	?	?	3.41E-05	6.52	14%	2%	2	0	23	5	70	96
rs16846161	2	2.12E+08	ERBB4,ERBB2	Silent,Silent	INTRON	3.72E-05	12.04	12%	1%	2	0	18	2	74	97
kgp22839559			?	?	?	3.97E-05	2.82	34%	16%	10	2	44	28	40	70
kgp12562255	1	2.01E+08	?	?	?	4.21E-05	21.79	9%	0%	0	0	17	1	78	100
kgp6990559	1	7014101	CAMTA1	Silent	INTRON,E	4.49E-05	0.44	35%	58%	15	35	36	42	43	20
rs6577395	1	6991925	CAMTA1	Silent	INTRON,E	5.34E-05	0.45	37%	59%	16	38	37	43	41	20
kgp4456934	2	2.18E+08	DIRC3	Silent	INTRON	5.68E-05	3.79	21%	7%	4	0	31	13	60	87
rs10495115	1	2.19E+08	?	?	?	6.04E-05	2.90	30%	13%	7	2	43	23	45	76
kgp4137144	1	2.19E+08	?	?	?	6.13E-05	6.19	14%	3%	2	0	22	5	70	95
rs3768769	2	1.14E+08	IL36A	Silent	INTRON	7.21E-05	4.30	17%	5%	2	0	29	10	64	91
kgp3488270	1	20335423	?	?	?	7.30E-05	0.27	6%	21%	1	4	10	33	84	63
rs2354380	2	51826155	?	?	?	7.48E-05	5.49	14%	3%	2	0	23	6	69	95
kgp7151153	3	79590648	ROBO1	Silent	INTRON	7.86E-05	3.98	18%	5%	4	1	27	8	64	92
rs28993969	2	1.14E+08	?	?	?	8.51E-05	3.67	20%	6%	4	0	30	13	61	88
rs12043743	1	1.97E+08	KCNT2	Silent	INTRON	8.61E-05	0.16	3%	13%	0	0	5	26	90	75
kgp24521552	2	1.44E+08	ARHGAP1	Silent	INTRON	8.86E-05	4.22	17%	5%	4	0	25	9	66	91
kgp11755256	2	42245135	?	?	?	8.99E-05	0.38	14%	32%	1	14	25	37	68	50
rs528065	2	23859449	KLHL29	Silent	INTRON	9.24E-05	2.45	44%	26%	19	3	46	46	30	52
rs13386874	2	51820543	?	?	?	9.25E-05	2.64	32%	15%	12	1	37	28	46	72
kgp956070	2	2.06E+08	PARD3B,P	Silent,Silent	INTRON	9.39E-05	0.37	14%	32%	2	11	23	41	70	48
rs35615951	2	1.34E+08	NCKAP5,N	Silent,Silent	INTRON	9.41E-05	2.32	48%	28%	22	8	46	41	26	52
kgp12253568	3	79428265	ROBO1	Silent	INTRON	9.55E-05	4.29	17%	4%	4	1	24	6	67	94
rs1397481	2	2.06E+08	PARD3B,P	Silent,Silent	INTRON	9.56E-05	0.37	14%	31%	2	10	23	43	70	48
kgp7161038	2	53521025	?	?	?	9.70E-05	0.09	1%	10%	0	0	2	20	92	81
rs1534647	2	62038088	?	?	?	9.72E-05	3.34	22%	8%	5	0	32	16	58	85
kgp7799142	3	13902000	WNT7A	Silent	INTRON	1.04E-04	0.12	2%	11%	0	0	3	22	91	79
kgp6029	2	1.69E+08	?	?	?	1.07E-04	0.37	13%	30%	2	11	21	39	72	51
kgp8142606	2	1.74E+08	?	?	?	1.10E-04	0.22	4%	17%	0	3	8	27	87	70
rs6737616	2	51807660	?	?	?	1.18E-04	5.98	13%	2%	1	0	22	5	72	96
kgp7713264	2	2.42E+08	GPR35,GPR35	Silent,Silent	INTRON	1.18E-04	0.45	30%	51%	10	27	37	47	47	26
kgp8055964	3	1.73E+08	SPATA16	Silent	INTRON	1.19E-04	Infinity	7%	0%	0	0	13	0	82	101
rs12712821	2	42238864	?	?	?	1.19E-04	0.39	15%	32%	1	14	26	37	68	50
rs13424176	2	42239532	?	?	?	1.19E-04	0.39	15%	32%	1	14	26	37	68	50
kgp9777128	2	42242872	?	?	?	1.19E-04	0.39	15%	32%	1	14	26	37	68	50
rs10195970	2	42249643	?	?	?	1.19E-04	0.39	15%	32%	1	14	26	37	68	50
rs10177811	2	42263580	?	?	?	1.19E-04	0.39	15%	32%	1	14	26	37	68	50

Table 15. Allelic Model, Genome Wide Placebo Cohort Analysis

GALA PLACEBO cohort															
Name	Chr	Position	Gene(s)	Mutation	Gene Locations	Fisher's Exact P	Odds Ratio (Minor Allele)	Allele Freq. (Cases)	Allele Freq. (Controls)	DD (Cases)	DD (Controls)	Dd (Cases)	Dd (Controls)	dd (Cases)	dd (Controls)
kgp5471255	11	57870219	OR9Q1	Silent	INTRON,E	1.16E-06	0.25	9%	29%	5	25	7	7	81	68
kgp11285883	9	2953403	?	?	?	2.68E-06	2.79	46%	23%	26	5	35	37	34	59
kgp433351	8	41496314	?	?	?	2.70E-06	0.35	23%	46%	6	19	32	55	57	27
kgp10148554	4	89767803	FAM13A	Silent	INTRON	3.69E-06	7.19	15%	2%	3	0	23	5	68	96
rs3858038	9	2988280	?	?	?	5.49E-06	2.63	53%	30%	33	7	34	46	28	48
kgp2877482	6	1644677	GMD5,GM	Silent,Sile	INTRON	6.08E-06	8.20	14%	2%	0	0	27	4	68	97
kgp6042557	3	1.94E+08	LOC10050	Silent	INTRON	6.53E-06	0.08	1%	12%	0	1	2	22	93	77
kgp22755512	X	27326117	?	?	?	6.61E-06	?	8%	0%	3	0	10	0	82	101
kgp10989246	4	89761443	FAM13A	Silent	INTRON	6.68E-06	7.11	15%	3%	3	0	23	5	68	95
rs7698655	4	89756076	FAM13A	Silent	INTRON	6.76E-06	7.10	15%	2%	3	0	23	5	69	96
kgp9409440	4	89759159	FAM13A	Silent	INTRON	6.76E-06	7.10	15%	2%	3	0	23	5	69	96
kgp6889327	4	89766553	FAM13A	Silent	INTRON	6.76E-06	7.10	15%	2%	3	0	23	5	69	96
rs7696391	4	89789287	FAM13A	Silent	INTRON	6.76E-06	7.10	15%	2%	3	0	23	5	69	96
rs11947777	4	89768744	FAM13A	Silent	INTRON	6.92E-06	7.02	15%	3%	3	0	23	5	69	95
kgp6301155	4	89766647	FAM13A	Silent	INTRON	7.20E-06	6.95	15%	3%	3	0	23	5	69	94
rs16846161	2	2.12E+08	ERBB4,ER	Silent,Sile	INTRON	7.44E-06	12.99	12%	1%	2	0	18	2	74	97
kgp7778345	9	2965090	?	?	?	9.91E-06	2.59	49%	27%	27	6	38	42	29	52
kgp6990559	1	7014101	CAMTA1	Silent	INTRON,E	1.01E-05	0.40	35%	58%	15	35	36	42	43	20
rs1393040	9	2985743	?	?	?	1.04E-05	2.57	48%	27%	28	6	35	42	31	53
rs6577395	1	6991925	CAMTA1	Silent	INTRON,E	1.27E-05	0.40	37%	59%	16	38	37	43	41	20
rs7846783	9	2958182	?	?	?	1.28E-05	2.58	45%	24%	25	6	36	37	34	58
kgp5747456	2	23932556	?	?	?	1.42E-05	?	8%	0%	0	0	15	0	80	101
kgp6429231	15	62931802	MGC1588	Silent	INTRON	1.42E-05	?	8%	0%	0	0	15	0	80	101
kgp30689515	X	56022365	?	?	?	1.42E-05	?	8%	0%	4	0	7	0	84	101
kgp1682126	5	2047397	?	?	?	1.56E-05	0.05	1%	10%	0	1	1	18	94	82
kgp2920925	17	39694480	?	?	?	1.56E-05	0.30	10%	27%	0	6	19	43	76	52
rs3894712	5	73973651	?	?	?	1.70E-05	0.29	9%	25%	3	5	11	41	81	55
rs7119480	11	84247636	DLG2,DLG	Silent,Sile	INTRON,E	1.71E-05	0.34	14%	33%	1	9	25	48	69	44
rs3858035	9	2968044	?	?	?	1.72E-05	2.51	48%	27%	27	7	37	41	30	53
rs3847233	9	2987835	?	?	?	1.95E-05	2.49	52%	30%	31	7	34	46	28	47
kgp12253568	3	79428265	ROBO1	Silent	INTRON	2.10E-05	4.91	17%	4%	4	1	24	6	67	94
kgp1977942	9	2938757	?	?	?	2.17E-05	2.52	46%	26%	28	7	32	37	35	56
kgp22744690	X	83601713	HDX,HDX,	Silent,Sile	INTRON	2.21E-05	7.50	13%	2%	7	0	11	4	77	97
rs8000689	13	41043438	TTL,TTL,TT	Silent,Sile	INTRON	2.22E-05	0.42	38%	60%	14	40	45	41	36	20
kgp4892427	9	2995617	?	?	?	2.27E-05	2.46	52%	30%	31	7	36	47	28	47
rs11562998	2	51814215	?	?	?	2.36E-05	6.53	14%	2%	2	0	23	5	70	96
rs11563025	2	51864372	?	?	?	2.36E-05	6.53	14%	2%	2	0	23	5	70	96
rs7680970	4	89772301	FAM13A	Missense	EXON	2.37E-05	5.88	15%	3%	3	0	23	6	69	95
kgp22836129	X	1.45E+08	?	?	?	2.38E-05	5.84	15%	3%	5	0	19	6	70	93
kgp11604017	11	1.18E+08	AMICA1,A	Silent,Sile	INTRON	2.39E-05	2.69	38%	18%	11	3	48	31	34	67
rs961090	15	40617414	?	?	?	2.40E-05	2.97	31%	13%	9	2	40	22	46	77
kgp22760557	X	3520721	?	?	?	2.40E-05	2.97	31%	13%	16	5	26	16	53	80
rs1393037	9	2968451	?	?	?	2.41E-05	2.50	48%	27%	27	7	37	40	30	52
rs4978567	9	1.17E+08	?	?	?	2.47E-05	0.41	32%	54%	10	27	41	52	44	20

Table 16. Genotypic Model, Genome Wide Placebo Cohort Analysis

GALA PLACEBO cohort														
Name	Chromosome	Position	Gene(s)	Mutation	Gene Locations (s)	Fisher's Exact P	Allele Freq. (Controls (Cases (Contr (Cases (Contr (Cases (Contr							
							Freq. (Cases)	Freq. (Controls)	DD (Cases)	DD (Contr ols)	Dd (Cases)	Dd (Contr ols)	dd (Cases)	dd (Contr ols)
kgp541892	5	73992881	HEXB	Missense	EXON	8.76E-07	9%	25%	3	3	11	44	81	54
kgp349487	14	91731724	?	?	?	1.53E-06	6%	17%	3	1	5	32	87	67
kgp211600	14	91744233	CCDC88C	Silent	INTRON	1.55E-06	6%	17%	3	1	5	32	86	67
kgp287748	6	1644677	GMDS, GM	Silent, Sile	INTRON	2.43E-06	14%	2%	0	0	27	4	68	97
rs1175074	5	73973220	?	?	?	2.71E-06	9%	25%	3	4	11	42	81	55
rs1223398	5	73975094	?	?	?	2.71E-06	9%	25%	3	4	11	42	81	55
rs1203094	1	67701765	IL23R	Silent	INTRON	3.44E-06	36%	37%	20	5	29	64	46	32
rs3894712	5	73973651	?	?	?	3.50E-06	9%	25%	3	5	11	41	81	55
rs3858038	9	2988280	?	?	?	4.13E-06	53%	30%	33	7	34	46	28	48
kgp625941	5	73973306	?	?	?	5.26E-06	9%	24%	3	4	11	41	81	56
rs7159692	14	91729406	?	?	?	6.22E-06	7%	18%	3	1	7	34	85	66
kgp433351	8	41496314	?	?	?	7.73E-06	23%	46%	6	19	32	55	57	27
kgp604255	3	1.94E+08	LOC10050	Silent	INTRON	8.38E-06	1%	12%	0	1	2	22	93	77
kgp891094	8	4818950	CSMD1	Silent	INTRON	8.91E-06	45%	33%	27	5	32	57	36	39
kgp481828	14	86277089	?	?	?	8.95E-06	45%	36%	10	18	66	36	19	47
kgp660175	19	28886975	?	?	?	9.85E-06	19%	31%	7	3	21	55	65	42
kgp574745	2	23932556	?	?	?	1.03E-05	8%	0%	0	0	15	0	80	101
kgp642925	15	62931802	MGC15885	Silent	INTRON	1.03E-05	8%	0%	0	0	15	0	80	101
kgp827624	14	91725476	?	?	?	1.22E-05	7%	17%	3	1	7	33	85	67
kgp682827	9	8373943	PTPRD, PT	Silent, Sile	INTRON	1.23E-05	26%	10%	3	2	43	17	48	82
rs3847233	9	2987835	?	?	?	1.32E-05	52%	30%	31	7	34	46	28	47
kgp3188	2	65804244	?	?	?	1.34E-05	36%	56%	13	25	41	63	40	13
rs1890118	6	82857479	?	?	?	1.48E-05	26%	32%	13	4	23	56	59	41
rs2282624	11	57001911	APLNR, AP	Silent, Sile	INTRON, E	1.54E-05	30%	35%	15	5	27	61	53	35
kgp489242	9	2995617	?	?	?	1.54E-05	52%	30%	31	7	36	47	28	47
kgp112858	9	2953403	?	?	?	1.66E-05	46%	23%	26	5	35	37	34	59
rs4740708	9	2993975	?	?	?	1.67E-05	51%	30%	31	7	34	47	29	47
rs695915	1	82664165	?	?	?	1.90E-05	34%	28%	6	17	51	23	37	61
rs2327006	6	1.31E+08	EPB41L2, E	Silent, Sile	INTRON	1.93E-05	22%	9%	1	2	39	13	55	84
kgp933491	6	1.31E+08	EPB41L2, E	Silent, Sile	INTRON	2.05E-05	22%	8%	2	2	38	13	55	86
rs193933	19	8331375	?	?	?	2.07E-05	27%	46%	11	17	30	59	54	25
kgp124750	4	1.86E+08	ACSL1	Silent	INTRON	2.11E-05	13%	3%	0	1	24	4	71	96
rs1247269	2	65804266	?	?	?	2.11E-05	31%	51%	10	21	39	62	46	18
rs1393040	9	2985743	?	?	?	2.31E-05	48%	27%	28	6	35	42	31	53
kgp292092	17	39694480	?	?	?	2.33E-05	10%	27%	0	6	19	43	76	52
rs209568	8	17612639	MTUS1, M	Synonym	EXON	2.34E-05	27%	11%	4	0	44	22	47	79
kgp125622	1	2.01E+08	?	?	?	2.42E-05	9%	0%	0	0	17	1	78	100
kgp262635	13	67483846	PCDH9, PC	Silent, Sile	INTRON, E	2.43E-05	34%	49%	4	28	56	43	34	30
kgp168212	5	2047397	?	?	?	2.51E-05	1%	10%	0	1	1	18	94	82
kgp101485	4	89767803	FAM13A	Silent	INTRON	2.55E-05	15%	2%	3	0	23	5	68	96
kgp576004	6	1.31E+08	EPB41L2, E	Silent, Sile	INTRON	2.61E-05	20%	7%	1	2	35	11	58	88
kgp783986	1	95321361	SLC44A3, S	Silent, Sile	INTRON	2.67E-05	20%	20%	0	11	38	19	57	71
rs1049917	6	1.31E+08	EPB41L2, E	Silent, Sile	INTRON	2.77E-05	19%	7%	1	2	35	11	59	88
kgp377815	19	28893126	?	?	?	2.80E-05	19%	32%	7	4	23	56	65	41
kgp765347	17	39694186	?	?	?	2.81E-05	10%	27%	0	5	19	44	76	52
rs1684616	2	2.12E+08	ERBB4, ER	Silent, Sile	INTRON	2.96E-05	12%	1%	2	0	18	2	74	97

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Example 9 Analysis for Extreme Responders vs. Extreme Non-Responders
Part 1 - Analysis of Candidate Variants

The initial analysis was analyzed to 35 genetic variants in high priority genes. Power (80%) with Bonferroni statistical correction
5 for multiple testing to identify significant genetic associations with an odds ratio >4, for variants with an allele frequency greater than 10%.

Results for Extreme Response Definition, Candidate Variants Selected a priori for Additive, Allelic and Genotypic models are presented in
10 tables 17-19, respectively.

In some embodiments genetic markers presented in Tables 17-19 are identified as predictive of response to glatiramer acetate if the p-value for the GALA cohort is less than about 0.15, less than about 0.13, less than about 0.07 or less than about 0.06.

15 In some embodiments genetic markers presented in Tables 17-19 are identified as predictive of response to glatiramer acetate if the p-value for the FORTE cohort is less than about 0.10, less than about 0.05, less than about 0.01, less than about 0.005 or less than about 0.001.

20 In some embodiments genetic markers presented in Tables 17-19 are identified as predictive of response to glatiramer acetate if the p-value for the Combined cohort is less than about 0.10, less than about 0.05, less than about 0.01, less than about 0.005 or less than about 0.001.

Table 17. Additive Model, Extreme Response Definition, Candidate Variants (Gala, Forte, and Combined cohorts)

GALA				FORTE				COMBINED					
Source	Name	Ch	Gene	Allele Freq. (Non-Resp.)	Allele Freq. (Non-Resp.)	Allele Freq. (Non-Resp.)	Allele Freq. (Non-Resp.)	Allele Freq. (Non-Resp.)	Allele Freq. (Non-Resp.)	Allele Freq. (Non-Resp.)	Allele Freq. (Non-Resp.)		
Tchelet GWAS	rs3135391	6	HLA-DRB1	0.060	0.58	18%	0.028	0.50	20%	0.064	0.57	19%	29%
Tchelet GWAS	rs3135388	6	HLA-DRB1	0.069	0.59	18%	0.028	0.50	20%	0.0075	0.58	19%	29%
Tchelet GWAS	rs2487896	10	HPSE2	0.130	0.60	11%	0.0017	0.33	12%	0.0044	0.51	11%	20%
Tchelet GWAS	rs1085360	18	MEX3C	0.149	0.70	36%	0.56	1.18	43%	0.54	0.90	40%	43%
Tchelet GWAS	rs1098808	9	SET	0.231	0.48	3%	0.0010	0.18	3%	0.0051	0.33	3%	8%
Comi	rs269976	18	SLC14A2	0.288	1.62	8%	0.28	2.33	6%	0.21	1.61	7%	5%
Tsareva 2011	rs231775	2	CTLA4	0.318	1.28	43%	0.46	1.22	37%	0.39	1.16	40%	36%
Grossman 2007	rs946685	1	IL12RB2	0.342	1.32	21%	0.84	0.92	15%	0.75	1.08	18%	17%
Tsareva 2011	rs1800629	6	TNF	0.355	0.74	13%	0.86	1.07	12%	0.39	0.82	13%	15%
Tchelet GWAS	rs1007328	15	AC012409.1	0.364	1.24	57%	0.051	0.57	45%	0.38	0.86	50%	54%
Tchelet GWAS	rs1225688	10	CYP26C1	0.366	0.79	30%	0.23	1.46	35%	0.93	1.02	33%	32%
Tchelet GWAS	rs1093109	2	AC074182.1	0.387	1.38	11%	0.42	0.69	7%	0.96	1.01	8%	8%
Tchelet GWAS	rs4148871	6	TAP2	0.421	0.79	17%	0.98	1.01	23%	0.83	0.95	20%	21%
Tchelet GWAS	rs947603	10	CEP55	0.436	1.26	23%	0.033	2.30	24%	0.06	1.51	24%	17%
Grossman 2007	rs2001791	3	CD86	0.439	1.29	16%	0.32	0.71	15%	0.93	1.02	15%	15%
Tsareva 2011	rs6897932	5	IL7Ra	0.493	0.82	21%	0.84	1.07	24%	0.77	0.94	23%	24%
Comi	rs1558896	7	TAC1	0.506	1.17	33%	0.27	0.71	26%	0.70	0.93	29%	31%
Grossman 2007	rs1415148	1	CTSS	0.555	0.86	36%	0.39	1.28	42%	0.79	1.05	40%	38%
Tchelet GWAS	rs1777193	8	AC016885.1	0.555	1.17	28%	0.000020	0.27	24%	0.067	0.71	26%	33%
Grossman 2007	rs2275235	1	CTSS	0.634	0.88	32%	0.16	1.52	40%	0.41	1.16	36%	33%
Tchelet GWAS	rs1573706	20	PTPRT	0.638	0.87	18%	0.00048	0.28	11%	0.0071	0.55	14%	23%
Tchelet GWAS	rs1159962	10	RP11-655H13.1	0.653	0.84	11%	0.98	1.01	10%	0.64	0.88	10%	12%
Comi	rs974060	7	TAC1	0.654	1.12	30%	0.19	0.67	25%	0.57	0.90	27%	29%
Comi	rs4890535	18	SLC14A2	0.656	1.19	9%	0.64	1.28	9%	0.52	1.21	9%	7%
Tchelet GWAS	rs1757545	2	AC078940.2	0.664	0.89	30%	0.018	0.52	30%	0.11	0.75	30%	37%
Tchelet GWAS	rs2521644	7	NPY	0.679	1.11	45%	0.83	1.06	44%	0.64	1.09	45%	43%
Grossman 2007	rs1129055	3	CD86	0.775	1.08	26%	0.19	0.68	30%	0.91	0.98	28%	29%
Tchelet GWAS	rs4343256	15	CRTC3	0.808	1.14	5%	0.044	0.37	6%	0.42	0.75	5%	7%
Tchelet GWAS	rs6097801	20	CYP24A1	0.823	0.93	14%	0.0057	0.41	9%	0.043	0.63	11%	17%
Tchelet GWAS	rs2177073	18	DTNA	0.864	0.94	12%	0.10	0.51	10%	0.23	0.74	11%	14%
Tchelet GWAS	rs1095035	7	AC074389.1	0.866	0.96	33%	0.15	1.62	29%	0.85	1.04	31%	30%
Tchelet GWAS	rs4369324	10	RP11-655H13.2	0.920	1.03	22%	0.35	1.42	20%	0.72	1.08	21%	19%
Tchelet GWAS	rs1161713	13	RP11-629E24.2	0.959	0.98	7%	0.0022	0.14	2%	0.052	0.49	4%	8%
Tchelet GWAS	rs4344916	2	AC083939.1	0.962	1.01	31%	0.08	0.63	26%	0.24	0.81	28%	33%
Tchelet GWAS	rs9944913	18	NOL4	0.981	1.01	13%	0.36	0.66	9%	0.42	0.80	11%	13%

Table 18. Allelic Model, Extreme Response Definition, Candidate Variants (Gala, Forte, and Combined cohorts)

GALA										FORTE										COMBINED									
Source	Name	Ch	Position	Gene	Odds			Allele			Odds			Allele			Odds			Allele			Odds			Allele			
					Ratio	(Minor	Allele)	Freq.	(Cases)	Freq.	(Controls)	Fisher's	Exact P	Ratio	(Minor	Allele)	Freq.	(Cases)	Freq.	(Controls)	Fisher's	Exact P	Ratio	(Minor	Allele)	Freq.	(Cases)	Freq.	(Controls)
Tchelet GWAS	rs3135388	6	32413051	HLA-DRB1	0.075234	0.599034	0.181818	0.270588	0.031164	0.500152	0.196629	0.328571	0.008221	0.582539	0.190323	0.2875	6	9	47	51	102	60							
Tchelet GWAS	rs3135391	6	32410987	HLA-DRB1	0.075291	0.591017	0.181818	0.273256	0.031164	0.500152	0.196629	0.328571	0.008266	0.577575	0.190323	0.289256	6	9	47	52	102	60							
Tchelet GWAS	rs2487896	10	1.01E+08	HPSE2	0.135493	0.576856	0.106061	0.170588	0.002228	0.334195	0.117978	0.285714	0.003985	0.496104	0.112903	0.204167	3	6	29	37	123	77							
Tchelet GWAS	rs1085360	18	48783342	MEX3C	0.195547	0.721805	0.363636	0.44186	0.570435	1.186638	0.426966	0.385714	0.601035	0.899676	0.4	0.42562	28	17	68	69	59	35							
Tchelet GWAS	rs1098808	9	1.31E+08	SET	0.281834	0.5	0.030303	0.058824	0.001601	0.17341	0.02809	0.142857	0.006355	0.328904	0.029032	0.083333	0	1	9	18	146	101							
Tsareva 2011	rs231775	2	2.05E+08	CTLA4	0.347935	1.251077	0.431818	0.377907	0.462029	1.285714	0.170767	0.314286	0.378507	1.171861	0.396774	0.359504	26	18	71	51	58	52							
Comi	rs269976	18	42781787	SLC14A2	0.351837	1.646465	0.083333	0.052326	0.361681	2.239521	0.061798	0.028571	0.277651	1.604167	0.070968	0.045455	0	1	22	9	133	111							
Grossman 2007	rs946685	1	67815715	IL12RB2	0.374886	1.327586	0.212121	0.168605	0.845141	0.929697	0.147727	0.157143	0.819741	1.073622	0.175325	0.165289	5	2	44	36	105	83							
Tchelet GWAS	rs1225688	10	94827183	CYP26C1	0.38939	0.803171	0.295455	0.343023	0.29301	1.434664	0.348315	0.271429	1	1.016072	0.325806	0.322314	15	11	71	56	69	54							
Tchelet GWAS	rs1007328	15	96703373	AC012409.1	0.417114	1.227085	0.568182	0.517442	0.065407	0.577402	0.449438	0.585714	0.392171	0.861538	0.5	0.53719	39	32	77	66	39	23							
Tchelet GWAS	rs1093109	2	1.85E+08	AC074182.1	0.417558	1.451108	0.106061	0.075581	0.428339	0.650602	0.067416	0.1	1	1.016197	0.083871	0.082645	2	3	22	14	131	104							
Tsareva 2011	rs1800629	6	31543031	TNF	0.419818	0.728936	0.128788	0.168605	1	1.092949	0.123596	0.114286	0.384855	0.797347	0.125806	0.152893	6	4	27	29	122	88							
Tchelet GWAS	rs4148871	6	32803316	TAP2	0.46037	0.782857	0.166667	0.203488	1	1.010036	0.230337	0.228571	0.832981	0.955227	0.203226	0.210744	4	7	55	37	96	77							
Tchelet GWAS	rs947603	10	95249605	CEP55	0.477454	1.238859	0.227273	0.19186	0.023852	2.505639	0.244318	0.114286	0.056786	1.522885	0.237013	0.169421	7	6	59	29	88	86							
Grossman 2007	rs2001791	3	1.22E+08	CD86	0.507354	1.289926	0.159091	0.127907	0.33832	0.684211	0.146067	0.2	1	1.022602	0.151613	0.14876	6	2	35	32	114	87							
Comi	rs1558896	7	97281912	TAC1	0.533334	1.186275	0.333333	0.296512	0.274375	0.712121	0.258427	0.328571	0.708106	0.928747	0.290323	0.305785	18	9	54	56	83	56							
Tsareva 2011	rs6897932	5	35874575	IL7Ra	0.582979	0.833333	0.212121	0.244186	0.870005	1.075	0.241573	0.228571	0.83943	0.942433	0.229032	0.239669	8	7	55	44	92	70							
Tchelet GWAS	rs1777193	8	94259105	AC016885.1	0.5999	1.168421	0.280303	0.25	2.18E-05	0.284084	0.241573	0.528571	0.072395	0.704348	0.258065	0.330579	9	16	62	48	84	57							
Grossman 2007	rs1415148	1	1.51E+08	CTSS	0.634082	0.87395	0.363636	0.395349	0.3899	1.30099	0.41954	0.357143	0.860062	1.047893	0.395425	0.384298	25	16	71	61	57	44							
Tchelet GWAS	rs1573706	20	40921149	PTPRT	0.66336	0.869841	0.181818	0.203488	0.000892	0.296742	0.106742	0.285714	0.009585	0.547566	0.13871	0.227273	2	7	39	41	114	73							
Comi	rs4890535	18	42760370	SLC14A2	0.676761	1.223077	0.090909	0.075581	0.801757	1.283951	0.089888	0.071429	0.53794	1.235619	0.090323	0.07438	1	3	26	12	128	106							
Comi	rs974060	7	97271508	TAC1	0.702366	1.123188	0.30303	0.27907	0.206336	0.670993	0.247191	0.328571	0.568262	0.895176	0.270968	0.293388	14	9	56	53	85	59							
Tchelet GWAS	rs1757545	2	76624220	AC078940.2	0.70994	0.900621	0.30303	0.325581	0.017315	0.483134	0.101136	0.471429	0.120633	0.743611	0.301948	0.367769	15	17	63	55	76	49							
Grossman 2007	rs2275235	1	1.51E+08	CTSS	0.712828	0.893785	0.318182	0.343023	0.187836	1.540881	0.397727	0.3	0.471074	1.157143	0.363636	0.330579	21	11	70	58	63	52							
Tchelet GWAS	rs1159962	10	1.11E+08	NPY	0.719551	0.853107	0.106061	0.122093	1	1.0125	0.101124	0.1	0.680358	0.879753	0.103226	0.115702	2	1	28	26	125	94							
Tchelet GWAS	rs2521644	7	24427969	NPY	0.726947	1.096078	0.44697	0.424419	0.887361	1.063973	0.44382	0.428571	0.666085	1.08275	0.445161	0.42562	28	22	82	59	45	40							
Grossman 2007	rs1129055	3	1.22E+08	CD86	0.79101	1.073858	0.257576	0.244186	0.227117	0.675239	0.297753	0.385714	0.924318	0.978163	0.280645	0.285124	12	8	63	53	80	60							
Tchelet GWAS	rs6097801	20	52767434	CYP24A1	0.869321	0.928421	0.136364	0.145349	0.002983	0.307916	0.089888	0.242857	0.034456	0.586611	0.109677	0.173554	7	3	20	36	128	82							
Tchelet GWAS	rs1095035	7	1800967	AC074389.1	0.903004	0.957627	0.333333	0.343023	0.153622	1.650794	0.292135	0.2	0.852865	1.038535	0.309677	0.301653	21	10	54	53	80	58							
Tchelet GWAS	rs1161713	13	30590793	RP11-629E24.2	1	0.97561	0.068182	0.069767	0.006286	0.154286	0.016834	0.1	0.061019	0.472625	0.03871	0.078512	1	1	10	17	144	103							
Tchelet GWAS	rs2177073	18	32054724	DTNA	1	0.940439	0.121212	0.127907	0.122899	0.510353	0.095505	0.171429	0.238954	0.728817	0.106452	0.140496	2	3	29	28	124	90							
Tchelet GWAS	rs4343256	15	91198415	CRTC3	1	1.134	0.05303	0.047059	0.065025	0.409439	0.05618	0.128571	0.477974	0.761092	0.054839	0.070833	0	0	17	17	138	103							
Tchelet GWAS	rs4344916	2	35597319	AC083939.1	1	1.011611	0.310606	0.30814	0.063797	0.563533	0.261364	0.335714	0.226351	0.797172	0.282468	0.330579	19	11	49	58	86	52							
Tchelet GWAS	rs4369324	10	1.11E+08	RP11-655H13.2	1	1.027289	0.219697	0.215116	0.364915	1.468531	0.196639	0.142857	0.749071	1.079398	0.206452	0.194215	6	5	52	37	97	79							
Tchelet GWAS	rs9944913	18	31926438	NOL4	1	1.007905	0.128788	0.127907	0.357373	0.66941	0.089888	0.128571	0.503205	0.810877	0.106452	0.128099	0	2	33	27	122	92							

Table 19. Genotypic Model, Extreme Response Definition, Candidate Variants (Gala, Forte, and Combined cohorts)

				GALA		FORTE		COMBINED					
Source	Name	Ch	Gene	Fisher's		Fisher's		DD		Dd		dd	
				Exact P	Fisher's Exact P	Exact P	Fisher's Exact P	s	rols	s	rols	s	rols
Comi	rs4890535	18	SLC14A2	0.051225	1	0.130308	1	3	26	12	128	106	
Tchelet GWAS	rs1085360	18	MEX3C	0.060784	0.807531	0.09938	28	17	68	69	59	35	
Comi	rs1558896	7	TAC1	0.108585	0.384407	0.129289	18	9	54	56	83	56	
Comi	rs269976	18	SLC14A2	0.131319	0.347736	0.068507	0	1	22	9	133	111	
Grossman 2007	rs2001791	3	CD86	0.163623	0.597721	0.466835	6	2	35	32	114	87	
Tchelet GWAS	rs947603	10	CEP55	0.175968	0.018504	0.03493	7	6	59	29	88	86	
Tchelet GWAS	rs3135391	6	HLA-DRB1	0.191442	0.061953	0.019534	6	9	47	52	102	60	
Tchelet GWAS	rs1225688	10	CYP26C1	0.211437	0.112697	1	15	11	71	56	69	54	
Tchelet GWAS	rs3135388	6	HLA-DRB1	0.229549	0.061953	0.023584	6	9	47	51	102	60	
Tchelet GWAS	rs1098808	9	SET	0.270151	0.003153	0.009817	0	1	9	18	146	101	
Tchelet GWAS	rs1095035	7	AC074389.1	0.290815	0.113948	0.194248	21	10	54	53	80	58	
Tchelet GWAS	rs1159962	10	RP11-655H13.1	0.319145	0.620619	0.808936	2	1	28	26	125	94	
Tsareva 2011	rs231775	2	CTLA4	0.323348	0.650864	0.641801	26	18	71	51	58	52	
Tchelet GWAS	rs2487896	10	HPSE2	0.339368	0.00344	0.016573	3	6	29	37	123	77	
Tchelet GWAS	rs1007328	15	AC012409.1	0.342331	0.160261	0.490428	39	32	77	66	39	23	
Tchelet GWAS	rs1093109	2	AC074182.1	0.399287	0.574087	0.674319	2	3	22	14	131	104	
Tchelet GWAS	rs1573706	20	PTPRT	0.421405	0.00156	0.022921	2	7	39	41	114	73	
Tchelet GWAS	rs4148871	6	TAP2	0.500007	0.725238	0.328473	4	7	55	37	96	77	
Comi	rs974060	7	TAC1	0.511178	0.294494	0.443883	14	9	56	53	85	59	
Grossman 2007	rs946685	1	IL12RB2	0.545787	0.760198	0.755453	5	2	44	36	105	83	
Tchelet GWAS	rs2521644	7	NPY	0.549577	0.965073	0.759357	28	22	82	59	45	40	
Tchelet GWAS	rs6097801	20	CYP24A1	0.583023	0.000194	0.001719	7	3	20	36	128	82	
Tsareva 2011	rs1800629	6	TNF	0.5881	0.209578	0.420205	6	4	27	29	122	88	
Tchelet GWAS	rs4344916	2	AC083939.1	0.607658	0.028396	0.025091	19	11	49	58	86	52	
Tchelet GWAS	rs1777193	8	AC016885.1	0.737475	2.95E-05	0.096795	9	16	62	48	84	57	
Tsareva 2011	rs6897932	5	IL7Ra	0.803461	0.772128	0.938197	8	7	55	44	92	70	
Grossman 2007	rs1415148	1	CTSS	0.848296	0.504217	0.708954	25	16	71	61	57	44	
Grossman 2007	rs2275235	1	CTSS	0.886713	0.22299	0.515363	21	11	70	58	63	52	
Tchelet GWAS	rs1757545	2	AC078940.2	0.911321	0.066946	0.276505	15	17	63	55	76	49	
Tchelet GWAS	rs9944913	18	NOL4	0.914654	0.312493	0.314049	0	2	33	27	122	92	
Tchelet GWAS	rs4369324	10	RP11-655H13.2	0.953211	0.311301	0.88185	6	5	52	37	97	79	
Tchelet GWAS	rs1161713	13	RP11-629E24.2	1	0.005284	0.060266	1	1	10	17	144	103	
Tchelet GWAS	rs4343256	15	CRTC3	1	0.054967	0.463072	0	0	17	17	138	103	
Tchelet GWAS	rs2177073	18	DTNA	1	0.177174	0.470055	2	3	29	28	124	90	
Grossman 2007	rs1129055	3	CD86	1	0.36822	0.877801	12	8	63	53	80	60	

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Example 10 Analysis for Extreme Responders vs. Extreme Non-Responders Part 2 - Analysis of Candidate Genes (30)

The second analysis was analyzed to a selected set of genetic variants in 30 priority candidate genes (4,012 variants). Power
5 (80%) to identify significant genetic associations with an odds ratio >7 , for variants with an allele frequency greater than 10%.

Results for Extreme Response Definition, Analysis of Candidate Genes (30) Selected a priori for Additive, Allelic and Genotypic models are presented in tables 20-22, respectively. No variants replicated
10 in both cohorts ($P < 0.05$). Less stringent ($P < 0.10 + P < 0.05$) values were used.

In some embodiments genetic markers presented in Tables 20-22 are identified as predictive of response to glatiramer acetate if the p-value for the GALA cohort is less than about 0.10, less than about
15 0.09, less than about 0.08, less than about 0.07 or less than about 0.02.

In some embodiments genetic markers presented in Tables 20-22 are identified as predictive of response to glatiramer acetate if the p-value for the FORTE cohort is less than about 0.05, less than about
20 0.02, less than about 0.01 or less than about 0.005.

In some embodiments genetic markers presented in Tables 20-22 are identified as predictive of response to glatiramer acetate if the p-value for the Combined cohort is less than about 0.05, less than about 0.01 or less than about 0.005.

Table 20. Additive Model, Extreme Response Definition Analysis of Candidate Genes (30) (Gala, Forte, and Combined cohorts)

			GALA				FORTE				COMBINED					
Columns	Gene	Chr	Regression		Regression		Regression		Regression		DD		Dd		dd	
			Armitage	n Odds	Armitage	n Odds	Armitage	n Odds	Armitage	n Odds	DD	(Contr	ols	DD	(Contr	ols
rs1894408	HLA-DOB/TAP2	6	0.089	1.50	0.003	2.85	0.0012	1.86	22	10	81	47	50	64		
rs1894407	HLA-DOB/TAP2	6	0.082	1.52	0.008	2.50	0.0024	1.78	21	10	82	48	51	63		
rs1894406	HLA-DOB/TAP2	6	0.072	1.54	0.009	2.52	0.0037	1.74	20	9	78	46	57	66		
rs12454490	SLC14A2	18	0.082	1.88	0.033	3.66	0.0119	2.10	2	1	40	16	113	104		

Table 21. Allelic Model, Extreme Response Definition, Analysis of Candidate Genes (30) (Gala, Forte, and Combined cohorts)

			GALA				FORTE				COMBINED								
Columns	Chr	Position	Fisher's		Odds		Fisher's		Odds		Fisher's		Odds						
			Exact	Allele Freq.	Ratio	Allele Freq.	Exact	Allele Freq.	Ratio	Allele Freq.	Exact	Allele Freq.	Ratio	Allele Freq.					
rs1894406	6	32787056	0.066	39%	1.58	28%	0.016	2.21	38%	21%	0.005	1.71	26%	20	9	78	46	57	66
rs17884784	4	123541500	0.082	5%	4.05	1%	0.024	0.09	1%	6%	1.000	0.91	2%	0	0	7	6	147	115
rs1894408	6	32786833	0.087	39%	1.53	30%	0.005	2.45	42%	23%	0.002	1.80	28%	22	10	81	47	50	64
rs1894407	6	32787036	0.087	39%	1.54	30%	0.018	2.16	41%	24%	0.003	1.72	28%	21	10	82	48	51	63

Table 22. Genotypic Model, Extreme Response Definition, Analysis of Candidate Genes (30) (Gala, Forte, and Combined cohorts)

			GALA				FORTE				COMBINED										
			Allele		Allele		Allele		Allele		Allele		Allele		Allele		Allele				
			Fisher's	Freq.	(Controls)	Fisher's	Freq.	(Controls)	Fisher's	Freq.	(Controls)	Fisher's	Freq.	(Controls)	Fisher's	Freq.	(Controls)	Fisher's	Freq.	(Controls)	
Columns	Gene	Chr	Position	Exact P	(Cases)	Exact P	(Cases)	Exact P	(Cases)	Exact P	(Cases)	Exact P	(Cases)	Exact P	(Cases)	Exact P	(Cases)	Exact P	(Cases)	Exact P	(Cases)
kgp11964392		18	74768870	0.0135	45%	49%	0.0288	53%	44%	0.0050	49%	48%	30	34	91	48	32	39			
kgp776593		11	1.21E+08	0.0711	11%	6%	0.0391	8%	1%	0.0074	10%	5%	0	1	30	10	125	110			
kgp8702370		3	1.32E+08	0.0747	17%	11%	0.0024	19%	3%	0.0033	18%	9%	7	0	43	21	105	99			
rs1894407	HLA-DOB/TAP2	6	32787036	0.0923	39%	30%	0.0155	41%	24%	0.0063	40%	28%	21	10	82	48	51	63			

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Example 11 Analysis for Extreme Responders vs. Extreme Non-Responders Part 3 - Analysis of Candidate Genes (180)

The third analysis was analyzed to a selected set of genetic variants in 180 priority candidate genes (25,461 variants). Power
5 (80%) to identify significant genetic associations with an odds ratio >7 , for variants with an allele frequency greater than 10%.

Results for Extreme Response Definition, Analysis of Candidate Genes (180) Selected a priori for Additive, Allelic and Genotypic models are presented in tables 23-25, respectively.

10 In some embodiments genetic markers presented in Tables 23-25 are identified as predictive of response to glatiramer acetate if the p-value for the GALA cohort is less than about 0.05, less than about 0.01, less than about 0.005, less than about 0.001, less than about 0.0005 or less than about 10^{-4} .

15 In some embodiments genetic markers presented in Tables 23-25 are identified as predictive of response to glatiramer acetate if the p-value for the FORTE cohort is less than about 0.05, less than about 0.01, less than about 0.005 or less than about 0.001.

20 In some embodiments genetic markers presented in Tables 23-25 are identified as predictive of response to glatiramer acetate if the p-value for the Combined cohort is less than about 0.05, less than about 0.01, less than about 0.005, less than about 0.001, less than about 0.0005 or less than about 10^{-4} .

Table 23. Additive Model, Extreme Response Definition Analysis of Candidate Genes (180) (Gala, Forte, and Combined cohorts)

GALA										FORTE										COMBINED									
Names	Ch	Gene	Func	Allele				Allele				Allele				Allele				Allele				Allele					
				Armitage	Odds	Freq.	(Non-Res)	Armitage	Odds	Freq.	(Non-Res)	Armitage	Odds	Freq.	(Non-Res)	Armitage	Odds	Freq.	(Non-Res)	Armitage	Odds	Freq.	(Non-Res)	Armitage	Odds	Freq.	(Non-Res)		
				P-valu	Rat	%	%	P-valu	%	P-valu	%	P-valu	%	P-valu	%	P-valu	%	P-valu	%	P-valu	%	P-valu	%	P-valu	%	P-valu	%		
rs6110157	20	MACROD2	intron	0.022	0.53	22%	33%	0.0078	0.45	18%	34%	0.00018	0.47	81%	67%	6	13	47	55	100	53								
kgp4017793	10	HIF1A	intron	0.025	0.25	2%	8%	0.023	?	0%	3%	0.00025	0.13	99%	93%	0	0	3	16	151	105								
kgp3496814	13	ALOX5AP	intron	0.029	0.60	39%	52%	0.00086	0.37	43%	67%	0.00061	0.55	58%	43%	28	39	73	59	54	23								
rs10162089	13	ALOX5AP	intron	0.006	1.93	56%	40%	0.0053	2.32	46%	26%	0.00094	1.78	50%	64%	43	14	69	57	42	48								
rs3885907	13	ALOX5AP	intron	0.016	1.73	52%	38%	0.0027	2.56	46%	24%	0.00097	1.77	52%	66%	41	13	68	56	46	52								
rs17238927	13	ALOX5AP	intron	0.042	0.15	1%	5%	0.023	?	0%	3%	0.0013	0.07	100%	96%	0	0	1	10	154	110								
rs9671124	13	ALOX5AP	intron	0.022	1.69	56%	42%	0.0020	2.57	49%	27%	0.0013	1.74	48%	62%	46	17	70	58	39	46								
rs4769060	13	ALOX5AP	intron	0.030	1.69	50%	38%	0.0037	2.43	47%	26%	0.0013	1.77	52%	66%	38	12	73	59	44	50								
rs4075692	13	ALOX5AP	intron	0.022	1.69	56%	42%	0.0023	2.55	49%	27%	0.0016	1.72	48%	62%	45	17	71	58	39	46								
rs11147439	13	ALOX5AP	intron	0.018	0.57	36%	50%	0.0089	0.48	42%	61%	0.0019	0.59	60%	47%	28	33	67	63	60	25								
kgp3276639	10	HIF1A	intron	0.044	1.90	19%	11%	0.036	2.48	21%	10%	0.0020	2.16	80%	90%	9	0	45	25	100	95								
kgp304921	20	MACROD2	intron	0.042	0.34	3%	10%	0.027	0.29	3%	10%	0.0021	0.32	97%	90%	1	2	7	19	144	98								
rs3803277	13	ALOX5AP	intron	0.016	0.57	37%	51%	0.012	0.49	43%	61%	0.0021	0.59	59%	46%	28	35	70	61	57	25								
kgp5440506	13	ALOX5AP	intron	0.017	0.57	36%	50%	0.011	0.49	43%	62%	0.0025	0.60	60%	47%	29	33	65	62	60	25								
rs9671182	13	ALOX5AP	intron	0.019	0.57	37%	51%	0.014	0.50	43%	61%	0.0028	0.60	59%	46%	29	33	68	63	58	24								
rs4254166	13	ALOX5AP	intron	0.025	0.59	37%	50%	0.011	0.49	43%	61%	0.0029	0.60	60%	47%	28	33	69	63	58	25								
rs4356336	13	ALOX5AP	intron	0.020	0.58	37%	51%	0.014	0.50	43%	61%	0.0029	0.60	59%	46%	29	34	68	62	58	25								
rs11002051	10	KCNMA1	intron	0.015	0.29	4%	11%	0.028	0.38	7%	16%	0.0031	0.39	95%	88%	0	1	17	28	138	92								
rs10278591	7	MAD1L1	intron	0.016	1.95	30%	19%	0.043	2.15	26%	14%	0.0032	1.88	72%	83%	13	2	61	38	81	81								
rs4360791	13	ALOX5AP	intron	0.018	0.57	38%	52%	0.021	0.53	44%	61%	0.0034	0.61	58%	45%	30	36	69	60	56	25								
kgp2715873	13	ALOX5AP	intron	0.025	0.59	37%	50%	0.014	0.50	43%	61%	0.0038	0.61	59%	47%	29	33	68	63	58	25								
rs9315047	13	ALOX5AP	intron	0.025	0.59	37%	50%	0.014	0.50	43%	61%	0.0038	0.61	59%	47%	29	33	68	63	58	25								
rs9670531	13	ALOX5AP	intron	0.025	0.59	37%	50%	0.014	0.50	43%	61%	0.0038	0.61	59%	47%	29	33	68	63	58	25								
rs4584668	13	ALOX5AP	intron	0.026	0.59	37%	50%	0.014	0.50	43%	61%	0.0039	0.61	59%	47%	29	33	68	62	58	25								
rs9508832	13	ALOX5AP	intron	0.022	1.73	49%	36%	0.011	2.21	41%	23%	0.0043	1.65	55%	68%	35	11	68	56	52	54								
kgp117398	7	MAD1L1	intron	0.023	1.88	30%	19%	0.043	2.15	26%	14%	0.0045	1.83	72%	82%	13	2	61	39	81	80								
kgp43370912	10	KCNMA1	intron	0.032	0.33	4%	10%	0.028	0.38	7%	16%	0.0074	0.42	95%	88%	0	1	17	26	138	93								

Table 24. Allelic Model, Extreme Response Definition, Analysis of Candidate Genes (180) (Gala, Forte, and Combined cohorts)

Columns	GALA										FORTE										COMBINED																																																																																																																																																																																																																																																																																																																																																																																																																																												
	Chr	Position	Odds					Odds					Odds					Odds					Odds																																																																																																																																																																																																																																																																																																																																																																																																																																										
			Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele	Freq.	Allele	Freq.	Fisher's	Ratio	Allele</

Table 25. Genotypic Model, Extreme Response Definition, Analysis of Candidate Genes (180) (Gala, Forte, and Combined cohorts)

Chromosomes			GALA				FORTE				COMBINED			
			GALA				FORTE				COMBINED			
			Position	Fisher's Exact	Allele Freq.	Allele Freq.	Fisher's Exact	Allele Freq.	Allele Freq.	Fisher's Exact	Allele Freq.	Allele Freq.	DD	DD
Columns	ome				(Cases)	(Cases)		(Cases)	(Cases)		(Cases)	(Cases)		
kgp17000984		6	32602425	0.434211	0.007576	0.007576	0.007576	0.007576	0.007576	0.007576	0.007576	0.007576	0	0
kgp460147		6	32602518	0.022	19%	12%	0.022	22%	16%	0.00020	21%	13%	1	4
kgp2535593		6	32602430	0.021	19%	12%	0.030	22%	16%	0.00037	21%	13%	1	4
kgp6312967		6	32603488	0.021	19%	12%	0.030	22%	16%	0.00037	21%	13%	1	4
kgp3668352		6	32603355	0.025	18%	12%	0.030	22%	16%	0.00039	20%	13%	1	4
kgp3752234		6	32626451	0.047	19%	12%	0.004	22%	13%	0.00048	21%	13%	1	3
rs6110157		20	14055947	0.042	22%	33%	0.013	18%	34%	0.00087	19%	33%	6	13
rs10162089		13	31316738	0.023	56%	40%	0.006	46%	26%	0.0021	50%	36%	43	14
rs11147439		13	31325643	0.041	36%	50%	0.029	42%	61%	0.0039	40%	53%	28	33
kgp5440506		13	31320543	0.033	36%	50%	0.032	43%	62%	0.0046	40%	53%	29	33
kgp11964392		18	74768870	0.013	45%	49%	0.029	53%	44%	0.0050	49%	48%	30	34
kgp3293283		13	31340117	0.038	8%	14%	0.007	8%	21%	0.0053	8%	16%	1	2
rs9671182		13	31321138	0.047	37%	51%	0.039	43%	61%	0.0055	41%	54%	29	33
rs11002051		10	78921392	0.023	4%	11%	0.041	7%	16%	0.0063	5%	12%	0	1
kgp5743538		13	31284424	0.013	9%	16%	0.040	13%	26%	0.0067	12%	19%	5	3
rs4617690		13	31296938	0.013	9%	16%	0.040	13%	26%	0.0067	12%	19%	5	3
rs3803277		13	31318308	0.050	37%	51%	0.042	43%	61%	0.0071	41%	54%	28	35
kgp4370912		10	78918297	0.037	4%	10%	0.041	7%	16%	0.015	5%	12%	0	1
rs17222919		13	31308329	0.026	11%	17%	0.028	14%	29%	0.017	13%	21%	4	4
rs7088816		10	1.01E+08	0.040	16%	21%	0.027	14%	29%	0.027	15%	23%	3	10
kgp11997323		10	1.01E+08	0.037	16%	20%	0.027	14%	29%	0.031	15%	23%	3	10
rs2801405		10	1.01E+08	0.037	16%	20%	0.027	14%	29%	0.031	15%	23%	3	10
kgp2044262		10	1.01E+08	0.040	16%	21%	0.044	15%	29%	0.033	15%	23%	3	10

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Example 12 Analysis for Extreme Responders vs. Extreme Non-Responders Part 4 - Genome Wide Analysis

A full genome-wide analysis (4 M variants) was then conducted. Power (80%) with Bonferroni statistical correction to identify significant
5 genetic associations with an odds ratio >11, for variants with an allele frequency greater than 10%. Approximately 4200 variants were selected for analysis in stage 2 (replication) ($P < 0.001$).

Results for Extreme Response Definition, Genome Wide Analysis for Additive, Allelic and Genotypic models are presented in tables 23-
10 25, respectively.

In some embodiments genetic markers presented in Tables 26-28 are identified as predictive of response to glatiramer acetate if the p-value for the GALA cohort is less than about 0.05, less than about 0.01, less than about 0.001, less than about 0.0005, less than about
15 10^{-4} or less than about $5 * 10^{-5}$.

In some embodiments genetic markers presented in Tables 26-28 are identified as predictive of response to glatiramer acetate if the p-value for the FORTE cohort is less than about 0.05, less than about 0.01, less than about 0.001, less than about 0.0005, less than about
20 10^{-4} or less than about $5 * 10^{-5}$.

In some embodiments genetic markers presented in Tables 26-28 are identified as predictive of response to glatiramer acetate if the p-value for the Combined cohort is less than about 10^{-4} , less than about $5 * 10^{-5}$, less than about 10^{-5} , less than about $5 * 10^{-6}$, less
25 than about 10^{-6} or less than about $5 * 10^{-7}$.

Stage 4. Placebo Cohort (n = 102: 23 R vs. 79 NR) - The placebo cohort (GALA placebo) was analyzed to identify variants associated with placebo response/non-response.

Results for Standard Response Definition, Placebo Cohort Results for
30 Additive, Allelic and Genotypic models are presented in tables 29-31, respectively.

