Supplementary information

Delineating significant genome-wide associations of variants with antipsychotic and antidepressant treatment response: Implications for clinical pharmacogenomics

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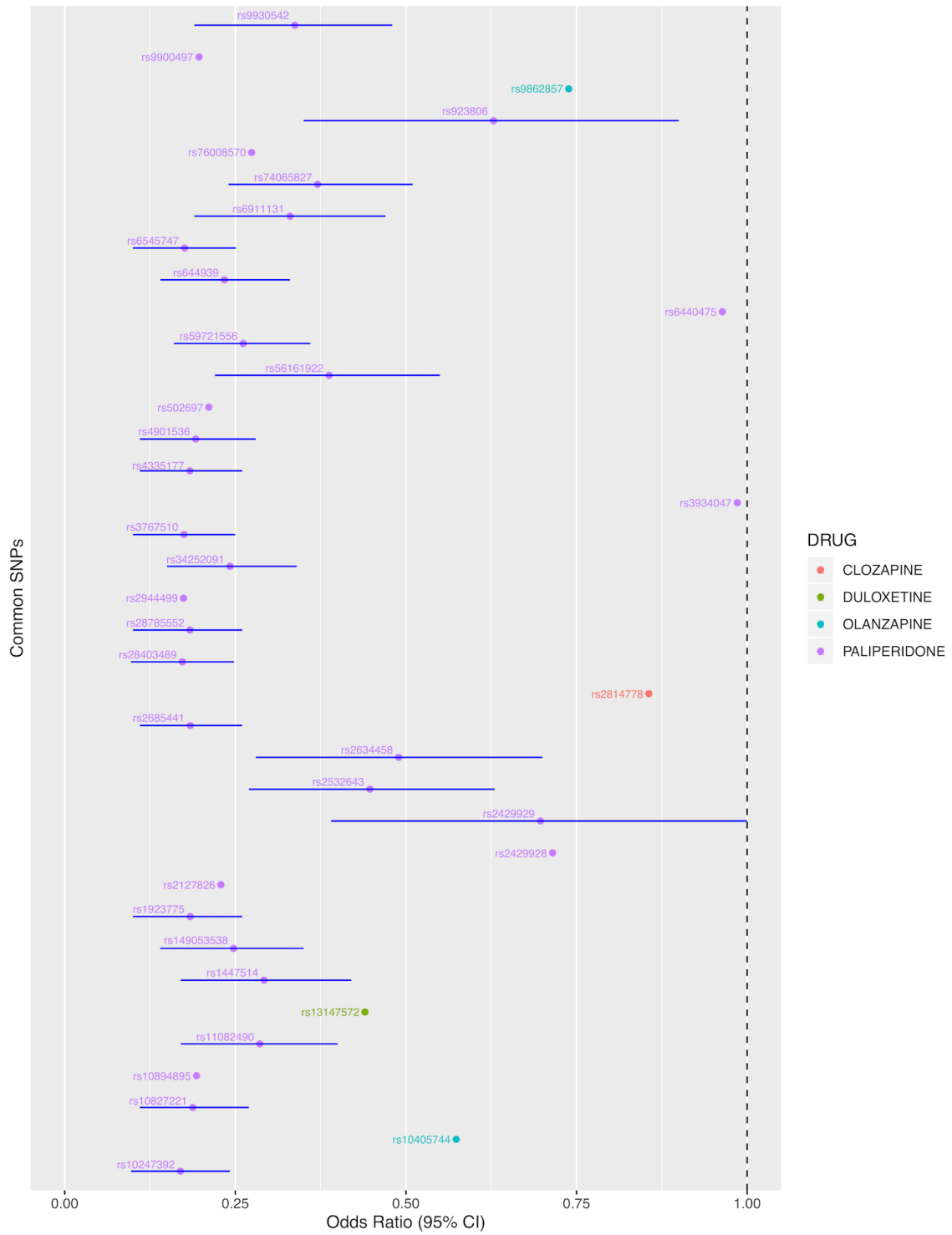
Figure S1. Odds ratio values (between 0-1) of pharmacogenomics (PGx) variants of common frequency (MAF > 0.10) are plotted alongside with the 95% of their confidence intervals. The PGx variants are colored based on the antipsychotic or antidepressant drug of the association.
