

American Journal of Human Genetics, Volume 90

## Supplemental Data

### ***RAD51* Haploinsufficiency Causes**

### **Congenital Mirror Movements in Humans**

Christel Depienne, Delphine Bouteiller, Aurélie Méneret, Ségolène Billot, Sergiu Groppa, Stephan Klebe, Fanny Charbonnier-Beaupel, Jean-Christophe Corvol, Jean-Paul Saraiva, Norbert Brueggemann, Kailash Bhatia, Massimo Cincotta, Vanessa Brochard, Constance Flamand-Roze, Wassila Carpentier, Sabine Meunier, Yannick Marie, Marion Gausсен, Giovanni Stevanin, Rosine Wehrle, Marie Vidailhet, Christine Klein, Isabelle Dusart, Alexis Brice, and Emmanuel Roze

**Table S1. Clinical features of patients with *RAD51* mutations**

| Family-Patient<br>Gender/age | MM severity <sup>a</sup> | MM location       | Associated disorders | Course <sup>c</sup> | Functional disability  | Treatment of MM |
|------------------------------|--------------------------|-------------------|----------------------|---------------------|--|-----------------|
| A-3<br>F/81                  | 0 <sup>b</sup>           | -                 | -                    | -                   | -  | -               |
| A-9<br>M/59                  | 3                        | Hands<br>Forearms | No                   | stable              | Difficulties in fine<br>bimanual activities<br>Pain/cramp during<br>sustained manual<br>activities<br>writing fatigability | No              |
| A-11<br>F/56                 | 0 <sup>b</sup>           | -                 | -                    | -                   | -  | -               |
| A-15<br>M/53                 | 2                        | Hands<br>Forearms | No                   | stable              | Pain/cramp during<br>sustained manual<br>activities  | No              |
| A-17<br>M/52                 | 2                        | Hands             | No                   | stable              | Pain/cramp during<br>sustained manual<br>activities  | No              |
| A-21<br>M/50                 | 0 <sup>b</sup>           | -                 | -                    | -                   | -  | -               |
| A-37<br>M/39                 | 0 <sup>b</sup>           | -                 | -                    | -                   | -  | -               |
| A-41<br>M/34                 | 0 <sup>b</sup>           | -                 | -                    | -                   | -  | -               |
| A-53<br>M/27                 | 3                        | Hands<br>Forearms | No                   | stable              | Difficulties in fine<br>bimanual activities<br>Pain/cramp during<br>sustained manual<br>activities                         | No              |
| A-54<br>F/31                 | 3                        | Hands<br>Forearms | No                   | stable              | Difficulties in fine<br>bimanual activities<br>Pain/cramp during<br>sustained manual<br>activities<br>writing fatigability | No              |
| A-56<br>M/33                 | 2                        | Hands<br>Forearms | No                   | Stable              | Difficulties in fine<br>bimanual activities<br>Pain/cramp during<br>sustained manual<br>activities                         | No              |

|                      |                |                           |    |        |  |    |
|----------------------|----------------|---------------------------|----|--------|--|----|
| <b>A-65<br/>F/17</b> | 3              | Hands<br>Forearms<br>Feet | No | stable | Difficulties in fine<br>bimanual activities<br>Pain/cramp during<br>sustained manual<br>activities<br>writing fatigability | No |
| <b>A-85<br/>F/14</b> | 0 <sup>b</sup> | -                         | -  | -      | -  | -  |
| <b>A-86<br/>F/16</b> | 0 <sup>b</sup> | -                         | -  | -      | -  | -  |
| <b>A-87<br/>F/20</b> | 0 <sup>b</sup> | -                         | -  | -      | -  | -  |
| <b>A-91<br/>M/13</b> | 2              | Hands<br>Forearms         | No | stable | Difficulties in fine<br>bimanual activities<br>Pain/cramp during<br>sustained manual<br>activities                         | No |
| <b>B-1<br/>F/58</b>  | 2              | Hands<br>Forearms         | No | stable | Difficulties in fine<br>bimanual activities  | No |
| <b>B-2<br/>M/31</b>  | 2              | Hands<br>Forearms         | No | stable | Difficulties in fine<br>bimanual activities  | No |

<sup>a</sup> according to the Woods and Teuber MM severity scale <sup>24</sup>; (0. No MM; 1. Barely discernible but repetitive MM; 2. Either slight but sustained MM, or stronger, but briefer MM; 3. Strong and sustained repetitive MM; 4. MM equal to that observed in the intended hand)

<sup>b</sup> asymptomatic carriers

<sup>c</sup> Course over decades from onset in infancy or early childhood

**Table S2. Statistics of SNPs and indels detected by whole exome analysis in patients 54 and 91 from Family A**

| Ind | SNP    |        |        |       |        |            |          |          | Indels |       |        |
|-----|--------|--------|--------|-------|--------|------------|----------|----------|--------|-------|--------|
|     | Total  | Htz    | Known  | New   | in CDS | New in CDS | Nonsense | Missense | Total  | Htz   | in CDS |
| 54  | 32 390 | 18 871 | 30 202 | 2 188 | 16 640 | 1 069      | 66       | 7 699    | 1 911  | 1 164 | 241    |
| 91  | 33 648 | 20 182 | 31 558 | 2 090 | 17 259 | 950        | 60       | 8 002    | 1 948  | 1 187 | 225    |

The coding regions of the genome of patients 54 and 91 (Family A) were sequenced by Integragen SA (Evry, France). Genomic DNA was captured using Agilent in-solution enrichment methodology (SureSelect Human All Exon Kits Version 1, Agilent) with the biotinylated oligonucleotide probe library (Human All Exon v1 – 38 Mb, Agilent), followed by paired-end 75 b massively parallel sequencing on Illumina GAIIx. Image analysis and base calling were performed using Illumina Real Time Analysis (RTA) Pipeline version 1.8 with default parameters. Bioinformatic analysis of sequencing data was based on the Illumina pipeline (CASAVA1.7). CASAVA performs alignment of a sequencing run to a reference genome (hg19), calls the SNPs based on the allele calls and read depth, and detects variants (SNPs & Indels). The alignment algorithm used was ELANDv2 (performs multiseed and gapped alignments). Htz, variants at the heterozygous state.

#### Supplemental Reference

24. Woods, B.T., and Teuber, H.L. (1978). Mirror movements after childhood hemiparesis. *Neurology* 28, 1152–1157.