Supplemental information

Germline variants in tumor suppressor *FBXW7*

lead to impaired ubiquitination

and a neurodevelopmental syndrome

Sarah E.M. Stephenson, Gregory Costain, Laura E.R. Blok, Michael A. Silk, Thanh Binh Nguyen, Xiaomin Dong, Dana E. Alhuzaimi, James J. Dowling, Susan Walker, Kimberly Amburgey, Robin Z. Hayeems, Lance H. Rodan, Marc A. Schwartz, Jonathan Picker, Sally A. Lynch, Aditi Gupta, Kristen J. Rasmussen, Lisa A. Schimmenti, Eric W. Klee, Zhiyv Niu, Katherine E. Agre, Ilana Chilton, Wendy K. Chung, Anya Revah-Politi, P.Y. Billie Au, Christopher Griffith, Melissa Racobaldo, Annick Raas-Rothschild, Bruria Ben Zeev, Ortal Barel, Sebastien Moutton, Fanny Morice-Picard, Virginie Carmignac, Jenny Cornaton, Nathalie Marle, Orrin Devinsky, Chandler Stimach, Stephanie Burns Wechsler, Bryan E. Hainline, Katie Sapp, Marjolaine Willems, Ange-line Bruel, Kerith-Rae Dias, Carey-Anne Evans, Tony Roscioli, Rani Sachdev, Suzanna E.L. Temple, Ying Zhu, Joshua J. Baker, Ingrid E. Scheffer, Fiona J. Gardiner, Amy L. Schneider, Alison M. Muir, Heather C. Mefford, Amy Crunk, Elizabeth M. Heise, Francisca Millan, Kristin G. Monaghan, Richard Person, Lindsay Rhodes, Sarah Richards, Ingrid M. Wentzensen, Benjamin Cogné, Bertrand Isidor, Mathilde Nizon, Marie Vincent, Thomas Besnard, Amelie Piton, Carlo Marcelis, Kohji Kato, Norihisa Koyama, Tomoo Ogi, Elaine Suk-Ying Goh, Christopher Richmond, David J. Amor, Jessica O. Boyce, Angela T. Morgan, Michael S. Hildebrand, Antony Kaspi, Melanie Bahlo, Rún Friðriksdóttir, Hildigunnur Katrínardóttir, Patrick Sulem, Kári Stefánsson, Hans Tómas Björnsson, Simone Mandelstam, Manuela Morleo, Milena Mariani, TUDP Study Group, Marcello Scala, Andrea Accogli, Annalaura Torella, Valeria Capra, Mathew Wallis, Sandra Jansen, Quinten Waisfisz, Hugoline de Haan, Simon Sadedin, Broad Center for Mendelian Genomics, Sze Chern Lim, Susan M. White, David B. Ascher, Annette Schenck, Paul J. Lockhart, John Christodoulou, and Tiong Yang Tan

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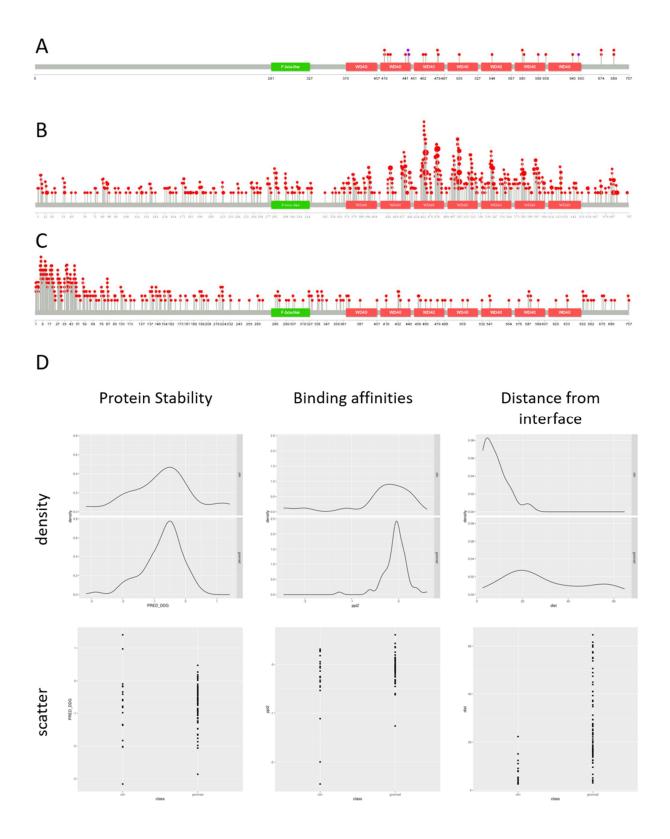


Figure S1: Distribution of neurodevelopment variants within FBXW7 relative to known COSMIC and gnomAD variants. (A) Location of patient-ascertained missense variants (red) and stop-gained and frameshift variants (purple). (B) Distribution of 1481 (440 unique) Catalogue Of Somatic Mutations In Cancer (COSMIC) somatic mutations (red) in FBXW7, where bubble size corresponds to the number of observations.

(C) Distribution of 280 missense variants (277 unique) in FBXW7 gnomAD v2.1 (140k exomes and genomes) variants with bubble size corresponding to the number of observations. (D) Comparison of structural predictors of neurodevelopmental disease variants to gnomAD variants. The gnomAD dataset was filtered to only those within the FBXW7 experimental structure, which includes residues 263 - 706, giving 78 variants only. Of these, the majority are very rare in the population (Allele Count: No. observations – 1:55, 2:14, 3:5, 6:2, 7:1, 12:1). Protein stability, determined using mutation Cutoff Scanning Matrix (mCSM), predicted the majority of gnomAD variants to also have a destabilizing effect, and to be similarly distributed to the patient cohort variants. Binding affinity, determined using mCSM-Protein–protein interactions (PPI) 1&2 ($\Delta\Delta$ G), suggests that gnomAD variants have a much smaller effect on binding affinity compared to the patient variants. Additionally, the gnomAD variants are dispersed throughout the structure and are, on average, further from the predicted interface with CYCLIN E1. See Table S3 for individual variant data.

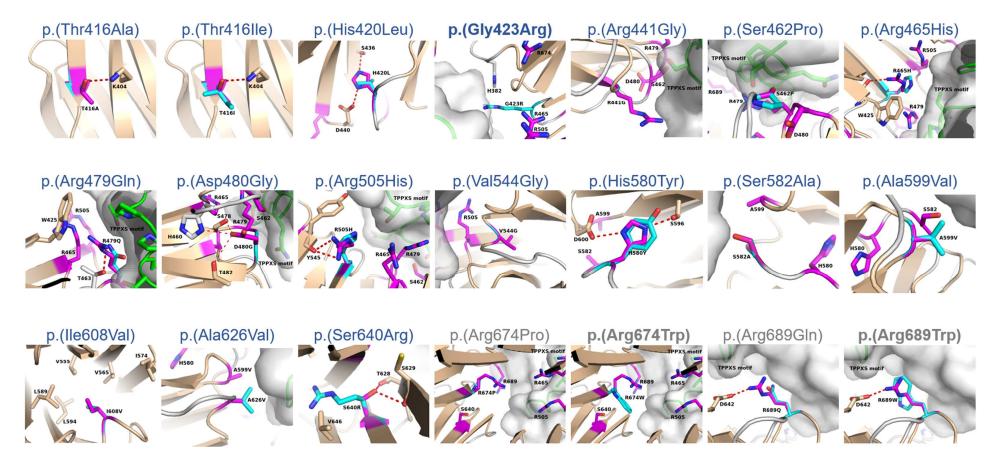


Figure S2: Change in interaction with CYCLIN E1 predicted by each variant

Zoom-in of the interaction of wild-type/variant residues of FBXW7 and its surrounding residues. The variant residues are overlaid on wild-type residues to identify the changes in interaction when variant occurs. FBXW7 is shown in brown ribbon, while CYCLIN E1 is shown in a light gray surface. All wild-type, and variant residues are shown in magenta and cyan sticks, respectively, while surrounding residues of FBXW7 and TPPXS motif of CYCLIN E1 are shown in brown and green sticks. The Oxygen and Nitrogen atoms are in red, and blue, respectively. Hydrogen bond interactions are shown in the red dash lines. Variants that reoccur are indicated by the bold title.

| ENSP00000474725/1-707 FBpp0073101/1-1326 | MERGCPAASSESVTSAGERTQSAVTSSTSTWVKSQASTSRKTEASEESGLGAVDAEVGAG |
|---|---|
| ENSP00000474725/1-707 FBpp0073101/1-1326 | G-GSL REAFVSMSTLREDVEDVCVSSNSQHGFAVVLDDESSTFEISSSNSLPTSAGAASTVGVVA :: :* .*:: : |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | RGNPSSSQVDE-EQM VDDSSSTDTLNGGHPDLGHPASSEHSRQGFFNEDNEDPPVVCLINDDDDDEEPEPEEDDE .:.**: :* * |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | NRVVEEEQQQQLRQQEEEHTARNGEELIEDEDEDAVDIVTGAISCPNTSQLALADGTIMAADGSKIFLETPVVEE |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | ::::*:* : |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | *:.* |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | :: |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | *.: *: *:: GSGTANSDDWPSSSNGRTVSSDSKYTYKDLSTTPTSSRKYTNSRLSKSTAKLNLGSSLGA |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | DEEDEEEEEMDQSDDSSRED SSCSQHRSGSSSTSKSMESSTSCTGAARTDVYTNTNSNDYPSLAPTTSGSSTSGGSCQQD . *. * * * * * * * * * * * * * * * * * |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | :*:. :*::. **::: EHTHTNSVTNSSSIVDLPVHQLSSP QEENVSASVSYSSVGSQTSQESGCSRTTAINPTAACSTGSACLGDSQASTSASTSSGAGA :.: * ** |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | FYTK-TTKMKRKLD-HGSE-VR-SFSLGKKPSNRCQYATTSTTKAARQVNASAQTQERFLTRSNPPAASGAGSVGANPTASVRQRRNGSSD |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | : *. *** : * * : *:* :*CKVSEYT-S VVHLEVVVEEGAGGGDGGVVEPGDFSAEEPWANCDEENNCSDLEEICTCQNGNGSSYGGS |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | TTGLVPCSA-TPTTFGDLRAANGQG NASLSETFDMDAMDPDEPISLSLSSASAGFTEYSLTNPSSLMSHQRKRKFNEGRLLDGGD :*:. * .*: * .*: * .*: * .*.: .*.: * .*.: .*.: * .*.: .*.: * .*.: |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | QTSVQP- YSVTISSSGEVGGPGSGVSDNCRKRIAYDFASTPRSSQHLGPTAVLSVTPSSHLTSSTPG *:** ** * |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | PTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIE SALGRRTPRSVPSRDNPPPELQHWLAQFQRWSHVERLLALDRLIDHCDPSQVRHMMKVIE * * ** ** ** ** ** ** ** ** ** ** ** ** |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | PQFQRDFISLLPKELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEE-GIDE PQFQRDFISLLPRELALFVLSYLEPKDLLRAAQTCRSWRFLCDDNLLWKEKCRKAQILAE ************************************ |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | PLHIKRRKV-IKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQF PRSDRPKRGRDGNMPP-IASPWKAAYMRQHIIEMNWRSRPVRKPKVLKGHDDHVITCLQF * ** : * * ****:*** *: *** :: ********* |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | CGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAE SGNRIVSGSDDNTLKVWSAVNGKCLRTLVGHTGGVWSSQMSGNIIISGSTDRTLKVWDMD *********************************** |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | TGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQY SGACVHTLQGHTSTVRCMHLHGSKVVSGSRDATLRVWDIEQGSCLHVLVGHLAAVRCVQY :* *:*** ************ : ************ * ****** |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | DGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVE DGKLIVSGAYDYMVKIWHPERQECLHTLQGHTNRVYSLQFDGLHVVSGSLDTSIRVWDVE **: :*****:***:***: ****************** |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | TGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTC TGNCKHTLMGHQSLTSGMELRQNILVSGNADSTVKVWDITTGQCLQTLSGPNKHHSAVTC |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | LQFNKNFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSR LQFNSRFVVTSSDDGTVKLWDVKTGDFIRNLVALDSGGSGGVVWRIRANDTKLICAVGSR |
| ENSP00000474725/1-707 FBpp0073101/1-1326 | ****.**:****************************** |
| A | t of human CDVW7 and Dresanbile Age convenees |

Figure S3: Amino acid alignment of human FBXW7 and Drosophila Ago sequences

Uniprot (www.uniprot.org) sequence alignment of Homo sapiens (ENSP00000474725/1-707) and Drosophila melanogaster (FBpp0073101/1-1326) FBXW7 (ago) proteins. Highlighted in yellow the F-Box, in gray the seven D40 repeats of the WD40 domain.

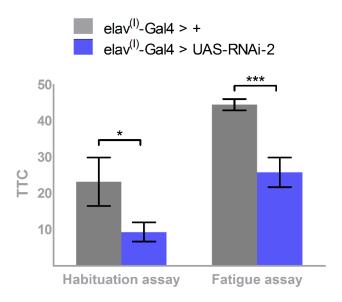


Figure S4: Knockdown of ago in Drosophila neurons induced by the elav^(I)-Gal4 driver causes faster decline of jump response due to fatigue

The knockdown of ago leads to a lower mTTC compared to the controls. Increasing the inter-trial interval in the fatigue assay, preventing habituation from being formed, demonstrates that this lower TTC is not due to improved habituation but due to motor fatigue. Precise genotypes tested in the fatigue assay: elav(1) C155-Gal4, GMR-wIR /Y; +/+; +/+ of genetic background control gray and elav(1) C155-Gal4. GMR-wIR /Y; +/+; UAS-RNAi-2/+ of RNAi-2 knockdown in blue. N_{control} = 42, N_{RNAi-2} = 48, mTTC_{control} = 44.53, mTTC_{RNAi-2} = 25.85, p = 1.35E-5. Statistical significance a linear model regression analysis on was assessed by the log transformed mTTC values, * P < 0.05, ** P < 0.01, *** P < 0.001.

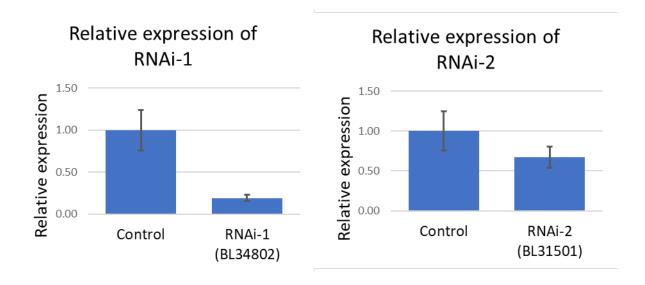


Figure S5: Relative expression of ago in Drosophila knockdown lines

Quantitative RT-PCR was performed on wandering L3 larva from RNAi-1 and RNAi-2 lines crossed to the ubiquitous Act-Gal4/TM3 Sb Tb driver to determine the level of *ago* expression using exon spanning primers to *ago* and β 'COP. Error bars represent standard deviation.