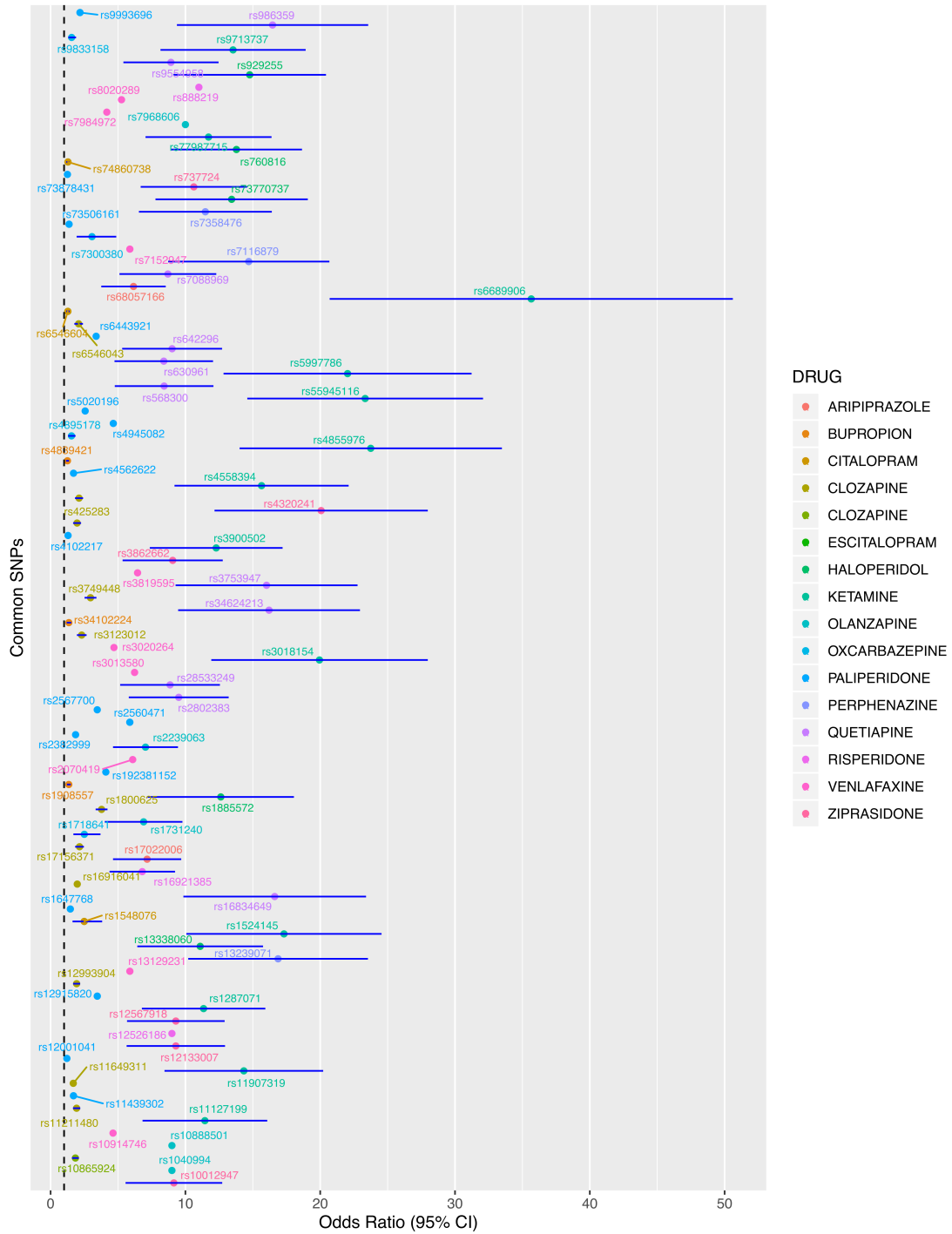
Figure S2. Odds ratio values (between 1-60) of pharmacogenomics (PGx) variants of common frequency (MAF > 0.10) are plotted alongside with the 95% of their confidence intervals. The PGx variants are colored based on the antipsychotic or antidepressant drug of the association.
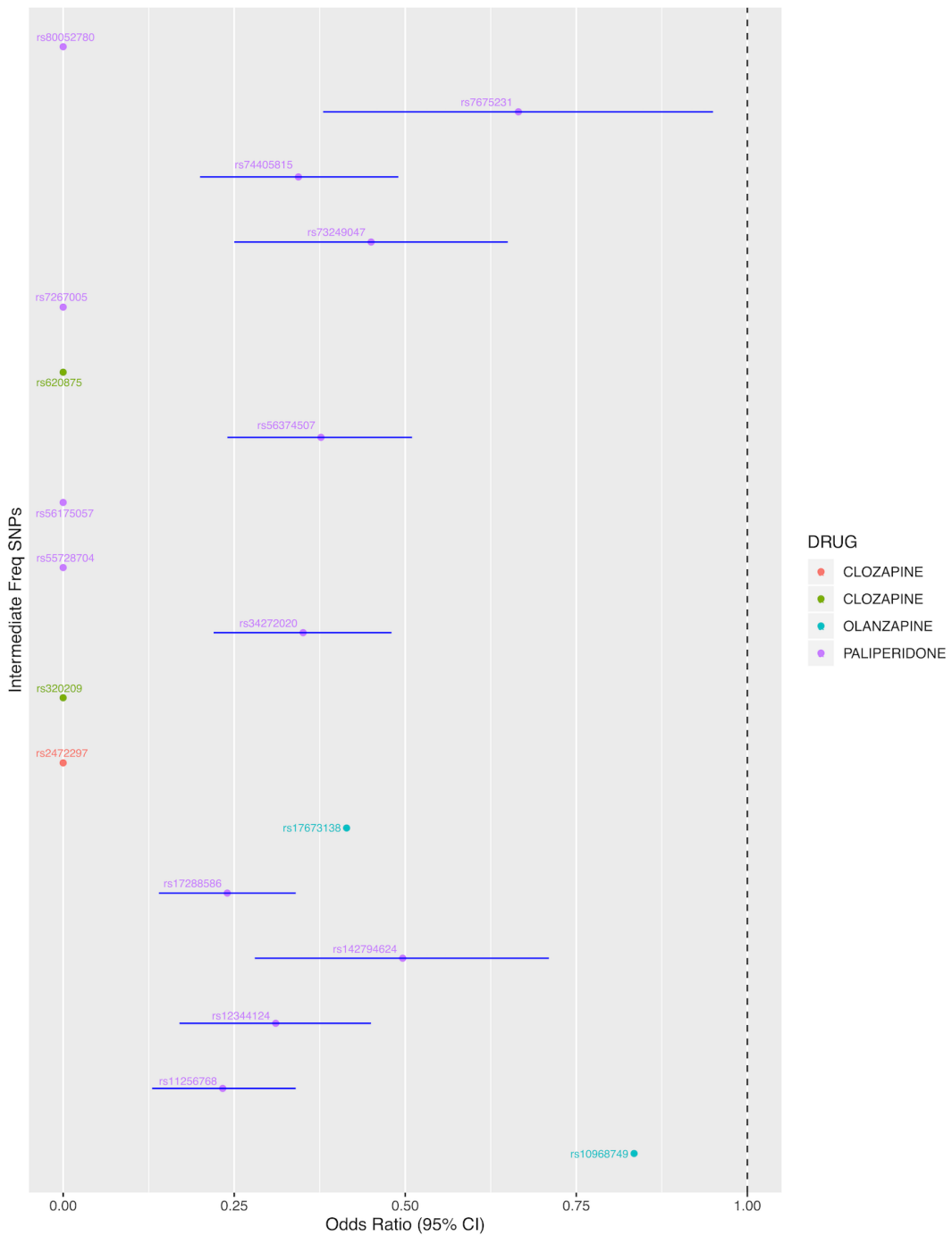
Figure S3. Odds ratio values (between 0-1) of pharmacogenomics (PGx) variants of intermediate frequency (0.05 < MAF < 0.10) are plotted alongside with the 95% of their confidence intervals. The