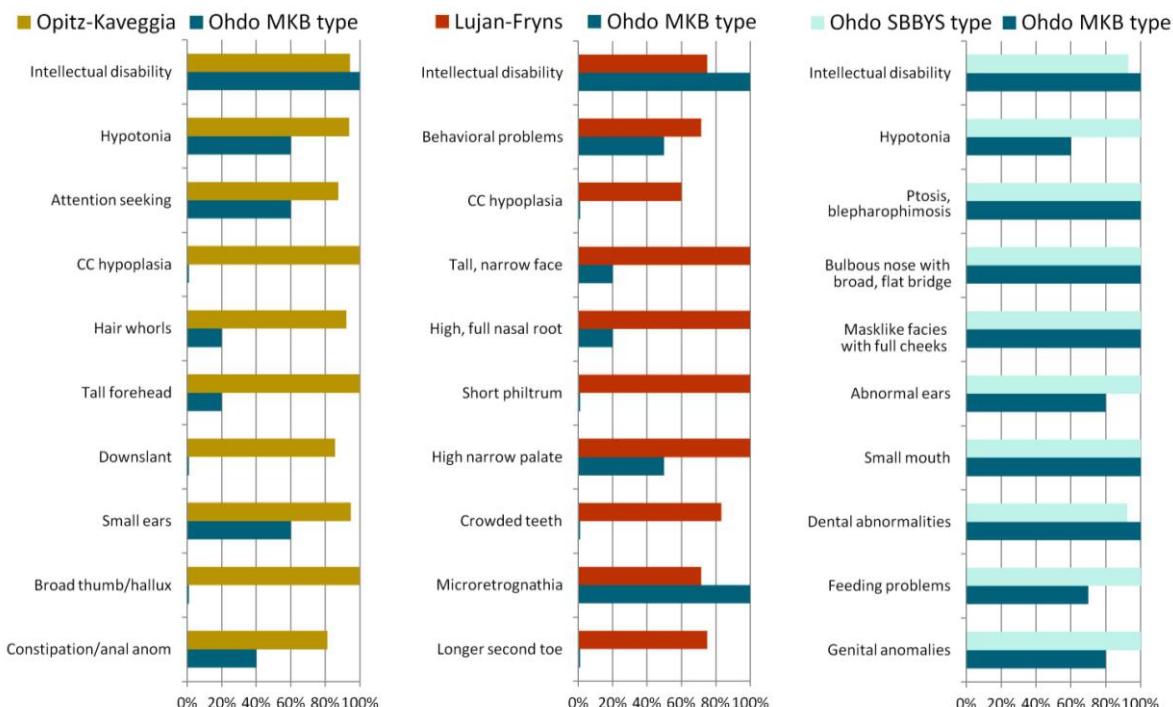


## Supplemental Data

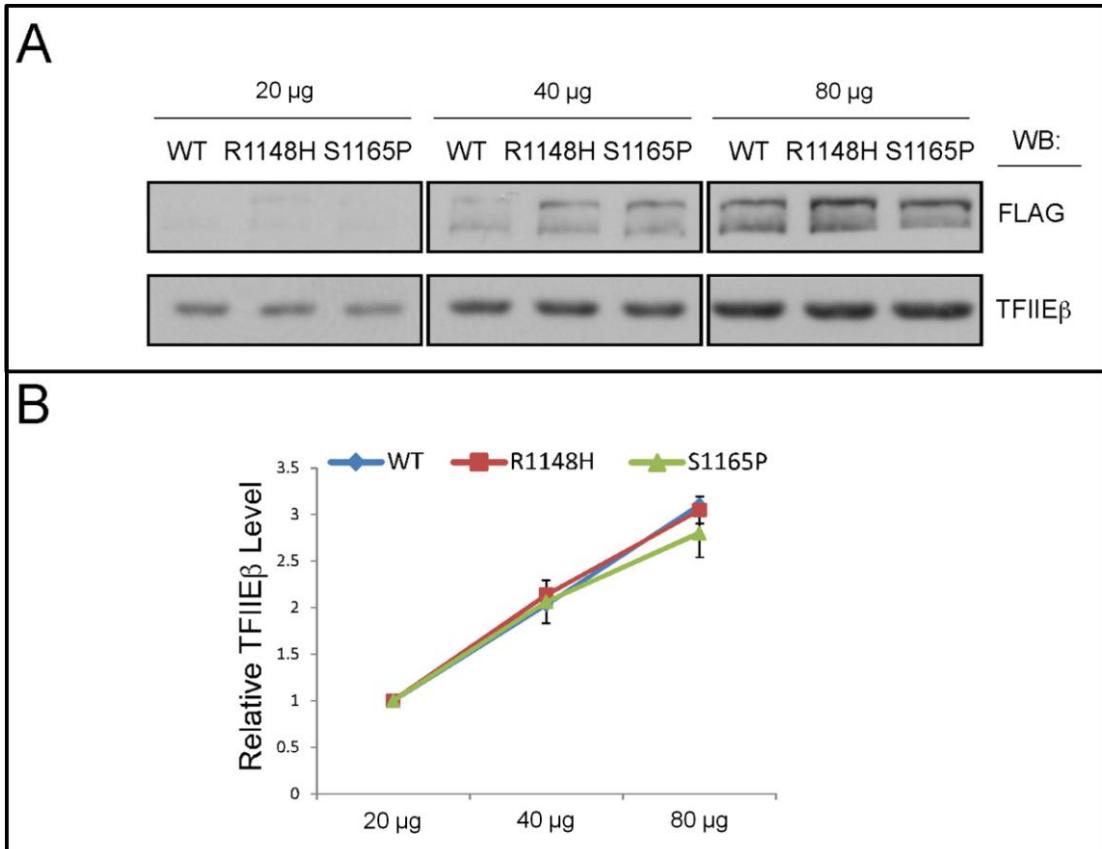
### Mutations in *MED12* Cause X-Linked Ohdo Syndrome

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**Figure S1. Phenotype Prevalence Plots**

Phenotype prevalence plots of persons with Ohdo syndrome MKB type (green) for the ten most prevalent features of the other *MED12*-related disorders Opitz-Kaveggia syndrome<sup>1</sup> (yellow) and Lujan-Fryns syndrome<sup>2</sup> (red) and of Ohdo syndrome SBBYS type<sup>3; 4</sup> (blue). Persons with Ohdo syndrome MKB type show largest overlap to Ohdo syndrome SBBYS type.



