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(54) Title: BIOMARKERS FOR HBV TREATMENT RESPONSE

(57) Abstract: The present invention relates to methods that are useful for predicting the response of hepatitis B virus (HBV) infected patients to pharmacological treatment.

Biomarkers for HBV treatment response

The present invention relates to methods that are useful for predicting the response of hepatitis B virus (HBV) infected patients to pharmacological treatment.

Background of the invention

The hepatitis B virus (HBV) infects 350-400 million people worldwide; one million deaths resulting from cirrhosis, liver failure, and hepatocellular carcinoma due to the infection are recorded annually. The infecting agent, hepatitis B virus (HBV), is a DNA virus which can be transmitted percutaneously, sexually, and perinatally. The prevalence of infection in Asia (≥ 8 %) is substantially higher than in Europe and North America (<2%) (Dienstag J.L., Hepatitis B Virus Infection., N. Engl. J. Med. 2008; 359: 1486-1500). The incidence of HBV acquired perinatally from an infected mother is much higher in Asia, leading to chronic infection in >90% of those exposed (WHO Fact Sheet No 204; revised August 2008). Additionally, 25% of adults who become chronically infected during childhood die from HBV-related liver cancer or cirrhosis (WHO Fact Sheet No 204; revised August 2008). Interferon alpha (IFNα) is a potent activator of anti-viral pathways and additionally mediates numerous immuno-regulatory functions (Muller U., Steinhoff U., Reis L.F. et al., Functional role of type I and type II interferons in antiviral defense, Science 1994; 264: 1918-21).

The efficacy of PEGASYS® (Pegylated IFN alfa 2a 40KD, Peg-IFN) at a dose of 180μg/week in the treatment of HBV was demonstrated in two large-scale pivotal studies. One study was in HBeAg-negative patients (WV16241) and the other in HBeAg-positive patients (WV16240).

WV16241 was conducted between June 2001 and August 2003; 552 HBeAg-negative CHB patients were randomized to one of three treatment arms: PEG-IFN monotherapy, PEG-IFN plus lamivudine or lamivudine alone for 48 weeks. Virologic response (defined as HBV DNA <20,000 copies/mL) assessed 24 weeks after treatment cessation was comparable in the groups

that received PEG-IFN (43% and 44%) and both arms were superior to the lamivudine group (29%) (Marcellin P., Lau G.K., Bonino F. et al., Peginterferon alfa-2a alone, lamivudine alone, and the two in combination in patients with HBeAg-negative chronic hepatitis B, N. Engl. J. Med. 2004; 351: 1206-17).

Study WV16240 was conducted between January 2002 and January 2004. In this study, 814 HBeAg-positive CHB patients were randomized to the same treatment arms as in WV16241, i.e. PEG-IFN monotherapy, PEG-IFN plus lamivudine or lamivudine alone for 48 weeks. Responses assessed 24 weeks after treatment cessation showed a 32% rate of HBeAg seroconversion in the PEG-IFN monotherapy group compared to 27% and 19% with PEG-IFN + lamivudine and lamivudine monotherapy respectively (Lau G.K., Piratvisuth T,. Luo K.X. et al., Peginterferon Alfa-2a, Lamivudine, and the Combination for HBeAg-Positive Chronic Hepatitis B, N. Engl. J. Med. 2005; 352: 2682-95). Metaanalysis of controlled HBV clinical studies has demonstrated that PEG-IFN-containing treatment facilitated significant HBsAg clearance or seroconversion in CHB patients over a lamivudine regimen (Li W.C., Wang M.R., Kong L.B. et al., Peginterferon alpha-based therapy for chronic hepatitis B focusing on HBsAg clearance or seroconversion: a meta-analysis of controlled clinical trials, BMC Infect. Dis. 2011; 11: 165-177).

More recently, the Neptune study (WV19432) was conducted between May 2007 and April 2010 and compared PEG-IFN administered as either 90 or 180 µg/week administered over either 24 or 48 weeks in HBeAg-positive patients (Liaw Y.F., Jia J.D., Chan H.L. et al., Shorter durations and lower doses of peginterferon alfa-2a are associated with inferior hepatitis B e antigen seroconversion rates in hepatitis B virus genotypes B or C, Hepatology 2011; 54: 1591-9). Efficacy was determined at 24 weeks following the end of treatment. This study, demonstrated that both the lower dose and shorter durations of treatment were inferior to the approved dose and duration previously used in the WV16240 study, thus confirming that the approved treatment regimen of i.e. 180µg/week for 48 weeks is the most beneficial for patients with HBeAg-positive CHB.

However, despite the fact that PEG-IFN has been successfully used in the treatment of CHB, little is known of the impact of host factors (genetic and non-genetic) and viral factors on treatment response.

Although viral and environmental factors play important roles in HBV pathogenesis, genetic influence is clearly present. While small genetic studies have suggested the possible implications of host immune/inflammation factors (e.g. HLA, cytokine, inhibitory molecule) in the outcomes of HBV infection, a genome-wide association study (GWAS) clearly demonstrated that 11 single nucleotide polymorphisms (SNPs) across the human leukocyte antigen (HLA)-DP gene region are significantly associated with the development of persistent chronic hepatitis B virus carriers in the Japanese and Thai HBV cohorts (Kamatani Y., Wattanapokayakit S., Ochi H. et al., A genome-wide association study identifies variants in the HLA-DP locus associated with chronic hepatitis B in Asians. Nat. Genet. 2009; 41: 591-595). Subsequently this finding was also confirmed in a separate Chinese cohort study using a TaqMan based genotyping assay (Guo X., Zhang Y., Li J. et al., Strong influence of human leukocyte antigen (HLA)-DP gene variants on development of persistent chronic hepatitis B virus carriers in the Han Chinese population, Hepatology 2011; 53: 422-8). Furthermore, a separate GWAS and replication analysis concluded similar results that there is significant association between the HLA-DP locus and the protective effects against persistent HBV infection in Japanese and Korean populations (Nishida N., Sawai H., Matsuura K. et al., Genome-wide association study confirming association of HLA-DP with protection against chronic hepatitis B and viral clearance in Japanese and Korean. PLos One 2012; 7: e39175). Finally, two additional SNPs (rs2856718 and rs7453920) within the HLA-DQ locus were found to have an independent effect of HLA-DQ variants on CHB susceptibility (Mbarek H., Ochi H., Urabe Y. et al., A genome-wide association study of chronic hepatitis B identified novel risk locus in a Japanese population, Hum. Mol. Genet. 2011; 20: 3884-92). Taken together, robust genetic evidence suggests that in the Asian population, polymorphic variations at the HLA region contribute significantly to the progression of chronic hepatitis B following acute infection in Asian populations.

Meta-analysis of controlled HBV clinical trials has demonstrated that conventional IFN alfa- or pegylated IFN alfa (2a or 2b)-containing treatment facilitated significant HBsAg clearance or seroconversion in CHB patients over lamivudine regimens (Li W.C., Wang M.R., Kong L.B. et al., Peginterferon alpha-based therapy for chronic hepatitis B focusing on HBsAg clearance or seroconversion: a meta-analysis of controlled clinical trials, BMC Infect. Dis. 2011; 11: 165-177). However, despite the fact that Peg-IFN has been successfully used in the treatment of CHB, little is known regarding the relationship between treatment response and the impact of host factors at the level of single nucleotide polymorphisms (SNPs). Pegylated interferon alfa, in

combination with ribavirin (RBV) has been successfully used in the treatment of chronic hepatitis C virus (HCV) infection. A major scientific finding in how HCV patients respond to Peg-IFN/RBV treatment is that via genome-wide association studies (GWAS), genetic polymorphisms around the gene IL28B on chromosome 19 are strongly associated with treatment outcome (Ge D., Fellay J., Thompson A.J. et al., Genetic variation in IL28B predicts hepatitis C treatment-induced viral clearance, Nature 2009; 461: 399-401; Tanaka Y., Nishida N., Sugiyama M. et al., Genome-wide association of IL28B with response to pegylated interferon-alpha and ribavirin therapy for chronic hepatitis C, Nat. Genet. 2009; 41: 1105-9; Suppiah V., Moldovan M., Ahlenstiel G. et al., IL28B is associated with response to chronic hepatitis C interferon-alpha and ribavirin therapy, Nat. Genet. 2009; 41: 1100-4). IL28B encoded protein is a type III IFN (IFN-λ3) and forms a cytokine gene cluster with IL28A and IL29 at the same chromosomal region. IL28B can be induced by viral infection and has antiviral activity. However, in CHB patients treated with Peg-IFN, there are limited and somewhat conflicting data on the association of specific SNPs (e.g. rs12989760, rs8099917, rs12980275) around IL28B region with treatment responses (Lampertico P., Vigano M., Cheroni C. et al., Genetic variation in IL28B polymorphism may predict HBsAg clearance in genotype D, HBeAg negative patients treated with interferon alfa, AASLD 2010; Mangia A., Santoro R., Mottola et al., Lack of association between IL28B variants and HBsAg clearance after interferon treatment, EASL 2011; de Niet A., Takkenberg R.B., Benayed R. et al., Genetic variation in IL28B and treatment outcome in HBeAg-positive and -negative chronic hepatitis B patients treated with Peg interferon alfa-2a and adefovir, Scand. J. Gastroenterol. 2012, 47: 475-81; Sonneveld M.J., Wong V.W., Woltman A.M. et al., Polymorphisms near IL28B and serologic response to peginterferon in HBeAg-positive patients with chronic hepatitis B, Gastroenterology 2012; 142: 513-520).

IL28B genotype predicts response to pegylated-interferon (peg-IFN)-based therapy in chronic hepatitis C. Holmes et al. investigated whether IL28B genotype is associated with peg-IFN treatment outcomes in a predominantly Asian CHB cohort. IL28B genotype was determined for 96 patients (Holmes et al., IL28B genotype is not useful for predicting treatment outcome in Asian chronic hepatitis B patients treated with pegylated interferon-alpha, J. Gastroenterol. Hepatol., 2013, 28(5): 861-6). 88% were Asian, 62% were HBeAg-positive and 13% were METAVIR stage F3-4. Median follow-up time was 39.3 months. The majority of patients carried the CC IL28B genotype (84%). IL28B genotype did not differ according to HBeAg status. The

primary endpoints were achieved in 27% of HBeAg-positive and 61% of HBeAg-negative patients. There was no association between IL28B genotype and the primary endpoint in either group. Furthermore, there was no difference in HBeAg loss alone, HBsAg loss, ALT normalisation or on-treatment HBV DNA levels according to IL28B genotype.

With whole blood sample collection in CHB patients who have been treated with Peg-IFN and have definite clinical outcomes, it is well justified that mechanistically understanding how host genetic factors affect treatment response and HBV disease biology will be tremendously beneficial to the future clinical practice of identifying patients who are likely to respond to Peg-IFN treatment and to the development of new HBV medicines.

Summary of the invention

The present invention provides for methods for identifying patients who will respond to an anti-HBV treatment with anti-HBV agents, such as an interferon.

One embodiment of the invention provides methods of identifying a patient who may benefit from treatment with an anti-HBV therapy comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *CADPS* on chromosome 3 in a sample obtained from the patient, wherein the presence of at least one A allele at rs7633796 indicates that the patient may benefit from the treatment with the anti-HBV treatment.

A further embodiment of the inventions provides methods of predicting responsiveness of a patient suffering from an HBV infection to treatment with an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *CADPS* on chromosome 3 in a sample obtained from the patient, wherein the presence of at least one A allele at rs7633796 indicates that the patient is more likely to be responsive to treatment with the anti-HBV treatment.

Yet another embodiment of the invention provides methods for determining the likelihood that a patient with an HBV infection will exhibit benefit from an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *CADPS* on chromosome 3 in a sample obtained from the patient, wherein the presence of at least one A allele at rs7633796 indicates that the patient has increased likelihood of benefit from the anti-HBV treatment.

Even another embodiment of the invention provides methods for optimizing the therapeutic efficacy of an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *CADPS* on chromosome 3 in a sample obtained from the patient, wherein the presence of at least one A allele at rs7633796 indicates that the patient has increased likelihood of benefit from the anti-HBV treatment.

A further embodiment of the invention provides methods for treating an HBV infection in a patient, the methods comprising: (i) determining the presence of at least one A allele at rs7633796 in gene *CADPS* on chromosome 3 in a sample obtained from the patient and (ii) administering an effective amount of an anti-HBV treatment comprising an interferon to said patient, whereby the HBV infection is treated.

Yet another embodiment of the present invention provides methods for predicting HBeAg seroconversion and HBV DNA <2000 IU/ml at >=24-week follow-up of treatment (responders vs. non-responders) of an HBe-positive patient infected with HBV to interferon treatment comprising: (i) providing a sample from said human subject, detecting the presence of a single nucleotide polymorphism in gene *CADPS* on chromosome 3 and (ii) determining that said patient has a high response rate to interferon treatment measured as HBeAg seroconversion and HBV DNA <2000 IU/ml at >=24-week follow-up of treatment (responders vs. non-responders) if at least one A allele at rs7633796 is present.

Another embodiment of the invention provides methods of identifying a patient who may benefit from treatment with an anti-HBV therapy comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *ARHGEF7* on chromosome 13 in a sample obtained from the patient, wherein the presence of at least one A allele at rs12584550 indicates that the patient may benefit from the treatment with the anti-HBV treatment.

A further embodiment of the inventions provides methods of predicting responsiveness of a patient suffering from an HBV infection to treatment with an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *ARHGEF7* on chromosome 13 in a sample obtained from the patient, wherein the presence of at least one A allele at rs12584550 indicates that the patient is more likely to be responsive to treatment with the anti-HBV treatment.

Yet another embodiment of the invention provides methods for determining the likelihood that a patient with an HBV infection will exhibit benefit from an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *ARHGEF7* on chromosome 13 in a sample obtained from the patient, wherein the presence of at least one A allele at rs12584550 indicates that the patient has increased likelihood of benefit from the anti-HBV treatment.

Even another embodiment of the invention provides methods for optimizing the therapeutic efficacy of an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *ARHGEF7* on chromosome 13 in a sample obtained from the patient, wherein the presence of at least one A allele at rs12584550 indicates that the patient has increased likelihood of benefit from the anti-HBV treatment.

A further embodiment of the invention provides methods for treating an HBV infection in a patient, the methods comprising: (i) determining the presence of at least one A allele at rs12584550 in gene *ARHGEF7* on chromosome 13 in a sample obtained from the patient and (ii) administering an effective amount of an anti-HBV treatment comprising an interferon to said patient, whereby the HBV infection is treated.

Yet another embodiment of the present invention provides methods for predicting HBeAg seroconversion and HBV DNA <2000 IU/ml at >=24-week follow-up of treatment (responders vs. non-responders) of an HBe-positive patient infected with HBV to interferon treatment comprising: (i) providing a sample from said human subject, detecting the presence of a single nucleotide polymorphism in gene *ARHGEF7* on chromosome 13 and (ii) determining that said patient has a high response rate to interferon treatment measured as HBeAg seroconversion and HBV DNA <2000 IU/ml at >=24-week follow-up of treatment (responders vs. non-responders) if at least one A allele at rs12584550 is present.

Another embodiment of the invention provides methods of identifying a patient who may benefit from treatment with an anti-HBV therapy comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *DOCK1* on chromosome 10 in a sample obtained from the patient, wherein the presence of at least one C allele at rs10765101 indicates that the patient may benefit from the treatment with the anti-HBV treatment.

A further embodiment of the inventions provides methods of predicting responsiveness of a patient suffering from an HBV infection to treatment with an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *DOCK1* on chromosome 10 in a sample obtained from the patient, wherein the presence of at least one C allele at rs10765101 indicates that the patient is more likely to be responsive to treatment with the anti-HBV treatment.

Yet another embodiment of the invention provides methods for determining the likelihood that a patient with an HBV infection will exhibit benefit from an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *DOCK1* on chromosome 10 in a sample obtained from the patient, wherein the presence of at least one C allele at rs10765101 indicates that the patient has increased likelihood of benefit from the anti-HBV treatment.

Even another embodiment of the invention provides methods for optimizing the therapeutic efficacy of an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *DOCK1* on chromosome 10 in a sample obtained from the patient, wherein the presence of at least one C allele at rs10765101 indicates that the patient has increased likelihood of benefit from the anti-HBV treatment.

A further embodiment of the invention provides methods for treating an HBV infection in a patient, the methods comprising: (i) determining the presence of at least one C allele at rs10765101 in gene *DOCK1* on chromosome 10 in a sample obtained from the patient and (ii) administering an effective amount of an anti-HBV treatment comprising an interferon to said patient, whereby the HBV infection is treated.

Yet another embodiment of the present invention provides methods for predicting HBeAg seroconversion and HBV DNA <2000 IU/ml at >=24-week follow-up of treatment (responders vs. non-responders) of an HBe-positive patient infected with HBV to interferon treatment comprising: (i) providing a sample from said human subject, detecting the presence of a single nucleotide polymorphism in gene *DOCK1* on chromosome 10 and (ii) determining that said patient has a high response rate to interferon treatment measured as HBeAg seroconversion and HBV DNA <2000 IU/ml at >=24-week follow-up of treatment (responders vs. non-responders) if at least one C allele at rs10765101 is present.

Another embodiment of the invention provides methods of identifying a patient who may benefit from treatment with an anti-HBV therapy comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *SYNJ1* on chromosome 21 in a sample obtained from the patient, wherein the presence of at least one G allele at rs10470165 indicates that the patient may benefit from the treatment with the anti-HBV treatment.

A further embodiment of the inventions provides methods of predicting responsiveness of a patient suffering from an HBV infection to treatment with an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *SYNJ1* on chromosome 21 in a sample obtained from the patient, wherein the presence of at least one G allele at rs10470165 indicates that the patient is more likely to be responsive to treatment with the anti-HBV treatment.

Yet another embodiment of the invention provides methods for determining the likelihood that a patient with an HBV infection will exhibit benefit from an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *SYNJ1* on chromosome 21 in a sample obtained from the patient, wherein the presence of at least one G allele at rs10470165 indicates that the patient has increased likelihood of benefit from the anti-HBV treatment.

Even another embodiment of the invention provides methods for optimizing the therapeutic efficacy of an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *SYNJ1* on chromosome 21 in a sample obtained from the patient, wherein the presence of at least one G allele at rs10470165 indicates that the patient has increased likelihood of benefit from the anti-HBV treatment.

A further embodiment of the invention provides methods for treating an HBV infection in a patient, the methods comprising: (i) determining the presence of at least one G allele at rs10470165 in gene *SYNJ1* on chromosome 21 in a sample obtained from the patient and (ii) administering an effective amount of an anti-HBV treatment comprising an interferon to said patient, whereby the HBV infection is treated.