Table S1: Analysis of FBXW7 neurodevelopmental syndrome variants

| arr[GRC | gDNA (Chr4; GRCh37) Exon g.153249446_153249447del 11 g.153249446dup 11 g.153245477_153245478del 13 g.153244218T>A 14 g.153250822A>T intror 10 GRCh37 4q31.3(152720434 153661857)x1 dn N/A | c.1331_1332del c.1332dup c.1713_1714del c.1939A>T | p.(Lys444Serfs*27) p.(Val445Serfs*27) p.(Asn572Leufs*32) p.(Lys647*) | Occurs within WD40 domain NMD predicted NMD predicted Truncation predicted | Same variant Absent Absent | Alternative change at same amino acid residue 3 LoF variants upstream 3 LoF variants upstream | Same variant Absent Absent | Alternative change at same amino acid residue p.(Lys444Glyfs*55), p.(Lys444fs*2), p.(Lys444fs*2), more than 10 NMD predicted variants p.(Val445Cysfs*53), | score rar sco | nk ore sco | rank score | predicted conseq- uence | score rank score | | rank score | rank score | ecore | core | edicted onseq- uence | rank score | predicted conseq- uence | score | nk ore predi cons uer | seq- score score | predicted conseq- uence | score rank |
|--|--|---|--|---|------------------------------|---|--|--|----------------------|---------------|---------------|-------------------------------|------------------------|------|---------------|---------------|---------|------|----------------------------|---------------|-------------------------------|---------|--------------------------------|------------------|-------------------------------|------------|
| 2 de novo 3 4 5 6 7 de novo 8 de novo 9 de novo arr[GRC dn dn,4 11 de novo 12 familial 13 de novo 14 de novo 15 | g.153249446dup 11 g.153245477_153245478del 13 g.153244218T>A 14 g.153250822A>T intror 10 | c.1332dup c.1713_1714del | p.(Val445Serfs*27) p.(Asn572Leufs*32) | NMD predicted | Absent | | | p.(Lys444Argfs*32), p.(Lys444fs*2), more than 10 NMD predicted variants p.(Val445Cysfs*53), | | - | - | - | | = | | = | - | - | | - | - | - | | | - | |
| 3 | g.153245477_153245478del 13 g.153244218T>A 14 g.153250822A>T intror 10 | c.1713_1714del | p.(Asn572Leufs*32) | | | 3 LoF variants upstream | Absent | | | | | | | | | | | | | | | | | | | |
| 5 familial f | g.153244218T>A 14 g.153250822A>T intror 10 | | | Truncation predicted | | | | p.(Val445Aspfs*27), more than 10 NMD predicted variants | | - | - | - | | - | | - | 1 - | - | | - | - | - | | | - | <u> </u> |
| 8 de novo arr[GR 10 de novo arr[GRC dn dn,4 11 de novo 12 familial 13 de novo 14 de novo 15 | g.153250822A>T intror 10 | c.1939A>T | p.(Lys647*) | 1 | Absent | 3 LoF variants upstream | Absent | More than 10 NMD predicted variants | | - | - | - | - | - | - | - | - | - | - | - | - | - | | | - | |
| 9 de novo arr[GRC dn dn,4 | | | 1 | Truncation predicted | Absent | 3 LoF variants upstream | Absent | p.(Lys647Asnfs*5) in stomach carcinoma, more than 10 NMD predicted variants | | - | - | - | | - | | - | - | - | | - | - | - | - | | - | |
| 10 de novo arr[GRC dn dn,4 11 de novo 12 familial 13 de novo 14 de novo 15 | (CDCh97) 4n91 9/159790494 159661957\v4 d- | n c.1236+2T>A | p.? | N/A | Absent | Alternative change at same nucleotide: Absent | Present (stomach carcinoma) | Alternative change at same nucleotide: c.1236+2T>C (large intestine adenocarcinoma) | | | | | | | | | | | | | | | | | | |
| 10 de novo dn dn,4 11 de novo 12 familial 13 de novo 14 de novo 15 | [GRCh37] 4q31.3(152720434_153661857)x1 dn N/A | N/A | Entire gene deleted | N/A | N/A | N/A | N/A | N/A | | | - | - | | - | | - | | - | | - | - | - | | | - | <u> </u> |
| 12 familial 13 de novo 14 de novo | RCH37] 4q31.3q32.1(152854578_156285170)x1 dn,4q32.1q34.1(161464002_175617314)x3 in,4q34.1q34.3(175858796_179802170)x3 dn | N/A | Entire gene deleted | N/A | N/A | N/A | N/A | N/A | | - | - | ÷ | | - | | = | - | - | | = | - | = | | | = | |
| 13 de novo 14 de novo 15 | g.153249531G>A 11 | c.1247C>T | p.(Thr416lle) | Yes | Absent | Absent | Absent | Absent | 4.22 0.8 | 36 0.1 | 13 0.61 | T | 5.90 0.95 | 2.78 | 0.99 0.5 | 6 0.97 | 1.37 0. | ე.34 | L -5.66 | 0.87 | D | 1.00 0. | 92 [| 0.05 0.56 | D | 0.78 0.80 |
| 14 de novo | g.153249532T>C 11 | c.1246A>G | p.(Thr416Ala) | Yes | Absent | Absent | Absent | Absent | 4.08 0.8 | 31 0.0 | 0.62 | Т | 5.90 0.95 | 2.40 | 0.97 0.5 | 6 0.97 | 1.71 0. |).44 | L -4.80 | 0.81 | D | 0.98 0. | B1 E | 0.02 0.59 | D | 0.80 0.81 |
| de novo | g.153249519T>A 11 | c.1259A>T | p.(His420Leu) | Yes | Absent | Absent | Absent | Multiple | 4.13 0.8 | 33 -1.5 | 50 0.81 | D | 5.90 0.95 | 3.08 | 0.99 0.8 | 7 0.59 | 4.72 1. | 1.00 | H -10.92 | 0.99 | D | 1.00 0. | 97 E | 0.00 0.91 | D | 0.94 0.95 |
| 16 de novo | g.153249511C>T 11 | c.1267G>A | p.(Gly423Arg) | Yes | Absent | Absent | Present (multiple tissue types) | Multiple | 4.35 0.8 | 39 0.1 | 16 0.61 | Т | 5.90 0.95 | 3.01 | 0.99 0.6 | 7 0.92 | 1.21 0. |).30 | L -7.94 | 0.96 | D | 1.00 0. | 97 🛭 | 0.00 0.91 | D | 0.94 0.96 |
| | g.153249457G>C 11 | c.1321C>G | p.(Arg441Gly) | Yes | Absent | Absent | Present (lung carcinoma, rhabdomyosarcoma) | Multiple | 3.72 0.7 | 70 2.0 | 0.21 | Т | 4.08 0.47 | 3.14 | 0.99 0.5 | 5 0.97 | 0.42 0. | ე.13 | N -6.83 | 0.93 | D | 0.99 0. | B0 E | 0.03 0.91 | D | 0.84 0.86 |
| 17 de novo | g.153249394A>G 11 | c.1384T>C | p.(Ser462Pro) | Yes | Absent | Absent | Absent | p.(Ser462Tyr), p.(Ser462Phe) | 4.33 0.8 | 39 0.8 | 36 0.74 | Т | 6.05 0.98 | 2.78 | 0.99 0.5 | 4 0.97 | 2.65 0. | ე.77 | M -4.96 | 0.82 | D | 0.93 0. | 92 E | 0.00 0.78 | D | 0.87 0.89 |
| 18 de novo | g.153249384C>T 11 | c.1394G>A | p.(Arg465His) | Yes | Absent | p.(Arg465Cys) (allele balance 45% or lower) | Present (more than 5 tissue types) | Multiple | 4.17 0.8 | 34 0.9 | 97 0.43 | Т | 6.05 0.98 | 3.08 | 0.99 0.6 | 1 0.95 | 1.26 0. |).32 | L -4.96 | 0.82 | D | 1.00 0. | 97 E | 0.02 0.91 | D | 0.78 0.79 |
| de novo (mosaic 14%) | g.153247366C>T 12 | c.1436G>A | p.(Arg479Gln) | Yes | Absent | p.(Arg479Gly) (allele balance 25-30%) | Present (more than 5 tissue types) | Multiple | 4.17 0.8 | 34 1.0 | 0.41 | Т | 5.72 0.89 | 2.93 | 0.99 0.8 | 0 0.75 | 0.84 0. | 0.21 | L -3.97 | 0.74 | D | 1.00 0. | 97 🛭 | 0.02 0.51 | D | 0.64 0.65 |
| 20 de novo | g.153247363T>C 12 | | p.(Asp480Gly) | Yes | Absent | Absent | Present (colon adenocarcinoma) | Multiple | 4.46 0.9 | | 49 0.89 | D | | 3.19 | | | | J.96 | H -6.95 | 0.93 | D | 1.00 0. | | | D | 0.99 0.99 |
| 21 de novo | g.153247288C>T 12 | c.1514G>A | p.(Arg505His) | Yes | Absent | Absent | Present (more than 5 tissue types) | Multiple | 4.17 0.8 | 35 0.0 | 0.62 | T | 4.87 0.63 | 3.08 | 0.99 0.5 | 5 0.97 | 1.50 0. |).38 | L -4.96 | 0.82 | D | 1.00 0. | 97 E | 0.01 0.78 | D | 0.75 0.75 |
| 22 de novo | g.153247171A>C 12 | c.1631T>G | p.(Val544Gly) | Yes | Absent | Absent | Present (large intestine adenocarcinoma) | p.(Val544Asp) (mouth squamous cell carcinoma) | 4.29 0.8 | -0.7 | 79 0.74 | Т | 5.72 0.89 | 3.18 | 0.99 0.5 | 5 0.97 | 4.32 0 |).98 | H -6.95 | 0.93 | D | 1.00 0. | 92 [| 0.00 0.91 | D | 0.64 0.66 |
| 23 de novo | g.153245453G>A 13 | c.1738C>T | p.(His580Tyr) | Yes | Absent | Absent | Present (large intestine adenocarcinoma) | Multiple | 4.09 0.8 | 32 -1.4 | 49 0.81 | Т | 5.70 0.89 | 2.95 | 0.99 0.7 | 5 0.84 | 4.04 0 |).97 | H -5.96 | 0.89 | D | 1.00 0. | 97 E | 0.01 0.56 | D | 0.89 0.89 |
| 24 de novo | g.153245447A>C 13 | c.1744T>G | p.(Ser582Ala) | Yes | Absent | Absent | Absent | Multiple | 4.02 0.7 | 79 1.0 | 00 0.41 | T | 5.70 0.89 | 0.97 | 0.97 0.7 | 6 0.83 | 1.46 0. | J.37 | L -2.70 | 0.61 | D | 0.98 0. | 75 E | 0.10 0.59 | Т | 0.66 0.67 |
| de novo (mosaic 23%) | g.153245395G>A 13 | c.1796C>T | p.(Ala599Val) | Yes | Absent | p.(Ala599Gly) (allele balance 35-40%) | Absent | Absent | 4.29 0.8 | 38 0.9 | 0.44 | Т | 5.45 0.80 | 2.69 | 0.99 0.8 | 6 0.62 | 0.86 0. | 0.21 | L -3.96 | 0.74 | D | 1.00 0. | 84 0 | 0.02 0.78 | D | 0.63 0.64 |
| 26 de novo | g.153244280G>A 14 | c.1877C>T | p.(Ala626Val) | Yes | Absent | Absent | Present (large intestine adenocarcinoma) | p.(Ala626Thr), p.(Ala626Pro), p.(Ala626Asp) | 4.13 0.8 | | 96 0.43 | Т | 5.67 0.88 | | 0.99 0.6 | 3 0.94 | 1.71 0. |).44 | L -3.91 | 0.74 | D | 1.00 0. | 91 E | 0.00 0.78 | D | 0.74 0.76 |
| 27 de novo | g.153244237G>T 14 | | p.(Ser640Arg) | Yes | Absent | Absent | Absent | Absent | 3.40 0.6 | | | T | 3.03 0.34 | | 0.99 0.8 | | | | M -4.91 | | D | 1.00 0. | | | T | 0.87 0.92 |
| 28 de novo | g.153245369T>C 13 | | p.(Ile608Val) | No | Absent | Absent | Absent | Absent | 2.43 0.4 | _ | | Т | 5.45 0.80 | | | | | | N -0.86 | + | + | 0.05 0. | | | Т | 0.36 0.41 |
| 29 de novo | g.153244136C>G 14 | | p.(Arg674Pro) | No No | Absent Absent | Absent | Absent Present (glioma, cervix squamous cell | p.(Arg674Trp), p.(Arg674Gln) p.(Arg674Gln) (colon adenocarcinoma, | 4.13 0.8 3.77 0.7 | | | Т | 4.82 0.62 1.62 0.23 | | 0.99 0.5 | | 2.67 0. | | M -6.83 | 0.93 | D D | | 92 E | | D D | 0.81 0.85 |
| de novo | g 159244197G> A | c.2020C>T | p.(Arg674Trp) | No No | | Absent | carcinoma, atypical meningioma, prostate adenocarcinoma) | stomach adenocarcinoma) | | | | | | | | | | | | | | | | | | 0.82 0.87 |
| 32 de novo | g.153244137G>A 14 | | p.(Arg689Gln) | | | | | | | | | | 400 000 | 260 | | | | | | | | | | | | |
| 33 de novo | g.153244137G>A 14 g.153244091C>T 14 | c.2066G>A | 1 | 140 | Absent | Absent | Present (more than 5 tissue types) | p.(Arg689Glu), p.(Arg689Trp) | 4.14 0.8 | 33 2.2 | 25 0.18 | Т | 4.82 0.62 | 2.62 | 0.98 0.4 | 0 0.99 | 2.70 (| 0.79 | M -3.92 | 0.73 | D | 1.00 0. | 89 E | 0.03 0.68 | D | 0.02 0.87 |

Tolerated (T); Deleterious (D); Low (L); Medium (M); High (H); Combined Annotation Dependent Depletion (CADD); Functional Analysis through Hidden Markov Models (FATHMM); Genomic Evolutionary Rate Profiling (GERP) ++ rejected substitutions" (RS) score; missense badness, PolyPhen-2; Sorting Intolerant From Tolerant (SIFT); Variant Effect Scoring Tool (VEST).

