

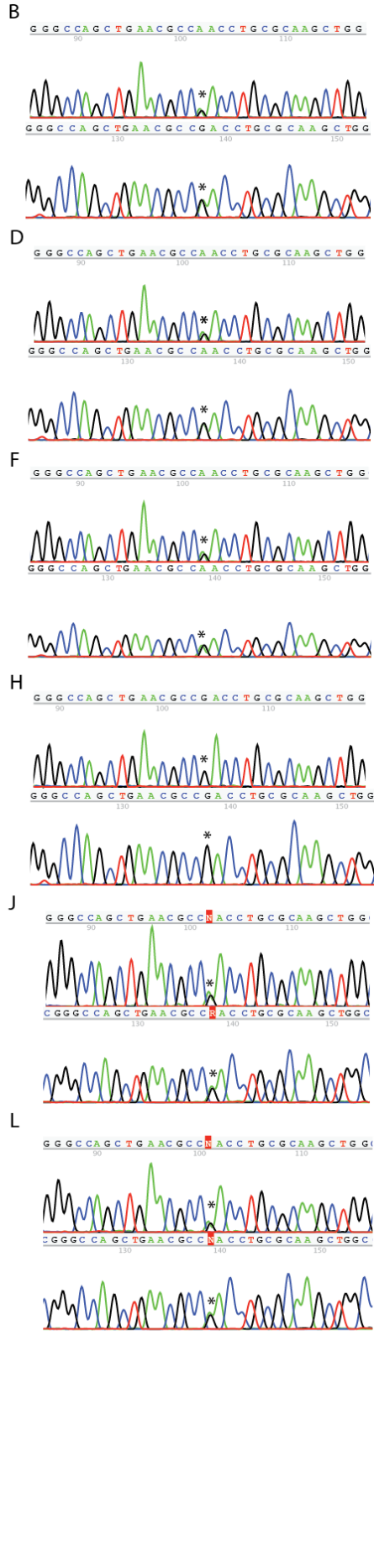
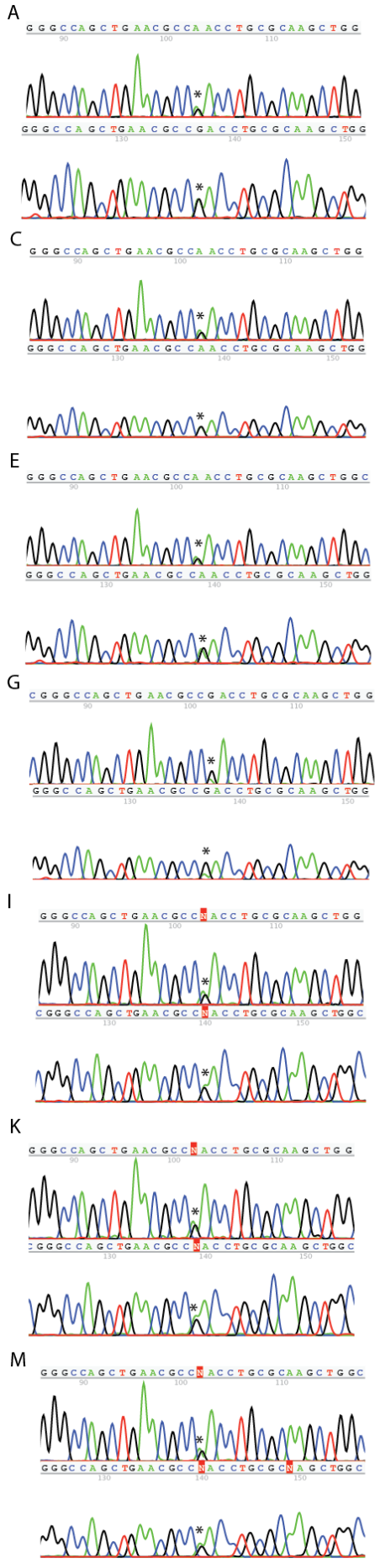
## **Supplemental Data**

### **A De Novo Mutation in the $\beta$ -Tubulin Gene *TUBB4A***

### **Results in the Leukoencephalopathy Hypomyelination**

### **with Atrophy of the Basal Ganglia and Cerebellum**

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## Figure S1. Validation of the *TUBB4A* c.G745A Variant