Yet another embodiment of the present invention provides methods for predicting HBeAg seroconversion and HBV DNA <2000 IU/ml at >=24-week follow-up of treatment (responders vs. non-responders) of an HBe-positive patient infected with HBV to interferon treatment comprising: (i) providing a sample from said human subject, detecting the presence of a single nucleotide polymorphism in gene *SYNJ1* on chromosome 21 and (ii) determining that said patient has a high response rate to interferon treatment measured as HBeAg seroconversion and HBV DNA <2000 IU/ml at >=24-week follow-up of treatment (responders vs. non-responders) if at least one G allele at rs10470165 is present.

Another embodiment of the invention provides methods of identifying a patient who may benefit from treatment with an anti-HBV therapy comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *EGFR* on chromosome 7 in a sample obtained from the patient, wherein the presence of at least one A allele at rs845562 indicates that the patient may benefit from the treatment with the anti-HBV treatment.

A further embodiment of the inventions provides methods of predicting responsiveness of a patient suffering from an HBV infection to treatment with an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *EGFR* on chromosome 7 in a sample obtained from the patient, wherein the presence of at least one A allele at rs845562 indicates that the patient is more likely to be responsive to treatment with the anti-HBV treatment.

Yet another embodiment of the invention provides methods for determining the likelihood that a patient with an HBV infection will exhibit benefit from an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *EGFR* on chromosome 7 in a sample obtained from the patient, wherein the presence of at least one A allele at rs845562 indicates that the patient has increased likelihood of benefit from the anti-HBV treatment.

Even another embodiment of the invention provides methods for optimizing the therapeutic efficacy of an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *EGFR* on chromosome 7 in a sample obtained from the patient, wherein the presence of at least one A allele at rs845562 indicates that the patient has increased likelihood of benefit from the anti-HBV treatment.

A further embodiment of the invention provides methods for treating an HBV infection in a patient, the methods comprising: (i) determining the presence of at least one A allele at rs845562 in gene *EGFR* on chromosome 7 in a sample obtained from the patient and (ii) administering an effective amount of an anti-HBV treatment comprising an interferon to said patient, whereby the HBV infection is treated.

Yet another embodiment of the present invention provides methods for predicting HBeAg seroconversion and HBV DNA <2000 IU/ml at >=24-week follow-up of treatment (responders vs. non-responders) of an HBe-positive patient infected with HBV to interferon treatment comprising: (i) providing a sample from said human subject, detecting the presence of a single nucleotide polymorphism in gene *EGFR* on chromosome 7 and (ii) determining that said patient has a high response rate to interferon treatment measured as HBeAg seroconversion and HBV DNA <2000 IU/ml at >=24-week follow-up of treatment (responders vs. non-responders) if at least one A allele at rs845562 is present.

Another embodiment of the invention provides methods of identifying a patient who may benefit from treatment with an anti-HBV therapy comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *HSPG2* on chromosome 1 in a sample obtained from the patient, wherein the presence of at least one G allele (major allele) at rs4654771 indicates that the patient may benefit from the treatment with the anti-HBV treatment.

A further embodiment of the inventions provides methods of predicting responsiveness of a patient suffering from an HBV infection to treatment with an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *HSPG2* on chromosome 1 in a sample obtained from the patient, wherein the presence of at least one G allele (major allele) at rs4654771 indicates that the patient is more likely to be responsive to treatment with the anti-HBV treatment.

Yet another embodiment of the invention provides methods for determining the likelihood that a patient with an HBV infection will exhibit benefit from an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *HSPG2* on chromosome 1 in a sample obtained from the patient, wherein the presence of at least one G allele (major allele) at rs4654771 indicates that the patient has increased likelihood of benefit from the anti-HBV treatment.

Even another embodiment of the invention provides methods for optimizing the therapeutic efficacy of an anti-HBV treatment comprising an interferon, the methods comprising: determining the presence of a single nucleotide polymorphism in gene *HSPG2* on chromosome 1 in a sample obtained from the patient, wherein the presence of at least one G allele (major allele) at rs4654771 indicates that the patient has increased likelihood of benefit from the anti-HBV treatment.

A further embodiment of the invention provides methods for treating an HBV infection in a patient, the methods comprising: (i) determining the presence of at least one G allele (major allele) at rs4654771 in gene *HSPG2* on chromosome 1 in a sample obtained from the patient and (ii) administering an effective amount of an anti-HBV treatment comprising an interferon to said patient, whereby the HBV infection is treated.

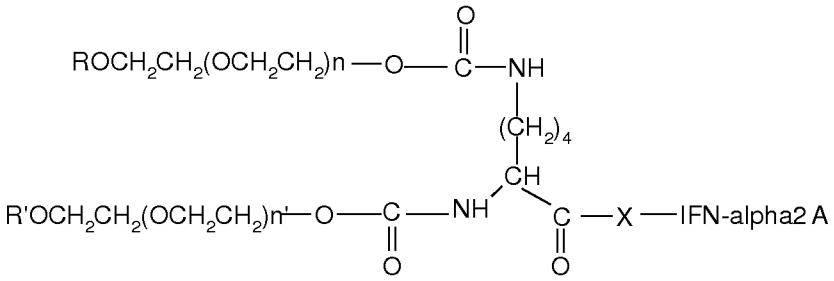
Yet another embodiment of the present invention provides methods for predicting HBeAg seroconversion and HBV DNA <2000 IU/ml at >=24-week follow-up of treatment (responders vs. non-responders) of an HBe-positive patient infected with HBV to interferon treatment comprising: (i) providing a sample from said human subject, detecting the presence of a single nucleotide polymorphism in gene *HSPG2* on chromosome 1 and (ii) determining that said patient has a high response rate to interferon treatment measured as HBeAg seroconversion and HBV DNA <2000 IU/ml at >=24-week follow-up of treatment (responders vs. non-responders) if at least one G allele (major allele) at rs4654771 is present.

Another embodiment of the present invention provides polymorphic signature that predicts responsiveness of a patient suffering from an HBV infection to treatment with an anti-HBV treatment comprising an interferon, said signature comprising the determination of the presence or absence of at least one the following single nucleotide polymorphisms (SNPs) rs2970471, rs4142734, rs10824875, rs9567867, rs2542943, rs604241, rs4899150, rs508636, rs12626242, rs7633796, rs7947950, rs12584550, rs10765101, rs12435908, rs845023, rs12627478, rs10470165, rs1867475, rs9856296, rs6776709, rs4684175, rs4685060, rs4539348, rs13297144, rs11072478, rs260010, rs13395925, rs845562, rs12568559, rs10193128, exm680251, rs4840946, rs4840947, exm680207, rs9288685, rs9322467, rs6733352, rs7633147, rs943172, rs4348723, rs6428677, rs4654771, rs2500499, rs4840939, rs10494323, exm-rs4133289, exm-rs10489849, exm114297, rs10489849, rs17403692, rs2662605, rs17094430, rs11110982, rs11177673, and rs736452, wherein the presence of at least one of these SNPs predicts responsiveness of a patient

suffering from an HBV infection to treatment with an anti-HBV treatment comprising an interferon.

In some embodiments, the interferon is selected from the group of peginterferon alfa-2a, peginterferon alfa-2b, interferon alfa-2a and interferon alfa-2b.

In some embodiments, the interferon is a peginterferon alfa-2a conjugate having the formula:



wherein R and R' are methyl, X is NH, and n and n' are individually or both either 420 or 520.

Brief description of the drawings

Fig. 1: Bar chart of the number of markers by chromosome in the *GWAS Marker Set*. Of 925,371 markers, 1,003 markers were not plotted due to unknown genomic location.

Fig. 2: Scree plot for ancestry analysis.

Fig. 3: The first two principal components of ancestry for HapMap individuals only. Population codes are as listed in Table 3.

Fig. 4: The first two principal components of ancestry for HapMap individuals ; coloured according to population group (Table 3). Overlaid are patients who will be incorporated into *PGx-CN-Interim1* (black crosses) and those that will be incorporated into *PGx-non-CN-Interim1* (grey crosses).

Fig. 5: Manhattan Plots for Endpoint 1

Fig. 6: QQ Plots for Endpoint 1

Fig. 7: Manhattan Plots for Endpoint 2

Fig. 8: QQ Plots for Endpoint 2

Fig. 9: Manhattan Plots for Endpoint 3

Fig. 10: QQ Plots for Endpoint 3

Fig. 11: Manhattan Plots for Endpoint 4

Fig. 12: QQ Plots for Endpoint 4

Fig. 13: Manhattan Plots for Endpoint 5

Fig. 14: QQ Plots for Endpoint 5

Fig. 15: Manhattan Plots for Endpoint 6

Fig. 16: QQ Plots for Endpoint 6

Fig. 17: Interactions among genes associated at the suggestive level with response to Pegasys

Detailed description of the invention

Definitions

To facilitate the understanding of this invention, a number of terms are defined below. Terms defined herein have meanings as commonly understood by a person of ordinary skill in the areas relevant to the present invention. Terms such as “a”, “an” and “the” are not intended to refer to only a singular entity, but include the general class of which a specific example may be used for illustration. The terminology herein is used to describe specific embodiments of the invention, but their usage does not delimit the invention, except as outlined in the claims.

The terms “sample” or "biological sample" refers to a sample of tissue or fluid isolated from an individual, including, but not limited to, for example, tissue biopsy, plasma, serum, whole blood, spinal fluid, lymph fluid, the external sections of the skin, respiratory, intestinal and genitourinary tracts, tears, saliva, milk, blood cells, tumors, organs. Also included are samples of in vitro cell culture constituents (including, but not limited to, conditioned medium resulting from the growth of cells in culture medium, putatively virally infected cells, recombinant cells, and cell components).

The terms "interferon" and "interferon-alpha" are used herein interchangeably and refer to the family of highly homologous species-specific proteins that inhibit viral replication and cellular proliferation and modulate immune response. Typical suitable interferons include, but are not limited to, recombinant interferon alpha-2b such as Intron® A interferon available from Schering Corporation, Kenilworth, N.J., recombinant interferon alpha-2a such as Roferon®-A interferon available from Hoffmann-La Roche, Nutley, N.J., recombinant interferon alpha-2C such as Berofor® alpha 2 interferon available from Boehringer Ingelheim Pharmaceutical, Inc., Ridgefield, Conn., interferon alpha-n1, a purified blend of natural alpha interferons such as Sumiferon® available from Sumitomo, Japan or as Wellferon® interferon alpha-n1 (INS) available from the Glaxo-Wellcome Ltd., London, Great Britain, or a consensus alpha interferon such as those described in U.S. Pat. Nos. 4,897,471 and 4,695,623 (especially Examples 7, 8 or 9 thereof) and the specific product available from Amgen, Inc., Newbury Park, Calif., or interferon alpha-n3 a mixture of natural alpha interferons made by Interferon Sciences and available from the Purdue Frederick Co., Norwalk, Conn., under the Alferon Tradename. The use of interferon alpha-2a or alpha-2b is preferred. Interferons can include pegylated interferons as defined below.

The terms "pegylated interferon", "pegylated interferon alpha" and "peginterferon" are used herein interchangeably and means polyethylene glycol modified conjugates of interferon alpha, preferably interferon alfa-2a and alfa-2b. Typical suitable pegylated interferon alpha include, but are not limited to, Pegasys® and Peg-Intron®.

As used herein, the terms "allele" and "allelic variant" refer to alternative forms of a gene including introns, exons, intron/exon junctions and 3′ and/or 5′ untranslated regions that are associated with a gene or portions thereof. Generally, alleles occupy the same locus or position on homologous chromosomes. When a subject has two identical alleles of a gene, the subject is said to be homozygous for the gene or allele. When a subject has two different alleles of a gene, the subject is said to be heterozygous for the gene. Alleles of a specific gene can differ from each other in a single nucleotide, or several nucleotides, and can include substitutions, deletions, and insertions of nucleotides.

As used herein, the term "polymorphism" refers to the coexistence of more than one form of a nucleic acid, including exons and introns, or portion (e.g., allelic variant) thereof. A portion of a gene of which there are at least two different forms, i.e., two different nucleotide sequences, is referred to as a polymorphic region of a gene. A polymorphic region can be a single nucleotide,

i.e. “single nucleotide polymorphism” or “SNP”, the identity of which differs in different alleles. A polymorphic region can also be several nucleotides long.

Numerous methods for the detection of polymorphisms are known and may be used in conjunction with the present invention. Generally, these include the identification of one or more mutations in the underlying nucleic acid sequence either directly (e.g., in situ hybridization) or indirectly (identifying changes to a secondary molecule, e.g., protein sequence or protein binding).

One well-known method for detecting polymorphisms is allele specific hybridization using probes overlapping the mutation or polymorphic site and having about 5, 10, 20, 25, or 30 nucleotides around the mutation or polymorphic region. For use in a kit, e.g., several probes capable of hybridizing specifically to allelic variants, such as single nucleotide polymorphisms, are provided for the user or even attached to a solid phase support, e.g., a bead or chip.

Abbreviations

AIC	Akaike Information Criterion
ALT	Alanine aminotransferase
Anti-HBs	Antibody to hepatitis B surface antigen
DNA	Deoxyribonucleic acid
GWAS	Genome-wide Association Study
HAV	Hepatitis A Virus
HBe	Hepatitis B 'e' Antigen
HBeAg	Hepatitis B 'e' Antigen
HBV	Hepatitis B Virus
HCV	Hepatitis C Virus
HIV	Human Immunodeficiency Virus
HLA	Human Leucocyte Antigen
HWE	Hardy-Weinberg Equilibrium
IU/ml	International units per milliliter
PCA	Principal Components Analysis
PEGASYS	Pegylated Interferon alpha 2a 40KD; Peg-IFN
Peg-IFN	Pegylated Interferon alpha 2a 40KD; PEGASYS

QC	Quality Checks
qHBsAg	Quantitative Hepatitis B Surface Antigen
S-loss	Surface Antigen Loss
SNP	Single Nucleotide Polymorphism
SPC	Summary of Product Characteristics
TLR	Toll-like Receptor
Tx	Treatment
Vs.	Versus

Examples

Objectives and Endpoints

The objective was to determine genetic variants associated with response to treatment with PEGASYS-containing regimen in patients with Chronic Hepatitis B.

The following primary endpoints were considered:

1. HBe-positive patients: E-seroconversion or S-loss at >=24-week follow-up
2. HBe-positive patients: (E-seroconversion plus HBV DNA<2000 IU/ml) or S-loss at >=24-week follow-up
3. HBe-negative patients: HBV DNA<2000 IU/ml or S-loss at >=24-week follow-up
4. E-seroconversion or S-loss at >=24-week follow-up if HBe-positive and HBV DNA<2000 IU/ml or S-loss at >=24-week follow-up if HBe-negative (1 and 3)
5. (E-seroconversion plus HBV DNA<2000 IU/ml) or S-loss at >=24-week follow-up if HBe-positive and HBV DNA<2000 IU/ml or S-loss at >=24-week follow-up if HBe-negative (2 and 3)
6. S-loss at >=24- week follow-upFor all endpoints and all markers, the null hypothesis of no association, between the genotype and the endpoint, was tested against the two-sided alternative that association exists.

Study Design

A cumulative meta-analysis, of data from company-sponsored clinical trials, and data from patients in General Practice care, is in progress. The combined data will, at the final analysis, comprise up to 1500 patients who have been treated with Pegasys for at least 24 weeks, with or without a nucleotide/ nucleoside analogue, and with 24 weeks of follow-up data available.

The following trials/ patient sources were considered for inclusion:

- RGT (ML22266)
- S-Collate (MV22009)
- SoN (MV22430)
- Switch (ML22265)
- Combo
- New Switch (ML27928)
- NEED
- Italian cohort of PEG.Be.Liver
- Professor Teerha (Thailand): clinical practice patients and some legacy Ph3 patients
- Professor Hongfei Zhang (Beijing, China): clinical practice patients and some legacy Ph3 patients
- Professor Yao Xie (Beijing, China): clinical practice patients
- Professor Xin Yue Chen (Beijing, China): clinical practice patients

Adult patients with chronic hepatitis B (male or female patients ≥18 years of age) must meet the following criteria for study entry:

- Previously enrolled in a Roche study and treated for chronic hepatitis B for at least 24 weeks with Peg-IFN ± nucleoside analogue (lamivudine or entacavir) or Peg-IFN ± nucleotide analogue (adefovir) with ≥24-week post-treatment follow-up or;
- Treated in general practice for chronic hepatitis B with Peg-IFN according to standard of care and in line with the current summary of product characteristics (SPC) / local labeling who have no contra-indication to Peg-IFN therapy as per the local label and have been treated with Peg-IFN for at least 24 weeks and have ≥24-week post-treatment response available at the time of blood collection.

- Patients are not infected with HAV, HCV, or HIV
- Patients should have the following medical record available (either from historical/ongoing study databases or from medical practice notes):
  - Demographics (e.g. age, gender, ethnic origin)
  - Pre-therapy HBeAg status, known or unknown HBV genotype
  - Quantitative HBV DNA by PCR Test in IU/ml over time (e.g. baseline, on-treatment: 12- and 24-week, post-treatment: 24-week)
  - Quantitative HBsAg test (if not available, qualitative HBsAg test) and anti-HBs over time (e.g. baseline, on-treatment: 12- and 24-week, post-treatment: 24-week)
  - Serum ALT over time (e.g. baseline, on-treatment: 12- and 24-week, post-treatment: 24-week)

It is noted that all patients will have received active regimen.

Analysis Populations

The majority of patients will be from China. For the purposes of statistical analysis, four analysis populations were defined as follows.

- *PGx-FAS* is all patients with at least one genotype
- *PGx-GT* is the subset of PGx-*FAS* whose genetic data passes quality checks
- *PGx-CN* is the subset of *PGx-GT* who share a common genetic background in the sense that they cluster with CHB and CHD reference subjects from HapMap version3 (see below)
- *PGx-non-CN* is the remainder of *PGx-GT* who do not fall within *PGx-CN*

Additional suffices are appended as *HBePos* or *HBeNeg* for the HBe-Positive and HBe-Negative subsets respectively, and as *interim1*,... *interim3,* and *final*, according to the stage of the analysis.

Genetic Markers

The GWAS marker panel was the Illumina OmniExpress Exome microarray (www.illumina.com), consisting of greater than 750,000 SNP markers and greater than 250,000

exonic markers. The group of markers which passed quality checks are referred to as the *GWAS Marker Set.*

General Considerations for Data Analysis

The GWAS is hypothesis-free. Markers with unadjusted $p<5x10^{-8}$ were considered to be genome-wide significant. In the interests of statistical power, no adjustment was made for multiple endpoints or multiple rounds of analysis.

Demographic and Baseline Characteristics

Table 1 below shows a brief summary of the baseline and demographic characteristics of the 137 patients in *PGx-FAS-interim1* and separately, of the 653 patients in current *PGx-FAS-interim2*. It was noted that members of the current interim tend to be older in age, and much less likely to self-report as 'Oriental', although a substantial number now self-report as 'Asian'.