Table 26. Additive Model, Extreme Response Definition, Genome Wide Analysis (Gala, Forte, and Combined cohorts)

Name	Cl	Gene	Location	GALA				FORTE				COMBINED							
				Allele				Allele				Allele				Allele			
				Armitage	Odds	Freq.	(Non-Resp)	Armitage	Odds	Freq.	(Non-Resp)	Armitage	Odds	Freq.	(Non-Resp)	Armitage	Odds	Freq.	(Non-Resp)
				P-value	Rati	(Resp	Resp	P-value	Rati	(Resp	Resp	P-value	Rati	(Resp	Resp	P-value	Rati	(Resp	Resp
kgp6214351	11	UVRAG	INTRON	2.4E-03	0.20	3%	13%	3.4E-05	0.12	3%	17%	9.1E-07	0.17	3%	14%	0	1	9	32
rs10026108	4	?	?	5.5E-05	3.06	62%	41%	8.3E-03	0.42	44%	61%	3.2E-06	0.39	42%	60%	21	36	87	72
kgp3984567	4	?	?	9.8E-05	0.34	38%	59%	6.9E-03	0.42	44%	61%	4.4E-06	0.40	41%	60%	21	36	86	72
kgp10948564	20	?	?	3.4E-03	0.41	20%	33%	4.4E-03	0.41	15%	31%	6.4E-06	0.37	17%	33%	4	8	44	63
kgp9627338	17	RPH3AL	INTRON	2.5E-03	0.36	8%	22%	2.3E-04	0.23	11%	29%	8.2E-06	0.34	10%	24%	1	7	28	44
kgp10788130	12	GRIN2B	INTRON	3.6E-03	?	0%	7%	1.5E-04	0.08	1%	11%	9.7E-06	0.07	1%	8%	0	1	2	18
kgp7077322	4	41334	INTRON	1.8E-03	0.13	2%	10%	3.6E-04	0.16	3%	16%	1.0E-05	0.18	3%	12%	0	0	8	28
rs7348267	20	?	?	3.4E-03	0.41	20%	33%	8.9E-03	0.44	15%	30%	1.1E-05	0.39	17%	32%	4	8	44	62
rs6032205	20	?	?	4.4E-03	0.41	20%	34%	1.0E-02	0.44	15%	30%	1.4E-05	0.39	17%	33%	4	8	44	62
kgp11768533	11	?	?	1.1E-03	2.52	50%	34%	1.8E-03	2.75	47%	26%	1.5E-05	2.37	48%	31%	32	5	85	66
rs502530	6	?	?	2.1E-02	0.19	2%	7%	6.2E-05	?	0%	9%	1.6E-05	0.07	1%	7%	0	0	2	18
rs1478682	11	?	?	7.5E-04	2.57	48%	31%	2.9E-03	2.60	45%	24%	1.7E-05	2.34	46%	29%	31	4	81	63
kgp11467007	5	STC2	INTRON	1.5E-03	0.17	2%	13%	1.2E-03	0.22	5%	17%	1.8E-05	0.24	4%	14%	0	2	12	30
rs196295	10	BAG3	EXON (Synon)	3.6E-04	0.35	11%	30%	6.1E-03	0.41	18%	34%	1.9E-05	0.42	15%	31%	4	15	39	46
rs196343	10	BAG3	INTRON	4.4E-04	0.36	11%	30%	5.3E-03	0.40	18%	34%	2.0E-05	0.42	15%	31%	4	15	39	45
rs7217872	17	PH3AL,RPH3AI	INTRON	3.7E-03	0.37	8%	22%	3.3E-04	0.24	11%	29%	2.0E-05	0.36	10%	24%	1	7	29	43
rs1079303	11	?	?	1.1E-03	2.52	50%	34%	2.3E-03	2.66	47%	26%	2.2E-05	2.33	48%	31%	32	5	85	66
rs10501082	11	?	?	1.1E-03	2.52	50%	34%	2.3E-03	2.66	47%	26%	2.2E-05	2.33	48%	31%	32	5	85	66
rs6718758	2	?	?	6.9E-03	0.53	31%	47%	9.2E-03	0.44	25%	41%	2.2E-05	0.46	28%	45%	10	27	66	56
rs7948420	11	?	?	6.0E-05	0.33	20%	42%	7.0E-03	0.46	33%	51%	2.2E-05	0.46	27%	45%	12	24	61	61
kgp18432055	9	TMEM38B	UTR	5.2E-04	3.51	20%	6%	8.3E-03	4.81	16%	4%	2.3E-05	3.61	18%	6%	5	0	46	14
rs10954782	8	?	?	3.1E-02	1.66	52%	39%	2.1E-03	0.40	37%	59%	2.4E-05	2.11	58%	40%	53	18	74	60
kgp9078300	2	KLHL29	INTRON	1.8E-02	2.18	21%	11%	1.0E-03	4.88	25%	7%	2.7E-05	2.95	23%	10%	6	1	60	22
rs7928078	11	?	?	1.8E-03	2.44	49%	34%	2.3E-03	2.66	47%	26%	3.0E-05	2.30	48%	31%	31	5	85	66
kgp9884626	2	?	?	4.2E-03	?	0%	6%	5.4E-03	?	0%	4%	3.1E-05	?	0%	5%	0	0	0	13
rs9579566	13	?	?	1.4E-03	?	0%	8%	7.8E-03	0.17	2%	9%	3.2E-05	0.11	1%	8%	0	1	3	18

Table 27. Allelic Model, Extreme Response Definition, Genome Wide Analysis (Gala, Forte, and Combined cohorts)

Chromosomes			GALA										FORTE										COMBINED											
			Gene					Locations					Allele					Allele					Allele					Allele						
			Name	Position	Gene(s)	Mutation	(s)	Locations	Fisher's	Ratio	Odds	Allele	Freq.	(Contr	Fisher's	Ratio	Odds	Allele	Freq.	(Contr	Fisher's	Ratio	Odds	Allele	Freq.	(Contr	Fisher's	Ratio	Odds	Allele	Freq.	(Contr	Fisher's	Ratio
kgp621435	11	75546691	UVRAG	Silent	INTRON		3.08E-03	0.21	3%	13%	2.29E-04	0.14	97%	83%	1.51E-06	0.18	3%	14%	0	1	9	32	145	88										
rs759458	2	65245365	SLC1A4,SLMissense	EXON			8.18E-05	2.97	36%	16%	4.98E-02	1.93	64%	77%	2.38E-06	2.61	36%	18%	20	3	71	37	63	81										
rs197523	21	19337261	CHODL,CH Silent,Silen	INTRON			5.54E-05	2.94	40%	19%	3.61E-02	1.99	63%	77%	2.67E-06	2.52	38%	20%	26	5	67	38	62	78										
rs7844274	8	72411302	?	?	?		1.13E-03	0.42	21%	39%	1.57E-02	0.45	83%	69%	2.87E-06	0.40	19%	37%	4	18	50	53	100	50										
kgp107881	12	13898682	GRIN2B	Silent	INTRON		1.51E-03	0.00	0%	7%	7.96E-04	0.09	99%	89%	5.83E-06	0.07	1%	8%	0	1	2	18	153	102										
rs5918137 X		41113080	?	?	?		1.69E-03	2.74	24%	10%	4.13E-02	2.05	68%	81%	6.58E-06	2.72	29%	13%	22	8	44	15	88	98										
kgp191253	2	1.38E+08	THSD7B	Silent	INTRON		1.04E-03	2.85	25%	10%	4.44E-03	3.45	76%	91%	6.88E-06	2.98	25%	10%	13	3	50	18	91	100										
kgp962733	17	90155	RPH3AL,RF Silent,Silen	INTRON			1.46E-03	0.32	8%	22%	1.58E-03	0.30	89%	71%	7.24E-06	0.34	10%	24%	1	7	28	44	125	70										
rs196343	10	1.21E+08	BAG3	Silent	INTRON		8.14E-05	0.30	11%	30%	7.18E-03	0.42	82%	66%	7.88E-06	0.39	15%	31%	4	15	39	45	112	60										
rs196295	10	1.21E+08	BAG3	Synonymo	EXON		7.94E-05	0.30	11%	30%	1.09E-02	0.43	82%	66%	8.19E-06	0.39	15%	31%	4	15	39	46	111	60										
rs343087	12	66260924	HMG2,HIP Silent,Silen	INTRON,EXON			3.77E-03	2.96	18%	7%	5.26E-03	3.70	78%	93%	8.46E-06	3.40	20%	7%	12	0	39	17	103	104										
kgp184320	9	1.09E+08	TMEM38B	Silent	UTR		3.76E-04	3.72	20%	6%	1.08E-02	4.35	84%	96%	1.53E-05	3.56	18%	6%	5	0	46	14	104	106										
rs7725112	5	1.74E+08	?	?	?		4.85E-04	3.59	21%	7%	3.71E-02	2.61	80%	91%	1.76E-05	3.17	20%	7%	5	1	53	16	97	104										
rs7028906	9	1.08E+08	?	?	?		8.10E-05	4.36	21%	6%	2.72E-02	3.65	86%	96%	1.76E-05	3.63	17%	5%	4	0	45	13	106	108										
rs9579566	13	30980265	?	?	?		3.90E-04	0.00	0%	8%	1.68E-02	0.18	98%	91%	1.80E-05	0.11	1%	8%	0	1	3	18	152	102										
kgp239141	2	43425645	?	?	?		7.83E-04	0.39	18%	36%	4.73E-03	0.41	76%	57%	1.81E-05	0.44	21%	38%	8	20	49	52	96	49										
kgp320293	12	13859947	GRIN2B	Silent	INTRON		8.78E-03	0.10	1%	7%	6.75E-04	0.09	99%	88%	1.87E-05	0.11	1%	8%	0	1	3	18	150	101										
kgp988462	2	2.07E+08	?	?	?		5.91E-03	0.00	0%	6%	2.23E-02	0.00	100%	96%	1.93E-05	0.00	0%	5%	0	0	0	13	154	108										
kgp227932 X		92601576	?	?	?		1.68E-03	0.47	34%	52%	4.17E-03	0.44	65%	44%	1.93E-05	0.47	35%	53%	32	41	42	47	78	33										
kgp568095	6	1.64E+08	?	?	?		6.18E-04	0.43	29%	48%	2.57E-02	0.51	70%	54%	1.94E-05	0.46	30%	48%	13	27	65	61	76	33										
kgp810745	6	1.64E+08	?	?	?		1.11E-03	0.45	35%	54%	2.91E-02	0.52	66%	50%	1.96E-05	0.47	34%	53%	17	32	72	64	65	25										
kgp114670	5	1.73E+08	STC2	Silent	INTRON		6.44E-04	0.16	2%	13%	4.17E-03	0.26	95%	83%	1.96E-05	0.25	4%	14%	0	2	12	30	143	89										
kgp109485	20	44082511	?	?	?		9.59E-03	0.49	20%	33%	4.00E-03	0.37	85%	69%	2.02E-05	0.42	17%	33%	4	8	44	63	107	50										
rs7217872	17	88988	RPH3AL,RF Silent,Silen	INTRON			2.31E-03	0.33	8%	22%	1.77E-03	0.32	89%	71%	2.05E-05	0.36	10%	24%	1	7	29	43	125	71										
rs343092	12	66250940	HMG2,HIP Silent,Silen	INTRON,EXON			6.14E-03	2.81	17%	7%	8.40E-03	3.53	79%	93%	2.18E-05	3.24	20%	7%	11	0	39	17	105	104										
rs7948420	11	27276450	?	?	?		4.80E-05	0.35	20%	42%	8.59E-03	0.46	67%	49%	2.27E-05	0.46	27%	45%	12	24	61	61	82	36										
rs9913349	17	68260070	?	?	?		2.63E-03	2.30	32%	17%	3.61E-02	1.99	63%	77%	2.31E-05	2.34	35%	19%	15	5	78	35	62	81										
rs6718758	2	60328802	?	?	?		6.51E-03	0.51	31%	47%	1.42E-02	0.48	75%	59%	2.36E-05	0.46	28%	45%	10	27	66	56	79	38										

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Table 29. Additive Model, Extreme Response Definition, Genome Wide Placebo Cohort Analysis

Placebo													
Name	Chr	Position	Gene(s)	Mutation	Gene Locations(s)	Armitage P	Regression Odds Ratio	DD (Cases)	DD (Controls)	Dd (Cases)	Dd (Controls)	dd (Cases)	dd (Controls)
rs1978721	19	30966217	ZNF536	Silent	INTRON	9.89E-09	35.3	0	0	11	2	12	77
kgp7344529	19	30967564	ZNF536	Silent	INTRON	9.89E-09	35.3	0	0	11	2	12	77
rs7252241	19	30967836	ZNF536	Silent	INTRON	9.89E-09	35.3	0	0	11	2	12	77
rs1978720	19	30968371	ZNF536	Silent	INTRON	9.89E-09	35.3	0	0	11	2	12	77
kgp146166	19	30965980	ZNF536	Silent	INTRON	1.92E-07	13.8	0	0	14	8	9	71
rs8112863	19	30965063	ZNF536	Silent	INTRON	2.37E-07	13.6	0	0	14	8	9	70
kgp2877482	6	1644677	GMDS, GMDS	Silent, Silent	INTRON	3.47E-07	17.2	0	0	11	4	12	75
kgp7851536	15	27960322	?	?	?	3.76E-07	?	0	0	7	0	16	79
kgp9348779	15	101900592	PCSK6, PCSK6, PCSK6, PCSK6	Silent, Silent, Silent, Silent	INTRON	3.76E-07	?	0	0	7	0	16	79
rs2289333	15	40617209	?	?	?	5.68E-07	17.9	1	0	9	3	13	76
kgp2471573	15	40633138	C15orf52	Synonymous_A5A	EXON	5.68E-07	17.9	1	0	9	3	13	76
kgp8598661	6	1627678	GMDS, GMDS	Silent, Silent	INTRON	6.01E-07	12.5	1	0	11	6	11	73
rs16846841	2	197063250	?	?	?	6.12E-07	41.6	0	0	8	1	15	78
rs7565256	2	79227275	?	?	?	6.17E-07	9.1	4	0	14	22	5	56
kgp12396787	22	27267611	?	?	?	7.21E-07	41.1	0	0	8	1	15	77
kgp6535349	15	40614200	?	?	?	7.54E-07	24.4	0	0	9	2	14	76
kgp9775757	1	23068465	EPHB2, EPHB2	Silent, Silent	INTRON	1.13E-06	9.2	3	0	15	22	5	57
kgp2151888	2	79295288	?	?	?	1.87E-06	8.2	3	0	13	19	6	60
kgp4985243	7	136556162	CHRM2, CHRM2, CHRM2, CHRM2, CHRM2, CHRM2, CHRM2, CHRM2	Silent, Silent, Silent, Silent, Silent, Silent, Silent, Silent	INTRON	2.25E-06	9.3	1	0	13	11	9	68
kgp6870400	2	79278036	?	?	?	2.38E-06	7.4	4	0	13	22	6	57
rs1077476	15	40619743	?	?	?	2.53E-06	13.1	1	0	9	4	13	74
kgp2136475	15	40623593	?	?	?	2.53E-06	13.1	1	0	9	4	13	74
rs4935590	10	57059483	?	?	?	2.59E-06	8.2	2	0	12	12	9	67
rs16907220	10	57059690	?	?	?	2.59E-06	8.2	2	0	12	12	9	67
rs1073665	10	57061057	?	?	?	2.59E-06	8.2	2	0	12	12	9	67
rs4477500	12	128645821	?	?	?	2.62E-06	7.3	9	2	10	37	3	39
kgp9016053	17	69386788	?	?	?	2.87E-06	10.5	1	0	10	7	10	71
kgp2617488	3	11849777	TAMM41	Silent	INTRON	2.88E-06	?	0	0	6	0	17	79
kgp3537954	5	103927513	?	?	?	2.88E-06	74935934087673200.0	0	0	6	0	17	79
kgp9400093	5	104031832	?	?	?	2.88E-06	74935934087673200.0	0	0	6	0	17	79
kgp3681524	7	145920329	CNTNAP2	Silent	INTRON	2.88E-06	45450941538370800.0	0	0	6	0	17	79
kgp788303	10	23646459	?	?	?	2.88E-06	74935934087672700.0	0	0	6	0	17	79
kgp7824246	12	11333716	?	?	?	2.88E-06	74935934087672700.0	0	0	6	0	17	79
kgp27533766	12	65501698	WIF1	Silent	INTRON	2.88E-06	74935934087672700.0	0	0	6	0	17	79
kgp4089310	18	7309451	?	?	?	2.88E-06	?	0	0	6	0	17	79
rs17225585	17	69370430	?	?	?	3.05E-06	10.2	1	0	11	7	11	69
rs13104183	4	113323634	ALPK1, ALPK1, ALPK1	Silent, Silent, Silent	INTRON, EXON	3.43E-06	6.7	4	0	10	16	8	63
kgp11962282	10	88223587	WAPAL	Silent	INTRON	3.61E-06	10.5	1	0	10	6	12	73
rs3934982	2	242926558	?	?	?	3.66E-06	11.5	1	0	9	5	12	74
kgp896539	3	135473872	?	?	?	3.77E-06	10.6	0	0	12	8	10	71
rs6743255	2	205363596	?	?	?	4.33E-06	7.7	2	0	13	15	8	64
kgp5046752	2	179650234	TTN, TTN, TTN, TTN, TTN	Silent	INTRON	4.67E-06	34.1	0	0	7	1	16	78
kgp3420885	13	112188913	?	?	?	4.67E-06	34.1	0	0	7	1	16	78
kgp3423367	19	54113722	?	?	?	4.67E-06	34.1	0	0	7	1	16	78
kgp9522435	19	30951753	ZNF536	Silent	INTRON	4.71E-06	20.5	0	0	8	2	15	77
kgp5544649	19	30958606	ZNF536	Silent	INTRON	4.71E-06	20.5	0	0	8	2	15	77
kgp3185857	22	27269249	?	?	?	4.71E-06	20.5	0	0	8	2	15	77
kgp5863276	22	27274898	?	?	?	4.71E-06	20.5	0	0	8	2	15	77
rs17825388	17	69380584	?	?	?	4.74E-06	9.2	1	0	11	8	11	71
rs1942396	18	69347308	?	?	?	4.74E-06	9.2	1	0	11	8	11	71
kgp2575625	2	218219226	DIRC3	Silent	INTRON	5.23E-06	8.6	1	0	12	10	10	69
kgp11688655	2	218219697	DIRC3	Silent	INTRON	5.23E-06	8.6	1	0	12	10	10	69
kgp3778675	2	218226516	DIRC3	Silent	INTRON	5.23E-06	8.6	1	0	12	10	10	69
rs10488907	4	113312105	ALPK1, ALPK1, ALPK1	Silent, Silent, Silent	INTRON, EXON	5.36E-06	7.5	2	0	12	13	9	66
kgp2832863	3	8820301	?	?	?	5.38E-06	33.7	0	0	7	1	16	77
kgp6643157	3	13145604	?	?	?	5.46E-06	20.3	0	0	8	2	15	76
kgp4292871	22	27274445	?	?	?	5.46E-06	20.3	0	0	8	2	15	76
rs6643055	X	111782861	?	?	?	5.65E-06	18.3	1	0	7	2	15	77
rs12005792	9	87236739	?	?	?	6.46E-06	6.8	3	1	15	22	5	56
rs882829	15	40607689	?	?	?	6.98E-06	10.6	1	0	9	5	13	74
kgp1305638	6	122195448	?	?	?	7.74E-06	29.6	1	0	6	1	16	78
rs6673115	1	23069649	EPHB2, EPHB2	Silent, Silent	INTRON	8.25E-06	6.7	5	1	14	30	4	48
kgp7380442	22	28746343	TTC28	Silent	INTRON	8.80E-06	?	1	0	5	0	17	79
kgp4898364	22	29092726	CHEK2, CHEK2, CHEK2	Silent, Silent, Silent	INTRON	8.80E-06	?	1	0	5	0	17	79
kgp9420863	1	105167334	?	?	?	9.42E-06	9.0	0	0	13	10	10	69
kgp100271	1	105186472	?	?	?	9.42E-06	9.0	0	0	13	10	10	69
kgp4009576	1	105189899	?	?	?	9.42E-06	9.0	0	0	13	10	10	69
kgp11130156	12	20871256	SLCO1C1, SLCO1C1, SLCO1C1, SLCO1C1	Silent, Silent, Silent, Silent	INTRON	9.52E-06	6.4	2	1	13	13	8	65
rs10746192	12	81942162	PPFIA2, PPFIA2, PPFIA2, PPFIA2, PPFIA2, PPFIA2, PPFIA2, PPFIA2	Silent, Silent, Silent, Silent, Silent, Silent, Silent, Silent	INTRON	9.87E-06	8.0	8	5	15	45	0	29
kgp8919080	7	84958459	?	?	?	9.94E-06	8.9	1	0	10	7	12	72

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Table 30. Allelic Model, Extreme Response Definition, Genome Wide Placebo Cohort Analysis

Placebo															
Name	Chr	Position	Gene(s)	Mutation	Gene Locations (s)	Fisher's Exact P	Odds Ratio	Allele Freq.	Allele Freq.	DD	DD	Dd	Dd	dd	dd
							(Minor Allele)	(Cases)	(Controls)	(Cases)	(Control s)	(Cases)	(Control s)	(Cases)	(Control s)
kgp106385	3	196573166	?	?	?	1.00E-06	0.1	7%	44%	0	17	3	35	20	27
rs1978721	19	30966217	ZNF536	Silent	INTRON	1.49E-06	24.5	24%	1%	0	0	11	2	12	77
kgp734452	19	30967564	ZNF536	Silent	INTRON	1.49E-06	24.5	24%	1%	0	0	11	2	12	77
rs7252241	19	30967836	ZNF536	Silent	INTRON	1.49E-06	24.5	24%	1%	0	0	11	2	12	77
rs1978720	19	30968371	ZNF536	Silent	INTRON	1.49E-06	24.5	24%	1%	0	0	11	2	12	77
kgp183404	3	196579489	?	?	?	2.26E-06	0.1	7%	42%	0	14	3	38	20	27
kgp860737	17	20459947	?	?	?	4.36E-06	0.0	2%	35%	0	10	1	35	20	34
rs2289333	15	40617209	?	?	?	5.79E-06	16.2	24%	2%	1	0	9	3	13	76
kgp247157	15	40633138	C15orf52	Synonymo	EXON	5.79E-06	16.2	24%	2%	1	0	9	3	13	76
rs7565256	2	79227275	?	?	?	7.04E-06	5.6	48%	14%	4	0	14	22	5	56
kgp859866	6	1627678	GMD5,GM	Silent,Siler	INTRON	8.30E-06	10.0	28%	4%	1	0	11	6	11	73
rs1310418	4	113323634	ALPK1,ALP	Silent,Siler	INTRON,E	9.26E-06	6.1	41%	10%	4	0	10	16	8	63
rs4477500	12	128645821	?	?	?	9.70E-06	4.9	64%	26%	9	2	10	37	3	39
kgp359896	4	7649861	SORCS2	Silent	INTRON	9.97E-06	0.0	2%	31%	0	7	1	35	22	37
kgp111645	17	20459328	?	?	?	1.07E-05	0.1	4%	35%	0	9	2	36	21	32
kgp146166	19	30965980	ZNF536	Silent	INTRON	1.22E-05	8.2	30%	5%	0	0	14	8	9	71
rs8112863	19	30965063	ZNF536	Silent	INTRON	1.38E-05	8.1	30%	5%	0	0	14	8	9	70
rs2555629	4	175430288	HPGD,HPG	Silent,Siler	INTRON,E	1.40E-05	4.6	61%	25%	11	4	6	32	6	43
kgp215188	2	79295288	?	?	?	1.44E-05	5.6	43%	12%	3	0	13	19	6	60
kgp553777	20	35531097	SAMHD1	Silent	INTRON	1.68E-05	5.5	41%	11%	4	1	11	16	8	62
kgp400475	20	35539858	SAMHD1	Silent	INTRON	1.68E-05	5.5	41%	11%	4	1	11	16	8	62
kgp977575	1	23068465	EPHB2,EPI	Silent,Siler	INTRON	1.68E-05	5.2	46%	14%	3	0	15	22	5	57
kgp687040	2	79278036	?	?	?	1.68E-05	5.2	46%	14%	4	0	13	22	6	57
rs763318	4	12963574	?	?	?	1.70E-05	5.4	83%	47%	15	20	8	33	0	25
rs4935590	10	57059483	?	?	?	1.73E-05	6.5	35%	8%	2	0	12	12	9	67
rs1690722	10	57059690	?	?	?	1.73E-05	6.5	35%	8%	2	0	12	12	9	67
rs1073665	10	57061057	?	?	?	1.73E-05	6.5	35%	8%	2	0	12	12	9	67
kgp596925	4	12976777	?	?	?	1.73E-05	4.5	70%	34%	11	10	10	33	2	36
kgp287748	6	1644677	GMD5,GM	Silent,Siler	INTRON	1.81E-05	12.1	24%	3%	0	0	11	4	12	75
rs4916561	3	196576109	?	?	?	1.84E-05	0.1	7%	38%	0	12	3	36	20	30
kgp228237	X	31244702	DMD,DMC	Silent,Siler	INTRON	1.91E-05	0.1	2%	30%	0	17	1	14	22	48
rs1077476	15	40619743	?	?	?	2.00E-05	11.9	24%	3%	1	0	9	4	13	74
kgp213647	15	40623593	?	?	?	2.00E-05	11.9	24%	3%	1	0	9	4	13	74
kgp785153	15	27960322	?	?	?	2.04E-05	?	15%	0%	0	0	7	0	16	79
kgp934877	15	101900592	PCSK6,PCS	Silent,Siler	INTRON	2.04E-05	?	15%	0%	0	0	7	0	16	79

Table 31. Genotype Model, Extreme Response Definition, Genome Wide Placebo Cohort Analysis

Placebo															
Name	Chr	Position	Gene(s)	Mutation	Gene Locations (s)	Fisher's Exact P	Allele								
							Allele Freq. (Cases)	Freq. (Controls)	DD (Case s)	DD (Cont rols)	Dd (Case s)	Dd (Cont rols)	dd (Case s)	dd (Cont rols)	
rs1978721	19	30966217	ZNF536	Silent	INTRON	4.57E-07	24%	1%	0	0	11	2	12	77	
kgp7344529	19	30967564	ZNF536	Silent	INTRON	4.57E-07	24%	1%	0	0	11	2	12	77	
rs7252241	19	30967836	ZNF536	Silent	INTRON	4.57E-07	24%	1%	0	0	11	2	12	77	
rs1978720	19	30968371	ZNF536	Silent	INTRON	4.57E-07	24%	1%	0	0	11	2	12	77	
kgp146166	19	30965980	ZNF536	Silent	INTRON	1.91E-06	30%	5%	0	0	14	8	9	71	
rs8112863	19	30965063	ZNF536	Silent	INTRON	2.19E-06	30%	5%	0	0	14	8	9	70	
rs7565256	2	79227275	?	?	?	2.25E-06	48%	14%	4	0	14	22	5	56	
kgp6295377	19	30953846	ZNF536	Silent	INTRON	3.08E-06	20%	2%	0	1	9	1	14	77	
rs4477500	12	128645821	?	?	?	3.54E-06	64%	26%	9	2	10	37	3	39	
rs11705401	22	37678096	?	?	?	3.97E-06	13%	37%	2	4	2	50	19	25	
kgp2536097	6	25181978	?	?	?	5.58E-06	74%	41%	14	8	6	48	3	23	
rs2109066	19	28835327	?	?	?	5.93E-06	9%	31%	2	5	0	39	21	35	
kgp2877482	6	1644677	GMD5,GM	Silent,Siler	INTRON	6.14E-06	24%	3%	0	0	11	4	12	75	
kgp9775757	1	23068465	EPHB2,EP	Silent,Siler	INTRON	6.34E-06	46%	14%	3	0	15	22	5	57	
kgp6601755	19	28886975	?	?	?	6.76E-06	11%	33%	2	3	1	45	19	30	
kgp8598661	6	1627678	GMD5,GM	Silent,Siler	INTRON	8.89E-06	28%	4%	1	0	11	6	11	73	
rs2159327	19	28835571	?	?	?	9.75E-06	9%	31%	2	5	0	39	20	35	
kgp2151888	2	79295288	?	?	?	9.91E-06	43%	12%	3	0	13	19	6	60	
rs2289333	15	40617209	?	?	?	1.01E-05	24%	2%	1	0	9	3	13	76	
kgp2471573	15	40633138	C15orf52	Synonymo	EXON	1.01E-05	24%	2%	1	0	9	3	13	76	
kgp6870400	2	79278036	?	?	?	1.27E-05	46%	14%	4	0	13	22	6	57	
kgp6850713	19	28885593	?	?	?	1.28E-05	7%	32%	1	3	1	44	20	32	
kgp7851536	15	27960322	?	?	?	1.33E-05	15%	0%	0	0	7	0	16	79	
kgp9348779	15	101900592	PCSK6,PCS	Silent,Siler	INTRON	1.33E-05	15%	0%	0	0	7	0	16	79	
rs995834	19	28866596	?	?	?	1.39E-05	11%	32%	2	4	1	43	20	32	
rs1773631	10	25665449	GPR158	Silent	INTRON	1.43E-05	27%	7%	0	2	12	7	10	70	
kgp8034516	8	97282138	PTDSS1	Silent	INTRON	1.46E-05	20%	3%	0	1	9	2	14	76	
rs13280716	8	97282560	PTDSS1	Silent	INTRON	1.46E-05	20%	3%	0	1	9	2	14	76	
kgp303315	8	97283313	PTDSS1	Silent	INTRON	1.46E-05	20%	3%	0	1	9	2	14	76	
kgp5433489	8	97302091	PTDSS1	Silent	INTRON	1.46E-05	20%	3%	0	1	9	2	14	76	
rs17707686	8	97312442	PTDSS1	Silent	INTRON	1.46E-05	20%	3%	0	1	9	2	14	76	
rs727047	22	37677719	?	?	?	1.48E-05	13%	35%	2	4	2	48	19	27	
kgp7521451	8	97297894	PTDSS1	Silent	INTRON	1.49E-05	20%	4%	0	2	9	2	13	74	
rs2056136	12	20867893	SLCO1C1,S	Silent,Siler	INTRON	1.50E-05	35%	9%	1	1	14	12	8	66	
rs10746192	12	81942162	PPFIA2,PPI	Silent,Siler	INTRON	1.54E-05	67%	35%	8	5	15	45	0	29	
rs2555629	4	175430288	HPGD,HPG	Silent,Siler	INTRON,E	1.57E-05	61%	25%	11	4	6	32	6	43	
kgp12537012	8	97285429	PTDSS1	Silent	INTRON	1.60E-05	20%	3%	0	1	9	2	14	75	
rs9969509	8	97293953	PTDSS1	Silent	INTRON	1.60E-05	20%	3%	0	1	9	2	14	75	
kgp6535349	15	40614200	?	?	?	1.60E-05	20%	1%	0	0	9	2	14	76	
rs16846841	2	197063250	?	?	?	1.73E-05	17%	1%	0	0	8	1	15	78	
kgp12396787	22	27267611	?	?	?	1.87E-05	17%	1%	0	0	8	1	15	77	
kgp4985243	7	136556162	CHRM2,Cf	Silent,Siler	INTRON	1.91E-05	33%	7%	1	0	13	11	9	68	
rs4935590	10	57059483	?	?	?	1.98E-05	35%	8%	2	0	12	12	9	67	
rs16907220	10	57059690	?	?	?	1.98E-05	35%	8%	2	0	12	12	9	67	
rs1073665	10	57061057	?	?	?	1.98E-05	35%	8%	2	0	12	12	9	67	
rs2292275	1	163292217	NUF2,NUF	Silent,Siler	INTRON,E	2.11E-05	57%	27%	4	6	18	30	1	42	
rs7962380	12	128643018	?	?	?	2.27E-05	67%	34%	11	5	9	44	3	30	
kgp10638512	3	196573166	?	?	?	2.34E-05	7%	44%	0	17	3	35	20	27	

Example 13 Association Analyses Corrected for Ancestry

A Principal Components Analysis (PCA) was performed in order to investigate potential population stratification among cases and controls. Sample-specific Eigen values were calculated to produce an output of 1st and 2nd Principal Components which can be used to infer patient ancestry.

An association analysis was performed using an Additive Genetic Model with Principal Components Analysis correction for population stratification; results are presented in Table 32.

Table 32. Regression, Additive Model, Corrected for ancestry by PCA

						GALA		FORTE				COMBINED															
						Gene		Allele		Allele		Allele		Allele		DD		DD		Dd		Dd		dd		dd	
						Locations		Allele		Allele		Allele		Allele		(Case		(Cont		(Case		(Cont		(Case		(Cont	
Name	Chr	Positio	Gene(s)	Mutati	(s)	on P	(Cases)	on P	(Cases)	on P	(Cases)	on P	(Cases)	on P	(Cases)	s)	rol	s)	rol	s)	rol	s)	rol	s)	rol	s)	rol
kgp24415	2	1.74E+08	?	?	?	1.91E-05	0%	5%	1.28E-02	0%	3%	2.24E-07	0%	4%	0	0	3	16	396	165							
kgp26026	13	79972606	RBM26	Silent	INTRON	1.47E-04	0%	3%	2.92E-04	0%	4%	2.54E-07	0%	4%	0	0	1	13	397	167							
kgp12008	2	73759636	ALMS1	Silent	INTRON	1.49E-04	0%	4%	2.26E-04	1%	5%	6.38E-07	0%	4%	0	0	3	16	396	165							
rs1688600	7	78021500	MAGI2	Silent	INTRON,E	1.93E-03	20%	11%	3.01E-05	20%	5%	8.60E-07	20%	9%	6	2	147	28	246	149							
kgp25952	13	80027089	?	?	?	4.30E-04	0%	3%	2.86E-04	0%	4%	8.77E-07	0%	3%	0	0	1	12	398	168							
kgp11141	20	35283733	NDRG3,N	Silent,Sile	INTRON	2.69E-03	2%	7%	3.18E-05	1%	6%	9.79E-07	1%	6%	0	1	11	21	388	158							
kgp34508	16	57268931	RSPRY1	Silent	INTRON	5.32E-03	1%	4%	1.47E-05	0%	7%	1.26E-06	1%	5%	0	0	5	17	394	164							
kgp22996	20	16933074	?	?	?	5.73E-03	2%	5%	3.71E-05	1%	8%	1.48E-06	1%	6%	0	0	11	23	388	158							
kgp12230	5	27037978	CDH9	Silent	INTRON	2.71E-03	1%	5%	7.14E-06	2%	9%	1.71E-06	1%	6%	0	0	10	22	386	159							
kgp96273	17	90155	RPH3AL,R	Silent,Sile	INTRON	6.18E-04	10%	21%	3.96E-03	13%	20%	1.87E-06	10%	21%	6	7	71	61	320	113							
rs1025179	7	78025427	MAGI2	Silent	INTRON,E	1.71E-03	20%	11%	3.76E-05	19%	5%	1.98E-06	20%	9%	6	2	145	29	248	150							
rs2816838	10	52714759	?	?	?	1.20E-03	14%	23%	1.38E-03	13%	22%	2.41E-06	13%	23%	4	8	92	67	303	106							
kgp62369	2	60301030	?	?	?	3.77E-04	31%	44%	4.52E-03	26%	39%	2.86E-06	28%	42%	30	34	166	85	203	62							
kgp23563	16	19771577	IQCK	Silent	INTRON	1.76E-04	12%	22%	1.39E-03	14%	26%	2.92E-06	13%	23%	4	5	98	75	297	101							
kgp77303	16	19740243	IQCK	Silent	INTRON	2.39E-04	13%	22%	1.06E-03	14%	26%	3.08E-06	13%	23%	4	5	99	74	295	101							
kgp47058	12	19907696	?	?	?	2.12E-05	30%	47%	3.99E-02	33%	43%	3.44E-06	31%	46%	41	38	169	89	189	54							
rs7191155	16	19800213	IQCK	Missense	EXON	2.52E-04	12%	22%	1.18E-03	14%	26%	4.02E-06	13%	23%	4	5	97	74	295	101							
kgp80307	8	6328607	MCPH1	Silent	INTRON	1.62E-02	2%	5%	1.78E-05	1%	7%	4.03E-06	1%	6%	0	1	9	18	388	162							
rs9931167	16	19792598	IQCK	Silent	INTRON	2.53E-04	12%	22%	1.39E-03	14%	26%	4.16E-06	13%	23%	4	5	98	74	297	101							
rs7217872	17	88988	RPH3AL,R	Silent,Sile	INTRON	1.35E-03	11%	20%	3.00E-03	13%	21%	4.20E-06	11%	21%	6	7	74	61	319	113							
rs1164812	16	19820694	IQCK	Silent	INTRON	3.15E-04	12%	22%	1.08E-03	14%	26%	4.25E-06	13%	23%	4	5	97	74	297	102							
rs3829539	16	19722366	C16orf88	Silent	INTRON	2.51E-04	12%	22%	1.40E-03	15%	26%	4.53E-06	13%	23%	4	5	98	74	296	101							
rs2660214	10	52732452	?	?	?	1.68E-03	14%	23%	1.84E-03	13%	22%	4.68E-06	13%	23%	4	8	94	66	301	107							
rs6718758	2	60328802	?	?	?	3.14E-03	33%	45%	4.38E-04	28%	44%	4.69E-06	31%	44%	35	38	175	85	189	58							
kgp10594	1	2.16E+08	USH2A	Silent	INTRON	2.20E-05	0%	5%	2.84E-02	1%	5%	4.94E-06	1%	5%	0	0	6	18	391	163							
rs1858973	16	19743649	IQCK	Silent	INTRON	3.15E-04	12%	22%	1.38E-03	15%	26%	5.09E-06	13%	23%	4	5	99	74	295	102							
kgp88178	6	32744440	?	?	?	6.70E-04	36%	49%	4.72E-04	42%	60%	5.13E-06	39%	53%	50	44	208	103	135	34							
kgp38541	16	19721806	C16orf88	Silent	INTRON	3.14E-04	12%	22%	1.29E-03	14%	26%	5.23E-06	13%	23%	4	5	98	74	297	102							
kgp29794	10	18397332	?	?	?	3.45E-03	2%	7%	2.96E-04	2%	8%	5.49E-06	2%	7%	0	0	16	26	382	155							
rs543122	3	1.24E+08	KALRN,KA	Silent,Sile	INTRON	2.87E-05	41%	57%	1.56E-02	44%	57%	5.65E-06	42%	57%	70	54	195	97	131	29							
kgp25216	1	23758427	ASAP3,AS	Silent,Sile	INTRON	1.03E-03	0%	3%	3.25E-03	0%	3%	5.69E-06	0%	3%	0	0	2	12	397	169							
rs8055485	16	19750051	IQCK	Silent	INTRON	3.15E-04	12%	22%	1.51E-03	15%	26%	5.77E-06	13%	23%	4	5	98	74	296	102							
rs9931211	16	19813605	IQCK	Silent	INTRON	3.15E-04	12%	22%	1.51E-03	15%	26%	5.77E-06	13%	23%	4	5	98	74	296	102							
rs9817308	3	1.24E+08	KALRN,KA	Silent,Sile	INTRON	2.46E-05	41%	58%	3.14E-02	45%	57%	5.89E-06	43%	57%	71	55	199	96	127	29							
kgp62143	11	75546691	UVRAG	Silent	INTRON	4.73E-03	5%	11%	1.34E-04	4%	13%	6.31E-06	5%	12%	0	2	37	39	361	140							
rs9579566	13	30980265	?	?	?	1.22E-04	2%	8%	1.55E-02	2%	7%	6.66E-06	2%	8%	0	1	18	27	381	153							
kgp50683	16	19756348	IQCK	Silent	INTRON	1.52E-04	16%	27%	2.10E-03	20%	34%	6.70E-06	18%	29%	10	12	126	82	262	86							
rs6497396	16	19735697	IQCK	Silent	INTRON	2.47E-04	13%	23%	1.48E-03	16%	29%	6.74E-06	14%	25%	6	6	102	77	290	98							
rs7228827	18	76900411	ATP9B	Silent	INTRON	2.53E-04	21%	11%	8.65E-03	20%	11%	6.90E-06	21%	11%	20	1	124	37	254	143							
rs950928	16	19824638	IQCK	Silent	INTRON	5.52E-04	13%	22%	1.64E-03	15%	26%	6.96E-06	14%	24%	4	5	102	75	293	100							
rs7579987	2	60307009	?	?	?	3.85E-03	36%	47%	4.94E-04	33%	48%	7.14E-06	33%	47%	40	41	184	87	175	52							
kgp10305	11	99881768	CNTN5,CN	Silent,Sile	INTRON,E	3.08E-03	10%	18%	1.45E-03	7%	16%	7.23E-06	8%	17%	3	6	61	50	334	123							
kgp10910	16	19803199	IQCK	Silent	INTRON	4.44E-04	12%	21%	1.39E-03	14%	26%	7.43E-06	13%	23%	4	5	98	73	297	102							
kgp16887	21	43016736	?	?	?	1.94E-03	5%	11%	3.96E-03	3%	11%	7.70E-06	4%	11%	1	2	30	37	368	142							
kgp11002	11	1.18E+08	CD3G	Silent	INTRON	4.13E-03	1%	3%	2.94E-04	0%	4%	8.07E-06	0%	4%	0	0	3	13	394	167							
rs6895094	5	1.41E+08	ARAP3	Silent	INTRON	6.18E-04	38%	52%	1.33E-02	35%	48%	8.17E-06	37%	51%	56	46	181	92	161	43							
rs2074037	16	19725130	C16orf88	Silent	INTRON	5.92E-04	13%	22%	1.25E-03	15%	26%	8.40E-06	14%	23%	4	5	101	73	294	101							
kgp27000	16	19750275	IQCK	Silent	INTRON	2.51E-04	13%	23%	2.90E-03	15%	28%	8.56E-06	14%	24%	6	6	102	76	291	98							

Example 14 Regression Analysis

Regression analysis was conducted using an additive genetic model to identify additional clinical and genetic variants that are highly associated with response after correction for the most significantly associated variables.

For clinical factors, regression analyses revealed two highly associated clinical covariates: "Log number of relapses in the last two years" significantly associated with response to glatiramer acetate (combined cohorts p-value 3.6×10^{-32} , odds ratio 14.5 (95%CI 8.6-24.4)) and "Baseline Expanded Disability Status Scale (EDSS) Score" (combined cohorts p-value 5.9×10^{-10} , odds ratio 0.62 (95%CI 8.6-24.4)) with higher baseline EDSS scores (increased MS disability) associated with increased likelihood of non-response to glatiramer acetate. Importantly, these clinical factors were significantly associated with glatiramer acetate response in both the GALA and FORTE patient cohorts.

Table 33. Clinical co-variates associated with response to glatiramer acetate.

Variable	GALA cohort (n = 318)			FORTE cohort (n = 262)			COMBINED cohorts (N = 580)		
	Odds Ratio	(95% CI)	P-Value	Odds Ratio	(95% CI)	P-Value	Odds Ratio	(95% CI)	P-Value
Log of No. of Relapses in Last 2 Years	16.78	8.4 - 33.4	2.3E-21	53.19	14.8 - 191.7	1.4E-11	14.50	8.6 - 24.4	3.6E-32
Baseline EDSS Score	0.62	0.5 - 0.8	3.0E-06	0.71	0.5 - 0.9	0.010	0.62	0.5 - 0.7	5.9E-10
Age	0.97	0.9 - 1.0	0.034	0.98	0.9 - 1.0	0.22	0.97	1.0 - 1.0	0.012
PCA Component 3 (EV = 2.41024)	Inf.		0.06	Inf.		0.07	Infinity		0.017
No. of Gd-T1 Lesions at Baseline	0.97	0.9 - 1.0	0.10	0.96	0.9 - 1.0	0.11	0.97	0.9 - 1.0	0.034

Results of regression analyses for the Additive Models are presented in Tables 34-37.

In some embodiments, all of the genetic markers presented in Tables 34-37 are identified as predictive of response to glatiramer acetate.

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Table 34. Regression Analysis, Additive Model (Gala cohort)

COMBINED					
Predictor	Chr	Position	Gene	P-Value	Odds Ratio
rs16886004	7	78021500	MAGI2	3.10E-07	2.79
kgp26026546	13	79972606		7.45E-07	0.03
rs10251797	7	78025427	MAGI2	7.93E-07	2.67
kgp8110667	22	32716792		9.48E-07	Infinity
kgp11210241	3	38537237		9.74E-07	Infinity
rs17687961	22	32716927		9.74E-07	Infinity
kgp12008955	2	73759636		1.08E-06	0.08
kgp24415534	2	1.74E+08		1.08E-06	0.08
kgp5976729	22	32675303		2.12E-06	Infinity
kgp25952891	13	80027089		2.38E-06	0.04
rs543122	3	1.24E+08		2.81E-06	0.54
kgp6236949	2	60301030		3.70E-06	0.54
rs9817308	3	1.24E+08		4.60E-06	0.55
kgp10372946	10	1.34E+08		4.62E-06	10.53
kgp8817856	6	32744440		4.90E-06	0.53
kgp11328629	10	1.21E+08		5.02E-06	2.95
kgp4705854	12	19907696		5.19E-06	0.55
rs4143493	6	51829939		5.24E-06	4.21
kgp3450875	16	57268931		5.60E-06	0.12
kgp1688752	21	43016736		5.79E-06	0.33
kgp9627338	17	90155		6.00E-06	0.45
rs17577980	6	32359821		6.15E-06	2.36
kgp3418770	10	59425598		6.31E-06	10.31
kgp2299675	20	16933074		6.55E-06	0.19
rs6718758	2	60328802		6.61E-06	0.55
rs7579987	2	60307009		6.71E-06	0.55
kgp10594414	1	2.16E+08		6.80E-06	0.14
rs10498793	6	51829707		7.20E-06	4.14
rs2816838	10	52714759		7.32E-06	0.46
kgp12230354	5	27037978		7.64E-06	0.19
rs13394010	2	60302746		8.16E-06	0.56
rs11029892	11	27269546		8.23E-06	1.94
kgp2356388	16	19771577		8.28E-06	0.46
rs11691553	2	60303554		8.55E-06	0.56
kgp5564995	6	26414060		9.08E-06	2.88
rs6895094	5	1.41E+08		9.18E-06	0.57
kgp10352965	7	30647900		9.40E-06	7.44
kgp26116630	6	48158833		9.42E-06	16.38
kgp7059449	2	41255455		9.98E-06	4.93
rs10203396	2	60305110		1.01E-05	0.56
kgp11843177	11	27316568		1.01E-05	1.95
rs9579566	13	30980265		1.04E-05	0.26
kgp11141512	20	35283733		1.06E-05	0.21

Table 35. Regression Analysis, Additive Model Corrected for Log Relapse and EDSS (Gala, Forte, Combined cohorts)

Chromos							Gene		GALA			FORTE			COMBINED		
Name	ome	Position	Gene(s)	Mutation	(s)	Locations	P-value*	Odds Ratio	P-value*	Odds Ratio	P-value*	Odds Ratio	P-value*	Odds Ratio			
kgp8817856	6	32744440	?	?	?		8.04E-29	0.48	1.18E-16	0.32	9.16E-43	0.39					
rs454748	6	32213210	?	?	?		1.60E-30	2.32	4.89E-14	1.78	6.67E-42	2.16					
kgp5447044	6	26501768	BTN1A1	Silent		INTRON	2.47E-29	0.31	2.37E-14	0.41	1.55E-41	0.35					
rs16901784	6	26555433	?	?	?		1.19E-29	0.29	2.19E-14	0.40	1.64E-41	0.34					
rs2143466	6	32309323	C6orf10	Silent		INTRON	6.41E-30	2.18	6.55E-14	1.75	1.88E-41	2.10					
kgp9938485	6	27021173	?	?	?		4.37E-29	0.42	5.52E-14	0.50	2.22E-41	0.42					
rs3799383	6	26510748	?	?	?		3.25E-29	0.31	2.37E-14	0.41	2.65E-41	0.34					
rs4897704	8	1.35E+08	?	?	?		6.20E-32	2.67	7.64E-14	1.72	2.78E-41	2.05					
kgp3478190	8	69080975	PREX2	Silent		INTRON	2.18E-29	2.07	4.90E-14	1.95	2.80E-41	2.09					
rs2820263	6	1.05E+08	?	?	?		8.15E-29	1.80	1.40E-15	2.53	2.82E-41	2.09					
kgp12230354	5	27037978	CDH9	Silent		INTRON	1.39E-28	0.13	5.86E-15	0.13	2.82E-41	0.12					
rs9393727	6	26500011	?	?	?		2.92E-29	0.31	2.87E-14	0.41	3.25E-41	0.34					
kgp31017880	X	97136288	?	?	?		3.71E-30	19.90	5.62E-14	Infinity	3.34E-41	24.31					
kgp3438641	5	98186154	?	?	?		1.24E-29	4.24	6.31E-15	7.61	3.46E-41	4.51					
kgp12113592	5	98160214	?	?	?		2.07E-29	4.18	6.70E-15	7.53	3.54E-41	4.45					
rs9650120	8	1.35E+08	?	?	?		6.72E-31	2.55	3.20E-14	1.90	4.40E-41	2.08					
kgp3931548	5	98146468	?	?	?		1.51E-29	4.17	6.31E-15	7.61	4.59E-41	4.45					
rs727637	5	98213991	CHD1	Silent		INTRON	1.51E-29	4.17	6.31E-15	7.61	4.59E-41	4.45					
kgp1892256	5	98257441	CHD1	Silent		INTRON	1.51E-29	4.17	6.31E-15	7.61	4.59E-41	4.45					
rs9501224	6	32792910	TAP2	Silent		INTRON	5.89E-29	2.07	7.52E-16	3.15	4.80E-41	2.24					
kgp11199573	2	2.02E+08	?	?	?		4.05E-29	2.00	5.40E-15	2.23	4.97E-41	2.04					
kgp7903189	5	98229104	CHD1	Silent		INTRON	1.15E-29	3.43	5.21E-15	7.77	5.73E-41	3.90					
rs2820259	6	1.05E+08	?	?	?		7.65E-29	1.80	8.55E-15	2.20	5.90E-41	1.99					
rs2857103	6	32791299	TAP2	Silent		INTRON	5.55E-29	2.13	7.52E-16	3.15	6.22E-41	2.27					
kgp9421884	19	11049860	?	?	?		8.34E-28	0.39	1.80E-15	0.24	6.64E-41	0.29					
rs6920256	6	26537801	?	?	?		8.77E-29	0.35	2.37E-14	0.41	6.74E-41	0.36					
kgp1688752	21	43016736	?	?	?		7.35E-30	0.22	2.38E-14	0.30	7.23E-41	0.28					
kgp6754792	6	26456074	?	?	?		1.63E-29	0.25	1.45E-13	0.49	7.65E-41	0.34					
kgp95865	9	14204068	NFIB,NFIB	Silent,Siler	INTRON		6.17E-29	3.29	2.80E-14	4.31	7.69E-41	3.78					
rs241451	6	32796480	TAP2,TAP2	Silent,Siler	INTRON		6.05E-29	2.11	2.29E-15	2.80	8.11E-41	2.15					

Table 36. Regression Analysis, Additive Model Corrected for top SNP rs1686004 (Gala, Forte, and Combined cohorts)

Name	Chr	Position	Gene(s)	Mutation	Gene Locations(s)	GALA		FORTE		COMBINED	
						P-value	Odds Ratio	P-value	Odds Ratio	P-value	Odds Ratio
kgp6996560	13	110124242	?	?	?	6.61E-05	0.17	2.43E-08	0.02	2.03E-11	0.09
rs4143493	6	51829939	PKHD1,PKHD1	Silent,Silent	INTRON	8.56E-05	3.34	3.58E-08	8.13	2.15E-11	4.60
kgp28541695	15	24985550	?	?	?	4.99E-07	~Infinity	2.77E-06	5.87	2.93E-11	17.52
rs10498793	6	51829707	PKHD1,PKHD1	Silent,Silent	INTRON	8.56E-05	3.34	5.18E-08	7.78	3.18E-11	4.50
kgp4705854	12	19907696	?	?	?	6.52E-07	0.47	3.84E-06	0.64	3.31E-11	0.53
kgp6236949	2	60301030	?	?	?	2.13E-05	0.55	7.45E-07	0.53	3.61E-11	0.53
kgp12230354	5	27037978	CDH9	Silent	INTRON	8.6E-05	0.18	1.21E-08	0.10	3.62E-11	0.16
kgp29794723	10	18397332	?	?	?	6.52E-05	0.26	5.1E-08	0.13	3.63E-11	0.20
kgp971582	6	51921703	PKHD1,PKHD1	Synonymous_N529N,Synonymous_N529N	EXON	4.38E-05	3.35	1.51E-07	5.24	4.17E-11	3.96
kgp4812831	6	51910905	PKHD1,PKHD1	Missense_N830S,Missense_N830S	EXON	4.38E-05	3.35	1.63E-07	5.34	4.7E-11	3.99
kgp4162414	6	51868165	PKHD1,PKHD1	Silent,Silent	INTRON	5.42E-05	3.29	1.63E-07	5.34	5.5E-11	3.96
kgp2688306	7	28560259	CREB5,CREB5,CREB5	Silent,Silent,Silent	INTRON	1.25E-05	3.03	4.92E-07	3.62	5.55E-11	3.15
rs7579987	2	60307009	?	?	?	0.000169	0.62	5.22E-08	0.44	5.73E-11	0.54
kgp9627338	17	90155	RPH3AL,RPH3AL,RPH3AL,RPH3AL	Silent,Silent,Silent,Silent	INTRON	9.23E-06	0.44	1.19E-06	0.45	5.92E-11	0.44
kgp11328629	10	120711084	?	?	?	5.3E-05	2.68	9.89E-08	4.12	6.08E-11	3.07
rs2816838	10	52714759	?	?	?	5.23E-05	0.50	2.7E-07	0.40	6.29E-11	0.45
kgp24415534	2	174156875	?	?	?	1.71E-06	0.05	5.58E-06	0.21	6.85E-11	0.09
rs10203396	2	60305110	?	?	?	0.000191	0.63	5.5E-08	0.44	7.36E-11	0.54
rs13394010	2	60302746	?	?	?	0.000193	0.63	5.22E-08	0.44	7.44E-11	0.54
rs6718758	2	60328802	?	?	?	0.000165	0.63	8.83E-08	0.45	7.74E-11	0.54
rs11691553	2	60303554	?	?	?	0.000235	0.63	4.41E-08	0.44	7.92E-11	0.54
kgp1009249	12	19838534	?	?	?	1.96E-06	0.43	2.46E-06	0.56	8.26E-11	0.49
rs13419758	2	60302920	?	?	?	0.000177	0.63	7.51E-08	0.45	8.34E-11	0.55
kgp93320791	2	60309952	?	?	?	0.000191	0.63	6.84E-08	0.45	9.04E-11	0.55
rs11029892	11	27269546	?	?	?	6.68E-05	1.82	1.98E-07	2.22	9.28E-11	1.98
kgp2350730	1	88444077	?	?	?	2.24E-06	4.82	3.98E-06	2.43	9.28E-11	3.62
kgp8192546	12	19903173	?	?	?	5.84E-07	0.43	4.85E-06	0.64	9.46E-11	0.52
rs17165909	7	93551606	GNNG11	Silent	INTRON	0.000131	5.91	4.06E-08	~Infinity	9.49E-11	10.50
rs10841337	12	19897179	?	?	?	3.73E-07	0.43	5.67E-06	0.68	9.49E-11	0.53
rs7217872	17	88988	RPH3AL,RPH3AL,RPH3AL,RPH3AL	Silent,Silent,Silent,Silent	INTRON	2.06E-05	0.46	7.59E-07	0.44	1.01E-10	0.45
rs17638791	6	51940816	PKHD1,PKHD1	Silent,Silent	INTRON	7.65E-05	3.02	1.63E-07	5.34	1.07E-10	3.67
rs10841322	12	19866642	?	?	?	2.66E-07	0.42	1.04E-05	0.71	1.1E-10	0.52
kgp3933330	7	28583709	CREB5,CREB5,CREB5	Silent,Silent,Silent	INTRON	4.2E-06	2.52	1.52E-06	2.41	1.16E-10	2.40
kgp10305127	11	99881768	CNTN5,CNTN5,CNTN5,CNTN5	Silent,Silent,Silent,Silent	INTRON,EXON	0.000109	0.49	2.85E-07	0.34	1.25E-10	0.41
kgp6507761	7	319681	?	?	?	0.000227	0.65	1.06E-07	0.49	1.25E-10	0.57
kgp7506434	1	13823114	LRRC38	Silent	INTRON	4.04E-05	0.10	7.69E-07	0.08	1.26E-10	0.08
rs11022778	11	13390860	ARNTL,ARNTL,ARNTL	Silent,Silent,Silent	INTRON	1.4E-05	1.98	2.46E-06	1.70	1.26E-10	1.91
kgp5908616	2	60329823	?	?	?	0.0002	0.64	1.12E-07	0.46	1.27E-10	0.56
kgp12122821	6	51938210	PKHD1,PKHD1	Silent,Silent	INTRON	7.65E-05	3.02	1.93E-07	5.16	1.29E-10	3.61
kgp10594414	1	216039833	USH2A	Silent	INTRON	1.05E-06	0.05	3.23E-06	0.26	1.31E-10	0.14

Table 37. Regression Analysis, Additive Model Corrected for rs1686004 + Log Relapse + EDSS (Gala, Forte, Combined cohorts)

GALA					FORTE					COMBINED				
Gene					Odds					Odds				
Name	Chr	Position	Gene(s)	Mutatio	Locations(s)	P-value	Ratio	P-value	Ratio	P-value	Ratio	P-value	Ratio	Odds Ratio
kgp8817856	6	32744440	HLA	?	?	2.41E-28	0.49	1.01E-19	0.32	7.56E-45	0.40	7.56E-45	0.32	0.40
kgp3438641	5	98186154	?	?	?	1.57E-29	4.50	9.08E-20	13.26	8.62E-45	5.49	8.62E-45	13.26	5.49
kgp12113592	5	98160214	?	?	?	2.60E-29	4.43	1.18E-19	13.10	1.06E-44	5.40	1.06E-44	13.10	5.40
kgp3931548	5	98146468	?	?	?	1.96E-29	4.42	9.08E-20	13.26	1.26E-44	5.39	1.26E-44	13.26	5.39
rs727637	5	98213991	CHD1	Silent	INTRON	1.96E-29	4.42	9.08E-20	13.26	1.26E-44	5.39	1.26E-44	13.26	5.39
kgp1892256	5	98257441	CHD1	Silent	INTRON	1.96E-29	4.42	9.08E-20	13.26	1.26E-44	5.39	1.26E-44	13.26	5.39
kgp31017880	X	97136288	?	?	?	3.74E-30	22.62	1.58E-17	Inf	1.59E-44	31.18	1.59E-44	Inf	31.18
kgp12230354	5	27037978	CDH9	Silent	INTRON	1.36E-28	0.11	5.47E-19	0.09	1.60E-44	0.10	1.60E-44	0.09	0.10
kgp3478190	8	69080975	PREX2	Silent	INTRON	2.47E-29	2.14	2.07E-18	2.34	1.67E-44	2.22	1.67E-44	2.34	2.22
kgp7903189	5	98229104	CHD1	Silent	INTRON	1.71E-29	3.60	8.77E-20	13.26	2.01E-44	4.68	2.01E-44	13.26	4.68
rs11956636	5	98159347	?	?	?	2.82E-29	4.27	9.46E-20	13.27	2.81E-44	5.21	2.81E-44	13.27	5.21
kgp11841858	5	98284488	?	?	?	1.46E-29	3.84	1.83E-18	7.04	4.78E-44	4.38	4.78E-44	7.04	4.38
kgp409852	5	98142161	?	?	?	1.96E-29	4.42	6.53E-19	7.99	5.38E-44	4.73	5.38E-44	7.99	4.73
rs1434781	8	69066793	PREX2	Silent	INTRON	4.93E-29	2.05	3.59E-18	2.21	6.24E-44	2.12	6.24E-44	2.21	2.12
rs2143466	6	32309323	C6orf10	Silent	INTRON	1.87E-29	2.13	1.04E-17	1.95	6.35E-44	2.12	6.35E-44	1.95	2.12
rs454748	6	32213210	?	?	?	6.95E-30	2.24	1.19E-17	1.87	6.51E-44	2.10	6.51E-44	1.87	2.10
rs2217788	8	69064811	PREX2	Silent	INTRON	4.02E-29	2.08	4.53E-18	2.22	7.01E-44	2.14	7.01E-44	2.22	2.14
rs2820263	6	1.05E+08	?	?	?	2.80E-28	1.71	1.22E-19	2.75	7.49E-44	2.11	7.49E-44	2.75	2.11
rs17166414	5	98202363	CHD1	Silent	INTRON	4.48E-29	4.14	9.87E-19	9.98	8.17E-44	4.82	8.17E-44	9.98	4.82
rs4713208	6	29283579	?	?	?	6.45E-33	0.26	1.83E-16	1.11	8.43E-44	0.47	8.43E-44	1.11	0.47
rs720831	6	29284518	?	?	?	6.45E-33	0.26	1.83E-16	1.11	8.43E-44	0.47	8.43E-44	1.11	0.47
kgp9832356	5	98262916	?	?	?	4.48E-29	4.14	5.42E-19	10.27	9.52E-44	4.86	9.52E-44	10.27	4.86
kgp5447044	6	26501768	BTN1A1	Silent	INTRON	7.65E-29	0.33	7.91E-18	0.43	9.64E-44	0.36	9.64E-44	0.43	0.36
rs2820259	6	1.05E+08	?	?	?	2.31E-28	1.71	3.55E-19	2.54	9.66E-44	2.02	9.66E-44	2.54	2.02
rs16901784	6	26555433	?	?	?	4.13E-29	0.31	6.44E-18	0.42	1.12E-43	0.35	1.12E-43	0.42	0.35
kgp4356222	5	98105883	RGMB, FLJ	Silent, Siler	INTRON, EXON	2.19E-29	4.75	2.36E-18	7.77	1.20E-43	5.03	1.20E-43	7.77	5.03
rs4897704	8	1.35E+08	?	?	?	3.72E-31	2.54	1.23E-17	1.89	1.23E-43	2.04	1.23E-43	1.89	2.04
kgp4269732	5	98275939	?	?	?	4.48E-29	4.14	6.76E-19	10.25	1.29E-43	4.86	1.29E-43	10.25	4.86
kgp9938485	6	27021173	?	?	?	9.70E-29	0.43	3.85E-17	0.57	1.45E-43	0.44	1.45E-43	0.57	0.44
kgp6703510	5	98296594	?	?	?	7.60E-29	3.91	5.36E-19	10.26	1.46E-43	4.73	1.46E-43	10.26	4.73
kgp3203641	5	98245912	CHD1	Silent	INTRON	4.48E-29	4.14	7.05E-19	10.23	1.54E-43	4.86	1.54E-43	10.23	4.86
kgp11324749	8	69066259	PREX2	Silent	INTRON	6.00E-29	2.04	4.09E-18	2.23	1.64E-43	2.12	1.64E-43	2.23	2.12
rs7737398	5	97974536	?	?	?	9.10E-30	5.46	8.14E-18	4.88	1.64E-43	4.77	1.64E-43	4.88	4.77

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Example 15 Selection of Genetic Markers Predictive of Response to Glatiramer Acetate.

