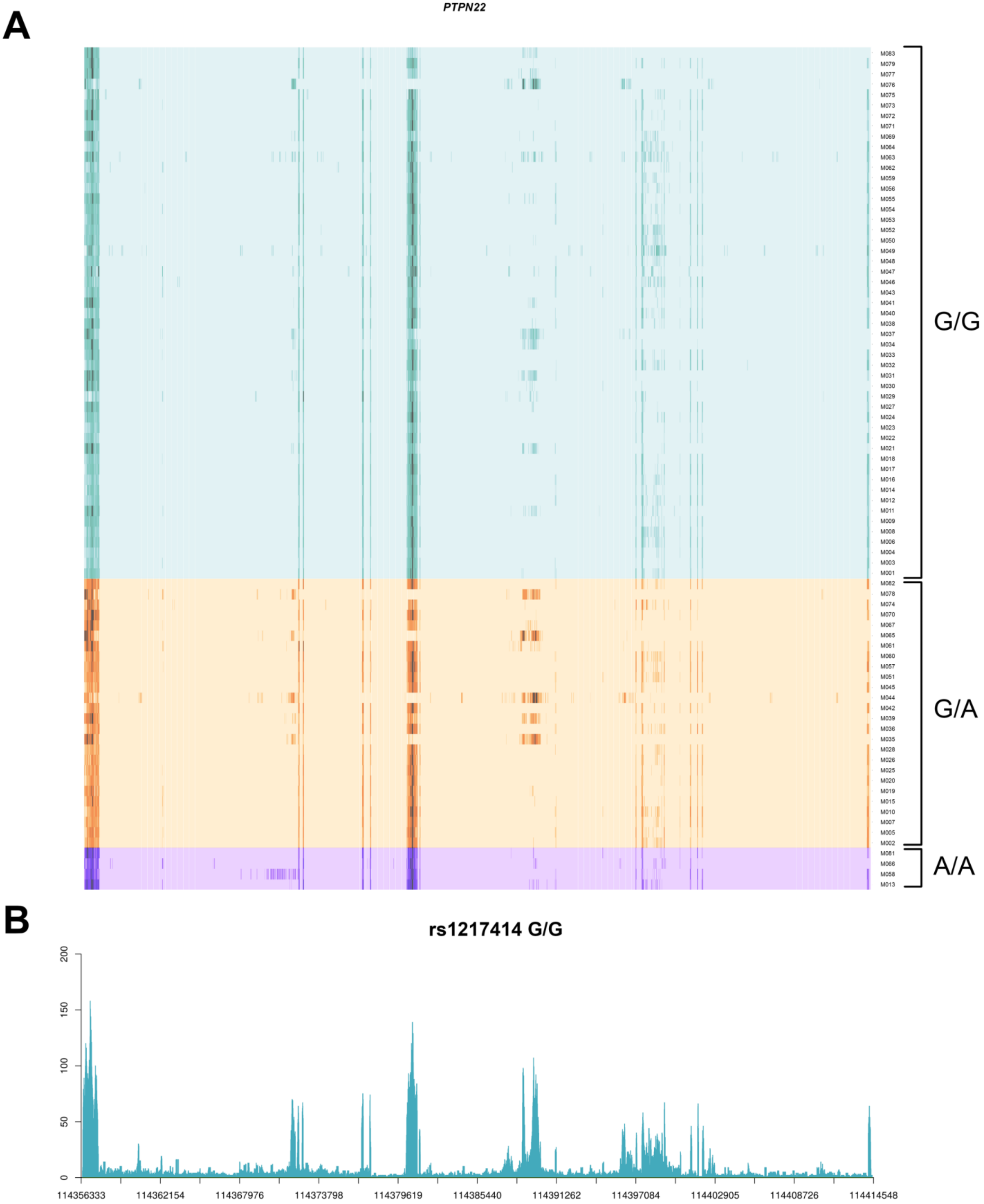A
PTPN22
M083
M079
M077
M076
M075
M073
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M071
M069
M064
M063
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M082
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M061
M060
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M045
M044
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M039
M036
M035
M028
M026
M025
M020
M019
M015
M010
M007
M005
M002
M081
M066
M058
M013
G/G
G/A
A/A
B
rs1217414 G/G
0
50
100
150
200
114356333
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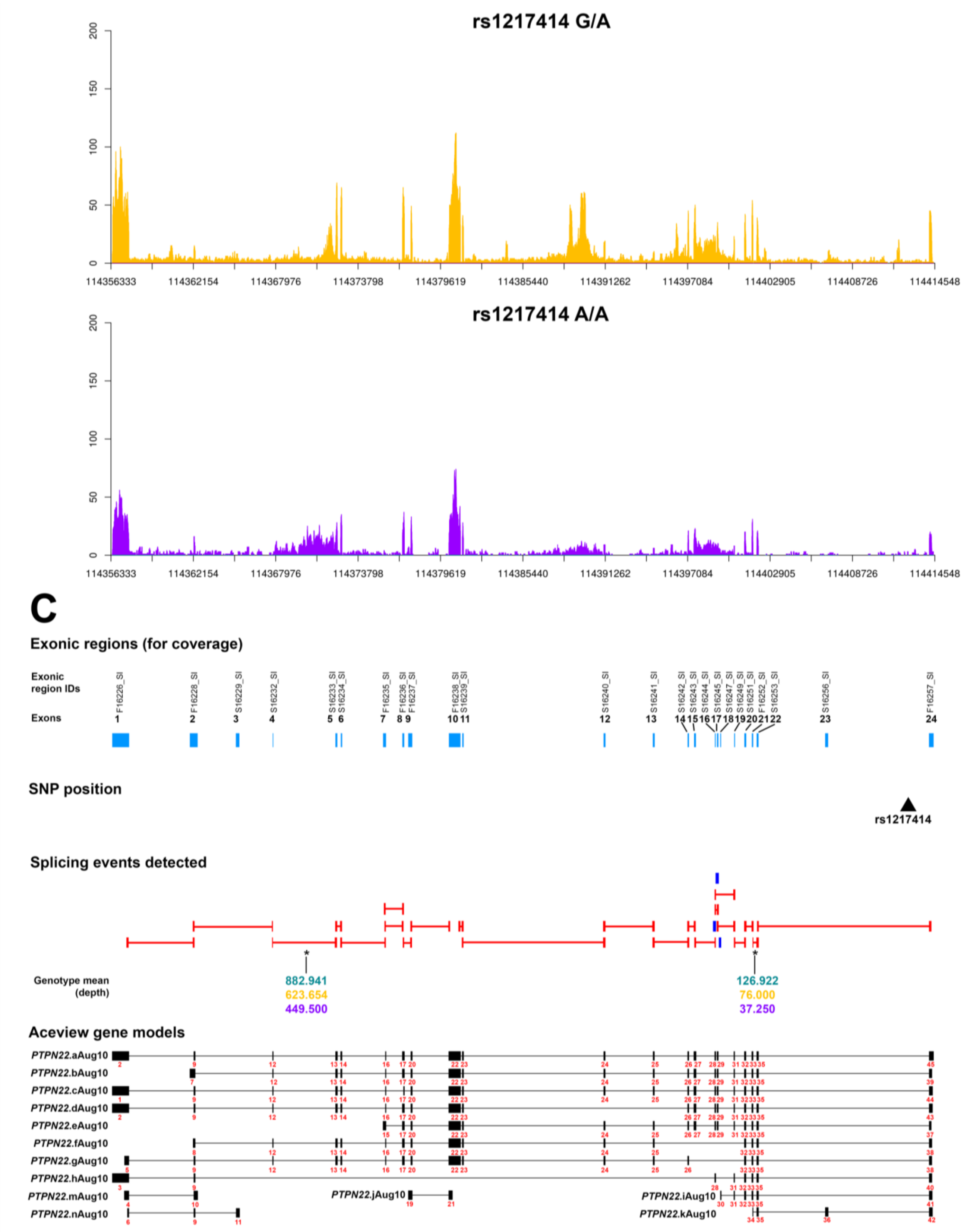

Supplemental Figure S6. *PTPN22* gene expression by rs1217414 genotypes in CD19+ T cells. (A) Sequencing coverage across the *PTPN22* gene (scaled by the maximum depth for the locus) for each individual subject. (B) Summary of the distribution of sequencing coverage across *PTPN22* for each genotype of rs1217414: G/G (teal), G/A (gold), A/A (purple). (C) Splicing events detected in *PTPN22* and *PTPN22* gene models from AceView annotations. Detected junctions are indicated by red bars and detected IR events are indicated by blue blocks. AceView gene models for *PTPN22* are indicated by black blocks and bars, and cyan blocks rs1217414 the collapsed gene model for *PTPN22*. Splicing events and exons associated with rs1893592 are denoted by an asterisk (*), and the mean coverage for the G/G (teal), G/A (gold), A/A (purple) genotypes are noted. Exons used for coverage (cyan blocks in collapsed gene models) are numbered sequentially by start and stop positions 5’ to 3’ on the + strand.