Table 1: Baseline and Demographic Characteristics for *PGx-FAS-interim1* and *PGx-FAS-interim2*

Variable	**Category**	**Statistics**
Count (n)		
Sex	Male	n (%)
	Female	n (%)
Age (yr)		Mean (SE)
Race	Oriental	n (%)
	White/ Caucasian	n (%)
	Asian	n (%)
	Other	n (%)
Height (cm)		Mean (SE)
Weight (kg)		Mean (SE)
BMI (kg/m^2)		Mean (SE)
Baseline ALT (U/L)		Median (IQR)

Variable	***PGx-FAS-interim1***	***PGx-FAS-interim2***
Count (n)	137	653
Sex	88 (64%)	433 (66%)
	49 (36%)	220 (34%)
Age (yr)	32.25 (0.848)	38.19 (0.451)
Race	119 (87%)	270 (41%)
	7 (5%)	229 (35%)

Variable	*PGx-FAS-interim1*	*PGx-FAS-interim2*
	0 (0%)	112 (17%)
	11 (8%)	42 (6%)
Height (cm)	168.26 (0.766)	167.9 (0.342)
Weight (kg)	67.74 (1.43)	66.93 (0.597)
BMI (kg/m^2)	23.78 (0.416)	23.58 (0.167)
Baseline ALT (U/L)	123 (119)	92 (104)

Analysis of Gentic Data

Quality Checks by Patient

Methods

The following criteria were assessed, on the basis of unfiltered GWAS data, in 653 patients of any self-reported race (*PGx-FAS-Interim2).*

- <30% heterozygosity genome-wide
- <5% missing genotype data
- Reported sex consistent with X-chromosome data
- <30% genotype-concordance with another sample

Results

All patients displayed <30% heterozygosity genome-wide. Three patients namely, 4360, 8529 and 8076 had 5% or more missing genotypes. Two samples, attributed to 5076 and 8554, were expected to be female, but showed high levels of X-chromosome homozygosity. Two pairs namely,6454 and 9850, and 9114 and 9180 were seen to be first-degree relative pairs so for each pair, the patient with a higher level of missing genotype data was excluded from consideration.

In this way, seven patients were excluded from further analysis; their details are provided in Table 2 below. The remaining 646 patients, whose genetic data satisfied the criteria above, were incorporated into the *PGx-GT-Interim2* Set.

Table 2: Seven patients whose genetic data failed quality checks; NA represents missing

ANONID	PROTO	AGE	SEX	RACE
4360	GV28855	61	MALE	WHITE
8529	GV28855	52	MALE	WHITE

ANONID	PROTO	AGE	SEX	RACE
8076	MV22430	28	MALE	ORIENTAL
5076	GV28855	45	FEMALE	WHITE
8554	MV22430	35	FEMALE	MAORI
6454	MV22430	55	FEMALE	CAUCASIAN
9114	GV28855	32	MALE	WHITE

ANONID	HGTCM	WGTKG	BMI	GENO	HBE_BS
4360	NA	NA	NA	A	POSITIVE
8529	NA	NA	NA	NA	NEGATIVE
8076	175	65	21.22449	B	POSITIVE
5076	NA	NA	NA	NA	NA
8554	173	77	25.72756	D	POSITIVE
6454	170	98.9	34.22145	B	POSITIVE
9114	NA	NA	NA	D	POSITIVE

Quality Checks by Marker

Methods

Markers were assessed for missing data. Those with greater than 5% missing data were excluded from further analysis.

Results

It was noted that all of the first interim data, and a subset of the second interim data, were derived from Human Omni Express Exome 8v1B, whereas the majority of the second interim data were derived from Human Omni Express Exome 8v1.2A.

In order to perform the meta-analysis, the overlapping set of 925,371 markers, with <5% missing overall, was incorporated into the *GWAS Marker Set*. Their distribution by chromosome is shown in Figure 1.

In the current interim analysis, markers were categorized as rare or non-rare, using a frequency threshold of 5%. In this way, a total of 323782 markers were considered rare; 601,589 were considered non-rare.

Multivariate Analysis of Ancestry

Principal Components Analysis (PCA) is a technique for reducing the dimensionality of a data set. It linearly transforms a set of variables into a smaller set of uncorrelated variables representing most of the information in the original set (Dunteman, 1989). In the current study, the marker variables were transformed into principal components which were compared to self-reported ethnic groupings. The objective is, in preparation for association testing, to determine clusters of individuals who share a homogeneous genetic background.

A suitable set of 134,575 markers for ancestry analysis was obtained as described in statistical report for Interim Analysis 1. Of this set, 131,924 had at least 5% frequency in interim 2 data. PCA was therefore applied using 131,924 markers, genotyped across 646 study individuals and 988 HapMap reference individuals (Table 3).

Table 3: Details of the HapMap version 3 reference subjects

Code	Description	Count
MKK	Maasai in Kinyawa, Kenya	143
LWK	Luhya in Webuye, Kenya	90
YRI	Yoruba in Ibadan, Nigeria	113
ASW	African ancestry in Southwest USA	49
CEU	Utah residents with Northern and Western European ancestry from the CEPH collection	112
TSI	Tuscans in Italy	88
MEX	Mexican ancestry in Los Angeles, California	50
GIH	Gujarati Indians in Houston, Texas	88
JPT	Japanese in Tokyo, Japan	86
CHD	Chinese in Metropolitan Denver, Colorado	85
CHB	Han Chinese in Bejing, China	84
	TOTAL	988

Fig. 2 shows the scree plot for the analysis. It is clear that the majority of information, indicated by the highest eigenvalues, was obtained from the first two principal components of ancestry, with little gain in information from subsequent components.

Fig. 3 shows the results of PCA for the HapMap reference data only. Four clusters are visible in this two-dimensional representation. Reading clockwise from top left, they are: African origin (blue/ orange/ pink/ maroon), Southeast Asian (yellow/ blue/ green), Mexican (dark green) and South Asian Origin (grey), and Northern and Western European (blue/ red).

Figure 4 shows the same data with study participants overlaid as crosses. Patients included in *PGx-CN-Interim2* are given by black crosses; patients included in *PGx-nonCN-Interim2* are given by grey crosses. As observed in the first interim analysis, the *PGx-CN-Interim2* study participants represent a genetically more diverse group of individuals than the reference set. The study participants are likely to have been drawn from different countries in South-East Asia.

For the purposes of genetic analysis, *PGx-CN-Interim2* was therefore made up of the 390 patients falling in a cluster around the Chinese and Japanese reference individuals. A total of 256 patients, whose plotted ancestry clearly departed from that cluster, made up *PGx-non-CN-Interim2*.

The number of patients in each planned analysis is given in Table 4 below. As stated earlier, the six endpoints are numbered as follows:

1. HBe-positive patients: E-seroconversion or S-loss at >=24-week follow-up
2. HBe-positive patients: (E-seroconversion plus HBV DNA<2000 IU/ml) or S-loss at >=24-week follow-up
3. HBe-negative patients: HBV DNA<2000 IU/ml or S-loss at >=24-week follow-up
4. E-seroconversion or S-loss at >=24-week follow-up if HBe-positive and HBV DNA<2000 IU/ml or S-loss at >=24-week follow-up if HBe-negative (1 and 3)
5. (E-seroconversion plus HBV DNA<2000 IU/ml) or S-loss at >=24-week follow-up if HBe-positive and HBV DNA<2000 IU/ml or S-loss at >=24-week follow-up if HBe-negative (2 and 3)
6. S-loss at >=24- week follow-up

It is noted that 24 patients did not have HBe data, so their response, as defined by endpoints 1-5, could not be determined. Furthermore, six of the analyses (each to be performed under two assumed modes of inheritance) contained at least one group with fewer than 30 patients, and so were not expected to be informative.

Table 4: Number of patients in each planned analysis

Endpoint	Analysis Set	Non-Responders	Responders	Total
1	*PGx-CN-HBePos*	247	92	339
	PGx-nonCN-HBePos	40	12	52
	PGx-GT-HBePos	287	104	391

Endpoint	Analysis Set	Non-Responders	Responders	Total
2	*PGx-CN-HBePos*	280	59	339
	PGx-nonCN-HBePos	41	11	52
	PGx-GT-HBePos	321	70	391
3	*PGx-CN-HBeNeg*	16	31	47
	PGx-nonCN-HBeNeg	79	93	172
	PGx-GT-HBeNeg	95	124	219
4	*PGx-CN*	263	123	386
	PGx-nonCN	119	105	224
	PGx-GT	382	228	610
5	*PGx-CN*	296	90	386
	PGx-nonCN	120	104	224
	PGx-GT	416	194	610
6	*PGx-CN*	364	14	378
	PGx-nonCN	209	12	221
	PGx-GT	573	26	599

Assessment of Covariates

In order to determine the covariates for the genome-wide association analysis, a series of variables were tested for association with each endpoint, using backwards stepwise regression. In accordance with the planned association analysis, the subject set for Endpoints 1,and 2 was *PGx-GT-HBe-Pos-Interim2* (n=391); the subject set for Endpoint 3 was *PGx-GT-HBe-Neg-Interim2* (n=231) and the subject set for endpoints 4, 5 and 6 was all members of *PGx-GT-Interim2* (n=646). Backwards steps were taken on the basis of the Akaike Information Criterion (AIC).

The covariates in the full model were as follows: Age, Sex, Baseline HBV DNA, Baseline ALT, HBV genotype, Concomitant use of nucleotide/ nucleoside analogues, and Study. Principal Components of Ancestry were included for Endpoints 4 and 5, due to inclusion of both HBe-positive and HBe-negative groups, together with reasonable responder counts. Baseline HBV and Baseline ALT were both log-transformed in order to improve symmetry.

Tables 5-10 show the covariates selected for Endpoints 1-6. It can be seen that baseline HBV DNA and baseline ALT were each selected in five out of six models.

Table 5: Covariates selected by backwards stepwise regression for Endpoint 1

Variable	Odds Ratio	95% CI	P-value
(Intercept)	1.23	0.16-9.56	0.8446
LOGDNA0	0.80	0.73-0.88	<0.0001
LOGALT0	2.05	1.46-2.89	<0.0001
NUCLO_N	0.33	0.16-0.66	0.0019
ML21827	0.36	0.14-0.96	0.0422
MV22430	0.62	0.28-1.37	0.2360

Table 6: Covariates selected by backwards stepwise regression for Endpoint 2

Variable	Odds Ratio	95% CI	P-value
(Intercept)	1.35	0.14-13.36	0.7992
LOGDNA0	0.81	0.73-0.90	<0.0001
LOGALT0	1.96	1.34-2.86	0.0005
NUCLO_N	0.26	0.10-0.67	0.0051
ML21827	0.16	0.05-0.54	0.0031
MV22430	0.30	0.11-0.81	0.0175

Table 7: Covariates selected by backwards stepwise regression for Endpoint 3

Variable	Odds Ratio	95% CI	P-value
(Intercept)	9.40	3.61-24.47	<0.0001
LOGDNA0	0.84	0.77-0.91	<0.0001

Table 8: Covariates selected by backwards stepwise regression for Endpoint 4

Variable	Odds Ratio	95% CI	P-value
(Intercept)	14.86	3.96-55.69	<0.0001
LOGDNA0	0.76	0.71-0.82	<0.0001
LOGALT0	1.64	1.26-2.14	0.0002
GENO_D	0.64	0.35-1.19	0.1584
NUCLO_N	0.28	0.13-0.56	0.0004
PC3	0.00	0.00-0.00	0.0020
ML21827	0.24	0.10-0.59	0.0020
MV22430	0.40	0.19-0.83	0.0145

Table 9: Covariates selected by backwards stepwise regression for Endpoint 5

Variable	Odds Ratio	95% CI	P-value
(Intercept)	26.04	5.71-118.84	<0.0001
LOGDNA0	0.76	0.71-0.81	<0.0001
LOGALT0	1.54	1.16-2.04	0.0025
GENO_D	0.62	0.33-1.17	0.1391
NUCLO_N	0.21	0.08-0.54	0.0013
PC3	0	0-0	0.0024
ML21827	0.09	0.03-0.30	<0.0001
MV22430	0.18	0.07-0.45	0.0003

Table 10: Covariates selected by backwards stepwise regression for Endpoint 6

Variable	Odds Ratio	95% CI	P-value
(Intercept)	0.15	0.01-2.10	0.1571
AGE	1.04	1.00-1.07	0.0365
LOGALT0	0.55	0.34-0.91	0.0197

Univariate Association Analysis

Methods

Due to the modest group counts in the current interim analysis, markers were excluded from single-point association analysis if they had frequency less than 5%. The remaining 601,589 markers were coded in two ways as follows. Firstly they were coded according to an additive model, given by the count of the number of minor alleles. Secondly they were coded according to a dominant model of inheritance, based upon carriage of the minor allele.

Thirty-six rounds of association analysis were conducted due to three patient sets and six endpoints, each under two modes of inheritance. The following model was fitted using multivariate logistic regression:

Endpoint=Intercept + [Covariates]+ Marker

Covariates were applied as selected above (Section 8.4). In addition, adjustments for study were applied in all analyses, and adjustments for first two principal components of ancestry were applied in analyses of subsets of *PGx-GT-Interim2* and *PGx-nonCN-Interim2*.

The significance of each marker was determined using a t-test. The genomic control lambda was calculated for each GWAS analysis and QQ-plots were examined, but no clear evidence of test-statistic inflation was found (Devlin and Roeder 1999). Maximum lambda was 1.06.

All markers were tested, using a chi-square test, for departure from Hardy-Weinberg Equilibrium (HWE) in *PGx-GT-Interim2* , *PGx-nonCN-Interim2* and *PGx-CN-Interim2*. The results were used to assist in the interpretation of association analysis output. In the tabulated results below, both the minor allele frequency (MAF) and the Hardy-Weinberg result are shown for the relevant, ancestry-defined patient-group.

Results for Endpoint 1

Figures 5 and 6 show the Manhattan plots and QQ plots respectively, for Endpoint 1. The first four QQ-plots are seen to track the 45-degree line, indicating that the p-value distributions are approximately as expected by chance. The QQ-plots for *PGx-nonCN-HBe-Pos-Interim2* both dip below the 45-degree line, indicating reduced statistical power; the final two Manhattan plots are correspondingly flat. It was noted that there were only 12 responders in these last two analyses.

Details of markers with $p<10^{-5}$ are given in Tables 11-14. No marker had $p<10^{-5}$ in *PGx-nonCN-HBe-Pos-Interim2*, under either mode of inheritance.

Table 11: Association Results with $p<10^{-5}$ for Endpoint 1 in *PGx-CN-HBe-Pos-Interim2,* additive model

Chr	SNP	BP	HWE(p)	MAF
7	rs2970471	101467854	1.0000	0.4192
10	rs4142734	54824741	0.5089	0.2577
10	rs10824875	54828992	0.5089	0.2577
13	rs9567867	48033401	0.8513	0.1615

Chr	SNP	Beta	p-value	Variant	Gene
7	rs2970471	2.6570	3.10e-06	INTRONIC	CUTL1
10	rs4142734	2.8220	9.45e-06	INTERGENIC	NA
10	rs10824875	2.8220	9.45e-06	INTERGENIC	NA
13	rs9567867	3.3960	6.18e-06	INTERGENIC	NA

Table 12: Association Results with $p<10^{-5}$ for Endpoint 1 in *PGx-CN-HBe-Pos-Interim2,* dominant model

Chr	SNP	BP	HWE(p)	MAF
2	rs2542943	172424963	0.7466	0.3769
11	rs604241	133883070	0.3933	0.3872
13	rs9567867	48033401	0.8513	0.1615
14	rs4899150	65344400	0.0986	0.4295

Chr	SNP	Beta	p-value	Variant	Gene
2	rs2542943	0.2862	5.09e-06	INTERGENIC	NA
11	rs604241	0.2907	9.58e-06	INTERGENIC	NA
13	rs9567867	3.9710	3.39e-06	INTERGENIC	NA
14	rs4899150	0.2996	9.96e-06	INTERGENIC	NA

Table 13: Association Results with $p<10^{-5}$ for Endpoint 1 in *PGx-GT-HBe-Pos-Interim2,* additive model

Chr	SNP	BP	HWE(p)	MAF
7	rs2970471	101467854	0.6282	0.4187
13	rs9567867	48033401	1.0000	0.1788

Chr	SNP	Beta	p-value	Variant	Gene
7	rs2970471	2.3950	5.01e-06	INTRONIC	CUTL1
13	rs9567867	3.3230	1.86e-06	INTERGENIC	NA

Table 14: Association Results with $p<10^{-5}$ for Endpoint 1 in *PGx-GT-HBe-Pos-Interim2,* dominant model

Chr	SNP	BP	HWE(p)	MAF
2	rs2542943	172424963	0.0044	0.4721
5	rs508636	80311835	0.1432	0.2248
13	rs9567867	48033401	1.0000	0.1788
14	rs4899150	65344400	2.69e-10	0.3909
21	rs12626242	34111588	1.0000	0.0759

Chr	SNP	Beta	p-value	Variant	Gene
2	rs2542943	0.2931	1.85e-06	INTERGENIC	NA
5	rs508636	3.1830	9.91e-06	INTRONIC	RASGRF2
13	rs9567867	3.9500	7.61e-07	INTERGENIC	NA
14	rs4899150	0.2958	8.41e-06	INTERGENIC	NA
21	rs12626242	3.8680	8.38e-06	INTRONIC	C21orf66

Results for Endpoint 2

Figures 7 and 8 show the Manhattan Plots and QQ plots respectively, for Endpoint 2. Details of markers with $p<10^{-5}$ are given in Tables 15-18. No marker had $p<10^{-5}$ in *PGx-nonCN-HBe-Pos-Interim2*, under either mode of inheritance however, there were only 11 responders in this group. The QQ-plots were seen to curve downwards and the Manhattan plots were depressed.