Based on the analyses above, genetic markers were selected as Predictive of Response to Glatiramer Acetate based on the following
5 p-value thresholds: Priority candidate variants: $P < 0.05$ (combined cohorts); Priority Genes: Replicated $P < 0.05$ in both cohorts; GWAS: $P < 10^{-4}$ (combined cohorts); and Placebo $P < 10^{-4}$ (placebo cohort).

The selected genetic markers are presented in Tables 38-41. Alleles associated with response are highlighted.

Table 38: Standard Response SNPs

STANDARD PHENOTYPE										Gala cohort				Porte cohort			
Prioritized Variants	Name	Chromosome	Position	Gene(s)	Major Allele (d)	Minor Allele (D)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)			
0 - Priority in Predictive Model	kgp24415534	2	174158875		G	A	3.40E-05	0.05	0.003	0.050	1.10E-02	0.14	0.005	0.033			
	kgp12088955	2	73759636	ALAC1	G	A	9.26E-05	Zero	0.000	0.038	3.65E-04	0.12	0.007	0.057			
	kgp26026546	13	79972606	R3H26	A	C	2.20E-04	Zero	0.000	0.034	4.46E-04	0.06	0.003	0.041			
	rs16886004	7	78021300	MAH2	A	G	2.28E-03	2.15	0.199	0.110	3.25E-03	5.56	0.199	0.049			
	kgp25952891	13	80827089		A	G	5.58E-04	Zero	0.000	0.029	4.80E-04	0.06	0.002	0.041			
	kgp5450873	16	37268931	RSPRY1	G	A	6.63E-03	0.19	0.008	0.038	1.51E-05	0.07	0.005	0.066			
0 - Priority in Predictive Model	rs10251797	7	78025427	MAH2	C	A	3.18E-03	2.07	0.199	0.113	4.05E-05	5.49	0.194	0.049			
	kgp2599675	20	16933074		G	A	4.43E-03	0.26	0.015	0.054	4.33E-05	0.13	0.012	0.082			
	kgp10594414	1	21803983	15H2A	A	G	3.57E-05	0.05	0.003	0.050	1.25E-02	0.24	0.013	0.049			
	kgp1688752	21	43016736		G	A	8.83E-04	0.34	0.045	0.113	1.48E-03	0.33	0.035	0.115			
	kgp12230354	5	27037978	CDH9	A	C	3.70E-03	0.21	0.010	0.046	3.31E-05	0.14	0.015	0.090			
	rs543122	3	124164156	KALRN	G	A	4.73E-05	0.50	0.407	0.571	1.39E-02	0.59	0.439	0.566			
	kgp6236940	2	60301030		A	G	6.37E-04	0.56	0.306	0.442	7.57E-03	0.55	0.261	0.385			
	kgp9627338	17	90155	RPH3AL	A	G	5.01E-04	0.47	0.104	0.208	3.13E-03	0.43	0.105	0.205			
	kgp11141512	20	35283733	MDR2	G	A	3.33E-03	0.30	0.020	0.067	3.65E-04	0.12	0.037	0.057			
	rs579566	13	30980265		G	A	2.08E-04	0.23	0.020	0.083	9.90E-03	0.30	0.035	0.074			
0 - Priority in Predictive Model	rs2816818	10	32714759		G	A	1.94E-03	0.51	0.139	0.233	1.80E-03	0.42	0.112	0.221			
	kgp4705854	12	19907696		G	A	5.01E-05	0.51	0.303	0.467	2.87E-02	0.63	0.326	0.434			
	rs9817308	3	124182136	KALRN	A	C	2.85E-05	0.49	0.406	0.576	2.64E-02	0.62	0.433	0.566			
	kgp8817856	6	32744440		G	A	6.03E-04	0.53	0.364	0.492	3.73E-04	0.46	0.419	0.598			
	kgp6214351	11	73546691	UVRAG	A	G	3.98E-03	0.42	0.031	0.113	2.63E-04	0.26	0.043	0.131			
	kgp2356388	16	19771577	KCK	G	A	1.88E-04	0.43	0.121	0.221	1.94E-03	0.45	0.144	0.262			
	kgp7418024	9	21453902		G	A	2.14E-03	0.13	0.005	0.038	3.81E-04	0.12	0.038	0.057			
	rs6718758	2	60328802		C	A	5.70E-03	0.63	0.333	0.446	5.96E-04	0.47	0.281	0.443			
	rs27579987	2	60307009		G	C	6.99E-03	0.64	0.336	0.466	3.91E-04	0.45	0.306	0.475			
	rs2217872	17	88988	RPH3AL	G	A	1.03E-03	0.49	0.106	0.204	2.42E-03	0.42	0.109	0.213			
0 - Priority in Predictive Model	rs12391010	2	60302746		A	G	7.74E-03	0.64	0.354	0.462	3.91E-04	0.45	0.306	0.475			
	rs7191155	16	19800213	KCK	A	G	5.38E-04	0.44	0.121	0.218	1.93E-03	0.45	0.144	0.262			
	rs9931167	16	19792596	KCK	G	A	5.38E-04	0.44	0.121	0.218	1.94E-03	0.45	0.144	0.262			
	rs11691553	2	60303554		C	A	8.54E-03	0.63	0.353	0.462	3.72E-04	0.45	0.305	0.475			
	rs11648129	16	19820604	KCK	A	G	6.54E-04	0.45	0.121	0.217	1.64E-03	0.44	0.143	0.262			
	kgp25216186	1	23758427	ASAP3	A	G	1.32E-03	0.07	0.003	0.033	2.45E-03	0.07	0.002	0.033			
	kgp29794723	10	18397332		A	G	4.77E-03	0.31	0.023	0.067	3.54E-04	0.18	0.018	0.082			
	rs3829539	16	19722366	C16orf88	A	G	5.38E-04	0.44	0.121	0.218	2.10E-03	0.45	0.145	0.262			
	rs6895094	5	14103737	ARAP3	A	C	6.58E-04	0.56	0.384	0.521	1.19E-02	0.60	0.353	0.484			
	kgp1009249	12	19838934		G	A	1.74E-04	0.48	0.179	0.307	1.03E-02	0.54	0.211	0.320			
0 - Priority in Predictive Model	rs10203596	2	60305110		A	G	8.67E-03	0.65	0.356	0.463	4.43E-04	0.46	0.308	0.475			
	kgp3834180	16	19721806	C16orf88	G	A	6.54E-04	0.45	0.121	0.217	1.94E-03	0.45	0.144	0.262			

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STANDARD PHENOTYPE										Galla cohort				Porte cohort			
Practiced Variants	Name	Chromo some	Position	Gene(s)	Major Allele (d)	Minor Allele (D)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)			
	rs6497396	16	19733697	LOC	A	G	1.30E-03	0.48	0.131	0.225	7.65E-04	0.43	0.153	0.287			
	rs13419758	2	60302920		G	A	8.67E-03	0.65	0.356	0.463	5.22E-04	0.47	0.308	0.475			
	rs8055485	16	19750051	LOC	A	G	6.54E-04	0.43	0.121	0.217	2.10E-03	0.45	0.145	0.262			
	rs9931211	16	19813605	LOC	A	G	6.54E-04	0.45	0.121	0.217	2.10E-03	0.45	0.145	0.262			
	kgp55869992	12	49219569	CACMB3	A	G	3.71E-04	0.57	0.389	0.542	2.00E-02	0.62	0.379	0.500			
	kgp8320791	2	60309952		C	G	8.67E-03	0.65	0.356	0.463	5.27E-04	0.46	0.310	0.475			
	kgp7730397	16	19740243	LOC	A	G	1.99E-03	0.47	0.126	0.218	1.64E-03	0.44	0.143	0.262			
	kgp116002881	11	118219897	CD3G	A	G	4.98E-03	0.14	0.005	0.034	4.46E-04	0.06	0.003	0.041			
	kgp3205849	10	121531725	INPP5F	A	G	8.42E-05	0.48	0.172	0.312	5.88E-02	0.63	0.183	0.262			
	kgp6127371	4	153856357		A	G	3.69E-04	0.18	0.013	0.063	9.38E-03	0.28	0.029	0.066			
	kgp10305127	11	99881768	CNTN3	A	G	4.21E-03	0.51	0.101	0.182	2.60E-03	0.39	0.068	0.156			
	rs6535882	4	153848128		G	A	3.83E-04	0.18	0.013	0.063	9.06E-03	0.27	0.020	0.066			
	kgp8700691	4	153849531		A	G	3.83E-04	0.18	0.013	0.063	9.06E-03	0.27	0.020	0.066			
	rs11029892	11	27269546		C	A	1.72E-03	1.83	0.343	0.229	3.44E-03	2.08	0.358	0.221			
	kgp2709301	16	19750275	LOC	G	A	1.08E-03	0.48	0.131	0.227	1.44E-03	0.45	0.154	0.279			
	kgp8192546	12	19903173		G	A	6.52E-05	0.47	0.215	0.358	2.64E-02	0.62	0.256	0.361			
	kgp5068397	16	19756348	LOC	A	G	7.59E-04	0.50	0.164	0.273	1.56E-03	0.47	0.203	0.336			
	kgp10910719	16	19803199	LOC	C	A	9.01E-04	0.46	0.121	0.214	1.94E-03	0.45	0.144	0.262			
	kgp2939751	6	38719342		G	A	0.81E-04	0.22	0.015	0.063	7.48E-03	0.24	0.015	0.057			
	rs930928	16	19824838	LOC	A	G	6.59E-04	0.45	0.126	0.223	3.11E-03	0.46	0.149	0.262			
	rs1858973	16	19743649	LOC	A	G	6.54E-04	0.45	0.121	0.217	2.67E-03	0.46	0.148	0.262			
	rs2660214	10	52732452		A	G	3.98E-03	0.54	0.141	0.229	2.37E-03	0.43	0.114	0.221			
	kgp2709692	18	30090808	LPIN2	C	A	2.36E-03	0.27	0.020	0.067	5.25E-03	0.19	0.010	0.049			
	kgp11210903	22	36898906	SEC14L4	G	A	3.70E-04	0.10	0.005	0.046	4.98E-02	0.19	0.005	0.025			
	kgp8030773	6	6328607	MCYH1	A	C	2.54E-02	0.36	0.018	0.050	1.69E-05	0.07	0.003	0.066			
	rs10841337	12	19897179		A	G	4.26E-05	0.47	0.217	0.367	4.27E-02	0.64	0.265	0.361			
	kgp8178358	14	70923024	ADAM421	A	G	3.36E-03	0.08	0.003	0.029	3.81E-04	0.12	0.008	0.057			
	kgp11843177	11	27316568		A	G	1.95E-03	1.85	0.321	0.210	4.13E-03	2.07	0.338	0.203			
	kgp23737989	7	97217288		G	A	3.27E-03	0.08	0.003	0.029	1.57E-03	Zero	0.000	0.025			
	rs7187976	16	19708196	C16orf62	A	G	1.08E-03	0.48	0.131	0.227	1.83E-03	0.45	0.157	0.279			
	rs17577980	6	32359821	HCG23	G	A	2.33E-04	2.36	0.228	0.106	5.31E-03	2.94	0.164	0.067			
	kgp5908616	2	60329823		A	C	8.71E-03	0.65	0.346	0.454	1.03E-03	0.48	0.295	0.451			
	kgp26995430	3	53359406	EXPT1A	G	A	3.40E-05	0.05	0.003	0.050	2.14E-01	0.39	0.010	0.025			
	kgp6996569	13	11012432		G	A	7.81E-03	0.23	0.010	0.042	4.30E-04	0.06	0.002	0.041			
	rs4782279	16	19759007	LOC	A	C	1.26E-03	0.49	0.136	0.233	1.99E-03	0.46	0.158	0.279			
	rs8053136	16	19767129	LOC	A	C	1.23E-03	0.53	0.179	0.288	1.68E-03	0.47	0.210	0.344			
	kgp11328629	10	12071084		G	A	2.03E-03	2.62	0.134	0.058	3.11E-03	3.81	0.140	0.041			
	kgp8200264	10	12858372	CAMK1D	A	G	8.64E-04	0.26	0.020	0.076	3.36E-03	0.31	0.033	0.098			
	kgp6836138	20	40712994	PTPRF	G	A	6.20E-05	0.08	0.005	0.054	1.26E-01	0.36	0.012	0.033			
	kgp841428	5	14103637	ARAP3	A	G	9.84E-04	0.57	0.384	0.517	1.52E-02	0.61	0.358	0.484			
	rs1915822	16	29872361	CDIPT	A	G	3.18E-03	1.02	0.490	0.367	4.87E-03	1.85	0.527	0.385			
	rs1579771	3	15727882	C1orf53	A	C	3.35E-04	2.02	0.376	0.246	1.64E-02	1.81	0.356	0.246			
	kgp4734301	11	27315427		A	G	2.36E-03	1.83	0.321	0.213	4.13E-03	2.07	0.338	0.205			

STANDARD PHENOTYPE										Gate cohort					Brite cohort				
Enriched Variants	Name	Chromo source	Position	Gene(s)	Major Allele (d)	Minor Allele (D)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non- Responders)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non- Responders)					
	rs11029928	11	27319188		G	A	2.36E-03	1.83	0.321	0.213	4.13E-03	2.07	0.338	0.205					
	rs10841322	12	19866642		G	A	3.20E-05	0.46	0.217	0.367	9.47E-02	0.69	0.251	0.328					
	kgp1786079	7	144701118		A	G	5.35E-04	0.48	0.106	0.213	9.86E-03	0.49	0.130	0.221					
	kgp3053636	2	295356730		C	A	1.01E-02	0.32	0.020	0.058	1.02E-04	0.22	0.028	0.115					
	kgp2601362	9	18959317	FAM154A	G	A	4.20E-03	0.40	0.038	0.097	2.94E-03	0.26	0.025	0.083					
	kgp8183049	13	40634155		G	A	5.58E-04	Zero	0.000	0.029	6.90E-02	Zero	0.000	0.008					
	kgp5564995	6	76414060	BTBD3A1	C	A	1.50E-04	3.35	0.153	0.057	3.98E-02	2.30	0.137	0.070					
	kgp27500525	8	30278677		A	G	3.79E-03	Zero	0.000	0.021	1.57E-03	Zero	0.000	0.025					
	rs11022778	11	13390860	ARMTL	A	C	4.49E-04	1.96	0.336	0.204	4.87E-02	1.58	0.366	0.270					
	kgp10826272	2	176263817		G	A	5.89E-04	Zero	0.000	0.029	6.96E-02	Zero	0.000	0.008					
	rs12494712	3	116796116		A	C	1.36E-02	1.74	0.220	0.142	1.24E-03	2.54	0.274	0.131					
	kgp1779254	12	73686930		A	G	3.12E-03	0.08	0.003	0.029	2.45E-03	0.07	0.002	0.033					
	kgp6190988	5	10699322	DAP	G	A	3.27E-03	0.08	0.003	0.029	2.22E-03	0.07	0.002	0.033					
	kgp4507761	7	319681		A	G	8.94E-03	0.65	0.457	0.567	2.90E-03	0.54	0.480	0.566					
	rs2074037	16	19725130	C16orf88	G	A	1.49E-03	0.47	0.126	0.216	2.46E-03	0.46	0.147	0.262					
	rs4143493	6	51829939	PKHD1	G	A	8.85E-03	3.00	0.078	0.029	1.57E-03	7.56	0.102	0.016					
	kgp1699628	6	18032535		A	G	1.73E-04	0.51	0.437	0.585	2.99E-02	0.63	0.430	0.582					
	rs7024953	8	18960334	FAM154A	A	G	4.68E-03	0.40	0.038	0.096	3.41E-03	0.27	0.025	0.082					
	kgp10974833	13	77339132		A	G	3.27E-03	0.08	0.003	0.029	2.99E-03	0.07	0.003	0.033					
	kgp10412303	2	29530350		G	A	1.21E-02	0.37	0.025	0.067	1.73E-04	0.21	0.027	0.107					
	kgp9666946	17	65734672	NOL11	A	C	1.28E-03	0.51	0.154	0.236	3.31E-03	0.50	0.179	0.303					
	rs17224858	3	124205297	KALRN	G	A	3.71E-05	0.45	0.172	0.313	1.22E-01	0.69	0.204	0.270					
	rs6849089	4	153715220	ARFIP1	G	A	8.57E-04	0.20	0.013	0.058	9.06E-03	0.27	0.020	0.066					
	rs7666442	4	153753101	ARFIP1	A	G	8.57E-04	0.20	0.013	0.058	9.06E-03	0.27	0.020	0.066					
	rs7672014	4	153818501	ARFIP1	G	A	8.57E-04	0.20	0.013	0.058	9.06E-03	0.27	0.020	0.066					
	rs7677801	4	153795067	ARFIP1	A	G	8.58E-04	0.20	0.013	0.059	9.38E-03	0.28	0.020	0.066					
	rs4669694	2	11263948	PLJ33534	G	A	1.85E-03	0.48	0.094	0.182	1.43E-02	0.46	0.083	0.156					
	kgp10523170	16	5221817		G	A	2.00E-02	0.12	0.003	0.021	9.95E-05	0.03	0.002	0.057					
	kgp5216209	3	16740453	SUC2A2	C	A	1.75E-03	0.21	0.013	0.055	4.56E-03	0.24	0.017	0.066					
	rs720176	16	19721515	C16orf88	A	G	1.77E-03	0.48	0.128	0.217	2.67E-03	0.46	0.148	0.262					
	kgp7481870	16	19729016	C16orf88, KCK	G	C	5.94E-03	0.45	0.133	0.231	8.16E-03	0.50	0.160	0.262					
	rs1532365	12	49204421		G	A	1.90E-03	0.61	0.336	0.487	1.26E-02	0.59	0.334	0.459					
	rs12943140	17	65738773	NOL11	G	A	1.45E-03	0.51	0.155	0.256	3.47E-03	0.50	0.179	0.303					
	kgp11702474	4	153712868	ARFIP1	A	G	8.97E-04	0.20	0.013	0.058	9.38E-03	0.28	0.020	0.066					
	rs10498793	6	31829707	PKHD1	G	A	8.85E-03	3.00	0.078	0.029	1.94E-03	7.33	0.100	0.016					
	kgp5539666	3	157292022	C3orf55	A	G	9.41E-04	1.94	0.354	0.238	1.61E-02	1.83	0.394	0.246					
	kgp10679353	16	19860133	KCK	G	A	1.51E-03	0.49	0.129	0.221	2.30E-03	0.46	0.159	0.279					
	kgp9410843	10	121484477		A	G	2.25E-04	0.50	0.173	0.364	6.76E-02	0.64	0.186	0.362					
	kgp6772915	9	18978739	FAM154A	A	C	8.72E-03	0.42	0.041	0.093	1.83E-03	0.24	0.023	0.082					
	kgp20478926	8	21050249		A	G	1.67E-03	0.38	0.023	0.092	2.91E-03	0.44	0.038	0.133					
	kgp10619195	4	99417717	TSPAP5	A	G	2.87E-04	0.29	0.013	0.104	3.30E-02	0.46	0.045	0.096					
	rs154352	16	19713882		A	G	2.28E-03	0.50	0.132	0.221	2.15E-03	0.45	0.153	0.270					
	kgp15990572	1	205017962	CNTN2	G	A	2.14E-03	0.13	0.003	0.038	1.37E-02	0.10	0.002	0.025					

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STANDARD PHENOTYPE														
Gain cohort					Loss cohort									
Prioritized Variants	Name	Chromosome	Position	Gene(s)	Major Allele (d)	Minor Allele (D)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)
	kgp24729706	22	49286157	LOC100128946	G	A	1.13E-03	0.24	0.018	0.067	4.15E-02	0.29	0.012	0.041
	rs931570	12	49193124		G	A	2.42E-03	0.61	0.156	0.483	1.11E-02	0.59	0.152	0.459
	kgp10991989	17	65697118		A	G	1.60E-03	0.48	0.111	0.200	9.17E-03	0.50	0.110	0.205
	kgp12357319	6	8794609		A	G	2.04E-02	0.12	0.003	0.021	3.27E-05	0.08	0.005	0.057
	kgp345301	16	19730554	KCK	A	C	2.05E-03	0.48	0.122	0.209	2.28E-03	0.45	0.146	0.262
	kgp8615910	5	38927198		A	T	1.47E-04	0.42	0.111	0.221	5.56E-02	0.59	0.135	0.205
	kgp2245773	13	91402306		G	A	2.67E-02	0.66	0.258	0.338	8.86E-04	0.43	0.185	0.320
	kgp29367521	4	14471944		G	A	4.84E-03	0.14	0.005	0.034	2.02E-03	0.11	0.005	0.042
	kgp2306434	1	13823114	LRRC38	A	G	3.24E-03	0.14	0.005	0.033	2.36E-03	0.09	0.002	0.041
	rs4780822	16	19727998	C16orf88, KCK	A	G	2.32E-03	0.50	0.129	0.217	1.71E-03	0.45	0.156	0.279
	kgp512180	16	10829457		G	A	2.02E-03	0.37	0.233	0.349	9.63E-03	0.55	0.229	0.344
	rs1604169	3	84213343		A	C	1.45E-02	0.66	0.386	0.483	2.13E-03	0.50	0.323	0.467
	kgp25921291	13	78418857		G	A	2.49E-03	0.18	0.008	0.046	7.68E-03	0.17	0.007	0.041
	rs16941784	6	26555433		C	A	1.37E-03	0.45	0.073	0.154	2.10E-03	0.43	0.105	0.213
	kgp6228750	1	110261382		A	G	1.92E-02	0.44	0.040	0.083	3.38E-04	0.26	0.030	0.113
	kgp9354820	13	93793636		G	A	2.86E-04	0.06	0.003	0.046	1.17E-01	0.29	0.007	0.025
	kgp8106690	12	128734969		A	G	2.00E-02	0.61	0.141	0.213	2.38E-04	0.40	0.128	0.270
	kgp5144181	2	30364733		G	A	3.79E-02	0.49	0.040	0.079	8.32E-05	0.16	0.017	0.090
	kgp9627406	8	112997137	KCS1	G	A	9.94E-04	0.39	0.070	0.163	2.89E-01	0.58	0.030	0.050
	kgp2262166	9	18960393	FAM154A	A	C	4.45E-03	0.40	0.038	0.096	5.93E-03	0.30	0.037	0.082
	kgp4223880	2	10584122	ODC1	A	G	4.98E-04	0.06	0.003	0.038	3.23E-02	0.22	0.008	0.033
	kgp61811	1	160346794		A	C	5.90E-03	0.20	0.008	0.042	2.45E-03	0.07	0.002	0.033
	kgp9421884	19	11049860		G	A	9.65E-02	0.56	0.048	0.079	3.73E-06	0.24	0.047	0.180
	rs9090872	16	19803846	KCK	G	A	1.99E-03	0.51	0.136	0.239	2.88E-03	0.47	0.162	0.279
	rs7864679	9	18945868	FAM154A	G	A	1.69E-02	0.48	0.046	0.096	7.87E-04	0.21	0.030	0.082
	kgp2446153	5	152980439	GRIK1	G	A	5.31E-04	0.06	0.003	0.038	3.17E-02	0.22	0.007	0.033
	kgp7804623	1	41125455	RPM33	G	A	2.90E-04	1.99	0.346	0.208	5.80E-02	1.57	0.336	0.246
	rs1792135	2	108062163	REV1	A	G	5.97E-04	0.48	0.120	0.227	3.49E-02	0.55	0.131	0.205
	rs8035836	15	94832144		C	A	4.54E-03	1.59	0.465	0.345	1.05E-02	1.76	0.513	0.385
	kgp85334	2	14574582		G	A	2.11E-04	0.13	0.008	0.055	1.26E-01	0.56	0.012	0.033
rs11192461	10	107266483		G	A	7.86E-03	0.49	0.081	0.146	7.33E-04	0.38	0.087	0.197	
kgp297178	9	19942835	FAM154A	G	A	2.48E-02	0.43	0.043	0.088	3.36E-04	0.18	0.017	0.082	
kgp2045074	6	51187450		C	A	4.03E-04	0.10	0.003	0.046	2.05E-01	0.30	0.005	0.016	
rs10649206	3	157233698		G	A	3.70E-04	1.97	0.369	0.246	2.77E-02	1.71	0.356	0.254	
rs8834010	3	157236222		C	A	5.70E-04	1.97	0.369	0.246	2.77E-02	1.71	0.356	0.254	
kgp971582	6	51921703	PKHD1	A	G	4.96E-03	2.99	0.091	0.033	4.76E-03	4.89	0.104	0.025	
kgp22793211	X	92601376		G	A	2.20E-03	0.63	0.391	0.538	8.20E-03	0.61	0.396	0.550	
kgp4373213	3	124199924	KALRN	A	G	5.14E-05	0.45	0.174	0.313	1.43E-01	0.71	0.208	0.270	
kgp19268724	14	21486590	MDRO2	G	A	1.32E-03	0.07	0.003	0.033	5.09E-03	0.19	0.010	0.049	
kgp9071685	9	21419168		G	A	1.19E-02	0.16	0.005	0.029	3.65E-04	0.12	0.007	0.057	
kgp632534	4	13612751	BODIL	C	G	2.84E-01	0.45	0.008	0.017	4.68E-07	0.05	0.005	0.002	
kgp1224440	1	247399991		A	C	3.76E-03	0.52	0.096	0.179	1.21E-03	0.41	0.122	0.238	
kgp2465184	9	18982204	FAM154A	A	C	2.48E-02	0.48	0.043	0.088	3.54E-04	0.18	0.018	0.082	

STANDARD PRESENTIVE														
Data cohort										Porte cohort				
Prioritized Variants	Name	Chromo some	Position	Gene(s)	Major Allele (d)	Minor Allele (D)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)
	kgp11543962	10	10957903		G	A	1.42E-02	0.21	0.008	0.034	3.81E-04	0.12	0.008	0.057
	kgp4543470	2	213559411		A	C	3.80E-06	0.36	0.106	0.246	4.45E-01	0.80	0.161	0.189
	kgp5579170	13	65681762	PITPNC1	G	A	2.00E-03	0.44	0.076	0.151	3.74E-03	0.45	0.093	0.192
	kgp4812831	6	51910905	PKHD1	A	G	4.96E-03	2.99	0.091	0.033	4.61E-03	4.95	0.102	0.025
	rs2598360	9	114153899	KIAA0368	G	A	4.06E-03	0.61	0.389	0.300	7.26E-03	0.58	0.361	0.500
	kgp10833631	8	17504188	MTUS1	A	G	9.73E-03	Zero	0.000	0.017	5.52E-04	Zero	0.000	0.041
	kgp3651767	16	84992155		G	A	6.93E-02	0.29	0.008	0.025	1.43E-03	0.09	0.007	0.074
	rs273829	9	114108079		A	C	1.84E-03	0.58	0.407	0.529	1.58E-02	0.61	0.391	0.516
	kgp279772	8	2105576		T	A	6.51E-03	0.61	0.237	0.338	8.63E-04	0.47	0.256	0.410
	kgp20163979	8	79366479		A	C	2.33E-04	Zero	0.000	0.033	3.69E-01	0.30	0.002	0.008
	kgp21171930	4	80362934		A	G	3.79E-03	Zero	0.000	0.021	2.45E-03	0.07	0.002	0.033
	kgp2092617	5	39635583		G	A	8.09E-03	0.10	0.003	0.025	1.57E-03	Zero	0.000	0.025
	kgp3594499	15	51652449	GLDN	G	A	5.89E-04	Zero	0.000	0.029	7.37E-02	0.15	0.002	0.016
	kgp649620	1	41235946	MFYC	G	A	1.54E-03	1.75	0.401	0.275	2.30E-02	1.66	0.418	0.303
	rs3818675	10	12858045	CAMK1D	G	A	1.81E-03	0.28	0.020	0.071	5.56E-03	0.32	0.030	0.090
	kgp0530088	11	30501054	MPTPD2	A	G	4.45E-02	0.70	0.276	0.350	2.34E-04	0.44	0.221	0.392
	rs2453478	12	49202743		A	G	1.81E-03	0.61	0.356	0.488	1.98E-02	0.62	0.341	0.459
	kgp10538725	18	3070717	MYO4B	G	A	7.81E-03	0.23	0.010	0.042	1.79E-03	0.14	0.008	0.049
	kgp26586329	8	6304848	MCPH1	A	G	8.09E-03	0.10	0.003	0.025	1.61E-03	Zero	0.000	0.025
	kgp50282494	5	72863824	UTP15	A	G	3.27E-03	0.08	0.003	0.029	1.02E-02	Zero	0.000	0.016
	rs7524868	1	41106774	RBM53	A	C	1.68E-04	2.05	0.351	0.208	9.59E-02	1.48	0.333	0.254
	kgp9806386	5	13806054		A	C	5.89E-04	Zero	0.000	0.029	7.57E-02	0.15	0.003	0.016
	kgp4127859	6	32434481		A	G	4.49E-04	2.42	0.205	0.100	1.43E-02	2.53	0.155	0.074
	kgp1753443	21	39811162	ERG	G	A	7.36E-03	2.09	0.162	0.092	2.76E-03	3.12	0.177	0.067
	kgp354462	2	149894403		A	C	2.89E-03	0.61	0.305	0.425	1.18E-02	0.58	0.290	0.410
	kgp26533576	6	99139642		A	C	2.40E-04	0.13	0.008	0.034	3.70E-01	0.45	0.008	0.016
	kgp2023214	16	76293345		A	G	5.03E-03	0.52	0.083	0.163	4.31E-03	0.45	0.078	0.172
	kgp6768546	4	153864174	FHRC1	G	A	1.95E-03	0.23	0.015	0.059	9.08E-03	0.27	0.020	0.066
	kgp1098237	9	114173681	KIAA0368	G	A	3.51E-03	0.61	0.379	0.496	9.79E-03	0.59	0.358	0.492
	kgp4559907	6	131253252		G	A	4.08E-04	0.56	0.311	0.454	3.11E-02	0.63	0.352	0.459
	rs1644418	10	12858409	CAMK1D	A	G	1.77E-03	0.26	0.018	0.067	5.33E-03	0.32	0.030	0.090
	kgp11804833	6	32396146		C	A	8.81E-04	2.34	0.190	0.092	9.98E-03	2.77	0.150	0.066
	rs7029123	9	114136169	KIAA0368	A	G	6.13E-03	0.63	0.391	0.500	6.39E-03	0.57	0.358	0.500
	kgp2688066	7	28560259	CREB5	A	G	1.51E-03	2.84	0.126	0.050	1.23E-02	3.21	0.118	0.041
	kgp2638591	8	108994382	RSP02	G	A	1.11E-03	0.32	0.035	0.096	1.32E-02	0.39	0.047	0.107
	rs2845371	22	17178213		G	A	5.95E-03	1.59	0.467	0.353	9.08E-03	1.78	0.508	0.377
	kgp5409955	9	18980841	FAM154A	G	A	2.34E-03	0.35	0.033	0.092	2.86E-02	0.35	0.025	0.066
	rs722827	18	76900411	ATP9B	G	A	6.44E-04	2.27	0.215	0.108	2.01E-02	1.98	0.198	0.107
	kgp1912591	2	137850215	THSD7B	A	G	4.12E-03	2.00	0.192	0.104	9.55E-03	2.22	0.215	0.107
	kgp4162414	6	51868165	PEL1D1	G	A	6.71E-03	2.89	0.088	0.033	4.61E-03	4.95	0.102	0.025
	rs2926455	10	107260501		A	G	8.73E-03	0.50	0.083	0.148	1.03E-03	0.99	0.090	0.197
	kgp3669685	7	78028723	M4G2	A	C	5.48E-03	1.80	0.254	0.160	3.26E-03	2.40	0.254	0.131
	kgp7059449	2	41255453		A	C	3.03E-02	2.89	0.056	0.021	1.57E-03	12.79	0.092	0.008

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STANDARD PHENOTYPE														
Prioritized Variants	Data cohort					Pilot cohort								
	Name	Chromosome	Position	Gene(s)	Major Allele (d)	Minor Allele (D)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)
rs3899755	X	68447361			C	A	7.42E-05	2.48	0.227	0.088	1.92E-01	1.42	0.204	0.148
rs2309760	4	183391332	ODZ3		A	G	1.87E-03	0.61	0.369	0.500	5.20E-02	0.67	0.320	0.418
kgp2788291	18	45153979			G	A	9.15E-03	0.57	0.119	0.197	1.21E-03	0.41	0.122	0.238
kgp3933330	7	28583709	CREB3		A	G	4.00E-04	2.42	0.198	0.088	3.21E-02	2.15	0.158	0.082
rs7062312	X	68447052			G	A	7.68E-05	2.49	0.228	0.088	1.92E-01	1.42	0.204	0.148
kgp337461	6	125019969	NKAIN2		A	G	2.96E-02	0.61	0.126	0.189	1.84E-04	0.39	0.119	0.262
rs6898068	5	126591501			G	A	6.36E-03	1.60	0.414	0.304	1.48E-03	2.19	0.396	0.246
kgp8046214	4	153726582	ARFIP1		A	G	8.57E-04	0.20	0.613	0.058	2.48E-02	0.31	0.020	0.058
rs6835202	4	152465186			C	A	1.75E-03	0.21	0.613	0.055	9.06E-03	0.27	0.020	0.066
kgp10620244	8	133472755	KCNQ3		G	A	1.29E-03	2.11	0.220	0.117	2.23E-02	1.96	0.219	0.123
kgp11407580	2	65096583			A	G	2.61E-04	0.25	0.025	0.092	3.43E-01	0.59	0.025	0.041
rs3799383	6	26510748			G	A	1.90E-03	0.45	0.071	0.150	2.58E-03	0.44	0.107	0.213
rs6845927	4	153798603	ARFIP1		A	C	2.20E-03	0.24	0.615	0.058	9.38E-03	0.28	0.020	0.066
rs10489312	1	175526526	TNR		A	G	1.28E-03	0.50	0.121	0.221	1.88E-02	0.53	0.133	0.221
kgp11633966	11	37301793			G	A	3.96E-03	0.56	0.172	0.267	2.75E-02	0.57	0.129	0.213
rs7496451	15	25718875			G	A	8.50E-03	1.82	0.220	0.138	6.16E-03	2.18	0.259	0.139
kgp3048169	4	78109391			G	A	5.55E-04	0.46	0.166	0.208	7.04E-02	0.60	0.109	0.172
kgp8990121	9	27215039	TEK		C	A	1.08E-03	2.57	0.157	0.071	3.93E-02	1.96	0.177	0.098
kgp26528455	6	72737785	RHRS1		G	A	2.26E-03	0.26	0.618	0.063	1.23E-02	0.32	0.017	0.066
kgp4755147	2	149894654			A	C	2.91E-03	0.61	0.308	0.429	1.57E-02	0.59	0.294	0.410
kgp10372946	10	133986657	JAKMIP3		G	A	1.26E-03	13.17	0.051	0.064	2.43E-02	7.37	0.055	0.008
rs1380706	2	57864042			A	G	2.87E-03	1.88	0.393	0.271	2.34E-02	1.67	0.424	0.311
kgp12182745	8	125465203	TRMT12		A	T	1.17E-03	0.41	0.654	0.133	8.88E-02	0.51	0.041	0.083
kgp3951463	3	157280172	C3orf55		C	A	1.42E-03	1.87	0.348	0.233	2.46E-02	1.75	0.348	0.246
kgp8602316	7	335911			G	A	8.14E-03	1.59	0.393	0.288	6.93E-03	1.77	0.440	0.295
rs16937077	11	10620629	MIR461-AS1		G	A	5.86E-03	0.53	0.106	0.183	4.35E-02	0.48	0.055	0.107
kgp6959492	4	153687676			A	G	1.89E-03	0.21	0.613	0.054	9.06E-03	0.27	0.020	0.066
kgp8793915	11	109012665			A	G	1.42E-03	Zero	0.600	0.023	6.90E-02	Zero	0.000	0.008
kgp13161760	21	18192806			G	A	3.27E-03	0.08	0.603	0.029	1.45E-02	Zero	0.000	0.025
kgp6567154	4	3482146			G	C	9.31E-03	0.64	0.274	0.375	1.81E-03	0.51	0.274	0.426
kgp2282938	22	32719612			G	A	1.70E-02	0.28	0.613	0.042	2.96E-04	0.18	0.018	0.083
kgp335723	8	75270402	QDAP1		A	G	2.94E-01	0.39	0.003	0.013	1.13E-06	Zero	0.000	0.037
rs10201643	2	149405641	LYPLAL3		C	A	3.22E-03	0.62	0.308	0.429	1.51E-02	0.59	0.294	0.410
kgp27640141	12	118805689	TACR3		G	A	2.02E-02	0.14	0.003	0.025	2.54E-04	Zero	0.000	0.033
rs7676525	4	153814538	ARFIP1		A	G	1.97E-03	0.21	0.613	0.054	9.98E-03	0.27	0.020	0.066
kgp28817122	8	122487115			A	G	9.13E-03	0.28	0.615	0.030	1.34E-03	0.21	0.018	0.074
kgp5014707	9	1702186			G	A	2.54E-02	Zero	0.600	0.013	2.54E-04	Zero	0.000	0.033
kgp7092772	14	22379841			G	A	9.73E-03	Zero	0.600	0.017	1.57E-03	Zero	0.000	0.025
kgp3477351	19	235864			G	A	2.54E-02	Zero	0.600	0.013	2.54E-04	Zero	0.000	0.033
kgp23296674	21	20962564			C	A	1.49E-03	Zero	0.000	0.025	6.90E-02	Zero	0.000	0.008
kgp12083934	16	10826979			A	G	3.15E-03	0.58	0.233	0.343	1.13E-02	0.56	0.230	0.344
kgp485315	7	15372018	ACOM3		G	A	8.50E-05	1.93	0.490	0.325	1.49E-01	1.36	0.443	0.369
kgp25191871	1	115687027			A	C	6.93E-03	0.38	0.030	0.081	5.66E-03	0.27	0.023	0.074

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STANDARD PHENOTYPE														
Prioritized Variants	Name	Chromo some	Position	Gene(s)	Major Allele (R)	Minor Allele (D)	Gala cohort				Forte cohort			
							P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)
	kgp24131116	2	213906695	IKZF2	G	A	9.91E-03	Zero	0.000	0.017	1.57E-03	Zero	0.000	0.025
	kgp9854133	3	31334098		G	A	6.08E-04	Zero	0.000	0.029	?	Zero	0.000	0.090
	kgp22811918	X	21960214	SRMS	C	A	4.90E-03	0.52	0.063	0.142	1.88E-02	0.45	0.047	0.115
	kgp7792268	13	23070499		C	A	6.43E-04	0.18	0.010	0.058	7.70E-02	0.35	0.015	0.041
	kgp11356379	11	9814612	LOC283104, SBR2	G	A	1.37E-02	0.66	0.353	0.457	1.59E-03	0.48	0.336	0.483
	kgp27571222	12	56245724		A	G	9.10E-03	0.11	0.003	0.029	1.65E-03	Zero	0.000	0.025
	rs1886214	13	42948531		A	G	4.17E-03	1.79	0.272	0.171	1.06E-02	1.99	0.285	0.172
	kgp1054273	12	67131774		G	A	2.33E-04	Zero	0.000	0.033	2.03E-01	0.30	0.005	0.016
	kgp9531947	18	42502140	SETBP1	G	A	3.79E-03	Zero	0.000	0.021	2.25E-03	0.11	0.005	0.041
	kgp5483926	3	144352913		A	C	6.84E-02	Zero	0.000	0.008	1.51E-05	0.07	0.005	0.066
	kgp1155998	1	124734012		G	A	2.76E-02	0.19	0.005	0.025	2.54E-04	Zero	0.000	0.033
	kgp2958113	5	163341388		A	C	2.76E-02	0.19	0.005	0.025	2.54E-04	Zero	0.000	0.033
	kgp8133515	11	4926211		G	A	8.09E-03	0.10	0.003	0.025	2.45E-03	0.07	0.002	0.033
	kgp2388938	8	79087167		G	A	9.28E-03	Zero	0.000	0.038	6.79E-01	0.60	0.005	0.008
	kgp28687699	8	79225285		C	A	9.28E-03	Zero	0.000	0.038	6.79E-01	0.60	0.005	0.008
	kgp11627539	14	78954642	NRXN3	A	G	2.83E-03	0.41	0.048	0.113	3.48E-03	0.40	0.070	0.156
	kgp24753479	1	26013940	MAN1C1	A	C	1.19E-02	0.16	0.005	0.029	1.61E-03	Zero	0.000	0.025
	kgp1283441	3	56931141	ARHGEF3	G	A	8.54E-04	0.49	0.124	0.225	3.75E-02	0.57	0.137	0.213
	rs17638791	6	51940816	PKHD1	A	G	7.32E-03	2.73	0.093	0.038	4.61E-03	4.95	0.102	0.025
	rs2325911	6	128027223	NEALN2	C	A	3.65E-02	0.61	0.121	0.179	1.48E-04	0.39	0.118	0.262
	kgp10967946	15	66274387	MIR3P11	G	A	5.49E-02	0.50	0.041	0.075	1.04E-04	0.24	0.030	0.123
	rs12013377	X	92620062		A	G	5.41E-03	0.67	0.409	0.342	6.48E-03	0.60	0.400	0.557
	kgp7186699	4	184878777	STOX2	G	A	1.79E-02	2.38	0.088	0.038	1.13E-03	13.37	0.100	0.008
	kgp93681119	7	11707419	THSD7A	A	G	1.06E-02	0.65	0.427	0.529	1.75E-02	0.60	0.343	0.459
	kgp124162	11	72356846	PDE2A	A	G	1.89E-03	0.21	0.013	0.054	1.55E-02	0.28	0.018	0.057
	kgp8446936	4	78053785		G	A	6.77E-04	0.25	0.018	0.075	9.68E-02	0.43	0.020	0.049
	rs4738738	8	58844234	TOX	A	C	1.63E-02	1.49	0.424	0.324	6.74E-04	2.22	0.425	0.254
	kgp7802182	18	56759170		A	G	2.53E-02	0.67	0.222	0.304	7.43E-04	0.44	0.194	0.336
	kgp2923815	19	43931355		G	A	3.62E-03	0.44	0.066	0.133	1.71E-02	0.42	0.063	0.131
	rs3767985	1	41104475	RIMS3	G	A	2.57E-04	2.00	0.351	0.213	1.04E-01	1.47	0.321	0.254
	kgp3418770	10	59425598		A	C	5.89E-03	6.24	0.048	0.008	6.50E-03	Infinity	0.056	0.000
	rs17449018	9	7060825	KDM4C	G	A	3.68E-04	2.03	0.326	0.195	7.93E-02	1.53	0.311	0.230
	kgp4524468	22	32724532		A	G	1.99E-04	2.16	0.304	0.169	7.14E-02	1.62	0.259	0.178
	kgp4418535	6	32431598		C	A	5.98E-04	2.37	0.202	0.100	1.80E-02	2.46	0.152	0.074
	kgp22823022	X	9742488		G	A	7.11E-02	0.71	0.151	0.214	8.53E-05	0.41	0.113	0.280
	kgp7863887	1	18992858		G	A	8.17E-03	0.48	0.058	0.123	1.47E-02	0.36	0.030	0.082
	rs1621509	7	2969680	CARD11	G	A	2.25E-03	2.06	0.226	0.133	3.02E-02	1.82	0.253	0.158
	kgp4842590	1	110249364		A	C	2.30E-02	0.37	0.020	0.035	8.15E-04	0.17	0.010	0.066
	rs11192469	10	107282331		A	G	1.11E-02	0.51	0.081	0.143	1.30E-03	0.39	0.083	0.189
	kgp8303520	7	154911294		C	A	5.76E-03	0.63	0.449	0.363	3.00E-02	0.64	0.376	0.492
	rs1341334	2	60324127		A	G	1.42E-02	0.67	0.374	0.475	2.98E-03	0.52	0.341	0.484
	rs9876830	3	157311299	C3orf55	G	A	1.55E-03	1.89	0.351	0.238	2.85E-02	1.72	0.346	0.246
	kgp11285862	21	18177980		A	G	1.56E-03	0.07	0.003	0.033	4.46E-02	0.19	0.002	0.025

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STANDARD PHENOTYPE										Gala cohort				Porte cohort			
Prioritized Variants	Name	Chromosome	Position	Genes	Major Allele (d)	Minor Allele (D)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)			
0 - Priority genes, Predictive Model	rs2824070	21	18205972		A	G	3.48E-03	0.20	0.010	0.046	1.11E-02	0.24	0.010	0.049			
	kgp7181058	14	98385698		G	A	2.11E-03	0.24	0.015	0.058	4.15E-02	0.29	0.012	0.041			
	kgp5002011	1	110267738		G	A	3.87E-02	0.46	0.035	0.071	2.96E-04	0.25	0.025	0.107			
	rs2139612	X	92614918		A	C	6.26E-03	0.68	0.412	0.342	7.28E-03	0.61	0.395	0.549			
	rs7860748	9	114202502	K1A0368	G	A	5.70E-03	0.63	0.381	0.492	9.79E-03	0.59	0.358	0.492			
	rs17029538	2	85996800		A	C	2.02E-04	0.26	0.028	0.097	4.36E-01	0.65	0.027	0.041			
	kgp1371881	16	76291607		A	G	6.85E-03	0.53	0.083	0.160	6.32E-03	0.46	0.075	0.164			
	rs10492882	16	76293394		A	G	1.03E-02	0.55	0.083	0.155	3.04E-03	0.44	0.075	0.172			
	rs9392727	6	26500011		C	G	2.78E-03	0.46	0.074	0.150	2.76E-03	0.44	0.108	0.213			
2 - Priority genes	rs1894408	6	32786633		C	G	3.02E-03	1.72	0.419	0.305	9.30E-03	1.82	0.407	0.279			
	rs2829117	21	47550754	COL6A2	G	A	1.24E-02	0.59	0.134	0.213	1.25E-03	0.45	0.137	0.262			
	kgp8437961	2	98960603	EF5B	G	A	2.79E-03	0.50	0.099	0.183	1.07E-02	0.48	0.110	0.197			
	rs1308102	11	116379889		G	A	4.99E-04	0.34	0.043	0.117	4.32E-02	0.50	0.060	0.115			
	rs4449139	2	124875366	CNTNAP5	G	A	5.12E-03	0.63	0.389	0.504	3.76E-03	0.55	0.408	0.557			
	rs11559024	19	45821183	CKM	A	G	2.50E-03	Zero	0.000	0.029	1.18E-02	0.15	0.003	0.033			
	rs1894407	6	32787036		C	A	1.75E-03	1.77	0.419	0.300	1.81E-02	1.72	0.403	0.287			
	rs2857103	6	32791299	TAP2	C	A	5.72E-03	1.70	0.369	0.269	4.13E-03	2.04	0.356	0.221			
	rs9601224	6	32792910	TAP2	G	A	6.53E-03	1.69	0.369	0.271	4.13E-03	2.04	0.356	0.221			
0 - Priority genes, Predictive Model	kgp8110667	22	32716792		G	A	5.97E-03	Infinity	0.030	0.000	1.46E-02	Infinity	0.050	0.090			
2 - Priority genes																	
	kgp6599438	20	40843626	PTPR	G	A	3.70E-03	0.21	0.010	0.046	1.55E-02	0.28	0.018	0.057			
	rs241431	6	32796480	TAP2	A	G	6.26E-03	1.69	0.369	0.267	1.13E-02	1.86	0.354	0.233			
	rs1894406	6	32787056		G	A	2.63E-03	1.74	0.402	0.288	1.73E-02	1.76	0.361	0.246			
	rs1218328	22	37524098	R2RB	G	A	1.09E-02	0.16	0.005	0.010	1.39E-02	0.10	0.003	0.025			
	rs241443	6	32797115	TAP2	A	C	1.05E-02	1.63	0.367	0.273	5.28E-03	2.01	0.340	0.217			
	rs6621323	6	32788707		A	G	1.90E-02	1.56	0.371	0.286	3.09E-03	2.07	0.363	0.221			
	kgp304921	20	14017077	MACROR2	A	G	3.43E-02	0.50	0.038	0.091	1.51E-02	0.32	0.020	0.066			
	rs241456	6	32795965	TAP2	G	A	2.12E-02	1.55	0.313	0.279	8.94E-03	2.00	0.299	0.180			