PGx variants are colored based on the antipsychotic or antidepressant drug of the association. Abbreviations: Intermediate Freq, intermediate frequency.
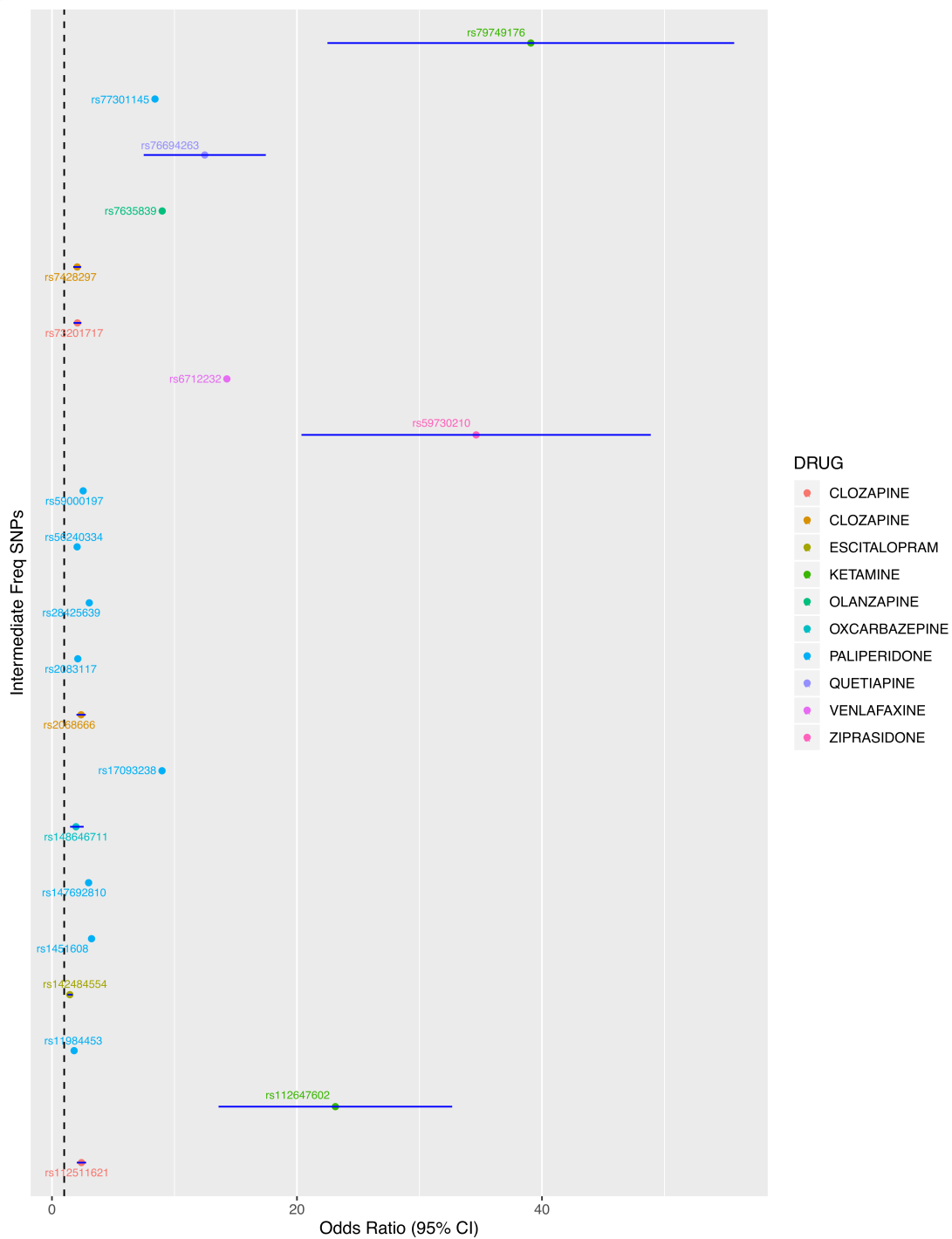
Figure S4. Odds ratio values (between 1-60) of pharmacogenomics (PGx) variants of intermediate frequency (0.05 < MAF < 0.10) are plotted alongside with the 95% of their confidence intervals. The PGx variants are colored based on the antipsychotic or antidepressant drug of the association. Abbreviations: Intermediate Freq, intermediate frequency.
