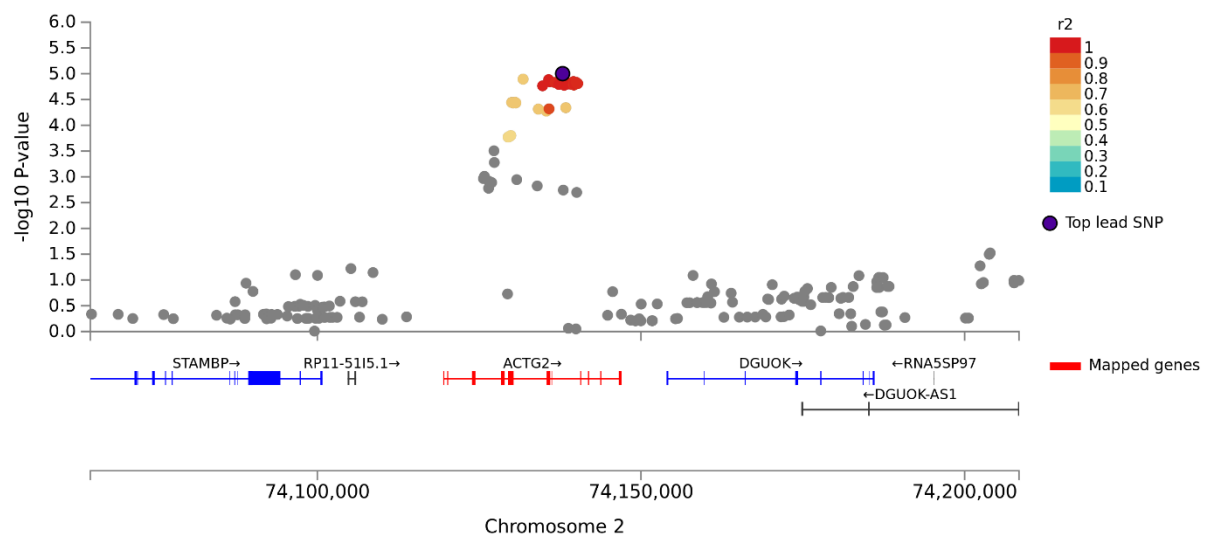


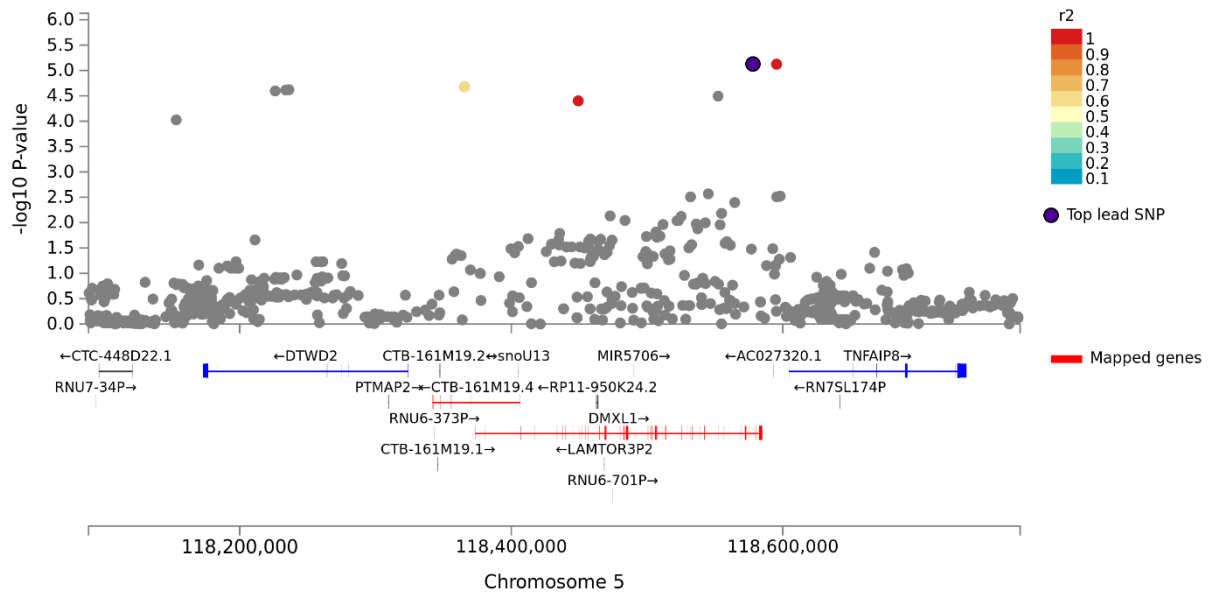
Evidence of polygenic regulation of the physiological presence of neurofilament light chain in human serum

