

**Supplement Table 2:** Analysis of the likelihood that an individual with an allele will more likely be in remission presented as odds ratios and 95% confidence intervals. Analyses are presented for the full PEER dataset as well as the full dataset adjusted by gender, age of onset, and race based on ancestral informative markers (AIMS). Adjusted odds ratios are also presented for the White and African-American cohorts. *P*-values < 0.05 are reported for the full cohort without correction and with Bonferroni correction (*q*).

Allele	Full DNA PEER	Full DNA PEER adjusted	European Ancestry adjusted	African Ancestry adjusted
A*01:01	1.17 (0.87,1.58)	1.12 (0.80,1.58)	1.07 (0.77,1.47)	0.92 (0.40,2.10)
A*02:01	1.39 (1.11,1.76) p=0.0048275 q=0.024	1.29 (0.99,1.68) p=0.056	1.37 (1.06,1.78) p=0.015	0.74 (0.42,1.33)
A*03:01	0.73 (0.51,1.04)	0.69 (0.48,1.00) p=0.050	0.70 (0.48,1.01) p=0.058	0.62 (0.26,1.50)
A*24:02	1.45 (1.04,2.01) p=0.028	1.24 (0.86,1.78) p=0.029	1.14 (0.79,1.63)	1.78 (0.72,4.43)
A*30:01	0.84 (0.52,1.37)	0.99 (0.58,1.69)	0.77 (0.32,1.89)	1.53 (0.86,2.73)
B*07:02	0.99 (0.71,1.39)	0.98 (0.69,1.39)	0.90 (0.62,1.30)	0.66 (0.31,1.41)
B*08:01	0.90 (0.63,1.30)	0.76 (0.51,1.13)	0.77 (0.52,1.13)	1.11 (0.48,2.57)
B*35:01	0.89 (0.57,1.39)	0.98 (0.62,.56)	0.94 (0.54,1.65)	1.45 (0.73,2.88)
B*44:02	<b>1.83 (1.35,2.47)</b> <b>p=0.0000964</b> <b>q=0.0003856</b>	1.42 (1.01,2.00) p =0.045	1.42 (1.03,1.97) p=0.033	2.95 (1.34,6.47) p=0.007
C*03:04	1.01 (0.70,1.45)	0.96 (0.65,1.42)	1.17 (0.79,1.73)	0.29 (0.08,1.02) P=0.054
C*04:01	0.81 (0.59,1.11)	0.97 (0.70,1.34)	0.85 (0.57,1.26)	0.99 (0.59,1.67)
C*05:01	1.44 (1.04,1.98) p=0.028 q=0.195062	1.20 (0.84,1.72)	1.13 (0.78,1.63)	1.87 (0.84,4.17)
C*06:02	1.30 (0.93,1.80)	1.06 (0.73,1.53)	1.13 (0.78,1.63)	1.36 (0.74,2.50)
C*07:01	0.88 (0.63,1.23)	0.86 (0.60,1.25)	0.82 (0.58,1.17)	0.80 (0.36,1.74)
C*07:02	1.11 (0.82,1.50)	1.06 (0.76,1.46)	0.88 (0.63,1.24)	0.85 (0.42,1.69)
C*16:01	0.86 (0.55,1.35)	0.85 (0.51,1.42)	1.13 (0.61,2.10)	1.00 (0.53,1.89)