

Supplementary Table 4: Effect of combinations of *KIR3DL1* and *HLA-B* on mean viral load set point (excluding samples that overlap with the progression analysis)

| | Without co-variables ¹ | | | | | | | | | | | | | | |
|--------------------------|-----------------------------------|-----------|------------|-----------|--------------------|--------|--------------|--------------|--------|------------|-------|--------------|----------------|------------|--------------------|
| | mVL <2000 | | mVL >10000 | | OR | 95% CI | p-value | mVL <2000 | | mVL >10000 | | mVL <2000 | mVL 2000-10000 | mVL >10000 | p for trend |
| | N (%) | N (%) | N (%) | N (%) | | | | OR | 95% CI | p-value | N (%) | | | | |
| <i>Bw6/Bw6</i> | 37 (32.5) | 81 (67.5) | 1.0 | | | | 37 (32.5) | 77 (67.5) | 1.00 | | | 37 (30.1) | 9 (7.3) | 77 (62.6) | |
| <i>3DL1*h/*y+Bw4-80I</i> | 55 (65.5) | 29 (34.5) | 0.2 | 0.14-0.52 | 9x10 ⁻⁵ | | 17 (63.0) | 10 (37.0) | 0.25 | 0.10-0.67 | 0.01 | 55 (61.1) | 6 (6.7) | 29 (32.2) | 6x10 ⁻⁵ |
| <i>3DL1*I/*x+Bw4-80I</i> | 22 (55.0) | 18 (45.0) | 0.4 | 0.18-0.89 | 0.02 | | 9 (50.0) | 9 (50.0) | 0.52 | 0.17-1.56 | 0.24 | 22 (51.2) | 3 (7.0) | 18 (41.8) | 0.02 |
| <i>3DL1*004+Bw4</i> | 36 (52.2) | 33 (47.8) | 1 | 0.21-0.78 | 0.01 | | 23 (60.5) | 15 (39.5) | 0.27 | 0.12-0.61 | 0.001 | 36 (50.0) | 3 (4.2) | 33 (45.8) | 7x10 ⁻³ |
| <i>3DL1*h/*y+B*57</i> | 36 (78.3) | 10 (21.7) | 0.1 | 0.06-0.36 | 2x10 ⁻⁵ | | | | | | | 36 (76.6) | 1 (2.1) | 10 (21.3) | 1x10 ⁻⁵ |
| <i>3DL1*I/*x+B*57</i> | 8 (53.3) | 7 (46.7) | 0.5 | 0.16-1.66 | 0.26 | | | | | | | 8 (50.0) | 1 (6.3) | 7 (43.7) | 0.22 |
| <i>3DL1*h/*y+B*27</i> | 7 (70.0) | 3 (30.0) | 0.1 | 0.04-0.78 | 0.02 | | | | | | | 7 (50.0) | 4 (28.6) | 3 (21.4) | 0.01 |
| <i>3DL1*I/*x+B*27</i> | 7 (77.8) | 2 (22.2) | 0.1 | 0.03-0.75 | 0.02 | | | | | | | 7 (70.0) | 1 (10.0) | 2 (20.0) | 0.02 |

¹For the *Bw4-80I* groups, all individuals with *KIR3DL1*004*, *B*57*, and *B*27* were removed from the analysis. For the *KIR3DL1*004* group, all individuals with *B*57*, *B*27*, and *3DL1*h/*y+Bw4-80I* were removed from the analysis.

p-values are based on comparisons between the genotypic variable listed and the *Bw6/Bw6* control group.

N = number of individuals; mVL = mean viral load; OR= odds ratio; 95% CI = 95% confidence interval