Table S2: Clinical details of Individuals with FBXW7 neurodevelopmental syndrome

| I able | 52: (| INICaاار | ai deta | IIIS OT | Indivi | duais | With | FBXW | // neu | Jrogev 10 IELETION | elopr | nenta | ıı sync | irome | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 |
|--|--|---|--|---|---|--|---|---|---|---|--|--|--|--|--|---|--|---|---|--|---|--|--|--|--|---|---|---|--|---|--|---|--|---|--|
| VARIANT TYPE Variant Details Mode of discovery | Trio WES (Broad) | Exome sequencing with parental variant segregation | Family-based WGS | Predicted Lo | ss of Function | Farth-hand WGS | See WES | Trin WE'S | GENE D | SIP array (Burina Infeium CoreCore-24 vf. 1, hgl9) | Gene Dx Trio WES | Solo WES | Tris WES (GeneDa) | Trio WES | Trio WES | Trio WES | Trio WGS | MISSENS Trio WES | Pair WES (Research) Deep | D DOMAIN | Trio WES (Mauri) | Trio WES | Trio WES (GeneDa) | Trio WES | Trio Exorne | Trio WES Tri | io WCS (research) | Trio WES | Tio WES (GeneDa) | MISSE Trio WES | NSE, NOT AFFECTI | NG WD40 DOMAIN | Solo WES | tio WES 1 | Dia WES |
| cDNA (NM_001349798.2) | c.1331_1332del | variant segregation c. 1333dup | c.1713_1714del | c.1713_1714del | c.1713_1714del | c.1713_1714del | c.1939A-T | c.1236+2T-A | NA NA | [VCGS] NA | c.1247C>T | c.1246AvG | c. 1259A-T | c.1267GsA | c.1267Gs-A | c.1321C-G | c.13847>G | c 1394GsA | depth for patient blood c.1436Qs-A | c.1439AvG | c.1514GsA | c.16317xG | c.1738C>T | c.1744T>G | c. 1796G>T | | c.1920C>A | c.1822A-G | c.2021G+C | c.2020C>T | c.2020C>T | c.2066Gs-A | | | c.2085C>T |
| gDNA (Chr4; GRCh57) | g 153249446_1532N9447del | g.153249446dup | g.1532N5477_1532N5478del | g.153245477_153245478del | g.153245477_153245478del | g 153045477_1530N5478del | g (532442)(8T)-A | g.153250822A-T | av (GRCh07) 4q01.3(152720434_153661857): | an(CRCHG7) 4q31.3q32.1(158554578_15658 5170)d1 xidn.4q32.1g34.1(161464032_175 617314)d dn.4q34.1q34.3(175858796_179 802170)xid dn | g.153249531GsA | g.153249532T>C | g.153249519T-A | g.153249511C>T | g 153249511C-T | g.153249457Gz-C | g 153249394AG | g.1532N928HC>T | g.153247369C>T | g 1532N7363T>C | g.153247288C>T | g.1533947171Av-C | g.153245453Q-A | g 1530N5447AvC | g.153045395G-A | g.153244280Gs-A | g 153244237GrT | g 1532453897-C | g.153244136C>G | g.153244137GsA | g 153244137Cs-A | g 153244291C>T | g.153244092GrA | g.153244092GsA g.15 | 4-1532044092Gz-A |
| | | | p.(Asr072Leu/s*32) | p.(Asr072Leufs*32) | p.(Asn572LeuIs*32) | p.(Aen572Leufs*32) | p.(Lys847*) | p.5 | 1 dn DEL | 617314)x3 dn,4q34.1q34.3(175858796_179 802170)x3 dn DEL NIA | p.(13x4165e) | p.(Tre415Ala) Absent | p.(He420Let.) | | p.(Sly423Arg) | | | p.(Arg465Hs) | p.(Arg479Cin) | p.(Asp480Cky) | | p.(Va544Gy) | p.(Ha5800yr) | p.(Ser582Ab) | p.(Ala599Vwl) | | p. (Ser646Arg) | | p. (Arg674Pro) | | | | | p.(Arg6891tp) p.(| p.(Arg6891p) |
| amino acid residue in gnomAC | p.(Lys444Serts' 27) Absent 3 LoF variants upstream | | | | | | | Absert Alternative change at same nucleotide: Absent | NA NA | NA NA | Absert Absert | Absent | Absent Absent | Absent Absent | Absert Absert | Absert Absert | Absert Absert | p.(Arg465Cyx) (allele balance 45% or lower) | p.(Arg479Gy) (allele balance 25-30%) | Absent Absent | Absert | Absent | Absent | Absort Absort | Absent p.(Aladis9Gly) (allele balance 35-40%) | Absert Absert | Absert Absert | Absert Absert | Absert Absert | Absent Absent Present (gloma, cervix | Absent Absent Present (gloms, centx | Absert Absert | Absent Absent | Absent Absent | Absert Absert |
| Same variant in COSMIC | Absent p.(Lys444Glyts*55), | Absent p./VeH45Cvefs*S31. | Absert | Absent | Absent | Absent | Absent o.(Lus647Asnfs*5) in storms | Present (stomach carcinoms) | NA. | NA NA | Absent | Absent | Absent | Present (multiple tissue types) | Present (multiple tissue types) | Present (lung carcinoms, rhabdomyosarcoma) | Absert | Present (more than 5 tissue types) | Present (more than 5 tissue types) | Present (colon adenocarcinoma) | Present (more than 5 tissue types) | Present (large intestine adenocarcinoma) | Present (large intestine adenocarcinoms) | Absent | Absent | Present (large intestine adenocarcinoma) | Absert | Absert | Absent | aquamous cell carcinoma, atypical meningloma, prostate adenocarcinoma) | adjumous cell carcinoma, atypical meningioma, prostate adenocarcinoma) | Present (more than 5 tissue lypes) | Present (more than 5 tissue Prese types) | | int (more than 5 tissue types) |
| Atternative change at same amino acid residue in COSMI Exon INM 001346798.20 | p.(Lys444Argts*32), p.(Lys444ts*2), more than 10 NMD predicted variants | p.(VaM45Cysfs*53), p.(VaM45Aspfs*27), more than 10 NMD predicted variants | More than 10 NMD predicted variants | More than 10 MMD predicted variants | More than 10 NMD predicted variants | More than 10 NMD predicted variants | p.(Lys647Asnts*5) in stoma d carcinoma, more than 10 MMD predicts variants | Afternative change at same nucleotide: c.1226-275-0 (targe intestine adenocarcinoma) | NA NA | NA NA | Absert | Absent | Multiple | Multiple | Multiple | Multiple | p.(Ser4627yr), p.(Ser4629he) | Multiple | Multiple 12 | Multiple 12 | Multiple P | p.(VsIS44Asp) (mouth squamous cell carcinoma) | Multiple | Multiple | Absent 13 | p. (Alat297hr), p. (Alat297hr), p. (Alat294kp) 14 | s (one in NCFs GDC) | Absort | p.(Arg674Trp), p.(Arg674Gin) | p.(ArgET4GIn) (colon adenocarcinoma, stomach adenocarcinoma) | p.(Ang674Gin) (colon adenocarcinoma, stomach adenocarcinoma) | р. (Arg689Glu), р. (Arg689Tp) | p.(Ang689Glu), p.(Ang689Glm) | p.(Arg689Gis), p.(i p.(Arg689Gis) p.(i | p.(Arg689Gb), p.(Arg689Gb) |
| Exen (NM_001540798.2) Occurs within W040 domain Inheritance | MAD predicted De novo | MMD predicted De nove | Truncation predicted Paternal | Truncation predicted Paternal | Truncation predicted Paternal | Truncation predicted Unknown | Truncation predicted De novo | NA De novo | NA De novo | NA De novo | Yes De rovo | Yes Inherited from mother with ID Yes | Yes De novo | Yes De novo | Yes De novo | Yes De novo | Yes De novo | Yes De novo | Yes De noso, post-aygotic (mossic: 14%) | Yes De rovo | Yes De rovo | Yes De novo | Yes De rovo | Yes De noio | Yes De novo (mossic: 23.3% of 103 reads) | Yes De rovo | Yes De novo | No De noio | No De roio | No De rovo | No De novo | No De novo | No De novo | No De novo | No De rovo |
| Other candidate variants | PDP2: de novo LoF variant | No | No | No. | No | No | No | No | Other inherited CNV (see below) | No i | arr[GRCh37] 23q11.23q11.23(22997609_249 61234)x3 pat | Yes NCOR1:NM_001190440:exer27 c.3734GxA:p.Arg1245Gh [mai] NCOR1:NM_001190440:exer3:c | No | No | No | No | No | No | Yes CACNA1A:NM_(02025.2:c.835 C>T p.(Arg279Cys) | No | No | No | No | No | No | No | No | No | No | No | No | KMT2D: de novo NM_003482.4:c.16012T>C p.(Cys5338Arg) | No | No | No |
| Demographic Features See | Male | Male | Ferals | Fernie | Ferrale | Malia | Male | Fernie | Male | Molis | Male | .244CsA:p.(Pro82Thr) [no known disease association] | Mak | Male | Male | Male | Male | Fernis | Molis | Molis | Vole | Ferrole | Male | Fernále | Vale | Male | Гетзів | Mile | Male | Vole | Male | Mile | Male | Mole | Male |
| Age at but assessment Other Medical History | 11 years | 3 years 2 months | 14 years 9 months | 11 years 9 months | 6 years 3 months | 44 years 6 months | Sy | 5 years | 7 years 2 months | 2 years 2 months | 18 yo | Эy | 10 years, 2 months | 14 yo | 15 Macedonian | 5 years | Information gathered from clinical record and obtained from parents | 9.5 years | (currently 6 years) | 16 years DDD4K02106 in DDD paper | 3 years | 23 months | 3 years | 6 years | 22 months | 3 yrs Csucaelan | 7 years | 11 years Caucasian | 2 years (currently 4 years) | 15 years | 14 years | 2 years | 10 years | 12 years | 7 y |
| accuminty | | | | | | | | | Feet malcostilon during | | | | | | | | Planned Cassanson after 42 | | | | | | | | 1565g, 33 weeks premature, | | | | Born at 42sks to a GSP6 41yo mother, BW = 7bs, Length = 48.5cm, HC = 34.5cm, NGU to 2 days due to mild resolutory | | | | | | |
| Prenatal history | Increased nuchal fold at 12/40; normal chromosomes on armiocentesis | suspicion of preeclampela | NAD | NAD | NAD | NAD | NAD | Born at 36+5 weeks, birth weight 3390 gr. Apgar scores 7 and 8. Neonatel jaundice treated with phototherapy. | pregnancy. Mother had positive syphilis serology. Blorn at 40 weeks: (weight 4,000g; height 51 cm; OFC 35.5 cm). Neonatal | 40+2/40 Emergency LUSCS for non-reassuring CRG. NI antensial concerns. Growth scans normal. | Unversarkable | no | ren-contributory, born at 38 weeks 1 day | uneventul | Unremarkable | | weeks of gestation, because of size and drop in fetal movement, weight at birth: 5230 g (<59 percentile, +2.4 5D), length: 57 om (<59 percentile, +2.6 5D), head circumference: 40 cm (59 percentile, +2.5 5D) | normal | Born at 40 weeks. Uneventful pregnancy. Weight at birth : 3520g. | Normal (well bar ear infection in mum and she took ear drops) | Delivered at 35 weeks, induced for maternal cholestasis. BW Bbs. 15cz., hospitalized for 6 days. | Normal | Unremarkable. Term delivery, Cesarean section for breech presentation | Normal | SGA, tracked small on US but no dx of IUGR, Vaginat, Mother GIPD, 30yans dd. NOU for 19 days for joundoe, hypoglycemia and feeding difficulties. Abnormal newborn hearing acreen. | Born at 41+4 wks. Uncomplicated pregnancy and delivery. BW 3872g. Circum | rentous cord insertion; rth and Appars 9/9; Birth ght, length, and head reference within normal | Normal | 2 days due to mild respiratory distress and poor feeding. Parents report a history of increased nuchal fold and extra skin fold in the back of the neck | Unremarkable pregnancy. Born at term. BW 3450g. Apgars 8.9. Morn recalls concerns re being by "blue" at delivery but no | Normal | Normal | Normal | Normal Hypotoni distress a | erechogenic kidneys; stonia and respiratory as at birth (Apgar 4-7- 9) |
| | | | | | | | | | serdogy at age 4 years | | | | | | | | head circumference: 40 cm (59 percentile, +2.5 SD) | | | | | | | | Abnormal newborn hearing screen. | | range | | increased nuchal fold and extra skin fold in the back of the neck at birth, which resolved. Mother look Priloses for GEPD during pregnancy. Newborn screen was normal. Net's was completed 3 times. | RELUCCION REGION. | | | | | |
| Neurological problems | Nyodonia, facile issues | Hypotonia | Hypotonia | NAD | NAD | NAD | NAD | No hypotonia | No neurological signs at testino. | Early hypotonia. No seizures. No | After creat of seizures at age 7 years, his academic and intellectual functions deteriorated. Now in special ed. | Unsteady call. Broad-based cal | hypotonia diagnosed shortly after birth | history of seizures: hypotonia | Nucloria: macrocephaly | Generalized hypotonia | hypotonia | neonatal hypotonia and failure to | Generalized severe hypotonia: | apgars 8 (81 min, 10 at 5 min, home day 4 fins, ducky episode day 12, floppy, generalised hypotonia; on CBZ for his | Hypotonia | Severe progressive spaticity: | Hypotonia. Broad-based galt but not trankly abolc. No selcures. Normal EMG/NCS. | no hypotonia, no selizures | motor developmental delay, mild hypotonia. Focal seizures (left arterior temporal area) confirmed by EEG and is now on artispileptic medication | Hypotenia. Tonic upgaze eye movements in infancy. Myclonic and mycolonic-lonic saturues from 4-5 months of ge. EEG findings suggesties of developmental epilepic encephalopathy with multifocal | nersized hypotonis; | Early Onset Absence Epilepsy EOAE: rose incided more boil- | Generalized hypotonia | Normal tone on exam (from 8 years). Achilles tendon contracture (right heel conds). Abnormality of coordination. | epilepsy started at 4yGm; hypotonia; ataxia; upper hand | Normal | hypotonia, language trouble | hypotoria Gotal | obal DD, hypotonia, drooling |
| | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, | | | | | . ,, | | regression. | intellectual functions deteriorated. Now in special ed. | | after birth | | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, | | ,, | thrise | | hypotonia; on CBZ for his seizures which has stabilised; | , | | Normal EMG/NCS. | | confirmed by EEG and is now on antiepileptic medication | ge. EDG findings suggestive of developmental epileptic encephalopathy with multifocal and generalised discharges. | ent-refractory seizures; | solzunes | | Abnormality of coordination. Possible staxis. Has history of migraines with photophobia. | dyskinetic involuntary movements and stereotypies | | | | drooling |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | FI x3 - Large cerebelum wided posterior fossa at 9 , the vermis continues to om 42mm to 46mm at 3.5 | | | MRI brain shows big cerebellum 46/mm with crowded posterior forces and tonsils low | | | Brain MFE (2 ye) : non | | |
| Brain imaging | CT brain only - no structural abnormalities reported | N/A | Large cerebellar vermis with low- lying torsals 3.5 mm below foramen magnum (Arnold-Chiari malformation) | NA NA | NA. | NA | NA | NA | NA. | NA | NA | thin corpus callosum | NA | N/A | agenesis of corpus calosum | Brain MFE (2 years of age) shows dyemorphic corpus calosum, scattered loci of T2 prolongation in periventricular white matter | NA. | NA | Brain MPE: cerebellar hypoplasis but large folia and big claterns | Crowded posterior fosses with enlarged cerebellum and thick. It vernis with low-lying tonsils just a above foramen magnum; thick is brainsiem, normal corpus callosum | Brain: abnormal suical pattern suggestive of polymicrogyris, thin corpus callosum, delayed myelination | Brain Atrophy per MRI Scattered small subcortical calcifications (Brain CT) | Normal brain MRI topine with MRS. | Delayed myelination; generally thin corous calineum | Brain MFE 3/2018: prominent extraoxist fluid but otherwise normal for age. | years, 8 to 41mm MRI brain abnormal suical be in pattern suggestive of polymicrogyria. corpus of | hereafter it mildly shrinks m at 9 years – this could elated to antiepilepsy stions. The dysmorphic callosum is not thickened | NA | NA | posterior fossa and tonsils low lying at foramen magnum; thick brainstem, scatened bilateral 872 hyperintensities in subcortical white matter, frontal, | normal brain MFII | NA | Etain MFE (2 ye): non specific white maiter hypersignals, widening of Virchou-Publin spaces, worsts upper ferits 4 ferm, low right torsit, mega claimers reagra; thick brainstern; normal myelination and corpus calcourn | NA Brain | Irain MPI: normal |
| | | | malformation) | | | | | | | | | | | | | white matter | | | magna | brainsten, normal corpus callosum | myelination | calcineasons (aran Ci) | | | norms to age. | poymerogyna. corpus of at 9 m and 9 y there went ico | calcaum is not included on the but is thick at 3.5 years. On the last scan re is generalised mild somegaly and increased of the extra-scial CSF spaces. | | | parietal and respond similar to Individual 25. Volume and myelination ok; thin corpus callosum | | | cistems magna; thick brainstern; normal myelination and corpus callosum | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | size | of the extra-axial CSF spaces | | | | | | | | |
| | | neonatal sucking difficulties delayed motor milestones : crawled on four legs at 18 | | | | | | Walking 18 months, first words 18 months. | Head control before 4 months, sit alone between 9 and 11 months, walk at age 16 months, | Markenia sistral desainomental | | | | | | | | | | | | | | | Developmental concerns at 2 months when he was not lifting his head or tracking. Rolled over at 9 months, sat on own at 10 months, pulled to stand at 14 | | | | Mid-moderate global developmental delay (Sitting at timo, talking at 13mo and walking at 24mo; at 10 evaluation showed assume complian with delayed | g Moderate ID. GDD - walked at 20 months Sowerh dates with | | | moderate global | | |
| Developmental / cognitive / psychiatric problems | Global developmental delay ; now borderline IQ, attends mainstream school with some assistance; some anxiety | months, walked independently at 21 months hypotonia and hyperbody. first words at 2,5 years. But at 3y 2 months : can | Global developmental delay, learning difficulty, ID, speechlanguage problems; delayed fire motor skills; sensory processing; 745D, no dx paed says not enough for diagnosis, but all have mid symptoms. | Debyed language; bite walker; delayed socially; attention, moot; learning disorder; psychiatrist involved; 7ASD, no | Delayed language: poor gross motor skills; attention/mood. PASD, WIL for ASD ax through Austin health | Borderline non-verbal IQ | walk at 14m/speech delay/learning difficulties | Speech development disorder. At the age of 4 years sentences of 3-4 words. Problems with pronounciation. | mild delayed speech, learning difficulties and global needucation since age 4 years (speech therapy, psychomotor | delay. Early gross motor delays. 1 with minimal weight-bearing and 1 lower limb use prior to age 2 years. First independent steps | Very mild delays in gross motor skills, mild cognitive delays (eg, color marring) until criset of seizures at age 7 yo, then more | Global moderate developmental delay, walking at 20m, first | nonmal | Developmental delay waled at age 3; intellectual disability. Very | Global dev delay all milestones/moderate intellectual | Moderate global developmental delay (language limited and has | motor developmental delay, normal language development, | Global developmental delay | Global developmental delay with marked generalized hypotonia, only syllabes for speech; (walking independently after 4 years) | Severe global developmental delay (babbling, mama dada but not consistent, non ambulatory); Sileop disturbance | Motor and speech delay | Severe progressive developmental delay with episodes of regression | Global developmental delay: gross molor (walking independently after 2 years) and expressive speech | Moderate global developmental delay (4 months head control 9 months sitting 31 months walking) | months, crawled at 14 months, crussing at 16 months, walking at 22 months is very wobbly and atil needs support. Speech - at 1 | Motor and speech delay. Walked at 1920 months of age. Global d | levelopmental delay (non- | Learning difficulties/Borderline IQ FSIQ-70 | at swing, its evaluation stroked average cognition with delayed expression language and motor skills. At 22mo his pediatrician reported that he was able to point and vocalize to show his. | first words at 4 years and sentence at 6 years, still not fully understandable at age 9. In grade 9 was operating at grad 4 | severe delay; no words; understands simple orders; walked at 32 m; | Speech delay | moderate global developmental delay, walking at 22 ms, global motor delay, global and facial hypotonia, fire motor trouble, fat words at 4yo, can say words, language trouble, good non-webal communication, conditional | roderate developmental psychoso | Global moderate somotor delay, delayed mited speech, dystalia |
| payoranic process | assistance; some anxiety | some letters, can count to five, recognizes colours. Can stay focused on an activity, nice. Speech iompediment but can | dx - paed says not enough for diagnosis, but all have mild symptoms | ds - paed says not enough for diagnosis, but all have mild symptoms | Austin health | | Geographic discussion | average level. Problems with loud noises, lives in her own world. No formal diagnosis of ASD. | Ansiety, low self-confidence, impulsivity, low teatment speed index (74) and normal indices (between 88 and 97) of WPPSI- | 22 months. No reported fine major concerns. Severe speech delay: grunts / vocalises. Only "mum" and "dad" at 2 years. | learning, attentional and cognitive delays. Sall with impaired coordination | deby, wasking at 20m, firts words at 2y | | few words. Dit of Autism spectrum disorder | deability | delay (tanguage limited and has speech aprasia, ambulatory) | normal fine motor development | | (walking independently after 4 years) | Sleep disturbance | | episodes of regression | expressive speech | 31 months walking) | 22 months has 2-3 spontaneous words, but usually only repeats or echos. Developmental delay, global, mild and making | Minimal speech at Dyrs of age. | bal, non-ambulatory) | in radio | wants, as well as use two word combinations, but he could not run without falling. By 25mo months he could use pronouns | 5 level for academics, and is in iffe skills program at school. Has computate behaviours, paricularly trichellomanis. NO | walked at 32 m; | | can say words, language trouble, good non-verbal communication, good level of understanding of simple orders, not tollet-trained | delay and limite | led speech, dystalia |
| | | produce more than 50 significant words | | | | | | Walking 18 months, first words 18 months. Speech development disorder. At the age of 4 years estetences of 3-4 words. Problems with Non-verbal development at low arrange level. Problems with loud noises, lives in her one word. No formal displayable of Acts. Mile skepting problems. | IV testing at age 5 years 3 months | | | | | | | | | | | | | | | | progress. Cruising age 16 mos; not walking yet 22 mos. Few words, mostly repeats words at 22 mos. Social and affectionals. | | | | reported that he was able to point and secalize to show his wants, as well as use how word combinations, but he could not run without failing. By 25mo months he could use pronouns and verbalize immediate experiences, but he could not walk up and down stains one step at a time. | P | | | Grand Inc. Companies | | |
| Ophthalmologic problems | No | Astignation | No | No | No | No | No | Hypermetropia, amblyopia | Hypermetopia, strabismus (orthoptic therapy) | No | No | strabismus | No | No | Bilateral esotropia hypermetropi | Mild hypermetropia, resolacrimal duct obstruction | No. | No | No | Esophoria | No | No | No reported concerns | No | Intermittent strabismus/esotropia. Hypermetropia but no rx for glasses. Amblyopia and treated with patching. | No Visus plosis; C | d impairment; Bilateral Cortical visual impairment | Myopia | No | Hypermetropia | No | No | No | No | No |
| | | | Acute CME, x2 sets of | | | | | | | | | | | | | | | | | | | | | | 5db bilsteral 5N/L. Hs 2 ear infections. Tubes placed at 17 months. Mixed hearing loss with mild sensorineural hearing loss. | N | | | | | | | | | |
| Audiology / hearing | Normal | Normal | grommets, no concerns with hearing | Normal | Acute CIM as beby, no gommets no concerns with hearing | Normal | Normal | Normal | Normal | Normal | Normal | Normal | bilateral mixed hearing loss requiring hearing sids | Normal | Normal | Chronic CM s/p TM tubes, normal audiometry | Normal | Normal | moderate conductive hearing loss | Normal | Normal | Normal | Normal | Normal | conductive hearing loss with chronic middle ear effusion sip ear tubes. "Note: pt is also compound heteropygote for 2 | Normal newborn hearing assessment. Normal assessment at 1 year of age. | Unclear | Normal | Failed NHS, but eventually had a normal ABPI in both ears | Normal | Normal | Normal | Normal | Normal | Normal |