Table 15: Association Results with $p<10^{-5}$ for Endpoint 2 in *PGx-CN-HBe-Pos-Interim2,* additive model

Chr	SNP	BP	HWE(p)	MAF
3	rs7633796	62758410	0.1011	0.1897
10	rs4142734	54824741	0.5089	0.2577
10	rs10824875	54828992	0.5089	0.2577
11	rs7947950	117312089	0.4865	0.1256
13	rs12584550	111769770	0.2126	0.3372

Chr	SNP	Beta	p-value	Variant	Gene
3	rs7633796	3.4130	1.17e-06	INTRONIC	CADPS
10	rs4142734	3.1980	8.96e-06	INTERGENIC	NA
10	rs10824875	3.1980	8.96e-06	INTERGENIC	NA
11	rs7947950	4.2420	4.43e-06	INTRONIC	DSCAML1
13	rs12584550	2.9350	7.14e-06	INTRONIC	ARHGEF7

Table 16: Association Results with $p<10^{-5}$ for Endpoint 2 in *PGx-CN-HBe-Pos-Interim2,* dominant model

Chr	SNP	BP	HWE(p)	MAF
11	rs7947950	117312089	0.4865	0.1256
14	rs4899150	65344400	0.0986	0.4295

Chr	SNP	Beta	p-value	Variant	Gene
11	rs7947950	4.4610	9.28e-06	INTRONIC	DSCAML1
14	rs4899150	0.2208	2.81e-06	INTERGENIC	NA

Table 17: Association Results with $p<10^{-5}$ for Endpoint 2 in *PGx-GT-HBe-Pos-Interim2,* additive model

Chr	SNP	BP	HWE(p)	MAF
3	rs7633796	62758410	0.0081	0.2786

Chr	SNP	Beta	p-value	Variant	Gene
3	rs7633796	2.7920	8.40e-06	INTRONIC	CADPS

Table 18: Association Results with $p<10^{-5}$ for Endpoint 2 in *PGx-GT-HBe-Pos-Interim2,* dominant model

Chr	SNP	BP	HWE(p)	MAF
10	rs10765101	129246566	0.4655	0.1602
14	rs4899150	65344400	2.69e-10	0.3909
14	rs12435908	66121468	5.65e-07	0.3104
21	rs845023	34000493	1.0000	0.0760
21	rs12627478	34114123	1.0000	0.0759
21	rs12626242	34111588	1.0000	0.0759
21	rs10470165	34020653	1.0000	0.0760

Chr	SNP	Beta	p-value	Variant	Gene
10	rs10765101	4.2420	3.97e-06	INTRONIC	DOCK1
14	rs4899150	0.2231	3.28e-06	INTERGENIC	NA
14	rs12435908	5.6830	8.29e-06	INTRONIC	FUT8
21	rs845023	4.3210	7.31e-06	DOWNSTREAM	NA
21	rs12627478	4.3720	6.38e-06	INTRONIC	C21orf66
21	rs12626242	4.5990	2.73e-06	INTRONIC	C21orf66
21	rs10470165	4.3290	7.14e-06	INTRONIC	SYNJ1

Results for Endpoint 3

Figures 9 and 10 show the Manhattan Plots and QQ plots respectively, for Endpoint 3. Details of markers with $p<10^{-5}$ are given in Tables 19-22. No marker had $p<10^{-5}$ in *PGx-CN-HBe-Neg-*

Interim2, under either mode of inheritance however, there were only 16 responders in this group. The QQ-plots were seen to curve downwards and the Manhattan plots were depressed.

Table 19: Association Results with $p<10^{-5}$ for Endpoint 3 in *PGx-GT-Hbe-Neg-Interim2,* additive model

Chr	SNP	BP	HWE(p)	MAF
17	rs1867475	76507025	0.7401	0.3870

Chr	SNP	Beta	p-value	Variant	Gene
17	rs1867475	0.3168	5.46e-06	INTERGENIC	NA

Table 20: Association Results with $p<10^{-5}$ for Endpoint 3 in *PGx-GT- Hbe-Neg-Interim2,* dominant model

Chr	SNP	BP	HWE(p)	MAF
3	rs9856296	14155453	0.8630	0.3498
3	rs6776709	13978803	1.0000	0.3787
3	rs4684175	14048394	0.8653	0.3651
3	rs4685060	14042534	0.7342	0.3646
17	rs1867475	76507025	0.7401	0.3870

Chr	SNP	Beta	p-value	Variant	Gene
3	rs9856296	4.4270	5.26e-06	INTRONIC	CHCHD4
3	rs6776709	4.0870	8.24e-06	INTERGENIC	NA
3	rs4684175	4.7410	1.23e-06	INTERGENIC	NA
3	rs4685060	4.6310	1.87e-06	INTERGENIC	NA
17	rs1867475	0.1408	1.10e-06	INTERGENIC	NA

Table 21: Association Results with $p<10^{-5}$ for Endpoint 3 in *PGx-nonCN- Hbe-Neg-Interim2,* additive model

Chr	SNP	BP	HWE(p)	MAF
11	rs4539348	71242461	0.6187	0.2480

Chr	SNP	Beta	p-value	Variant	Gene
11	rs4539348	4.4530	8.89e-06	INTRONIC	KRTAP5-7; KRTAP5-8

Table 22: Association Results with $p<10^{-5}$ for Endpoint 3 in *PGx-nonCN- Hbe-Neg-Interim2,* dominant model

Chr	SNP	BP	HWE(p)	MAF
9	rs13297144	6788085	0.2541	0.2598
17	rs1867475	76507025	0.6155	0.4668

Chr	SNP	Beta	p-value	Variant	Gene
9	rs13297144	0.1848	8.41e-06	INTRONIC	JMJD2C
17	rs1867475	0.0844	3.48e-06	INTERGENIC	NA

Results for Endpoint 4

Figures 11 and 12 show the Manhattan Plots and QQ plots respectively, for Endpoint 4. Details of markers with $p<10^{-5}$ are given in Tables 23-28.

Table 23: Association Results with $p<10^{-5}$ for Endpoint 4 in *PGx-CN-Interim2,* additive model

Chr	SNP	BP	HWE(p)	MAF
15	rs11072478	74615507	0.3785	0.3551
20	rs260010	57764298	0.9140	0.3756

Chr	SNP	Beta	p-value	Variant	Gene
15	rs11072478	2.3750	7.69e-06	INTRONIC	CCDC33
20	rs260010	0.3921	3.87e-06	UPSTREAM	NA

Table 24: Association Results with $p<10^{-5}$ for Endpoint 4 in *PGx-CN-Interim2,* dominant model

Chr	SNP	BP	HWE(p)	MAF
2	rs13395925	7893850	0.3211	0.2859
2	rs2542943	172424963	0.7466	0.3769
7	rs845562	55254805	0.6640	0.3705
14	rs4899150	65344400	0.0986	0.4295

Chr	SNP	Beta	p-value	Variant	Gene
2	rs13395925	0.3121	7.87e-06	INTERGENIC	NA
2	rs2542943	0.3149	6.07e-06	INTERGENIC	NA
7	rs845562	3.8440	1.91e-06	INTRONIC	EGFR
14	rs4899150	0.2940	4.15e-06	INTERGENIC	NA

Table 25: Association Results with $p<10^{-5}$ for Endpoint 4 in *PGx-GT-Interim2,* additive model

Chr	SNP	BP	HWE(p)	MAF
1	rs12568559	116223259	1.0000	0.3297
2	rs10193128	233987722	0.5085	0.3909
NA	exm680251	NA	0.0226	0.4938
8	rs4840946	8231793	0.0335	0.4961
8	rs4840947	8232143	0.0145	0.4837
NA	exm680207	NA	0.0277	0.4961

Chr	SNP	Beta	p-value	Variant	Gene
1	rs12568559	0.4741	2.69e-06	INTRONIC	VANGL1
2	rs10193128	0.5201	6.18e-06	INTRONIC	ENSG00000168918
NA	exm680251	1.8990	8.12e-06	NA	NA
8	rs4840946	1.8980	7.53e-06	INTRONIC	ENSG00000182319
8	rs4840947	1.8830	8.19e-06	INTRONIC	ENSG00000182319
NA	exm680207	1.9370	4.43e-06	NA	NA

Table 26: Association Results with $p<10^{-5}$ for Endpoint 4 in *PGx-GT-Interim2,* dominant model

Chr	SNP	BP	HWE(p)	MAF
2	rs10193128	233987722	0.5085	0.3909
2	rs9288685	233987114	0.6287	0.4218
6	rs9322467	154771277	0.0324	0.1796
7	rs845562	55254805	0.0329	0.2833

Chr	SNP	Beta	p-value	Variant	Gene
2	rs10193128	0.3693	9.53e-07	INTRONIC	ENSG00000168918
2	rs9288685	0.3791	3.60e-06	INTRONIC	ENSG00000168918
6	rs9322467	2.5710	9.31e-06	SYNONYMOUS CODING	CNKSR3
7	rs845562	2.6040	8.61e-06	INTRONIC	EGFR

Table 27: Association Results with $p<10^{-5}$ for Endpoint 4 in *PGx-nonCN-Interim2,* additive model

Chr	SNP	BP	HWE(p)	MAF
2	rs6733352	209472769	0.0138	0.4118
3	rs7633147	55161838	1.0000	0.2246
11	rs4539348	71242461	0.6187	0.2480

Chr	SNP	Beta	p-value	Variant	Gene
2	rs6733352	0.2659	7.73e-07	INTERGENIC	NA
3	rs7633147	0.2355	4.76e-06	INTERGENIC	NA
11	rs4539348	4.4900	4.08e-06	INTRONIC	KRTAP5-7; KRTAP5-8

Table 28: Association Results with $p<10^{-5}$ for Endpoint 4 in *PGx-nonCN-Interim2,* dominant model

Chr	SNP	BP	HWE(p)	MAF
2	rs6733352	209472769	0.0138	0.4118
3	rs7633147	55161838	1.0000	0.2246

Chr	SNP	Beta	p-value	Variant	Gene
2	rs6733352	0.1382	2.40e-06	INTERGENIC	NA
3	rs7633147	0.1857	2.71e-06	INTERGENIC	NA

Results for Endpoint 5

Figures 13 and 14 show the Manhattan Plots and QQ plots respectively, for Endpoint 5. Details of markers with $p<10^{-5}$ are given in Tables 29-33.

Table 29: Association Results with $p<10^{-5}$ for Endpoint 5 in *PGx-CN- Interim2,* dominant model

Chr	SNP	BP	HWE(p)	MAF
9	rs943172	7403305	0.6864	0.4833
14	rs4899150	65344400	0.0986	0.4295

Chr	SNP	Beta	p-value	Variant	Gene
9	rs943172	0.2428	1.54e-06	INTERGENIC	NA
14	rs4899150	0.2515	5.05e-06	INTERGENIC	NA

Table 30: Association Results with $p<10^{-5}$ for Endpoint 5 in *PGx-GT- Interim2,* additive model

Chr	SNP	BP	HWE(p)	MAF
1	rs12568559	116223259	1.0000	0.3297
1	rs4348723	116239633	0.2267	0.3034
1	rs6428677	116240026	0.1912	0.3019
1	rs4654771	22158363	0.0332	0.4745
1	rs2500499	244271051	0.1647	0.1711
8	rs4840939	8215349	0.3844	0.4659

Chr	SNP	Beta	p-value	Variant	Gene
1	rs12568559	0.4597	7.41e-06	INTRONIC	VANGL1
1	rs4348723	0.4420	5.07e-06	3PRIME_UTR	VANGL1
1	rs6428677	0.4447	5.84e-06	3PRIME_UTR	VANGL1
1	rs4654771	0.5019	8.30e-06	INTRONIC	HSPG2
1	rs2500499	2.3800	5.44e-06	INTERGENIC	NA
8	rs4840939	0.5054	8.19e-06	INTRONIC	ENSG00000182319

Table 31: Association Results with $p<10^{-5}$ for Endpoint 5 in *PGx-GT- Interim2,* dominant model

Chr	SNP	BP	HWE(p)	MAF
1	rs4348723	116239633	0.2267	0.3034
1	rs6428677	116240026	0.1912	0.3019
1	rs4654771	22158363	0.0332	0.4745
6	rs9322467	154771277	0.0324	0.1796
14	rs12435908	66121468	5.65e-07	0.3104

Chr	SNP	Beta	p-value	Variant	Gene
1	rs4348723	0.3687	6.06e-06	3PRIME_UTR	VANGL1
1	rs6428677	0.3720	7.24e-06	3PRIME_UTR	VANGL1
1	rs4654771	0.2781	1.81e-07	INTRONIC	HSPG2
6	rs9322467	2.8850	2.74e-06	SYNONYMOUS CODING	CNKSR3
14	rs12435908	3.3790	5.40e-06	INTRONIC	FUT8

Table 32: Association Results with $p<10^{-5}$ for Endpoint 5 in *PGx-nonCN- Interim2,* additive model

Chr	SNP	BP	HWE(p)	MAF
2	rs6733352	209472769	0.0138	0.4118
3	rs7633147	55161838	1.0000	0.2246
11	rs4539348	71242461	0.6187	0.2480

Chr	SNP	Beta	p-value	Variant	Gene
2	rs6733352	0.2849	1.79e-06	INTERGENIC	NA
3	rs7633147	0.2460	8.05e-06	INTERGENIC	NA
11	rs4539348	4.6940	2.46e-06	INTRONIC	KRTAP5-7;KRTAP5-8

Table 33: Association Results with $p<10^{-5}$ for Endpoint 5 in *PGx-nonCN- Interim2,* dominant model

Chr	SNP	BP	HWE(p)	MAF
2	rs6733352	209472769	0.0138	0.4118
3	rs7633147	55161838	1.0000	0.2246

Chr	SNP	Beta	p-value	Variant	Gene
2	rs6733352	0.1577	5.91e-06	INTERGENIC	NA
3	rs7633147	0.1958	4.93e-06	INTERGENIC	NA

Results for Endpoint 6

Figures 15 and 16 show the Manhattan Plots and QQ plots respectively, for Endpoint 6. Details of markers with $p<10^{-5}$ are given in Tables 34-37.

Table 34: Association Results with $p<10^{-5}$ for Endpoint 6 in *PGx-CN- Interim2,* additive model

Chr	SNP	BP	HWE(p)	MAF
1	rs10494323	159374604	1.0000	0.0205
NA	exm-rs4133289	NA	1.0000	0.0218
NA	exm-rs10489849	NA	1.0000	0.0167
NA	exm114297	NA	1.0000	0.0205
1	rs10489849	159196765	1.0000	0.0167
3	rs17403692	65104083	0.1494	0.0961

Chr	SNP	BP	HWE(p)	MAF
5	rs2662605	17999554	1.0000	0.0295
14	rs17094430	97244170	1.0000	0.0180

Chr	SNP	Beta	p-value	Variant	Gene
1	rs10494323	25.9100	1.47e-06	INTRONIC	OR10J1
NA	exm-rs4133289	23.3500	2.20e-06	NA	NA
NA	exm-rs10489849	22.0200	9.15e-06	NA	NA
NA	exm114297	25.8000	1.57e-06	NA	NA
1	rs10489849	22.0200	9.15e-06	INTERGENIC	NA
3	rs17403692	8.7050	5.71e-06	INTERGENIC	NA
5	rs2662605	24.7700	2.84e-06	INTERGENIC	NA
14	rs17094430	26.7600	8.62e-06	INTERGENIC	NA

Table 35: Association Results with $p<10^{-5}$ for Endpoint 6 in *PGx-CN- Interim2,* dominant model

Chr	SNP	BP	HWE(p)	MAF
1	rs10494323	159374604	1.0000	0.0205
NA	exm-rs4133289	NA	1.0000	0.0218
NA	exm-rs10489849	NA	1.0000	0.0167
NA	exm114297	NA	1.0000	0.0205
1	rs10489849	159196765	1.0000	0.0167
5	rs2662605	17999554	1.0000	0.0295
12	rs11110982	102118934	0.2016	0.0244
14	rs17094430	97244170	1.0000	0.0180

Chr	SNP	Beta	p-value	Variant	Gene
1	rs10494323	25.9100	1.47e-06	INTRONIC	OR10J1
NA	exm-rs4133289	23.3500	2.20e-06	NA	NA
NA	exm-rs10489849	22.0200	9.15e-06	NA	NA
NA	exm114297	25.8000	1.57e-06	NA	NA
1	rs10489849	22.0200	9.15e-06	INTERGENIC	NA
5	rs2662605	24.7700	2.84e-06	INTERGENIC	NA
12	rs11110982	19.0800	6.07e-06	INTRONIC	CHPT1
14	rs17094430	26.7600	8.62e-06	INTERGENIC	NA

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Table 36: Association Results with $p<10^{-5}$ for Endpoint 6 in *PGx-GT- Interim2,* additive model

Chr	SNP	BP	HWE(p)	MAF
3	rs17403692	65104083	8.71e-06	0.2183
12	rs11177673	69832861	0.6131	0.1927

Chr	SNP	Beta	p-value	Variant	Gene
3	rs17403692	5.5880	1.54e-06	INTERGENIC	NA
12	rs11177673	5.2320	2.94e-06	INTERGENIC	NA

Table 37: Association Results with $p<10^{-5}$ for Endpoint 6 in *PGx-nonCN- Interim2,* additive model

Chr	SNP	BP	HWE(p)	MAF
19	rs736452	33145645	1.0000	0.0352

Chr	SNP	Beta	p-value	Variant	Gene
19	rs736452	47.9600	9.31e-06	INTRONIC	ANKRD27

A total of 23 genes were implicated at the suggestive level ($p<10^{-5}$). Of these, five interact closely with each other and with guanine (Figure 17). The genes in question were ARHGEF7 (Rho Guanine Nucleotide Exchange Factor 7), DOCK1 (Dedicator of Cytokinesis 1), HSPG2 (Heparan Sulfate Proteoglycan 2), SYNJ1 (Synaptojanin 1), and EGFR (Epidermal Growth Factor). It is noted that guanine nucleoside analogues under investigation in the treatment of hepatitis B (Rivkin, 2007) and EGFR has been shown to interact with the hepatitis B virus (Menzo et al, 1993).

Software

Custom-written perl scripts (Wall et al, 1996) were used to reformat the data, select markers for ancestry analysis and produce tables. PLINK version 1.07 (Purcell et al, 2007) was used to perform the genetic QC analyses, to merge study data with HapMap data, and for association analysis. EIGENSOFT 4.0 (Patterson et al, 2006; Price et al, 2006) was used for PCA. R version 2.15.2 (R Core Team, 2012) was used for the production of graphics.

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All of the compositions and/or methods disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations may be applied to the compositions and/or methods and in the steps or in the sequence of steps of the method described herein without departing from the concept, spirit and scope of the invention. All such similar substitutes and

modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.

Claims

1. A method of identifying a patient who may benefit from treatment with an anti-HBV therapy comprising an interferon, the method comprising:
determining the presence of a single nucleotide polymorphism in gene *CADPS* on chromosome 3 in a sample obtained from the patient, wherein the presence of at least one A allele at rs7633796 indicates that the patient may benefit from the treatment with the anti-HBV treatment.

2. A method of predicting responsiveness of a patient suffering from an HBV infection to treatment with an anti-HBV treatment comprising an interferon, the method comprising:
determining the presence of a single nucleotide polymorphism in gene *CADPS* on chromosome 3 in a sample obtained from the patient, wherein the presence of at least one A allele at rs7633796 indicates that the patient is more likely to be responsive to treatment with the anti-HBV treatment.

3. A method for determining the likelihood that a patient with an HBV infection will exhibit benefit from an anti-HBV treatment comprising an interferon, the method comprising:
determining the presence of a single nucleotide polymorphism in gene *CADPS* on chromosome 3 in a sample obtained from the patient, wherein the presence of at least one A allele at rs7633796 indicates that the patient has increased likelihood of benefit from the anti-HBV treatment.