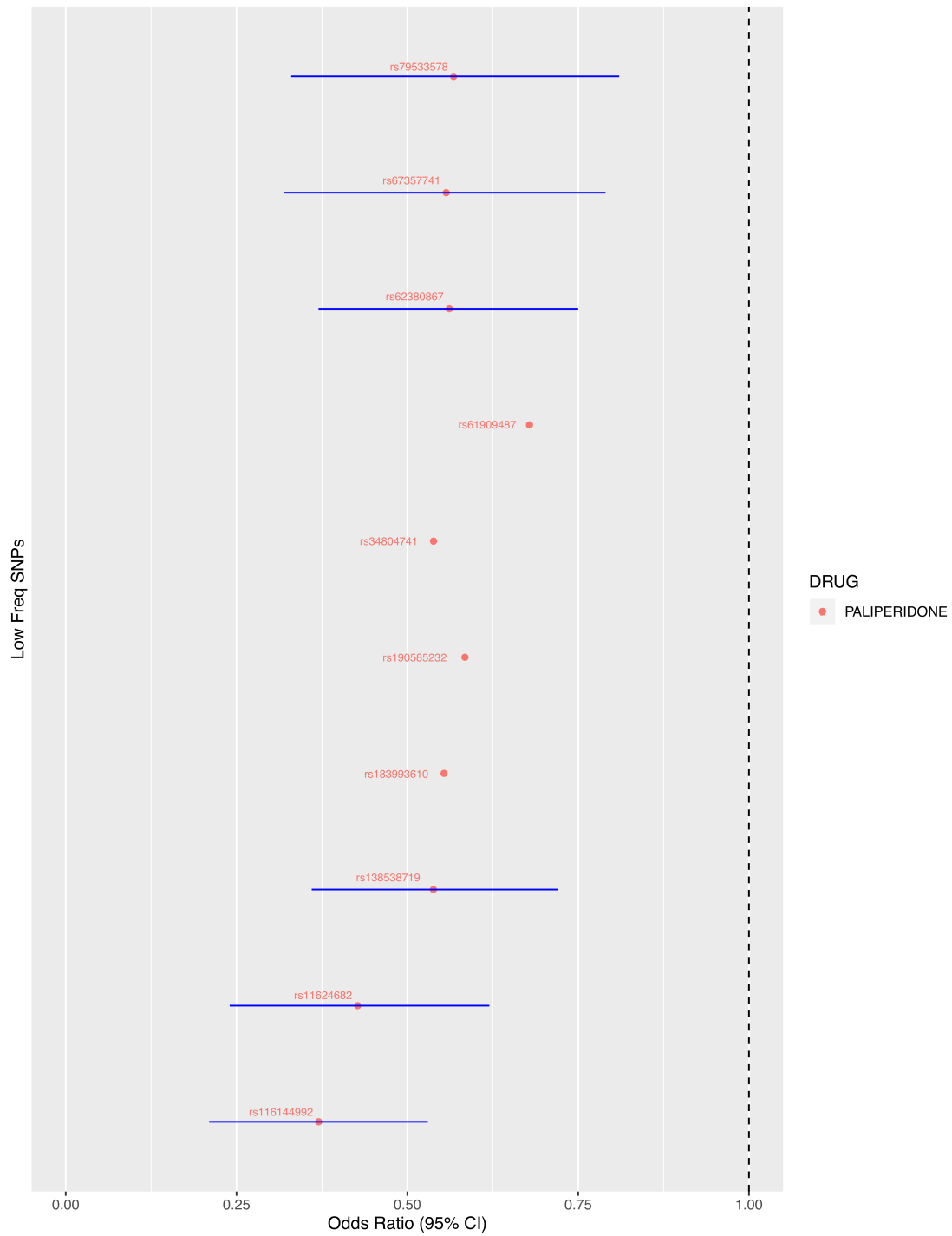
Figure S5. Odds ratio values (between 0-1) of pharmacogenomics (PGx) variants of low frequency (0.05 < MAF < 0.10) are plotted alongside with the 95% of their confidence intervals. The PGx variants are colored based on the antipsychotic or antidepressant drug of the association. Abbreviations: Low Freq, low frequency.