| Oral / dentition / other ENT | Submucous cleft palate | High polate, widely spaced teeth | tonsillectomy; cleft soft palate; Class III meloculation; orthodontics; on WL for thinoplasty | Submucous cleft palate; tonsillectomy; orthodontics | tonellectomy and superior adenoidectomy after speech assessment; orthodontics; | | D Normal | Normal | no | Ankylogiossis. Poor suck/swellow coordination. Obstructive/noisy upper airway breathing. | No | hypoplastic usula | ronmal | High points | High painte | Normal dentition, no caries | No | Anterior open-bite malocolusion | No. | Carlous teeth | Laryngeal deft | High palate | No reported concerns | No | GUB2* delayed teeth eruption and in unusual order | Fongue Se release at 2 months of age. | Dental caries | No | Debyed dental eruption - first tooth at 12mo | No | Normal | Laryngomalacia; Lip and longue | Narrow palate | Dysmouth, I | emorphic ears, amail oth, high palete, billd is, nasal voice, nasal septum deviation |
| Oral / dentition / other ENT problems | Salitocos cen passe | Trigo passe, money spaces man | orthodontics; on WL for rhinoplasty | tonsillactomy; orthodontics | speech did not improve after T&As on sailing list for pharyngoplasty | midface retrusion | 70.118 | 10.110 | 10 | Obstructive/holey upper sirvery breathing. | | TOPOGRASIO, UNIX | TO THE | | rigii jaaa | PETRO OFFICE, TO CARRE | | Surgical correction for patent | | Caron men | Layigaa oni | regs passas | TO RECORD CONCERNS | | unusual order | | | | tooth at 12mo | | 7,0110 | tie at birth - clipped | THE TANK SAME | usala, n sep | nasal voice, nasal splum deviation |
| Cardiac problems | Bicuspid sortic valve, PDA requiring surgical closure | Atrial septel defect | No | No. | Heart mumur when born, innocent, no follow up needed, ECG and echo normal | No | No | No | No | No(referred for echocardiogram, pending) | No | spontaneously resolving VSD | No | interrupted acriic arch; multiple ASD and VSDs; subscriic stencels. Severe LV dysfunction. | No | Normal ECHO | delay in ductus arteriosus closure after birth, but normal echocardiogram at 3 weeks of age | ductus artericeus, now she has minimal shunts for perimembranous interventricular defect and cellum secundum intervental defect | No. | No | No | Pensistent left superior vena cava to coronary sinus | No | Atrial Septel Defect | No | Small PFO noted at birth. Ven Normal ECHO at 2yrs of age. (spx | tricular septal defect ordeneously closed); Mesocardia | No | No | No | No | Elicuspid sortic valve | No | No Patent into | dent foramen quale, interstrial defect |
| Respiratory problems | No | No | Moderate OSA; no asthma | OSA and snoring; hospitalised for pneumonia at 3, no asthma | OSA, now resolved | Mild asthma as child, flares up every once in a while | P No | No | No | No. | No | No | respiratory distress at birth, no current issues | No | No | No | No | Recurrent pneumonia, low citar functioning | No. | No. | No | recurrent pneumonia | No. | No | No F | Recurrent upper respiratory tract pneum infections disease | ecurrent sepiration vonias; Reactive sinvay se; Sinuses essentially | No | No | No | No | CT scan performed secondary to frequent sinus infections showed "underdeveloped | No. | No | No |
| | | | | | | | | | | | | | facilità d'advention in interv | | | | | | | | | | | | Hx leading difficulty. Still structure with hard books due to | | | | Hypoor sucking and feeding difficulties as infant leading to FTT by 3mo. Formulas were tried with no success. Barium | | | FTT and poor suck/swallow coordination. GERD and blood in | | | |
| Gastrointestinal problems' feeding difficulties | Poor feeding in newborn period requiring NGT feeds; Chronic constipation | neonatal sucking difficulties. Nocturnal salva swellowing difficulties responsible for coughing and nocturnal wakings. | Cleft-related feeding difficulties; fussy eater; mainly carbs | Hyperphagia; eats good variety of toods and textures; constipation | fusey eater | No | No | No | No | Early difficulties with latching and ongoing poor coordination of suck and sealow. Early difficulty initiating solids. | No | No | requiring Glube, Nassen fundoplication (GERD), currently eats by mouth with no vomiting, diarrhea or constipation | Glube fed; Constipation | Severe persistent constipation | Severe feeding difficulties with velopharyngeal insufficiency, GERD, constipation | poor feeding, constipation | Episodic constipation | Constipation | Chronic constipation, gastro- oesophageal reflux | onstipation (negative testing for Hirschprung); G-tube dependence; GEPD | failure to gain weight | Severe constitution. Negative rectal biopsy for Hirschprung. | No | His feeding difficulty. Still struggles with hard foods due to distryed teeth emption. Prefers soit toods and struggles at little to chew and swallow hard foods; uses a sippy cup and can drink from a straw. | Diarrhoea Constip dysfund | ation; Ono-motor feeding ction; GEPID; G-tube fed | No | swellow showed GERD - to Prevacid and Zentac with minimal improvement. Normal upper GI and small bowel series. | intermittent diamhea, of unclear eliology | No | stool prompting several formula changes. He was diagnosed with milk protein allergy as infant, but skin test negative and now able to tolerate milk without symptoms. / blood in stools. | Constipation r | severe constipation O | Constipation |
| | Bilateral cryptorchidam; non- | Initial inquinal testis but now | | | | | | | | | | | | | | | | | | | | | | | | | | | endoscopy showed some mild inflammation, but was otherwise wnl. Hx chronic constipation. | Small peris and testicies | | | | | |
| Renal / genitourinary problems Hematologic problems | functioning right multicystic dysplastic kidney No | normal. Normal abdominal and kidneys US No | No No | No No Seem by Endo at PICH; above 1 | No No | No No | No No | No No | No No | No No | No No | No No | No No | Cryptorchidiem Neutropenia; Thrombocytopenia | Nephromegaly/Normal function No | Nocturia Neutropenia (resolved) and Intermittent normocytic anemia | normal renal ultrasound at 14 mo iron deficiency (4 µmol/L at 5 mo) | No neoratal anemia | No No | Cryptorchidam No | No No | No No | No No | No No | No No | No Blac | teral inguinal hernias | Incontinence, resolved at 8 yr with seizure control No | No No | (history of delayed puberty). Normal renal ultrasound No | No No | Bilateral cryptorchidam No | Incomplete foreskin | No Increase di No | ased corsicomedulary differentiation No |
| Endocrine problems | No | No | No | charts for both height and weight; lost 20kg in a year, high BMI; involved in study related to diabetes, does not have | High end of Yule charts on height and weight, no official measurements yet because of COVID, but Mum said heading in same direction as Marcelle | No | No | No | No | No | No | testosterone assay and pelvis ultrasound normal | No | No | No | No | No | No | No | Warnin D deficiency | No | No | No | No | No | No No | onatal hypoglycemia (resolved) | No | Hypothyroidem (KGF-1 41 rg/mL, TSH 15.2 uLl/mL, free T4 1.43 rg/dL) ix w synthroid .05mg. N thyroid utnaound | 6 Delayed puberty | No | No | No | No | No |
| | | | | diabeles; no longer linked in wit Endo at RCH | h in same direction as Marcelle | | | | | | | | | | Normal birth centiles;subsequen overgrowth with all centile being >>> 97th; review at age 15 | | | | | | | | | | | | | | | | | | - | | |
| Musculoskeletal problems | Sprengel deformity scapulae, webbed neck | Joint body | No | No | No | No | No | No | No | Small fingers, broad thumbs. | No | Joint body | muscle faligue | Tall | growth now normalizing with centiles; as adolescent more Murtan like habitus with long tons and US-15 ratio 0.79 & arm apan -length by 3.7 cm; amall chest with mild pectus exceedure; | Left sided hemityperplasia | No | Beighton score 6/9 + pectus carinatum + mild scollosis | dacrete limb length asymetry (Left-Right) | Dislocated hip | No | increased muscle tone | No | No | No joint problems or muscle concerns. Hypotonis has improved with time | Mid kyphosis. Hypotonia has Right or improved with time. | alcaneovalgus deformity at birth (resolved) | No | No | mild valgue deformity of knees. Decreased coverage of R femoral head on pelvic way. Short stature at 3rd centile | No | No | Joint body | early hypotonia | Joint body |
| Immunological problems | No. | No | No | No. | No. | No. | No | No | No | No. | No. | No | No | | span >length by 3.7 cm; small chest with mild pectus excavatum; No | Hypogammaglobulinemia | No | IgG1 deficit | No. | No Re | ecurrent infections/pneumonia, Possible IgA deficiency | No | No. | No | No. | No R | ecurrent infections | No | Episodes of fevers | Bacterial moningitis at age By, | No | | few offis, bronchills | | No |
| | | | | | | | | | | | | | | No | | | | | No Pigmentary mosaicism including cafe-au-lait spots in a patichy pattern without midline separation and | | | | | | | | | | | no history of recurrent infections | | | | | |
| Skin | Normal | Normal | Acne, on roacculane | Acre, on reaccutane | Normal | Normal | Normal | Normal | Skin telanglectasia (cheeks, upper part of the back), regression of a congenital blue new of the back | Normal | Normal | hypertrichosis | Normal | Normal | Pigmented raseuus on lower righ bultook | Normal | white patches on skin and a rash | Hypopigmented skin across Blaschko lines | pattern without midline separation and hyperpigmentation in a blaschkolinear pattern. Naevus. flammeus. | Normal | Normal | Normal | Normal | Normal | Normal | Eczerra Capitar | ry hemangiomas; Nevus | Normal | Normal | sensitive skin to temperature change | Normal | May have immunological abnormalities (per parents report, we didn't have anything to review). | Normal | Normal | Normal |
| Maligrancy | No. | No | No Sensory processing difficulties: | No On medication for analety www | No WL for phary ngoplasty, post | No On medication for anxiety *** | No d | No | No. | No | No | No | No normal microarray in 2013, | No Admission to ICU for | No | No Severe fatigue, drop attack* | No. | No | No | No. | No | No | No CMA, MS-MLPA for Angelman, and FMRI testing negative | No | No Failure to thrive. Weight percentile <1%, length <1%, weight for length <32%, head | No. | No | No | No. | No array CGH (60K) normal, free | No No | No No | No | No D | No Dolicocephaly, |
| Other Family History | | | on medication for anxiety and depression | On medication for anxiety and depression | pharyngeal wall flap, 'non-cleft VPI'; arviety, but not medicated | On medication for arrively and depression | | | fragile X syndrome | | | | midly low carritine responding to supplementation | Admission to ICU for hyperammonemia | | Severe fatigue, drop attacks (unclear etiology) | narrow shoulders | | | | | | and FMRI testing negative | | circumference 2%, All growth parametes are increasing along his own curve indicating normal growth velocity. | Narrowisloping shoulders | | NI | | array CGH (60K) normal, frax normal | NO. | NO NO | No | No macroce | Dollocosphaly, rocephaly (DFC = 54 cm at 3 y), |
| | | | | | | | | | Difficult to assess, child growing in a foster tamily, mother has possibly similar difficulties but no evaluation data during her | 9 | | | | | | | | | | | | | | | | | | | | | | | | | |
| Similarly affected family members | No | no | 3 | 3 | 3 | 3 (daughters) | no | No | possery similar diminuses out in evaluation data during her scholing, she did her first year of primary school taice and specialized education at age 10 years; tather had mild learning difficulties with attention deliciency, difficulties in writing | No No | Father had absence epilepsy in childhood, shares the same duplication listed above | mother with ID and hypertrichosis, father with ID and microcephaly (-3.55D), | no | None | NI | 7 year old brother with hemityperplasia, but developmentally normal. Does not carry FEXW7 variant. | No | no | No | No | NO | none | No | No. She is an only child, from healthy unrelated Japanese parents. | No. First child to both parents | No | No | No | No | no | no | No | no | no | No. |
| | | | | | | | | | difficulties with attention deficiency, difficulties in writing and general clumeiness without attack or neurological deficit | i. | | | | | | | | | | | | | | | | | | | | | | | | | |
| Consanguistly Full siblings | No 1 | No | No 2 | No 2 | No 2 | No NA | No NA | No 0, two half sidens | No 2 | No No | Older brother - healthy, 5 | fetus with ventriculomegaly, hypoplastic thumbs, IUGP, anal imperforation, pelalic kidney, | ro yes | No Full Slater - 16 yo - Healthy | NI 2- well and developmentally age appropriate | No 1 | No 1 | no 1 male, 1 female | No No | No 0 | ND 5 | no | No 2 | No | None None | No 1 | No. | No 2 | No 7 | no 3 | no | No | 10 | | No No |
| Other Physical Examination | Paternal SLE | | Father | Father | Father | Daughters | | Brother of mother with ADHD and dev delay. Other brother of mother with ADHD only. | 3 paternal half brother from 2 somen, mother pregnant from another partner | Mother learning difficulties (16p13.11 duplication) | | right sortic arch. | | | | Non-contributory | Parents unaffected | | No. | One half sibling | NO | | | | Ashkenazi Jewish ancestry. | No. Malern | ral uncle with congenital heart disease | NI | Mother had two spontaneous fire trimester abortions; AJ ancestry | nane contributory | 5/700 | | | | - |
| Physical Examination | 50th centile | 105.1cm (+35D) | Age 17 y: 160 cm (32nd centile) | Age 15 y: 175 cm (98th centile) | Age 10 y: 156 cm (>98h certile) | Age 47 y: 187 cm (92nd centil | le) 152 cm (+45D) | At age 3 years 6 months 110.2 cm (2.02 SD) | 127 cm (+1.4 5D) | 72nd centile (2y) | 159.4 cm (1st-3rd centile) | 88 (+0,55D) | 142.3 cm (72nd centile) | 167 cm (53rd centile) | All consistently above 97th centile till about age 13 then has started normalizing and at last exam (age 15) head | 89th centile | At 10 mo: 75 cm (64th percentile) | 141 (75-90%) | 120 cm (+1,5 5D) at 6 years | Age 5 m: 66 cm (52nd certile) | 107.0 cm (95th percentile) | 142.3 cm | 102 cm (65th centile) | 103 cm, -1.9 5D | 76.20cm (Z=2.85) | 91 cm (10th centile) 125 cm | n (Gänd centile) at 7y5m | 136.2 at 11 yes (22nd percentile) | <<1% (Normal at birth, by 3 months length was 30%, and by 12mo it was <2%) | 154 2 on (Indicential) at 15y (was previously at 25th centile) | 397m 114.5 cm (+1.50) | 92nd centile | 147 cm (+1.5 5D) | 166 cm (+1.5 SD) 116.5 cm | cm (50th centile) at 6 y and 3 m |
| | 10th centile | | Age 17 y: 53 kg (36th centile) | Age 15 y: 82kg (98th centile) | | | | | | | 53.1 kg (3rd-10th centile) | | | | circumference remains above 97th centile but other centiles or | | | | | | 15.1 kg (90-95th percentile) | | | | | | (74th centile) at 7y5m 3 | | | | 20 kg (+1 SD) | 99h certile | | ' | g (59th centile) at 6 y |
| Head circumference | 50th centile | 54.5 cm (+3.2 SD) | Age 13 y: 2nd centile | Age 5y3m: 53 cm (98th centile) | Age 4y3m: 52.5 cm (95th certile) | NA | 54.5 cm (+15D) | 29.1 kg (0.97 SD) 53.5 cm (2.28 SD) | 52.4 cm (median) | 80th centile (2y) | 50.6 cm (<2nd certile) | 44 (-35D) | | | | | | 57 (>97%) | 54.2 cm (+2.50) at 6 years | Age 5 y: 52 cm (66th centile) M | facrocephaly - 54.6 cm (>95th centile) | 46 at 2y | 52cm (83nd centile) | 48.5cm, -1.55D | | 12.3 kg (7th centile) 25 kg 50 cm (58th centile) 51.0 cm | (34th centile) at 6y10m S | 52 cm at 5 yrs (85% percentile) | 25% (consistent since birth) | 55.8cm (75th centile) at 15y | 53 cm (+1 50) | 90-90th centile | 55.5 (+1.5 50) | 60cm (+3 SD) 54.5 cm | and 3 m cm (+2.5 SD) at 6 y and 3 m |
| | | | | | | | | | | | | | | | Long palpebral feaures which | somewhat flat face, short nose, downturned corners of mouth | | | | | Ald dysmorphic facial features- Overlokked halices, Stateral epicanthal folds, down | | | | mild fattering of the occiput but otherwise normal head shape with anterior and posterior hairlines normal. Carrly, dark brown hair. Level palpabral fatteres with normal eye spaces. Pupite equally round and reactive to light with estraccular rouvements in tradem. I stess are brown. Ears normal formed and brown. Ears normal formed and brown. Ears normal formed and behaved. These says no reservisions. | | | | | | | Ears that are mildy prominent and posteriorly rotated but | | | |
| Facial features | Broad forehead, high nasal root, deeply set eyes, periorbital fullnass, make fattering, short philhrum, thin upper and lover lips vermillon, webbed neck, underdeveloped superior onus of ears with left-sided presuricular pit | "de novo posinatal macrosomia", epicanthus, thick eyebrows, synophris, large lobules of ears, | Deeply set eyes, periorbital fullness | Not dysmorphic | Deeply set eyes, periorbital fullness | Midface retrusion | Not dysmorphic | Prominent normals, no nomes bossing. Upshlant, hypertelorism/feliscarchus, almond shaped eyes. Nose normal. This upper lip. Ears low set and goateriorly rotated, normal shape. | Mid facial saymmetry with low set right ear, thick eyebrows, | Prominent metopic subme. Flat occiput. Broad nasal bridge / hyperielorism. Lateral eversion of eyelids. Small ears with thickened helices. Mild micrographs. This upper lip with flat phillrum. | Midly dysmorphic | Downturned corner of the mouth, synophrys, highly arches eyeldross | d Not dysmorphic | Myopathic facies; Hypoteloric, thin upper and lower lips vermillor, highly arched | were down starting with long thick curly eyelbahes upfilled nose with a flat fig; low set posterior rotated ears with overfolded helices and prominer | somewhat flat face, short nose, downturned corners of mouth | small chin, deep set eyes | long face, bulbous nose, posteriorly rotated ears, high | Mild dysmorphic facial -metopic ridge, overloided helices, epicanthal folds, bulbous nose, | Long palpebral fissures, dimple | anted palpebral fissures, deep- set eyes, periorbital fullness, P fish sorbed naiste. Wide nased | Pully eyelds and cheeks ,small mouth slightly broad nose | mild frontal bossing, raised philtrum, thin upper lip, | Deep-set eyes, periorbital fullness, anleveried ears, depressed rasal bridge and broa- rasal lip. | Pupils equally round and reactive to light with estraccular movements in tandem. Hisses are brown. Ears normal formed and b | Epicanthic folds, depressed & Lowar oad rasel bridge, blue sclerae, plosis; 1 | nterior hairline; Blateral Prin ear helix; Synophrys | Normal | Depressed rasal bridge, high arched pales, terted upper lip | Deep set eyes, mildly narrow pts. fland eyebnows, long philtrum, prominent lips, longe appearing frontal incisors | no | Ears that are mildy prominent and posteriorly noised but otherwise normally formed and set, normal nease bridge, good destition, forwhead is tall with a somewhat receded anterior habitine. Noticetal with mildly long polipishost fissures, perioribite I fallesse noted and gives impression of eyes being somewhat deep set, biblieral epicanthal folds. | small mouth front | Dysmorp forehead side and uplifted e small ears | norphic features: high read, dolichocephaly, and protrudin ears with of earlobes, flat masal lithum, amail mouth, icharion, oglisif palate, usula, chin hypophala. |
| | underdeveloped superior crus of ears with left-sided presuricular pit | deeply set eyes, periorbibli fulness, downturned mouth, | | | | | | normal. Thin upper lip. Ears low set and posteriorly rotated, normal shape. | thin upper lip | thickened helices. Mid micrographia. Thin upper lip with flat phillinum. | | eyebrows | | eyebrows with synophrys; thick eyelashes, left presuricular pit. | inferior and superior crus; jow! like cheeks and his mouth was small with down turned corners; high palate | | | narrow palate, rasal voice | uptented upper lip, | b P | bridge, Scaphocephalic with a prominent occiput, Metopic but not sagital ridging. | | | rosal Sp. | placed. There are no presuricular pits or tages. Prominent, somewhat high nasel bridge with normal nose and philtrum. Thin | | | | | appearing frontal incisors | | long palpebral fissures, periorbital fullness noted and gives impression of eyes being somewhat deep set, bilateral | | philtrus' | um, amail mouth, dusion, oglval palate, sula, chin hypoplasia |
| | | | | | | | | | | | | | | | | | | | | | | | | | placed. There are no presurricular pits or tages. Prominent, somewhat high read bridge with normal nose and philtrum. Thin lips. Palate is intact and not high with single middine usuks. Teeth are privary leath with normal enamel. | | | | | | | epicarihal folds. | | | |
| Hands / feet | Tapering fingers, single palmar crease on R, small feet with pes planus and overlapping toes | Single palmar crease, clinodactyly | Normal | Normal | Normal | Normal | Normal | Toes 2-5 clirodactyly. | Metabaraus varus (surgery at age 2.5 years, intermittent physiotherapy and networns- | Small, feetly hands & lingers with broad thumbs. Small loss. Single palmar creases. | Normal | flat feet, right single transverse palmar fold | Normal | Normal | Although his hands were large consistent with the next of his habitus, his fingers were actually short (10th certile); broad thumbs, splayed forefeet with 2- 3 syndactyly. | hemityperplasis of left leg | fat pad on top of foot | Normal | finger hyperlaxity and mild proximal rigidity | Tapered digits, hypermobile joints, single palms crease biblierally, persistent fetal finger pads, broad small feet | Thickening of palms | Pinger availing | Normal | Normal | Mid fifth finger brachydactyly. Normal otherwise. | Disteral Cree Normal Interph of fine | single transverse palmar see; Tapered fingers; slangeal joint contracture ser; Short phalances of | Normal | Persistent fetal pads, single palmer crease | 2-3 toe syndactyly | Normal | 2nd toes bilaterally have a more donal insertion point and the 2nd toe overlaps toes 1 and 3, right > left, lymphedema of the donaum of each hand that was not noted in the feet. | Normal | Normal Pes p | es planus, bilateral |
| | planus and overlapping toes | | | | | - | | | | | | | - | | humbs, splayed forefeet with 2- 3 syndactyly. | | | | p | pads, broad small feet | | - | | | | finger Py | stangeal joint contracture per; Short phalanges of re; 2-3 toe syndactyly; continent calcaneus | | para trans | | | dorsum of each hand that was not noted in the feet. | | | |
| Other findings | No | unaffected Mother 170 cm (+1,250) OFC 54,8 (-0,550) ; tather 174 cm (-0,250) OFC 58 cm (+1,550) | | Obesity | No | No | other people in the materns family with over weightheig | Aralyses pelcorrect FMR1, SNF-array, WES and relabolic acreening. With metabolic acreening low activity of very long chain acyl-CoA delydrogerase (VLCAD). She turned out to be a carrier of VLCADD. | 4q31.3(1527)344_153661857): 5ds, 6q21(114465667_114548253);d mat, | s S No | No | No | No | No | arrail chest with mild pectus excavature; arrail umbilical bernia; | No | long eyelsehes | No | No | BW 3.40kg, HC 35.5cm at birth | hymus bulge with valsalvs. TEA removed | No | No | No | No | No | No | No | No | Supernumerary ripple | No | Mid datel pectus excavatum | No | No Sometic potentials | malosensory evoked data and EMG: normal |
| | | om (+1,550) at birth : 38+2WG : 3240g51cm/CFC35cm | | | | <u> </u> | | | | | | | <u> </u> | | - | | | | | | | 1532H7171A-C | | | | Was n | eported in cohort paper PMID 32960281 | | | | | | | | |
| | | 3240g/51cm/CPC35cm | | | | | | | Intragenic DPPS duplication inherited from the father HS3STS exon 3 duplication (UTR) inherited from the mother | | | | | | | | | | | | | - India | | | | | PSeD 32960281 | | | | | | - | $\overline{}$ | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | • | | | | | |

Fable S3: HPO terms associated with FBXW7 Neurodevelopmental syndrome

| Table 53 | : HPO terms associated | with FE |
|-----------------------|---|---|
| Prenatal history | Thickened nuchal skin fold HP:0000474 Jaundice HP:0000952 Breech presentation HP:0001623 Neonatal hypoglycemia HP:0001998 Hyperechogenic kidneys HP:0004719 Neonatal respiratory distress HP:0002643 | |
| Neurological problems | Hypotonia HP:0001252 Seizure HP:0001250 Progressive spasticity HP:0002191 Unsteady gait HP:0002317 Broad-based gait HP:0002136 Paroxysmal tonic upgaze HP:003980 Early onset absence seizures HP:0011152 Achilles tendro contracture HP:001771 Abnormality of coordination HP:001143 | Developme cognitive / psy problem |
| | Migraine HP:0002076 Photophobia HP:0000613 Ataxia HP:0001251 Dyskinesia HP:0100660 Stereotypy HP:0000733 Drooling HP:0002307 Atonic seizure HP:0010819 | Ophthalmo problem |
| | Enlarged cerebellum HP:0012081 Arnold-Chiari type I malformation HP:0007099 Thin corpus callosum HP:0033725 | |
| Brain Imaging | Agenesis of corpus callosum HP:0001274 Abnormal corpus callosum morphology HP:0001273 Punctate periventricular 72 hyperintense foci HP:0030081 Aplasia/Hypoplasia of the cerebellum HP:0007360 Enlarged cisterna magna HP:0002280 Abnormal brainstem morphology HP:0002363 Brain atrophy HP:0012444 Subcortical white matter calcifications HP:0007346 Delayed myelination HP:0012448 Extra-axial cerebrospinal fluid accumulation HP:0012510 Polymicrogyria HP:00021126 Ventriculomegaly HP:0002119 Dilation of Virnow-Robin spaces HP:0012520 | Audiology / h |

| Developmental / cognitive / psychiatric problems | Global developmental delay HP:0001263 Intellectual dissability, borderline HP:0006889 Anxiety HP:0000739 Poor suck HP:00002033 Motor delay HP:0001270 Specific learning disability HP:0001328 Delayed speech and language development HP:0000750 Speech articulation difficulties HP:0009088 Sleep disturbance HP:0002360 Impulsivity HP:0100710 Short attention span HP:0000750 Autistic behavior HP:0000729 Speech apraxia HP:0011098 Developmental regression HP:0002376 Hair-pulling HP:0012167 Depression HP:0000716 |
|--|--|
| | Astigmatism HP:0000483 |
| Ophthalmologic problems | Assignitatish HP.:0000540 Amblyopia HP:0000646 Strabismus HP:0000486 Nasolacrimal duct obstruction HP:0000579 Esophoria HP:0025312 Bilateral ptosis HP:0001488 Cerebral Visual impairment HP:0100704 Myopia HP:0000545 |
| Audiology / hearing | Mixed hearing impairment HP:0000410 Conductive hearing impairment HP:0000405 Sensorineural hearing impairment HP:0000407 |
| Oral / dentition / other ENT problems | Otitis media with effusion HP:0031353 Submucous cleft of soft and hard palate HP:0410031 High palate HP:0000218 Widely spaced teeth HP:0000687 Cleft soft palate HP:0000185 Dental maloculsion HP:0000689 Midface retrusion HP:001089 Modiface retrusion HP:001089 Poor suck HP:0002033 Impaired oropharyngeal swallow response HP:0031162 Episodic upper airway obstruction HP:0012271 Short uvula HP:0010812 Anterior open-bite malocclusion HP:0009102 Carious teeth HP:0000670 Laryngeal cleft HP:0008751 Delayed eruption of teeth HP:0000684 Laryngomalacia HP:0001601 Narrow palate HP:000189 Abnormal ear morphology HP:0031703 Biflid uvula HP:0000193 Nasal speech HP:0001611 Deviated nasal septum HP:0004411 |