4. A method for optimizing the therapeutic efficacy of an anti-HBV treatment comprising an interferon, the method comprising:
determining the presence of a single nucleotide polymorphism in gene *CADPS* on chromosome 3 in a sample obtained from the patient, wherein the presence of at least one A allele at rs7633796 indicates that the patient has increased likelihood of benefit from the anti-HBV treatment.

5. A method for treating an HBV infection in a patient, the method comprising:

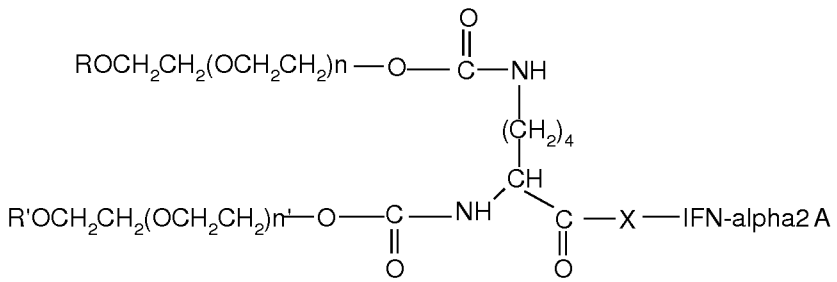
(i) determining the presence of at least one A allele at rs7633796 in gene *CADPS* on chromosome 3 in a sample obtained from the patient and

(ii) administering an effective amount of an anti-HBV treatment comprising an interferon to said patient, whereby the HBV infection is treated.

6. A method for predicting HBeAg seroconversion and HBV DNA <2000 IU/ml at >=24-week follow-up of treatment (responders vs. non-responders) of an HBe-positive patient infected with HBV to interferon treatment comprising:
providing a sample from said human subject, detecting the presence of a single nucleotide polymorphism in gene *CADPS* on chromosome 3 and determining that said patient has a high response rate to interferon treatment measured as HBeAg seroconversion and HBV DNA <2000 IU/ml at >=24-week follow-up of treatment (responders vs. non-responders) if at least one A allele at rs7633796 is present.

7. The method of any of claims 1 to 6, wherein the interferon is selected from the group of peginterferon alfa-2a, peginterferon alfa-2b, interferon alfa-2a and interferon alfa-2b.

8. The method of claim 7, wherein the interferon is a peginterferon alfa-2a conjugate having the formula:



wherein R and R' are methyl, X is NH, and n and n' are individually or both either 420 or 520.

Fig.1

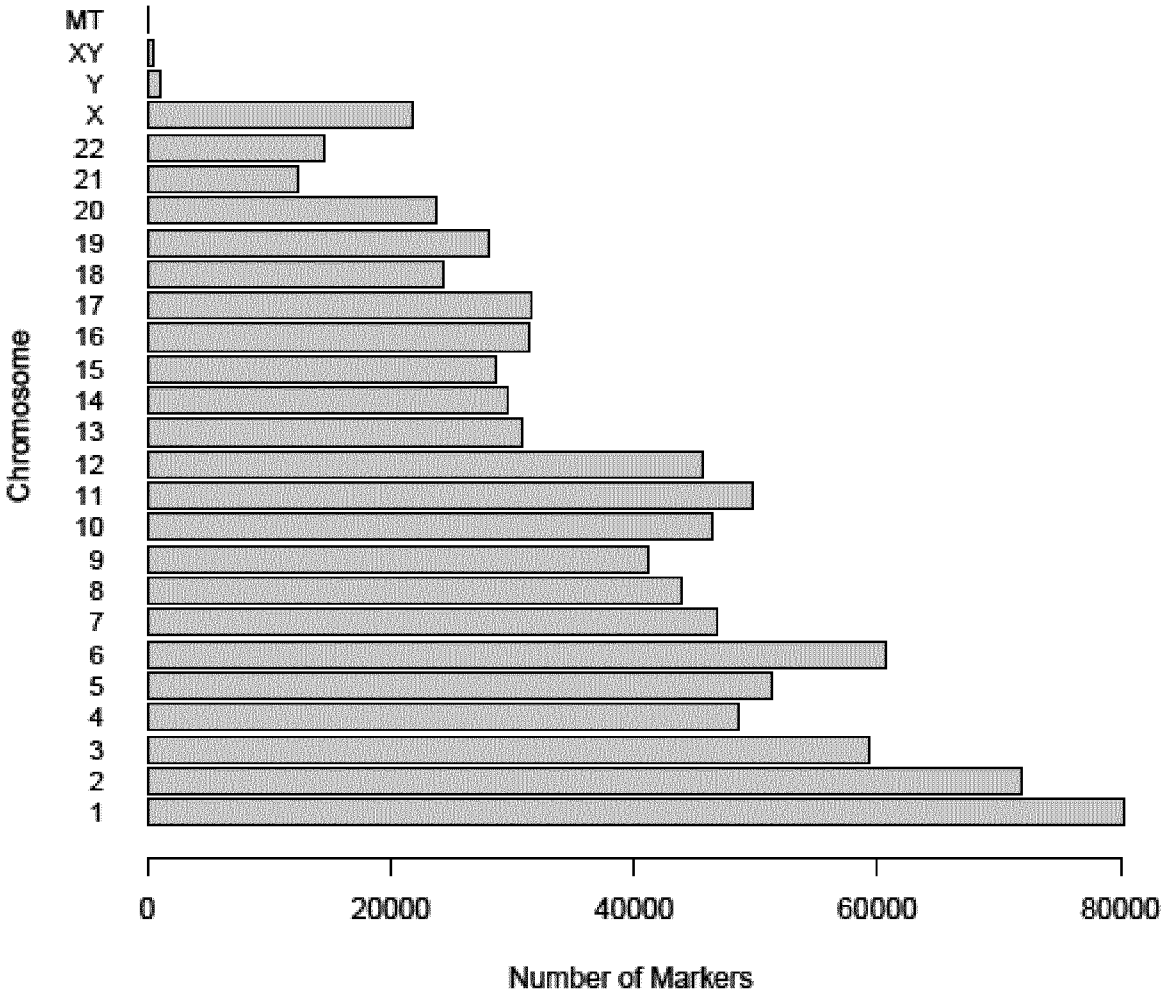

MT
XY
Y
X
22
21
20
19
18
17
16
15
14
13
12
11
10
9
8
7
6
5
4
3
2
1
Chromosome
0
20000
40000
60000
80000
Number of Markers

Fig. 2

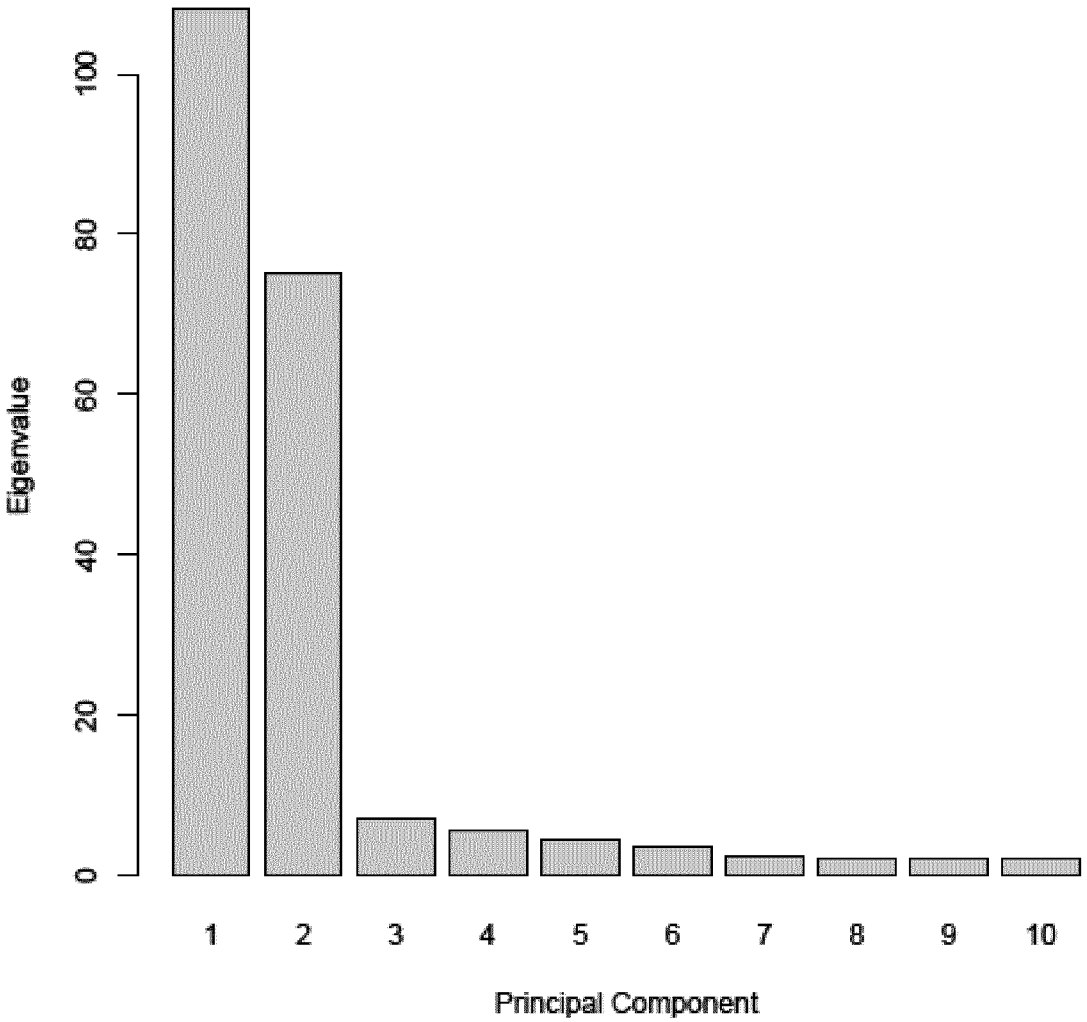

Eigenvalue
0
20
40
60
80
100
1
2
3
4
5
6
7
8
9
10
Principal Component

Fig. 3

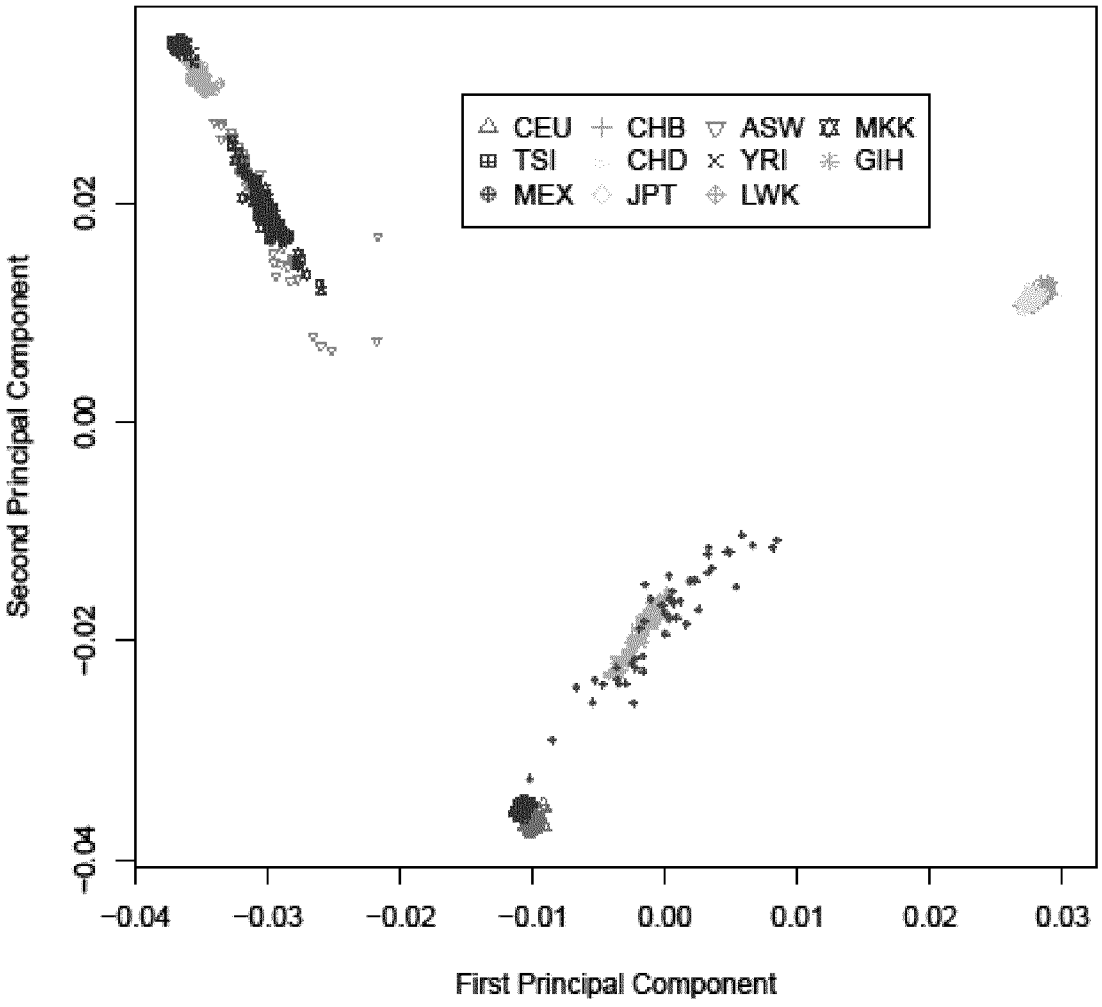

CEU
CHB
ASW
MKK
TSI
CHD
YRI
GIH
MEX
JPT
LWK
Second Principal Component
First Principal Component
0.02
0.00
−0.02
−0.04
−0.04
−0.03
−0.02
−0.01
0.00
0.01
0.02
0.03

Fig. 4

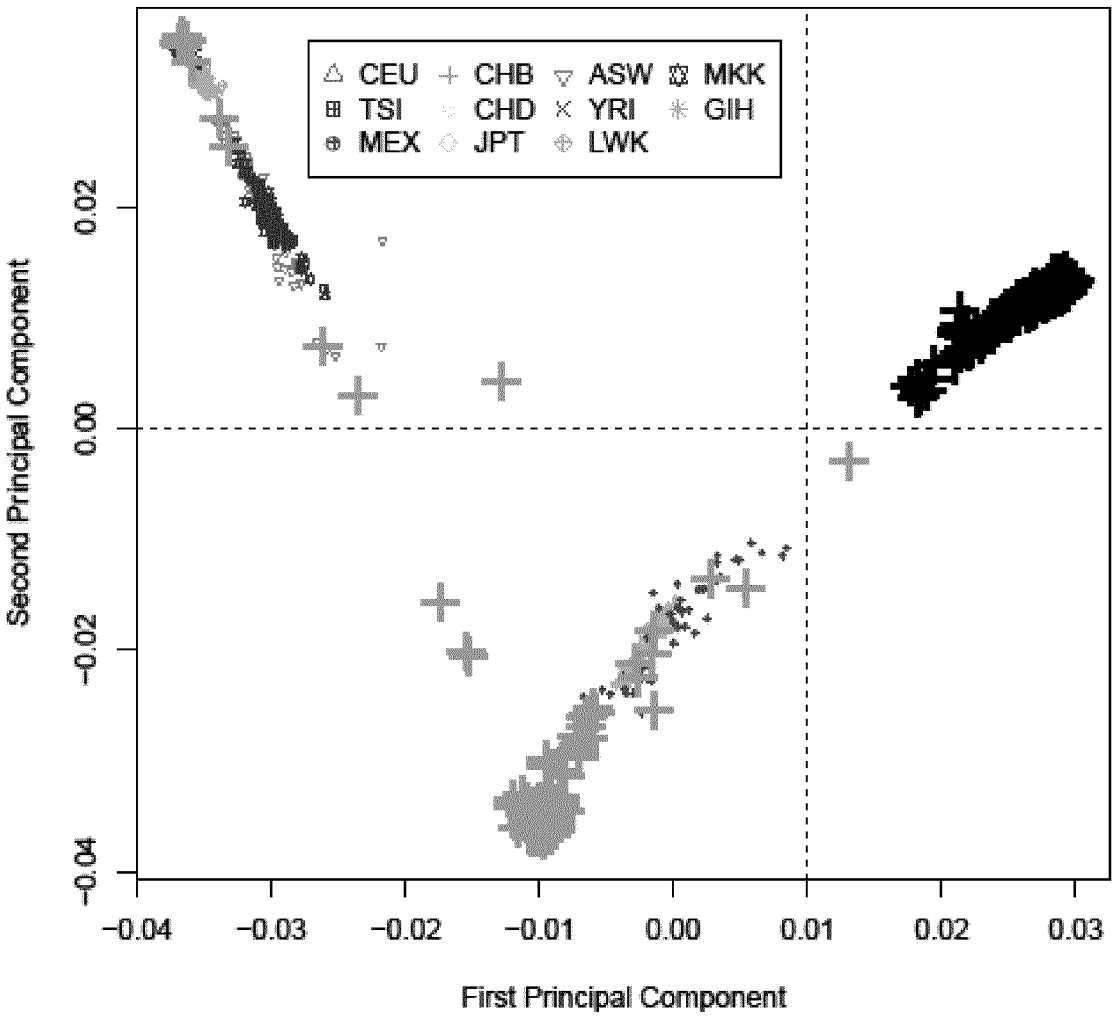

CEU
CHB
ASW
MKK
TSI
CHD
YRI
GIH
MEX
JPT
LWK
Second Principal Component
First Principal Component
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0.00
−0.02
−0.04
−0.04
−0.03
−0.02
−0.01
0.00
0.01
0.02
0.03