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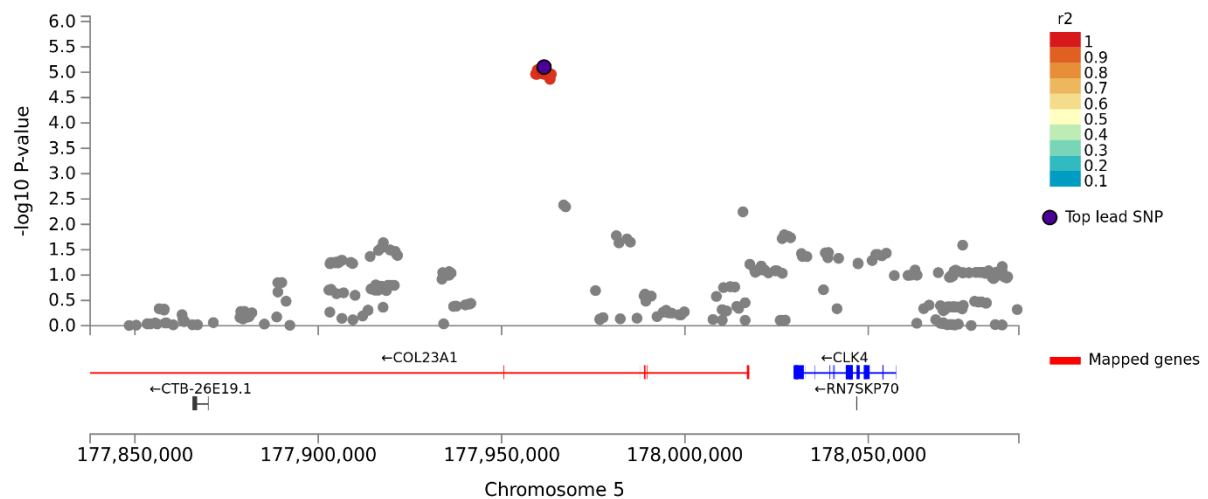
Supplementary Figures



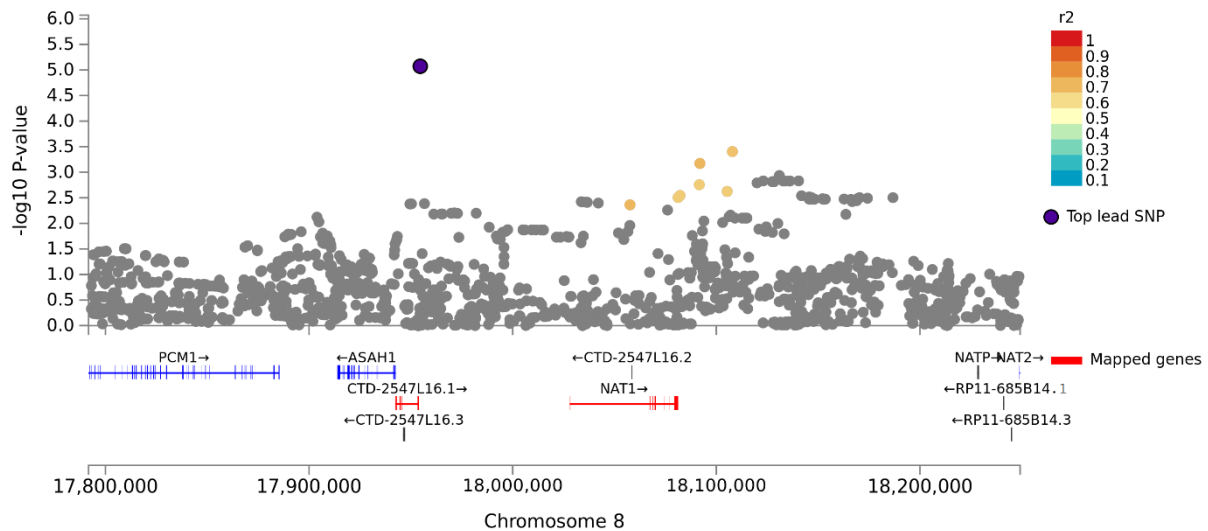
Suppl.Figure.1. Regional association plot for the suggestive locus #1 identified for serum NfL through meta-analysis of the BiDirect and ASPS-Fam studies (N=2,186). Lead variant: rs2462121 ($p = 9.98 \times 10^{-6}$; $z = -4.418$). Number of supporting variants in locus: 39 ($p < 0.05$, $r^2 \geq 0.6$ in 500 kb window from lead variant).