STANDARD PHENOTYPE										Case cohort				Pilot cohort			
Priority Variant	Name	Chromosome	Position	Gene(s)	Major Allele (G)	Minor Allele (D)	P-value (Amitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	P-value (Amitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)			
0 - Priority genes, Predictive Model	kgp7747883	18	74804150	MBP	G	A	3.55E-02	0.70	0.346	0.429	9.82E-03	0.57	0.325	0.451			
2 - Priority genes	rs2621321	6	32789480		A	G	2.30E-02	1.54	0.316	0.233	7.19E-03	2.05	0.308	0.180			
2 - Priority genes	rs2837104	6	32790167	TAP2	G	C	2.38E-02	1.54	0.316	0.233	7.89E-03	2.03	0.299	0.180			
2 - Priority genes	rs241454	6	32796144	TAP2	A	G	2.57E-02	1.53	0.315	0.233	7.80E-03	2.02	0.300	0.180			
2 - Priority genes	rs241447	6	32796751	TAP2	A	G	2.85E-02	1.52	0.313	0.233	8.34E-03	2.01	0.303	0.183			
2 - Priority genes	kgp74569	6	32796057	TAP2	G	A	2.85E-02	1.52	0.313	0.233	7.80E-03	2.02	0.300	0.180			
2 - Priority genes	rs2837101	6	32794676	TAP2	A	G	2.48E-02	1.53	0.313	0.231	9.33E-03	2.00	0.296	0.180			
2 - Priority genes	kgp1024254	6	32785904		C	A	5.85E-03	1.63	0.424	0.317	4.44E-02	1.58	0.386	0.287			
2 - Priority genes	rs241444	6	32797109	TAP2	G	A	2.65E-02	1.52	0.313	0.233	8.54E-03	2.00	0.299	0.180			
2 - Priority genes	kgp4479467	6	32629331	HLA-DQA1	A	G	2.03E-02	1.50	0.391	0.300	1.59E-02	1.80	0.374	0.262			
2 - Priority genes	kgp10632945	20	4682507		G	A	1.87E-02	0.82	0.177	0.254	3.48E-02	0.59	0.170	0.254			
2 - Priority genes	rs241446	6	32796967	TAP2	G	A	2.49E-02	1.53	0.311	0.229	1.09E-02	1.96	0.298	0.180			
2 - Priority genes	rs241453	6	32796226	TAP2	G	A	3.40E-02	1.30	0.311	0.233	7.89E-03	2.02	0.300	0.180			
2 - Priority genes	rs241449	6	32796653	TAP2	C	A	3.25E-02	1.50	0.308	0.229	9.22E-03	1.99	0.298	0.180			
0 - Priority genes, Predictive Model	rs18162089	13	31316738	ALOX5AP	G	A	7.79E-03	1.56	0.508	0.398	3.16E-02	1.58	0.457	0.344			
2 - Priority genes	rs2071469	6	32794783	HLA-DQB1	G	A	6.76E-03	1.62	0.426	0.321	4.44E-02	1.58	0.386	0.287			
2 - Priority genes	p1_M_061310_6_159_P	6	32795505	TAP2	T	D	3.66E-02	1.49	0.310	0.233	7.89E-03	2.02	0.300	0.180			
2 - Priority genes	rs241452	6	32796346	TAP2	A	G	3.31E-02	1.50	0.313	0.233	8.43E-03	2.01	0.299	0.180			
2 - Priority genes	kgp2388352	6	32797297	TAP2	A	G	4.25E-02	1.47	0.311	0.235	7.04E-03	2.02	0.304	0.180			
2 - Priority genes	kgp8036704	6	32796521	TAP2	G	A	3.51E-02	1.50	0.310	0.233	8.61E-03	2.02	0.296	0.180			

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STANDARD PHENOTYPE					Case cohort					Pilot cohort				
Variant	Name	Chromosome	Position	Gene(s)	Major Allele (M)	Minor Allele (m)	p-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	p-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)
2 - Priority genes	rs241442	6	32797168	TAP2	G	A	3.94E-02	1.48	0.311	0.235	7.80E-03	2.02	0.300	0.180
2 - Priority genes	rs241445	6	32797072	TAP2	G	A	3.57E-02	1.49	0.312	0.235	8.54E-03	2.00	0.299	0.180
2 - Priority genes	rs1410779	9	9083173	JAK2	G	A	1.93E-02	0.61	0.145	0.217	1.29E-02	0.54	0.178	0.279
2 - Priority genes	kgp23672937	7	18685891	HEXAC9	G	A	4.94E-02	0.15	0.003	0.017	9.97E-03	Zero	0.000	0.016
2 - Priority genes	kgp4348717	18	74810199	MEP	G	A	4.94E-02	0.15	0.003	0.017	9.97E-03	Zero	0.000	0.016
2 - Priority genes	kgp9699734	10	79358319	KCNMA1	A	G	2.70E-02	Infinity	0.020	0.008	4.11E-02	Infinity	0.033	0.000
2 - Priority genes	rs241440	6	32797361	TAP2	G	A	3.40E-02	1.50	0.311	0.233	1.69E-02	1.96	0.295	0.180
2 - Priority genes	kgp5134770	6	32828420	HLA-DQB1	G	A	1.68E-02	1.53	0.391	0.298	2.74E-02	1.73	0.362	0.262
2 - Priority genes	kgp4898179	6	32629347	HLA-DQB1	A	G	2.53E-02	1.48	0.391	0.304	1.87E-02	1.77	0.372	0.262
0 - Priority in Predictive Model	rs759458	2	65245365	SLC1A4	G	A	1.08E-03	1.90	0.303	0.183	4.74E-01	1.18	0.288	0.254
2 - Priority genes	rs2071472	6	32784620	HLA-DQB	G	A	2.91E-02	1.49	0.348	0.267	1.86E-02	1.79	0.331	0.221
2 - Priority genes	rs2071470	6	32784753	HLA-DQB	A	G	2.91E-02	1.49	0.348	0.267	1.86E-02	1.79	0.331	0.221
2 - Priority genes	kgp25543811	18	74774894	MIR488P	G	A	4.81E-02	0.15	0.003	0.017	1.37E-02	0.10	0.002	0.023
2 - Priority genes	kgp293787	20	4995092	PTPR	G	A	4.88E-03	0.15	0.005	0.028	2.19E-02	0.39	0.032	0.082
2 - Priority genes	rs1043136	3	30720304	TGFBR2	A	G	4.42E-02	1.47	0.306	0.233	3.75E-02	1.67	0.308	0.208
2 - Priority genes	rs4769080	13	31337877	ALOX5AP	A	G	3.14E-02	1.42	0.472	0.383	3.13E-02	1.60	0.439	0.328
2 - Priority genes	kgp6037617	13	31287981	ALOX5AP	A	G	1.11E-02	0.68	0.212	0.292	4.38E-02	0.62	0.233	0.320
2 - Priority genes	kgp5441587	6	32827356	PSM29	G	A	4.56E-02	0.14	0.003	0.017	1.97E-02	0.23	0.010	0.041
2 - Priority genes	rs241435	6	32798243	TAP2, TAP2	G	A	4.94E-02	0.15	0.003	0.017	1.97E-02	0.23	0.010	0.041
2 - Priority genes	kgp3182607	6	32829948	PSM29	G	A	4.94E-02	0.15	0.003	0.017	1.97E-02	0.23	0.010	0.041
2 - Priority genes	kgp22778566	7	1950337	MADH1	G	A	1.10E-02	1.56	0.276	0.199	2.87E-02	1.95	0.216	0.131

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STANDARD PHENOTYPE										Data cohort					Forfe cohort				
Predefined Variants	Name	Chromosome	Position	Gene(s)	Major Allele (M)	Minor Allele (m)	P-value (A vs M)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	P-value (A vs M)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)					
2 - Priority genes	kgp97310	9	5122932	JAK2	A	G	4.58E-02	0.68	0.174	0.242	1.99E-02	0.58	0.225	0.128					
2 - Priority genes	kgp5440506	13	31320543	ALOX5AP	G	A	3.52E-02	0.71	0.393	0.479	2.50E-02	0.63	0.462	0.583					
2 - Priority genes	rs11147439	13	31325643	ALOX5AP	C	A	4.34E-02	0.72	0.396	0.479	2.16E-02	0.62	0.460	0.582					
2 - Priority genes	rs4360791	13	31318020	ALOX5AP	G	A	4.65E-02	0.72	0.409	0.492	2.32E-02	0.63	0.470	0.590					
2 - Priority genes	rs9671182	13	31321138	ALOX5AP	C	G	3.90E-02	0.71	0.398	0.483	2.76E-02	0.64	0.465	0.582					
2 - Priority genes	rs4366336	13	31319548	ALOX5AP	A	G	3.98E-02	0.71	0.399	0.483	2.76E-02	0.64	0.463	0.582					
2 - Priority genes	rs10815180	9	5116636	JAK2	A	C	3.98E-02	0.66	0.180	0.232	3.69E-02	0.62	0.234	0.328					
2 - Priority genes	rs4354166	13	31322949	ALOX5AP	A	G	4.97E-02	0.72	0.399	0.479	2.40E-02	0.63	0.463	0.582					
2 - Priority genes	kgp2715873	13	31320249	ALOX5AP	G	A	4.97E-02	0.72	0.399	0.479	2.76E-02	0.64	0.465	0.582					
2 - Priority genes	rs9670531	13	31321069	ALOX5AP	A	G	4.97E-02	0.72	0.399	0.479	2.76E-02	0.64	0.465	0.582					
1 - Priority variants	rs2487896	10	100802380	HPSE2	G	A	5.73E-01	0.88	0.139	0.155	5.50E-04	0.39	0.122	0.246					
0 - Priority variants, Predictive Model	rs1135391	6	32410987	HLA-DRA	G	A	1.99E-02	0.66	0.174	0.242	4.99E-02	0.64	0.231	0.320					
2 - Priority genes	kgp26271138	6	32823393	PSMB9	G	A	4.94E-02	0.15	0.003	0.017	4.15E-02	0.29	0.012	0.041					
1 - Priority variants	rs2135388	6	32413951		G	A	4.72E-02	0.87	0.174	0.239	4.09E-02	0.64	0.231	0.320					
2 - Priority genes	kgp11281589	7	1941003	MAD1L1	A	G	4.53E-02	1.49	0.282	0.211	4.24E-02	1.85	0.210	0.131					
1 - Priority variants	rs17575455	2	76624220		C	A	4.13E-01	0.87	0.331	0.383	6.21E-03	0.96	0.308	0.443					
1 - Priority variants	rs947603	10	95249605		A	G	5.39E-02	1.48	0.258	0.192	1.59E-01	1.45	0.225	0.164					

(Note: Odds Ratio >1 = Minor Allele is associated with Response, Odds Ratio <1 = Minor Allele Associated with Non-Response)

Table 38: Standard Response SNP%
STANDARD PHENOTYPE

STANDARD PHENOTYPE														
Combined														
Prioritized Variants	Name	Chromosome	Position	Gene(s)	Major Allele (M)	Minor Allele (m)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	DD (Responders)	DD (Non-responders)	DD (Non-responders)	Ad (Non-responders)
D - Priority in Predictive Model	kgp24415534	2	174156875		G	A	3.98E-07	0.08	0.004	0.044	0	0	3	165
	kgp12008953	2	73759636	ALMS1	G	A	3.98E-07	0.08	0.004	0.044	0	0	3	165
	kgp26026346	13	79972606	RBBP2	A	C	4.46E-07	0.03	0.001	0.036	0	0	1	167
D - Priority in Predictive Model	rs18886004	7	78021500	MARCH2	A	G	9.81E-07	2.79	0.199	0.089	6	2	147	149
	kgp250522891	13	80027089		A	G	1.41E-06	0.04	0.001	0.033	0	0	1	168
	kgp3430875	16	57268931	RSPRY1	G	A	1.99E-06	0.12	0.006	0.047	0	0	5	164
	rs10251797	7	78025427	MARCH2	C	A	2.21E-06	2.67	0.197	0.091	6	2	145	150
	kgp2299675	20	16933074		G	A	2.28E-06	0.19	0.014	0.064	0	0	11	155
	kgp10594414	1	216039833	USH2A	A	G	2.44E-06	0.14	0.008	0.050	0	0	6	163
	kgp1688752	21	43016736		G	A	2.53E-06	0.33	0.040	0.113	1	2	30	142
	kgp12230354	5	27037978	CDR8	A	C	2.74E-06	0.19	0.013	0.061	0	0	10	199
	rs543122	3	124164136	KALRN	G	A	3.17E-06	0.54	0.423	0.569	70	54	195	29
	kgp6236949	2	60301030		A	G	3.26E-06	0.54	0.283	0.423	30	34	166	62
	kgp9627338	17	90155	RPH3AL	A	G	3.52E-06	0.45	0.105	0.207	6	7	71	113
	kgp11141512	20	35283733	MDRC3	G	A	4.12E-06	0.21	0.014	0.064	0	1	11	152
	rs9379386	13	30980265		G	A	4.19E-06	0.26	0.023	0.080	0	1	18	153
	rs2316838	10	52714759		G	A	4.79E-06	0.46	0.125	0.229	4	8	92	106
	kgp4705854	12	19907696		G	A	4.80E-06	0.53	0.115	0.456	41	38	169	54
	rs9817308	3	124182136	KALRN	A	C	5.18E-06	0.55	0.429	0.572	71	55	199	29
D - Priority in Predictive Model	kgp8817856	6	32744440		G	A	5.33E-06	0.53	0.392	0.528	50	44	208	34
	kgp6214351	11	75546691	UVRAG	A	G	5.51E-06	0.35	0.046	0.119	0	2	27	140
	kgp2356388	16	19771577	RCK	G	A	5.78E-06	0.46	0.133	0.235	4	5	98	101
D - Priority in Predictive Model	kgp7416074	9	21453902		G	A	6.06E-06	0.13	0.006	0.044	0	0	5	165
	rs6718758	2	60328802		C	A	6.08E-06	0.55	0.307	0.445	35	38	175	58
	rs7579987	2	60307009		G	C	6.43E-06	0.55	0.331	0.469	40	41	184	52
	rs7217872	17	58988	RPH3AL	G	A	7.50E-06	0.47	0.108	0.207	6	7	74	113
	rs13394010	2	60302746		A	G	7.81E-06	0.56	0.350	0.467	39	41	185	53
	rs7191155	16	19800213	RCK	A	G	7.89E-06	0.56	0.350	0.467	39	41	185	53
	rs9931167	16	19792598	RCK	G	A	7.89E-06	0.46	0.133	0.233	4	5	97	101
	rs11691553	2	60303354		C	A	8.07E-06	0.46	0.133	0.233	4	5	98	101
	rs11648129	16	19820694	RCK	A	G	8.19E-06	0.56	0.350	0.467	39	41	183	53
	kgp25216186	1	23758427	ASAP3	A	G	8.23E-06	0.47	0.132	0.232	4	5	97	102
	kgp29794723	10	18397332		A	G	8.36E-06	0.07	0.003	0.033	0	0	2	169
	rs3829539	16	19722366	C16orf88	A	G	8.64E-06	0.25	0.020	0.072	0	0	16	155
	rs6893994	5	141037277	ARAP3	A	C	8.80E-06	0.47	0.133	0.233	4	5	98	101
	kgp1099249	12	19838534		G	A	9.24E-06	0.57	0.368	0.508	56	46	181	43
	rs10203396	2	60305110		A	G	9.55E-06	0.51	0.195	0.311	10	16	136	84
	kgp3654180	16	19721806	C16orf88	G	A	9.72E-06	0.56	0.332	0.467	39	41	186	53

STANDARD PHENOTYPE										Combined									
Prioritized Variants	Name	Chromosome	Position	Gene(s)	Major Allele (A)	Minor Allele (B)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	EB (Responders)	DB (Non-responders)	DB (Non-responders)	DB (Non-responders)	DB (Non-responders)	DB (Non-responders)	DB (Non-responders)	DB (Non-responders)	DB (Non-responders)
	rs6497396	16	19733697	LOC100000000	A	G	1.02E-05	0.48	0.143	0.246	6	6	102	77	290	98			
	rs13419758	2	60302920		G	A	1.09E-05	0.56	0.332	0.467	40	41	183	87	174	53			
	rs8055485	16	19750031	LOC100000000	A	G	1.09E-05	0.47	0.133	0.232	4	5	98	74	296	102			
	rs9931211	16	19813605	LOC100000000	A	G	1.09E-05	0.47	0.133	0.232	4	5	98	74	296	102			
	kgp5869992	12	49219569	CACNB3	A	G	1.13E-05	0.58	0.384	0.528	60	58	184	74	152	48			
	kgp9320791	2	60309952		C	G	1.15E-05	0.56	0.333	0.467	39	41	187	87	172	53			
	kgp7730397	16	19740243	LOC100000000	A	G	1.17E-05	0.47	0.134	0.233	4	5	99	74	293	101			
	kgp11002881	11	118219897	CD3G	A	G	1.17E-05	0.10	0.094	0.036	0	0	3	13	394	167			
	kgp3205849	10	121531725	INPP5F	A	G	1.18E-05	0.53	0.178	0.295	13	18	115	69	269	91			
	kgp6127371	4	153856357		A	G	1.23E-05	0.23	0.016	0.064	0	0	13	23	384	157			
	kgp10305127	11	99881768	CNTN5	A	G	1.23E-05	0.44	0.084	0.173	3	6	61	50	334	123			
	rs653882	4	153448128		G	A	1.24E-05	0.23	0.016	0.064	0	0	13	23	386	158			
	kgp6706691	4	153449531		A	G	1.24E-05	0.23	0.016	0.064	0	0	13	23	386	158			
	rs11629892	11	27269546		G	A	1.25E-05	1.94	0.351	0.227	44	5	192	72	183	104			
	kgp270801	16	19750275	LOC100000000	G	A	1.27E-05	0.48	0.143	0.244	6	6	102	76	291	98			
	kgp8192546	12	19803173		G	A	1.29E-05	0.55	0.236	0.359	21	23	146	84	232	74			
	kgp5068397	16	19756348	LOC100000000	A	G	1.37E-05	0.51	0.183	0.294	10	12	126	82	262	86			
	kgp16910719	16	19803199	LOC100000000	C	A	1.39E-05	0.47	0.133	0.231	4	5	98	73	297	102			
	kgp2939751	6	38719342		G	A	1.39E-05	0.22	0.015	0.061	0	0	12	22	387	159			
	rs959928	16	19824838	LOC100000000	A	G	1.43E-05	0.48	0.138	0.236	4	5	102	75	293	100			
	rs1858973	16	19743849	LOC100000000	A	G	1.44E-05	0.48	0.134	0.232	4	5	99	74	295	102			
	rs2660214	10	52352452		A	G	1.45E-05	0.48	0.138	0.227	4	8	94	68	301	107			
	kgp2709692	18	30808008	LPIN2	C	A	1.45E-05	0.22	0.015	0.061	0	0	12	22	386	159			
	kgp11210903	22	30808906	SEC14L4	G	A	1.48E-05	0.12	0.005	0.039	0	0	4	14	395	167			
	kgp6030773	8	63286607	MCPH1	A	C	1.48E-05	0.26	0.011	0.055	0	1	9	18	388	162			
	rs10841337	12	19877179		A	G	1.56E-05	0.55	0.241	0.365	22	24	147	84	227	73			
	kgp8178358	14	70923024	ADAM21	A	G	1.57E-05	0.12	0.005	0.039	0	0	4	14	393	167			
	kgp11843177	11	27316568		A	G	1.59E-05	1.95	0.330	0.208	39	4	185	67	175	109			
	kgp23737989	7	97217288		G	A	1.60E-05	0.04	0.001	0.028	0	0	1	10	398	171			
	rs7187976	16	19768196	C16orf62	A	G	1.63E-05	0.49	0.144	0.244	6	6	103	76	290	98			
	rs17577980	6	12359821	HCC23	G	A	1.66E-05	2.36	0.196	0.093	13	5	130	23	255	150			
	kgp5908816	2	60359823		A	C	1.67E-05	0.57	0.320	0.433	37	42	181	80	180	59			
	kgp26995430	3	53359406	ECTP1A	G	A	1.68E-05	0.14	0.008	0.041	0	0	5	15	394	166			
	kgp6996560	13	110124242		G	A	1.69E-05	0.14	0.006	0.041	0	0	5	15	394	166			
	rs4782279	16	19756607	LOC100000000	A	C	1.71E-05	0.50	0.147	0.249	7	7	103	76	288	98			
	rs8053136	16	19746129	LOC100000000	A	C	1.76E-05	0.52	0.195	0.307	12	14	131	83	255	84			
	kgp11328629	10	120711084		G	A	1.79E-05	2.95	0.137	0.052	6	0	97	19	295	162			
	kgp8200264	10	12856372	CAMK1D	A	G	1.87E-05	0.30	0.026	0.083	0	2	21	26	376	152			
	kgp6835138	20	40712994	P1PR1	G	A	1.88E-05	0.17	0.009	0.047	0	0	7	17	392	164			
	kgp841428	5	14106337	ARAP3	A	G	1.93E-05	0.58	0.371	0.506	56	46	183	91	159	44			
	rs3815822	16	29872361	CDIPT	A	C	1.96E-05	1.74	0.509	0.373	102	26	202	83	95	72			
	rs1579771	9	157278882	C3orf55	A	C	1.96E-05	1.91	0.366	0.346	39	9	213	71	146	101			
	kgp4734301	11	27315427		A	G	1.96E-05	1.93	0.330	0.210	39	4	185	68	175	109			

STANDARD PHENOTYPE										Combined									
Prioritized Variants	Name	Chromosome	Position	Gene(s)	Major Allele (d)	Minor Allele (D)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	DD (Responders) (n)	DD (Non-Responders) (n)	DD (Non-Responders) (n)	DD (Non-Responders) (n)	DD (Non-Responders) (n)	DD (Non-Responders) (n)	DD (Non-Responders) (n)	DD (Non-Responders) (n)	DD (Non-Responders) (n)
	rs11029928	11	27319188		G	A	1.96E-03	1.93	0.330	0.210	39	185	4	175	108				
	rs10841322	12	1986642		G	A	2.00E-03	0.53	0.234	0.354	20	147	21	232	74				
	kgp1786679	7	14470118		A	G	2.09E-03	0.49	0.118	0.315	4	86	11	308	114				
	kgp5053636	2	205336730		C	A	2.13E-03	0.29	0.024	0.077	1	17	0	378	153				
	kgp9601362	9	18959317	FAM154A	G	A	2.21E-03	0.33	0.031	0.092	0	25	3	372	149				
	kgp8183049	13	40634155		G	A	2.23E-03	Zero	0.000	0.022	0	0	0	399	172				
	kgp5564993	6	36414060	BTBD3A1	C	A	2.28E-03	2.88	0.145	0.061	1	109	0	274	151				
	kgp27500525	9	30278677		A	G	2.35E-03	2.69	0.090	0.032	0	0	0	399	173				
	rs11022778	11	13390860	ARNTL	A	C	2.37E-03	1.06	0.351	0.227	52	176	5	171	104				
	kgp10826273	2	176263817		G	A	2.41E-03	Zero	0.000	0.022	0	0	0	398	173				
	rs12494712	3	116796116		A	G	2.44E-03	2.08	0.247	0.138	23	151	2	225	33				
	kgp1779254	12	73686930		A	G	2.47E-03	0.08	0.003	0.031	0	0	0	397	169				
	kgp6190988	5	10699522	DAP	G	A	2.47E-03	0.08	0.003	0.031	0	0	0	397	169				
	kgp4507761	7	319681		A	G	2.55E-03	0.59	0.428	0.566	78	185	61	135	37				
	rs2074037	16	19725130	C16orf58	G	A	2.55E-03	0.49	0.137	0.232	4	101	5	294	101				
	rs4133493	6	51829939	PKHD1	G	A	2.57E-03	4.21	0.090	0.035	0	0	0	327	172				
	kgp1699628	6	18032535		A	G	2.72E-03	0.57	0.454	0.584	72	218	62	109	32				
	rs7624953	9	18460334	FAM154A	A	G	2.74E-03	0.34	0.031	0.091	0	0	3	372	151				
	kgp10974813	13	77339132		A	G	2.78E-03	0.08	0.003	0.030	0	0	0	395	170				
	kgp10412303	2	205303530		G	A	2.83E-03	0.50	0.026	0.080	0	0	1	378	153				
	kgp8669946	17	85735872	NOL1	A	G	2.86E-03	0.53	0.167	0.272	12	109	10	378	92				
	rs17224858	3	124305297	KALRN	G	A	2.89E-03	0.54	0.188	0.298	10	130	19	259	92				
	rs8840089	4	153713220	ARFP1	G	A	3.06E-03	0.34	0.016	0.061	0	0	0	386	159				
	rs7666442	4	153753101	ARFP1	A	G	3.06E-03	0.34	0.016	0.061	0	0	0	386	159				
	rs7672013	4	153818501	ARFP1	G	A	3.06E-03	0.24	0.016	0.061	0	0	0	386	159				
	rs7671801	4	153795067	ARFP1	A	G	3.15E-03	0.24	0.016	0.061	0	0	0	383	158				
	rs4669694	2	11767948	FLJ33534	G	A	3.15E-03	0.46	0.088	0.173	2	66	6	328	123				
	kgp10523170	16	5221617		G	A	3.16E-03	0.08	0.003	0.033	0	0	1	397	170				
	kgp5216209	3	170740453	SLC2A2	C	A	3.18E-03	0.23	0.015	0.058	0	0	0	387	159				
	rs720176	16	19721515	C16orf28	A	G	3.20E-03	0.49	0.138	0.232	4	101	5	290	102				
	kgp7481890	16	19729016	C16orf28	G	C	3.20E-03	0.49	0.146	0.242	4	107	5	282	98				
	rs1532305	12	49204421		G	A	3.23E-03	0.59	0.345	0.478	43	188	52	166	60				
	rs12943140	17	85738773	NOL1	G	A	3.24E-03	0.53	0.167	0.272	12	108	10	275	92				
	kgp11702474	4	153712868	ARFP1	A	G	3.31E-03	0.24	0.016	0.061	0	0	0	384	159				
	rs10498793	6	51829707	PKHD1	A	G	3.34E-03	4.14	0.089	0.025	0	0	0	328	172				
	kgp559666	3	197292022	C3orf55	G	A	3.39E-03	1.90	0.354	0.240	34	213	7	150	101				
	kgp10679353	16	19800133	KNX	G	A	3.39E-03	0.50	0.144	0.240	5	105	7	289	101				
	kgp9410843	10	121484477		A	G	3.48E-03	0.55	0.180	0.290	13	116	18	266	94				
	kgp6772915	9	18978739	FAM154A	A	C	3.50E-03	0.33	0.032	0.089	0	0	2	371	149				
	kgp20478926	8	21050249		A	G	3.53E-03	0.44	0.030	0.106	5	14	15	377	156				
	kgp10619195	4	94417717	TSPAN5	A	G	3.54E-03	0.36	0.040	0.102	0	0	2	366	146				
	rs1541392	16	19713882		A	G	3.54E-03	0.50	0.142	0.238	6	101	5	290	103				
	kgp15390522	1	205017962	CNTN2	G	A	3.59E-03	0.11	0.004	0.033	0	0	0	396	169				

STANDARD PHENOTYPE														
Combined														
Prioritized Variants	Name	Chromosome	Position	Gene(s)	Major Allele (A)	Minor Allele (B)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	BD (Responders)	BD (Non-Responders)	BD (Responders)	BD (Non-Responders)
	kgp24729705	22	49286357	LXK1101128946	G	A	3.61E-05	0.24	0.015	0.033	0	0	12	388
	rs931570	12	49195124		G	A	3.61E-05	0.59	0.344	0.475	43	51	187	167
	kgp10591989	17	65697118		A	G	3.63E-05	0.49	0.111	0.292	7	5	74	317
	kgp12557319	6	8794609		A	G	3.69E-05	0.11	0.004	0.033	0	0	3	395
	kgp345201	16	19730554	LXK	A	C	3.69E-05	0.49	0.134	0.228	4	5	98	293
	kgp8615910	5	30927198		A	T	3.72E-05	0.49	0.123	0.215	4	7	90	304
	kgp2245775	13	91402506		G	A	3.76E-05	0.55	0.221	0.331	13	18	150	235
	kgp29367521	4	134471944		G	A	3.81E-05	0.13	0.005	0.036	0	0	4	395
	kgp7506534	1	13623114	LRRIC38	A	G	3.83E-05	0.11	0.004	0.036	0	1	3	395
	rs4780822	16	19727998	C16orf88, RCK	A	G	3.85E-05	0.50	0.143	0.238	5	6	103	288
	kgp312180	16	10529457		G	A	3.89E-05	0.56	0.232	0.347	19	22	147	233
	rs1604169	3	84215343		A	C	3.91E-05	0.57	0.355	0.478	41	40	201	157
	kgp25921291	13	78418857		G	A	3.92E-05	0.17	0.008	0.044	0	1	6	393
	rs16991784	6	26555433		C	A	4.02E-05	0.47	0.089	0.174	2	8	67	329
	kgp6228750	1	110261382		A	G	4.06E-05	0.35	0.035	0.094	1	1	26	372
	kgp9354820	19	93793636		G	A	4.07E-05	0.14	0.005	0.039	0	1	4	395
	kgp8108690	12	128734869		A	G	4.09E-05	0.51	0.135	0.232	8	9	90	296
	kgp5144181	2	30364733		G	A	4.10E-05	0.32	0.029	0.083	1	0	21	377
	kgp9627406	9	132997137	NCSI	G	A	4.10E-05	0.38	0.048	0.120	0	4	35	328
	kgp2352166	9	18960393	FAM154A	A	C	4.15E-05	0.35	0.033	0.091	0	3	26	373
	kgp4223880	2	10584127	CDK3	A	G	4.19E-05	0.13	0.005	0.036	0	0	4	394
	kgp61811	1	160346794		A	C	4.19E-05	0.14	0.005	0.039	0	1	4	394
	kgp9421834	19	11049860		G	A	4.23E-05	0.39	0.048	0.113	0	3	38	361
	rs2050872	18	19801346	RCK	G	A	4.27E-05	0.51	0.149	0.246	7	7	105	287
	rs7864679	9	18945868	FAM154A	G	A	4.34E-05	0.35	0.033	0.091	0	3	26	372
	kgp2146153	5	152980439	GRU1	G	A	4.35E-05	0.13	0.005	0.036	0	0	4	395
	kgp7804623	1	41125465	RIMS3	G	A	4.36E-05	1.82	0.341	0.221	47	8	178	174
	rs3792135	2	100062163	REV1	A	G	4.38E-05	0.51	0.125	0.219	4	10	91	303
	rs2055826	15	94832144		C	A	4.40E-05	1.71	0.489	0.358	97	22	195	106
	kgp85534	2	14574582		G	A	4.57E-05	0.20	0.010	0.047	0	0	8	391
	rs11192461	10	107366483		G	A	4.60E-05	0.45	0.084	0.183	1	4	65	333
	kgp207178	9	18942635	FAM154A	G	A	4.66E-05	0.34	0.030	0.086	0	2	24	375
	kgp2045074	8	51187450		C	A	4.74E-05	0.13	0.005	0.036	0	0	4	392
	rs10899206	3	157233698		G	A	4.80E-05	1.85	0.362	0.249	38	9	213	148
	rs9834010	3	157236222		C	A	4.80E-05	1.85	0.362	0.249	38	9	213	148
	kgp971582	6	51921703	PKHD1	A	G	4.82E-05	3.60	0.898	0.830	2	0	74	323
	kgp22793211	X	92601576		G	A	4.82E-05	0.64	0.394	0.542	93	65	126	177
	kgp4573213	3	124199924	KALRN	A	G	4.83E-05	0.55	0.191	0.298	10	19	132	256
	kgp19568724	14	21486590	MDR2	G	A	4.84E-05	0.15	0.006	0.039	0	0	5	394
	kgp9071686	9	21419168		G	A	4.84E-05	0.15	0.006	0.039	0	0	5	394
	kgp652534	4	15612751	BCD1L	C	G	4.84E-05	0.15	0.006	0.039	0	0	5	394
	kgp1224440	1	247399991		A	C	4.87E-05	0.50	0.109	0.199	2	11	83	314
	kgp2465134	9	18942204	FAM154A	A	C	4.87E-05	0.34	0.030	0.086	0	2	24	374

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STANDARD PHENOTYPE										Combined									
Protein-coding Variant	Name	Chromosome	Position	Gene(s)	Major Allele (G)	Minor Allele (A)	P-value (Association Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	BD (Responders) (n)	BD (Non-Responders) (n)	BD (Non-Responders) (n)	BD (Non-Responders) (n)	BD (Non-Responders) (n)	BD (Non-Responders) (n)	BD (Non-Responders) (n)	BD (Non-Responders) (n)	BD (Non-Responders) (n)
	kgp11543462	10	109579303		G	A	4.88E-05	0.17	0.008	0.042	0	0	0	0	0	0	0	0	0
	kgp4343470	2	213559411		A	C	4.90E-05	0.51	0.134	0.227	5	7	5	7	5	7	5	7	5
	kgp5379170	12	65681762	PTPRM1	G	A	4.94E-05	0.46	0.084	0.165	5	2	5	2	5	2	5	2	5
	kgp4812831	6	51910905	PKHD1	A	G	4.94E-05	3.62	0.096	0.030	1	0	1	0	1	0	1	0	1
	rs2598360	9	114155899	KIAA0368	G	A	5.01E-05	0.59	0.373	0.500	51	48	51	48	51	48	51	48	51
	kgp10633631	8	17504188	MTUS1	A	G	5.02E-05	2.49	0.000	0.025	0	1	0	1	0	1	0	1	0
	kgp3631767	16	84992155		G	A	5.08E-05	0.17	0.008	0.041	0	0	0	0	0	0	0	0	0
	rs23820	9	114103079		A	C	5.10E-05	0.59	0.398	0.525	57	52	57	52	57	52	57	52	57
	kgp279772	8	2103376		T	A	5.15E-05	0.57	0.247	0.362	25	20	25	20	25	20	25	20	25
	kgp20163979	8	79366479		A	C	5.17E-05	0.05	0.001	0.025	0	0	0	0	0	0	0	0	0
	kgp21171930	4	80362934		A	G	5.17E-05	0.05	0.001	0.025	0	0	0	0	0	0	0	0	0
	kgp2092817	5	39632583		G	A	5.17E-05	0.05	0.001	0.025	0	0	0	0	0	0	0	0	0
	kgp3398409	15	51652449	GLDN	G	A	5.17E-05	0.05	0.001	0.025	0	0	0	0	0	0	0	0	0
	kgp6469620	1	41235946	NEFC	G	A	5.21E-05	1.74	0.410	0.285	64	18	64	18	64	18	64	18	64
	rs3818675	10	12858045	CAMK1D	G	A	5.23E-05	0.32	0.025	0.077	0	2	0	2	0	2	0	2	0
	kgp9530088	11	30501054	MPTP2	A	G	5.23E-05	0.57	0.248	0.364	25	21	25	21	25	21	25	21	25
	rs2353478	12	49202743		A	G	5.23E-05	0.60	0.348	0.478	45	52	45	52	45	52	45	52	45
	kgp10558725	18	3070717	KYOM4	G	A	5.25E-05	0.18	0.009	0.044	0	0	0	0	0	0	0	0	0
	kgp28586329	8	6304848	KCTD11	A	G	5.30E-05	0.05	0.001	0.025	0	0	0	0	0	0	0	0	0
	kgp30282494	5	72863824	UTP15	A	G	5.30E-05	0.05	0.001	0.025	0	0	0	0	0	0	0	0	0
	rs7524868	1	41106774	RIMS3	A	C	5.35E-05	1.81	0.342	0.224	47	8	47	8	47	8	47	8	47
	kgp9806386	5	138688054		A	C	5.42E-05	0.05	0.001	0.025	0	0	0	0	0	0	0	0	0
	kgp4127859	6	52434481		A	G	5.43E-05	2.12	0.180	0.091	8	0	8	0	8	0	8	0	8
	kgp1753445	21	39811162	ERG	G	A	5.45E-05	2.40	0.169	0.083	6	0	6	0	6	0	6	0	6
	kgp9354462	2	149894403		A	C	5.45E-05	0.59	0.297	0.420	37	32	37	32	37	32	37	32	37
	kgp26533576	6	98139642		A	C	5.57E-05	0.17	0.008	0.041	0	0	0	0	0	0	0	0	0
	kgp2023214	16	76293345		A	G	5.66E-05	0.49	0.080	0.166	8	8	8	8	8	8	8	8	8
	kgp6768546	4	153864174	HHDC1	G	A	5.80E-05	0.26	0.018	0.061	0	0	0	0	0	0	0	0	0
	kgp1098237	9	114173681	KIAA0368	G	A	5.98E-05	0.60	0.368	0.494	52	46	52	46	52	46	52	46	52
	kgp4559002	8	13255322		G	A	6.02E-05	0.60	0.331	0.456	46	37	46	37	46	37	46	37	46
	rs1644418	10	12858409	CAMK1D	A	G	6.11E-05	0.31	0.024	0.075	0	2	0	2	0	2	0	2	0
	kgp11804835	6	22396146		C	A	6.12E-05	2.35	0.170	0.083	8	1	8	1	8	1	8	1	8
	rs7029123	9	114136169	KIAA0368	A	G	6.19E-05	0.60	0.375	0.500	52	48	52	48	52	48	52	48	52
	kgp2688306	7	28560259	CREB5	A	G	6.20E-05	2.90	0.122	0.047	3	1	3	1	3	1	3	1	3
	kgp2638591	8	108994382	RSPO2	G	A	6.21E-05	0.36	0.041	0.099	0	0	0	0	0	0	0	0	0
	rs3643371	22	17178213		G	A	6.21E-05	1.70	0.487	0.361	93	21	93	21	93	21	93	21	93
	kgp5409955	9	18980841	FAM134A	G	A	6.27E-05	0.34	0.020	0.083	0	2	0	2	0	2	0	2	0
	rs7228827	18	76900411	ATP9B	G	A	6.28E-05	2.12	0.206	0.108	20	1	20	1	20	1	20	1	20
	kgp1912531	2	137950215	THSD7B	A	G	6.34E-05	2.12	0.204	0.105	18	4	18	4	18	4	18	4	18
	kgp4162414	6	51668165	PKHD1	C	A	6.35E-05	3.56	0.095	0.030	1	0	1	0	1	0	1	0	1
	rs2926455	10	107360501		A	G	6.37E-05	0.46	0.086	0.165	1	4	1	4	1	4	1	4	1
	kgp3666685	7	78028723	MA3H2	A	C	6.38E-05	1.98	0.254	0.190	21	4	21	4	21	4	21	4	21
	kgp7059449	1	41255455		A	C	6.39E-05	4.93	0.074	0.017	1	0	1	0	1	0	1	0	1

Continued															
Prioritized Variants	Name	Chromosome	Position	Gene(s)	Major Allele (d)	Minor Allele (D)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	DD (Responders) (rs)	DD (Non-Responders) (rs)	Bd (Responders) (rs)	Bd (Non-Responders) (rs)	Id (Non-Responders) (rs)
	rs3899755	X	68447361		C	A	6.44E-03	2.00	0.216	0.168	34	4	104	31	261
	rs2308760	4	181391332	ODZ3	A	G	6.56E-03	0.61	0.144	0.472	53	44	168	83	177
	kgp2786291	18	45153979		G	A	6.64E-05	0.51	0.120	0.211	5	9	86	58	108
	kgp3933330	7	28583709	CRFB5	A	G	6.67E-05	2.26	0.178	0.086	15	1	111	29	271
	rs7052312	X	68447052		G	A	6.68E-05	2.01	0.215	0.168	33	4	103	31	260
	kgp337461	6	123019669	NKAIN2	A	G	6.76E-03	0.51	0.123	0.214	9	5	80	67	310
	rs6899668	5	126591501		G	A	6.78E-03	1.75	0.405	0.285	62	13	199	77	138
	kgp6046214	4	153726582	AKBP1	A	G	6.80E-05	0.25	0.016	0.058	0	0	13	21	386
	rs6835202	4	153855186		C	A	6.80E-05	0.25	0.016	0.058	0	0	13	21	386
	kgp14607560	8	133472755	KCNQ3	G	A	6.83E-03	2.05	0.219	0.119	20	4	135	35	244
	rs3795383	2	63056383		A	G	6.84E-03	0.31	0.025	0.075	1	0	18	27	380
	rs6845927	6	26510748		G	A	6.85E-03	0.48	0.089	0.171	2	8	67	46	329
	rs10489112	4	153799603	AKBP1	A	C	6.87E-05	0.26	0.018	0.061	0	0	14	22	383
	kgp11633966	11	175526526	TNR	A	G	6.87E-05	0.52	0.128	0.221	6	10	90	60	302
	rs7496431	13	37701793		G	A	6.88E-05	0.54	0.130	0.249	11	10	98	70	290
	kgp3048169	13	25718875		G	A	6.89E-05	2.01	0.239	0.138	23	0	145	50	231
	kgp8990121	4	78109591		G	A	6.94E-03	0.51	0.168	0.196	5	9	76	53	318
	kgp26528455	9	77215039	TEK	C	A	6.94E-05	2.35	0.167	0.080	10	0	113	29	278
	kgp4755147	6	72337785	RIMS1	G	A	6.96E-05	0.28	0.018	0.064	1	1	12	21	388
	kgp10372946	2	149894654		A	C	7.15E-05	0.59	0.301	0.422	38	32	161	88	195
	rs1390766	10	133900657	JAKMIP3	G	A	7.17E-03	10.53	0.053	0.046	0	0	42	2	357
	kgp12182745	2	57864042		A	G	7.29E-05	1.72	0.409	0.285	64	17	190	68	135
	kgp3951463	8	125465203	TNAT12	A	T	7.30E-05	0.43	0.047	0.117	3	6	31	30	357
	kgp8602316	3	157280172	C3orf55	C	A	7.32E-05	1.83	0.348	0.238	36	8	205	70	157
	rs16927077	7	335911		G	A	7.36E-05	1.79	0.417	0.291	74	18	184	68	140
	kgp6939492	11	10620629	MRVI1-AS1	G	A	7.38E-05	0.47	0.080	0.157	2	5	60	47	337
	kgp8793915	4	153687676		A	G	7.39E-05	0.26	0.016	0.058	0	0	13	21	386
	kgp13161760	11	109012665		A	G	7.40E-05	2.69	0.000	0.019	0	0	0	7	399
	kgp6567154	21	18192806		G	A	7.40E-05	0.05	0.001	0.028	0	1	1	8	398
	kgp2282938	4	3442146		G	C	7.47E-05	0.59	0.274	0.392	28	32	161	78	207
	kgp353723	22	32719612		G	A	7.47E-05	0.25	0.015	0.056	0	0	12	20	386
	rs10201643	8	75270402	G2AP1	A	G	7.54E-05	0.08	0.003	0.028	0	0	2	10	396
	kgp27648141	2	149905641	LYPD6B	C	A	7.56E-05	0.60	0.301	0.422	40	32	160	88	199
	rs7670525	12	118005689	TACX3	G	A	7.57E-05	0.05	0.001	0.028	0	1	1	8	397
	kgp28817122	4	153814538	ARBP1	A	G	7.66E-03	0.26	0.016	0.058	0	0	13	21	385
	kgp5014707	8	122487115		A	G	7.66E-03	0.26	0.016	0.058	0	0	13	21	385
	kgp7092772	9	1702186		G	A	7.78E-05	2.69	0.000	0.019	0	0	0	7	399
	kgp3477351	14	22379841		G	A	7.78E-05	2.69	0.000	0.019	0	0	0	7	398
	kgp23298674	19	295864		G	A	7.75E-05	2.69	0.000	0.019	0	0	0	7	399
	kgp12033934	21	20962564		C	A	7.75E-03	2.69	0.000	0.019	0	0	0	7	399
	kgp485316	16	10828979		A	G	7.75E-03	0.58	0.232	0.344	20	22	143	79	232
	kgp25191871	7	15372018	ACMRO	G	A	7.80E-05	1.67	0.466	0.340	94	17	183	89	121
		1	115687027		A	C	7.84E-05	0.33	0.036	0.078	0	2	21	24	376

STANDARD PHENOTYPE										Combined									
Proteinized Variants	Name	Chromosome	Position	Gene(s)	Major Allele (d)	Minor Allele (D)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	RD (Responders) (ers)	RD (Non-Responders) (ers)	DR (Non-Responders) (ers)	DR (Non-Responders) (ers)	DR (Non-Responders) (ers)	DR (Non-Responders) (ers)	DR (Non-Responders) (ers)	DR (Non-Responders) (ers)	DR (Non-Responders) (ers)
	kgp24131116	2	213906695	KZFP1	G	A	7.91E-05	Zero	0.000	0.019	0	0	0	0	7	398	174	174	174
	kgp0854133	3	31334098		G	A	7.91E-05	Zero	0.000	0.019	0	0	0	0	7	398	174	174	174
	kgp22811918	X	21960214	SMS	C	A	8.00E-05	0.48	0.055	0.133	5	12	34	24	360	145	145	145	145
	kgp7792268	13	23070499		C	A	8.06E-05	0.24	0.013	0.052	0	1	10	17	388	163	163	163	163
	kgp11356379	11	9814612	LXC2R3104,SBF2	G	A	8.09E-05	0.59	0.344	0.466	41	37	186	89	162	48	48	48	48
	kgp27571222	12	56245724		A	G	8.10E-05	0.05	0.001	0.028	0	1	1	8	394	172	172	172	172
	rs1886214	13	42948331		A	G	8.21E-05	1.89	0.278	0.171	31	3	159	56	207	122	122	122	122
	kgp1034273	12	67131774		G	A	8.21E-05	0.09	0.003	0.028	0	0	2	10	397	171	171	171	171
	kgp9531947	18	42502140	SEI1BP1	G	A	8.21E-05	0.09	0.003	0.028	0	0	2	10	397	171	171	171	171
	kgp5483926	3	14352913		A	C	8.21E-05	0.09	0.003	0.028	0	0	2	10	397	171	171	171	171
	kgp4155998	1	184734012		G	A	8.21E-05	0.09	0.003	0.028	0	0	2	10	397	171	171	171	171
	kgp2938113	5	163341388		A	C	8.21E-05	0.09	0.003	0.028	0	0	2	10	397	171	171	171	171
	kgp8135515	11	4936211		G	A	8.21E-05	0.09	0.003	0.028	0	0	2	10	397	171	171	171	171
	kgp5388938	8	79087167		G	A	8.21E-05	0.09	0.003	0.028	0	0	2	10	397	171	171	171	171
	kgp28687698	8	79225285		C	A	8.21E-05	0.09	0.003	0.028	0	0	2	10	397	171	171	171	171
	kgp11627530	14	78934642	NRX33	A	G	8.35E-05	0.43	0.039	0.128	0	5	47	36	352	139	139	139	139
	kgp24753470	1	26013940	MA41C1	A	C	8.41E-05	0.09	0.003	0.028	0	0	2	10	396	171	171	171	171
	kgp1285441	3	36931141	ARHGEF3	G	A	8.44E-05	0.52	0.130	0.221	8	6	88	68	303	107	107	107	107
	rs17638791	6	31940816	PKHD1	A	G	8.49E-05	3.35	0.098	0.033	1	0	76	12	322	189	189	189	189
	rs2325911	6	125027223	NRX1N2	C	A	8.57E-05	0.51	0.119	0.207	9	3	27	69	312	189	189	189	189
	kgp10967046	13	66274367	MEU3F11	G	A	8.61E-05	0.36	0.035	0.091	1	1	26	31	371	149	149	149	149
	rs12013377	X	92620062		A	G	8.64E-05	0.85	0.405	0.547	97	66	129	66	173	49	49	49	49
	kgp7186699	4	184878777	STOX2	G	A	8.64E-05	3.55	0.094	0.028	4	1	67	8	328	172	172	172	172
	kgp9368119	7	11707419	TESD7A	A	G	8.76E-05	0.60	0.365	0.506	52	47	203	59	144	45	45	45	45
	kgp124162	11	72356846	PDE2A	A	G	8.78E-05	0.25	0.015	0.055	0	0	12	20	386	161	161	161	161
	kgp8440036	4	780538785		G	A	8.79E-05	0.30	0.019	0.066	1	2	13	20	353	159	159	159	159
	rs4736738	8	59844254	TOX	A	C	8.80E-05	1.69	0.424	0.300	80	13	177	82	140	85	85	85	85
	kgp7802182	18	36759170		A	G	8.96E-05	0.57	0.208	0.315	19	16	128	82	252	83	83	83	83
	kgp2923813	19	43921355		G	A	8.97E-05	0.43	0.064	0.133	1	2	49	44	348	135	135	135	135
	rs3767955	1	41104475	R2483	G	A	8.91E-05	1.78	0.341	0.227	46	8	180	66	173	107	107	107	107
	kgp3418770	10	59425598		A	G	8.92E-05	10.31	0.052	0.006	0	0	41	2	354	178	178	178	178
	rs17449018	9	7060825	KDR4C	G	A	8.97E-05	1.82	0.318	0.207	41	4	172	66	166	169	169	169	169
	kgp4524468	22	32724532		A	G	8.98E-05	1.89	0.281	0.172	27	8	165	45	198	124	124	124	124
	kgp4418535	6	32421538		C	A	9.00E-05	2.26	0.177	0.091	8	0	125	33	266	148	148	148	148
	kgp22825022	X	9742468		G	A	9.00E-05	0.56	0.133	0.246	17	16	70	51	305	169	169	169	169
	kgp7063887	1	189928568		G	A	9.14E-05	0.41	0.044	0.108	0	6	35	27	363	148	148	148	148
	rs1621509	7	2969680	CARD11	G	A	9.29E-05	2.60	0.239	0.142	15	4	160	43	222	133	133	133	133
	kgp4842590	1	110242364		A	C	9.32E-05	0.27	0.015	0.058	1	1	10	19	387	160	160	160	160
	rs11192469	10	107282331		A	G	9.38E-05	0.47	0.083	0.158	1	4	64	49	333	127	127	127	127
	kgp8302520	7	154911234		C	A	9.41E-05	0.61	0.412	0.539	68	56	188	82	137	42	42	42	42
	rs13415334	2	60323127		A	G	9.46E-05	0.60	0.357	0.478	47	42	191	88	161	50	50	50	50
	rs9876830	3	157311299	C3orf53	G	A	9.48E-05	1.82	0.348	0.240	35	8	208	71	156	102	102	102	102
	kgp11285862	21	18177980		A	G	9.56E-05	0.09	0.093	0.030	0	1	2	9	396	171	171	171	171

STANDARD PHENOTYPE										Combined									
Prioritized Variants	Name	Chromosome	Position	Genotype	Major Allele (G)	Minor Allele (A)	P-value (Association Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	DB (Responders) (rs)	DD (Non-responders) (rs)	DD (Responders) (rs)	DD (Non-responders) (rs)	DD (Non-responders) (rs)	DD (Non-responders) (rs)	DD (Non-responders) (rs)	DD (Non-responders) (rs)	DD (Non-responders) (rs)
0 - Priority genes, Predictive Model	rs28234070	21	18205972		A	G	9.57E-05	0.22	0.010	0.047	0	1	8	15	389	164			
	kgp7181088	14	98285698		G	A	9.62E-05	0.24	0.014	0.052	0	0	11	19	398	162			
	kgp5002011	1	110365738		G	A	9.68E-05	0.35	0.030	0.083	1	1	22	28	376	152			
	rs2139612	X	92814918		A	C	9.68E-05	0.65	0.403	0.544	98	65	129	67	173	49			
	rs7880748	9	114202303	K1A0368	G	A	9.73E-05	0.81	0.370	0.492	52	46	191	86	156	49			
	rs17029528	2	69096880		A	C	9.73E-05	0.33	0.028	0.078	1	0	20	28	378	152			
	kgp1371881	16	76391607		A	G	9.74E-05	0.50	0.079	0.161	8	8	47	42	344	130			
	rs10492882	16	76291394		A	G	9.74E-05	0.50	0.079	0.161	8	8	47	42	344	130			
	rs9393727	8	26500011		C	G	9.75E-05	0.49	0.091	0.171	2	8	68	46	327	127			
	rs1894408	6	32786833		C	G	9.82E-05	1.73	0.413	0.296	58	16	211	74	127	89			
2 - Priority genes	rs2829117	21	47550754	COR6A2	G	A	9.85E-05	0.54	0.135	0.229	9	11	90	61	300	109			
	kgp8437961	2	99060803	EHSB	G	A	9.85E-05	0.50	0.105	0.188	4	6	75	56	318	119			
	rs1508102	11	11639889		G	A	9.87E-05	0.42	0.052	0.116	0	4	41	34	357	143			
	rs4449139	2	124875366	CNTNAP3	G	A	9.93E-05	0.81	0.398	0.522	61	53	195	83	142	45			
	rs11559024	19	45821183	CKM	A	G	1.06E-04	0.09	0.003	0.030	0	1	2	9	394	171			
	rs1894407	6	32787036		C	A	1.06E-04	1.73	0.411	0.296	57	16	213	75	128	90			
	rs2827103	6	32791299	TAP2	C	A	1.13E-04	1.78	0.362	0.253	39	11	211	69	149	100			
	rs9301274	6	32792910	TAP2	G	A	1.32E-04	1.77	0.362	0.254	39	11	211	70	149	100			
	kgp8110667	22	32716792		G	A	1.44E-04	Infinity	0.940	0.000	1	0	30	0	367	181			
	kgp8599438	20	40943626	FIPR1	G	A	2.48E-04	0.26	0.014	0.050	0	0	11	18	386	163			
2 - Priority genes	rs241451	6	32796480	TAP2	A	G	2.58E-04	1.72	0.360	0.256	39	12	207	68	150	100			
	rs1894406	6	32787036		G	A	2.66E-04	1.68	0.381	0.273	51	13	202	73	146	95			
	rs3118328	22	37524608	IL2RB	G	A	2.96E-04	0.13	0.004	0.028	0	0	3	10	395	169			
	rs241443	6	32797115	TAP2	A	C	3.02E-04	1.71	0.358	0.254	40	11	202	69	152	99			
	rs2621323	6	32788707		A	G	3.33E-04	1.69	0.367	0.264	43	12	207	71	149	97			
	kgp304921	20	14017977	MACROD2	A	G	8.00E-04	0.41	0.029	0.075	2	2	19	23	373	154			
	rs241456	6	32795965	TAP2	G	A	8.63E-04	1.66	0.306	0.213	32	9	180	59	187	113			

STANDARD PHENOTYPE															Combined									
Stratified Variants	Name	Chromosome	Position	Gene(s)	Major Allele (d)	Minor Allele (D)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	DD (Responders) (rs)	DD (Non-Responders) (rs)	Did (Responders) (rs)	Did (Non-Responders) (rs)										
0 - Priority genes, Predictive Model	kgp7747883	18	74804250	MEP	G	A	8.64E-04	0.64	0.135	0.436	43	33	181	174	56									
2 - Priority genes	rs2621321	6	32789480		A	G	9.00E-04	1.66	0.308	0.215	31	9	183	184	112									
2 - Priority genes	rs2877161	6	32790167	TAP2	G	C	9.87E-04	1.65	0.307	0.215	31	9	183	185	112									
2 - Priority genes	rs241454	6	32796144	TAP2	A	G	1.02E-03	1.65	0.307	0.215	32	9	180	185	112									
2 - Priority genes	rs241447	6	32796751	TAP2	A	G	1.11E-03	1.64	0.308	0.217	32	9	180	184	111									
2 - Priority genes	kgp974569	6	32796637	TAP2	G	A	1.12E-03	1.64	0.307	0.215	32	9	180	186	112									
2 - Priority genes	rs2877161	6	32796676	TAP2	A	G	1.15E-03	1.64	0.305	0.214	31	9	181	187	112									
2 - Priority genes	kgp10224254	6	32785904		C	A	1.15E-03	1.56	0.405	0.307	59	18	205	135	88									
2 - Priority genes	rs241444	6	32797109	TAP2	G	A	1.22E-03	1.63	0.306	0.215	32	9	180	187	112									
2 - Priority genes	kgp4479467	6	32629331	HLA-DQB1	A	G	1.25E-03	1.58	0.383	0.287	54	11	195	147	88									
2 - Priority genes	kgp10632945	20	4692507		G	A	1.25E-03	0.81	0.173	0.254	10	11	118	270	100									
2 - Priority genes	rs241446	6	32796967	TAP2	G	A	1.26E-03	1.63	0.303	0.213	32	9	176	188	113									
2 - Priority genes	rs241453	6	32796226	TAP2	G	A	1.31E-03	1.63	0.305	0.215	32	9	179	187	112									
2 - Priority genes	rs241449	6	32796655	TAP2	C	A	1.35E-03	1.63	0.303	0.212	32	9	175	188	112									
0 - Priority genes, Predictive Model	rs10162089	13	31316738	ALOX5AP	G	A	1.40E-03	1.51	0.482	0.380	96	24	190	110	67									
2 - Priority genes	rs2071469	6	32784783	HLA-DQB	G	A	1.40E-03	1.55	0.406	0.309	59	18	205	134	87									
2 - Priority genes	PL_M_061510_6_159_P	6	32795305	TAP2	T	D	1.41E-03	1.62	0.305	0.215	32	9	178	187	112									
2 - Priority genes	rs241452	6	32796346	TAP2	A	G	1.42E-03	1.62	0.306	0.217	32	9	179	186	111									
2 - Priority genes	kgp2328352	6	32797297	TAP2	A	G	1.46E-03	1.62	0.307	0.216	34	10	173	185	111									
2 - Priority genes	kgp8036764	6	32796521	TAP2	G	A	1.55E-03	1.63	0.303	0.215	29	9	183	186	112									

