**Supplementary material**

**Supplementary figure legends**

**Supplementary Fig. 1.** Modified partial screenshot from DECIPHER showing all terminal 1q deletions overlapping our patient’s deletion. In this, we highlight (red shading) the spanning of the present deletion. In addition, we show just one patient (ISCA patient nssv577260) with practically the same breakpoint as that of our patient’s deletion as well as eight other patients with similar deletions (DECIPHER patients 2219 and 4092; ISCA patients nssv577258, nssv577264, nssv584387, nssv1415047, nssv3396736, and nssv13655372) (see also Table 1). Vertical black arrows indicate some morbid genes relevant to the 1q43-q44 deletion syndrome. Furthermore, we delimit by dotted lines, a potential gene involved in cardiac defects. Note that this gene displays a high HI index of 17.76 score (most likely haploinsufficient) to a particular instance (mentioned as “Affected patient”) used to open the DECIPHER’s graphic. Although not showed in this graphic, the LoF/pLI score to *SMYD3* is 0.00, which means a low score for haploinsufficiency sensitivity. Note: The last accession to this online graphic was at October 6, 2018.

**Supplementary Fig. 2.** Modified partial screenshot from UCSC Genome Browser. This graphic shows deletions (and duplications) overlapping our patient’s deletion. We delimit by dotted lines the *SMYD3* gene as well as indicate with arrows those deletions spanning or contiguously flanking said gene and related to heart defects. It seems relevant that, except for one case, all deletions (in this chromosomal segment) out of the said delimited region (dotted lines) or not involving *SMYD3* were not associated to cardiac defects. However, it would denote both a potential incomplete penetrance from alterations in said gene and the need of a complete clinical description from several reported deletions. Note: The last accession to this online graphic was at October 6, 2018.

**Supplementary Fig. 3.** Modified partial screenshot from DECIPHER showing all terminal 10q duplications overlapping our patient’s duplication. In this, we highlight (blue shading) the spanning of the present duplication. Also, we show just one patient (ISCA patient nssv578582) with practically the same breakpoint as that of our patient’s duplication. Furthermore, we indicate by a vertical red arrow, a relevant morbid gene for partial 10q trisomy syndrome. Note that the instance mentioned as “Affected patient”, was used just to open the DECIPHER’s graphic. Note: The last accession to this online graphic was at October 6, 2018.