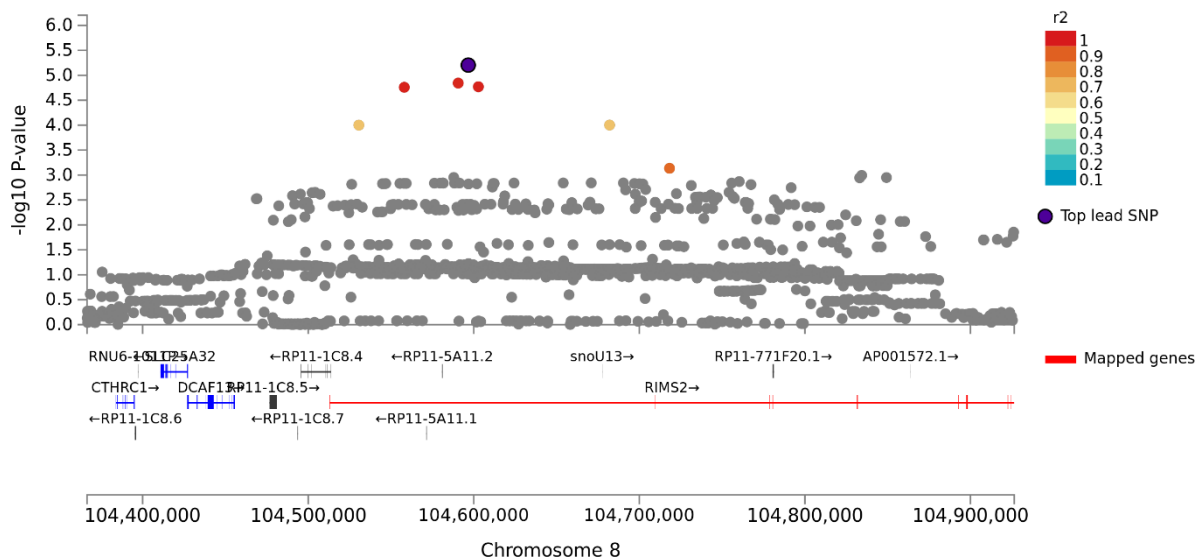
Suppl.Figure.2. Regional association plot for the suggestive locus #2 identified for serum NfL through meta-analysis of the BiDirect and ASPS-Fam studies (N=2,186). Lead variant: rs114956339 ($p = 7.46 \times 10^{-6}$; $z = 4.48$). Number of supporting variants in locus: 3 ($p < 0.05$, $r^2 \geq 0.6$ in 500 kb window from lead variant).



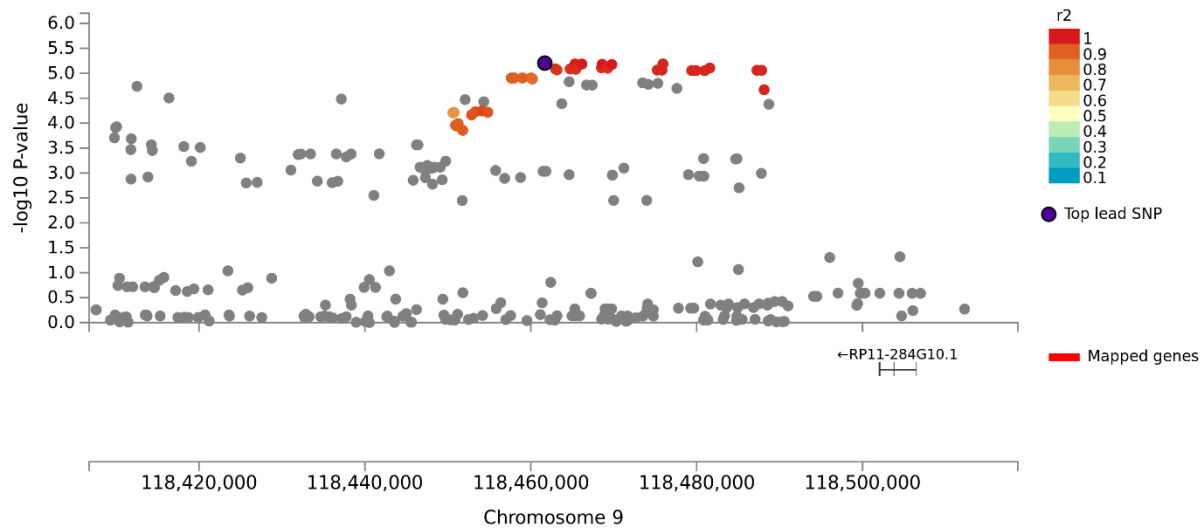
Suppl.Figure.3. Regional association plot for the suggestive locus #3 identified for serum NfL through meta-analysis of the BiDirect and ASPS-Fam studies (N=2,186). Lead variant: rs529938 ($p = 7.9 \times 10^{-6}$; $z = 4.468$). Number of supporting variants in locus: 20 ($p < 0.05$, $r^2 \geq 0.6$ in 500 kb window from lead variant).