| Cardiac problems | Bicuspid aortic valve HP:0001647 Patent ductus arleriosus HP:0001643 Atrial septal defect HP:0001631 Ventricular septal defect HP:0001629 Interrupted aortic arch HP:0011611 Subvalvular aortic stenosis HP:0001682 |
|---|--|
| | Abnormal left ventricular function HP:0005162 Secundum atrial septal defect HP:0001684 Persistent left superior vena cava HP:0005301 Patent foramen ovale HP:0001655 Mesocardia HP:0011599 |
| Respiratory problems | Obstructive sleep apnea HP:0002870 Snoring HP:0025267 Asthma HP:0002099 Recurrent pneumonia HP:0006532 Recurrent sinusitis HP:0011108 Abnormality of the maxillary sinus HP:0430023 Recurrent upper respiratory tract infections HP:0002788 Bronchitis HP:0012387 |
| Gastrointestinal problems/ feeding difficulties | Feeding difficulties HP:0011968 Nasogastric tube feeding in infancy HP:0011470 Chronic constipation HP:0012450 Polyphagia HP:0002591 Gastroesophageal reflux HP:0002020 Velopharyngeal insufficiency HP:0000220 Constipation HP:0002019 Failure to thrive HP:0001508 Diarrhea HP:0002014 |
| Renal / genitourinary problems | Bilateral cryptorchidism HP:0008689 Multicystic kidney dysplasia HP:000003 Enlarged kidney HP:0000105 Nocturia HP:000017 Inguinal hernia HP:0000023 Urinary incontinence HP:0000020 Micropenis HP:0000054 Decreased testicular size HP:0012435 Abnormal renal corticomedullary differentiation HP:000593 |

| Hematologic problems | Neutropenia HP:0001875 Thrombocytopenia HP:0001873 Normocytic anemia HP:0001897 Iron deficiency anemia HP:0001891 Anemia HP:0001903 |
|-----------------------------|--|
| Endocrine problems | Low levels of vitamin D HP:0100512 Neonatal hypoglycemia HP:0001998 Hypothyroidism HP:0000821 |
| Musculoskeletal problems | Sprengel anomaly HP:0000912 Webbed neck HP:0000465 Joint laxly HP:0001388 Short linger HP:000381 Broad thumb HP:0011304 Increased muscle fatiguability HP:0003750 Pectus excavatum HP:0000767 Pectus excavatum HP:0000768 Hemihyperfrophy HP:0001528 Scollosis HP:0002650 Hijp dislocation HP:0002827 Hypertonia HP:0001276 Kyphosis HP:0002808 Calcaneovalgus deformity HP:0001848 Genu valgum HP:0002857 |
| Immunological problems | Decreased circulating antibody level HP:00043 Recurrent fever HP:0001954 |
| Skin problems | Acne HP:0001061 Telangiectasia HP:0001009 Blue nevus HP:0100814 Hypertrichosis HP:000998 Melancoytic nevus HP:0000995 Poliosis HP:0002290 Hypopigmentation of the skin HP:0001010 Distributed along Blaschko lines HP:0025293 Cafe-au-lait spot HP:0000957 Hyperpigmentation of the skin HP:0000953 Nevus flammeus HP:0001052 |

| Growth | Obesity HP:0001513 |
|-----------------|--|
| | Macrocephaly HP:0000256 |
| | Microcephaly HP:0000252 |
| | |
| | Broad forehead HP:0000337 |
| | Abnormal nasal bridge morphology HP:0000422 |
| | Periorbital fullness HP:0000629 |
| | Malar flattening HP:0000272 |
| | Deeply set eye HP:0000490 |
| | Thin vermilion border HP:0000233 |
| | Underdeveloped superior crus of antihelix HP:0011246 |
| | Preauricular pit HP:0004467 |
| | Epicanthus HP:0000286 |
| | Thick eyebrow HP:0000574 |
| | Synophrys HP:0000664 |
| | Large earlobe HP:0009748 |
| | Downturned corners of mouth HP:0002714 |
| | Prominent forehead HP:0011220 Hypertelorism HP:0000316 |
| | Telecanthus HP:0000516 |
| | Almond-shaped palpebral fissure HP:0007874 |
| | Low-set, posteriorly rotated ears HP:0000368 |
| | Prominent metopic ridge HP:0005487 |
| | Dolichocephaly HP:0000268 |
| | Flat occiput HP:0005469 |
| | Wide nasal bridge HP:0000431 |
| | Eversion of lateral third of lower eyelids HP:0007655 |
| | Thickened helices HP:0000391 |
| Facial features | Microtia HP:0008551 |
| | Micrognathia HP:0000347 |
| | Smooth philtrum HP:0000319 |
| | Highly arched eyebrow HP:0002553 |
| | Myopathic facies HP:0002058 |
| | Hypotelorism HP:0000601 |
| | Prominent eyelashes HP:0011231 |
| | Long palpebral fissure HP:0000637 |
| | Downslanted palpebral fissures HP:0000494 |
| | Anteverted nares HP:0000463 |
| | Overfolded helix HP:0000396 |
| | Prominent inferior crus of antihelix HP:0011238 |
| | Narrow mouth HP:0000160 |
| | Short nose HP:0003196 |
| | Prominent nasal tip HP:0005274 |
| | Tented upper lip vermilion HP:0010804 |
| | Deep philtrum HP:0002002 |
| | Scaphocephaly HP:0030799 |
| | Prominent occiput HP:0000269 Anteverted ears HP:0040080 |
| | Depressed nasal bridge HP:0005280 |
| | Low anterior hairline HP:0000294 |
| | Thick vermilion border HP:0000294 |
| | Incisor macrodontia HP:0011081 |
| | moles mas buonta in solitori |

Short stature HP:0004322 Tall stature HP:0000098

| | Tapered finger HP:0001182 Single transverse palmar crease HP:0000954 |
|------------|---|
| | Short foot HP:0001773 |
| | Pes planus HP:0001763 |
| | Overlapping toe HP:0001845 Clinodactyly HP:0030084 |
| | Metatarsus adductus HP:0001840 |
| Hands/feet | 2-3 toe syndactyly HP:0004691 |
| | Prominent fingertip pads HP:0001212 |
| | Finger swelling HP:0025131 |
| | Short 5th finger HP:0009237 |
| | Interphalangeal joint contracture of finger HP:0001220 |
| | Prominent calcaneus HP:0012428 |
| | Abnormality of the 2nd toe HP:0010319 |

Supernumerary nipple HP:0002558 Narrow chest HP:0000774 Umbilical hernia HP:0001537

Table S4: Impact of neurodevelopmental syndrome variants on protein stability and interaction with CYCLIN E1.

| | mCSM- | | | | | | | | |
|---------------|--------------------------------------|-----------------------------|-----------------------------|------------------------------------|---------------------------|--------------------------------------|----------|----------|----------------------------|
| | Stability (ΔΔG) - previous structure | mCSM- Stability (ΔΔG) | Change in protein stability | Distance to interface (Å) | mCSM- PPI 1&2 (ΔΔG) | Change in PPI binding affinity | Δ Charge | Δ Volume | Δ Residue nature |
| p.(Thr416lle) | -0.134 | -0.179 | Decrease | 15.1 | -0.07 | Decrease | 0 | 50.6 | Polar -> Hydrophobic |
| p.(Thr416Ala) | | -0.788 | Decrease | 15.1 | -0.134 | Decrease | 0 | -27.5 | Polar -> Hydrophobic |
| p.(His420Leu) | | -0.823 | Decrease | 12.4 | -0.469 | Decrease | Partial | 13.5 | Partial charge -> Neutral |
| p.(Gly423Arg) | -1.031 | -0.985 | Decrease | 7.8 | -0.264 | Decrease | 1 | 113.3 | Neutral -> Basic |
| p.(Arg441Gly) | -1.258 | -1.367 | Decrease | 2.8 | 0.179 | Increase | -1 | -113.3 | Basic -> Neutral |
| p.(Ser462Pro) | | 0.973 | Increase | 2.6 | -2.449 | Decrease | 0 | 23.7 | Polar -> Hydrophobic |
| p.(Arg465His) | | -1.834 | Decrease | 5.1 | 0.286 | Increase | Partial | -20.2 | Basic -> Partial charge |
| p.(Arg479Gln) | -0.625 | -1.346 | Decrease | 3.1 | 0.054 | Increase | -1 | -29.6 | Basic -> Unchanged |
| p.(Asp480Gly) | 0.327 | 1.401 | Increase | 4.5 | -1.998 | Decrease | 1 | -51 | Acidic -> Neutral |
| p.(Arg505His) | -2.019 | -2.032 | Decrease | 5.4 | -0.038 | Neutral | Partial | -20.2 | Basic -> Partial charge |
| p.(Val544Gly) | -3.203 | -3.16 | Decrease | 9.1 | -1.114 | Decrease | 0 | -79.9 | Hydrophobic -> Hydrophobic |
| p.(His580Tyr) | -0.414 | -0.422 | Decrease | 9.1 | 0.311 | Increase | Partial | 40.4 | Partial charge -> Aromatic |
| p.(Ser582Ala) | | 0.033 | Increase | 3.54 | -0.422 | Decrease | 0 | -0.4 | Polar -> Hydrophobic |
| p.(Ala599Val) | -0.451 | -0.093 | Neutral | 4 | 0.265 | Increase | 0 | 51.4 | Hydrophobic -> Hydrophobic |
| p.(Ala626Val) | | -0.106 | Decrease | 4.4 | 0.291 | Increase | 0 | 51.4 | Hydrophobic -> Hydrophobic |
| p.(Ser640Arg) | -0.639 | -0.586 | Decrease | 11.1 | -0.355 | Decrease | 1 | 84.4 | Polar -> Basic |
| p.(Ile608Val) | | -2.019 | Decrease | 22.3 | -0.244 | Decrease | 0 | -33.4 | Hydrophobic -> Hydrophobic |
| p.(Arg674Pro) | -0.648 | -0.614 | Decrease | 8.1 | -0.321 | Decrease | -1 | -60.7 | Basic -> Neutral |
| p.(Arg674Trp) | -0.283 | -0.157 | Decrease | 8.1 | 0.013 | Neutral | -1 | 54.4 | Basic -> Aromatic |
| p.(Arg689Gln) | -0.079 | -0.353 | Decrease | 3.4 | -0.54 | Decrease | -1 | -29.6 | Basic -> Neutral |
| p.(Arg689Trp) | | -0.357 | Decrease | 3.4 | -0.437 | Decrease | -1 | 54.4 | Basic -> Aromatic |

mutation Cutoff Scanning Matrix (mCSM); Protein-protein interactions (PPI)

Table S5: Comparison of the impact of neurodevelopmental syndrome variants and gnomAD variants on protein stability and substrate binding