STANDARD PHENOTYPE										Combined									
Prioritized Variants	Name	Chromosome	Position	Gene(s)	Major Allele (G)	Minor Allele (A)	P-value (A-ratio Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	Did (Responders)	Did (Non-Responders)	Did (Responders)	Did (Non-Responders)	Did (Responders)	Did (Non-Responders)	Did (Responders)	Did (Non-Responders)	Did (Responders)
2 - Priority genes	rs241442	6	32797168	TAP2	G	A	1.56E-03	1.62	0.305	0.217	32	9	179	60	187	111			
2 - Priority genes	rs241443	6	32797072	TAP2	G	A	1.56E-03	1.62	0.305	0.217	32	9	179	60	187	111			
2 - Priority genes	rs1410779	9	5093173	LAK2	G	A	1.73E-03	0.61	0.161	0.238	8	10	112	66	277	103			
2 - Priority genes	kgp23672937	7	18685891	HEAC9	G	A	1.74E-03	0.07	0.001	0.017	0	0	1	6	398	173			
2 - Priority genes	kgp4348717	18	74816199	MBP	G	A	1.74E-03	0.07	0.001	0.017	0	0	1	6	398	173			
2 - Priority genes	kgp9697734	10	79338319	KCNMA1	A	G	1.74E-03	Infinity	0.026	0.000	0	0	21	0	377	179			
2 - Priority genes	rs241440	6	32797161	TAP2	G	A	1.79E-03	1.61	0.303	0.215	32	9	177	60	189	112			
2 - Priority genes	kgp5334779	6	32628420	HLA-DQB1	G	A	1.87E-03	1.56	0.377	0.286	50	10	199	83	142	87			
2 - Priority genes	kgp4898179	6	32629347	HLA-DQB1	A	G	1.91E-03	1.55	0.382	0.290	54	11	195	83	148	87			
2 - Priority in Predictive Model	rs759458	2	65243365	SLC1A4	G	A	2.01E-03	1.59	0.295	0.207	38	7	139	61	201	113			
2 - Priority genes	rs2071472	6	32794620	HLA-DQB	G	A	2.21E-03	1.56	0.340	0.251	40	12	191	67	188	102			
2 - Priority genes	rs2071470	6	32784753	HLA-DQB	A	G	2.21E-03	1.56	0.340	0.251	40	12	191	67	188	102			
2 - Priority genes	kgp23543811	18	74774894	MBP,MBP	G	A	2.20E-03	0.12	0.003	0.019	0	0	2	7	397	173			
2 - Priority genes	kgp293787	20	40905098	PTPR	G	A	2.55E-03	0.37	0.019	0.052	0	2	15	15	384	164			
2 - Priority genes	rs2043136	3	30720304	TOX2	A	G	4.11E-03	1.53	0.307	0.225	38	7	167	67	191	106			
2 - Priority genes	rs4769060	13	31337877	ALOX5AP	A	G	4.43E-03	1.45	0.455	0.365	87	22	189	88	123	71			
2 - Priority genes	kgp6032617	13	31287981	ALOX5AP	A	G	4.44E-03	0.67	0.222	0.301	23	15	131	29	344	87			
2 - Priority genes	kgp5441587	6	32827356	PSM29	G	A	6.10E-03	0.24	0.006	0.025	0	0	5	9	394	169			
2 - Priority genes	rs241435	6	32798243	TAP2,TAP2	G	A	6.85E-03	0.24	0.006	0.025	0	0	5	9	394	172			
2 - Priority genes	kgp3182607	6	32820948	PSM29	G	A	6.85E-03	0.24	0.006	0.025	0	0	5	9	394	172			
2 - Priority genes	kgp2278566	7	1958337	MAAD1L1	G	A	7.00E-03	1.57	0.246	0.175	19	4	136	53	220	117			

STANDARD PHENOTYPE										Combined					
Variant	Name	Chromosome	Position	Gene(s)	Major Allele (R)	Minor Allele (D)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	DD (Responders)	DD (Non-Responders)	DD (Responders)	DD (Non-Responders)	dd (Non-Responders)
2 - Priority genes	kgp97310	9	3122952	JAK2	A	G	7.79E-03	0.68	0.203	0.271	17	14	125	70	256
2 - Priority genes	kgp5440806	13	31320543	ALOX5AP	G	A	7.94E-03	0.72	0.428	0.514	81	45	175	95	138
2 - Priority genes	rs1147439	13	31325643	ALOX5AP	C	A	8.10E-03	0.72	0.429	0.514	81	45	180	96	138
2 - Priority genes	rs4360791	13	31318020	ALOX5AP	G	A	8.60E-03	0.72	0.440	0.525	85	48	181	94	133
2 - Priority genes	rs9671182	13	31321138	ALOX5AP	C	G	8.78E-03	0.72	0.432	0.517	82	45	180	96	136
2 - Priority genes	rs4358336	13	31319346	ALOX5AP	A	G	8.93E-03	0.72	0.432	0.517	82	46	181	93	136
2 - Priority genes	rs10815160	9	3116616	JAK2	A	C	9.34E-03	0.68	0.207	0.278	19	14	124	71	248
2 - Priority genes	rs4254166	13	31322949	ALOX5AP	A	G	9.96E-03	0.72	0.431	0.514	81	45	182	98	136
2 - Priority genes	kgp2713673	13	31320249	ALOX5AP	G	A	1.13E-02	0.73	0.432	0.514	82	45	181	96	136
2 - Priority genes	rs9670531	13	31321069	ALOX5AP	A	G	1.13E-02	0.73	0.432	0.514	82	45	181	96	136
1 - Priority variants	rs2487896	10	100803380	HPSE2	G	A	1.29E-02	0.65	0.130	0.186	6	6	92	55	201
0 - Priority variants, Predictive Model	rs3155391	6	32410987	HLA-DRA	G	A	1.44E-02	0.70	0.203	0.268	20	10	122	77	257
2 - Priority genes	kgp26271158	6	32823393	PSMD9	G	A	1.47E-02	0.29	0.088	0.025	0	0	6	9	393
1 - Priority variants	rs3155388	6	32413051		G	A	1.66E-02	0.70	0.203	0.267	20	10	122	76	257
2 - Priority genes	kgp11281589	7	1041003	MAD1L1	A	G	1.76E-02	1.48	0.246	0.184	19	5	133	55	219
1 - Priority variants	rs17575455	2	76628220		C	A	1.94E-02	0.73	0.319	0.380	42	26	170	84	186
1 - Priority variants	rs947603	10	95249603		A	G	2.65E-02	1.42	0.241	0.182	22	8	148	50	228

(Note: Odds Ratio > 1 = Minor Allele is associated with Response.
Odds Ratio < 1 = Minor Allele Associated with Non-Response)

Table 39: Extreme Response SNPs

EXTREME PHENOTYPE										Cats cohort					Forre cohort				
Prioritized Variants	Name	Chromosome	Position	Gene(s)	Major Allele (d)	Minor Allele (D)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)	P-value (Armitage Test)	Odds Ratio (Minor Allele)	Minor Allele Freq. (Responders)	Allele Freq. (Non-Responders)					
U - Priority - Model	kgp6214351	11	75546691	UVRAG	A	G	2.44E-03	0.20	0.030	0.128	3.36E-05	0.12	0.028	0.111					
	rs759458	2	65245365	SLC1A4	G	A	4.44E-05	3.31	0.356	0.157	4.89E-02	1.86	0.364	0.229					
	rs7844274	8	72411302		C	A	1.13E-03	0.42	0.212	0.390	1.39E-02	0.45	0.170	0.314					
	kgp5924567	4	40379680		G	A	9.89E-05	0.34	0.379	0.587	6.90E-03	0.42	0.428	0.614					
	kgp11580685	16	3856653		G	A	5.50E-05	0.18	0.053	0.212	1.07E-01	0.59	0.073	0.143					
	kgp10948564	20	44082511		G	C	3.35E-03	0.41	0.197	0.331	4.38E-03	0.41	0.146	0.314					
	rs197523	21	19337261	CHODL	G	A	6.01E-05	2.89	0.402	0.186	4.34E-02	1.86	0.371	0.229					
	kgp12371737	9	19458272		G	A	4.17E-05	0.21	0.068	0.244	6.77E-02	0.49	0.112	0.260					
	kgp4627438	17	90155	RPH3AL	A	G	2.55E-03	0.36	0.083	0.221	2.77E-04	0.23	0.108	0.286					
	rs7860	2	65249922	SLC1A4	C	A	5.39E-07	8.99	0.212	0.035	2.42E-01	1.74	0.140	0.086					
	kgp7189498	2	65250677	SLC1A4	G	C	8.57E-07	8.77	0.215	0.037	2.08E-01	1.82	0.145	0.086					
	kgp10788130	12	13898682	GRIN2B	G	A	3.62E-03	2.00	0.090	0.070	1.48E-04	0.08	0.011	0.114					
	kgp7242489	2	65250541	SLC1A4	A	T	6.51E-07	8.88	0.212	0.035	2.42E-01	1.74	0.140	0.086					
	kgp7077322	4	164661252		A	C	1.82E-03	0.13	0.015	0.100	3.59E-04	0.16	0.054	0.157					
	rs7348267	20	44084386		G	A	3.35E-03	0.41	0.197	0.331	8.93E-03	0.44	0.146	0.300					
	kgp7121374	2	65246727	SLC1A4	A	G	6.51E-07	8.88	0.212	0.035	3.18E-01	1.57	0.148	0.100					
	kgp4127859	6	32434481		A	G	1.28E-04	3.79	0.235	0.076	2.87E-02	2.89	0.193	0.086					
	kgp8107491	6	164295151		G	A	7.53E-04	0.43	0.348	0.541	2.00E-02	0.50	0.341	0.500					
	rs16889310	6	164319963		G	A	1.81E-04	0.33	0.162	0.335	9.67E-02	0.55	0.382	0.271					
	rs6932205	20	44082709		C	A	4.36E-03	0.41	0.203	0.335	9.99E-03	0.44	0.148	0.300					
	kgp11768553	11	27279451		G	A	1.14E-03	2.52	0.390	0.337	1.79E-03	2.75	0.472	0.257					
	rs502530	6	145584096		C	A	2.10E-02	0.19	0.015	0.070	6.33E-03	2.80	0.000	0.086					
	rs1478682	11	27315009		G	A	7.52E-04	2.57	0.485	0.314	2.93E-03	2.60	0.449	0.243					
	kgp1124492	1	105554880		G	A	9.05E-04	0.26	0.068	0.194	6.10E-02	0.41	0.057	0.129					
	kgp11843177	11	27316568		A	G	4.45E-04	2.69	0.594	0.218	1.53E-02	2.28	0.371	0.214					
	kgp11467007	5	172730436	STC2	G	A	1.49E-03	0.17	0.023	0.128	1.24E-03	0.22	0.051	0.171					
	rs196295	10	121436362	BAG3	G	A	3.99E-04	0.35	0.114	0.302	6.11E-03	0.41	0.182	0.343					
	rs11029892	11	27269546		G	A	5.83E-04	2.63	0.417	0.244	1.11E-02	2.36	0.393	0.229					
	rs9911349	17	68260070		A	G	2.13E-03	2.39	0.318	0.169	2.74E-02	2.10	0.371	0.229					
	kgp5680955	6	164297121		G	A	6.88E-04	0.43	0.288	0.483	2.10E-02	0.51	0.391	0.457					
kgp6236940	2	60301030		A	G	1.20E-03	0.45	0.280	0.465	6.45E-02	0.56	0.242	0.357						
rs196343	10	121417957	BAG3	G	A	4.43E-04	0.36	0.114	0.309	5.34E-03	0.40	0.180	0.343						
rs7217872	17	88988	RPH3AL	G	A	3.72E-03	0.37	0.083	0.215	3.34E-04	0.24	0.112	0.286						
kgp4634875	7	11794583	THSD7A	G	A	3.67E-03	2.01	0.545	0.378	1.13E-02	0.46	0.416	0.588						
kgp4418555	6	32431558		C	A	2.45E-04	3.58	0.227	0.076	2.93E-02	2.84	0.151	0.096						
rs1079303	11	27269598		A	G	1.14E-03	2.52	0.500	0.337	2.32E-03	2.66	0.466	0.257						
rs10501082	11	27270978		G	A	1.14E-03	2.52	0.500	0.337	2.32E-03	2.66	0.466	0.257						
rs6718758	2	60328802		C	A	6.94E-03	0.53	0.311	0.471	9.16E-03	0.44	0.253	0.414						
rs7723112	5	173998604		G	A	2.09E-04	2.94	0.212	0.070	3.76E-02	2.58	0.197	0.086						
kgp4734301	11	27315427		A	G	5.37E-04	2.64	0.394	0.221	1.53E-02	2.28	0.371	0.214						
rs11029928	11	27319188		G	A	5.37E-04	2.64	0.394	0.221	1.53E-02	2.28	0.371	0.214						
rs7948420	11	27776450		A	G	6.04E-05	0.33	0.205	0.424	6.96E-03	0.46	0.328	0.514						

DEMANDE OU BREVET VOLUMINEUX

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NOM DU FICHER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

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What is claimed is:

1. A method for treating a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis with a pharmaceutical composition comprising glatiramer acetate and a pharmaceutically acceptable carrier, comprising the steps of:

- (i) determining a genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of: kgp10090631, kgp1009249, kgp10152733, kgp10224254, kgp10305127, kgp10351364, kgp10372946, kgp10404633, kgp10412303, kgp10523170, kgp1054273, kgp10558725, kgp10564659, kgp10591989, kgp10594414, kgp10619195, kgp10620244, kgp10632945, kgp10633631, kgp10679353, kgp10788130, kgp10826273, kgp10910719, kgp10922969, kgp10948564, kgp10967046, kgp10974833, kgp1098237, kgp11002881, kgp11010680, kgp11077373, kgp11141512, kgp11206453, kgp11210903, kgp1124492, kgp11281589, kgp11285862, kgp11328629, kgp11356379, kgp11407560, kgp11453406, kgp11467007, kgp11514107, kgp11543962, kgp11580695, kgp11627530, kgp11633966, kgp11686146, kgp11702474, kgp11711524, kgp11768533, kgp11804835, kgp11843177, kgp12008955, kgp12083934, kgp12182745, kgp12230354, kgp1224440, kgp12371757, kgp124162, kgp12426624, kgp12557319, kgp1285441, kgp13161760, kgp1355977, kgp1371881, kgp15390522, kgp1683448, kgp1688752, kgp1699628, kgp1753445, kgp1779254, kgp1786079, kgp18379774, kgp18432055, kgp18525257, kgp1912531, kgp19568724, kgp20163979, kgp2023214, kgp2045074, kgp20478926, kgp2092817, kgp21171930, kgp2245775, kgp2262166, kgp22778566, kgp22793211, kgp22811918, kgp22823022, kgp2282938, kgp2299675, kgp23298674, kgp2356388, kgp23672937, kgp23737989, kgp2388352, kgp2391411, kgp24131116, kgp24415534, kgp2446153, kgp2451249, kgp2465184, kgp24729706, kgp24753470, kgp25191871, kgp25216186, kgp25543811,

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kgp25921291, kgp25952891, kgp26026546, kgp26271158,
kgp2638591, kgp26528455, kgp26533576, kgp2688306,
kgp26995430, kgp270001, kgp2709692, kgp2715873, kgp27500525,
kgp27571222, kgp27640141, kgp2788291, kgp279772, kgp28532436,
kgp28586329, kgp28687699, kgp28817122, kgp2923815,
kgp29367521, kgp293787, kgp2958113, kgp2959751, kgp297178,
kgp29794723, kgp30282494, kgp3048169, kgp304921, kgp3182607,
kgp3202939, kgp3205849, kgp3218351, kgp3267884, kgp3276689,
kgp337461, kgp3418770, kgp3450875, kgp345301, kgp3477351,
kgp3496814, kgp355027, kgp355723, kgp3593828, kgp3598409,
kgp3651767, kgp3669685, kgp3730395, kgp3812034, kgp3854180,
kgp3933330, kgp3951463, kgp3984567, kgp3991733, kgp4011779,
kgp4056892, kgp4096263, kgp4127859, kgp4155998, kgp4162414,
kgp4223880, kgp4346717, kgp4370912, kgp4418535, kgp4420791,
kgp4479467, kgp4524468, kgp4543470, kgp4559907, kgp4573213,
kgp4634875, kgp4705854, kgp4734301, kgp4755147, kgp4812831,
kgp4842590, kgp485316, kgp487328, kgp4898179, kgp5002011,
kgp5014707, kgp5017029, kgp5053636, kgp5068397, kgp512180,
kgp5144181, kgp5159037, kgp5216209, kgp5292386, kgp5334779,
kgp5388938, kgp5409955, kgp5440506, kgp5441587, kgp5483926,
kgp55646, kgp5564995, kgp5579170, kgp5680955, kgp5869992,
kgp5908616, kgp6023196, kgp6032617, kgp6038357, kgp6076976,
kgp6091119, kgp6127371, kgp61811, kgp6190988, kgp6214351,
kgp6228750, kgp6236949, kgp6469620, kgp6505544, kgp6507761,
kgp652534, kgp6539666, kgp6567154, kgp6599438, kgp6603796,
kgp6666134, kgp6700691, kgp6737096, kgp6768546, kgp6772915,
kgp6835138, kgp6959492, kgp6996560, kgp7059449, kgp7063887,
kgp7077322, kgp7092772, kgp7117398, kgp7121374, kgp7178233,
kgp7181058, kgp7186699, kgp7189498, kgp7242489, kgp7331172,
kgp7416024, kgp7481870, kgp7506434, kgp7521990, kgp759150,
kgp767200, kgp7714238, kgp7730397, kgp7747883, kgp7792268,
kgp7802182, kgp7804623, kgp7924485, kgp8030775, kgp8036704,
kgp8046214, kgp8106690, kgp8107491, kgp8110667, kgp8169636,
kgp8174785, kgp8178358, kgp8183049, kgp8192546, kgp8200264,
kgp8303520, kgp8335515, kgp8372910, kgp841428, kgp8437961,

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kgp8440036, kgp85534, kgp8599417, kgp8602316, kgp8615910,
kgp8767692, kgp8777935, kgp8793915, kgp8796185, kgp8817856,
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kgp9421884, kgp9450430, kgp9530088, kgp9551947, kgp9601362,
kgp9627338, kgp9627406, kgp9669946, kgp9699754, kgp971582,
kgp97310, kgp974569, kgp9795732, kgp9806386, kgp9854133,
kgp9884626, rs10049206, rs10124492, rs10125298, rs10162089,
rs10201643, rs10203396, rs10251797, rs10278591, rs10489312,
rs10492882, rs10498793, rs10501082, rs10510774, rs10512340,
rs1079303, rs10815160, rs10816302, rs10841322, rs10841337,
rs10954782, rs11002051, rs11022778, rs11029892, rs11029907,
rs11029928, rs11083404, rs11085044, rs11136970, rs11147439,
rs11192461, rs11192469, rs11559024, rs1157449, rs11648129,
rs11691553, rs12013377, rs12494712, rs12943140, rs13002663,
rs13394010, rs13415334, rs13419758, rs1380706, rs1387768,
rs1410779, rs1478682, rs1508102, rs1532365, rs1544352,
rs1545223, rs1579771, rs1604169, rs1621509, rs1644418,
rs16886004, rs16895510, rs16901784, rs16927077, rs16930057,
rs17029538, rs17224858, rs17238927, rs17329014, rs17400875,
rs17449018, rs17577980, rs17638791, rs1858973, rs1886214,
rs1894406, rs1894407, rs1894408, rs196295, rs196341,
rs196343, rs197523, rs1979992, rs1979993, rs2043136,
rs2058742, rs2071469, rs2071470, rs2071472, rs2074037,
rs2136408, rs2139612, rs2175121, rs2241883, rs2309760,
rs2325911, rs241435, rs241440, rs241442, rs241443, rs241444,
rs241445, rs241446, rs241447, rs241449, rs241451, rs241452,
rs241453, rs241454, rs241456, rs2453478, rs2598360,
rs2621321, rs2621323, rs2660214, rs2816838, rs2824070,
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rs2926455, rs2934491, rs3135388, rs3218328, rs343087,
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rs3815822, rs3818675, rs3829539, rs3885907, rs3899755,
rs4075692, rs4143493, rs419132, rs423239, rs4254166,
rs4356336, rs4360791, rs4449139, rs4584668, rs4669694,

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rs4709792, rs4738738, rs4769060, rs4780822, rs4782279,
rs4822644, rs484482, rs4894701, rs5024722, rs502530,
rs543122, rs6032205, rs6032209, rs6110157, rs623011,
rs6497396, rs6535882, rs6687976, rs6718758, rs6835202,
rs6840089, rs6845927, rs6895094, rs6899068, rs7020402,
rs7024953, rs7028906, rs7029123, rs7062312, rs714342,
rs7187976, rs7191155, rs720176, rs7217872, rs7228827,
rs7348267, rs7496451, rs7524868, rs7563131, rs7579987,
rs759458, rs7666442, rs7670525, rs7672014, rs7677801,
rs7725112, rs7844274, rs7850, rs7860748, rs7862565,
rs7864679, rs7928078, rs7948420, rs8035826, rs8050872,
rs8053136, rs8055485, rs823829, rs858341, rs9315047,
rs931570, rs9346979, rs9376361, rs9393727, rs9501224,
rs9508832, rs950928, rs9579566, rs9597498, rs9670531,
rs9671124, rs9671182, rs9817308, rs9834010, rs9876830,
rs9913349, rs9931167 and rs9931211,

- (ii) identifying the subject as a predicted responder to
glatiramer acetate if the genotype of the subject contains

one or more A alleles at the location of kgp10152733,
kgp10224254, kgp10305127, kgp10351364, kgp10372946,
kgp10404633, kgp10564659, kgp10591989, kgp10594414,
kgp10619195, kgp10620244, kgp10633631, kgp10974833,
kgp11002881, kgp11285862, kgp11328629, kgp11407560,
kgp11514107, kgp11627530, kgp11702474, kgp11711524,
kgp11768533, kgp11804835, kgp12083934, kgp12182745,
kgp12230354, kgp1224440, kgp124162, kgp12557319, kgp1371881,
kgp1699628, kgp1753445, kgp1779254, kgp1786079, kgp18379774,
kgp18525257, kgp20163979, kgp2023214, kgp20478926,
kgp21171930, kgp2262166, kgp22778566, kgp2465184,
kgp24753470, kgp25191871, kgp25216186, kgp25952891,
kgp26026546, kgp26533576, kgp27500525, kgp27571222,
kgp28532436, kgp28586329, kgp28817122, kgp2958113,
kgp29794723, kgp30282494, kgp304921, kgp3205849, kgp3218351,
kgp3276689, kgp337461, kgp345301, kgp355027, kgp355723,

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kgp3593828, kgp3812034, kgp3951463, kgp4162414, kgp4223880,
kgp4418535, kgp4543470, kgp4573213, kgp4634875, kgp4755147,
kgp4842590, kgp485316, kgp5068397, kgp5334779, kgp5483926,
kgp5564995, kgp5869992, kgp5908616, kgp6032617, kgp6038357,
kgp6076976, kgp6091119, kgp6127371, kgp61811, kgp6214351,
kgp6228750, kgp6236949, kgp6469620, kgp6505544, kgp6507761,
kgp6666134, kgp6700691, kgp6772915, kgp6959492, kgp7077322,
kgp7117398, kgp7178233, kgp7186699, kgp7506434, kgp759150,
kgp7730397, kgp7802182, kgp7804623, kgp7924485, kgp8030775,
kgp8036704, kgp8046214, kgp8106690, kgp8110667, kgp8178358,
kgp8200264, kgp8372910, kgp841428, kgp8602316, kgp8615910,
kgp8793915, kgp8796185, kgp8990121, kgp9018750, kgp9354462,
kgp9368119, kgp9410843, kgp9450430, kgp9530088, kgp9627338,
kgp9669946, kgp97310, kgp974569, kgp9806386, kgp9884626,
rs10049206, rs10124492, rs10125298, rs10162089, rs10203396,
rs10251797, rs10278591, rs10489312, rs10492882, rs10498793,
rs10501082, rs10510774, rs10512340, rs10815160, rs10816302,
rs10841337, rs11029892, rs11029928, rs11192469, rs11559024,
rs11648129, rs12013377, rs13394010, rs13415334, rs1478682,
rs1544352, rs1545223, rs1604169, rs1621509, rs1644418,
rs17029538, rs17400875, rs17449018, rs17577980, rs1858973,
rs1894406, rs1894407, rs197523, rs2058742, rs2071469,
rs2071472, rs2139612, rs2241883, rs2309760, rs241440,
rs241442, rs241444, rs241445, rs241446, rs241449, rs241453,
rs241456, rs2453478, rs2660214, rs2824070, rs2845371,
rs2857103, rs2926455, rs343087, rs343092, rs3767955,
rs3792135, rs3829539, rs3899755, rs4075692, rs4143493,
rs423239, rs4254166, rs4356336, rs4584668, rs4780822,
rs4782279, rs5024722, rs6032209, rs6110157, rs623011,
rs6497396, rs6845927, rs6895094, rs6899068, rs7024953,
rs7028906, rs7029123, rs7062312, rs7187976, rs7191155,
rs720176, rs7228827, rs7496451, rs7563131, rs759458,
rs7666442, rs7670525, rs7677801, rs7725112, rs7850,
rs7862565, rs7948420, rs8035826, rs8053136, rs8055485,
rs823829, rs9315047, rs9501224, rs9508832, rs950928,

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rs9597498, rs9670531, rs9671124, rs9817308, rs9834010,
rs9876830 or rs9931211,

one or more C alleles at the location of kgp10910719,
kgp11077373, kgp11453406, kgp12426624, kgp2045074,
kgp22811918, kgp23298674, kgp2709692, kgp28687699,
kgp3496814, kgp3669685, kgp3730395, kgp4056892, kgp4370912,
kgp5053636, kgp5216209, kgp5292386, kgp6023196, kgp652534,
kgp7059449, kgp7189498, kgp7521990, kgp7792268, kgp8303520,
kgp9320791, kgp9795732, rs10201643, rs11022778, rs11136970,
rs11147439, rs11691553, rs1579771, rs16901784, rs2136408,
rs2325911, rs241443, rs2857104, rs3803277, rs3885907,
rs4738738, rs4894701, rs502530, rs6032205, rs6687976,
rs6718758, rs6835202, rs714342, rs7524868, rs7844274,
rs9393727 or rs9671182,

one or more G alleles at the location of kgp10090631,
kgp1009249, kgp10412303, kgp10523170, kgp1054273,
kgp10558725, kgp10632945, kgp10679353, kgp10788130,
kgp10826273, kgp10922969, kgp10948564, kgp10967046,
kgp1098237, kgp11010680, kgp11141512, kgp11206453,
kgp11210903, kgp1124492, kgp11281589, kgp11356379,
kgp11467007, kgp11543962, kgp11580695, kgp11633966,
kgp11686146, kgp11843177, kgp12008955, kgp12371757,
kgp1285441, kgp13161760, kgp1355977, kgp15390522, kgp1683448,
kgp1688752, kgp1912531, kgp19568724, kgp2092817, kgp2245775,
kgp22793211, kgp22823022, kgp2282938, kgp2299675, kgp2356388,
kgp23672937, kgp23737989, kgp2388352, kgp2391411,
kgp24131116, kgp24415534, kgp2446153, kgp2451249,
kgp24729706, kgp25543811, kgp25921291, kgp26271158,
kgp2638591, kgp26528455, kgp2688306, kgp26995430, kgp270001,
kgp2715873, kgp27640141, kgp2788291, kgp2923815, kgp29367521,
kgp293787, kgp2959751, kgp297178, kgp3048169, kgp3182607,
kgp3202939, kgp3267884, kgp3418770, kgp3450875, kgp3477351,
kgp3598409, kgp3651767, kgp3854180, kgp3933330, kgp3984567,
kgp4011779, kgp4096263, kgp4127859, kgp4155998, kgp4346717,
kgp4420791, kgp4479467, kgp4524468, kgp4559907, kgp4705854,

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kgp4734301, kgp4812831, kgp487328, kgp4898179, kgp5002011,
 kgp5014707, kgp5017029, kgp512180, kgp5144181, kgp5159037,
 kgp5388938, kgp5409955, kgp5440506, kgp5441587, kgp55646,
 kgp5579170, kgp5680955, kgp6190988, kgp6539666, kgp6567154,
 kgp6599438, kgp6603796, kgp6737096, kgp6768546, kgp6835138,
 kgp6996560, kgp7063887, kgp7092772, kgp7121374, kgp7181058,
 kgp7331172, kgp7416024, kgp7481870, kgp767200, kgp7714238,
 kgp7747883, kgp8107491, kgp8169636, kgp8174785, kgp8183049,
 kgp8192546, kgp8335515, kgp8437961, kgp8440036, kgp85534,
 kgp8599417, kgp8767692, kgp8777935, kgp8817856, kgp8869954,
 kgp9071686, kgp9078300, kgp9354820, kgp9421884, kgp9551947,
 kgp9601362, kgp9627406, kgp9699754, kgp971582, kgp9854133,
 rs1079303, rs10841322, rs10954782, rs11002051, rs11029907,
 rs11083404, rs11085044, rs11192461, rs1157449, rs12494712,
 rs12943140, rs13002663, rs13419758, rs1380706, rs1387768,
 rs1410779, rs1508102, rs1532365, rs16886004, rs16895510,
 rs16927077, rs16930057, rs17224858, rs17238927, rs17329014,
 rs17638791, rs1886214, rs1894408, rs196295, rs196341,
 rs196343, rs1979992, rs1979993, rs2043136, rs2071470,
 rs2074037, rs2175121, rs241435, rs241447, rs241451, rs241452,
 rs241454, rs2598360, rs2621321, rs2621323, rs2816838,
 rs2839117, rs2857101, rs2934491, rs3135388, rs3218328,
 rs3799383, rs3815822, rs3818675, rs419132, rs4360791,
 rs4449139, rs4669694, rs4709792, rs4769060, rs4822644,
 rs484482, rs543122, rs6535882, rs6840089, rs7020402,
 rs7217872, rs7348267, rs7579987, rs7672014, rs7860748,
 rs7864679, rs7928078, rs8050872, rs858341, rs931570,
 rs9346979, rs9376361, rs9579566, rs9913349 or rs9931167, or
 one or more T alleles at the location of kgp18432055,
 kgp279772, kgp3991733 or kgp7242489; and

- (iii) administering the pharmaceutical composition comprising glatiramer acetate and a pharmaceutically acceptable carrier to the subject only if the subject is identified as a predicted responder to glatiramer acetate.

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2. The method of claim 1, wherein step (i) further comprises determining a genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of: rs10988087, rs1573706, rs17575455, rs2487896, rs3135391, rs6097801 and rs947603, and wherein step (ii) further comprises identifying the subject as a predicted responder to glatiramer acetate if the genotype of the subject contains one or more A alleles at the location of rs10988087, one or more C alleles at the location of rs17575455, or one or more G alleles at the location of rs1573706, rs2487896, rs3135391, rs6097801 or rs947603.
3. The method of claim 1 or claim 2, wherein administering the pharmaceutical composition comprising glatiramer acetate and a pharmaceutically acceptable carrier comprises administering to the human subject three subcutaneous injections of the pharmaceutical composition over a period of seven days with at least one day between every subcutaneous injection.
4. The method of any one of claims 1-3, wherein the pharmaceutical composition is a unit dose of a 1 ml aqueous solution comprising 40 mg of glatiramer acetate.
5. The method of any one of claims 1-3, wherein the pharmaceutical composition is a unit dose of a 1 ml aqueous solution comprising 20 mg of glatiramer acetate.
6. The method of any one of claims 1-3, wherein the pharmaceutical composition is a unit dose of a 0.5 ml aqueous solution comprising 20 mg of glatiramer acetate.
7. The method of any one of claims 1-5, wherein the pharmaceutical composition comprising glatiramer acetate and a pharmaceutically acceptable carrier is administered as a monotherapy.
8. The method of any one of claims 1-7, wherein the pharmaceutical composition comprising glatiramer acetate and a pharmaceutically

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acceptable carrier is administered in combination with at least one other multiple sclerosis drug.

9. A method of identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the method comprising determining the genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of kgp10090631, kgp1009249, kgp10152733, kgp10224254, kgp10305127, kgp10351364, kgp10372946, kgp10404633, kgp10412303, kgp10523170, kgp1054273, kgp10558725, kgp10564659, kgp10591989, kgp10594414, kgp10619195, kgp10620244, kgp10632945, kgp10633631, kgp10679353, kgp10788130, kgp10826273, kgp10910719, kgp10922969, kgp10948564, kgp10967046, kgp10974833, kgp1098237, kgp11002881, kgp11010680, kgp11077373, kgp11141512, kgp11206453, kgp11210903, kgp1124492, kgp11281589, kgp11285862, kgp11328629, kgp11356379, kgp11407560, kgp11453406, kgp11467007, kgp11514107, kgp11543962, kgp11580695, kgp11627530, kgp11633966, kgp11686146, kgp11702474, kgp11711524, kgp11768533, kgp11804835, kgp11843177, kgp12008955, kgp12083934, kgp12182745, kgp12230354, kgp1224440, kgp12371757, kgp124162, kgp12426624, kgp12557319, kgp1285441, kgp13161760, kgp1355977, kgp1371881, kgp15390522, kgp1683448, kgp1688752, kgp1699628, kgp1753445, kgp1779254, kgp1786079, kgp18379774, kgp18432055, kgp18525257, kgp1912531, kgp19568724, kgp20163979, kgp2023214, kgp2045074, kgp20478926, kgp2092817, kgp21171930, kgp2245775, kgp2262166, kgp22778566, kgp22793211, kgp22811918, kgp22823022, kgp2282938, kgp2299675, kgp23298674, kgp2356388, kgp23672937, kgp23737989, kgp2388352, kgp2391411, kgp24131116, kgp24415534, kgp2446153, kgp2451249, kgp2465184, kgp24729706, kgp24753470, kgp25191871, kgp25216186, kgp25543811, kgp25921291, kgp25952891, kgp26026546, kgp26271158, kgp2638591, kgp26528455, kgp26533576, kgp2688306, kgp26995430, kgp270001, kgp2709692, kgp2715873, kgp27500525, kgp27571222, kgp27640141, kgp2788291, kgp279772, kgp28532436, kgp28586329, kgp28687699, kgp28817122, kgp2923815,

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kgp29367521, kgp293787, kgp2958113, kgp2959751, kgp297178,
kgp29794723, kgp30282494, kgp3048169, kgp304921, kgp3182607,
kgp3202939, kgp3205849, kgp3218351, kgp3267884, kgp3276689,
kgp337461, kgp3418770, kgp3450875, kgp345301, kgp3477351,
kgp3496814, kgp355027, kgp355723, kgp3593828, kgp3598409,
kgp3651767, kgp3669685, kgp3730395, kgp3812034, kgp3854180,
kgp3933330, kgp3951463, kgp3984567, kgp3991733, kgp4011779,
kgp4056892, kgp4096263, kgp4127859, kgp4155998, kgp4162414,
kgp4223880, kgp4346717, kgp4370912, kgp4418535, kgp4420791,
kgp4479467, kgp4524468, kgp4543470, kgp4559907, kgp4573213,
kgp4634875, kgp4705854, kgp4734301, kgp4755147, kgp4812831,
kgp4842590, kgp485316, kgp487328, kgp4898179, kgp5002011,
kgp5014707, kgp5017029, kgp5053636, kgp5068397, kgp512180,
kgp5144181, kgp5159037, kgp5216209, kgp5292386, kgp5334779,
kgp5388938, kgp5409955, kgp5440506, kgp5441587, kgp5483926,
kgp55646, kgp5564995, kgp5579170, kgp5680955, kgp5869992,
kgp5908616, kgp6023196, kgp6032617, kgp6038357, kgp6076976,
kgp6091119, kgp6127371, kgp61811, kgp6190988, kgp6214351,
kgp6228750, kgp6236949, kgp6469620, kgp6505544, kgp6507761,
kgp652534, kgp6539666, kgp6567154, kgp6599438, kgp6603796,
kgp6666134, kgp6700691, kgp6737096, kgp6768546, kgp6772915,
kgp6835138, kgp6959492, kgp6996560, kgp7059449, kgp7063887,
kgp7077322, kgp7092772, kgp7117398, kgp7121374, kgp7178233,
kgp7181058, kgp7186699, kgp7189498, kgp7242489, kgp7331172,
kgp7416024, kgp7481870, kgp7506434, kgp7521990, kgp759150,
kgp767200, kgp7714238, kgp7730397, kgp7747883, kgp7792268,
kgp7802182, kgp7804623, kgp7924485, kgp8030775, kgp8036704,
kgp8046214, kgp8106690, kgp8107491, kgp8110667, kgp8169636,
kgp8174785, kgp8178358, kgp8183049, kgp8192546, kgp8200264,
kgp8303520, kgp8335515, kgp8372910, kgp841428, kgp8437961,
kgp8440036, kgp85534, kgp8599417, kgp8602316, kgp8615910,
kgp8767692, kgp8777935, kgp8793915, kgp8796185, kgp8817856,
kgp8869954, kgp8990121, kgp9018750, kgp9071686, kgp9078300,
kgp9320791, kgp9354462, kgp9354820, kgp9368119, kgp9410843,
kgp9421884, kgp9450430, kgp9530088, kgp9551947, kgp9601362,

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kgp9627338, kgp9627406, kgp9669946, kgp9699754, kgp971582,
kgp97310, kgp974569, kgp9795732, kgp9806386, kgp9854133,
kgp9884626, rs10049206, rs10124492, rs10125298, rs10162089,
rs10201643, rs10203396, rs10251797, rs10278591, rs10489312,
rs10492882, rs10498793, rs10501082, rs10510774, rs10512340,
rs1079303, rs10815160, rs10816302, rs10841322, rs10841337,
rs10954782, rs11002051, rs11022778, rs11029892, rs11029907,
rs11029928, rs11083404, rs11085044, rs11136970, rs11147439,
rs11192461, rs11192469, rs11559024, rs1157449, rs11648129,
rs11691553, rs12013377, rs12494712, rs12943140, rs13002663,
rs13394010, rs13415334, rs13419758, rs1380706, rs1387768,
rs1410779, rs1478682, rs1508102, rs1532365, rs1544352, rs1545223,
rs1579771, rs1604169, rs1621509, rs1644418, rs16886004,
rs16895510, rs16901784, rs16927077, rs16930057, rs17029538,
rs17224858, rs17238927, rs17329014, rs17400875, rs17449018,
rs17577980, rs17638791, rs1858973, rs1886214, rs1894406,
rs1894407, rs1894408, rs196295, rs196341, rs196343, rs197523,
rs1979992, rs1979993, rs2043136, rs2058742, rs2071469, rs2071470,
rs2071472, rs2074037, rs2136408, rs2139612, rs2175121, rs2241883,
rs2309760, rs2325911, rs241435, rs241440, rs241442, rs241443,
rs241444, rs241445, rs241446, rs241447, rs241449, rs241451,
rs241452, rs241453, rs241454, rs241456, rs2453478, rs2598360,
rs2621321, rs2621323, rs2660214, rs2816838, rs2824070, rs2839117,
rs2845371, rs2857101, rs2857103, rs2857104, rs2926455, rs2934491,
rs3135388, rs3218328, rs343087, rs343092, rs3767955, rs3792135,
rs3799383, rs3803277, rs3815822, rs3818675, rs3829539, rs3885907,
rs3899755, rs4075692, rs4143493, rs419132, rs423239, rs4254166,
rs4356336, rs4360791, rs4449139, rs4584668, rs4669694, rs4709792,
rs4738738, rs4769060, rs4780822, rs4782279, rs4822644, rs484482,
rs4894701, rs5024722, rs502530, rs543122, rs6032205, rs6032209,
rs6110157, rs623011, rs6497396, rs6535882, rs6687976, rs6718758,
rs6835202, rs6840089, rs6845927, rs6895094, rs6899068, rs7020402,
rs7024953, rs7028906, rs7029123, rs7062312, rs714342, rs7187976,
rs7191155, rs720176, rs7217872, rs7228827, rs7348267, rs7496451,
rs7524868, rs7563131, rs7579987, rs759458, rs7666442, rs7670525,

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rs7672014, rs7677801, rs7725112, rs7844274, rs7850, rs7860748, rs7862565, rs7864679, rs7928078, rs7948420, rs8035826, rs8050872, rs8053136, rs8055485, rs823829, rs858341, rs9315047, rs931570, rs9346979, rs9376361, rs9393727, rs9501224, rs9508832, rs950928, rs9579566, rs9597498, rs9670531, rs9671124, rs9671182, rs9817308, rs9834010, rs9876830, rs9913349, rs9931167 and rs9931211, and

identifying the human subject as a predicted responder to glatiramer acetate if the genotype of the subject contains

one or more A alleles at the location of kgp10152733, kgp10224254, kgp10305127, kgp10351364, kgp10372946, kgp10404633, kgp10564659, kgp10591989, kgp10594414, kgp10619195, kgp10620244, kgp10633631, kgp10974833, kgp11002881, kgp11285862, kgp11328629, kgp11407560, kgp11514107, kgp11627530, kgp11702474, kgp11711524, kgp11768533, kgp11804835, kgp12083934, kgp12182745, kgp12230354, kgp1224440, kgp124162, kgp12557319, kgp1371881, kgp1699628, kgp1753445, kgp1779254, kgp1786079, kgp18379774, kgp18525257, kgp20163979, kgp2023214, kgp20478926, kgp21171930, kgp2262166, kgp22778566, kgp2465184, kgp24753470, kgp25191871, kgp25216186, kgp25952891, kgp26026546, kgp26533576, kgp27500525, kgp27571222, kgp28532436, kgp28586329, kgp28817122, kgp2958113, kgp29794723, kgp30282494, kgp304921, kgp3205849, kgp3218351, kgp3276689, kgp337461, kgp345301, kgp355027, kgp355723, kgp3593828, kgp3812034, kgp3951463, kgp4162414, kgp4223880, kgp4418535, kgp4543470, kgp4573213, kgp4634875, kgp4755147, kgp4842590, kgp485316, kgp5068397, kgp5334779, kgp5483926, kgp5564995, kgp5869992, kgp5908616, kgp6032617, kgp6038357, kgp6076976, kgp6091119, kgp6127371, kgp61811, kgp6214351, kgp6228750, kgp6236949, kgp6469620, kgp6505544, kgp6507761, kgp6666134, kgp6700691, kgp6772915, kgp6959492, kgp7077322, kgp7117398, kgp7178233, kgp7186699, kgp7506434,

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kgp759150, kgp7730397, kgp7802182, kgp7804623,
kgp7924485, kgp8030775, kgp8036704, kgp8046214,
kgp8106690, kgp8110667, kgp8178358, kgp8200264,
kgp8372910, kgp841428, kgp8602316, kgp8615910,
kgp8793915, kgp8796185, kgp8990121, kgp9018750,
kgp9354462, kgp9368119, kgp9410843, kgp9450430,
kgp9530088, kgp9627338, kgp9669946, kgp97310, kgp974569,
kgp9806386, kgp9884626, rs10049206, rs10124492,
rs10125298, rs10162089, rs10203396, rs10251797,
rs10278591, rs10489312, rs10492882, rs10498793,
rs10501082, rs10510774, rs10512340, rs10815160,
rs10816302, rs10841337, rs11029892, rs11029928,
rs11192469, rs11559024, rs11648129, rs12013377,
rs13394010, rs13415334, rs1478682, rs1544352, rs1545223,
rs1604169, rs1621509, rs1644418, rs17029538, rs17400875,
rs17449018, rs17577980, rs1858973, rs1894406, rs1894407,
rs197523, rs2058742, rs2071469, rs2071472, rs2139612,
rs2241883, rs2309760, rs241440, rs241442, rs241444,
rs241445, rs241446, rs241449, rs241453, rs241456,
rs2453478, rs2660214, rs2824070, rs2845371, rs2857103,
rs2926455, rs343087, rs343092, rs3767955, rs3792135,
rs3829539, rs3899755, rs4075692, rs4143493, rs423239,
rs4254166, rs4356336, rs4584668, rs4780822, rs4782279,
rs5024722, rs6032209, rs6110157, rs623011, rs6497396,
rs6845927, rs6895094, rs6899068, rs7024953, rs7028906,
rs7029123, rs7062312, rs7187976, rs7191155, rs720176,
rs7228827, rs7496451, rs7563131, rs759458, rs7666442,
rs7670525, rs7677801, rs7725112, rs7850, rs7862565,
rs7948420, rs8035826, rs8053136, rs8055485, rs823829,
rs9315047, rs9501224, rs9508832, rs950928, rs9597498,
rs9670531, rs9671124, rs9817308, rs9834010, rs9876830 or
rs9931211,

one or more C alleles at the location of kgp10910719,
kgp11077373, kgp11453406, kgp12426624, kgp2045074,
kgp22811918, kgp23298674, kgp2709692, kgp28687699,

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kgp3496814, kgp3669685, kgp3730395, kgp4056892,
kgp4370912, kgp5053636, kgp5216209, kgp5292386,
kgp6023196, kgp652534, kgp7059449, kgp7189498,
kgp7521990, kgp7792268, kgp8303520, kgp9320791,
kgp9795732, rs10201643, rs11022778, rs11136970,
rs11147439, rs11691553, rs1579771, rs16901784, rs2136408,
rs2325911, rs241443, rs2857104, rs3803277, rs3885907,
rs4738738, rs4894701, rs502530, rs6032205, rs6687976,
rs6718758, rs6835202, rs714342, rs7524868, rs7844274,
rs9393727 or rs9671182,

one or more G alleles at the location of kgp10090631,
kgp1009249, kgp10412303, kgp10523170, kgp1054273,
kgp10558725, kgp10632945, kgp10679353, kgp10788130,
kgp10826273, kgp10922969, kgp10948564, kgp10967046,
kgp1098237, kgp11010680, kgp11141512, kgp11206453,
kgp11210903, kgp1124492, kgp11281589, kgp11356379,
kgp11467007, kgp11543962, kgp11580695, kgp11633966,
kgp11686146, kgp11843177, kgp12008955, kgp12371757,
kgp1285441, kgp13161760, kgp1355977, kgp15390522,
kgp1683448, kgp1688752, kgp1912531, kgp19568724,
kgp2092817, kgp2245775, kgp22793211, kgp22823022,
kgp2282938, kgp2299675, kgp2356388, kgp23672937,
kgp23737989, kgp2388352, kgp2391411, kgp24131116,
kgp24415534, kgp2446153, kgp2451249, kgp24729706,
kgp25543811, kgp25921291, kgp26271158, kgp2638591,
kgp26528455, kgp2688306, kgp26995430, kgp270001,
kgp2715873, kgp27640141, kgp2788291, kgp2923815,
kgp29367521, kgp293787, kgp2959751, kgp297178,
kgp3048169, kgp3182607, kgp3202939, kgp3267884,
kgp3418770, kgp3450875, kgp3477351, kgp3598409,
kgp3651767, kgp3854180, kgp3933330, kgp3984567,
kgp4011779, kgp4096263, kgp4127859, kgp4155998,
kgp4346717, kgp4420791, kgp4479467, kgp4524468,
kgp4559907, kgp4705854, kgp4734301, kgp4812831,
kgp487328, kgp4898179, kgp5002011, kgp5014707,

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kgp5017029, kgp512180, kgp5144181, kgp5159037,
kgp5388938, kgp5409955, kgp5440506, kgp5441587, kgp55646,
kgp5579170, kgp5680955, kgp6190988, kgp6539666,
kgp6567154, kgp6599438, kgp6603796, kgp6737096,
kgp6768546, kgp6835138, kgp6996560, kgp7063887,
kgp7092772, kgp7121374, kgp7181058, kgp7331172,
kgp7416024, kgp7481870, kgp767200, kgp7714238,
kgp7747883, kgp8107491, kgp8169636, kgp8174785,
kgp8183049, kgp8192546, kgp8335515, kgp8437961,
kgp8440036, kgp85534, kgp8599417, kgp8767692, kgp8777935,
kgp8817856, kgp8869954, kgp9071686, kgp9078300,
kgp9354820, kgp9421884, kgp9551947, kgp9601362,
kgp9627406, kgp9699754, kgp971582, kgp9854133, rs1079303,
rs10841322, rs10954782, rs11002051, rs11029907,
rs11083404, rs11085044, rs11192461, rs1157449,
rs12494712, rs12943140, rs13002663, rs13419758,
rs1380706, rs1387768, rs1410779, rs1508102, rs1532365,
rs16886004, rs16895510, rs16927077, rs16930057,
rs17224858, rs17238927, rs17329014, rs17638791,
rs1886214, rs1894408, rs196295, rs196341, rs196343,
rs1979992, rs1979993, rs2043136, rs2071470, rs2074037,
rs2175121, rs241435, rs241447, rs241451, rs241452,
rs241454, rs2598360, rs2621321, rs2621323, rs2816838,
rs2839117, rs2857101, rs2934491, rs3135388, rs3218328,
rs3799383, rs3815822, rs3818675, rs419132, rs4360791,
rs4449139, rs4669694, rs4709792, rs4769060, rs4822644,
rs484482, rs543122, rs6535882, rs6840089, rs7020402,
rs7217872, rs7348267, rs7579987, rs7672014, rs7860748,
rs7864679, rs7928078, rs8050872, rs858341, rs931570,
rs9346979, rs9376361, rs9579566, rs9913349 or rs9931167,
or

one or more T alleles at the location of kgp18432055,
kgp279772, kgp3991733 or kgp7242489,

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or identifying the human subject as a predicted non-responder to glatiramer acetate if the genotype of the subject contains

no A alleles at the location of kgp10152733, kgp10224254, kgp10305127, kgp10351364, kgp10372946, kgp10404633, kgp10564659, kgp10591989, kgp10594414, kgp10619195, kgp10620244, kgp10633631, kgp10974833, kgp11002881, kgp11285862, kgp11328629, kgp11407560, kgp11514107, kgp11627530, kgp11702474, kgp11711524, kgp11768533, kgp11804835, kgp12083934, kgp12182745, kgp12230354, kgp1224440, kgp124162, kgp12557319, kgp1371881, kgp1699628, kgp1753445, kgp1779254, kgp1786079, kgp18379774, kgp18525257, kgp20163979, kgp2023214, kgp20478926, kgp21171930, kgp2262166, kgp22778566, kgp2465184, kgp24753470, kgp25191871, kgp25216186, kgp25952891, kgp26026546, kgp26533576, kgp27500525, kgp27571222, kgp28532436, kgp28586329, kgp28817122, kgp2958113, kgp29794723, kgp30282494, kgp304921, kgp3205849, kgp3218351, kgp3276689, kgp337461, kgp345301, kgp355027, kgp355723, kgp3593828, kgp3812034, kgp3951463, kgp4162414, kgp4223880, kgp4418535, kgp4543470, kgp4573213, kgp4634875, kgp4755147, kgp4842590, kgp485316, kgp5068397, kgp5334779, kgp5483926, kgp5564995, kgp5869992, kgp5908616, kgp6032617, kgp6038357, kgp6076976, kgp6091119, kgp6127371, kgp61811, kgp6214351, kgp6228750, kgp6236949, kgp6469620, kgp6505544, kgp6507761, kgp6666134, kgp6700691, kgp6772915, kgp6959492, kgp7077322, kgp7117398, kgp7178233, kgp7186699, kgp7506434, kgp759150, kgp7730397, kgp7802182, kgp7804623, kgp7924485, kgp8030775, kgp8036704, kgp8046214, kgp8106690, kgp8110667, kgp8178358, kgp8200264, kgp8372910, kgp841428, kgp8602316, kgp8615910, kgp8793915, kgp8796185, kgp8990121, kgp9018750, kgp9354462, kgp9368119, kgp9410843, kgp9450430, kgp9530088, kgp9627338, kgp9669946, kgp97310, kgp974569, kgp9806386,

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kgp9884626, rs10049206, rs10124492, rs10125298,
rs10162089, rs10203396, rs10251797, rs10278591,
rs10489312, rs10492882, rs10498793, rs10501082,
rs10510774, rs10512340, rs10815160, rs10816302,
rs10841337, rs11029892, rs11029928, rs11192469,
rs11559024, rs11648129, rs12013377, rs13394010,
rs13415334, rs1478682, rs1544352, rs1545223, rs1604169,
rs1621509, rs1644418, rs17029538, rs17400875, rs17449018,
rs17577980, rs1858973, rs1894406, rs1894407, rs197523,
rs2058742, rs2071469, rs2071472, rs2139612, rs2241883,
rs2309760, rs241440, rs241442, rs241444, rs241445,
rs241446, rs241449, rs241453, rs241456, rs2453478,
rs2660214, rs2824070, rs2845371, rs2857103, rs2926455,
rs343087, rs343092, rs3767955, rs3792135, rs3829539,
rs3899755, rs4075692, rs4143493, rs423239, rs4254166,
rs4356336, rs4584668, rs4780822, rs4782279, rs5024722,
rs6032209, rs6110157, rs623011, rs6497396, rs6845927,
rs6895094, rs6899068, rs7024953, rs7028906, rs7029123,
rs7062312, rs7187976, rs7191155, rs720176, rs7228827,
rs7496451, rs7563131, rs759458, rs7666442, rs7670525,
rs7677801, rs7725112, rs7850, rs7862565, rs7948420,
rs8035826, rs8053136, rs8055485, rs823829, rs9315047,
rs9501224, rs9508832, rs950928, rs9597498, rs9670531,
rs9671124, rs9817308, rs9834010, rs9876830 or rs9931211,

no C alleles at the location of kgp10910719, kgp11077373,
kgp11453406, kgp12426624, kgp2045074, kgp22811918,
kgp23298674, kgp2709692, kgp28687699, kgp3496814,
kgp3669685, kgp3730395, kgp4056892, kgp4370912,
kgp5053636, kgp5216209, kgp5292386, kgp6023196,
kgp652534, kgp7059449, kgp7189498, kgp7521990,
kgp7792268, kgp8303520, kgp9320791, kgp9795732,
rs10201643, rs11022778, rs11136970, rs11147439,
rs11691553, rs1579771, rs16901784, rs2136408, rs2325911,
rs241443, rs2857104, rs3803277, rs3885907, rs4738738,
rs4894701, rs502530, rs6032205, rs6687976, rs6718758,

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rs6835202, rs714342, rs7524868, rs7844274, rs9393727 or
rs9671182,

no G alleles at the location of kgp10090631, kgp1009249,
kgp10412303, kgp10523170, kgp1054273, kgp10558725,
kgp10632945, kgp10679353, kgp10788130, kgp10826273,
kgp10922969, kgp10948564, kgp10967046, kgp1098237,
kgp11010680, kgp11141512, kgp11206453, kgp11210903,
kgp1124492, kgp11281589, kgp11356379, kgp11467007,
kgp11543962, kgp11580695, kgp11633966, kgp11686146,
kgp11843177, kgp12008955, kgp12371757, kgp1285441,
kgp13161760, kgp1355977, kgp15390522, kgp1683448,
kgp1688752, kgp1912531, kgp19568724, kgp2092817,
kgp2245775, kgp22793211, kgp22823022, kgp2282938,
kgp2299675, kgp2356388, kgp23672937, kgp23737989,
kgp2388352, kgp2391411, kgp24131116, kgp24415534,
kgp2446153, kgp2451249, kgp24729706, kgp25543811,
kgp25921291, kgp26271158, kgp2638591, kgp26528455,
kgp2688306, kgp26995430, kgp270001, kgp2715873,
kgp27640141, kgp2788291, kgp2923815, kgp29367521,
kgp293787, kgp2959751, kgp297178, kgp3048169, kgp3182607,
kgp3202939, kgp3267884, kgp3418770, kgp3450875,
kgp3477351, kgp3598409, kgp3651767, kgp3854180,
kgp3933330, kgp3984567, kgp4011779, kgp4096263,
kgp4127859, kgp4155998, kgp4346717, kgp4420791,
kgp4479467, kgp4524468, kgp4559907, kgp4705854,
kgp4734301, kgp4812831, kgp487328, kgp4898179,
kgp5002011, kgp5014707, kgp5017029, kgp512180,
kgp5144181, kgp5159037, kgp5388938, kgp5409955,
kgp5440506, kgp5441587, kgp55646, kgp5579170, kgp5680955,
kgp6190988, kgp6539666, kgp6567154, kgp6599438,
kgp6603796, kgp6737096, kgp6768546, kgp6835138,
kgp6996560, kgp7063887, kgp7092772, kgp7121374,
kgp7181058, kgp7331172, kgp7416024, kgp7481870,
kgp767200, kgp7714238, kgp7747883, kgp8107491,
kgp8169636, kgp8174785, kgp8183049, kgp8192546,

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kgp8335515, kgp8437961, kgp8440036, kgp85534, kgp8599417,
 kgp8767692, kgp8777935, kgp8817856, kgp8869954,
 kgp9071686, kgp9078300, kgp9354820, kgp9421884,
 kgp9551947, kgp9601362, kgp9627406, kgp9699754,
 kgp971582, kgp9854133, rs1079303, rs10841322, rs10954782,
 rs11002051, rs11029907, rs11083404, rs11085044,
 rs11192461, rs1157449, rs12494712, rs12943140,
 rs13002663, rs13419758, rs1380706, rs1387768, rs1410779,
 rs1508102, rs1532365, rs16886004, rs16895510, rs16927077,
 rs16930057, rs17224858, rs17238927, rs17329014,
 rs17638791, rs1886214, rs1894408, rs196295, rs196341,
 rs196343, rs1979992, rs1979993, rs2043136, rs2071470,
 rs2074037, rs2175121, rs241435, rs241447, rs241451,
 rs241452, rs241454, rs2598360, rs2621321, rs2621323,
 rs2816838, rs2839117, rs2857101, rs2934491, rs3135388,
 rs3218328, rs3799383, rs3815822, rs3818675, rs419132,
 rs4360791, rs4449139, rs4669694, rs4709792, rs4769060,
 rs4822644, rs484482, rs543122, rs6535882, rs6840089,
 rs7020402, rs7217872, rs7348267, rs7579987, rs7672014,
 rs7860748, rs7864679, rs7928078, rs8050872, rs858341,
 rs931570, rs9346979, rs9376361, rs9579566, rs9913349 or
 rs9931167, or

no T alleles at the location of kgp18432055, kgp279772,
 kgp3991733 or kgp7242489.

