

**Table S3. Chromosome rearrangements characterized by SNP microarray**

| Proband                                             | Cytogenetic description    | Detection      |                | Physical position     | Size (Mb) | Genes affected | Structural variants at breakpoints | Sequence features at breakpoints                          | DNA source  |
|-----------------------------------------------------|----------------------------|----------------|----------------|-----------------------|-----------|----------------|------------------------------------|-----------------------------------------------------------|-------------|
|                                                     |                            | <i>de novo</i> | method         |                       |           |                |                                    |                                                           |             |
| <b>(A) Probands with known rearrangements</b>       |                            |                |                |                       |           |                |                                    |                                                           |             |
| 8399                                                | Del (7)(q11.22q21.11)      | Y              | FISH           | 7:70243900-80836222*  | 10.79     | 91             | -/-                                | Unique / Unique                                           | LBL         |
| 9061                                                | Del (7)(q11.23q11.23)      | F              | FISH           | 7:73022752-73525602*  | 0.50      | 13             | -/-                                | AluSc / AluSx                                             | PBL/LBL     |
| 9101                                                | Del (5)(p15.2p14.3)        | Y              | 500K SNP array | 5:11612493-19014517*  | 7.38      | 13             | +/+                                | TTTAAAN <sub>36</sub> TTTAAAN <sub>36</sub> TTTAA / Uniqu | PBL/LBL     |
|                                                     | Inv(5)(p14.3p14.2)         | Y              | Sequencing     | 5:19014518-24615888*  | 5.60      | 1              | +/-                                | Unique / Unique                                           |             |
|                                                     | Del (7)(q11.23q11.23)      | Y              | FISH           | 7:72556311-76960517*  | 4.40      | 71             | +/-                                | LCR(L1MD2) / AluYd8                                       |             |
| 9164**                                              | t(7;11)(q21.1;p14)         | Y              | Karyotype      | NA                    | NA        | NA             | NA                                 | NA                                                        |             |
|                                                     | Del (1)(q21.1q21.1)        | Y              | 500K SNP array | 1:146101297-147808115 | 1.46      | 14             | +/+                                | LCR/LCR                                                   | LBL         |
|                                                     | Dup (7)(q11.23q11.23)      | Y              | aCGH, FISH     | 7:72755520-74289929   | 1.53      | 26             | +/+                                | LCR/LCR                                                   |             |
| <b>(B) Probands with unsuspected rearrangements</b> |                            |                |                |                       |           |                |                                    |                                                           |             |
| 9239                                                | Del (5)(q15q15)            | ?              | 500K SNP array | 5:93028002-95601249*  | 2.57      | 15             | -/+                                | L1PA7 / LTR MLT2B2                                        | PBL         |
| 9152                                                | Del (7)(q11.23q11.23)      | Y              | 500K SNP array | 7:74137882-76242236*  | 2.13      | 34             | -/+                                | AluSx / LCR(AluSg)                                        | PBL/LBL     |
| 8772                                                | Mosaic Del (2)(p11.2p11.2) | Y              | 500K SNP array | 2:87756166-89121981   | 1.37      | 14             | +/+                                | LCR / LCR                                                 | LBL         |
| 8293                                                | Dup (1)(p36.11p35.3)       | ?              | 500K SNP array | 1:27264555-28339257   | 1.07      | 25             | +/-                                | NA                                                        | LBL         |
| 9148                                                | Dup (2)(p22.1p16.1)        | Y              | 500K SNP array | 2:40289097-57450235   | 17.16     | 74             | -/+                                | NA                                                        | PBL         |
| 8464                                                | Dup (16)(p12.2p11.2)       | Y              | 500K SNP array | 16:21534304-29358350  | 7.82      | 61             | +/+                                | LCR / LCR                                                 | PBL/LBL/FIB |

Physical positions are based on the Feb 2009 Human genome assembly [43, 44]; \* denotes positional information based on sequence of breakpoints; The presence or absence of structural variants associated with breakpoints was determined using the UCSC Genome Browser [38] and Database of Genomic Variants [39] along with data generated by this study. \*\* The rearrangements in proband 9164 are stereotypical of 1q21.1 deletion and 7q11.23 duplication disorders, respectively. Abbreviations are: F, familial; FIB, fibroblast; LBL, lymphoblastoid cell line; PBL, peripheral blood