| riant | Amino acid reference | Amino acid position | amino acid change | mCSM- Stability (ΔΔG) | Distance to interface (Å) | mCSM-PPI 1&2 (ΔΔG) | Allele Count | Class | Chromosome | Position | rsID | Reference | Alternate | Source | Protein Consequence | Transcript Conseque |
|---|---|--|-----------------------|---|--|---|--|--|---|--|---|---|---|--|---|--|
| 16A | Ţ | 416 | A | -0.788 | 15.1 | -0.134 | 1 | clin | 4 | 153247315 | - | G T | A | This study | p.(Thr416lle) | c.1247C>T |
| 16I 20L | H | 416 420 | | -0.179 -0.823 | 15.1 12.4 | -0.07 -0.469 | 1 | clin clin | 4 | 153249532 153249519 | - | T T | C A | This study This study | p.(Thr416Ala) p.(His420Leu) | c.1246A>G c.1259 A>T |
| 23R | G | 423 | R | -0.985 | 7.8 | -0.264 | 2 | clin | 4 | 153249511 | - | Ċ | T | This study | p.(Gly423Arg) | c.1267G>A |
| 41G | R | 441 | G | -1.367 | 2.8 | 0.179 | 1 | clin | 4 | 153249457 | - | G | С | This study | p.(Arg441Gly) | c.1321C>G |
| 62P | S | 462 | P | 0.973 | 2.6 | -2.449 | 1 | clin | 4 | 153249394 | - | A | G | This study | p.(Ser462Pro) | c.1384T>C |
| 55H | R R | 465* 479* | H Q | -1.834 -1.346 | 5.1 3.1 | 0.286 0.054 | 1 | clin clin | 4 | 153249384 153247366 | - | C C | T | This study This study | p.(Arg465His) | c.1394G>A c.1436G>A |
| 79Q 30G | D | 480 | G | 1.401 | 4.5 | -1.998 | 1 | clin | 4 | 153247363 | - | T | C | This study This study | p.(Arg479Gln) p.(Asp480Gly) | c.1439A>G |
|)5H | R | 505 | H | -2.032 | 5.4 | -0.038 | 1 | clin | 4 | 153247288 | - | Ċ | Ť | This study | p.(Arg505His) | c.1514G>A |
| 4G | V | 544 | G | -3.16 | 9.1 | -1.114 | 1 | clin | 4 | 153247171 | - | Α | С | This study | p.(Val544Gly) | c.1631T>G |
| 0Y | Н | 580 | Y | -0.422 | 9.1 | 0.311 | 1 | clin | 4 | 153245453 | - | G | Α | This study | p.(His580Tyr) | c.1738C>T |
| 9V | A | 599* | V | -0.093 | 4 22.3 | 0.265 | 1 | clin clin | 4 | 153245395 | - | G T | A C | This study | p.(Ala599Val) | c.1796C>T |
| V R | S | 608 640 | R | -2.019 -0.586 | 11.1 | -0.244 -0.355 | 1 | clin | 4 | 153245369 153244237 | - | G | T | This study This study | p.(lle608Val) p.(Ser640Arg) | c.1822A>G c.1920C>A |
| IP | R | 674 | P | -0.614 | 8.1 | -0.321 | 1 | clin | 4 | 153244136 | - | C | G | This study | p.(Arg674Pro) | c.2021G>C |
| W | R | 674 | W | -0.157 | 8.1 | 0.013 | 1 | clin | 4 | 153244137 | - | G | Α | This study | p.(Arg674Trp) | c.2020C>T |
| Q | R | 689 | Q | -0.353 | 3.4 | -0.54 | 1 | clin | 4 | 153244091 | - | С | T | This study | p.(Arg689Gln) | c.2066G>A |
| W | R | 689 | W | -0.357 | 3.4 | -0.437 | 2 | clin | 4 | 153244092 | | G | A T | This study | p.(Arg689Trp) | c.2065C>T |
| SI 'R | V H | 265 267 | R | -1.029 -0.581 | 57.368 61.633 | 0.119 -0.111 | 1 | gnomad | 4 | 153259022 153259015 | rs1393933844 rs1172754641 | C | C | gnomAD Genomes gnomAD Exomes | p.Val265lle p.His267Arg | c.793G>A c.800A>G |
| M | V | 271 | M | -0.254 | 64.686 | -0.311 | 1 | gnomad | 4 | 153259004 | rs764074483 | C | T | gnomAD Exomes | p.Val271Met | c.811G>A |
| E | K | 286 | E | -0.462 | 60.444 | -0.046 | 1 | gnomad | 4 | 153258959 | rs1490325931 | T | Ċ | gnomAD Exomes | p.Lys286Glu | c.856A>G |
| F | L | 288 | F | -0.908 | 59.843 | 0.132 | 6 | gnomad | 4 | 153253869 | - | C | Α | gnomAD Exomes | p.Leu288Phe | c.864G>T |
| S | A | 289 | S | -1.765 | 57.647 | 0.121 | 6 | gnomad | 4 | 153253868 | rs1444335835 | Ç | A | gnomAD Exomes | p.Ala289Ser | c.865G>T |
| C N | Y | 291 291 | C N | -0.467 -0.601 | 55.112 55.112 | -0.254 -0.017 | 2 | gnomad | 4 | 153253861 153253862 | rs948405432 rs369187069 | T A | C T | gnomAD Exomes | p.Tyr291Cys | c.872A>G c.871T>A |
| N E | K K | 291 | E N | 0.02 | 55.112 40.936 | 0.004 | 1 | gnomad | 4 | 153253862 | rs750051282 | T | C | gnomAD Exomes gnomAD Exomes | p.Tyr291Asn p.Lys299Glu | c.8/11>A c.895A>G |
| 1 | Ĺ | 302 | I | -0.922 | 44.101 | -0.084 | 1 | gnomad | 4 | 153253829 | rs150506693 | G | T | gnomAD Exomes | p.Leu302lle | c.904C>A |
| 1 | T | 307 | | -0.413 | 54.949 | -0.006 | 1 | gnomad | 4 | 153253813 | rs764174613 | G | A | gnomAD Exomes | p.Thr307lle | c.920C>T |
| Н | R | 309 | H | -0.992 | 59.667 | 0.003 | 1 | gnomad | 4 | 153253807 | rs760675122 | C | T | gnomAD Exomes | p.Arg309His | c.926G>A |
| <u></u> | L | 319 | | -0.533 | 49.037 | -0.066 | 1 | gnomad | 4 | 153253778 | rs1369661240 | G | T | gnomAD Genomes | p.Leu319lle | c.955C>A |
| R T | K K | 326 326 | R T | -0.425 -0.52 | 39.317 39.317 | 0.12 -0.056 | 1 | gnomad | 4 | 153253756 153253756 | rs773325030 rs773325030 | T T | C G | gnomAD Exomes gnomAD Exomes | p.Lys326Arg p.Lys326Thr | c.977A>G c.977A>C |
| <u> </u> D | E | 326 | D | -0.52 | 37.333 | 0.1 | 1 | gnomad | 4 | 153253756 | rs148769501 | † | G | gnomAD Exomes gnomAD Exomes | p.Clu327Asp | c.981A>C |
| E | G | 329 | E | -1.067 | 34.737 | 0.145 | 1 | gnomad | 4 | 153252020 | rs1358178925 | C | T | gnomAD Genomes | p.Gly329Glu | c.986G>A |
| ٧ | I | 330 | V | -1.265 | 36.875 | -0.056 | 1 | gnomad | 4 | 153252018 | rs767438108 | Т | С | gnomAD Exomes | p.lle330Val | c.988A>G |
| <u> </u> | 1 | 336 | M | -0.569 | 45.102 | 0.19 | 1 | gnomad | 4 | 153251998 | rs1046708929 | G | C | gnomAD Exomes | p.lle336Met | c.1008C>G |
| Q K | K R | 337 338 | Q K | -0.295 -0.216 | 47.538 50.737 | 0.194 0.251 | 3 | gnomad gnomad | 4 | 153251997 153251993 | rs750480880 rs1185005670 | T C | G T | gnomAD Exomes gnomAD Exomes | p.Lys337Gln p.Arg338Lys | c.1009A>C c.1013G>A |
| <u>\</u> | V | 341 | A | -0.210 | 55.273 | -0.144 | 1 | gnomad | 4 | 153251984 | rs1485389861 | A | G | gnomAD Exomes | p.Val341Ala | c.1022T>C |
| Ė | i | 342 | T | -0.67 | 57.24 | -0.602 | 2 | gnomad | 4 | 153251981 | rs765495879 | A | Ğ | gnomAD Exomes | p.lle342Thr | c.1025T>C |
| 1 | | 342 | V | -0.424 | 57.24 | 0.344 | 1 | gnomad | 4 | 153251982 | rs1247097813 | T | С | gnomAD Exomes | p.lle342Val | c.1024A>G |
| / | | 347 | V | -0.956 | 53.902 | -0.016 | 1 | gnomad | 4 | 153251967 | rs762013076 | T | С | gnomAD Exomes | p.lle347Val | c.1039A>G |
| R | H T | 359 363 | R N | -0.889 -1.29 | 35.47 31.186 | 0.035 -0.004 | 3 | gnomad | 4 | 153251930 153251918 | rs1014611334 rs1381320045 | T G | C T | gnomAD Genomes | p.His359Arg | c.1076A>G c.1088C>A |
| N S | N N | 364 | S | -1.29 | 29.412 | -0.004 | 2 | gnomad | 4 | 153251918 | rs775885576 | T | C | gnomAD Exomes gnomAD Exomes | p.Thr363Asn p.Asn364Ser | c.1088C>A c.1091A>G |
| Q | R | 367 | Q | -0.102 | 29.26 | -0.019 | 7 | gnomad | 4 | 153251906 | rs745418631 | Ċ | T | gnomAD Exomes,gnomAD Genomes | p.Arg367Gln | c.1100G>A |
| R | K | 371 | R | -0.371 | 27.686 | 0.115 | 1 | gnomad | 4 | 153251894 | rs761747465 | T | С | gnomAD Exomes | p.Lys371Arg | c.1112A>G |
| 3R | P | 373 | R | -0.297 | 23.003 | -0.033 | 1 | gnomad | 4 | 153251888 | rs748952220 | G | С | gnomAD Exomes | p.Pro373Arg | c.1118C>G |
| 4 <u>E</u> 7V | I I | 374 387 | E V | 0.473 -1.645 | 21.263 13.766 | -0.168 0.063 | 1 | gnomad | 4 | 153251886 153250901 | rs937391131 rs1338105130 | A | C C | gnomAD Exomes gnomAD Exomes | p.Lys374Glu p.Leu387Val | c.1120A>G c.1159T>G |
| <u>·</u> L | S | 407 | Ĺ | -0.153 | 23.243 | -0.1 | 1 | gnomad | 4 | 153250840 | - | G | A | gnomAD Genomes | p.Ser407Leu | c.1220C>T |
| L | V | 418 | L | -0.209 | 15.903 | -0.155 | 2 | gnomad | 4 | 153249526 | rs755422880 | С | Α | gnomAD Exomes | p.Val418Leu | c.1252G>T |
| M | V | 418 | M | -0.517 | 15.903 | -0.098 | 2 | gnomad | 4 | 153249526 | rs755422880 | C | Ţ | gnomAD Exomes | p.Val418Met | c.1252G>A |
| <u>!</u> | N I | 432 433 | l F | 0.078 -1.662 | 26.504 23.411 | -0.075 0.361 | 2 | gnomad | 4 | 153249483 153249481 | rs772668762 rs761173677 | I T | A A | gnomAD Exomes gnomAD Exomes | p.Asn432lle p.lle433Phe | c.1295A>T c.1297A>T |
| , | | 433 | V | -1.662 -1.665 | 23.411 | -0.172 | 2 | gnomad | 4 | 153249481 | rs761173677 | T | C | gnomAD Exomes gnomAD Exomes | p.lle433Pne p.lle433Val | c.1297A>I c.1297A>G |
| ' - | i | 435 | V | -1.87 | 16.772 | -0.377 | 1 | gnomad | 4 | 153249475 | rs1190126709 | Ť | C | gnomAD Exomes | p.lle435Val | c.1303A>G |
| L | V | 445 | L | -0.729 | 18.426 | -0.093 | 1 | gnomad | 4 | 153249445 | rs776371212 | С | Α | gnomAD Exomes | p.Val445Leu | c.1333G>T |
| N | T | 456 | N | -0.895 | 14.647 | -0.131 | 1 | gnomad | 4 | 153249411 | rs775244232 | G | T | gnomAD Exomes | p.Thr456Asn | c.1367C>A |
| F V | L G | 457 459 | F V | -1.16 -0.347 | 12.355 9.584 | 0.603 -0.311 | 1 1 | gnomad | 4 | 153249407 153249402 | rs1433184454 rs772056210 | T C | A A | gnomAD Exomes gnomAD Exomes | p.Leu457Phe p.Gly459Val | c.1371A>T c.1376G>T |
| <u>v</u> | R | 459 465* | C | -0.347 | 9.584 5.148 | 0.035 | 1 | gnomad | 4 | 153249402 | rs867384286 | G | A | gnomAD Exomes gnomAD Exomes | p.Giy459Vai p.Arg465Cys | c.1376G>T |
| 3 | E | 471 | G | -0.856 | 25.356 | -0.243 | 12 | gnomad | 4 | 153249366 | rs756238684 | Ť | C | gnomAD Exomes | p.Glu471Gly | c.1412A>G |
| 3 | R | 479* | G | -0.614 | 3.072 | -1.265 | 1 | gnomad | 4 | 153247367 | rs747241612 | G | C | gnomAD Exomes | p.Arg479Gly | c.1435C>G |
| | V | 485 | <u> </u> | -1.163 | 17.029 | -0.053 | 2 | gnomad | 4 | 153247349 | rs1325363774 | C | T | gnomAD Exomes | p.Val485lle | c.1453G>A |
| | | 488 | T R | -2.861 -1.47 | 20.45 17.376 | -0.025 0.073 | 1 3 | gnomad | 4 | 153247339 153247318 | rs1222797439 rs750717620 | A T | G C | gnomAD Exomes anomAD Exomes | p.lle488Thr p.His495Arg | c.1463T>C c.1484A>G |
| | l u | 40E | | -1.47 | 17.376 | -0.627 | 2 | gnomad | 4 | 153247318 | rs1334352027 | T T | C | gnomAD Exomes gnomAD Exomes | p.His495Arg p.Tyr509Cys | c.1484A>G c.1526A>G |
| ? | H Y | 495 509 | С | | | | - | | | | | | (, | | F, | |
| R C | | 495 509 515 | C I | -0.697 | 16.152 | -0.323 | 1 | gnomad | 4 | 153247259 | rs757683191 | C | T | gnomAD Exomes | p.Val515lle | c.1543G>A |
| R C I | Y V T | 509 515 532 | Ī | -0.697 -0.371 | 20.341 | -0.005 | 1 | gnomad | 4 | 153247259 153247207 | rs757683191 rs1179476070 | C G | T A | gnomAD Exomes | p.Thr532lle | c.1595C>T |
| R C I | Y V T T | 509 515 532 541 | I I S | -0.697 -0.371 -0.708 | 20.341 6.634 | -0.005 0.083 | 1 | gnomad gnomad | 4 4 4 | 153247259 153247207 153247181 | rs757683191 rs1179476070 rs1184403966 | С | T A A | gnomAD Exomes gnomAD Exomes | p.Thr532lle p.Thr541Ser | c.1595C>T c.1621A>T |
| R C I S | Y V T T | 509 515 532 541 542 | I I S S | -0.697 -0.371 -0.708 -1.271 | 20.341 6.634 3.775 | -0.005 0.083 -0.02 | 1 1 | gnomad gnomad gnomad | 4 4 4 4 | 153247259 153247207 153247181 153247177 | rs757683191 rs1179476070 rs1184403966 rs1462861861 | C G T T | T A A C | gnomAD Exomes gnomAD Exomes gnomAD Exomes | p.Thr532lle p.Thr541Ser p.Asn542Ser | c.1595C>T c.1621A>T c.1625A>G |
| | Y V T T | 509 515 532 541 | I I S | -0.697 -0.371 -0.708 | 20.341 6.634 | -0.005 0.083 | 1 | gnomad gnomad | 4 4 4 | 153247259 153247207 153247181 | rs757683191 rs1179476070 rs1184403966 | C G | T A A | gnomAD Exomes gnomAD Exomes | p.Thr532lle p.Thr541Ser | c.1595C>T c.1621A>T |
| R C I S | Y V T T N R | 509 515 532 541 542 564 | I I S S C | -0.697 -0.371 -0.708 -1.271 -1.983 | 20.341 6.634 3.775 15.026 | -0.005 0.083 -0.02 -0.448 | 1 1 1 1 | gnomad gnomad gnomad gnomad | 4 4 4 4 4 | 153247259 153247207 153247181 153247177 153245501 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 | C G T T G | T A A C A | gnomAD Exomes gnomAD Exomes gnomAD Exomes gnomAD Genomes | p.Thr532lle p.Thr541Ser p.Asn542Ser p.Arg564Cys | c.1595C>T c.1621A>T c.1625A>G c.1690C>T |
| 8 | Y V T T N R T M E | 509 515 532 541 542 564 576 587 588 | | -0.697 -0.371 -0.708 -1.271 -1.983 -0.072 -0.303 -1.234 | 20.341 6.634 3.775 15.026 16.356 12.55 15.447 | -0.005 0.083 -0.02 -0.448 -0.047 -0.345 0.029 | 1 1 1 1 2 1 2 | gnomad gnomad gnomad gnomad gnomad gnomad gnomad | 4 4 4 4 4 4 4 | 153247259 153247207 153247181 153247177 153245501 153245464 153245430 153245427 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 rs1429385222 | C G T T G G C | T A A C A A T A | gnomAD Exomes gnomAD Exomes gnomAD Exomes gnomAD Genomes gnomAD Exomes gnomAD Exomes gnomAD Exomes | p.Thr532lle p.Thr541Ser p.Asn542Ser p.Asn542Ser p.Arg564Cys p.Thr576Met p.Met587lle p.Glu588Asp | c.1595C>T c.1621A>T c.1625A>G c.1690C>T c.1727C>T c.1761G>A c.1764A>T |
| | Y V T T T N R T M M E E K | 509 515 532 541 542 564 576 587 588 590 | | -0.697 -0.371 -0.708 -1.271 -1.983 -0.072 -0.303 -1.234 -0.269 | 20.341 6.634 3.775 15.026 16.356 12.55 15.447 22.181 | -0.005 0.083 -0.02 -0.448 -0.047 -0.345 0.029 -0.234 | 1 1 1 1 2 1 2 1 | gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad | 4 4 4 4 4 4 4 4 4 | 153247259 153247207 153247181 153247177 153245501 153245464 153245430 153245427 153245423 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 rs1429385222 rs1269436440 rs751435265 | C G T T G G C T | T A A C A A T A C C | gnomAD Exomes gnomAD Exomes gnomAD Exomes gnomAD Genomes gnomAD Exomes gnomAD Exomes gnomAD Exomes gnomAD Exomes gnomAD Exomes | p.Thr532lle p.Thr541Ser p.Asn542Ser p.Arg564Cys p.Thr576Met p.Met587lle p.Glu588Asp p.Lys590Glu | c.1595C>T c.1621A>T c.1625A>G c.1690C>T c.1727C>T c.1761G>A c.1764A>T c.1768A>G |