Fig. 5

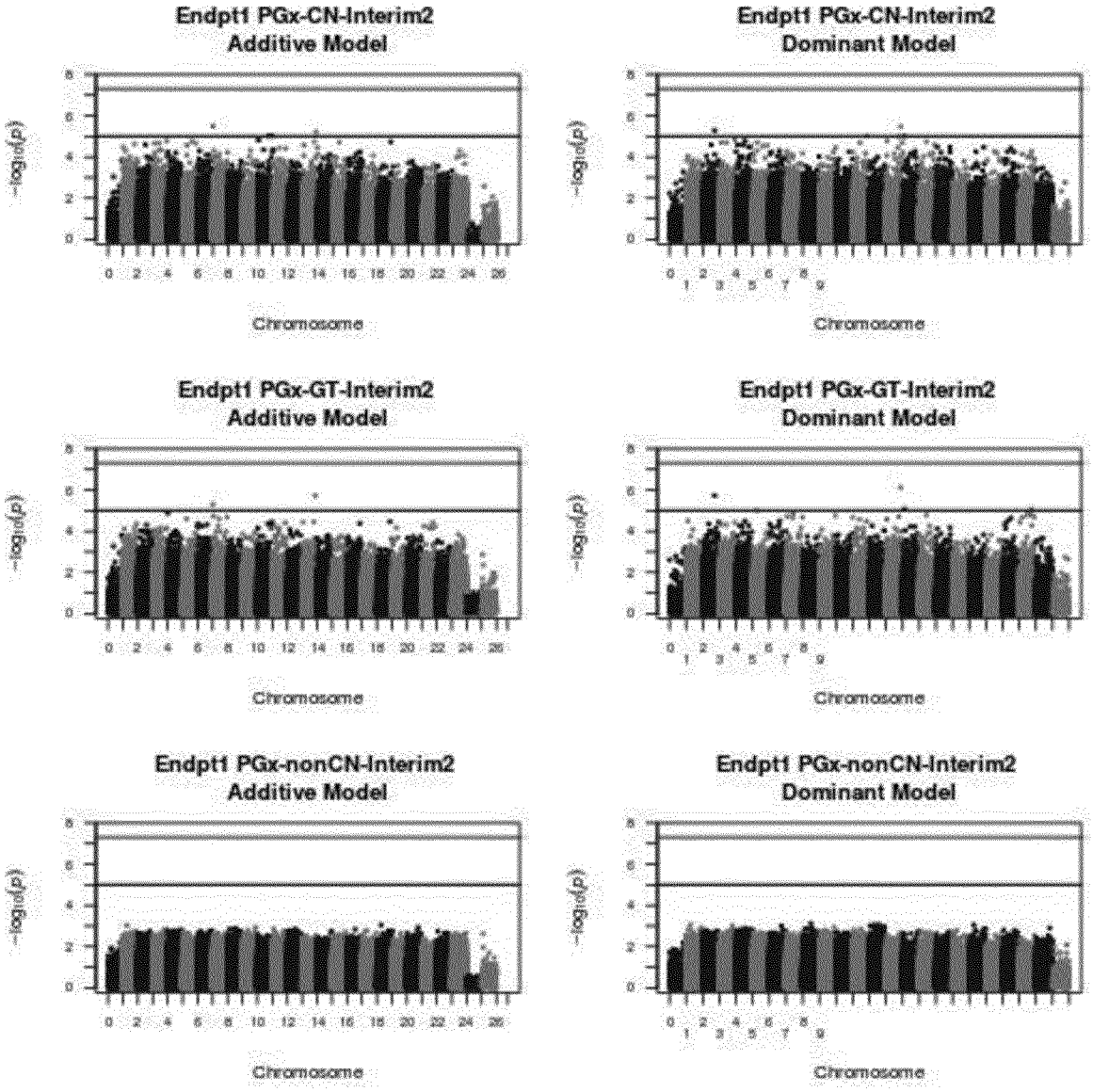

Endpt1 PGx-CN-Interim2
Additive Model
Endpt1 PGx-CN-Interim2
Dominant Model
Endpt1 PGx-GT-Interim2
Additive Model
Endpt1 PGx-GT-Interim2
Dominant Model
Endpt1 PGx-nonCN-Interim2
Additive Model
Endpt1 PGx-nonCN-Interim2
Dominant Model
Chromosome

Fig. 6

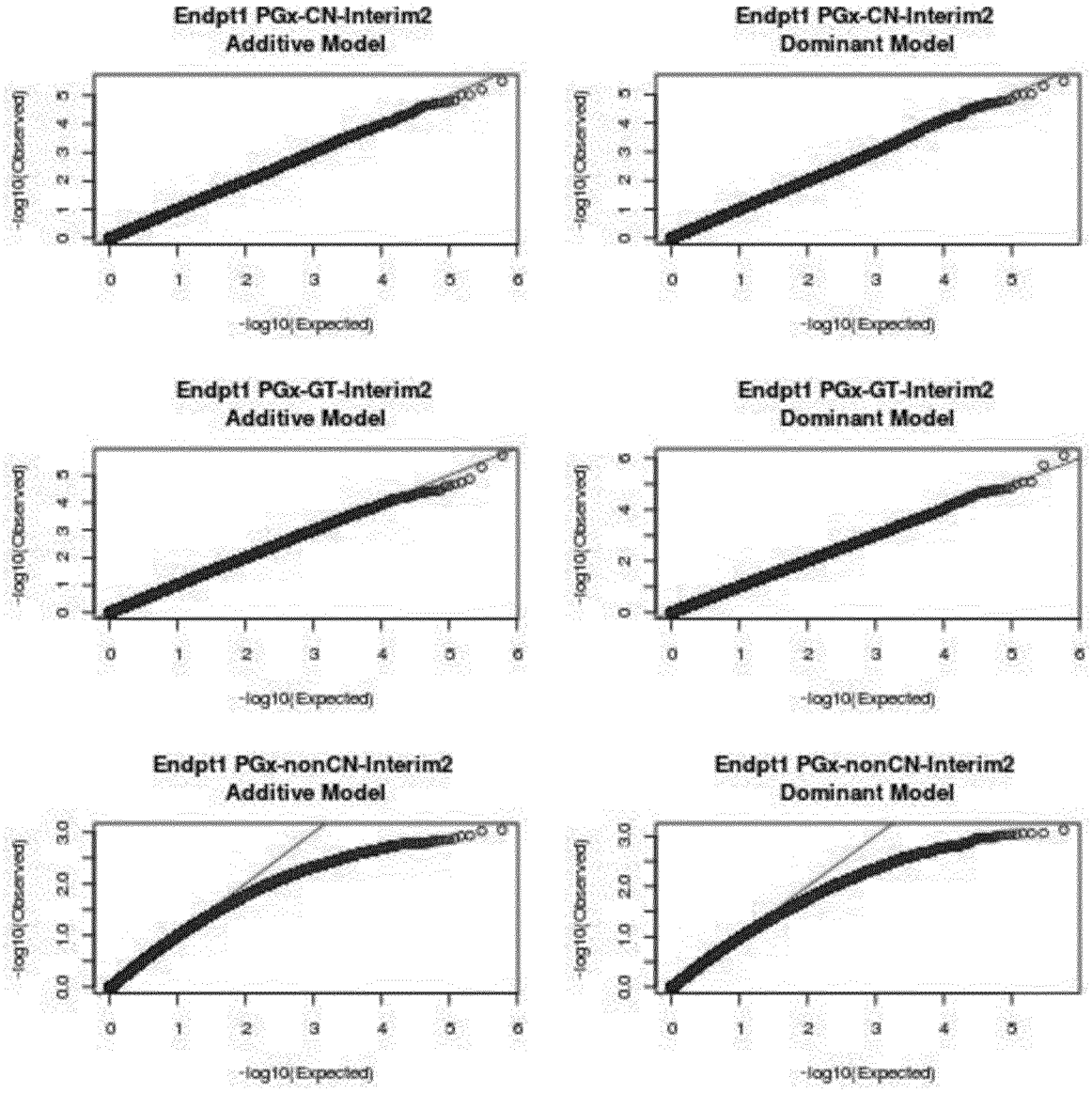

Endpt1 PGx-CN-Interim2
Additive Model
-log10(Observed)
-log10(Expected)
Endpt1 PGx-CN-Interim2
Dominant Model
-log10(Observed)
-log10(Expected)
Endpt1 PGx-GT-Interim2
Additive Model
-log10(Observed)
-log10(Expected)
Endpt1 PGx-GT-Interim2
Dominant Model
-log10(Observed)
-log10(Expected)
Endpt1 PGx-nonCN-Interim2
Additive Model
-log10(Observed)
-log10(Expected)
Endpt1 PGx-nonCN-Interim2
Dominant Model
-log10(Observed)
-log10(Expected)

Fig. 7

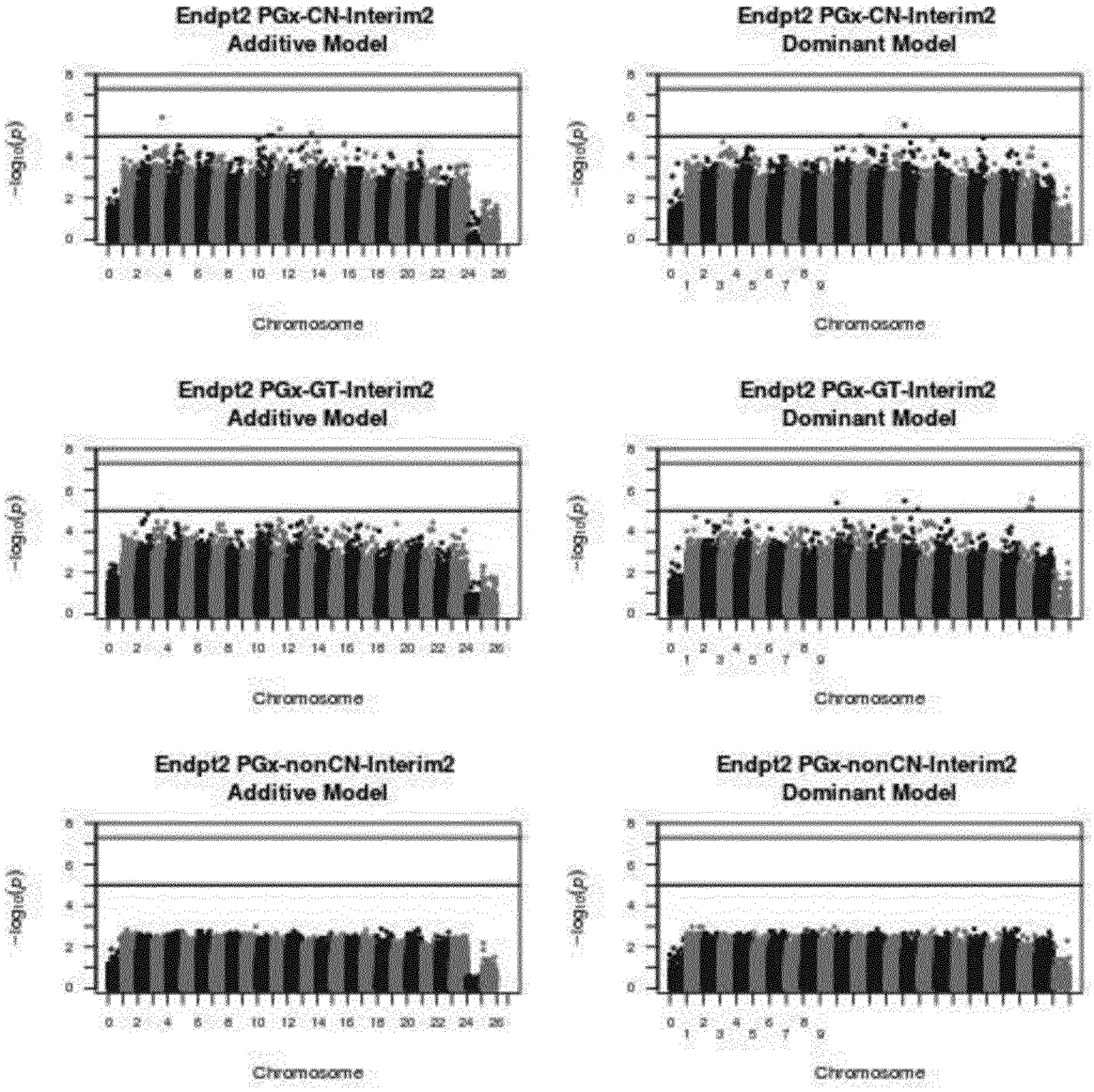

Endpt2 PGx-CN-Interim2
Additive Model
Endpt2 PGx-CN-Interim2
Dominant Model
Endpt2 PGx-GT-Interim2
Additive Model
Endpt2 PGx-GT-Interim2
Dominant Model
Endpt2 PGx-nonCN-Interim2
Additive Model
Endpt2 PGx-nonCN-Interim2
Dominant Model
−log10(p)
Chromosome

Fig. 8

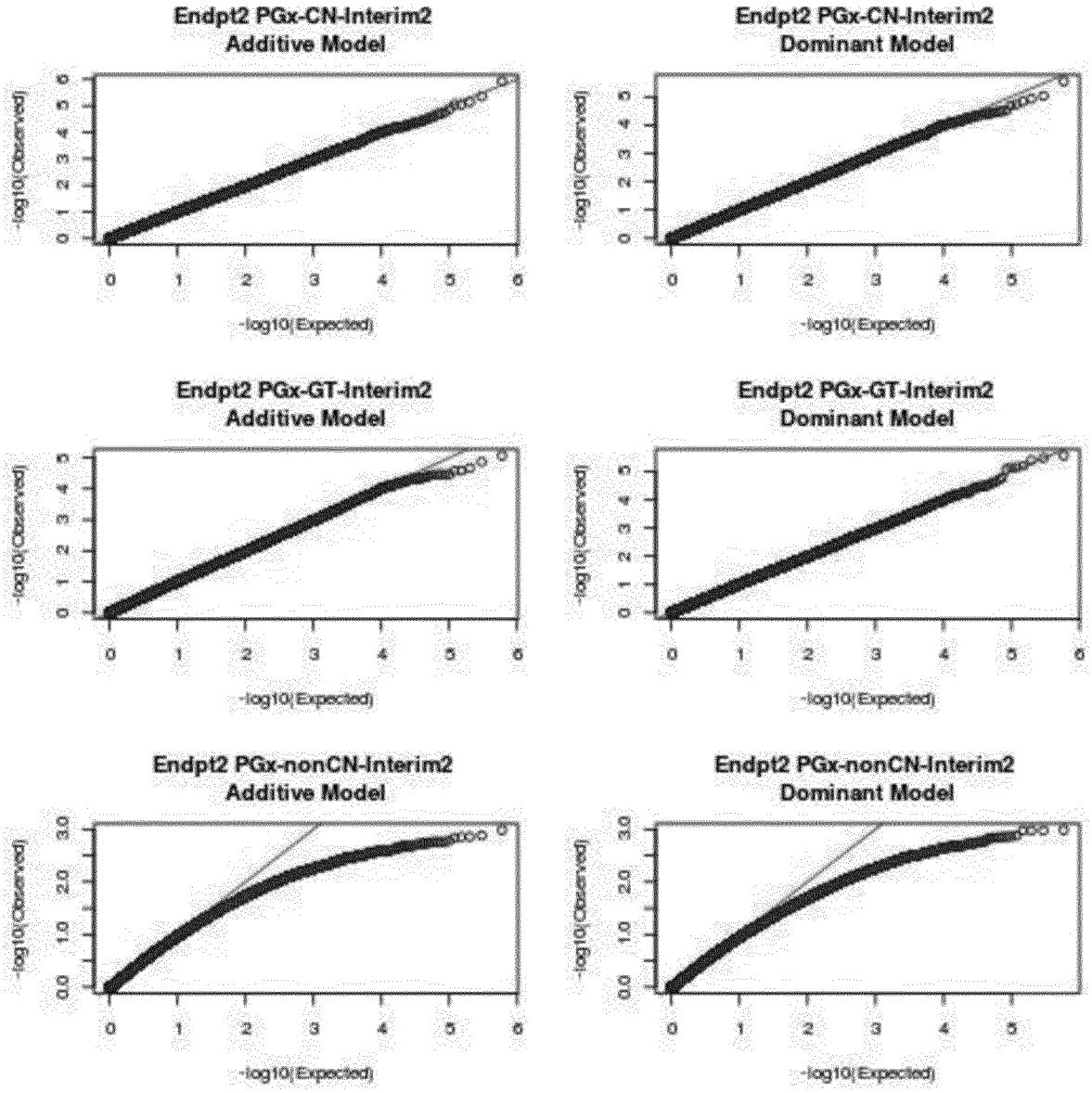

Endpt2 PGx-CN-Interim2
Additive Model
-log10(Observed)
-log10(Expected)
Endpt2 PGx-CN-Interim2
Dominant Model
-log10(Observed)
-log10(Expected)
Endpt2 PGx-GT-Interim2
Additive Model
-log10(Observed)
-log10(Expected)
Endpt2 PGx-GT-Interim2
Dominant Model
-log10(Observed)
-log10(Expected)
Endpt2 PGx-nonCN-Interim2
Additive Model
-log10(Observed)
-log10(Expected)
Endpt2 PGx-nonCN-Interim2
Dominant Model
-log10(Observed)
-log10(Expected)

Fig. 9

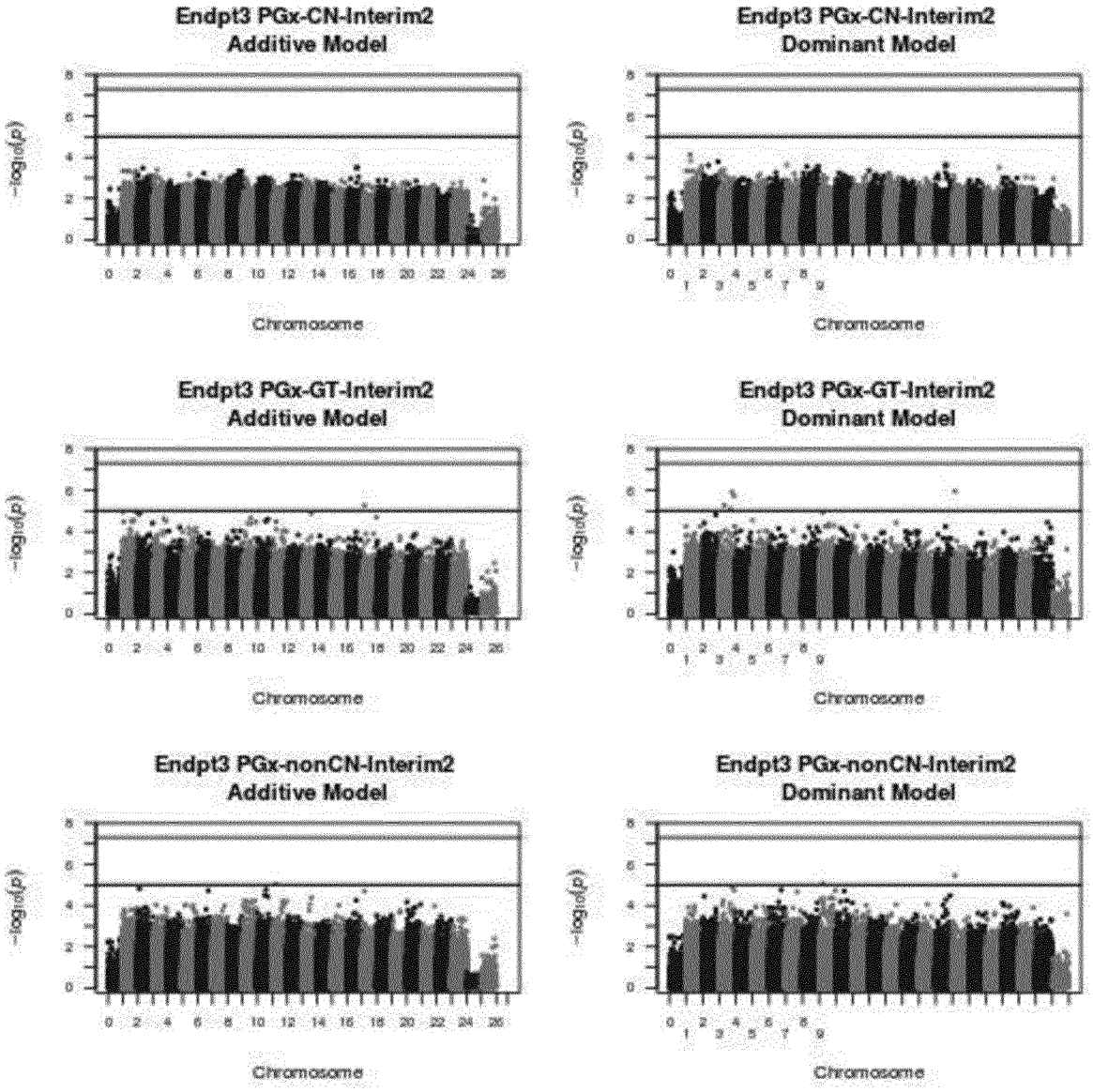

Endpt3 PGx-CN-Interim2
Additive Model
Endpt3 PGx-CN-Interim2
Dominant Model
Endpt3 PGx-GT-Interim2
Additive Model
Endpt3 PGx-GT-Interim2
Dominant Model
Endpt3 PGx-nonCN-Interim2
Additive Model
Endpt3 PGx-nonCN-Interim2
Dominant Model
Chromosome