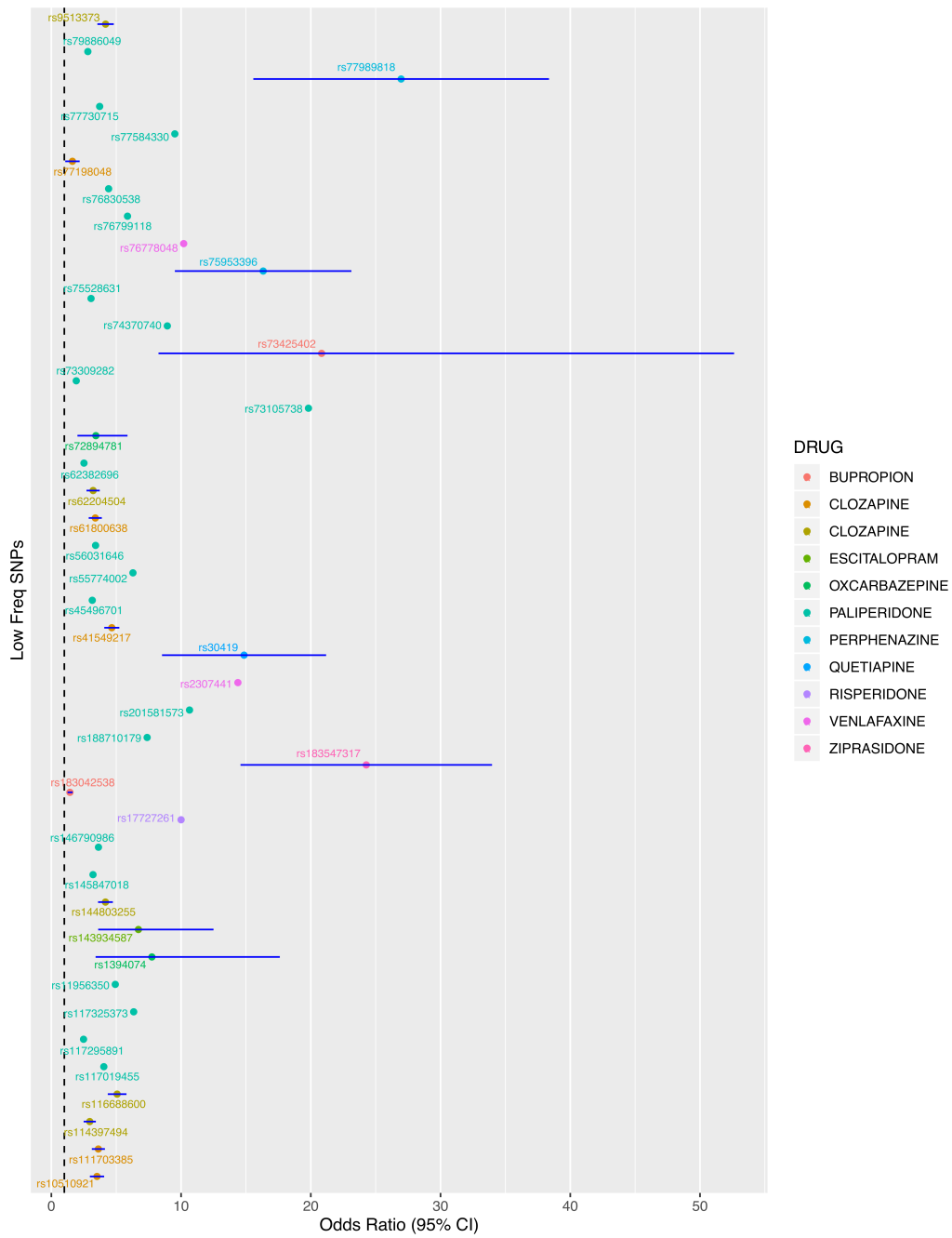
Figure S6. Odds ratio values (between 1-60) of pharmacogenomics (PGx) variants of low frequency (0.05 < MAF < 0.10) are plotted alongside with the 95% of their confidence intervals. The PGx variants are colored based on the antipsychotic or antidepressant drug of the association. Abbreviations: Low Freq, low frequency.
