

**Supplementary Table 2. FBAT Results for All 20 Markers of *DTNBPI*<sup>a</sup>**

| Markers <sup>b</sup> | LD bins  | Distance <sup>c</sup> | Genotyping Completion Rate | SNP        | Allele   | All Families |             |                 | EA Subset   |             |                 |
|----------------------|----------|-----------------------|----------------------------|------------|----------|--------------|-------------|-----------------|-------------|-------------|-----------------|
|                      |          |                       |                            |            |          | Freq.        | Z Score     | <i>p</i> -value | Freq.       | Z Score     | <i>p</i> -value |
| rs742102             |          | 6,815                 | 0.99                       | C/T        | T        | 0.04         | 1.07        | 0.28            | 0.03        | 1.01        | 0.31            |
| rs17470454           |          | 1,032                 | 0.99                       | C/T        | C        | 0.95         | 0.67        | 0.50            | 0.93        | 0.63        | 0.53            |
| rs742106             |          | 13,956                | 0.98                       | C/T        | T        | 0.31         | 0.26        | 0.79            | 0.33        | 0.64        | 0.52            |
| <b>rs875462</b>      | <b>A</b> | 7,427                 | <b>0.99</b>                | <b>A/G</b> | <b>A</b> | <b>0.80</b>  | <b>2.65</b> | <b>0.008</b>    | <b>0.75</b> | <b>2.30</b> | <b>0.021</b>    |
| rs10949305           | B        | 16,887                | 0.98                       | T/A        | A        | 0.18         | 0.27        | 0.79            | 0.10        | -0.07       | 0.95            |
| rs2743553            | B        | 10,324                | 0.99                       | C/T        | T        | 0.14         | 1.53        | 0.13            | 0.09        | 1.06        | 0.29            |
| rs742105             | C        | 16,047                | 0.98                       | G/A        | A        | 0.40         | 0.45        | 0.65            | 0.43        | 0.72        | 0.47            |
| <b>rs760666</b>      | <b>A</b> | 4,119                 | <b>0.98</b>                | <b>C/T</b> | <b>C</b> | <b>0.81</b>  | <b>2.76</b> | <b>0.006</b>    | <b>0.77</b> | <b>2.14</b> | <b>0.032</b>    |
| <b>rs7758659</b>     | <b>A</b> | 27,615                | <b>0.99</b>                | <b>G/A</b> | <b>G</b> | <b>0.81</b>  | <b>2.84</b> | <b>0.004</b>    | <b>0.77</b> | <b>2.16</b> | <b>0.030</b>    |
| rs2619539            | C        | 5,448                 | 0.99                       | C/G        | G        | 0.40         | 0.55        | 0.58            | 0.44        | 0.43        | 0.67            |
| rs2743865            | B        | 1,799                 | 0.99                       | C/T        | T        | 0.17         | 0.87        | 0.38            | 0.10        | 0.47        | 0.64            |
| rs3213207            | D        | 5,330                 | 0.98                       | A/G        | A        | 0.90         | 0.55        | 0.58            | 0.87        | 0.64        | 0.52            |

|           |   |        |      |     |   |      |      |      |      |       |      |
|-----------|---|--------|------|-----|---|------|------|------|------|-------|------|
| rs1011313 | E | 16,397 | 0.98 | G/A | A | 0.09 | 0.14 | 0.89 | 0.10 | -0.31 | 0.76 |
| rs2619528 | F | 1,303  | 0.98 | G/A | A | 0.28 | 0.02 | 0.99 | 0.23 | -0.54 | 0.59 |
| rs760761  | F | 2,517  | 0.99 | C/T | C | 0.72 | 0.38 | 0.71 | 0.77 | 1.18  | 0.24 |
| rs2619522 | F | 3,421  | 0.98 | T/G | T | 0.72 | 0.22 | 0.83 | 0.77 | 0.82  | 0.41 |
| rs1018381 | B | 3,801  | 0.99 | C/T | T | 0.17 | 0.81 | 0.42 | 0.10 | 0.43  | 0.66 |
| rs909706  | G | 4,338  | 0.98 | A/G | G | 0.31 | 1.33 | 0.18 | 0.32 | 1.43  | 0.15 |
| rs2619538 |   | 3,452  | 0.99 | A/T | T | 0.43 | 0.58 | 0.56 | 0.42 | 1.09  | 0.27 |
| rs742208  |   | N/A    | 0.96 | T/C | C | 0.17 | 1.00 | 0.32 | 0.11 | -0.12 | 0.90 |

<sup>a</sup> FBAT results for all 20 screening SNPs are shown in the whole current sample and EA subset. SNP = nucleotide changes listed as major allele / minor allele. Allele nucleotides were converted to a unified format by ensuring they were from the minus strand. Nominal *p*-value and associated allele are shown. Freq. = frequency of the more often transmitted allele. Significant SNP (rs7758659) row is bolded, as are the two rows with SNPs in high LD with rs7758659 (rs875462 and rs760666).

<sup>b</sup> rs numbers are in first column, and LD bins (see Figure 2b) if any in the second column. Markers are in the order from the 3' to the 5' flanking regions.

<sup>c</sup> Distance to next marker in base pairs (bp). The position for the first marker is nucleotide 15,624,612 in the UCSC May 2004 freeze of chromosome 6.