Fig. 10

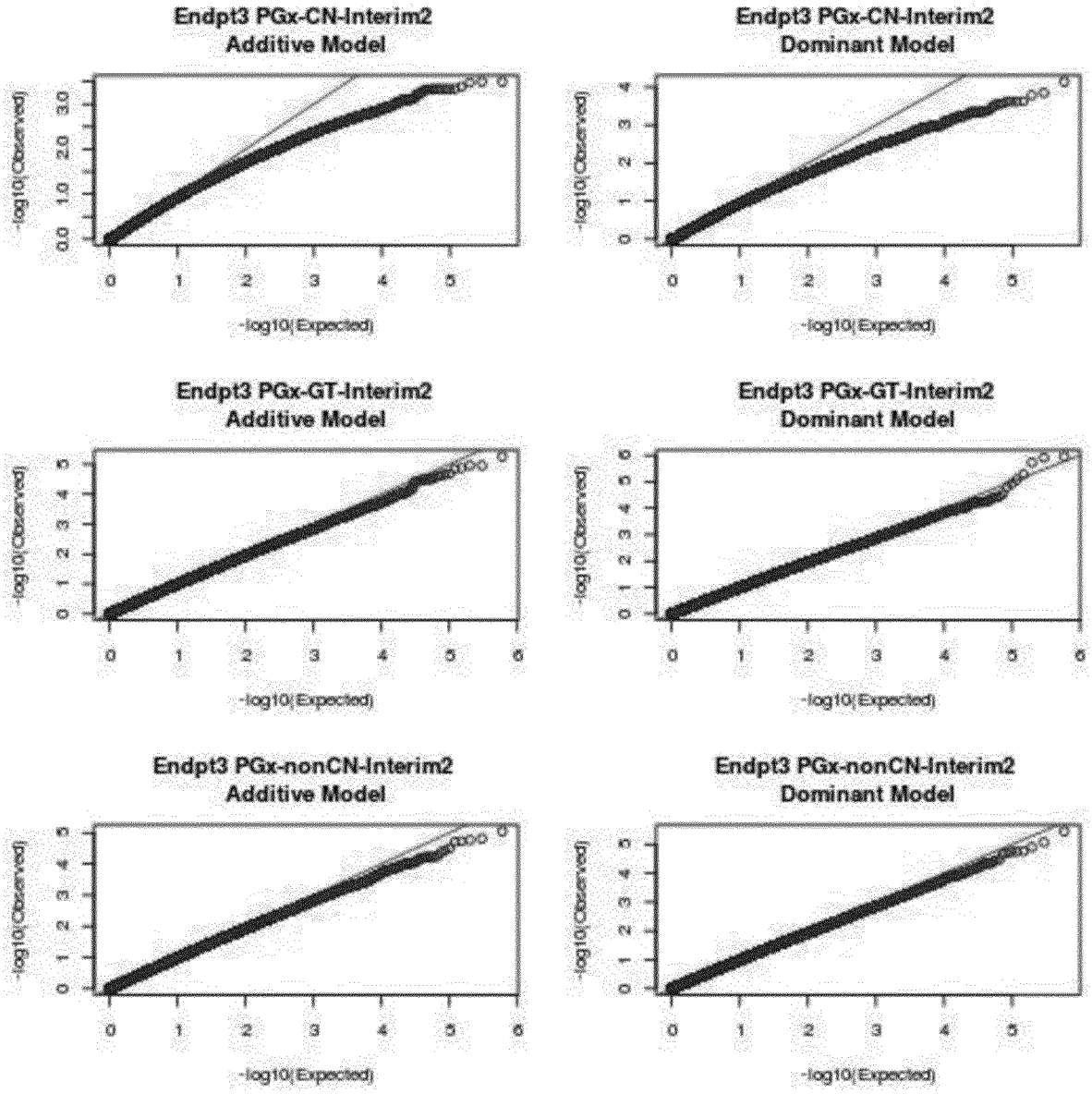

Endpt3 PGx-CN-Interim2
Additive Model
-log10(Observed)
-log10(Expected)
Endpt3 PGx-CN-Interim2
Dominant Model
-log10(Observed)
-log10(Expected)
Endpt3 PGx-GT-Interim2
Additive Model
-log10(Observed)
-log10(Expected)
Endpt3 PGx-GT-Interim2
Dominant Model
-log10(Observed)
-log10(Expected)
Endpt3 PGx-nonCN-Interim2
Additive Model
-log10(Observed)
-log10(Expected)
Endpt3 PGx-nonCN-Interim2
Dominant Model
-log10(Observed)
-log10(Expected)

Fig. 11

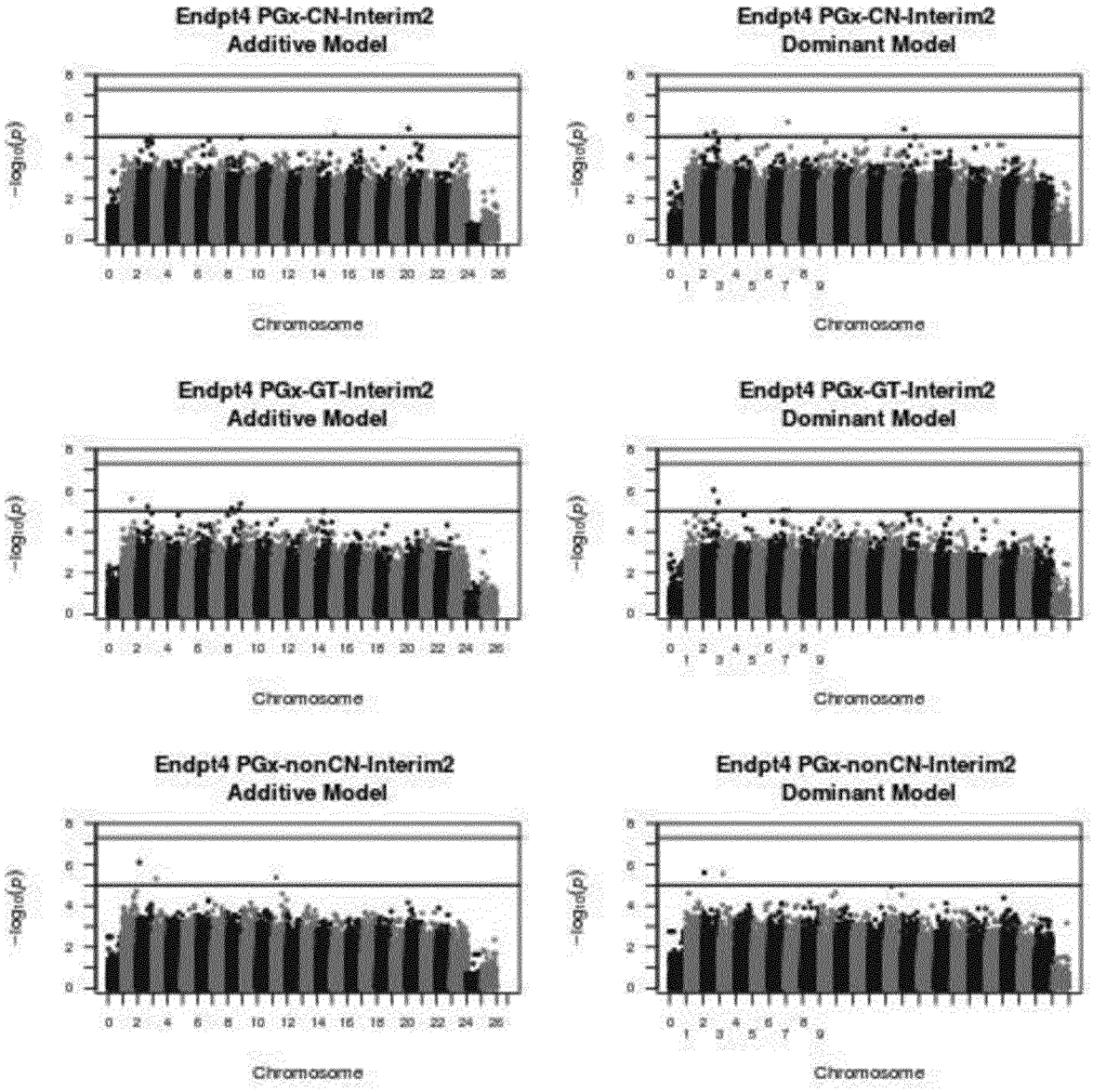

Endpt4 PGx-CN-Interim2
Additive Model
Endpt4 PGx-CN-Interim2
Dominant Model
Endpt4 PGx-GT-Interim2
Additive Model
Endpt4 PGx-GT-Interim2
Dominant Model
Endpt4 PGx-nonCN-Interim2
Additive Model
Endpt4 PGx-nonCN-Interim2
Dominant Model
−log10(p)
Chromosome

Fig. 12

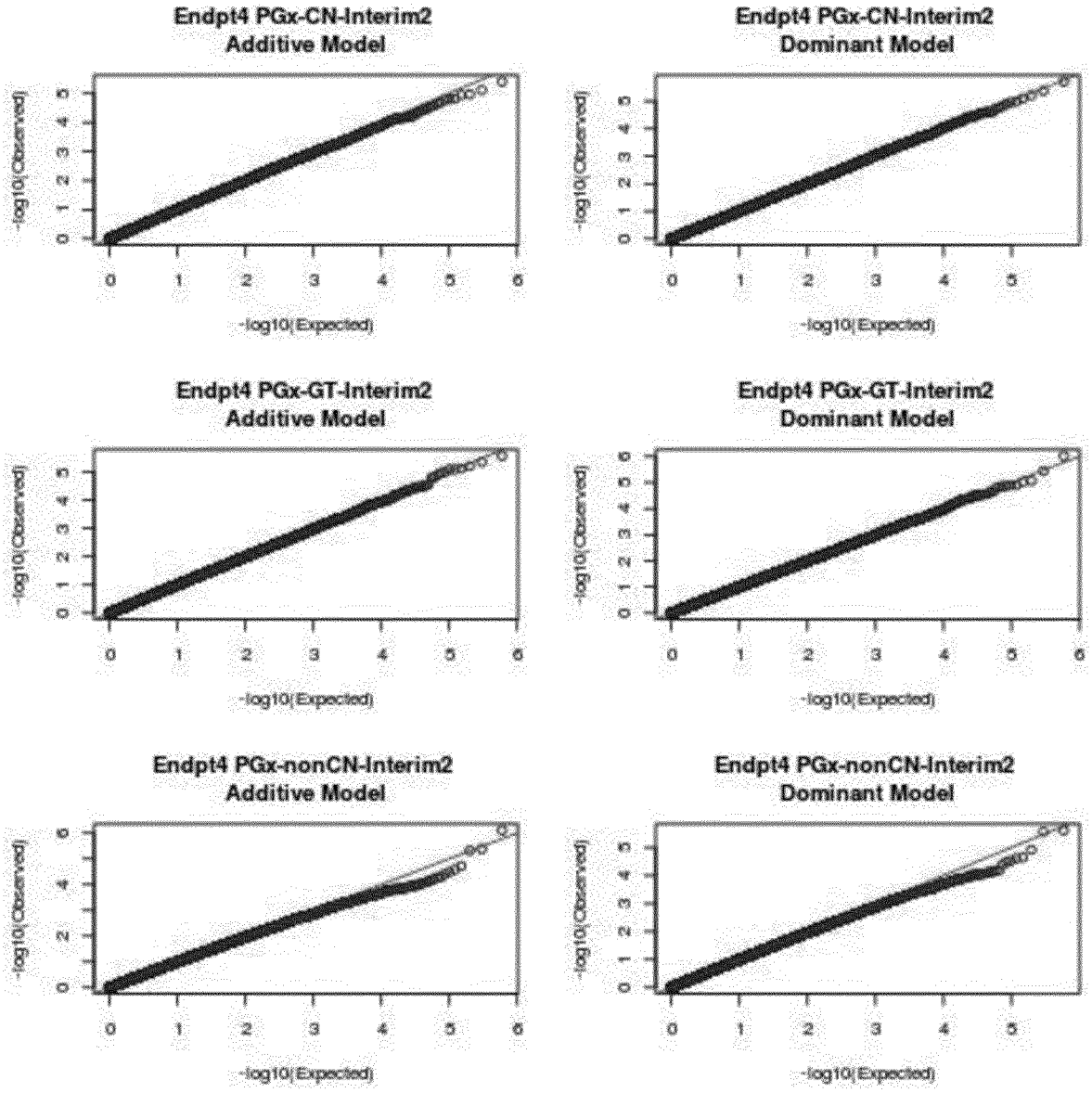

Endpt4 PGx-CN-Interim2
Additive Model
Endpt4 PGx-CN-Interim2
Dominant Model
Endpt4 PGx-GT-Interim2
Additive Model
Endpt4 PGx-GT-Interim2
Dominant Model
Endpt4 PGx-nonCN-Interim2
Additive Model
Endpt4 PGx-nonCN-Interim2
Dominant Model
-log10(Observed)
-log10(Expected)

Fig. 13

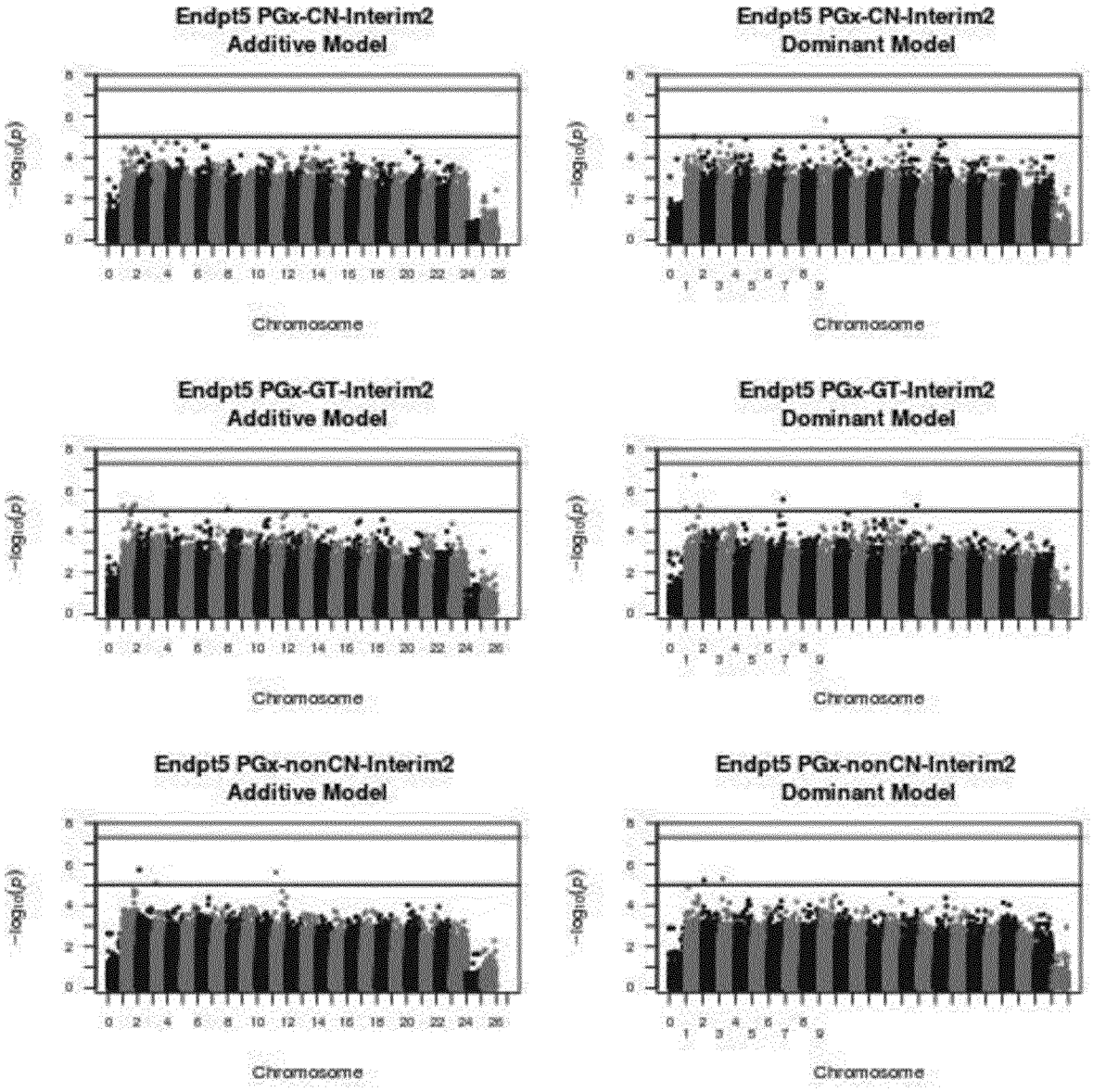

Endpt5 PGx-CN-Interim2
Additive Model
Endpt5 PGx-CN-Interim2
Dominant Model
Endpt5 PGx-GT-Interim2
Additive Model
Endpt5 PGx-GT-Interim2
Dominant Model
Endpt5 PGx-nonCN-Interim2
Additive Model
Endpt5 PGx-nonCN-Interim2
Dominant Model
−log10(p)
Chromosome