Sanger sequence of blood DNA from eleven affected individuals from ten unrelated families and the parents of the LD\_0638 family. Position c.G745 is indicated with a "\*" in each panel, forward (top) and reverse (bottom) reads are given for each individual. Samples: LD\_0313.0A (A), LD\_0345.0A (B), LD\_0440.0A (C), LD\_0605.0A (D), LD\_0638.0A (E), LD\_0638.0B (F), LD\_0638.1 (G; mosaic) LD\_0638.2 (H; wild-type), HA04 (I), HA07 (J), HA23 (K), HA27 (L) and HA107 (M).

**Table S1. Summary of Exome Sequencing Statistics**

| Family  | Individual | Affected | Mapped Sequence (Gb) | Target Bases <sup>a</sup> |           |                            |
|---------|------------|----------|----------------------|---------------------------|-----------|----------------------------|
|         |            |          |                      | Mean Depth                | Q20 Depth | Percent > 18x <sup>b</sup> |
| LD_0313 | LD_0313.0A | Yes      | 14.7                 | 87.8                      | 84.7      | 97.2                       |
|         | LD_0313.1  | No       | 21.3                 | 40.6                      | 39.9      | 96.8                       |
|         | LD_0313.2  | No       | 13.8                 | 33.6                      | 32.8      | 95.6                       |
| LD_0345 | LD_0345.0A | Yes      | 9.9                  | 40.5                      | 39.1      | 93.5                       |
|         | LD_0345.1  | No       | 27.9                 | 21.1                      | 20.6      | 93.1                       |
|         | LD_0345.2  | No       | 21.0                 | 36.5                      | 35.5      | 95.9                       |
| LD_0440 | LD_0440.0A | Yes      | 7.7                  | 56.0                      | 53.7      | 94.4                       |
|         | LD_0440.01 | No       | 10.2                 | 49.1                      | 47.0      | 90.8                       |
|         | LD_0440.1  | No       | 19.6                 | 26.5                      | 26.0      | 94.6                       |
|         | LD_0440.2  | No       | 17.6                 | 102.1                     | 98.0      | 97.2                       |
| LD_0605 | LD_0605.0A | Yes      | 30.2                 | 156.6                     | 149.5     | 98.0                       |
|         | LD_0605.1  | No       | 15.9                 | 58.4                      | 56.6      | 96.0                       |
|         | LD_0605.2  | No       | 12.9                 | 58.9                      | 56.5      | 95.5                       |
| LD_0638 | LD_0638.0A | Yes      | 10.3                 | 75.2                      | 72.1      | 95.7                       |
|         | LD_0638.0B | Yes      | 10.7                 | 79.4                      | 76.1      | 95.9                       |
|         | LD_0638.1  | No       | 10.4                 | 80.0                      | 77.2      | 95.6                       |
|         | LD_0638.2  | No       | 13.8                 | 103.2                     | 99.2      | 97.1                       |
| HA27    | HA27       | Yes      | 20.1                 | 237.5                     | 229.4     | 92.0                       |
|         | HA28       | No       | 7.1                  | 73.3                      | 70.1      | 84.0                       |
|         | HA29       | No       | 7.8                  | 80.1                      | 77.4      | 84.5                       |
| HA107   | HA107      | Yes      | 10.8                 | 91.7                      | 86.1      | 96.0                       |
|         | HA108      | No       | 14.0                 | 113.5                     | 106.4     | 96.9                       |
|         | HA109      | No       | 12.5                 | 103.1                     | 99.6      | 96.5                       |
| HA04    | HA04       | Yes      | 17.3                 | 205.7                     | 199.5     | 91.9                       |
| HA07    | HA07       | Yes      | 18.4                 | 218.9                     | 212.2     | 91.5                       |
| HA23    | HA23       | Yes      | 20.6                 | 240.4                     | 232.0     | 91.5                       |

<sup>a</sup>Bases captured by SeqCap EZ Human Exome Library v3.0 kit.

<sup>b</sup>The percentage of target bases covered by a minimum of 18 reads.