10. The method of claim 9, further comprising determining a genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of: rs10988087, rs1573706, rs17575455, rs2487896, rs3135391, rs6097801 and rs947603, and

identifying the human subject as a predicted responder to glatiramer acetate if the genotype of the subject contains one or more A alleles at the location of rs10988087, one or more C alleles at the location of rs17575455, or one or more G alleles

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at the location of rs1573706, rs2487896, rs3135391, rs6097801 or rs947603, or

identifying the human subject as a predicted non-responder to glatiramer acetate if the genotype of the subject contains no A alleles at the location of rs10988087, no C alleles at the location of rs17575455, or no G alleles at the location of rs1573706, rs2487896, rs3135391, rs6097801 or rs947603.

11. The method of any one of claims 1-10, wherein the genotype is determined from a nucleic acid-containing sample that has been obtained from the subject.
12. The method of any one of claims 1-11, wherein determining the genotype comprises using a method selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of mismatch (CCM), denaturing high performance liquid chromatography (DHPLC), Polymerase Chain Reaction (PCR) and an array, or a combination thereof.
13. The method of claim 12, wherein the genotype is determined using at least one pair of PCR primers and at least one probe.
14. The method of claim 12, wherein the array is selected from the group consisting of a gene chip, and a TaqMan Open Array.
15. The method of claim 14, wherein the gene chip is selected from the group consisting of a DNA array, a DNA microarray, a DNA chip, and a whole genome genotyping array.
16. The method of claim 12, wherein the array is a TaqMan Open Array.
17. The method of any of claims 14-15, wherein the gene chip is a whole genome genotyping array.

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18. The method of any one of claims 1-17, wherein determining the genotype of the subject at the location corresponding to the location of the said one or more SNPs comprises:
- (i) obtaining DNA from a sample that has been obtained from the subject;
 - (ii) optionally amplifying the DNA; and
 - (iii) subjecting the DNA or the amplified DNA to a method selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of mismatch (CCM), denaturing high performance liquid chromatography (DHPLC), Polymerase Chain Reaction (PCR) and an array, or a combination thereof, for determining the identity the one or more SNPs.
19. The method of claim 18, wherein the array comprises a plurality of probes suitable for determining the identity of the one or more SNPs.
20. The method of any of claims 17-18, wherein the array is a gene chip.
21. The method of claim 20, wherein the gene chip is a whole genome genotyping array.
22. The method of any one of claims 1-21, wherein the human subject is a naïve patient.
23. The method of any of claims 1-21, wherein the human subject has been previously administered glatiramer acetate.
24. The method of any of claims 1-21, wherein the human subject has been previously administered a multiple sclerosis drug other than glatiramer acetate.
25. The method of any one of claims 1-24, wherein the genotype is determined at locations corresponding to the locations of 2, 3,

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4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16 or more single nucleotide polymorphisms (SNPs).

26. The method of any one of claims 1-24, wherein the one or more SNPs is selected from the group consisting of kgp24415534, kgp6214351, kgp6599438, kgp7747883, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, and rs759458.
27. The method of claim 26, wherein the one or more SNPs comprise 2, 3, 4, 5, 6, 7, 8, 9 or 10 of the SNPs selected from the group consisting of kgp24415534, kgp6214351, kgp6599438, kgp7747883, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, and rs759458.
28. The method of claim 26 or 27, wherein if rs3135391 is the one SNP selected, then selecting at least one SNP other than rs3135391.
29. The method of any one of claims 1-24, wherein the one or more SNPs is selected from the group consisting of kgp24415534, kgp6214351, kgp6599438, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, and rs759458.
30. The method of claim 26, wherein the one or more SNPs comprise 2, 3, 4, 5, 6, 7, 8, 9 or 10 of the SNPs selected from the group consisting of kgp24415534, kgp6214351, kgp6599438, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, and rs759458.
31. The method of claim 29 or 30, wherein if rs3135391 is the one SNP selected, then selecting at least one SNP other than rs3135391.
32. The method of any one of claims 1-31, wherein the genotype of the subject at the location corresponding to the location of one or more of the SNPs is determined indirectly by determining the genotype of the subject at a location corresponding to the

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location of at least one SNP that is in linkage disequilibrium with the one or more SNPs.

33. The method of any one of claims 1-31, wherein the genotype of the subject at the location corresponding to the location of the one or more SNPs is determined by indirect genotyping.
34. The method of claim 33, wherein the indirect genotyping allows identification of the genotype of the subject at the location corresponding to the location of the one or more SNPs with a probability of at least 85%.
35. The method of claim 34, wherein the indirect genotyping allows identification of the genotype of the subject at the location corresponding to the location of the one or more SNPs with a probability of at least 90%.
36. The method of claim 35, wherein the indirect genotyping allows identification of the genotype of the subject at the location corresponding to the location of the one or more SNPs with a probability of at least 99%.
37. The method of any one of claims 1-36, further comprising the step of determining the log number of relapses in the last two years for the human subject.
38. The method of any one of claims 1-37, further comprising the step of determining the baseline Expanded Disability Status Scale (EDSS) score for the human subject.
39. The method of any one of claims 1-38, further comprising applying the algorithm depicted in Figure 8 or in Figure 9 to identify the subject as a predicted responder or as a predicted non-responder to glatiramer acetate.
40. The method of any one of claims 1-38, further comprising determining the genotype of the subject at a location corresponding to the location of one or more single nucleotide

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polymorphisms (SNPs) selected from the group consisting of:
 kgp10148554, kgp10215554, kgp10762962, kgp10836214, kgp10989246,
 kgp11285883, kgp11604017, kgp11755256, kgp1211163, kgp12253568,
 kgp12562255, kgp1432800, kgp1682126, kgp1758575, kgp2176915,
 kgp22839559, kgp24521552, kgp2877482, kgp2920925, kgp2993366,
 kgp3188, kgp3287349, kgp3420309, kgp3488270, kgp3598966,
 kgp3624014, kgp3697615, kgp394638, kgp4037661, kgp4137144,
 kgp433351, kgp4456934, kgp4575797, kgp4591145, kgp4892427,
 kgp4970670, kgp4985243, kgp5252824, kgp5326762, kgp541892,
 kgp5691690, kgp5747456, kgp5894351, kgp5924341, kgp5949515,
 kgp6042557, kgp6081880, kgp6194428, kgp6213972, kgp625941,
 kgp6301155, kgp6429231, kgp6828277, kgp6889327, kgp6990559,
 kgp7006201, kgp7151153, kgp7161038, kgp7653470, kgp7778345,
 kgp7932108, kgp8145845, kgp8644305, kgp8847137, kgp9143704,
 kgp9409440, kgp956070, kgp9909702, kgp9927782, rs10038844,
 rs1026894, rs10495115, rs11562998, rs11563025, rs11750747,
 rs11947777, rs12043743, rs12233980, rs12341716, rs12472695,
 rs12881439, rs13168893, rs13386874, rs1357718, rs1393037,
 rs1393040, rs1397481, rs1474226, rs1508515, rs1534647,
 rs16846161, rs1715441, rs17187123, rs17245674, rs17419416,
 rs1793174, rs1883448, rs1905248, rs209568, rs2354380, rs2618065,
 rs263247, rs2662, rs28993969, rs34647183, rs35615951, rs3768769,
 rs3847233, rs3858034, rs3858035, rs3858036, rs3858038,
 rs3894712, rs4740708, rs4797764, rs4978567, rs528065, rs6459418,
 rs6577395, rs6811337, rs7119480, rs7123506, rs7231366,
 rs7680970, rs7684006, rs7696391, rs7698655, rs7819949,
 rs7846783, rs7949751, rs7961005, rs8000689, rs8018807, rs961090,
 rs967616, rs9948620 and rs9953274, and

identifying the human subject as a predicted responder to
 glatiramer acetate if the genotype of the subject contains

one or more A alleles at the location of kgp10762962,
 kgp11285883, kgp11604017, kgp1211163, kgp12253568, kgp12562255,
 kgp2176915, kgp24521552, kgp2877482, kgp2993366, kgp3188,
 kgp3624014, kgp394638, kgp4037661, kgp433351, kgp4456934,

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kgp4575797, kgp4591145, kgp4892427, kgp4970670, kgp4985243,
 kgp5252824, kgp5326762, kgp541892, kgp5747456, kgp5894351,
 kgp6042557, kgp6081880, kgp6194428, kgp6429231, kgp7006201,
 kgp7151153, kgp7161038, kgp7653470, kgp8145845, kgp8644305,
 kgp9143704, kgp9409440, kgp9909702, kgp9927782, rs10038844,
 rs10495115, rs11750747, rs12341716, rs12881439, rs13168893,
 rs1393040, rs1474226, rs1534647, rs1715441, rs17187123,
 rs17245674, rs17419416, rs1793174, rs1883448, rs1905248,
 rs263247, rs34647183, rs35615951, rs3847233, rs3858038,
 rs4740708, rs528065, rs6459418, rs6577395, rs6811337, rs7680970,
 rs7684006, rs7698655, rs7961005, rs8018807, rs9948620 or
 rs9953274,

one or more C alleles at the location of kgp10836214, kgp1432800,
 kgp22839559, kgp6301155, kgp6828277, rs2354380, rs2662,
 rs3858035, rs3894712, rs4797764 or rs7696391,

one or more G alleles at the location of kgp10148554,
 kgp10215554, kgp10989246, kgp11755256, kgp1682126, kgp1758575,
 kgp2920925, kgp3287349, kgp3420309, kgp3488270, kgp3598966,
 kgp3697615, kgp4137144, kgp5691690, kgp5924341, kgp5949515,
 kgp6213972, kgp625941, kgp6889327, kgp6990559, kgp7778345,
 kgp7932108, kgp8847137, kgp956070, rs1026894, rs11562998,
 rs11563025, rs11947777, rs12233980, rs12472695, rs13386874,
 rs1357718, rs1393037, rs1397481, rs1508515, rs16846161, rs209568,
 rs2618065, rs28993969, rs3768769, rs3858034, rs3858036,
 rs4978567, rs7119480, rs7123506, rs7231366, rs7819949, rs7846783,
 rs7949751, rs8000689, rs961090 or rs967616, or

one or more T alleles at the location of rs12043743.

41. The method of claim 40, wherein the genotype of the subject at the location corresponding to the location of one or more of the SNPs is determined indirectly by determining the genotype of the subject at a location corresponding to the location of at least one SNP that is in linkage disequilibrium with the one or more SNPs.

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42. A kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the kit comprising at least one probe specific for the location of a SNP selected from the group consisting of kgp10090631, kgp1009249, kgp10152733, kgp10224254, kgp10305127, kgp10351364, kgp10372946, kgp10404633, kgp10412303, kgp10523170, kgp1054273, kgp10558725, kgp10564659, kgp10591989, kgp10594414, kgp10619195, kgp10620244, kgp10632945, kgp10633631, kgp10679353, kgp10788130, kgp10826273, kgp10910719, kgp10922969, kgp10948564, kgp10967046, kgp10974833, kgp1098237, kgp11002881, kgp11010680, kgp11077373, kgp11141512, kgp11206453, kgp11210903, kgp1124492, kgp11281589, kgp11285862, kgp11328629, kgp11356379, kgp11407560, kgp11453406, kgp11467007, kgp11514107, kgp11543962, kgp11580695, kgp11627530, kgp11633966, kgp11686146, kgp11702474, kgp11711524, kgp11768533, kgp11804835, kgp11843177, kgp12008955, kgp12083934, kgp12182745, kgp12230354, kgp1224440, kgp12371757, kgp124162, kgp12426624, kgp12557319, kgp1285441, kgp13161760, kgp1355977, kgp1371881, kgp15390522, kgp1683448, kgp1688752, kgp1699628, kgp1753445, kgp1779254, kgp1786079, kgp18379774, kgp18432055, kgp18525257, kgp1912531, kgp19568724, kgp20163979, kgp2023214, kgp2045074, kgp20478926, kgp2092817, kgp21171930, kgp2245775, kgp2262166, kgp22778566, kgp22793211, kgp22811918, kgp22823022, kgp2282938, kgp2299675, kgp23298674, kgp2356388, kgp23672937, kgp23737989, kgp2388352, kgp2391411, kgp24131116, kgp24415534, kgp2446153, kgp2451249, kgp2465184, kgp24729706, kgp24753470, kgp25191871, kgp25216186, kgp25543811, kgp25921291, kgp25952891, kgp26026546, kgp26271158, kgp2638591, kgp26528455, kgp26533576, kgp2688306, kgp26995430, kgp270001, kgp2709692, kgp2715873, kgp27500525, kgp27571222, kgp27640141, kgp2788291, kgp279772, kgp28532436, kgp28586329, kgp28687699, kgp28817122, kgp2923815, kgp29367521, kgp293787, kgp2958113, kgp2959751, kgp297178, kgp29794723, kgp30282494, kgp3048169, kgp304921, kgp3182607, kgp3202939, kgp3205849, kgp3218351, kgp3267884, kgp3276689, kgp337461, kgp3418770, kgp3450875, kgp345301,

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kgp3477351,	kgp3496814,	kgp355027,	kgp355723,	kgp3593828,
kgp3598409,	kgp3651767,	kgp3669685,	kgp3730395,	kgp3812034,
kgp3854180,	kgp3933330,	kgp3951463,	kgp3984567,	kgp3991733,
kgp4011779,	kgp4056892,	kgp4096263,	kgp4127859,	kgp4155998,
kgp4162414,	kgp4223880,	kgp4346717,	kgp4370912,	kgp4418535,
kgp4420791,	kgp4479467,	kgp4524468,	kgp4543470,	kgp4559907,
kgp4573213,	kgp4634875,	kgp4705854,	kgp4734301,	kgp4755147,
kgp4812831,	kgp4842590,	kgp485316,	kgp487328,	kgp4898179,
kgp5002011,	kgp5014707,	kgp5017029,	kgp5053636,	kgp5068397,
kgp512180,	kgp5144181,	kgp5159037,	kgp5216209,	kgp5292386,
kgp5334779,	kgp5388938,	kgp5409955,	kgp5440506,	kgp5441587,
kgp5483926,	kgp55646,	kgp5564995,	kgp5579170,	kgp5680955,
kgp5869992,	kgp5908616,	kgp6023196,	kgp6032617,	kgp6038357,
kgp6076976,	kgp6091119,	kgp6127371,	kgp61811,	kgp6190988,
kgp6214351,	kgp6228750,	kgp6236949,	kgp6469620,	kgp6505544,
kgp6507761,	kgp652534,	kgp6539666,	kgp6567154,	kgp6599438,
kgp6603796,	kgp6666134,	kgp6700691,	kgp6737096,	kgp6768546,
kgp6772915,	kgp6835138,	kgp6959492,	kgp6996560,	kgp7059449,
kgp7063887,	kgp7077322,	kgp7092772,	kgp7117398,	kgp7121374,
kgp7178233,	kgp7181058,	kgp7186699,	kgp7189498,	kgp7242489,
kgp7331172,	kgp7416024,	kgp7481870,	kgp7506434,	kgp7521990,
kgp759150,	kgp767200,	kgp7714238,	kgp7730397,	kgp7747883,
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kgp8036704,	kgp8046214,	kgp8106690,	kgp8107491,	kgp8110667,
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kgp8437961,	kgp8440036,	kgp85534,	kgp8599417,	kgp8602316,
kgp8615910,	kgp8767692,	kgp8777935,	kgp8793915,	kgp8796185,
kgp8817856,	kgp8869954,	kgp8990121,	kgp9018750,	kgp9071686,
kgp9078300,	kgp9320791,	kgp9354462,	kgp9354820,	kgp9368119,
kgp9410843,	kgp9421884,	kgp9450430,	kgp9530088,	kgp9551947,
kgp9601362,	kgp9627338,	kgp9627406,	kgp9669946,	kgp9699754,
kgp971582,	kgp97310,	kgp974569,	kgp9795732,	kgp9806386,
kgp9854133,	kgp9884626,	rs10049206,	rs10124492,	rs10125298,
rs10162089,	rs10201643,	rs10203396,	rs10251797,	rs10278591,

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rs10489312, rs10492882, rs10498793, rs10501082, rs10510774,
rs10512340, rs1079303, rs10815160, rs10816302, rs10841322,
rs10841337, rs10954782, rs11002051, rs11022778, rs11029892,
rs11029907, rs11029928, rs11083404, rs11085044, rs11136970,
rs11147439, rs11192461, rs11192469, rs11559024, rs1157449,
rs11648129, rs11691553, rs12013377, rs12494712, rs12943140,
rs13002663, rs13394010, rs13415334, rs13419758, rs1380706,
rs1387768, rs1410779, rs1478682, rs1508102, rs1532365, rs1544352,
rs1545223, rs1579771, rs1604169, rs1621509, rs1644418,
rs16886004, rs16895510, rs16901784, rs16927077, rs16930057,
rs17029538, rs17224858, rs17238927, rs17329014, rs17400875,
rs17449018, rs17577980, rs17638791, rs1858973, rs1886214,
rs1894406, rs1894407, rs1894408, rs196295, rs196341, rs196343,
rs197523, rs1979992, rs1979993, rs2043136, rs2058742, rs2071469,
rs2071470, rs2071472, rs2074037, rs2136408, rs2139612, rs2175121,
rs2241883, rs2309760, rs2325911, rs241435, rs241440, rs241442,
rs241443, rs241444, rs241445, rs241446, rs241447, rs241449,
rs241451, rs241452, rs241453, rs241454, rs241456, rs2453478,
rs2598360, rs2621321, rs2621323, rs2660214, rs2816838, rs2824070,
rs2839117, rs2845371, rs2857101, rs2857103, rs2857104, rs2926455,
rs2934491, rs3135388, rs3218328, rs343087, rs343092, rs3767955,
rs3792135, rs3799383, rs3803277, rs3815822, rs3818675, rs3829539,
rs3885907, rs3899755, rs4075692, rs4143493, rs419132, rs423239,
rs4254166, rs4356336, rs4360791, rs4449139, rs4584668, rs4669694,
rs4709792, rs4738738, rs4769060, rs4780822, rs4782279, rs4822644,
rs484482, rs4894701, rs5024722, rs502530, rs543122, rs6032205,
rs6032209, rs6110157, rs623011, rs6497396, rs6535882, rs6687976,
rs6718758, rs6835202, rs6840089, rs6845927, rs6895094, rs6899068,
rs7020402, rs7024953, rs7028906, rs7029123, rs7062312, rs714342,
rs7187976, rs7191155, rs720176, rs7217872, rs7228827, rs7348267,
rs7496451, rs7524868, rs7563131, rs7579987, rs759458, rs7666442,
rs7670525, rs7672014, rs7677801, rs7725112, rs7844274, rs7850,
rs7860748, rs7862565, rs7864679, rs7928078, rs7948420, rs8035826,
rs8050872, rs8053136, rs8055485, rs823829, rs858341, rs9315047,
rs931570, rs9346979, rs9376361, rs9393727, rs9501224, rs9508832,

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rs950928, rs9579566, rs9597498, rs9670531, rs9671124, rs9671182, rs9817308, rs9834010, rs9876830, rs9913349, rs9931167 and rs9931211.

43. A kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the kit comprising at least one pair of PCR primers designed to amplify a DNA segment which includes the location of a SNP selected from the group consisting of kgp10090631, kgp1009249, kgp10152733, kgp10224254, kgp10305127, kgp10351364, kgp10372946, kgp10404633, kgp10412303, kgp10523170, kgp1054273, kgp10558725, kgp10564659, kgp10591989, kgp10594414, kgp10619195, kgp10620244, kgp10632945, kgp10633631, kgp10679353, kgp10788130, kgp10826273, kgp10910719, kgp10922969, kgp10948564, kgp10967046, kgp10974833, kgp1098237, kgp11002881, kgp11010680, kgp11077373, kgp11141512, kgp11206453, kgp11210903, kgp1124492, kgp11281589, kgp11285862, kgp11328629, kgp11356379, kgp11407560, kgp11453406, kgp11467007, kgp11514107, kgp11543962, kgp11580695, kgp11627530, kgp11633966, kgp11686146, kgp11702474, kgp11711524, kgp11768533, kgp11804835, kgp11843177, kgp12008955, kgp12083934, kgp12182745, kgp12230354, kgp1224440, kgp12371757, kgp124162, kgp12426624, kgp12557319, kgp1285441, kgp13161760, kgp1355977, kgp1371881, kgp15390522, kgp1683448, kgp1688752, kgp1699628, kgp1753445, kgp1779254, kgp1786079, kgp18379774, kgp18432055, kgp18525257, kgp1912531, kgp19568724, kgp20163979, kgp2023214, kgp2045074, kgp20478926, kgp2092817, kgp21171930, kgp2245775, kgp2262166, kgp22778566, kgp22793211, kgp22811918, kgp22823022, kgp2282938, kgp2299675, kgp23298674, kgp2356388, kgp23672937, kgp23737989, kgp2388352, kgp2391411, kgp24131116, kgp24415534, kgp2446153, kgp2451249, kgp2465184, kgp24729706, kgp24753470, kgp25191871, kgp25216186, kgp25543811, kgp25921291, kgp25952891, kgp26026546, kgp26271158, kgp2638591, kgp26528455, kgp26533576, kgp2688306, kgp26995430, kgp270001, kgp2709692, kgp2715873, kgp27500525, kgp27571222, kgp27640141, kgp2788291, kgp279772, kgp28532436, kgp28586329, kgp28687699, kgp28817122,

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kgp2923815, kgp29367521, kgp293787, kgp2958113, kgp2959751,
kgp297178, kgp29794723, kgp30282494, kgp3048169, kgp304921,
kgp3182607, kgp3202939, kgp3205849, kgp3218351, kgp3267884,
kgp3276689, kgp337461, kgp3418770, kgp3450875, kgp345301,
kgp3477351, kgp3496814, kgp355027, kgp355723, kgp3593828,
kgp3598409, kgp3651767, kgp3669685, kgp3730395, kgp3812034,
kgp3854180, kgp3933330, kgp3951463, kgp3984567, kgp3991733,
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kgp4420791, kgp4479467, kgp4524468, kgp4543470, kgp4559907,
kgp4573213, kgp4634875, kgp4705854, kgp4734301, kgp4755147,
kgp4812831, kgp4842590, kgp485316, kgp487328, kgp4898179,
kgp5002011, kgp5014707, kgp5017029, kgp5053636, kgp5068397,
kgp512180, kgp5144181, kgp5159037, kgp5216209, kgp5292386,
kgp5334779, kgp5388938, kgp5409955, kgp5440506, kgp5441587,
kgp5483926, kgp55646, kgp5564995, kgp5579170, kgp5680955,
kgp5869992, kgp5908616, kgp6023196, kgp6032617, kgp6038357,
kgp6076976, kgp6091119, kgp6127371, kgp61811, kgp6190988,
kgp6214351, kgp6228750, kgp6236949, kgp6469620, kgp6505544,
kgp6507761, kgp652534, kgp6539666, kgp6567154, kgp6599438,
kgp6603796, kgp6666134, kgp6700691, kgp6737096, kgp6768546,
kgp6772915, kgp6835138, kgp6959492, kgp6996560, kgp7059449,
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kgp7792268, kgp7802182, kgp7804623, kgp7924485, kgp8030775,
kgp8036704, kgp8046214, kgp8106690, kgp8107491, kgp8110667,
kgp8169636, kgp8174785, kgp8178358, kgp8183049, kgp8192546,
kgp8200264, kgp8303520, kgp8335515, kgp8372910, kgp841428,
kgp8437961, kgp8440036, kgp85534, kgp8599417, kgp8602316,
kgp8615910, kgp8767692, kgp8777935, kgp8793915, kgp8796185,
kgp8817856, kgp8869954, kgp8990121, kgp9018750, kgp9071686,
kgp9078300, kgp9320791, kgp9354462, kgp9354820, kgp9368119,
kgp9410843, kgp9421884, kgp9450430, kgp9530088, kgp9551947,

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kgp9601362, kgp9627338, kgp9627406, kgp9669946, kgp9699754,
kgp971582, kgp97310, kgp974569, kgp9795732, kgp9806386,
kgp9854133, kgp9884626, rs10049206, rs10124492, rs10125298,
rs10162089, rs10201643, rs10203396, rs10251797, rs10278591,
rs10489312, rs10492882, rs10498793, rs10501082, rs10510774,
rs10512340, rs1079303, rs10815160, rs10816302, rs10841322,
rs10841337, rs10954782, rs11002051, rs11022778, rs11029892,
rs11029907, rs11029928, rs11083404, rs11085044, rs11136970,
rs11147439, rs11192461, rs11192469, rs11559024, rs1157449,
rs11648129, rs11691553, rs12013377, rs12494712, rs12943140,
rs13002663, rs13394010, rs13415334, rs13419758, rs1380706,
rs1387768, rs1410779, rs1478682, rs1508102, rs1532365, rs1544352,
rs1545223, rs1579771, rs1604169, rs1621509, rs1644418,
rs16886004, rs16895510, rs16901784, rs16927077, rs16930057,
rs17029538, rs17224858, rs17238927, rs17329014, rs17400875,
rs17449018, rs17577980, rs17638791, rs1858973, rs1886214,
rs1894406, rs1894407, rs1894408, rs196295, rs196341, rs196343,
rs197523, rs1979992, rs1979993, rs2043136, rs2058742, rs2071469,
rs2071470, rs2071472, rs2074037, rs2136408, rs2139612, rs2175121,
rs2241883, rs2309760, rs2325911, rs241435, rs241440, rs241442,
rs241443, rs241444, rs241445, rs241446, rs241447, rs241449,
rs241451, rs241452, rs241453, rs241454, rs241456, rs2453478,
rs2598360, rs2621321, rs2621323, rs2660214, rs2816838, rs2824070,
rs2839117, rs2845371, rs2857101, rs2857103, rs2857104, rs2926455,
rs2934491, rs3135388, rs3218328, rs343087, rs343092, rs3767955,
rs3792135, rs3799383, rs3803277, rs3815822, rs3818675, rs3829539,
rs3885907, rs3899755, rs4075692, rs4143493, rs419132, rs423239,
rs4254166, rs4356336, rs4360791, rs4449139, rs4584668, rs4669694,
rs4709792, rs4738738, rs4769060, rs4780822, rs4782279, rs4822644,
rs484482, rs4894701, rs5024722, rs502530, rs543122, rs6032205,
rs6032209, rs6110157, rs623011, rs6497396, rs6535882, rs6687976,
rs6718758, rs6835202, rs6840089, rs6845927, rs6895094, rs6899068,
rs7020402, rs7024953, rs7028906, rs7029123, rs7062312, rs714342,
rs7187976, rs7191155, rs720176, rs7217872, rs7228827, rs7348267,
rs7496451, rs7524868, rs7563131, rs7579987, rs759458, rs7666442,

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rs7670525, rs7672014, rs7677801, rs7725112, rs7844274, rs7850, rs7860748, rs7862565, rs7864679, rs7928078, rs7948420, rs8035826, rs8050872, rs8053136, rs8055485, rs823829, rs858341, rs9315047, rs931570, rs9346979, rs9376361, rs9393727, rs9501224, rs9508832, rs950928, rs9579566, rs9597498, rs9670531, rs9671124, rs9671182, rs9817308, rs9834010, rs9876830, rs9913349, rs9931167 and rs9931211.

44. A kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the kit comprising a reagent for performing a method selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of mismatch (CCM), gene chip and denaturing high performance liquid chromatography (DHPLC) for determining the genotype of the subject at a location corresponding to the location of at least one SNP selected from the group consisting of kgp10090631, kgp1009249, kgp10152733, kgp10224254, kgp10305127, kgp10351364, kgp10372946, kgp10404633, kgp10412303, kgp10523170, kgp1054273, kgp10558725, kgp10564659, kgp10591989, kgp10594414, kgp10619195, kgp10620244, kgp10632945, kgp10633631, kgp10679353, kgp10788130, kgp10826273, kgp10910719, kgp10922969, kgp10948564, kgp10967046, kgp10974833, kgp1098237, kgp11002881, kgp11010680, kgp11077373, kgp11141512, kgp11206453, kgp11210903, kgp1124492, kgp11281589, kgp11285862, kgp11328629, kgp11356379, kgp11407560, kgp11453406, kgp11467007, kgp11514107, kgp11543962, kgp11580695, kgp11627530, kgp11633966, kgp11686146, kgp11702474, kgp11711524, kgp11768533, kgp11804835, kgp11843177, kgp12008955, kgp12083934, kgp12182745, kgp12230354, kgp1224440, kgp12371757, kgp124162, kgp12426624, kgp12557319, kgp1285441, kgp13161760, kgp1355977, kgp1371881, kgp15390522, kgp1683448, kgp1688752, kgp1699628, kgp1753445, kgp1779254, kgp1786079, kgp18379774, kgp18432055, kgp18525257, kgp1912531, kgp19568724, kgp20163979, kgp2023214, kgp2045074, kgp20478926, kgp2092817,

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kgp21171930, kgp2245775, kgp2262166, kgp22778566, kgp22793211,
kgp22811918, kgp22823022, kgp2282938, kgp2299675, kgp23298674,
kgp2356388, kgp23672937, kgp23737989, kgp2388352, kgp2391411,
kgp24131116, kgp24415534, kgp2446153, kgp2451249, kgp2465184,
kgp24729706, kgp24753470, kgp25191871, kgp25216186, kgp25543811,
kgp25921291, kgp25952891, kgp26026546, kgp26271158, kgp2638591,
kgp26528455, kgp26533576, kgp2688306, kgp26995430, kgp270001,
kgp2709692, kgp2715873, kgp27500525, kgp27571222, kgp27640141,
kgp2788291, kgp279772, kgp28532436, kgp28586329, kgp28687699,
kgp28817122, kgp2923815, kgp29367521, kgp293787, kgp2958113,
kgp2959751, kgp297178, kgp29794723, kgp30282494, kgp3048169,
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kgp3593828, kgp3598409, kgp3651767, kgp3669685, kgp3730395,
kgp3812034, kgp3854180, kgp3933330, kgp3951463, kgp3984567,
kgp3991733, kgp4011779, kgp4056892, kgp4096263, kgp4127859,
kgp4155998, kgp4162414, kgp4223880, kgp4346717, kgp4370912,
kgp4418535, kgp4420791, kgp4479467, kgp4524468, kgp4543470,
kgp4559907, kgp4573213, kgp4634875, kgp4705854, kgp4734301,
kgp4755147, kgp4812831, kgp4842590, kgp485316, kgp487328,
kgp4898179, kgp5002011, kgp5014707, kgp5017029, kgp5053636,
kgp5068397, kgp512180, kgp5144181, kgp5159037, kgp5216209,
kgp5292386, kgp5334779, kgp5388938, kgp5409955, kgp5440506,
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kgp7121374, kgp7178233, kgp7181058, kgp7186699, kgp7189498,
kgp7242489, kgp7331172, kgp7416024, kgp7481870, kgp7506434,
kgp7521990, kgp759150, kgp767200, kgp7714238, kgp7730397,

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kgp7747883, kgp7792268, kgp7802182, kgp7804623, kgp7924485,
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kgp9551947, kgp9601362, kgp9627338, kgp9627406, kgp9669946,
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rs10278591, rs10489312, rs10492882, rs10498793, rs10501082,
rs10510774, rs10512340, rs1079303, rs10815160, rs10816302,
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rs11136970, rs11147439, rs11192461, rs11192469, rs11559024,
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rs12943140, rs13002663, rs13394010, rs13415334, rs13419758,
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rs2839117, rs2845371, rs2857101, rs2857103, rs2857104, rs2926455,
rs2934491, rs3135388, rs3218328, rs343087, rs343092, rs3767955,
rs3792135, rs3799383, rs3803277, rs3815822, rs3818675, rs3829539,

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rs3885907, rs3899755, rs4075692, rs4143493, rs419132, rs423239, rs4254166, rs4356336, rs4360791, rs4449139, rs4584668, rs4669694, rs4709792, rs4738738, rs4769060, rs4780822, rs4782279, rs4822644, rs484482, rs4894701, rs5024722, rs502530, rs543122, rs6032205, rs6032209, rs6110157, rs623011, rs6497396, rs6535882, rs6687976, rs6718758, rs6835202, rs6840089, rs6845927, rs6895094, rs6899068, rs7020402, rs7024953, rs7028906, rs7029123, rs7062312, rs714342, rs7187976, rs7191155, rs720176, rs7217872, rs7228827, rs7348267, rs7496451, rs7524868, rs7563131, rs7579987, rs759458, rs7666442, rs7670525, rs7672014, rs7677801, rs7725112, rs7844274, rs7850, rs7860748, rs7862565, rs7864679, rs7928078, rs7948420, rs8035826, rs8050872, rs8053136, rs8055485, rs823829, rs858341, rs9315047, rs931570, rs9346979, rs9376361, rs9393727, rs9501224, rs9508832, rs950928, rs9579566, rs9597498, rs9670531, rs9671124, rs9671182, rs9817308, rs9834010, rs9876830, rs9913349, rs9931167 and rs9931211.

45. The kit of claim 44, wherein the gene chip is a whole genome genotyping array.

46. The kit of any one of claims 42-45, the kit comprising

- (i) at least one pair of PCR primers designed to amplify a DNA segment which includes the location a SNP selected from the group consisting of kgp10090631, kgp1009249, kgp10152733, kgp10224254, kgp10305127, kgp10351364, kgp10372946, kgp10404633, kgp10412303, kgp10523170, kgp1054273, kgp10558725, kgp10564659, kgp10591989, kgp10594414, kgp10619195, kgp10620244, kgp10632945, kgp10633631, kgp10679353, kgp10788130, kgp10826273, kgp10910719, kgp10922969, kgp10948564, kgp10967046, kgp10974833, kgp1098237, kgp11002881, kgp11010680, kgp11077373, kgp11141512, kgp11206453, kgp11210903, kgp1124492, kgp11281589, kgp11285862, kgp11328629, kgp11356379, kgp11407560, kgp11453406, kgp11467007, kgp11514107, kgp11543962, kgp11580695, kgp11627530, kgp11633966, kgp11686146, kgp11702474, kgp11711524, kgp11768533,

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kgp11804835, kgp11843177, kgp12008955, kgp12083934,
kgp12182745, kgp12230354, kgp1224440, kgp12371757,
kgp124162, kgp12426624, kgp12557319, kgp1285441,
kgp13161760, kgp1355977, kgp1371881, kgp15390522,
kgp1683448, kgp1688752, kgp1699628, kgp1753445, kgp1779254,
kgp1786079, kgp18379774, kgp18432055, kgp18525257,
kgp1912531, kgp19568724, kgp20163979, kgp2023214,
kgp2045074, kgp20478926, kgp2092817, kgp21171930,
kgp2245775, kgp2262166, kgp22778566, kgp22793211,
kgp22811918, kgp22823022, kgp2282938, kgp2299675,
kgp23298674, kgp2356388, kgp23672937, kgp23737989,
kgp2388352, kgp2391411, kgp24131116, kgp24415534,
kgp2446153, kgp2451249, kgp2465184, kgp24729706,
kgp24753470, kgp25191871, kgp25216186, kgp25543811,
kgp25921291, kgp25952891, kgp26026546, kgp26271158,
kgp2638591, kgp26528455, kgp26533576, kgp2688306,
kgp26995430, kgp270001, kgp2709692, kgp2715873, kgp27500525,
kgp27571222, kgp27640141, kgp2788291, kgp279772,
kgp28532436, kgp28586329, kgp28687699, kgp28817122,
kgp2923815, kgp29367521, kgp293787, kgp2958113, kgp2959751,
kgp297178, kgp29794723, kgp30282494, kgp3048169, kgp304921,
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kgp5002011, kgp5014707, kgp5017029, kgp5053636, kgp5068397,
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kgp5483926, kgp55646, kgp5564995, kgp5579170, kgp5680955,

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kgp8036704, kgp8046214, kgp8106690, kgp8107491, kgp8110667,
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rs11147439, rs11192461, rs11192469, rs11559024, rs1157449,
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rs1644418, rs16886004, rs16895510, rs16901784, rs16927077,
rs16930057, rs17029538, rs17224858, rs17238927, rs17329014,
rs17400875, rs17449018, rs17577980, rs17638791, rs1858973,

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rs1886214, rs1894406, rs1894407, rs1894408, rs196295,
 rs196341, rs196343, rs197523, rs1979992, rs1979993,
 rs2043136, rs2058742, rs2071469, rs2071470, rs2071472,
 rs2074037, rs2136408, rs2139612, rs2175121, rs2241883,
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 rs2824070, rs2839117, rs2845371, rs2857101, rs2857103,
 rs2857104, rs2926455, rs2934491, rs3135388, rs3218328,
 rs343087, rs343092, rs3767955, rs3792135, rs3799383,
 rs3803277, rs3815822, rs3818675, rs3829539, rs3885907,
 rs3899755, rs4075692, rs4143493, rs419132, rs423239,
 rs4254166, rs4356336, rs4360791, rs4449139, rs4584668,
 rs4669694, rs4709792, rs4738738, rs4769060, rs4780822,
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 rs623011, rs6497396, rs6535882, rs6687976, rs6718758,
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 rs714342, rs7187976, rs7191155, rs720176, rs7217872,
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 rs7579987, rs759458, rs7666442, rs7670525, rs7672014,
 rs7677801, rs7725112, rs7844274, rs7850, rs7860748,
 rs7862565, rs7864679, rs7928078, rs7948420, rs8035826,
 rs8050872, rs8053136, rs8055485, rs823829, rs858341,
 rs9315047, rs931570, rs9346979, rs9376361, rs9393727,
 rs9501224, rs9508832, rs950928, rs9579566, rs9597498,
 rs9670531, rs9671124, rs9671182, rs9817308, rs9834010,
 rs9876830, rs9913349, rs9931167 and rs9931211, and

- (ii) at least one probe specific for the location of a SNP selected from the group consisting of kgp10090631, kgp1009249, kgp10152733, kgp10224254, kgp10305127, kgp10351364, kgp10372946, kgp10404633, kgp10412303, kgp10523170, kgp1054273, kgp10558725, kgp10564659,

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kgp10591989, kgp10594414, kgp10619195, kgp10620244,
kgp10632945, kgp10633631, kgp10679353, kgp10788130,
kgp10826273, kgp10910719, kgp10922969, kgp10948564,
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kgp11010680, kgp11077373, kgp11141512, kgp11206453,
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kgp11328629, kgp11356379, kgp11407560, kgp11453406,
kgp11467007, kgp11514107, kgp11543962, kgp11580695,
kgp11627530, kgp11633966, kgp11686146, kgp11702474,
kgp11711524, kgp11768533, kgp11804835, kgp11843177,
kgp12008955, kgp12083934, kgp12182745, kgp12230354,
kgp1224440, kgp12371757, kgp124162, kgp12426624,
kgp12557319, kgp1285441, kgp13161760, kgp1355977,
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kgp1753445, kgp1779254, kgp1786079, kgp18379774,
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kgp2092817, kgp21171930, kgp2245775, kgp2262166,
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kgp26533576, kgp2688306, kgp26995430, kgp270001, kgp2709692,
kgp2715873, kgp27500525, kgp27571222, kgp27640141,
kgp2788291, kgp279772, kgp28532436, kgp28586329,
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kgp3205849, kgp3218351, kgp3267884, kgp3276689, kgp337461,
kgp3418770, kgp3450875, kgp345301, kgp3477351, kgp3496814,
kgp355027, kgp355723, kgp3593828, kgp3598409, kgp3651767,
kgp3669685, kgp3730395, kgp3812034, kgp3854180, kgp3933330,

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kgp3951463, kgp3984567, kgp3991733, kgp4011779, kgp4056892,
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rs10815160, rs10816302, rs10841322, rs10841337, rs10954782,

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rs11002051, rs11022778, rs11029892, rs11029907, rs11029928,
rs11083404, rs11085044, rs11136970, rs11147439, rs11192461,
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rs4143493, rs419132, rs423239, rs4254166, rs4356336,
rs4360791, rs4449139, rs4584668, rs4669694, rs4709792,
rs4738738, rs4769060, rs4780822, rs4782279, rs4822644,
rs484482, rs4894701, rs5024722, rs502530, rs543122,
rs6032205, rs6032209, rs6110157, rs623011, rs6497396,
rs6535882, rs6687976, rs6718758, rs6835202, rs6840089,
rs6845927, rs6895094, rs6899068, rs7020402, rs7024953,
rs7028906, rs7029123, rs7062312, rs714342, rs7187976,
rs7191155, rs720176, rs7217872, rs7228827, rs7348267,
rs7496451, rs7524868, rs7563131, rs7579987, rs759458,
rs7666442, rs7670525, rs7672014, rs7677801, rs7725112,
rs7844274, rs7850, rs7860748, rs7862565, rs7864679,
rs7928078, rs7948420, rs8035826, rs8050872, rs8053136,

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rs8055485, rs823829, rs858341, rs9315047, rs931570,
rs9346979, rs9376361, rs9393727, rs9501224, rs9508832,
rs950928, rs9579566, rs9597498, rs9670531, rs9671124,
rs9671182, rs9817308, rs9834010, rs9876830, rs9913349,
rs9931167 and rs9931211.

47. A kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the kit comprising reagents for TaqMan Open Array assay designed for determining the genotype of the subject at a location corresponding to the location of at least one SNP selected from the group consisting of kgp10090631, kgp1009249, kgp10152733, kgp10224254, kgp10305127, kgp10351364, kgp10372946, kgp10404633, kgp10412303, kgp10523170, kgp1054273, kgp10558725, kgp10564659, kgp10591989, kgp10594414, kgp10619195, kgp10620244, kgp10632945, kgp10633631, kgp10679353, kgp10788130, kgp10826273, kgp10910719, kgp10922969, kgp10948564, kgp10967046, kgp10974833, kgp1098237, kgp11002881, kgp11010680, kgp11077373, kgp11141512, kgp11206453, kgp11210903, kgp1124492, kgp11281589, kgp11285862, kgp11328629, kgp11356379, kgp11407560, kgp11453406, kgp11467007, kgp11514107, kgp11543962, kgp11580695, kgp11627530, kgp11633966, kgp11686146, kgp11702474, kgp11711524, kgp11768533, kgp11804835, kgp11843177, kgp12008955, kgp12083934, kgp12182745, kgp12230354, kgp1224440, kgp12371757, kgp124162, kgp12426624, kgp12557319, kgp1285441, kgp13161760, kgp1355977, kgp1371881, kgp15390522, kgp1683448, kgp1688752, kgp1699628, kgp1753445, kgp1779254, kgp1786079, kgp18379774, kgp18432055, kgp18525257, kgp1912531, kgp19568724, kgp20163979, kgp2023214, kgp2045074, kgp20478926, kgp2092817, kgp21171930, kgp2245775, kgp2262166, kgp22778566, kgp22793211, kgp22811918, kgp22823022, kgp2282938, kgp2299675, kgp23298674, kgp2356388, kgp23672937, kgp23737989, kgp2388352, kgp2391411, kgp24131116, kgp24415534, kgp2446153, kgp2451249, kgp2465184, kgp24729706, kgp24753470, kgp25191871, kgp25216186, kgp25543811, kgp25921291, kgp25952891, kgp26026546, kgp26271158, kgp2638591, kgp26528455, kgp26533576, kgp2688306,

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kgp26995430, kgp270001, kgp2709692, kgp2715873, kgp27500525,
kgp27571222, kgp27640141, kgp2788291, kgp279772, kgp28532436,
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kgp293787, kgp2958113, kgp2959751, kgp297178, kgp29794723,
kgp30282494, kgp3048169, kgp304921, kgp3182607, kgp3202939,
kgp3205849, kgp3218351, kgp3267884, kgp3276689, kgp337461,
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kgp355027, kgp355723, kgp3593828, kgp3598409, kgp3651767,
kgp3669685, kgp3730395, kgp3812034, kgp3854180, kgp3933330,
kgp3951463, kgp3984567, kgp3991733, kgp4011779, kgp4056892,
kgp4096263, kgp4127859, kgp4155998, kgp4162414, kgp4223880,
kgp4346717, kgp4370912, kgp4418535, kgp4420791, kgp4479467,
kgp4524468, kgp4543470, kgp4559907, kgp4573213, kgp4634875,
kgp4705854, kgp4734301, kgp4755147, kgp4812831, kgp4842590,
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kgp5017029, kgp5053636, kgp5068397, kgp512180, kgp5144181,
kgp5159037, kgp5216209, kgp5292386, kgp5334779, kgp5388938,
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kgp5564995, kgp5579170, kgp5680955, kgp5869992, kgp5908616,
kgp6023196, kgp6032617, kgp6038357, kgp6076976, kgp6091119,
kgp6127371, kgp61811, kgp6190988, kgp6214351, kgp6228750,
kgp6236949, kgp6469620, kgp6505544, kgp6507761, kgp652534,
kgp6539666, kgp6567154, kgp6599438, kgp6603796, kgp6666134,
kgp6700691, kgp6737096, kgp6768546, kgp6772915, kgp6835138,
kgp6959492, kgp6996560, kgp7059449, kgp7063887, kgp7077322,
kgp7092772, kgp7117398, kgp7121374, kgp7178233, kgp7181058,
kgp7186699, kgp7189498, kgp7242489, kgp7331172, kgp7416024,
kgp7481870, kgp7506434, kgp7521990, kgp759150, kgp767200,
kgp7714238, kgp7730397, kgp7747883, kgp7792268, kgp7802182,
kgp7804623, kgp7924485, kgp8030775, kgp8036704, kgp8046214,
kgp8106690, kgp8107491, kgp8110667, kgp8169636, kgp8174785,
kgp8178358, kgp8183049, kgp8192546, kgp8200264, kgp8303520,
kgp8335515, kgp8372910, kgp841428, kgp8437961, kgp8440036,
kgp85534, kgp8599417, kgp8602316, kgp8615910, kgp8767692,
kgp8777935, kgp8793915, kgp8796185, kgp8817856, kgp8869954,

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kgp8990121, kgp9018750, kgp9071686, kgp9078300, kgp9320791,
kgp9354462, kgp9354820, kgp9368119, kgp9410843, kgp9421884,
kgp9450430, kgp9530088, kgp9551947, kgp9601362, kgp9627338,
kgp9627406, kgp9669946, kgp9699754, kgp971582, kgp97310,
kgp974569, kgp9795732, kgp9806386, kgp9854133, kgp9884626,
rs10049206, rs10124492, rs10125298, rs10162089, rs10201643,
rs10203396, rs10251797, rs10278591, rs10489312, rs10492882,
rs10498793, rs10501082, rs10510774, rs10512340, rs1079303,
rs10815160, rs10816302, rs10841322, rs10841337, rs10954782,
rs11002051, rs11022778, rs11029892, rs11029907, rs11029928,
rs11083404, rs11085044, rs11136970, rs11147439, rs11192461,
rs11192469, rs11559024, rs1157449, rs11648129, rs11691553,
rs12013377, rs12494712, rs12943140, rs13002663, rs13394010,
rs13415334, rs13419758, rs1380706, rs1387768, rs1410779,
rs1478682, rs1508102, rs1532365, rs1544352, rs1545223,
rs1579771, rs1604169, rs1621509, rs1644418, rs16886004,
rs16895510, rs16901784, rs16927077, rs16930057, rs17029538,
rs17224858, rs17238927, rs17329014, rs17400875, rs17449018,
rs17577980, rs17638791, rs1858973, rs1886214, rs1894406,
rs1894407, rs1894408, rs196295, rs196341, rs196343, rs197523,
rs1979992, rs1979993, rs2043136, rs2058742, rs2071469,
rs2071470, rs2071472, rs2074037, rs2136408, rs2139612,
rs2175121, rs2241883, rs2309760, rs2325911, rs241435, rs241440,
rs241442, rs241443, rs241444, rs241445, rs241446, rs241447,
rs241449, rs241451, rs241452, rs241453, rs241454, rs241456,
rs2453478, rs2598360, rs2621321, rs2621323, rs2660214,
rs2816838, rs2824070, rs2839117, rs2845371, rs2857101,
rs2857103, rs2857104, rs2926455, rs2934491, rs3135388,
rs3218328, rs343087, rs343092, rs3767955, rs3792135, rs3799383,
rs3803277, rs3815822, rs3818675, rs3829539, rs3885907,
rs3899755, rs4075692, rs4143493, rs419132, rs423239, rs4254166,
rs4356336, rs4360791, rs4449139, rs4584668, rs4669694,
rs4709792, rs4738738, rs4769060, rs4780822, rs4782279,
rs4822644, rs484482, rs4894701, rs5024722, rs502530, rs543122,
rs6032205, rs6032209, rs6110157, rs623011, rs6497396, rs6535882,

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rs6687976, rs6718758, rs6835202, rs6840089, rs6845927,
rs6895094, rs6899068, rs7020402, rs7024953, rs7028906,
rs7029123, rs7062312, rs714342, rs7187976, rs7191155, rs720176,
rs7217872, rs7228827, rs7348267, rs7496451, rs7524868,
rs7563131, rs7579987, rs759458, rs7666442, rs7670525, rs7672014,
rs7677801, rs7725112, rs7844274, rs7850, rs7860748, rs7862565,
rs7864679, rs7928078, rs7948420, rs8035826, rs8050872,
rs8053136, rs8055485, rs823829, rs858341, rs9315047, rs931570,
rs9346979, rs9376361, rs9393727, rs9501224, rs9508832, rs950928,
rs9579566, rs9597498, rs9670531, rs9671124, rs9671182,
rs9817308, rs9834010, rs9876830, rs9913349, rs9931167 and
rs9931211.

48. The kit of any of claims 42-47, further comprising instructions for use of the kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate.

49. The kit of any one of claims 42-48, wherein the one or more single nucleotide polymorphisms (SNPs) are selected from the group consisting of kgp24415534, kgp6214351, kgp6599438, kgp7747883, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, and rs759458.

50. The kit of claim 49, wherein the one or more single nucleotide polymorphisms (SNPs) comprise 2, 3, 4, 5, 6, 7, 8, 9 or 10 of the SNPs selected from the group consisting of kgp24415534, kgp6214351, kgp6599438, kgp7747883, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, and rs759458.

51. The kit of claim 49 or 50, wherein if rs3135391 is the one SNP selected, then selecting at least one SNP other than rs3135391.

52. The kit of claims 42-48, wherein the one or more SNPs is selected from the group consisting of kgp24415534, kgp6214351,

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kgp6599438, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, and rs759458.

53. The kit of claim 52, wherein the one or more SNPs comprise 2, 3, 4, 5, 6, 7, 8, 9 or 10 of the SNPs selected from the group consisting of kgp24415534, kgp6214351, kgp6599438, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, and rs759458.

54. The method of claim 52 or 53, wherein if rs3135391 is the one SNP selected, then selecting at least one SNP other than rs3135391.