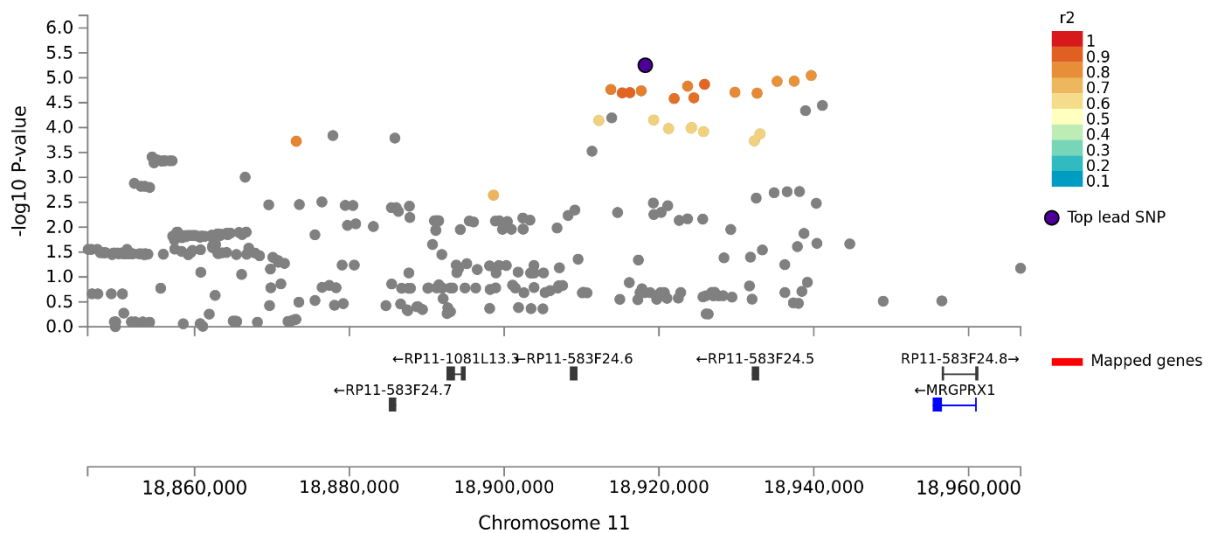
Suppl.Figure.4. Regional association plot for the suggestive locus #4 identified for serum NfL through meta-analysis of the BiDirect and ASPS-Fam studies (N=2,186). Lead variant: rs73198093 ($p = 8.48 \times 10^{-6}$; $z = 4.453$). Number of supporting variants in locus: 7 ($p < 0.05$, $r^2 \geq 0.6$ in 500 kb window from lead variant).



Suppl.Figure.5. Regional association plot for the suggestive locus #5 identified for serum NfL through meta-analysis of the BiDirect and ASPS-Fam studies (N=2,186). Lead variant: rs34372929 ($p = 6.25 \times 10^{-6}$; $z = 4.518$). Number of supporting variants in locus: 6 ($p < 0.05$, $r^2 \geq 0.6$ in 500 kb window from lead variant).



Suppl.Figure.6. Regional association plot for the suggestive locus #6 identified for serum NfL through meta-analysis of the BiDirect and ASPS-Fam studies (N=2,186). Lead variant: rs10982883 ($p = 6.25 \times 10^{-6}$; $z = 4.518$). Number of supporting variants in locus: 39 ($p < 0.05$, $r^2 \geq 0.6$ in 500 kb window from lead variant).



Suppl.Figure.7. Regional association plot for the suggestive locus #7 identified for serum NfL through meta-analysis of the BiDirect and ASPS-Fam studies (N=2,186). Lead variant: rs1842909 ($p = 5.61 \times 10^{-6}$; $z = 4.541$). Number of supporting variants in locus: 23 ($p < 0.05$, $r^2 \geq 0.6$ in 500 kb window from lead variant).