**Figure S2. Quantification of Relative TFIIE $\beta$  Protein Expression Levels in Serially Diluted Nuclear Extracts from Four Independent Transient Expression Experiments**

(A) Representative western blot (WB) of nuclear extracts from HEK293 cells transiently expressing FLAG-MED12 WT or its Ohto syndrome mutant derivatives p.(Arg1148His) (R1148H) and p.(Ser1165Pro) (S1165P). MED12 was detected using antibodies specific for the FLAG epitope on FLAG-MED12 derivatives and TFIIE $\beta$  by antibodies directly directed against this protein.

(B) TFIIE $\beta$  levels were quantified using ImageQuant TL software and expressed relative to the level of TFIIE $\beta$  in 20 µg nuclear extract. Values represent the average +/- SEM of the four independent transient expression experiments. The linear range of TFIIE $\beta$  immunoblot signals occurs between 20 and 80 µg of nuclear extracts. To derive relative FLAG-MED12 WT and mutant protein levels shown in Figure 2, WB signals for FLAG-MED12 derivatives were quantified in 40 µg of nuclear extracts.

**Table S1. Detailed Phenotype Description of Persons with Ohdo Syndrome MKB Type and Mutations in *MED12***

C: cryptorchidism, H: hypermetropia, Mi: microcornea/microphthalmus, N: nystagmus, ND: not determined, S: strabismus, SP: small penis SS: shawl scrotum, yo: years old

**Table S2. Exome Sequencing Results and Prioritization of Variants of Families 1 and 2**

|                                  | Family 1 | Family 2 | Overlapping Genes |
|----------------------------------|----------|----------|-------------------|
| Total number of variants         | 39175    | 40105    | 9846              |
| Exonic/canonical splice sites    | 16820    | 16655    | 6108              |
| Non synonymous changes           | 8197     | 8118     | 3411              |
| Not present in dbSNP132          | 719      | 744      | 174               |
| Not present in in-house database | 420      | 438      | 54                |
| X chromosomal variants           | 15       | 15       | 4                 |
| Hemizygous (>70% variation)      | 4        | 5        | 1                 |

**Table S3. Variants Remaining after Prioritization in Families 1 and 2**

| Family | Chr         | Position        | Gene Name    | cDNA Change         | Protein Change        |
|--------|-------------|-----------------|--------------|---------------------|-----------------------|
| 1      | chrX        | 44703940        | DUSP21       | c.562A>G            | p.(Ile188Val)         |
|        | chrX        | 53573686        | HUWE1        | c.10737C>G          | p.(Asn3579Lys)        |
|        | <b>chrX</b> | <b>70348536</b> | <b>MED12</b> | <b>c.3443G&gt;A</b> | <b>p.(Arg1148His)</b> |
|        | chrX        | 153609403       | EMD          | c.611G>A            | p.(Arg204His)         |
| 2      | <b>chrX</b> | <b>70348981</b> | <b>MED12</b> | <b>c.3493T&gt;C</b> | <b>p.(Ser1165Pro)</b> |
|        | chrX        | 76891467        | ATRX         | c.4638A>C           | p.(Lys1546Asn)        |
|        | chrX        | 118250601       | KIAA1210     | c.508C>A            | p.(Leu170Ile)         |
|        | chrX        | 125685583       | DCAF12L1     | c.1009G>A           | p.(Asp337Asn)         |
|        | chrX        | 134156452       | FAM127C      | c.38C>T             | p.(Ala13Val)          |

*MED12* mutations are depicted in bold.

## References

1. Clark, R.D., Graham, J.M., Jr., Friez, M.J., Hoo, J.J., Jones, K.L., McKeown, C., Moeschler, J.B., Raymond, F.L., Rogers, R.C., Schwartz, C.E., et al. (2009). FG syndrome, an X-linked multiple congenital anomaly syndrome: the clinical phenotype and an algorithm for diagnostic testing. *Genet Med* 11, 769-775.
2. Schwartz, C.E., Tarpey, P.S., Lubs, H.A., Verloes, A., May, M.M., Risheg, H., Friez, M.J., Futreal, P.A., Edkins, S., Teague, J., et al. (2007). The original Lujan syndrome family has a novel missense mutation (p.N1007S) in the MED12 gene. *J Med Genet* 44, 472-477.
3. Clayton-Smith, J., O'Sullivan, J., Daly, S., Bhaskar, S., Day, R., Anderson, B., Voss, A.K., Thomas, T., Biesecker, L.G., Smith, P., et al. (2011). Whole-exome-sequencing identifies mutations in histone acetyltransferase gene KAT6B in individuals with the Say-Barber-Biesecker variant of Ohdo syndrome. *Am J Hum Genet* 89, 675-681.
4. Day, R., Beckett, B., Donnai, D., Fryer, A., Heidenblad, M., Howard, P., Kerr, B., Mansour, S., Maye, U., McKee, S., et al. (2008). A clinical and genetic study of the Say/Barber/Biesecker/Young-Simpson type of Ohdo syndrome. *Clin Genet* 74, 434-444.