55. A kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate, the kit comprising

- a) at least one probe specific for a location corresponding to the location of at least one SNP;
- b) at least one pair of PCR primers designed to amplify a DNA segment which includes a location corresponding to the location of at least one SNP;
- c) at least one pair of PCR primers designed to amplify a DNA segment which includes a location corresponding to the location of at least one SNP and at least one probe specific for a location corresponding to the location of at least one SNP;
- d) a reagent for performing a method selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of mismatch (CCM), gene chip and denaturing high performance liquid chromatography (DHPLC) for determining the identity of at least one SNP; or

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e) reagents for TaqMan Open Array assay designed for determining the genotype at a location corresponding to the location of at least one SNP,

wherein the at least one SNP is selected from the group consisting of kgp10090631, kgp1009249, kgp10152733, kgp10224254, kgp10305127, kgp10351364, kgp10372946, kgp10404633, kgp10412303, kgp10523170, kgp1054273, kgp10558725, kgp10564659, kgp10591989, kgp10594414, kgp10619195, kgp10620244, kgp10632945, kgp10633631, kgp10679353, kgp10788130, kgp10826273, kgp10910719, kgp10922969, kgp10948564, kgp10967046, kgp10974833, kgp1098237, kgp11002881, kgp11010680, kgp11077373, kgp11141512, kgp11206453, kgp11210903, kgp1124492, kgp11281589, kgp11285862, kgp11328629, kgp11356379, kgp11407560, kgp11453406, kgp11467007, kgp11514107, kgp11543962, kgp11580695, kgp11627530, kgp11633966, kgp11686146, kgp11702474, kgp11711524, kgp11768533, kgp11804835, kgp11843177, kgp12008955, kgp12083934, kgp12182745, kgp12230354, kgp1224440, kgp12371757, kgp124162, kgp12426624, kgp12557319, kgp1285441, kgp13161760, kgp1355977, kgp1371881, kgp15390522, kgp1683448, kgp1688752, kgp1699628, kgp1753445, kgp1779254, kgp1786079, kgp18379774, kgp18432055, kgp18525257, kgp1912531, kgp19568724, kgp20163979, kgp2023214, kgp2045074, kgp20478926, kgp2092817, kgp21171930, kgp2245775, kgp2262166, kgp22778566, kgp22793211, kgp22811918, kgp22823022, kgp2282938, kgp2299675, kgp23298674, kgp2356388, kgp23672937, kgp23737989, kgp2388352, kgp2391411, kgp24131116, kgp24415534, kgp2446153, kgp2451249, kgp2465184, kgp24729706, kgp24753470, kgp25191871, kgp25216186, kgp25543811, kgp25921291, kgp25952891, kgp26026546, kgp26271158, kgp2638591, kgp26528455, kgp26533576, kgp2688306, kgp26995430, kgp270001, kgp2709692, kgp2715873, kgp27500525, kgp27571222, kgp27640141, kgp2788291, kgp279772, kgp28532436, kgp28586329, kgp28687699, kgp28817122, kgp2923815, kgp29367521, kgp293787, kgp2958113, kgp2959751, kgp297178, kgp29794723, kgp30282494, kgp3048169, kgp304921, kgp3182607, kgp3202939, kgp3205849, kgp3218351, kgp3267884, kgp3276689, kgp337461, kgp3418770, kgp3450875, kgp345301, kgp3477351, kgp3496814, kgp355027, kgp355723, kgp3593828,

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kgp3598409,	kgp3651767,	kgp3669685,	kgp3730395,	kgp3812034,
kgp3854180,	kgp3933330,	kgp3951463,	kgp3984567,	kgp3991733,
kgp4011779,	kgp4056892,	kgp4096263,	kgp4127859,	kgp4155998,
kgp4162414,	kgp4223880,	kgp4346717,	kgp4370912,	kgp4418535,
kgp4420791,	kgp4479467,	kgp4524468,	kgp4543470,	kgp4559907,
kgp4573213,	kgp4634875,	kgp4705854,	kgp4734301,	kgp4755147,
kgp4812831,	kgp4842590,	kgp485316,	kgp487328,	kgp4898179,
kgp5002011,	kgp5014707,	kgp5017029,	kgp5053636,	kgp5068397,
kgp512180,	kgp5144181,	kgp5159037,	kgp5216209,	kgp5292386,
kgp5334779,	kgp5388938,	kgp5409955,	kgp5440506,	kgp5441587,
kgp5483926,	kgp55646,	kgp5564995,	kgp5579170,	kgp5680955,
kgp5869992,	kgp5908616,	kgp6023196,	kgp6032617,	kgp6038357,
kgp6076976,	kgp6091119,	kgp6127371,	kgp61811,	kgp6190988,
kgp6214351,	kgp6228750,	kgp6236949,	kgp6469620,	kgp6505544,
kgp6507761,	kgp652534,	kgp6539666,	kgp6567154,	kgp6599438,
kgp6603796,	kgp6666134,	kgp6700691,	kgp6737096,	kgp6768546,
kgp6772915,	kgp6835138,	kgp6959492,	kgp6996560,	kgp7059449,
kgp7063887,	kgp7077322,	kgp7092772,	kgp7117398,	kgp7121374,
kgp7178233,	kgp7181058,	kgp7186699,	kgp7189498,	kgp7242489,
kgp7331172,	kgp7416024,	kgp7481870,	kgp7506434,	kgp7521990,
kgp759150,	kgp767200,	kgp7714238,	kgp7730397,	kgp7747883,
kgp7792268,	kgp7802182,	kgp7804623,	kgp7924485,	kgp8030775,
kgp8036704,	kgp8046214,	kgp8106690,	kgp8107491,	kgp8110667,
kgp8169636,	kgp8174785,	kgp8178358,	kgp8183049,	kgp8192546,
kgp8200264,	kgp8303520,	kgp8335515,	kgp8372910,	kgp841428,
kgp8437961,	kgp8440036,	kgp85534,	kgp8599417,	kgp8602316,
kgp8615910,	kgp8767692,	kgp8777935,	kgp8793915,	kgp8796185,
kgp8817856,	kgp8869954,	kgp8990121,	kgp9018750,	kgp9071686,
kgp9078300,	kgp9320791,	kgp9354462,	kgp9354820,	kgp9368119,
kgp9410843,	kgp9421884,	kgp9450430,	kgp9530088,	kgp9551947,
kgp9601362,	kgp9627338,	kgp9627406,	kgp9669946,	kgp9699754,
kgp971582,	kgp97310,	kgp974569,	kgp9795732,	kgp9806386,
kgp9854133,	kgp9884626,	rs10049206,	rs10124492,	rs10125298,
rs10162089,	rs10201643,	rs10203396,	rs10251797,	rs10278591,
rs10489312,	rs10492882,	rs10498793,	rs10501082,	rs10510774,

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rs10512340, rs1079303, rs10815160, rs10816302, rs10841322,
rs10841337, rs10954782, rs11002051, rs11022778, rs11029892,
rs11029907, rs11029928, rs11083404, rs11085044, rs11136970,
rs11147439, rs11192461, rs11192469, rs11559024, rs1157449,
rs11648129, rs11691553, rs12013377, rs12494712, rs12943140,
rs13002663, rs13394010, rs13415334, rs13419758, rs1380706,
rs1387768, rs1410779, rs1478682, rs1508102, rs1532365, rs1544352,
rs1545223, rs1579771, rs1604169, rs1621509, rs1644418,
rs16886004, rs16895510, rs16901784, rs16927077, rs16930057,
rs17029538, rs17224858, rs17238927, rs17329014, rs17400875,
rs17449018, rs17577980, rs17638791, rs1858973, rs1886214,
rs1894406, rs1894407, rs1894408, rs196295, rs196341, rs196343,
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rs2071470, rs2071472, rs2074037, rs2136408, rs2139612, rs2175121,
rs2241883, rs2309760, rs2325911, rs241435, rs241440, rs241442,
rs241443, rs241444, rs241445, rs241446, rs241447, rs241449,
rs241451, rs241452, rs241453, rs241454, rs241456, rs2453478,
rs2598360, rs2621321, rs2621323, rs2660214, rs2816838, rs2824070,
rs2839117, rs2845371, rs2857101, rs2857103, rs2857104, rs2926455,
rs2934491, rs3135388, rs3218328, rs343087, rs343092, rs3767955,
rs3792135, rs3799383, rs3803277, rs3815822, rs3818675, rs3829539,
rs3885907, rs3899755, rs4075692, rs4143493, rs419132, rs423239,
rs4254166, rs4356336, rs4360791, rs4449139, rs4584668, rs4669694,
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rs484482, rs4894701, rs5024722, rs502530, rs543122, rs6032205,
rs6032209, rs6110157, rs623011, rs6497396, rs6535882, rs6687976,
rs6718758, rs6835202, rs6840089, rs6845927, rs6895094, rs6899068,
rs7020402, rs7024953, rs7028906, rs7029123, rs7062312, rs714342,
rs7187976, rs7191155, rs720176, rs7217872, rs7228827, rs7348267,
rs7496451, rs7524868, rs7563131, rs7579987, rs759458, rs7666442,
rs7670525, rs7672014, rs7677801, rs7725112, rs7844274, rs7850,
rs7860748, rs7862565, rs7864679, rs7928078, rs7948420, rs8035826,
rs8050872, rs8053136, rs8055485, rs823829, rs858341, rs9315047,
rs931570, rs9346979, rs9376361, rs9393727, rs9501224, rs9508832,
rs950928, rs9579566, rs9597498, rs9670531, rs9671124, rs9671182,

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rs9817308, rs9834010, rs9876830, rs9913349, rs9931167 and rs9931211.

56. The kit of claim 55, wherein the at least one single nucleotide polymorphisms (SNPs) are selected from the group consisting of kgp24415534, kgp6214351, kgp6599438, kgp7747883, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, and rs759458,

preferably wherein the kit further comprises instructions for use of the kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate.

57. The kit of claim 55, wherein the at least one single nucleotide polymorphisms (SNPs) comprise 2, 3, 4, 5, 6, 7, 8, 9 or 10 of the SNPs selected from the group consisting of kgp24415534, kgp6214351, kgp6599438, kgp7747883, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391 and rs759458.

58. The kit of claim 56 or 57, wherein if rs3135391 is the at least one SNP selected, then selecting at least one SNP other than rs3135391.

59. The kit of claim 55, wherein the at least one single nucleotide polymorphisms (SNPs) are selected from the group consisting of kgp24415534, kgp6214351, kgp6599438, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391 and rs759458,

preferably wherein the kit further comprises instructions for use of the kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis as a predicted responder or as a predicted non-responder to glatiramer acetate.

60. The kit of claim 59, wherein the at least one single nucleotide polymorphisms (SNPs) further comprise 2, 3, 4, 5, 6, 7, 8, or 9

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of the SNPs selected from the group consisting of kgp24415534, kgp6214351, kgp6599438, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391 and rs759458.

61. The kit of any one of claims 42-60, wherein the genotype of the subject at the location corresponding to the location of one or more of the SNPs is determined by indirect genotyping.

62. The kit of any one of claims 42-60, wherein the genotype of the subject at the location corresponding to the location of one or more of the SNPs is determined indirectly by determining the genotype of the subject at a location corresponding to the location of at least one SNP that is in linkage disequilibrium with the one or more SNPs.

63. The kit of claim 55-62, comprising

- a) at least one probe specific for a location corresponding to the location of at least one SNP;
- b) at least one pair of PCR primers designed to amplify a DNA segment which includes a location corresponding to the location of at least one SNP;
- c) at least one pair of PCR primers designed to amplify a DNA segment which includes a location corresponding to the location of at least one SNP and at least one probe specific for a location corresponding to the location of at least one SNP;
- d) a reagent for performing a method selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of mismatch (CCM), gene chip and denaturing high performance liquid chromatography (DHPLC) for determining the identity of at least one SNP; or

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e) reagents for TaqMan Open Array assay designed for determining the genotype at a location corresponding to the location of at least one SNP,

wherein the at least one SNP is in linkage disequilibrium with the one or more SNPs.

64. The kit of any one of claims 42-63, wherein determining the genotype of the subject at a location corresponding to the location of at least one SNP that is in linkage disequilibrium with the one or more SNPs allows identification of the genotype of the subject at the location corresponding to the location of the one or more SNPs with a probability of at least 85%.

65. The kit of claim 64, wherein determining the genotype of the subject at a location corresponding to the location of at least one SNP that is in linkage disequilibrium with the one or more SNPs allows identification of the genotype of the subject at the location corresponding to the location of the one or more SNPs with a probability of at least 90%.

66. The kit of claim 65, wherein determining the genotype of the subject at a location corresponding to the location of at least one SNP that is in linkage disequilibrium with the one or more SNPs allows identification of the genotype of the subject at the location corresponding to the location of the one or more SNPs with a probability of at least 99%.

67. A probe for identifying the genotype of a location corresponding to the location of a SNP selected from the group consisting of kgp10090631, kgp1009249, kgp10148554, kgp10152733, kgp10215554, kgp10224254, kgp10305127, kgp10351364, kgp10372946, kgp10404633, kgp10412303, kgp10523170, kgp1054273, kgp10558725, kgp10564659, kgp10591989, kgp10594414, kgp10619195, kgp10620244, kgp10632945, kgp10633631, kgp10679353, kgp10762962, kgp10788130, kgp10826273, kgp10836214, kgp10910719, kgp10922969, kgp10948564, kgp10967046, kgp10974833, kgp1098237, kgp10989246, kgp11002881, kgp11010680,

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kgp11077373, kgp11141512, kgp11206453, kgp11210903, kgp1124492,
kgp11281589, kgp11285862, kgp11285883, kgp11328629, kgp11356379,
kgp11407560, kgp11453406, kgp11467007, kgp11514107, kgp11543962,
kgp11580695, kgp11604017, kgp11627530, kgp11633966, kgp11686146,
kgp11702474, kgp11711524, kgp11755256, kgp11768533, kgp11804835,
kgp11843177, kgp12008955, kgp12083934, kgp1211163, kgp12182745,
kgp12230354, kgp1224440, kgp12253568, kgp12371757, kgp124162,
kgp12426624, kgp12557319, kgp12562255, kgp1285441, kgp13161760,
kgp1355977, kgp1371881, kgp1432800, kgp15390522, kgp1682126,
kgp1683448, kgp1688752, kgp1699628, kgp1753445, kgp1758575,
kgp1779254, kgp1786079, kgp18379774, kgp18432055, kgp18525257,
kgp1912531, kgp19568724, kgp20163979, kgp2023214, kgp2045074,
kgp20478926, kgp2092817, kgp21171930, kgp2176915, kgp2245775,
kgp2262166, kgp22778566, kgp22793211, kgp22811918, kgp22823022,
kgp2282938, kgp22839559, kgp2299675, kgp23298674, kgp2356388,
kgp23672937, kgp23737989, kgp2388352, kgp2391411, kgp24131116,
kgp24415534, kgp2446153, kgp2451249, kgp24521552, kgp2465184,
kgp24729706, kgp24753470, kgp25191871, kgp25216186, kgp25543811,
kgp25921291, kgp25952891, kgp26026546, kgp26271158, kgp2638591,
kgp26528455, kgp26533576, kgp2688306, kgp26995430, kgp270001,
kgp2709692, kgp2715873, kgp27500525, kgp27571222, kgp27640141,
kgp2788291, kgp279772, kgp28532436, kgp28586329, kgp28687699,
kgp2877482, kgp28817122, kgp2920925, kgp2923815, kgp29367521,
kgp293787, kgp2958113, kgp2959751, kgp297178, kgp29794723,
kgp2993366, kgp30282494, kgp3048169, kgp304921, kgp3182607,
kgp3188, kgp3202939, kgp3205849, kgp3218351, kgp3267884,
kgp3276689, kgp3287349, kgp337461, kgp3418770, kgp3420309,
kgp3450875, kgp345301, kgp3477351, kgp3488270, kgp3496814,
kgp355027, kgp355723, kgp3593828, kgp3598409, kgp3598966,
kgp3624014, kgp3651767, kgp3669685, kgp3697615, kgp3730395,
kgp3812034, kgp3854180, kgp3933330, kgp394638, kgp3951463,
kgp3984567, kgp3991733, kgp4011779, kgp4037661, kgp4056892,
kgp4096263, kgp4127859, kgp4137144, kgp4155998, kgp4162414,
kgp4223880, kgp433351, kgp4346717, kgp4370912, kgp4418535,
kgp4420791, kgp4456934, kgp4479467, kgp4524468, kgp4543470,

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kgp4559907, kgp4573213, kgp4575797, kgp4591145, kgp4634875,
kgp4705854, kgp4734301, kgp4755147, kgp4812831, kgp4842590,
kgp485316, kgp487328, kgp4892427, kgp4898179, kgp4970670,
kgp4985243, kgp5002011, kgp5014707, kgp5017029, kgp5053636,
kgp5068397, kgp512180, kgp5144181, kgp5159037, kgp5216209,
kgp5252824, kgp5292386, kgp5326762, kgp5334779, kgp5388938,
kgp5409955, kgp541892, kgp5440506, kgp5441587, kgp5483926,
kgp55646, kgp5564995, kgp5579170, kgp5680955, kgp5691690,
kgp5747456, kgp5869992, kgp5894351, kgp5908616, kgp5924341,
kgp5949515, kgp6023196, kgp6032617, kgp6038357, kgp6042557,
kgp6076976, kgp6081880, kgp6091119, kgp6127371, kgp61811,
kgp6190988, kgp6194428, kgp6213972, kgp6214351, kgp6228750,
kgp6236949, kgp625941, kgp6301155, kgp6429231, kgp6469620,
kgp6505544, kgp6507761, kgp652534, kgp6539666, kgp6567154,
kgp6599438, kgp6603796, kgp6666134, kgp6700691, kgp6737096,
kgp6768546, kgp6772915, kgp6828277, kgp6835138, kgp6889327,
kgp6959492, kgp6990559, kgp6996560, kgp7006201, kgp7059449,
kgp7063887, kgp7077322, kgp7092772, kgp7117398, kgp7121374,
kgp7151153, kgp7161038, kgp7178233, kgp7181058, kgp7186699,
kgp7189498, kgp7242489, kgp7331172, kgp7416024, kgp7481870,
kgp7506434, kgp7521990, kgp759150, kgp7653470, kgp767200,
kgp7714238, kgp7730397, kgp7747883, kgp7778345, kgp7792268,
kgp7802182, kgp7804623, kgp7924485, kgp7932108, kgp8030775,
kgp8036704, kgp8046214, kgp8106690, kgp8107491, kgp8110667,
kgp8145845, kgp8169636, kgp8174785, kgp8178358, kgp8183049,
kgp8192546, kgp8200264, kgp8303520, kgp8335515, kgp8372910,
kgp841428, kgp8437961, kgp8440036, kgp85534, kgp8599417,
kgp8602316, kgp8615910, kgp8644305, kgp8767692, kgp8777935,
kgp8793915, kgp8796185, kgp8817856, kgp8847137, kgp8869954,
kgp8990121, kgp9018750, kgp9071686, kgp9078300, kgp9143704,
kgp9320791, kgp9354462, kgp9354820, kgp9368119, kgp9409440,
kgp9410843, kgp9421884, kgp9450430, kgp9530088, kgp9551947,
kgp956070, kgp9601362, kgp9627338, kgp9627406, kgp9669946,
kgp9699754, kgp971582, kgp97310, kgp974569, kgp9795732,
kgp9806386, kgp9854133, kgp9884626, kgp9909702, kgp9927782,

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P1_M_061510_11_106_M, P1_M_061510_18_342_P, P1_M_061510_6_159_P,
rs10038844, rs10049206, rs10124492, rs10125298, rs10162089,
rs10201643, rs10203396, rs10251797, rs1026894, rs10278591,
rs10489312, rs10492882, rs10495115, rs10498793, rs10501082,
rs10510774, rs10512340, rs1079303, rs10815160, rs10816302,
rs10841322, rs10841337, rs10954782, rs11002051, rs11022778,
rs11029892, rs11029907, rs11029928, rs11083404, rs11085044,
rs11136970, rs11147439, rs11192461, rs11192469, rs11559024,
rs11562998, rs11563025, rs1157449, rs11648129, rs11691553,
rs11750747, rs11947777, rs12013377, rs12043743, rs12233980,
rs12341716, rs12472695, rs12494712, rs12881439, rs12943140,
rs13002663, rs13168893, rs13386874, rs13394010, rs13415334,
rs13419758, rs1357718, rs1380706, rs1387768, rs1393037,
rs1393040, rs1397481, rs1410779, rs1474226, rs1478682, rs1508102,
rs1508515, rs1532365, rs1534647, rs1544352, rs1545223, rs1579771,
rs1604169, rs1621509, rs1644418, rs16846161, rs16886004,
rs16895510, rs16901784, rs16927077, rs16930057, rs17029538,
rs1715441, rs17187123, rs17224858, rs17238927, rs17245674,
rs17329014, rs17400875, rs17419416, rs17449018, rs17577980,
rs17638791, rs1793174, rs1858973, rs1883448, rs1886214,
rs1894406, rs1894407, rs1894408, rs1905248, rs196295, rs196341,
rs196343, rs197523, rs1979992, rs1979993, rs2043136, rs2058742,
rs2071469, rs2071470, rs2071472, rs2074037, rs209568, rs2136408,
rs2139612, rs2175121, rs2241883, rs2309760, rs2325911, rs2354380,
rs241435, rs241440, rs241442, rs241443, rs241444, rs241445,
rs241446, rs241447, rs241449, rs241451, rs241452, rs241453,
rs241454, rs241456, rs2453478, rs2598360, rs2618065, rs2621321,
rs2621323, rs263247, rs2660214, rs2662, rs2816838, rs2824070,
rs2839117, rs2845371, rs2857101, rs2857103, rs2857104,
rs28993969, rs2926455, rs2934491, rs3135388, rs3218328, rs343087,
rs343092, rs34647183, rs35615951, rs3767955, rs3768769,
rs3792135, rs3799383, rs3803277, rs3815822, rs3818675, rs3829539,
rs3847233, rs3858034, rs3858035, rs3858036, rs3858038, rs3885907,
rs3894712, rs3899755, rs4075692, rs4143493, rs419132, rs423239,
rs4254166, rs4356336, rs4360791, rs4449139, rs4584668, rs4669694,

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rs4709792, rs4738738, rs4740708, rs4769060, rs4780822, rs4782279, rs4797764, rs4822644, rs484482, rs4894701, rs4978567, rs5024722, rs502530, rs528065, rs543122, rs6032205, rs6032209, rs6110157, rs623011, rs6459418, rs6497396, rs6535882, rs6577395, rs6687976, rs6718758, rs6811337, rs6835202, rs6840089, rs6845927, rs6895094, rs6899068, rs7020402, rs7024953, rs7028906, rs7029123, rs7062312, rs7119480, rs7123506, rs714342, rs7187976, rs7191155, rs720176, rs7217872, rs7228827, rs7231366, rs7348267, rs7496451, rs7524868, rs7563131, rs7579987, rs759458, rs7666442, rs7670525, rs7672014, rs7677801, rs7680970, rs7684006, rs7696391, rs7698655, rs7725112, rs7819949, rs7844274, rs7846783, rs7850, rs7860748, rs7862565, rs7864679, rs7928078, rs7948420, rs7949751, rs7961005, rs8000689, rs8018807, rs8035826, rs8050872, rs8053136, rs8055485, rs823829, rs858341, rs9315047, rs931570, rs9346979, rs9376361, rs9393727, rs9501224, rs9508832, rs950928, rs9579566, rs9597498, rs961090, rs9670531, rs9671124, rs9671182, rs967616, rs9817308, rs9834010, rs9876830, rs9913349, rs9931167, rs9931211, rs9948620 and rs9953274.

68. A probe for identifying the genotype of a location corresponding to the location of a SNP selected from the group consisting of kgp24415534, kgp6214351, kgp6599438, kgp7747883, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, and rs759458.

69. The probe of claim 68 wherein the location of a SNP selected from the group consisting of kgp24415534, kgp6214351, kgp6599438, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391 and rs759458.

70. The probe of claim 67-69, wherein if rs3135391 is the one SNP selected, then selecting a SNP other than rs3135391.

71. The probe of any one of claims 67-70, wherein the SNP is in linkage disequilibrium with the one or more SNPs.

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72. The probe of any one of claims 67-70, wherein the location of the SNP is determined indirectly by determining the genotype at a location corresponding to the location of the SNP that is in linkage disequilibrium with the one or more SNPs.

73. Glatiramer acetate or a pharmaceutical composition comprising glatiramer acetate for use in treating a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis which human subject is identified as a predicted responder to glatiramer acetate by:

a) determining a genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of:

kgp10090631,	kgp1009249,	kgp10152733,	kgp10224254,
kgp10305127,	kgp10351364,	kgp10372946,	kgp10404633,
kgp10412303,	kgp10523170,	kgp1054273,	kgp10558725,
kgp10564659,	kgp10591989,	kgp10594414,	kgp10619195,
kgp10620244,	kgp10632945,	kgp10633631,	kgp10679353,
kgp10788130,	kgp10826273,	kgp10910719,	kgp10922969,
kgp10948564,	kgp10967046,	kgp10974833,	kgp1098237,
kgp11002881,	kgp11010680,	kgp11077373,	kgp11141512,
kgp11206453,	kgp11210903,	kgp1124492,	kgp11281589,
kgp11285862,	kgp11328629,	kgp11356379,	kgp11407560,
kgp11453406,	kgp11467007,	kgp11514107,	kgp11543962,
kgp11580695,	kgp11627530,	kgp11633966,	kgp11686146,
kgp11702474,	kgp11711524,	kgp11768533,	kgp11804835,
kgp11843177,	kgp12008955,	kgp12083934,	kgp12182745,
kgp12230354,	kgp1224440,	kgp12371757,	kgp124162,
kgp12426624,	kgp12557319,	kgp1285441,	kgp13161760,
kgp1355977,	kgp1371881,	kgp15390522,	kgp1683448,
kgp1688752,	kgp1699628,	kgp1753445,	kgp1779254,
kgp1786079,	kgp18379774,	kgp18432055,	kgp18525257,
kgp1912531,	kgp19568724,	kgp20163979,	kgp2023214,
kgp2045074,	kgp20478926,	kgp2092817,	kgp21171930,
kgp2245775,	kgp2262166,	kgp22778566,	kgp22793211,
kgp22811918,	kgp22823022,	kgp2282938,	kgp2299675,
kgp23298674,	kgp2356388,	kgp23672937,	

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kgp23737989, kgp2388352, kgp2391411, kgp24131116, kgp24415534,
kgp2446153, kgp2451249, kgp2465184, kgp24729706, kgp24753470,
kgp25191871, kgp25216186, kgp25543811, kgp25921291,
kgp25952891, kgp26026546, kgp26271158, kgp2638591,
kgp26528455, kgp26533576, kgp2688306, kgp26995430, kgp270001,
kgp2709692, kgp2715873, kgp27500525, kgp27571222, kgp27640141,
kgp2788291, kgp279772, kgp28532436, kgp28586329, kgp28687699,
kgp28817122, kgp2923815, kgp29367521, kgp293787, kgp2958113,
kgp2959751, kgp297178, kgp29794723, kgp30282494, kgp3048169,
kgp304921, kgp3182607, kgp3202939, kgp3205849, kgp3218351,
kgp3267884, kgp3276689, kgp337461, kgp3418770, kgp3450875,
kgp345301, kgp3477351, kgp3496814, kgp355027, kgp355723,
kgp3593828, kgp3598409, kgp3651767, kgp3669685, kgp3730395,
kgp3812034, kgp3854180, kgp3933330, kgp3951463, kgp3984567,
kgp3991733, kgp4011779, kgp4056892, kgp4096263, kgp4127859,
kgp4155998, kgp4162414, kgp4223880, kgp4346717, kgp4370912,
kgp4418535, kgp4420791, kgp4479467, kgp4524468, kgp4543470,
kgp4559907, kgp4573213, kgp4634875, kgp4705854, kgp4734301,
kgp4755147, kgp4812831, kgp4842590, kgp485316, kgp487328,
kgp4898179, kgp5002011, kgp5014707, kgp5017029, kgp5053636,
kgp5068397, kgp512180, kgp5144181, kgp5159037, kgp5216209,
kgp5292386, kgp5334779, kgp5388938, kgp5409955, kgp5440506,
kgp5441587, kgp5483926, kgp55646, kgp5564995, kgp5579170,
kgp5680955, kgp5869992, kgp5908616, kgp6023196, kgp6032617,
kgp6038357, kgp6076976, kgp6091119, kgp6127371, kgp61811,
kgp6190988, kgp6214351, kgp6228750, kgp6236949, kgp6469620,
kgp6505544, kgp6507761, kgp652534, kgp6539666, kgp6567154,
kgp6599438, kgp6603796, kgp6666134, kgp6700691, kgp6737096,
kgp6768546, kgp6772915, kgp6835138, kgp6959492, kgp6996560,
kgp7059449, kgp7063887, kgp7077322, kgp7092772, kgp7117398,
kgp7121374, kgp7178233, kgp7181058, kgp7186699, kgp7189498,
kgp7242489, kgp7331172, kgp7416024, kgp7481870, kgp7506434,
kgp7521990, kgp759150, kgp767200, kgp7714238, kgp7730397,
kgp7747883, kgp7792268, kgp7802182, kgp7804623, kgp7924485,
kgp8030775, kgp8036704, kgp8046214, kgp8106690, kgp8107491,

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kgp8110667, kgp8169636, kgp8174785, kgp8178358, kgp8183049,
kgp8192546, kgp8200264, kgp8303520, kgp8335515, kgp8372910,
kgp841428, kgp8437961, kgp8440036, kgp85534, kgp8599417,
kgp8602316, kgp8615910, kgp8767692, kgp8777935, kgp8793915,
kgp8796185, kgp8817856, kgp8869954, kgp8990121, kgp9018750,
kgp9071686, kgp9078300, kgp9320791, kgp9354462, kgp9354820,
kgp9368119, kgp9410843, kgp9421884, kgp9450430, kgp9530088,
kgp9551947, kgp9601362, kgp9627338, kgp9627406, kgp9669946,
kgp9699754, kgp971582, kgp97310, kgp974569, kgp9795732,
kgp9806386, kgp9854133, kgp9884626, rs10049206, rs10124492,
rs10125298, rs10162089, rs10201643, rs10203396, rs10251797,
rs10278591, rs10489312, rs10492882, rs10498793, rs10501082,
rs10510774, rs10512340, rs1079303, rs10815160, rs10816302,
rs10841322, rs10841337, rs10954782, rs11002051, rs11022778,
rs11029892, rs11029907, rs11029928, rs11083404, rs11085044,
rs11136970, rs11147439, rs11192461, rs11192469, rs11559024,
rs1157449, rs11648129, rs11691553, rs12013377, rs12494712,
rs12943140, rs13002663, rs13394010, rs13415334, rs13419758,
rs1380706, rs1387768, rs1410779, rs1478682, rs1508102,
rs1532365, rs1544352, rs1545223, rs1579771, rs1604169,
rs1621509, rs1644418, rs16886004, rs16895510, rs16901784,
rs16927077, rs16930057, rs17029538, rs17224858, rs17238927,
rs17329014, rs17400875, rs17449018, rs17577980, rs17638791,
rs1858973, rs1886214, rs1894406, rs1894407, rs1894408,
rs196295, rs196341, rs196343, rs197523, rs1979992, rs1979993,
rs2043136, rs2058742, rs2071469, rs2071470, rs2071472,
rs2074037, rs2136408, rs2139612, rs2175121, rs2241883,
rs2309760, rs2325911, rs241435, rs241440, rs241442, rs241443,
rs241444, rs241445, rs241446, rs241447, rs241449, rs241451,
rs241452, rs241453, rs241454, rs241456, rs2453478, rs2598360,
rs2621321, rs2621323, rs2660214, rs2816838, rs2824070,
rs2839117, rs2845371, rs2857101, rs2857103, rs2857104,
rs2926455, rs2934491, rs3135388, rs3218328, rs343087,
rs343092, rs3767955, rs3792135, rs3799383, rs3803277,
rs3815822, rs3818675, rs3829539, rs3885907, rs3899755,

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rs4075692, rs4143493, rs419132, rs423239, rs4254166,
rs4356336, rs4360791, rs4449139, rs4584668, rs4669694,
rs4709792, rs4738738, rs4769060, rs4780822, rs4782279,
rs4822644, rs484482, rs4894701, rs5024722, rs502530, rs543122,
rs6032205, rs6032209, rs6110157, rs623011, rs6497396,
rs6535882, rs6687976, rs6718758, rs6835202, rs6840089,
rs6845927, rs6895094, rs6899068, rs7020402, rs7024953,
rs7028906, rs7029123, rs7062312, rs714342, rs7187976,
rs7191155, rs720176, rs7217872, rs7228827, rs7348267,
rs7496451, rs7524868, rs7563131, rs7579987, rs759458,
rs7666442, rs7670525, rs7672014, rs7677801, rs7725112,
rs7844274, rs7850, rs7860748, rs7862565, rs7864679, rs7928078,
rs7948420, rs8035826, rs8050872, rs8053136, rs8055485,
rs823829, rs858341, rs9315047, rs931570, rs9346979, rs9376361,
rs9393727, rs9501224, rs9508832, rs950928, rs9579566,
rs9597498, rs9670531, rs9671124, rs9671182, rs9817308,
rs9834010, rs9876830, rs9913349, rs9931167 and rs9931211, and

b) identifying the subject as a predicted responder to glatiramer acetate if the genotype of the subject contains

one or more A alleles at the location of kgp10152733,
kgp10224254, kgp10305127, kgp10351364, kgp10372946,
kgp10404633, kgp10564659, kgp10591989, kgp10594414,
kgp10619195, kgp10620244, kgp10633631, kgp10974833,
kgp11002881, kgp11285862, kgp11328629, kgp11407560,
kgp11514107, kgp11627530, kgp11702474, kgp11711524,
kgp11768533, kgp11804835, kgp12083934, kgp12182745,
kgp12230354, kgp1224440, kgp124162, kgp12557319,
kgp1371881, kgp1699628, kgp1753445, kgp1779254,
kgp1786079, kgp18379774, kgp18525257, kgp20163979,
kgp2023214, kgp20478926, kgp21171930, kgp2262166,
kgp22778566, kgp2465184, kgp24753470, kgp25191871,
kgp25216186, kgp25952891, kgp26026546, kgp26533576,
kgp27500525, kgp27571222, kgp28532436, kgp28586329,
kgp28817122, kgp2958113, kgp29794723, kgp30282494,
kgp304921, kgp3205849, kgp3218351, kgp3276689, kgp337461,

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kgp345301, kgp355027, kgp355723, kgp3593828, kgp3812034,
kgp3951463, kgp4162414, kgp4223880, kgp4418535,
kgp4543470, kgp4573213, kgp4634875, kgp4755147,
kgp4842590, kgp485316, kgp5068397, kgp5334779,
kgp5483926, kgp5564995, kgp5869992, kgp5908616,
kgp6032617, kgp6038357, kgp6076976, kgp6091119,
kgp6127371, kgp61811, kgp6214351, kgp6228750, kgp6236949,
kgp6469620, kgp6505544, kgp6507761, kgp6666134,
kgp6700691, kgp6772915, kgp6959492, kgp7077322,
kgp7117398, kgp7178233, kgp7186699, kgp7506434,
kgp759150, kgp7730397, kgp7802182, kgp7804623,
kgp7924485, kgp8030775, kgp8036704, kgp8046214,
kgp8106690, kgp8110667, kgp8178358, kgp8200264,
kgp8372910, kgp841428, kgp8602316, kgp8615910,
kgp8793915, kgp8796185, kgp8990121, kgp9018750,
kgp9354462, kgp9368119, kgp9410843, kgp9450430,
kgp9530088, kgp9627338, kgp9669946, kgp97310, kgp974569,
kgp9806386, kgp9884626, rs10049206, rs10124492,
rs10125298, rs10162089, rs10203396, rs10251797,
rs10278591, rs10489312, rs10492882, rs10498793,
rs10501082, rs10510774, rs10512340, rs10815160,
rs10816302, rs10841337, rs11029892, rs11029928,
rs11192469, rs11559024, rs11648129, rs12013377,
rs13394010, rs13415334, rs1478682, rs1544352, rs1545223,
rs1604169, rs1621509, rs1644418, rs17029538, rs17400875,
rs17449018, rs17577980, rs1858973, rs1894406, rs1894407,
rs197523, rs2058742, rs2071469, rs2071472, rs2139612,
rs2241883, rs2309760, rs241440, rs241442, rs241444,
rs241445, rs241446, rs241449, rs241453, rs241456,
rs2453478, rs2660214, rs2824070, rs2845371, rs2857103,
rs2926455, rs343087, rs343092, rs3767955, rs3792135,
rs3829539, rs3899755, rs4075692, rs4143493, rs423239,
rs4254166, rs4356336, rs4584668, rs4780822, rs4782279,
rs5024722, rs6032209, rs6110157, rs623011, rs6497396,
rs6845927, rs6895094, rs6899068, rs7024953, rs7028906,

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rs7029123, rs7062312, rs7187976, rs7191155, rs720176,
rs7228827, rs7496451, rs7563131, rs759458, rs7666442,
rs7670525, rs7677801, rs7725112, rs7850, rs7862565,
rs7948420, rs8035826, rs8053136, rs8055485, rs823829,
rs9315047, rs9501224, rs9508832, rs950928, rs9597498,
rs9670531, rs9671124, rs9817308, rs9834010, rs9876830 or
rs9931211,

one or more C alleles at the location of kgp10910719,
kgp11077373, kgp11453406, kgp12426624, kgp2045074,
kgp22811918, kgp23298674, kgp2709692, kgp28687699,
kgp3496814, kgp3669685, kgp3730395, kgp4056892,
kgp4370912, kgp5053636, kgp5216209, kgp5292386,
kgp6023196, kgp652534, kgp7059449, kgp7189498,
kgp7521990, kgp7792268, kgp8303520, kgp9320791,
kgp9795732, rs10201643, rs11022778, rs11136970,
rs11147439, rs11691553, rs1579771, rs16901784, rs2136408,
rs2325911, rs241443, rs2857104, rs3803277, rs3885907,
rs4738738, rs4894701, rs502530, rs6032205, rs6687976,
rs6718758, rs6835202, rs714342, rs7524868, rs7844274,
rs9393727 or rs9671182,

one or more G alleles at the location of kgp10090631,
kgp1009249, kgp10412303, kgp10523170, kgp1054273,
kgp10558725, kgp10632945, kgp10679353, kgp10788130,
kgp10826273, kgp10922969, kgp10948564, kgp10967046,
kgp1098237, kgp11010680, kgp11141512, kgp11206453,
kgp11210903, kgp1124492, kgp11281589, kgp11356379,
kgp11467007, kgp11543962, kgp11580695, kgp11633966,
kgp11686146, kgp11843177, kgp12008955, kgp12371757,
kgp1285441, kgp13161760, kgp1355977, kgp15390522,
kgp1683448, kgp1688752, kgp1912531, kgp19568724,
kgp2092817, kgp2245775, kgp22793211, kgp22823022,
kgp2282938, kgp2299675, kgp2356388, kgp23672937,
kgp23737989, kgp2388352, kgp2391411, kgp24131116,
kgp24415534, kgp2446153, kgp2451249, kgp24729706,

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kgp25543811, kgp25921291, kgp26271158, kgp2638591,
kgp26528455, kgp2688306, kgp26995430, kgp270001,
kgp2715873, kgp27640141, kgp2788291, kgp2923815,
kgp29367521, kgp293787, kgp2959751, kgp297178,
kgp3048169, kgp3182607, kgp3202939, kgp3267884,
kgp3418770, kgp3450875, kgp3477351, kgp3598409,
kgp3651767, kgp3854180, kgp3933330, kgp3984567,
kgp4011779, kgp4096263, kgp4127859, kgp4155998,
kgp4346717, kgp4420791, kgp4479467, kgp4524468,
kgp4559907, kgp4705854, kgp4734301, kgp4812831,
kgp487328, kgp4898179, kgp5002011, kgp5014707,
kgp5017029, kgp512180, kgp5144181, kgp5159037,
kgp5388938, kgp5409955, kgp5440506, kgp5441587, kgp55646,
kgp5579170, kgp5680955, kgp6190988, kgp6539666,
kgp6567154, kgp6599438, kgp6603796, kgp6737096,
kgp6768546, kgp6835138, kgp6996560, kgp7063887,
kgp7092772, kgp7121374, kgp7181058, kgp7331172,
kgp7416024, kgp7481870, kgp767200, kgp7714238,
kgp7747883, kgp8107491, kgp8169636, kgp8174785,
kgp8183049, kgp8192546, kgp8335515, kgp8437961,
kgp8440036, kgp85534, kgp8599417, kgp8767692, kgp8777935,
kgp8817856, kgp8869954, kgp9071686, kgp9078300,
kgp9354820, kgp9421884, kgp9551947, kgp9601362,
kgp9627406, kgp9699754, kgp971582, kgp9854133, rs1079303,
rs10841322, rs10954782, rs11002051, rs11029907,
rs11083404, rs11085044, rs11192461, rs1157449,
rs12494712, rs12943140, rs13002663, rs13419758,
rs1380706, rs1387768, rs1410779, rs1508102, rs1532365,
rs16886004, rs16895510, rs16927077, rs16930057,
rs17224858, rs17238927, rs17329014, rs17638791,
rs1886214, rs1894408, rs196295, rs196341, rs196343,
rs1979992, rs1979993, rs2043136, rs2071470, rs2074037,
rs2175121, rs241435, rs241447, rs241451, rs241452,
rs241454, rs2598360, rs2621321, rs2621323, rs2816838,
rs2839117, rs2857101, rs2934491, rs3135388, rs3218328,

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rs3799383, rs3815822, rs3818675, rs419132, rs4360791,
rs4449139, rs4669694, rs4709792, rs4769060, rs4822644,
rs484482, rs543122, rs6535882, rs6840089, rs7020402,
rs7217872, rs7348267, rs7579987, rs7672014, rs7860748,
rs7864679, rs7928078, rs8050872, rs858341, rs931570,
rs9346979, rs9376361, rs9579566, rs9913349 or rs9931167,
or

one or more T alleles at the location of kgp18432055,
kgp279772, kgp3991733 or kgp7242489.

74. The glatiramer acetate or a pharmaceutical composition comprising glatiramer acetate for use of claim 73 wherein determining a genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of: kgp24415534, kgp6214351, kgp6599438, kgp7747883, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, and rs759458.

75. The glatiramer acetate or a pharmaceutical composition comprising glatiramer acetate for use of claim 73 wherein determining a genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of: kgp24415534, kgp6214351, kgp6599438, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391 and rs759458.

76. The glatiramer acetate or a pharmaceutical composition comprising glatiramer acetate for use of claim 73-75, wherein if rs3135391 is the one or more SNP selected, then selecting a SNP other than rs3135391.

77. Glatiramer acetate for use according to claim 73-76, wherein the genotype of the subject at the location corresponding to the location of one or more of the SNPs is determined indirectly by determining the genotype of the subject at a location

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corresponding to the location of at least one SNP that is in linkage disequilibrium with the one or more SNPs.

78. Glatiramer acetate for use according to claim 73 -76, wherein determining the genotype of the subject at a location corresponding to the location of at least one SNP that is in linkage disequilibrium with the one or more SNPs allows identification of the genotype of the subject at the location corresponding to the location of the one or more SNPs with a probability of at least 85%, 90%, or 99%.

79. A method of determining the genotype of a human subject comprising identifying whether the genotype of a human subject contains

one or more A alleles at the location of kgp10152733,
 kgp10224254, kgp10305127, kgp10351364, kgp10372946,
 kgp10404633, kgp10564659, kgp10591989, kgp10594414,
 kgp10619195, kgp10620244, kgp10633631, kgp10974833,
 kgp11002881, kgp11285862, kgp11328629, kgp11407560,
 kgp11514107, kgp11627530, kgp11702474, kgp11711524,
 kgp11768533, kgp11804835, kgp12083934, kgp12182745,
 kgp12230354, kgp1224440, kgp124162, kgp12557319, kgp1371881,
 kgp1699628, kgp1753445, kgp1779254, kgp1786079, kgp18379774,
 kgp18525257, kgp20163979, kgp2023214, kgp20478926,
 kgp21171930, kgp2262166, kgp22778566, kgp2465184, kgp24753470,
 kgp25191871, kgp25216186, kgp25952891, kgp26026546,
 kgp26533576, kgp27500525, kgp27571222, kgp28532436,
 kgp28586329, kgp28817122, kgp2958113, kgp29794723,
 kgp30282494, kgp304921, kgp3205849, kgp3218351, kgp3276689,
 kgp337461, kgp345301, kgp355027, kgp355723, kgp3593828,
 kgp3812034, kgp3951463, kgp4162414, kgp4223880, kgp4418535,
 kgp4543470, kgp4573213, kgp4634875, kgp4755147, kgp4842590,
 kgp485316, kgp5068397, kgp5334779, kgp5483926, kgp5564995,
 kgp5869992, kgp5908616, kgp6032617, kgp6038357, kgp6076976,
 kgp6091119, kgp6127371, kgp61811, kgp6214351, kgp6228750,

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kgp6236949, kgp6469620, kgp6505544, kgp6507761, kgp6666134,
kgp6700691, kgp6772915, kgp6959492, kgp7077322, kgp7117398,
kgp7178233, kgp7186699, kgp7506434, kgp759150, kgp7730397,
kgp7802182, kgp7804623, kgp7924485, kgp8030775, kgp8036704,
kgp8046214, kgp8106690, kgp8110667, kgp8178358, kgp8200264,
kgp8372910, kgp841428, kgp8602316, kgp8615910, kgp8793915,
kgp8796185, kgp8990121, kgp9018750, kgp9354462, kgp9368119,
kgp9410843, kgp9450430, kgp9530088, kgp9627338, kgp9669946,
kgp97310, kgp974569, kgp9806386, kgp9884626, rs10049206,
rs10124492, rs10125298, rs10162089, rs10203396, rs10251797,
rs10278591, rs10489312, rs10492882, rs10498793, rs10501082,
rs10510774, rs10512340, rs10815160, rs10816302, rs10841337,
rs11029892, rs11029928, rs11192469, rs11559024, rs11648129,
rs12013377, rs13394010, rs13415334, rs1478682, rs1544352,
rs1545223, rs1604169, rs1621509, rs1644418, rs17029538,
rs17400875, rs17449018, rs17577980, rs1858973, rs1894406,
rs1894407, rs197523, rs2058742, rs2071469, rs2071472,
rs2139612, rs2241883, rs2309760, rs241440, rs241442, rs241444,
rs241445, rs241446, rs241449, rs241453, rs241456, rs2453478,
rs2660214, rs2824070, rs2845371, rs2857103, rs2926455,
rs343087, rs343092, rs3767955, rs3792135, rs3829539,
rs3899755, rs4075692, rs4143493, rs423239, rs4254166,
rs4356336, rs4584668, rs4780822, rs4782279, rs5024722,
rs6032209, rs6110157, rs623011, rs6497396, rs6845927,
rs6895094, rs6899068, rs7024953, rs7028906, rs7029123,
rs7062312, rs7187976, rs7191155, rs720176, rs7228827,
rs7496451, rs7563131, rs759458, rs7666442, rs7670525,
rs7677801, rs7725112, rs7850, rs7862565, rs7948420, rs8035826,
rs8053136, rs8055485, rs823829, rs9315047, rs9501224,
rs9508832, rs950928, rs9597498, rs9670531, rs9671124,
rs9817308, rs9834010, rs9876830 or rs9931211,
one or more C alleles at the location of kgp10910719,
kgp11077373, kgp11453406, kgp12426624, kgp2045074,
kgp22811918, kgp23298674, kgp2709692, kgp28687699, kgp3496814,
kgp3669685, kgp3730395, kgp4056892, kgp4370912, kgp5053636,

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kgp5216209, kgp5292386, kgp6023196, kgp652534, kgp7059449,
kgp7189498, kgp7521990, kgp7792268, kgp8303520, kgp9320791,
kgp9795732, rs10201643, rs11022778, rs11136970, rs11147439,
rs11691553, rs1579771, rs16901784, rs2136408, rs2325911,
rs241443, rs2857104, rs3803277, rs3885907, rs4738738,
rs4894701, rs502530, rs6032205, rs6687976, rs6718758,
rs6835202, rs714342, rs7524868, rs7844274, rs9393727 or
rs9671182,

one or more G alleles at the location of kgp10090631,
kgp1009249, kgp10412303, kgp10523170, kgp1054273, kgp10558725,
kgp10632945, kgp10679353, kgp10788130, kgp10826273,
kgp10922969, kgp10948564, kgp10967046, kgp1098237,
kgp11010680, kgp11141512, kgp11206453, kgp11210903,
kgp1124492, kgp11281589, kgp11356379, kgp11467007,
kgp11543962, kgp11580695, kgp11633966, kgp11686146,
kgp11843177, kgp12008955, kgp12371757, kgp1285441,
kgp13161760, kgp1355977, kgp15390522, kgp1683448, kgp1688752,
kgp1912531, kgp19568724, kgp2092817, kgp2245775, kgp22793211,
kgp22823022, kgp2282938, kgp2299675, kgp2356388, kgp23672937,
kgp23737989, kgp2388352, kgp2391411, kgp24131116, kgp24415534,
kgp2446153, kgp2451249, kgp24729706, kgp25543811, kgp25921291,
kgp26271158, kgp2638591, kgp26528455, kgp2688306, kgp26995430,
kgp270001, kgp2715873, kgp27640141, kgp2788291, kgp2923815,
kgp29367521, kgp293787, kgp2959751, kgp297178, kgp3048169,
kgp3182607, kgp3202939, kgp3267884, kgp3418770, kgp3450875,
kgp3477351, kgp3598409, kgp3651767, kgp3854180, kgp3933330,
kgp3984567, kgp4011779, kgp4096263, kgp4127859, kgp4155998,
kgp4346717, kgp4420791, kgp4479467, kgp4524468, kgp4559907,
kgp4705854, kgp4734301, kgp4812831, kgp487328, kgp4898179,
kgp5002011, kgp5014707, kgp5017029, kgp512180, kgp5144181,
kgp5159037, kgp5388938, kgp5409955, kgp5440506, kgp5441587,
kgp55646, kgp5579170, kgp5680955, kgp6190988, kgp6539666,
kgp6567154, kgp6599438, kgp6603796, kgp6737096, kgp6768546,
kgp6835138, kgp6996560, kgp7063887, kgp7092772, kgp7121374,
kgp7181058, kgp7331172, kgp7416024, kgp7481870, kgp767200,

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kgp7714238, kgp7747883, kgp8107491, kgp8169636, kgp8174785,
 kgp8183049, kgp8192546, kgp8335515, kgp8437961, kgp8440036,
 kgp85534, kgp8599417, kgp8767692, kgp8777935, kgp8817856,
 kgp8869954, kgp9071686, kgp9078300, kgp9354820, kgp9421884,
 kgp9551947, kgp9601362, kgp9627406, kgp9699754, kgp971582,
 kgp9854133, rs1079303, rs10841322, rs10954782, rs11002051,
 rs11029907, rs11083404, rs11085044, rs11192461, rs1157449,
 rs12494712, rs12943140, rs13002663, rs13419758, rs1380706,
 rs1387768, rs1410779, rs1508102, rs1532365, rs16886004,
 rs16895510, rs16927077, rs16930057, rs17224858, rs17238927,
 rs17329014, rs17638791, rs1886214, rs1894408, rs196295,
 rs196341, rs196343, rs1979992, rs1979993, rs2043136,
 rs2071470, rs2074037, rs2175121, rs241435, rs241447, rs241451,
 rs241452, rs241454, rs2598360, rs2621321, rs2621323,
 rs2816838, rs2839117, rs2857101, rs2934491, rs3135388,
 rs3218328, rs3799383, rs3815822, rs3818675, rs419132,
 rs4360791, rs4449139, rs4669694, rs4709792, rs4769060,
 rs4822644, rs484482, rs543122, rs6535882, rs6840089,
 rs7020402, rs7217872, rs7348267, rs7579987, rs7672014,
 rs7860748, rs7864679, rs7928078, rs8050872, rs858341,
 rs931570, rs9346979, rs9376361, rs9579566, rs9913349 or
 rs9931167, or
 one or more T alleles at the location of kgp18432055,
 kgp279772, kgp3991733 or kgp7242489.

80. The method of claim 79, wherein identifying whether the genotype of a human subject contains

one or more A alleles at the location of kgp10152733,
 kgp10224254, kgp10305127, kgp10351364, kgp10372946,
 kgp10404633, kgp10564659, kgp10591989, kgp10594414,
 kgp10619195, kgp10620244, kgp10633631, kgp10974833,
 kgp11002881, kgp11285862, kgp11328629, kgp11407560,
 kgp11514107, kgp11627530, kgp11702474, kgp11711524,
 kgp11768533, kgp11804835, kgp12083934, kgp12182745,
 kgp12230354, kgp1224440, kgp124162, kgp12557319, kgp1371881,
 kgp1699628, kgp1753445, kgp1779254, kgp1786079, kgp18379774,

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kgp18525257, kgp20163979, kgp2023214, kgp20478926,
kgp21171930, kgp2262166, kgp22778566, kgp2465184, kgp24753470,
kgp25191871, kgp25216186, kgp25952891, kgp26026546,
kgp26533576, kgp27500525, kgp27571222, kgp28532436,
kgp28586329, kgp28817122, kgp2958113, kgp29794723,
kgp30282494, kgp304921, kgp3205849, kgp3218351, kgp3276689,
kgp337461, kgp345301, kgp355027, kgp355723, kgp3593828,
kgp3812034, kgp3951463, kgp4162414, kgp4223880, kgp4418535,
kgp4543470, kgp4573213, kgp4634875, kgp4755147, kgp4842590,
kgp485316, kgp5068397, kgp5334779, kgp5483926, kgp5564995,
kgp5869992, kgp5908616, kgp6032617, kgp6038357, kgp6076976,
kgp6091119, kgp6127371, kgp61811, kgp6214351, kgp6228750,
kgp6236949, kgp6469620, kgp6505544, kgp6507761, kgp6666134,
kgp6700691, kgp6772915, kgp6959492, kgp7077322, kgp7117398,
kgp7178233, kgp7186699, kgp7506434, kgp759150, kgp7730397,
kgp7802182, kgp7804623, kgp7924485, kgp8030775, kgp8036704,
kgp8046214, kgp8106690, kgp8110667, kgp8178358, kgp8200264,
kgp8372910, kgp841428, kgp8602316, kgp8615910, kgp8793915,
kgp8796185, kgp8990121, kgp9018750, kgp9354462, kgp9368119,
kgp9410843, kgp9450430, kgp9530088, kgp9627338, kgp9669946,
kgp97310, kgp974569, kgp9806386, kgp9884626, rs10049206,
rs10124492, rs10125298, rs10162089, rs10203396, rs10251797,
rs10278591, rs10489312, rs10492882, rs10498793, rs10501082,
rs10510774, rs10512340, rs10815160, rs10816302, rs10841337,
rs11029892, rs11029928, rs11192469, rs11559024, rs11648129,
rs12013377, rs13394010, rs13415334, rs1478682, rs1544352,
rs1545223, rs1604169, rs1621509, rs1644418, rs17029538,
rs17400875, rs17449018, rs17577980, rs1858973, rs1894406,
rs1894407, rs197523, rs2058742, rs2071469, rs2071472,
rs2139612, rs2241883, rs2309760, rs241440, rs241442, rs241444,
rs241445, rs241446, rs241449, rs241453, rs241456, rs2453478,
rs2660214, rs2824070, rs2845371, rs2857103, rs2926455,
rs343087, rs343092, rs3767955, rs3792135, rs3829539,
rs3899755, rs4075692, rs4143493, rs423239, rs4254166,
rs4356336, rs4584668, rs4780822, rs4782279, rs5024722,

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rs6032209, rs6110157, rs623011, rs6497396, rs6845927,
rs6895094, rs6899068, rs7024953, rs7028906, rs7029123,
rs7062312, rs7187976, rs7191155, rs720176, rs7228827,
rs7496451, rs7563131, rs759458, rs7666442, rs7670525,
rs7677801, rs7725112, rs7850, rs7862565, rs7948420, rs8035826,
rs8053136, rs8055485, rs823829, rs9315047, rs9501224,
rs9508832, rs950928, rs9597498, rs9670531, rs9671124,
rs9817308, rs9834010, rs9876830 or rs9931211,
one or more C alleles at the location of kgp10910719,
kgp11077373, kgp11453406, kgp12426624, kgp2045074,
kgp22811918, kgp23298674, kgp2709692, kgp28687699, kgp3496814,
kgp3669685, kgp3730395, kgp4056892, kgp4370912, kgp5053636,
kgp5216209, kgp5292386, kgp6023196, kgp652534, kgp7059449,
kgp7189498, kgp7521990, kgp7792268, kgp8303520, kgp9320791,
kgp9795732, rs10201643, rs11022778, rs11136970, rs11147439,
rs11691553, rs1579771, rs16901784, rs2136408, rs2325911,
rs241443, rs2857104, rs3803277, rs3885907, rs4738738,
rs4894701, rs502530, rs6032205, rs6687976, rs6718758,
rs6835202, rs714342, rs7524868, rs7844274, rs9393727 or
rs9671182,

one or more G alleles at the location of kgp10090631,
kgp1009249, kgp10412303, kgp10523170, kgp1054273, kgp10558725,
kgp10632945, kgp10679353, kgp10788130, kgp10826273,
kgp10922969, kgp10948564, kgp10967046, kgp1098237,
kgp11010680, kgp11141512, kgp11206453, kgp11210903,
kgp1124492, kgp11281589, kgp11356379, kgp11467007,
kgp11543962, kgp11580695, kgp11633966, kgp11686146,
kgp11843177, kgp12008955, kgp12371757, kgp1285441,
kgp13161760, kgp1355977, kgp15390522, kgp1683448, kgp1688752,
kgp1912531, kgp19568724, kgp2092817, kgp2245775, kgp22793211,
kgp22823022, kgp2282938, kgp2299675, kgp2356388, kgp23672937,
kgp23737989, kgp2388352, kgp2391411, kgp24131116, kgp24415534,
kgp2446153, kgp2451249, kgp24729706, kgp25543811, kgp25921291,
kgp26271158, kgp2638591, kgp26528455, kgp2688306, kgp26995430,
kgp270001, kgp2715873, kgp27640141, kgp2788291, kgp2923815,

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kgp29367521, kgp293787, kgp2959751, kgp297178, kgp3048169,
kgp3182607, kgp3202939, kgp3267884, kgp3418770, kgp3450875,
kgp3477351, kgp3598409, kgp3651767, kgp3854180, kgp3933330,
kgp3984567, kgp4011779, kgp4096263, kgp4127859, kgp4155998,
kgp4346717, kgp4420791, kgp4479467, kgp4524468, kgp4559907,
kgp4705854, kgp4734301, kgp4812831, kgp487328, kgp4898179,
kgp5002011, kgp5014707, kgp5017029, kgp512180, kgp5144181,
kgp5159037, kgp5388938, kgp5409955, kgp5440506, kgp5441587,
kgp55646, kgp5579170, kgp5680955, kgp6190988, kgp6539666,
kgp6567154, kgp6599438, kgp6603796, kgp6737096, kgp6768546,
kgp6835138, kgp6996560, kgp7063887, kgp7092772, kgp7121374,
kgp7181058, kgp7331172, kgp7416024, kgp7481870, kgp767200,
kgp7714238, kgp7747883, kgp8107491, kgp8169636, kgp8174785,
kgp8183049, kgp8192546, kgp8335515, kgp8437961, kgp8440036,
kgp85534, kgp8599417, kgp8767692, kgp8777935, kgp8817856,
kgp8869954, kgp9071686, kgp9078300, kgp9354820, kgp9421884,
kgp9551947, kgp9601362, kgp9627406, kgp9699754, kgp971582,
kgp9854133, rs1079303, rs10841322, rs10954782, rs11002051,
rs11029907, rs11083404, rs11085044, rs11192461, rs1157449,
rs12494712, rs12943140, rs13002663, rs13419758, rs1380706,
rs1387768, rs1410779, rs1508102, rs1532365, rs16886004,
rs16895510, rs16927077, rs16930057, rs17224858, rs17238927,
rs17329014, rs17638791, rs1886214, rs1894408, rs196295,
rs196341, rs196343, rs1979992, rs1979993, rs2043136,
rs2071470, rs2074037, rs2175121, rs241435, rs241447, rs241451,
rs241452, rs241454, rs2598360, rs2621321, rs2621323,
rs2816838, rs2839117, rs2857101, rs2934491, rs3135388,
rs3218328, rs3799383, rs3815822, rs3818675, rs419132,
rs4360791, rs4449139, rs4669694, rs4709792, rs4769060,
rs4822644, rs484482, rs543122, rs6535882, rs6840089,
rs7020402, rs7217872, rs7348267, rs7579987, rs7672014,
rs7860748, rs7864679, rs7928078, rs8050872, rs858341,
rs931570, rs9346979, rs9376361, rs9579566, rs9913349 or
rs9931167, or

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one or more T alleles at the location of kgp18432055, kgp279772, kgp3991733 or kgp7242489 is determined indirectly by determining the genotype of the subject at a location corresponding to the location of at least one SNP that is in linkage disequilibrium with the one or more SNPs.