Fig. 14

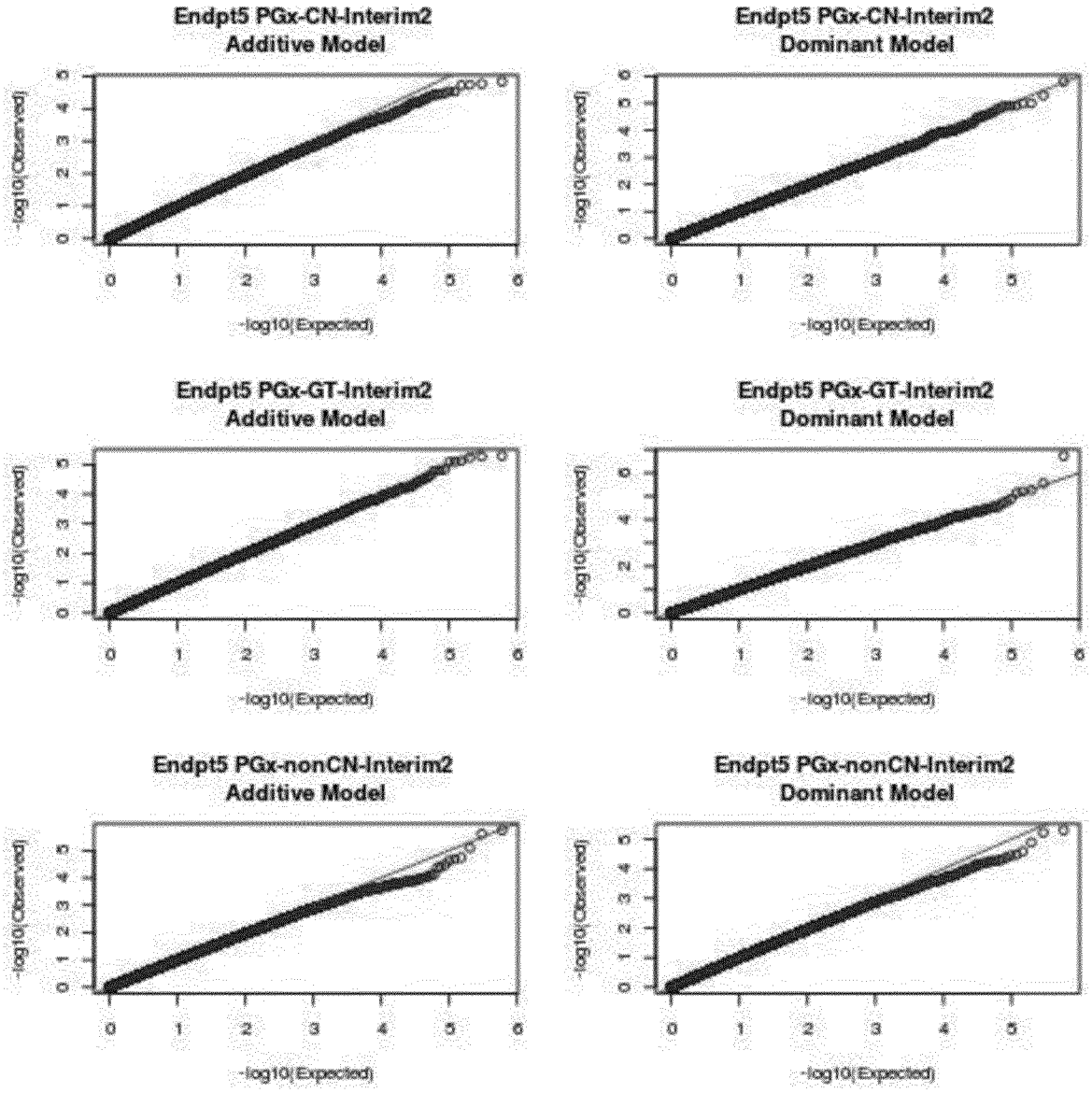

Endpt5 PGx-CN-Interim2
Additive Model
Endpt5 PGx-CN-Interim2
Dominant Model
Endpt5 PGx-GT-Interim2
Additive Model
Endpt5 PGx-GT-Interim2
Dominant Model
Endpt5 PGx-nonCN-Interim2
Additive Model
Endpt5 PGx-nonCN-Interim2
Dominant Model
-log10(Observed)
-log10(Expected)

Fig. 15

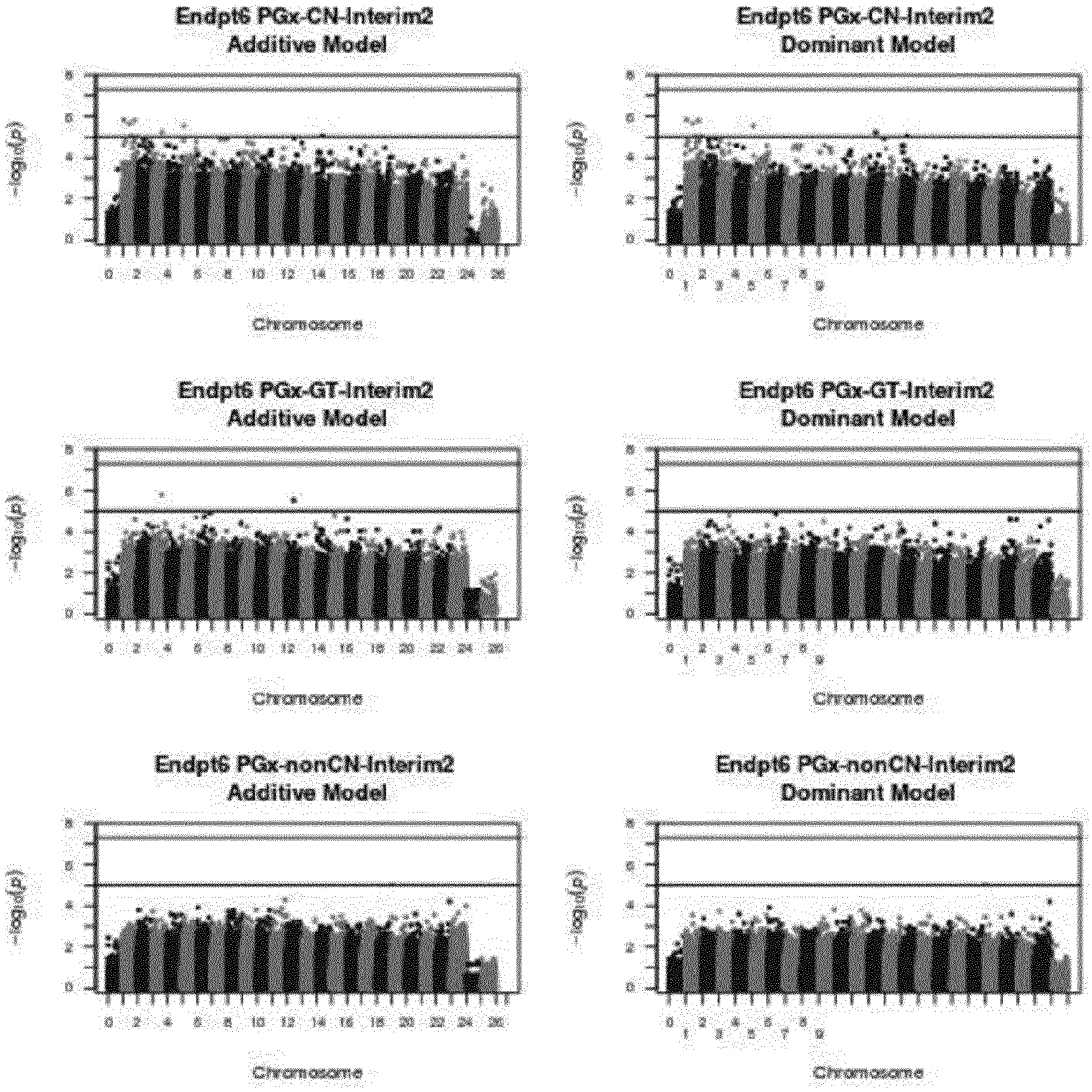

Endpt6 PGx-CN-Interim2
Additive Model
Endpt6 PGx-CN-Interim2
Dominant Model
Endpt6 PGx-GT-Interim2
Additive Model
Endpt6 PGx-GT-Interim2
Dominant Model
Endpt6 PGx-nonCN-Interim2
Additive Model
Endpt6 PGx-nonCN-Interim2
Dominant Model
−log10(p)
Chromosome

Fig. 16

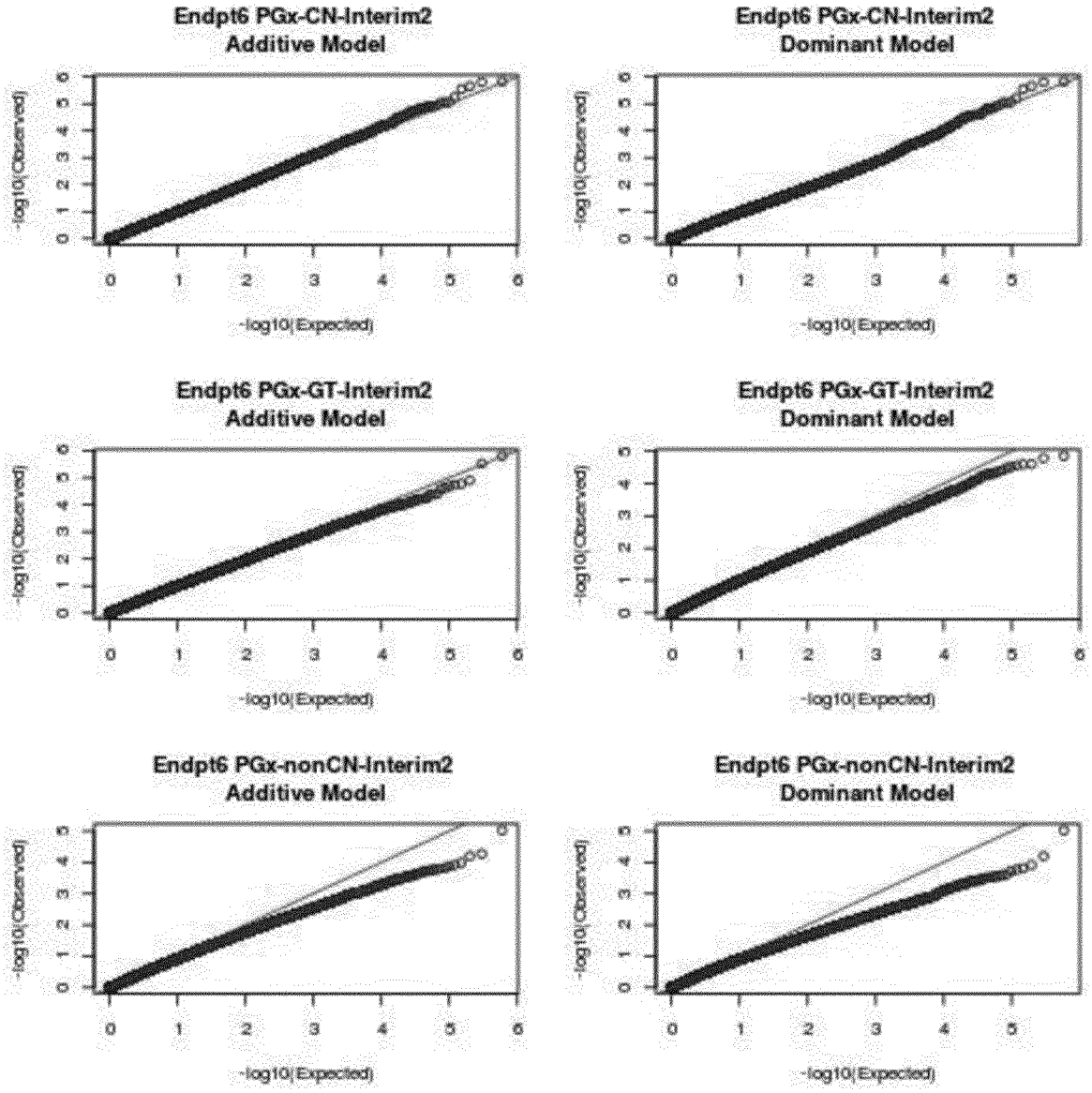
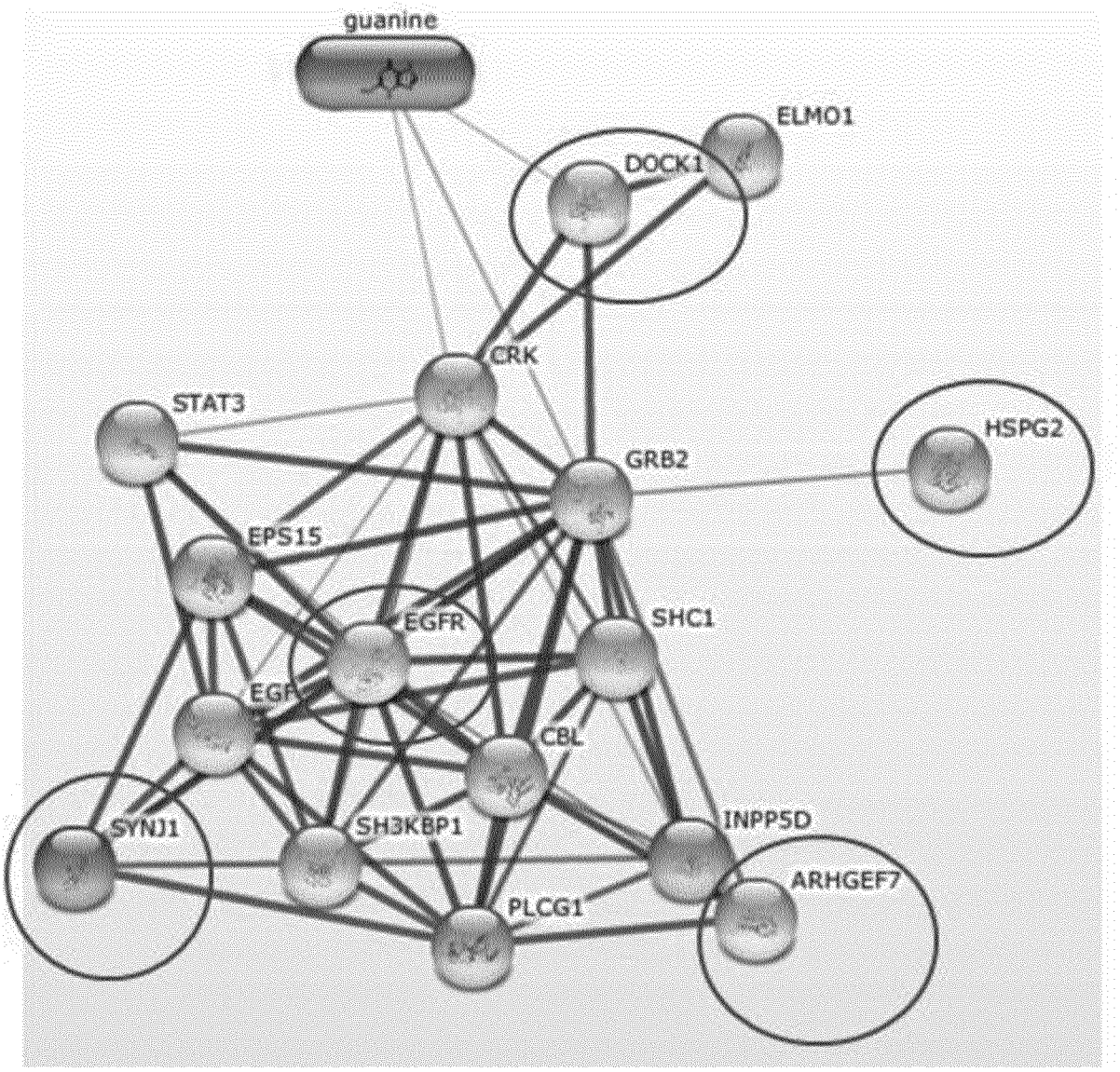

Endpt6 PGx-CN-Interim2
Additive Model
Endpt6 PGx-CN-Interim2
Dominant Model
Endpt6 PGx-GT-Interim2
Additive Model
Endpt6 PGx-GT-Interim2
Dominant Model
Endpt6 PGx-nonCN-Interim2
Additive Model
Endpt6 PGx-nonCN-Interim2
Dominant Model
-log10(Observed)
-log10(Expected)

Fig. 17


guanine
ELMO1
DOCK1
CRK
STAT3
HSPG2
GRB2
EPS15
SHC1
EGFR
EGF
CBL
SYNJ1
SH3KBP1
INPPSD
ARHGEF7
PLCG1

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2015/079719

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/68 C12Q1/70
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, WPI Data, BIOSIS, CHEM ABS Data, Sequence Search, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 2011/115914 A1 (GLOBEIMMUNE INC [US]; APELIAN DAVID [US]; FRANZUSOFF ALEX [US]) 22 September 2011 (2011-09-22) claims 19-22; page 7, [0016]-[0018]; page 91	1-8
X,P	WO 2015/091306 A1 (HOFFMANN LA ROCHE [CH]; HOFFMANN LA ROCHE [US]) 25 June 2015 (2015-06-25) tables 15 and 17; claims	1-8

-/--

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

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"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
16 February 2016	29/02/2016

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Hennard, Christophe

2

Form PCT/ISA/210 (second sheet) (April 2005)

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	MILAN J. SONNEVELD ET AL: "Polymorphisms Near IL28B and Serologic Response to Peginterferon in HBeAg-Positive Patients With Chronic Hepatitis B", GASTROENTEROLOGY, vol. 142, no. 3, 1 March 2012 (2012-03-01) , pages 513-520.e1, XP055070037, ISSN: 0016-5085, DOI: 10.1053/j.gastro.2011.11.025 figure 4; page 516 column 2	1-8
A	WU XIAOPAN ET AL: "Evaluation of susceptibility locus for response to interferon-[alpha] based therapy in chronic hepatitis B patients in Chinese", ANTIVIRAL RESEARCH, vol. 93, no. 2, 19 December 2011 (2011-12-19), pages 297-300, XP028886860, ISSN: 0166-3542, DOI: 10.1016/J.ANTIVIRAL.2011.12.009 page 298	1-8
A	L. BOGLIONE ET AL: "Role of CYP27B1+2838 promoter polymorphism in the treatment of chronic hepatitis B HBeAg negative with PEG-interferon", JOURNAL OF VIRAL HEPATITIS., vol. 22, no. 3, 24 July 2014 (2014-07-24), pages 318-327, XP055250350, OXFORD, UK ISSN: 1352-0504, DOI: 10.1111/jvh.12288 page 319	1-8
A	CN 102 188 598 B (JIANGSU PROVINCE HOSPITAL TCM) 22 August 2012 (2012-08-22) abstract	1-8

2

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/EP2015/079719

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2011115914 A1	22-09-2011	EP 2547792 A1	23-01-2013
		JP 2013522302 A	13-06-2013
		US 2013121964 A1	16-05-2013
		WO 2011115914 A1	22-09-2011
WO 2015091306 A1	25-06-2015	NONE	
CN 102188598 B	22-08-2012	NONE	