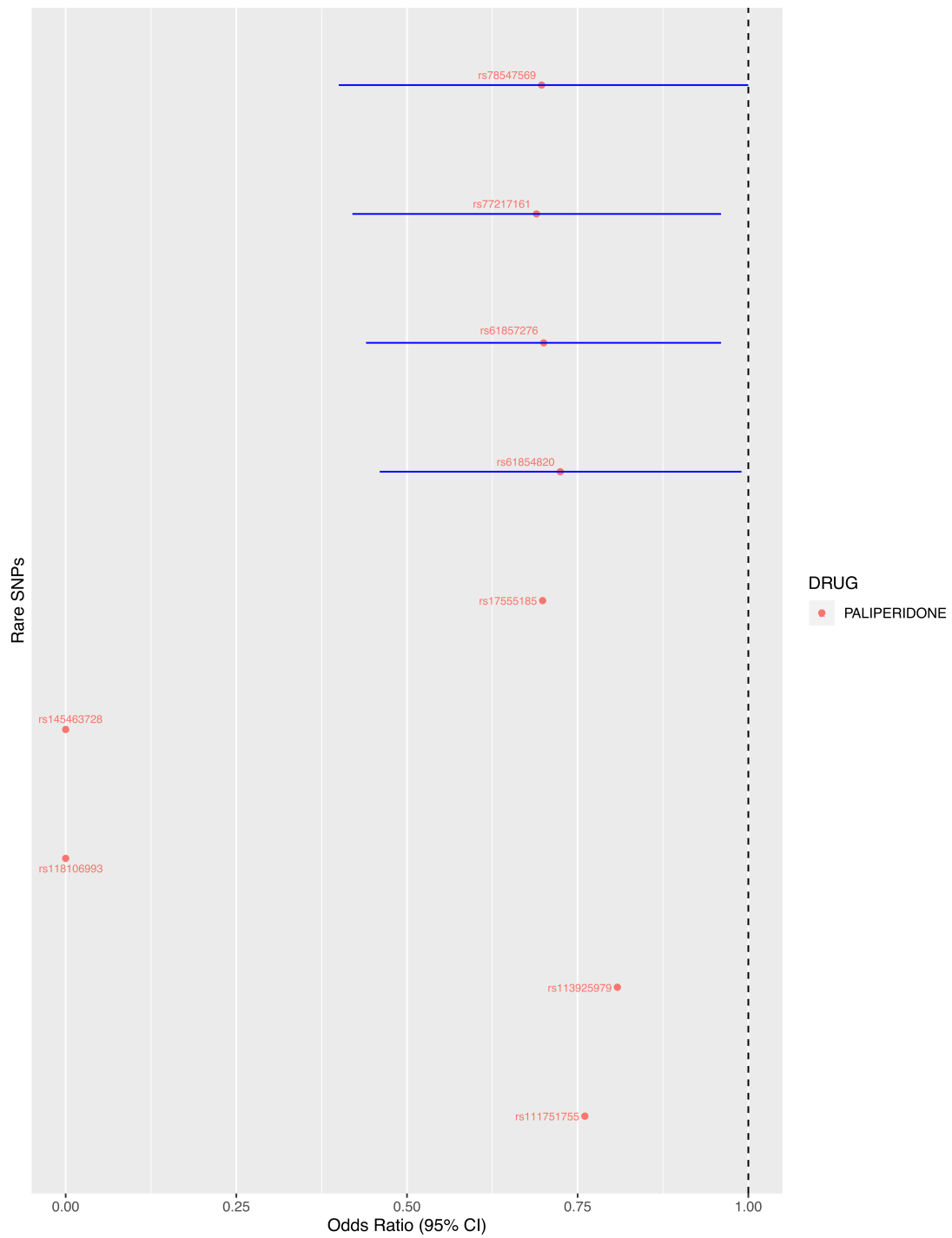
Figure S7. Odds ratio values (between 0-1) of pharmacogenomics (PGx) variants of rare frequency (0.05 < MAF < 0.10) are plotted alongside with the 95% of their confidence intervals. The PGx variants are colored based on the antipsychotic or antidepressant drug of the association.

Figure S8. Odds ratio values (between 1-60) of pharmacogenomics (PGx) variants of rare frequency (0.05 < MAF < 0.10) are plotted alongside with the 95% of their confidence intervals. The PGx variants are colored based on the antipsychotic or antidepressant drug of the association.