81. The method of claim 78 or 80, wherein identifying the genotype of a human subject at the location of kgp24415534, kgp6214351, kgp6599438, kgp7747883, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391, or rs759458.

82. The method of claim 81, wherein identifying the genotype of a human subject at the location of kgp24415534, kgp6214351, kgp6599438, kgp8110667, kgp8817856, rs10162089, rs16886004, rs1894408, rs3135391 and rs759458.

83. The method of any one of claims 78-81, wherein if rs3135391 is the SNP selected, then selecting a SNP other than rs3135391.

84. The method of any one of claims 78-83, wherein the SNP is in linkage disequilibrium with the one or more SNPs.

85. The method of any one of claims 78-83, wherein the genotype of the human subject is determined indirectly by determining the genotype of the human subject at a location corresponding to the location of the SNP that is in linkage disequilibrium with the one or more SNPs.

86. A method of identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis who is predicted to have a slower course of disease progression, comprising the steps of:

(i) determining a genotype of the subject at a location corresponding to the location of one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of: kgp10148554, kgp10215554, kgp10762962,

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kgp10836214, kgp10989246, kgp11285883, kgp11604017,
 kgp11755256, kgp1211163, kgp12253568, kgp12562255,
 kgp1432800, kgp1682126, kgp1758575, kgp2176915,
 kgp22839559, kgp24521552, kgp2877482, kgp2920925,
 kgp2993366, kgp3188, kgp3287349, kgp3420309, kgp3488270,
 kgp3598966, kgp3624014, kgp3697615, kgp394638, kgp4037661,
 kgp4137144, kgp433351, kgp4456934, kgp4575797, kgp4591145,
 kgp4892427, kgp4970670, kgp4985243, kgp5252824, kgp5326762,
 kgp541892, kgp5691690, kgp5747456, kgp5894351, kgp5924341,
 kgp5949515, kgp6042557, kgp6081880, kgp6194428, kgp6213972,
 kgp625941, kgp6301155, kgp6429231, kgp6828277, kgp6889327,
 kgp6990559, kgp7006201, kgp7151153, kgp7161038, kgp7653470,
 kgp7778345, kgp7932108, kgp8145845, kgp8644305, kgp8847137,
 kgp9143704, kgp9409440, kgp956070, kgp9909702, kgp9927782,
 rs10038844, rs1026894, rs10495115, rs11562998, rs11563025,
 rs11750747, rs11947777, rs12043743, rs12233980, rs12341716,
 rs12472695, rs12881439, rs13168893, rs13386874, rs1357718,
 rs1393037, rs1393040, rs1397481, rs1474226, rs1508515,
 rs1534647, rs16846161, rs1715441, rs17187123, rs17245674,
 rs17419416, rs1793174, rs1883448, rs1905248, rs209568,
 rs2354380, rs2618065, rs263247, rs2662, rs28993969,
 rs34647183, rs35615951, rs3768769, rs3847233, rs3858034,
 rs3858035, rs3858036, rs3858038, rs3894712, rs4740708,
 rs4797764, rs4978567, rs528065, rs6459418, rs6577395,
 rs6811337, rs7119480, rs7123506, rs7231366, rs7680970,
 rs7684006, rs7696391, rs7698655, rs7819949, rs7846783,
 rs7949751, rs7961005, rs8000689, rs8018807, rs961090,
 rs967616, rs9948620 and rs9953274, and

- (ii) identifying the subject as predicted to have a slower course of disease progression if the genotype of the subject contains

one or more A alleles at the location of kgp10762962,
 kgp11285883, kgp11604017, kgp1211163, kgp12253568,
 kgp12562255, kgp2176915, kgp24521552, kgp2877482, kgp2993366,
 kgp3188, kgp3624014, kgp394638, kgp4037661, kgp433351,

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kgp4456934, kgp4575797, kgp4591145, kgp4892427, kgp4970670,
 kgp4985243, kgp5252824, kgp5326762, kgp541892, kgp5747456,
 kgp5894351, kgp6042557, kgp6081880, kgp6194428, kgp6429231,
 kgp7006201, kgp7151153, kgp7161038, kgp7653470, kgp8145845,
 kgp8644305, kgp9143704, kgp9409440, kgp9909702, kgp9927782,
 rs10038844, rs10495115, rs11750747, rs12341716, rs12881439,
 rs13168893, rs1393040, rs1474226, rs1534647, rs1715441,
 rs17187123, rs17245674, rs17419416, rs1793174, rs1883448,
 rs1905248, rs263247, rs34647183, rs35615951, rs3847233,
 rs3858038, rs4740708, rs528065, rs6459418, rs6577395,
 rs6811337, rs7680970, rs7684006, rs7698655, rs7961005,
 rs8018807, rs9948620 or rs9953274,
 one or more C alleles at the location of kgp10836214,
 kgp1432800, kgp22839559, kgp6301155, kgp6828277, rs2354380,
 rs2662, rs3858035, rs3894712, rs4797764 or rs7696391,
 one or more G alleles at the location of kgp10148554,
 kgp10215554, kgp10989246, kgp11755256, kgp1682126,
 kgp1758575, kgp2920925, kgp3287349, kgp3420309, kgp3488270,
 kgp3598966, kgp3697615, kgp4137144, kgp5691690, kgp5924341,
 kgp5949515, kgp6213972, kgp625941, kgp6889327, kgp6990559,
 kgp7778345, kgp7932108, kgp8847137, kgp956070, rs1026894,
 rs11562998, rs11563025, rs11947777, rs12233980, rs12472695,
 rs13386874, rs1357718, rs1393037, rs1397481, rs1508515,
 rs16846161, rs209568, rs2618065, rs28993969, rs3768769,
 rs3858034, rs3858036, rs4978567, rs7119480, rs7123506,
 rs7231366, rs7819949, rs7846783, rs7949751, rs8000689,
 rs961090 or rs967616, or
 one or more T alleles at the location of rs12043743.

87. The method of claim 86, wherein the genotype of the subject at the location corresponding to the location of one or more of the SNPs is determined indirectly by determining the genotype of the subject at a location corresponding to the location of at least one SNP that is in linkage disequilibrium with the one or more SNPs.

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88. A kit for identifying a human subject afflicted with multiple sclerosis or a single clinical attack consistent with multiple sclerosis who is predicted to have a slower course of disease progression, the kit comprising

- a) at least one probe specific for a location corresponding to the location of at least one SNP;
- b) at least one pair of PCR primers designed to amplify a DNA segment which includes a location corresponding to the location of at least one SNP;
- c) at least one pair of PCR primers designed to amplify a DNA segment which includes a location corresponding to the location of at least one SNP and at least one probe specific for a location corresponding to the location of at least one SNP;
- d) a reagent for performing a method selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, sequencing, single strand conformation polymorphism analysis (SSCP), chemical cleavage of mismatch (CCM), gene chip and denaturing high performance liquid chromatography (DHPLC) for determining the identity of at least one SNP; or
- e) reagents for TaqMan Open Array assay designed for determining the genotype at a location corresponding to the location of at least one SNP,

wherein the at least one SNP is selected from the group consisting of kgp10148554, kgp10215554, kgp10762962, kgp10836214, kgp10989246, kgp11285883, kgp11604017, kgp11755256, kgp1211163, kgp12253568, kgp12562255, kgp1432800, kgp1682126, kgp1758575, kgp2176915, kgp22839559, kgp24521552, kgp2877482, kgp2920925, kgp2993366, kgp3188, kgp3287349, kgp3420309, kgp3488270, kgp3598966, kgp3624014, kgp3697615, kgp394638, kgp4037661, kgp4137144, kgp433351, kgp4456934, kgp4575797, kgp4591145, kgp4892427, kgp4970670, kgp4985243, kgp5252824, kgp5326762,

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kgp541892, kgp5691690, kgp5747456, kgp5894351, kgp5924341,
kgp5949515, kgp6042557, kgp6081880, kgp6194428, kgp6213972,
kgp625941, kgp6301155, kgp6429231, kgp6828277, kgp6889327,
kgp6990559, kgp7006201, kgp7151153, kgp7161038, kgp7653470,
kgp7778345, kgp7932108, kgp8145845, kgp8644305, kgp8847137,
kgp9143704, kgp9409440, kgp956070, kgp9909702, kgp9927782,
rs10038844, rs1026894, rs10495115, rs11562998, rs11563025,
rs11750747, rs11947777, rs12043743, rs12233980, rs12341716,
rs12472695, rs12881439, rs13168893, rs13386874, rs1357718,
rs1393037, rs1393040, rs1397481, rs1474226, rs1508515, rs1534647,
rs16846161, rs1715441, rs17187123, rs17245674, rs17419416,
rs1793174, rs1883448, rs1905248, rs209568, rs2354380, rs2618065,
rs263247, rs2662, rs28993969, rs34647183, rs35615951, rs3768769,
rs3847233, rs3858034, rs3858035, rs3858036, rs3858038, rs3894712,
rs4740708, rs4797764, rs4978567, rs528065, rs6459418, rs6577395,
rs6811337, rs7119480, rs7123506, rs7231366, rs7680970, rs7684006,
rs7696391, rs7698655, rs7819949, rs7846783, rs7949751, rs7961005,
rs8000689, rs8018807, rs961090, rs967616, rs9948620 and
rs9953274.

89. The kit of claims 42-66, or claim 88, further comprising applying the algorithm depicted in Figure 8 or Figure 9 to identify the subject as a predicted responder or as a predicted non-responder to glatiramer acetate.

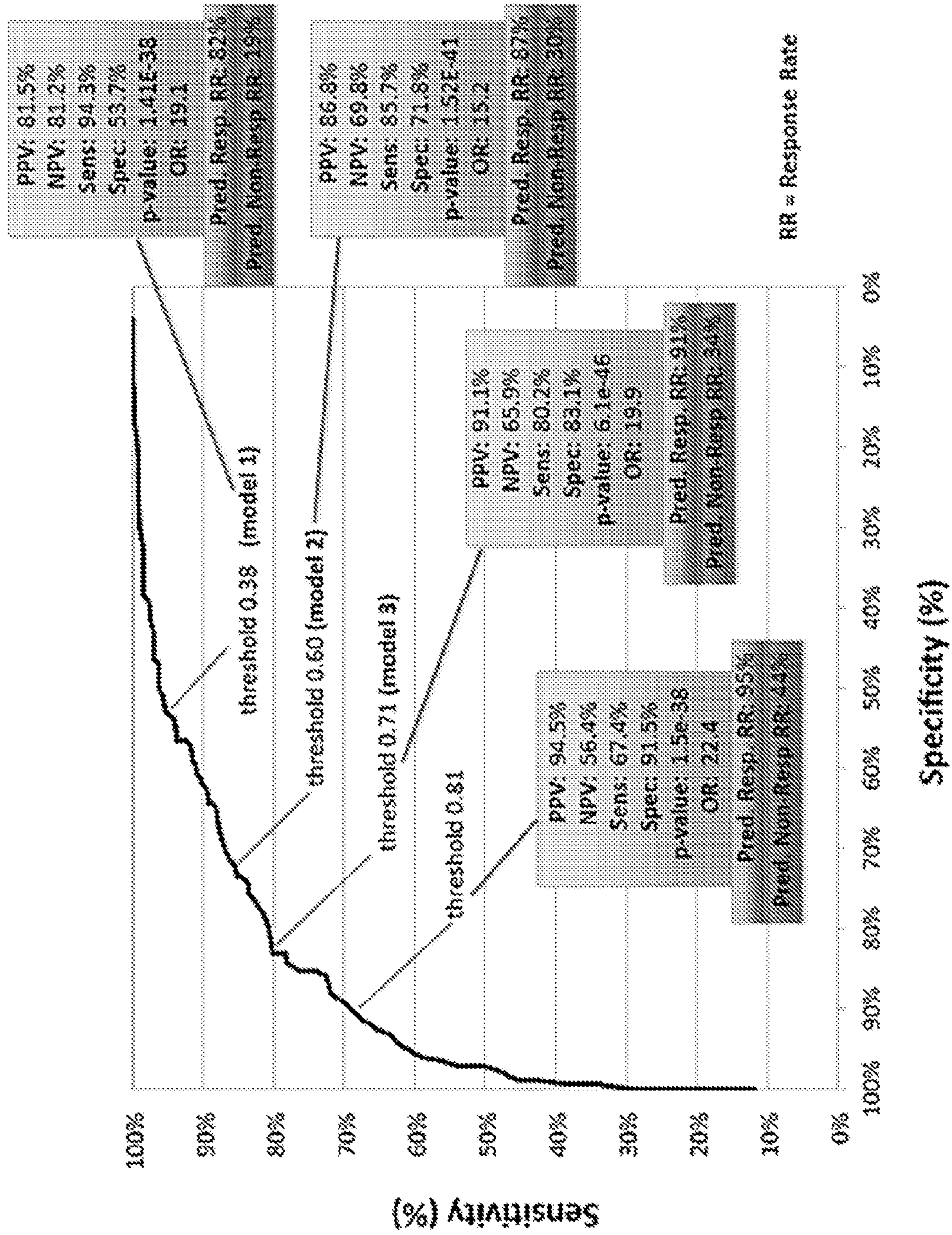


Figure 1

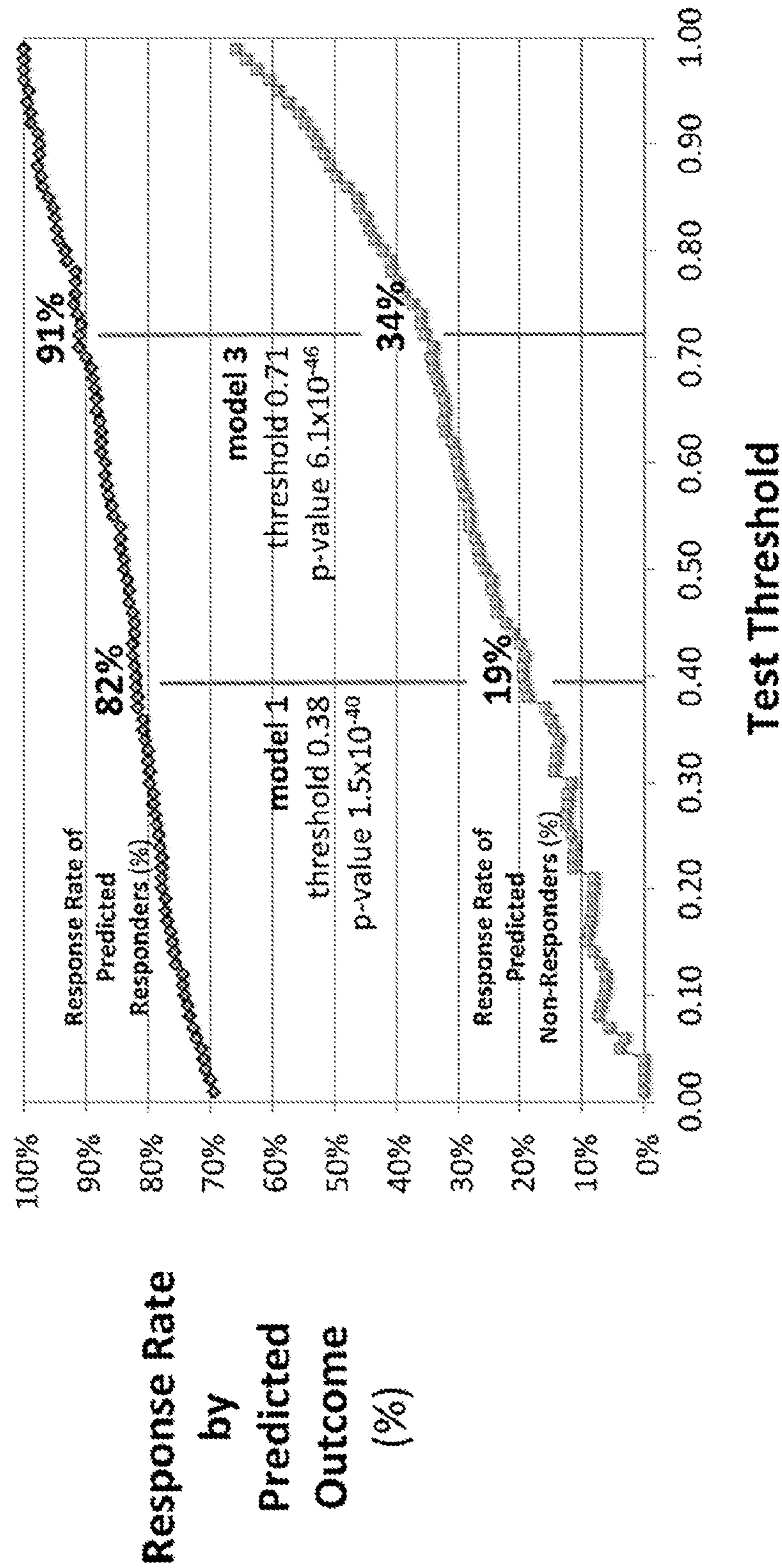


Figure 2

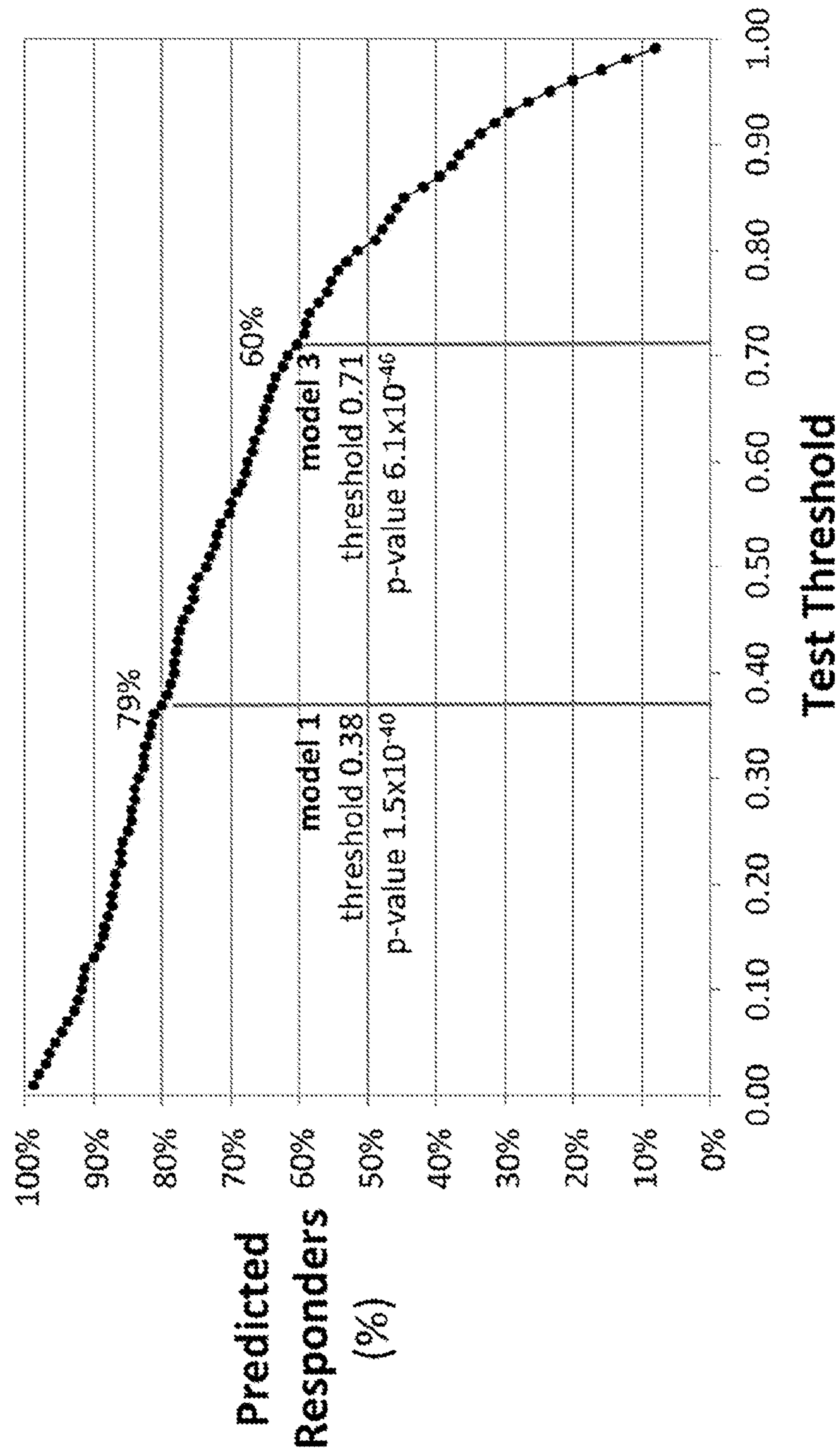


Figure 3

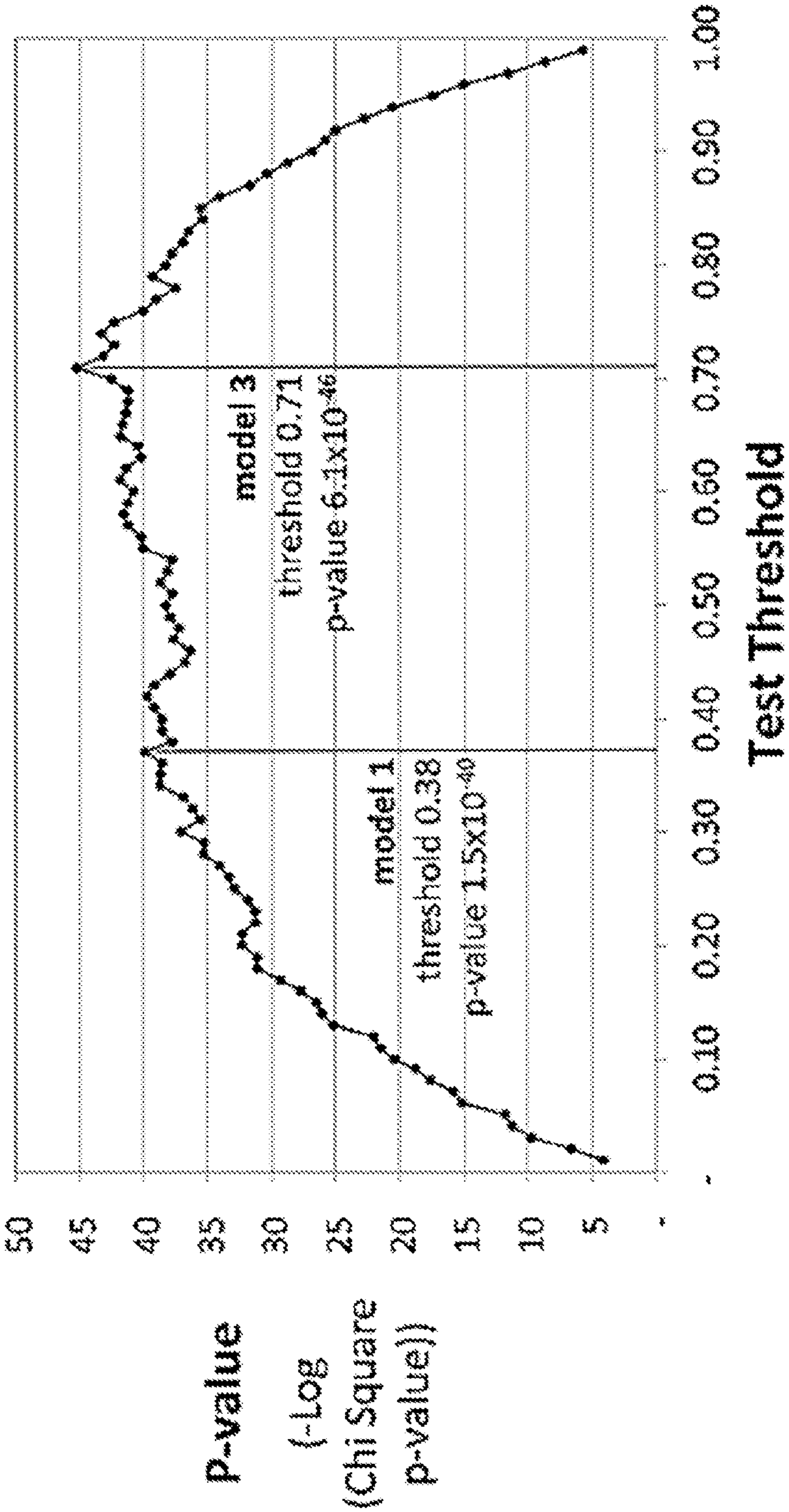


Figure 4

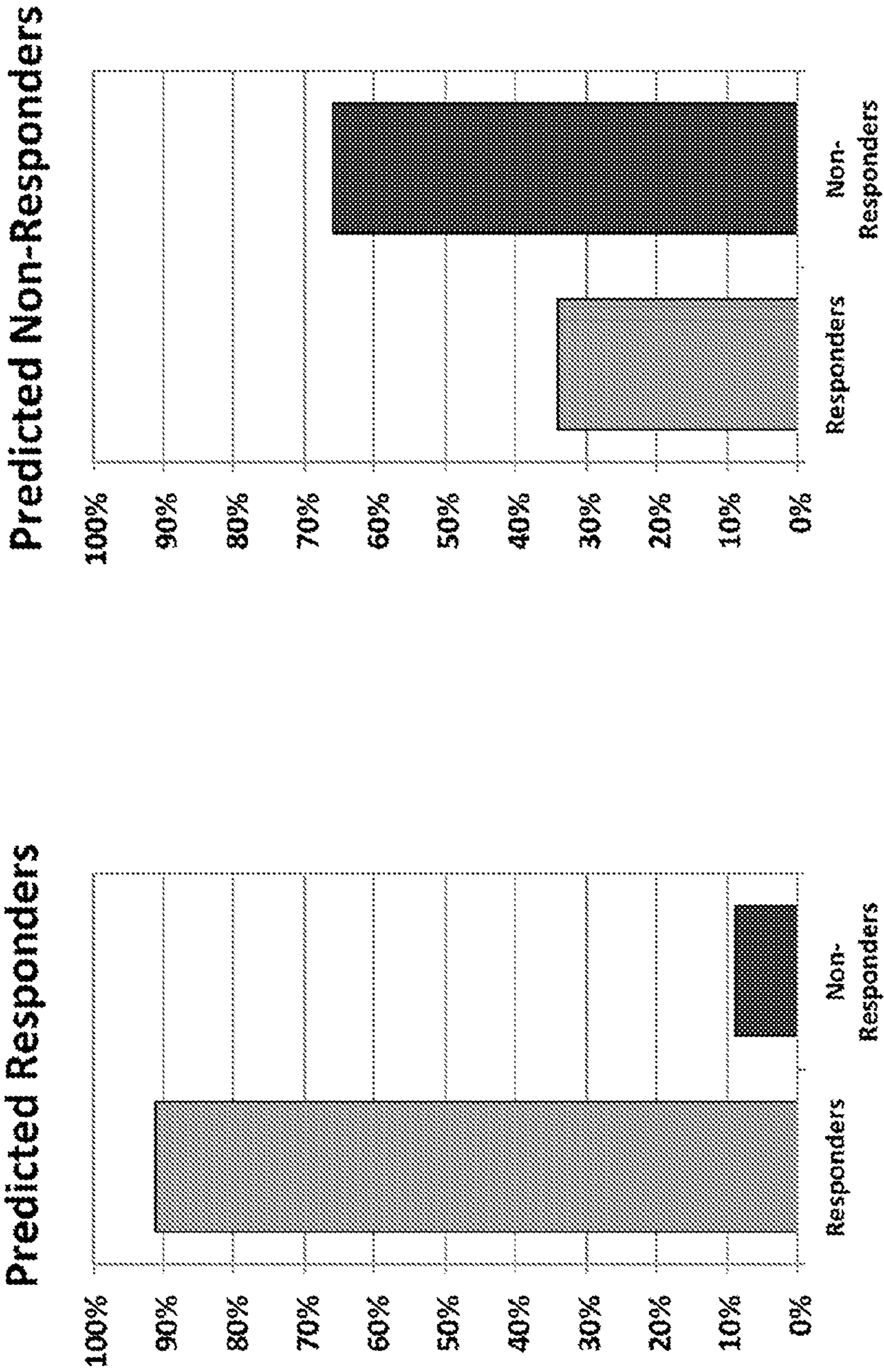


Figure 5

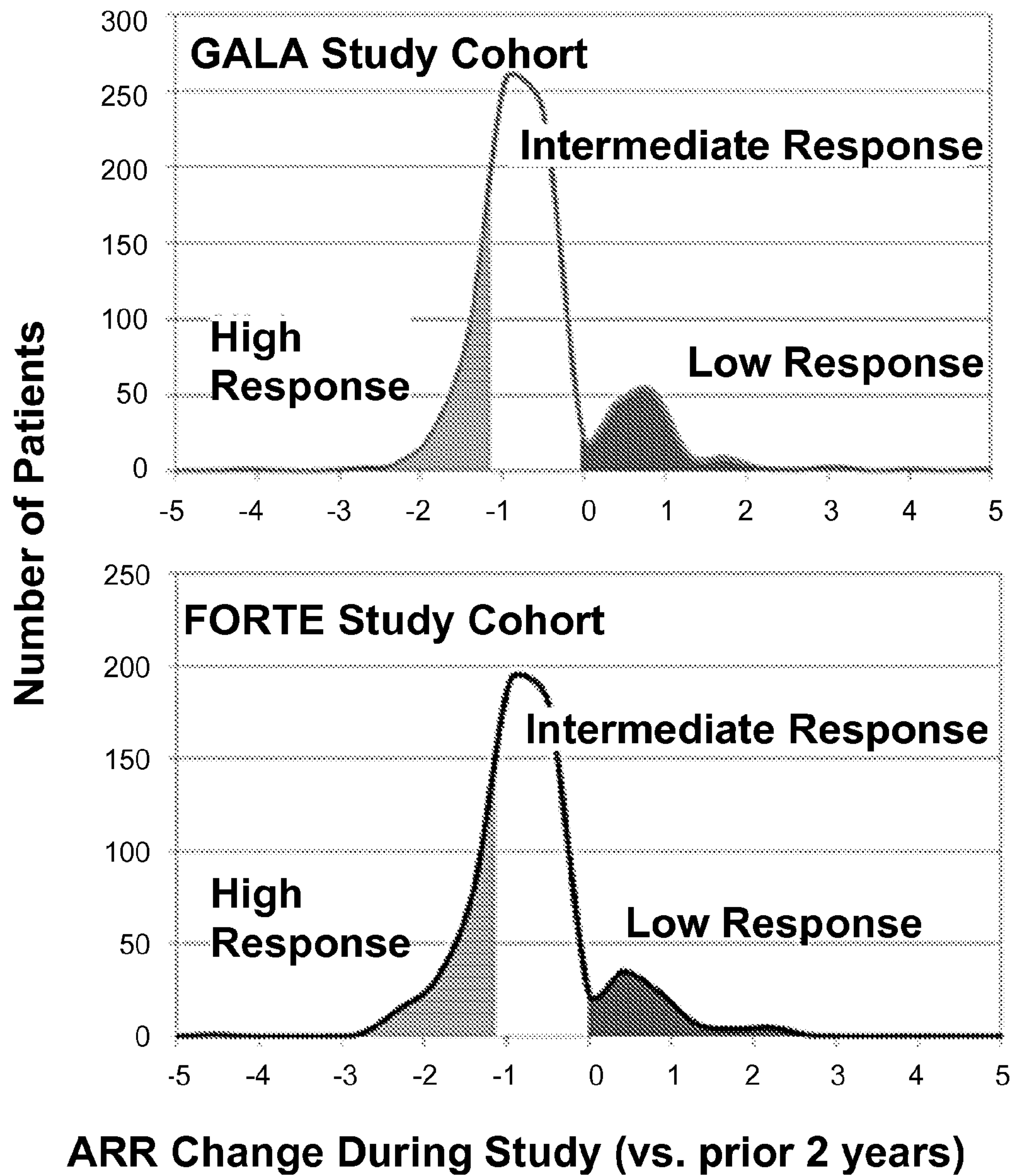
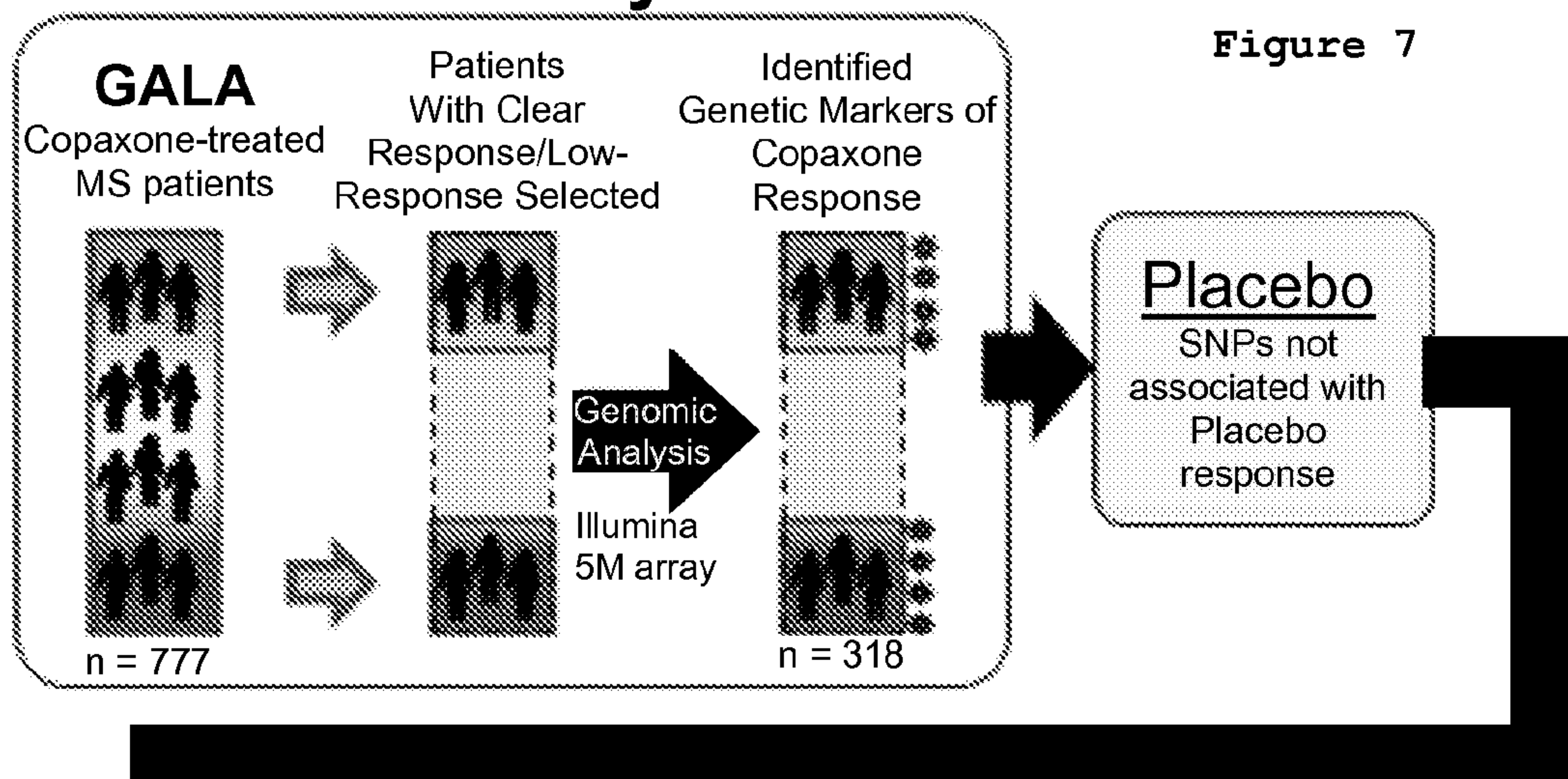
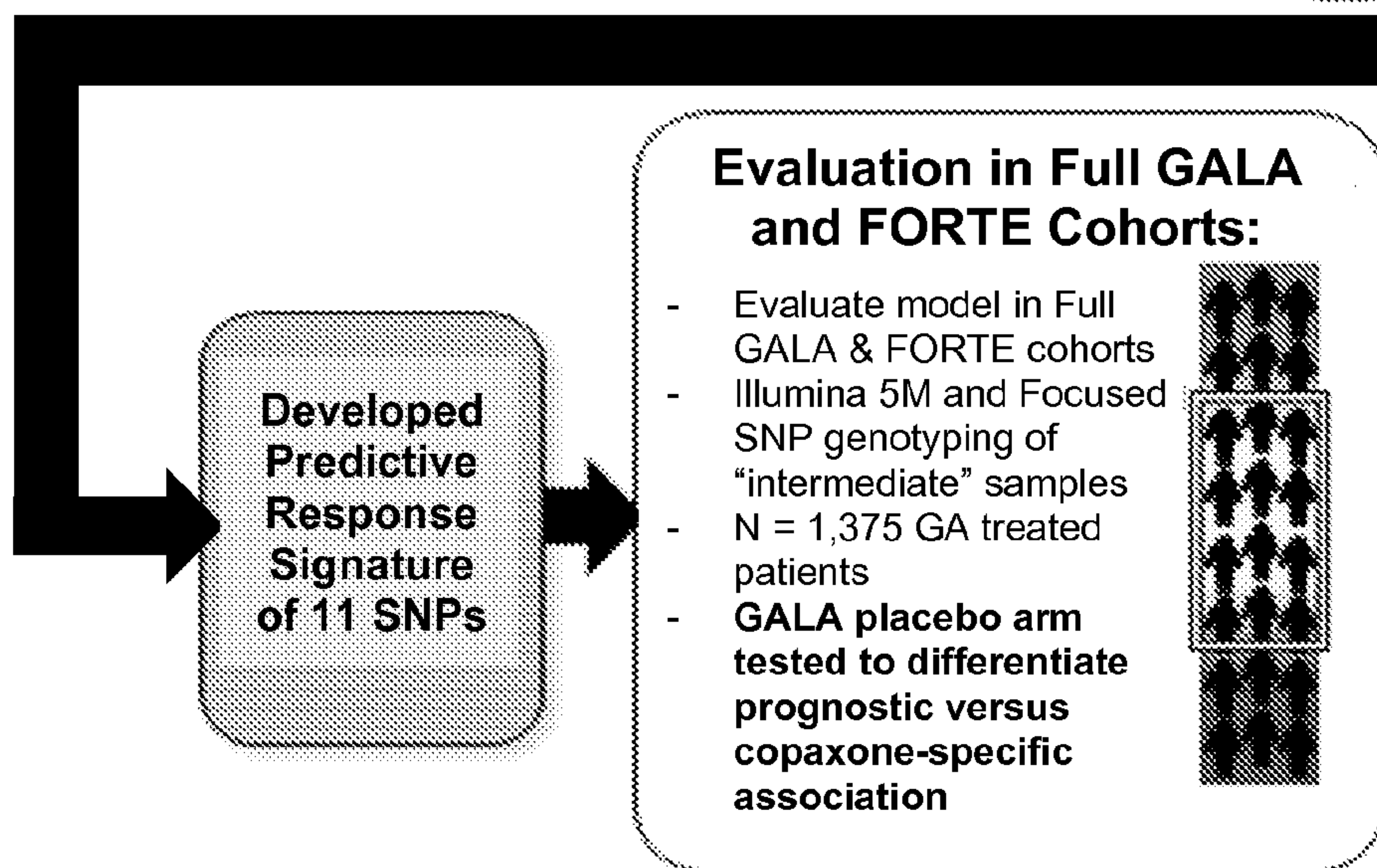
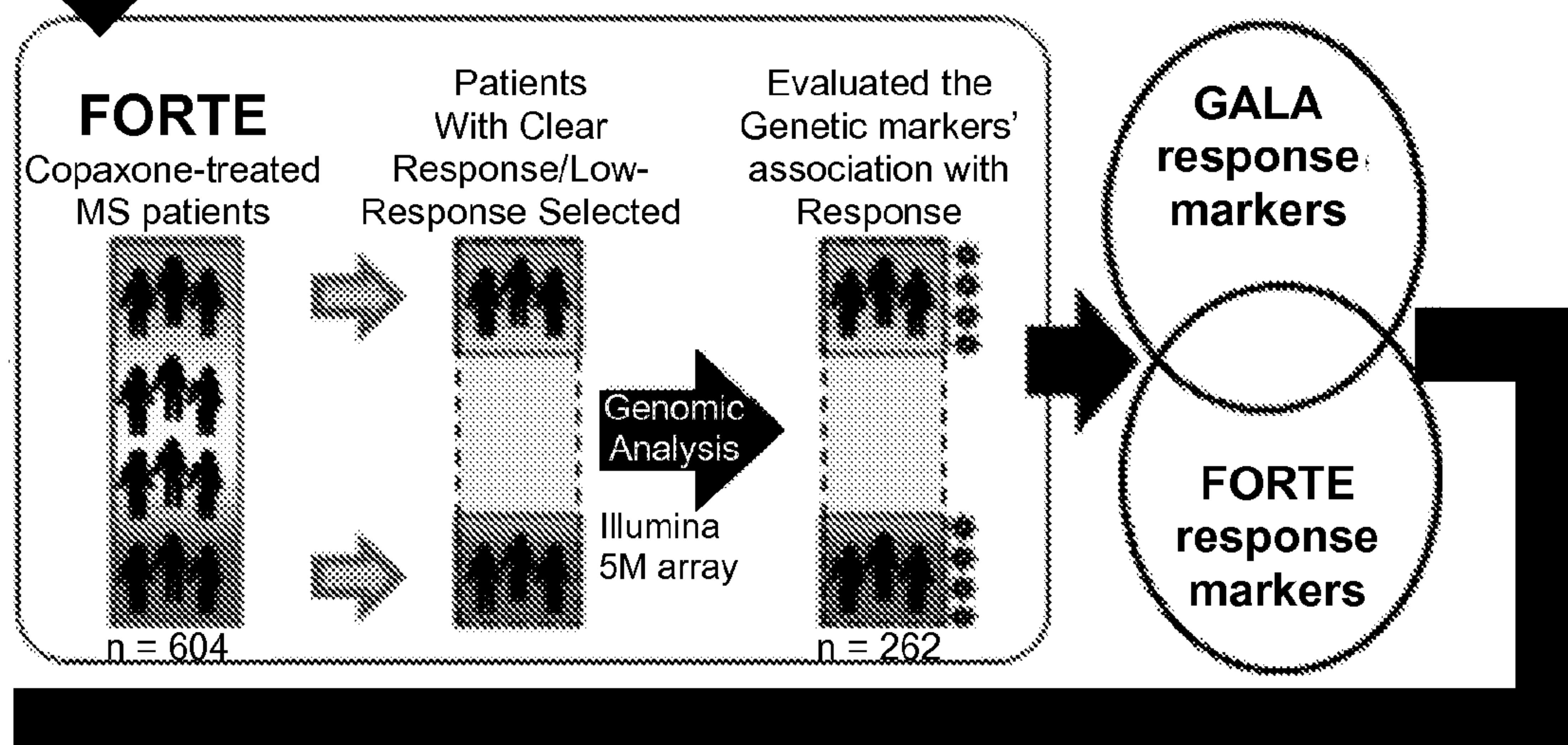


Figure 6

Discovery



Confirmation



Equation for Predicted Response Score =

$$= ([(.0105265)+(Clinical1*coefficient)+ (Clinical2*coefficient)+(SNP1*coefficient)+(SNP2*coefficient)+ \dots+(SNP11*coefficient)]+7.43905)/85.991086$$

The value of clinical covariates and SNPs 1-11 to be input in the equation are determined according to this table:

Variable	Item/SNP ID	Genotype	Recoded
Clinical 1	Log of No. of Relapses in Last 2 Years	n/a	Input patient Log No. of Relapses in Last 2 Years
Clinical 2	Baseline EDSS Score	n/a	Input patient Baseline EDSS Score
SNP 1	rs759458	G G	0
		A G	1
		A A	2
SNP 2	kgp24415534	G G	0
		A G	1
		A A	2
SNP 3	rs3135391	G G	0
		A G	1
		A A	2
SNP 4	kgp8817856	G G	0
		A G	1
		A A	2
SNP 5	rs1894408	C C	0
		C G	1
		G G	2
SNP 6	rs16886004	A A	0
		A G	1
		G G	2
SNP 7	kgp6214351	A A	0
		A G	1
		G G	2
SNP 8	rs10162089	G G	0
		A G	1
		A A	2
SNP 9	kgp7747883	G G	0
		A G	1
		A A	2
SNP 10	kgp6599438	G G	0
		A G	1
		A A	2
SNP 11	kgp8110667	G G	0
		A G	1
		A A	2

The coefficients for each clinical factor and SNP are:

Code	Covariate Name	Coefficient
Clinical 1	Log of No. of Relapses in Last 2 Years	2.92986372
Clinical 2	Baseline EDSS Score	-0.60903763
SNP 1	rs759458	0.58926846
SNP 2	kgp24415534	-2.3993415
SNP 3	rs3135391	-0.1604137
SNP 4	kgp8817856	-0.662872
SNP 5	rs1894408	0.31917131
SNP 6	rs16886004	0.80544267
SNP 7	kgp6214351	-1.03736
SNP 8	rs10162089	0.44599906
SNP 9	kgp7747883	-0.4871921
SNP 10	kgp6599438	-1.6183459
SNP 11	kgp8110667	37.3339568

Threshold:

Patients with a predicted response score of greater than 0.09641 are predicted to be high responders and patients with a predicted response scores of less than 0.09641 are predicted to be less likely to respond.

Figure 8

Equation for Predicted Response Score =

$$= [(0.0105265) + (\text{SNP1} * \text{coefficient}) + (\text{SNP2} * \text{coefficient}) + \dots + (\text{SNP11} * \text{coefficient})] + 5.260164102 / 79.091729112$$

The value of SNPs 1-11 to be input in the equation are determined according to this table:

SNP #	SNP ID	Genotype	Recoded
SNP 1	rs759458	G G	0
		A G	1
		A A	2
SNP 2	kgp24415534	G G	0
		A G	1
		A A	2
SNP 3	rs3135391	G G	0
		A G	1
		A A	2
SNP 4	kgp8817856	G G	0
		A G	1
		A A	2
SNP 5	rs1894408	C C	0
		C G	1
		G G	2
SNP 6	rs16886004	A A	0
		A G	1
		G G	2
SNP 7	kgp6214351	A A	0
		A G	1
		G G	2
SNP 8	rs10162089	G G	0
		A G	1
		A A	2
SNP 9	kgp7747883	G G	0
		A G	1
		A A	2
SNP 10	kgp6599438	G G	0
		A G	1
		A A	2
SNP 11	kgp8110667	G G	0
		A G	1
		A A	2

The coefficients for each SNP are:

Code	Covariate Name	Coefficient
SNP 1	rs759458	0.58926846
SNP 2	kgp24415534	-2.3993415
SNP 3	rs3135391	-0.1604137
SNP 4	kgp8817856	-0.662872
SNP 5	rs1894408	0.31917131
SNP 6	rs16886004	0.80544267
SNP 7	kgp6214351	-1.03736
SNP 8	rs10162089	0.44599906
SNP 9	kgp7747883	-0.4871921
SNP 10	kgp6599438	-1.6183459
SNP 11	kgp8110667	37.3339568

Threshold:

Patients with a predicted response score of greater than 0.075 are predicted to be high responders and patients with a predicted response scores of less than 0.075 are predicted to be less likely to respond.

Figure 9

Sensitivity (%)

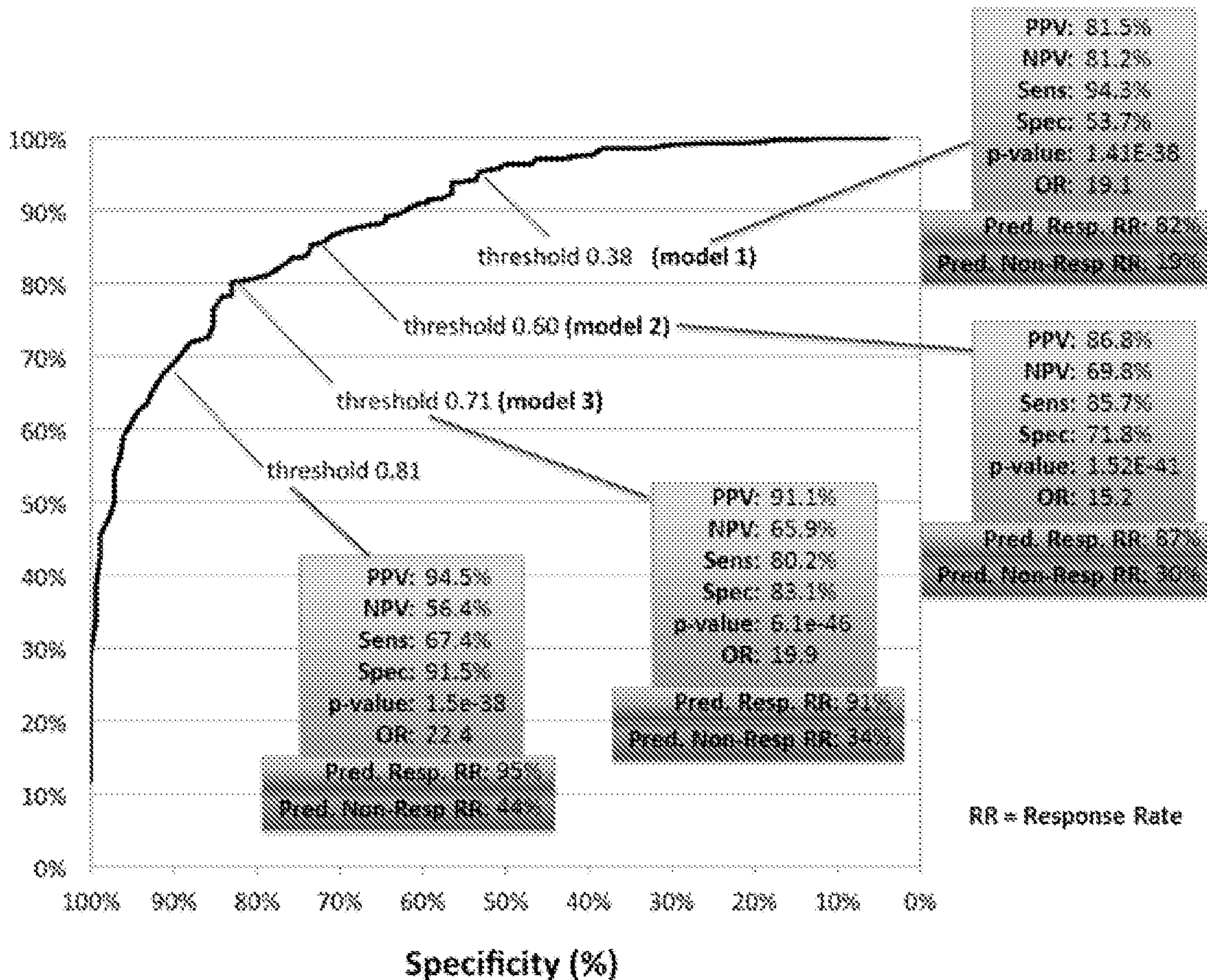


Figure 1