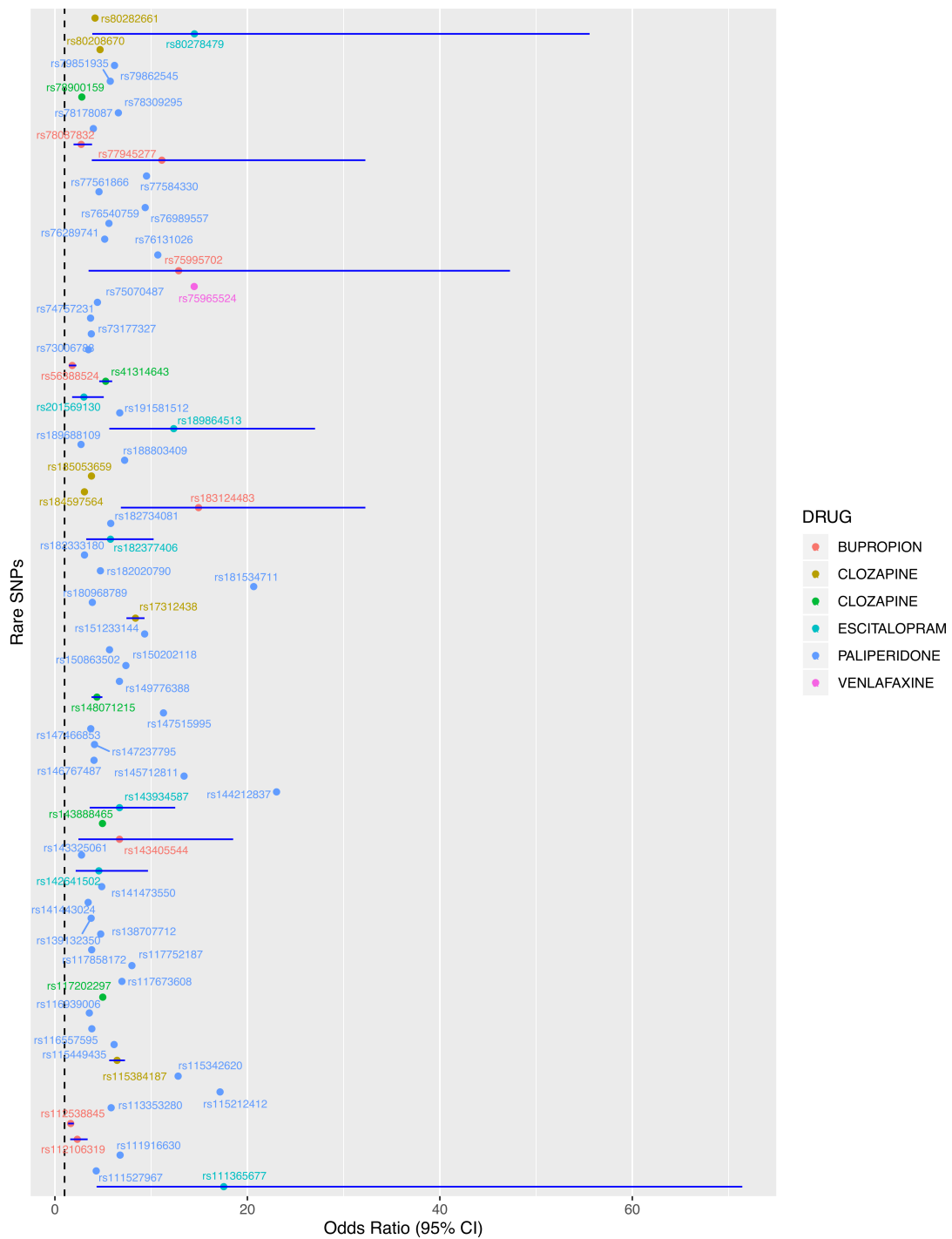
Figure S9. Odds ratio values (between 0-1) of pharmacogenomics (PGx) variants, which were not found in 1000Genomes Project, are plotted alongside with the 95% of their confidence intervals. The PGx variants are colored based on the antipsy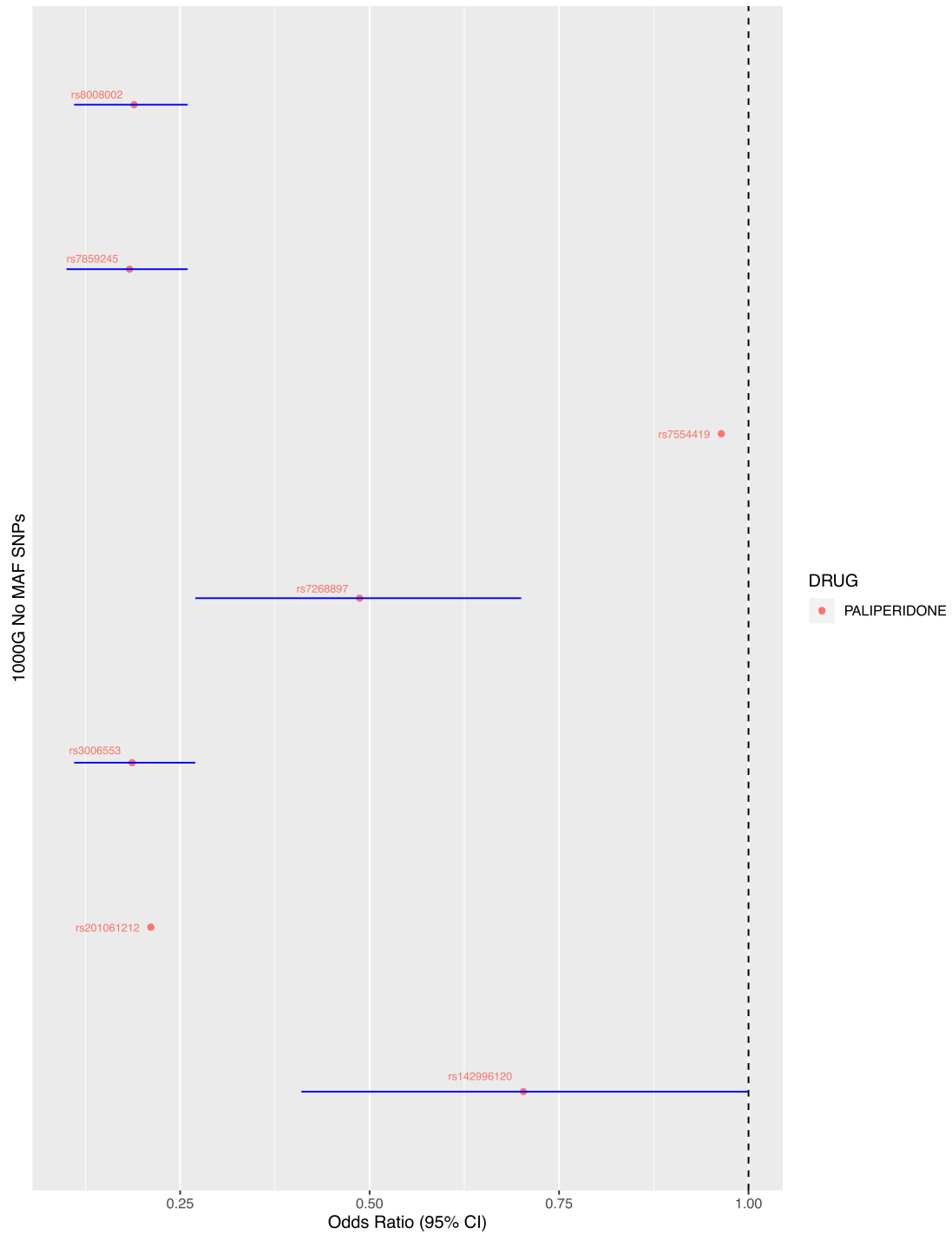chotic or antidepressant drug of the association. Abbreviations: 1000G No MAF, not found in 1000Genomes Project (no MAF was found).

Figure S10. Odds ratio values (between 1-60) of pharmacogenomics (PGx) variants, which were not found in 1000Genomes Project, are plotted alongside with the 95% of their confidence intervals. The PGx variants are colored based on the antipsychotic or antidepressant drug of the association. Abbreviations: 1000G No MAF, not found 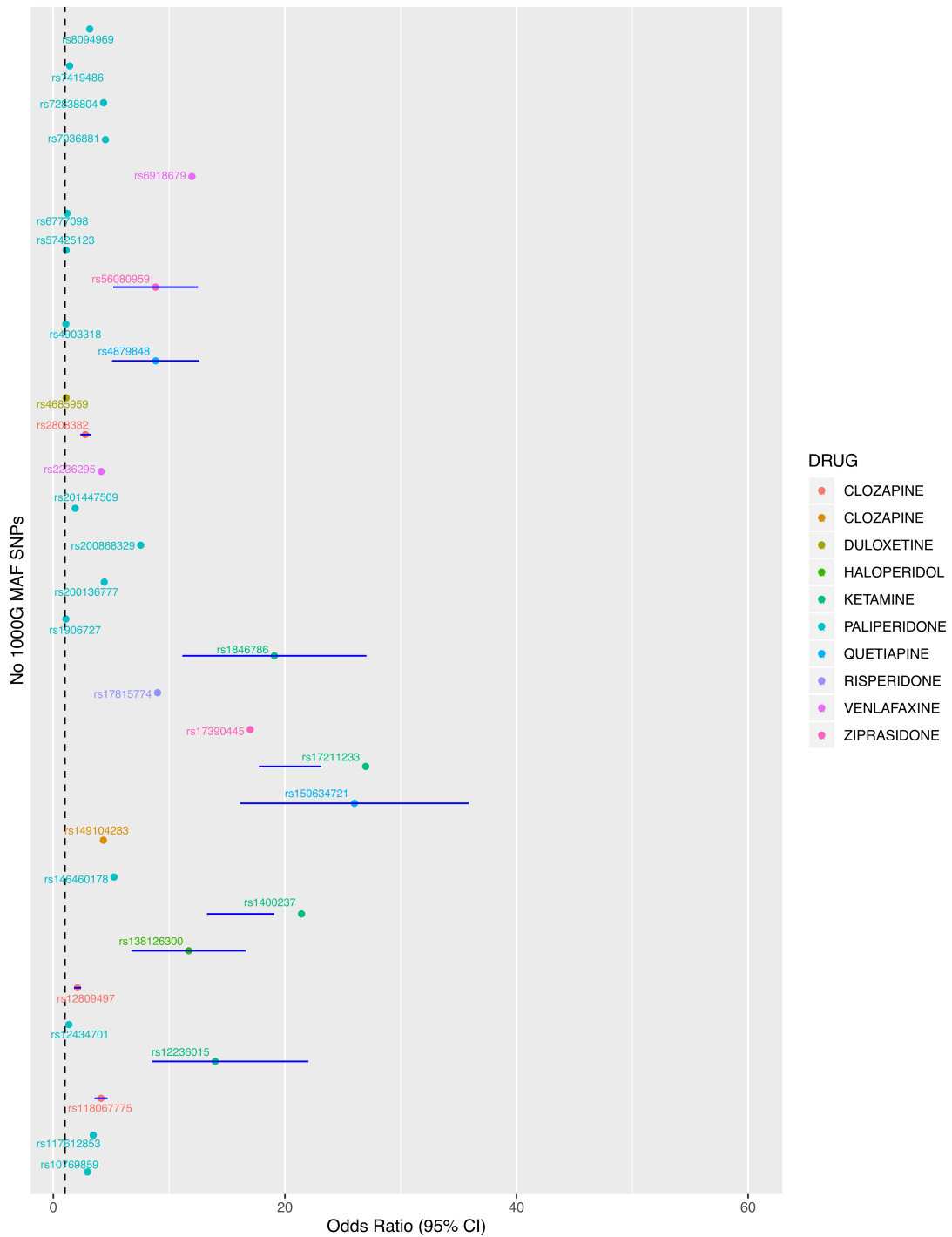in 1000Genomes Project (no MAF was found).