| 8 | Y V T T N R T M E K K K | 509 515 532 541 542 564 576 587 588 590 590 | | -0.697 -0.371 -0.708 -1.271 -1.983 0.072 -0.303 -1.234 0.269 -0.309 | 20.341 6.634 3.775 15.026 16.356 12.55 15.447 22.181 22.181 | -0.005 0.083 -0.02 -0.448 -0.047 -0.345 0.029 -0.234 -0.109 | 1 1 1 1 1 2 1 2 1 2 | gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad | 4 4 4 4 4 4 4 4 4 | 153247259 153247207 153247181 153247177 1532455464 153245464 153245427 153245423 153245423 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 rs1429385222 rs1269436440 rs751435265 - rs1290448722 | C G T T G G T T T T | T A A C A A T A C C C C | gnomAD Exomes gnomAD Exomes gnomAD Exomes gnomAD Genomes gnomAD Exomes | p.Thr532lle p.Thr541Ser p.Asn542Ser p.Asp542Ser p.Arg564Cys p.Thr576Met p.Met587ile p.Glu588Asp p.Lys590Glu p.Lys590Arg | c.1595C>T c.1621A>T c.1625A>G c.1690C>T c.1727C>T c.1761G>A c.1764A>T c.1768A>G c.1769A>G |
| 3 | Y V T T T N R T M M E E K | 509 515 532 541 542 564 576 587 588 590 | | -0.697 -0.371 -0.708 -1.271 -1.983 -0.072 -0.303 -1.234 -0.269 | 20.341 6.634 3.775 15.026 16.356 12.55 15.447 22.181 | -0.005 0.083 -0.02 -0.448 -0.047 -0.345 0.029 -0.234 | 1 1 1 1 2 1 2 1 | gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad | 4 4 4 4 4 4 4 4 4 | 153247259 153247207 153247181 153247177 153245501 153245464 153245430 153245427 153245423 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 rs1429385222 rs1269436440 rs751435265 | C G T T G G C T | T A A C A A T A C C | gnomAD Exomes gnomAD Exomes gnomAD Exomes gnomAD Genomes gnomAD Exomes gnomAD Exomes gnomAD Exomes gnomAD Exomes gnomAD Exomes | p.Thr532lle p.Thr541Ser p.Asn542Ser p.Arg564Cys p.Thr576Met p.Met587lle p.Glu588Asp p.Lys590Glu | c.1595C>T c.1621A>T c.1625A>G c.1690C>T c.1727C>T c.1761G>A c.1764A>T c.1768A>G |
| 3 1 1 1 6 6 7 7 8 | Y V V T T T T N R T T M E K K A A | 509 515 532 541 542 564 576 587 588 590 590 599* | | -0.697 -0.371 -0.708 -1.271 -1.983 -0.072 -0.303 -1.234 -0.269 -0.309 -0.412 | 20.341 6.634 3.775 15.026 16.356 12.55 15.447 22.181 22.181 3.998 | -0.005 0.083 -0.02 -0.448 -0.047 -0.345 0.029 -0.234 -0.109 -0.372 | 1 1 1 1 2 1 2 1 1 2 1 | gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad | 4 4 4 4 4 4 4 4 4 4 4 4 | 153247259 153247207 153247181 153247177 153245501 153245464 153245427 153245427 153245422 153245422 153245395 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 rs1429385222 rs1269436440 rs751435265 - rs1290448722 rs766088325 | C G T T G G T T G | T A A A A T A C C C C C | gnomAD Exomes gnomAD Exomes gnomAD Exomes gnomAD Genomes gnomAD Exomes | p.Thr532lle p.Thr541Ser p.Asn542Ser p.Asn542Ser p.Arg564Cys p.Thr576Met p.Met587lle p.Glu588Asp p.Lys590Glu p.Lys590Arg p.Ala599Gly | c.1595C>T c.1621A>T c.1625A>G c.1690C>T c.1727C>T c.1761G>A c.1764A>T c.1768A>G c.1769A>G |
| R C I I I I I I I I I I I I I I I I I I | Y V V T T T N N R T M E K K A P P N K K | 509 515 532 541 542 564 576 587 588 590 590 590 620 633 634 | | -0.697 -0.371 -0.708 -1.271 -1.983 -1.234 -0.269 -0.309 -0.412 -0.557 -0.757 -0.757 | 20.341 6.634 3.775 15.026 16.356 12.55 15.447 22.181 22.181 3.998 16.899 23.914 27.347 | -0.005 0.083 -0.02 -0.448 -0.047 -0.345 0.029 -0.234 -0.109 -0.372 -0.062 -0.073 -0.05 | 1 1 1 1 2 1 2 1 1 2 1 1 | gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 153247259 153247207 153247181 153247187 153245501 153245464 153245430 153245423 153245423 153245423 153245429 153244299 153244259 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 rs1429385222 rs1269436440 rs751435265 - rs1290448722 rs766088325 rs1375643251 rs758163453 rs1199177582 | C G T T G G C T T T G G | T A A G C C C C C C C C C C C C C C C C C | gnomAD Exomes gnomAD Exomes gnomAD Exomes gnomAD Exomes gnomAD Genomes gnomAD Exomes | p.Thr532lle p.Thr541Ser p.Asn542Ser p.Asn542Ser p.Arg564Cys p.Thr576Met p.Met587lle p.Glu588Asp p.Lys590Glu p.Lys590Glu p.Lys590Arg p.Ala599Gly p.Pro620Ser p.Asn633Ser p.Lys634Arg | c.1595C>T c.1621A>T c.1625A>G c.1690C>T c.1727C>T c.1761G>A c.1764A>T c.1768A>G c.1796C>G c.1796C>G c.1858C>T c.1858C>T |
| R C S S C M I I D E R G S S R | Y V V T T T N N R T T M M E K K A P P N K K K K K K K K K K K K K K K K K | 509 515 532 541 542 564 576 587 588 590 590 620 633 634 652 | | -0.697 -0.371 -0.708 -1.271 -1.983 -0.072 -0.303 -1.234 -0.269 -0.309 -0.412 -0.557 -0.757 -0.026 -0.136 | 20.341 6.634 3.775 15.026 16.356 12.55 15.447 22.181 22.181 23.998 16.899 23.914 27.347 26.65 | -0.005 0.083 -0.02 -0.448 -0.047 -0.345 0.029 -0.234 -0.109 -0.372 -0.062 -0.073 -0.05 0.13 | 1 1 1 1 2 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 | gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 153247259 153247207 153247181 153247187 153247187 153245501 153245501 153245430 153245427 153245423 153245425 153245295 153244259 153244256 153244256 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 rs1429385225 rs1269436440 rs751435265 - rs1290448722 rs766088325 rs1375643251 rs758163453 rs1199177582 rs1182453513 | C G T T T T G G G G T T T T T T T T T T | T A A C A A T A C C C C A A C C C G G | gnomAD Exomes | p.Thr532lle p.Thr541Ser p.Asn542Ser p.Asn542Ser p.Arg564Cys p.Thr576Met p.Met587lle p.Glu588Asp p.Lys59OGlu p.Lys59OGlu p.Lys59Odrg p.Ala599Gly p.Pro62OSer p.Asn633Ser p.Lys652Gln | c.1595C>T c.1621A>T c.1625A>G c.1690C>T c.1727C>T c.1761G>A c.1764A>T c.1768A>G c.1769A>G c.1769A>G c.1788A>G c.1858C>T c.1858C>T c.1898A>G |
| R C III II S S S C III II I S S S C II I I I | Y V T T T T N R R T M M K K K K K K K K K K K K K K K K K | 509 515 532 541 542 564 576 587 588 590 590 590 620 633 634 652 653 | | -0.697 -0.371 -0.708 -1.271 -1.983 -0.072 -0.303 -1.234 -0.269 -0.309 -0.412 -0.557 -0.757 -0.757 -0.266 -0.363 | 20.341 6.634 3.775 15.026 16.356 12.55 15.447 22.181 22.181 22.181 22.398 16.899 23.914 27.347 26.65 24.831 | -0.005 0.083 -0.02 -0.448 -0.047 -0.345 0.029 -0.234 -0.109 -0.372 -0.062 -0.073 -0.05 0.13 | 1 1 1 1 2 1 2 1 1 1 1 1 1 3 1 1 | gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 153247259 153247207 153247181 153247187 153245501 153245464 153245427 153245423 153245425 153245425 153244259 153244259 153244259 153244259 153244259 153244259 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 rs1429385222 rs1269436440 rs751435265 - rs1290448722 rs766088325 rs13975643251 rs758163453 rs1199177582 rs1182453513 rs775781675 | C G T T T G G T T T G G T T T T G G T T T T G G T T T T T G G T T T T T G G G T T T T T G G G T T T T T G G G T T T T T G G G T T T T T G G G T T T T T G G G T T T T T T G G G T T T T T T G G G T | T A A C A A T T A C C C C C C C C C C C | gnomAD Exomes | p.Thr532lle p.Thr541Ser p.Asn542Ser p.Asn542Ser p.Arq564Cys p.Thr576Met p.Met587ile p.Glu588Asp p.Lys590Glu p.Lys590Arg p.Ala599Gly p.Pro620Ser p.Asn633Ser p.Lys634Arg p.Lys636Alrg p.Lys636Alrg | c.1595C>T c.1621A>T c.1625A>G c.1690C>T c.1727C>T c.1761G>A c.1764A>T c.1768A>G c.1769A>G c.1769C>G c.1858C>T c.1898A>G c.1901A>G |
| R C I I I S S S C M I I D E R G S S R | Y V V T T T N N R T T M M E K K A A P N K K K T T T T T T T T T T T T T T T T | 509 515 532 541 542 564 576 587 588 590 590 599* 620 633 634 652 653 653 | | -0.697 -0.371 -0.708 -1.271 -1.983 -1.234 -0.269 -0.309 -0.412 -0.557 -0.757 -0.757 -0.266 -0.363 -0.363 -0.363 -0.363 | 20.341 6.634 3.775 15.026 16.356 12.55 15.447 22.181 22.181 3.998 16.899 23.914 27.347 26.65 24.831 24.831 | -0.005 0.083 -0.02 -0.448 -0.047 -0.345 0.029 -0.234 -0.109 -0.372 -0.062 -0.073 -0.05 0.13 -0.116 0.066 | 1 1 1 1 2 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 | gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 153247259 153247207 153247181 153247177 153245501 153245460 153245430 153245427 153245422 153245422 153244259 153244259 153244259 15324429 15324429 15324429 15324429 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 rs1429385222 rs1269436440 rs751435265 - rs1290448722 rs766088325 rs1375643251 rs758163453 rs1199177582 rs1182453513 rs775781675 | C G T T T G G G T T T G G G G G G G G G | T A A G G A T A G G G G G G G G A A A T A G G G G | gnomAD Exomes | p.Thr532lle p.Thr541Ser p.Asn542Ser p.Asn542Ser p.Arg564Cys p.Thr576Met p.Met587lle p.Glu588Asp p.Lys590Glu p.Lys590Glu p.Lys590Gly p.Pro620Ser p.Asn633Ser p.Lys634Arg p.Lys652Gln p.Thr653Lys p.Thr653Lys | c.1595C>T c.1621A>T c.1625A>G c.1690C>T c.1727C>T c.1761G>A c.1764A>T c.1768A>G c.1796C>G c.1796C>G c.1858C>T c.189A>G c.1901A>G |
| R C S S S C M M D E R G G S S S R Q K M Y | Y V T T T T N R R T M M K K K K K K K K K K K K K K K K K | 509 515 532 541 542 564 576 587 588 590 590 590 620 633 634 652 653 | | -0.697 -0.371 -0.708 -1.271 -1.983 -0.072 -0.303 -1.234 -0.269 -0.309 -0.412 -0.557 -0.757 -0.757 -0.266 -0.363 | 20.341 6.634 3.775 15.026 16.356 12.55 15.447 22.181 22.181 22.181 22.398 16.899 23.914 27.347 26.65 24.831 | -0.005 0.083 -0.02 -0.448 -0.047 -0.345 0.029 -0.234 -0.109 -0.372 -0.062 -0.073 -0.05 0.13 | 1 1 1 1 2 1 2 1 1 1 1 1 1 3 1 1 1 1 1 1 | gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 153247259 153247207 153247181 153247187 153245501 153245464 153245427 153245423 153245425 153245425 153244259 153244259 153244259 153244259 153244259 153244259 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 rs1429385222 rs1269436440 rs751435265 - rs1290448722 rs766088325 rs13975643251 rs758163453 rs1199177582 rs1182453513 rs775781675 | C G T T T G G T T T G G T T T T G G T T T T G G T T T T T G G T T T T T G G G T T T T T G G G T T T T T G G G T T T T T G G G T T T T T G G G T T T T T G G G T T T T T T G G G T T T T T T G G G T | T A A C A A T T A C C C C C C C C C C C | gnomAD Exomes | p.Thr532lle p.Thr541Ser p.Asn542Ser p.Asn542Ser p.Arg564Cys p.Thr576Met p.Met587lle p.Glu588Asp p.Lys590Glu p.Lys590Glu p.Lys590Arg p.Ala599Gly p.Pro620Ser p.Asn633Ser p.Lys652Gln p.Thr653Lys p.Thr653Met | c.1595C>T c.1621A>T c.1625A>G c.1690C>T c.1727C>T c.1761G>A c.1768A>G c.1769A>G c.1769A>G c.1769A>G c.1769A>G c.1769A>G c.1769C>G c.1858C>T c.1898A>G c.1991A>G |
| R C I I I I S S S C I I I I S S S C I I I I | Y V V T T T T N N R T T M M E K K A A P P N K K K T T T T T T T T T T T T T T T T | 509 515 532 541 542 564 576 587 588 590 590 590 620 633 634 652 653 653 656 658 666 | | -0.697 -0.371 -0.708 -1.271 -1.983 -1.234 -0.269 -0.309 -0.412 -0.557 -0.026 0.136 -0.363 0.115 -0.584 -0.906 -0.612 | 20.341 6.634 3.775 15.026 16.356 12.55 15.447 22.181 3.998 16.899 23.914 27.347 26.65 24.831 24.831 18.778 20.288 17.859 | -0.005 0.083 -0.02 -0.448 -0.047 -0.345 0.029 -0.234 -0.109 -0.372 -0.062 -0.073 -0.05 0.13 -0.116 0.066 -0.201 0.191 -0.022 | 1 1 1 1 2 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 | gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad gnomad | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 153247259 153247207 153247181 153247177 153245501 153245464 153245430 153245422 153245422 153245422 153245425 153244259 153244259 15324426 15324426 153244199 15324419 153244194 153244184 153244184 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 rs1429385222 rs1269436440 rs751435265 - rs1290448722 rs766088325 rs1375643251 rs758163453 rs1199177582 rs1182453513 rs775781675 rs1776237755 rs1776249 rs974902950 | C G G C T T T G G G G G A C C T T T T T T T T T T T T T T T T T | T A A C C C C C C G T A T T C C C C C C C C C C C C C C C C | gnomAD Exomes gnomAD Genomes gnomAD Exomes | p.Thr532lle p.Thr532lle p.Thr541Ser p.Asn542Ser p.Asn542Ser p.Arg564Cys p.Thr576Met p.MetS87lle p.Glu588Asp p.Lys590Glu p.Lys590Glu p.Lys590Arg p.Ala599Gly p.Pro620Ser p.Asn633Ser p.Lys634Arg p.Lys632Gln p.Thr653Lys p.Thr653Lys p.Thr653Met p.Phe656Tyr p.Arg658Gln p.Thr6658In | C.1595C>T C.1621A>T C.1625A>G C.1690C>T C.1727C>T C.1761G>A C.1764A>T C.1768A>G C.1769A>G C.1769A>G C.1769A>G C.1788A>G C.1796C>G C.1858C>T C.1898A>G C.1954A>C C.1954A>C C.1954A>C C.1958C>A C.1958C>A C.1958C>A C.1958C>A |
| 3 C C C C C C C C C C C C C C C C C C C | Y V T T T T N N R T T M M E K K A A P N K K T T T T R R T T R R R T T T R R R T T R | 509 515 532 541 542 564 576 587 588 590 590 620 633 634 652 653 656 658 666 662 665 | | -0.697 -0.371 -0.708 -1.271 -1.983 -1.234 -0.269 -0.309 -0.412 -0.557 -0.757 -0.026 -0.136 -0.363 -0.115 -0.584 -0.906 -0.612 -0.629 | 20.341 6.634 3.775 15.026 16.356 12.55 15.447 22.181 22.181 22.181 27.347 26.65 24.831 18.778 20.288 17.859 11.47 | -0.005 0.083 -0.02 -0.448 -0.047 -0.345 0.029 -0.234 -0.109 -0.372 -0.062 -0.073 -0.013 -0.116 0.066 -0.201 0.191 -0.022 -0.132 | 1 1 1 1 1 2 1 2 1 1 1 1 1 1 1 1 1 1 1 1 | gnomad | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 153247259 153247207 153247181 153247181 153245501 153245460 153245430 153245422 153245422 153245422 153244259 153244250 153244256 153244199 153244199 153244191 153244191 153244191 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 rs1429385222 rs1269436440 rs751435265 - rs1290448722 rs766088325 rs1375643251 rs758163453 rs1199177582 rs1182453513 rs775781675 rs775781675 rs775781675 rs7559610249 rs974902950 rs957874517 | C G T T T G G G A C C T T C C C C C C C C C C C C C C C | T A A C C C C C G G T T A T C C A A | gnomAD Exomes gnomAD Exomes gnomAD Exomes gnomAD Exomes gnomAD Genomes gnomAD Exomes | p.Thr532lle p.Thr541Ser p.Asn542Ser p.Asn542Ser p.Asrg564Cys p.Thr576Met p.Met587lle p.Glu588Asp p.Lys590Glu p.Lys590Glu p.Lys590Arg p.Ala599Gly p.Pr0620Ser p.Asn633Ser p.Lys652Gln p.Thr653Lys p.Thr653Met p.Pre656Tyr p.Arg658Gln p.Thr652Ala p.Ser665lle | c.1595C>T c.1621A>T c.1625A>G c.1690C>T c.1727C>T c.17761G>A c.1764A>T c.1768A>G c.1769A>G c.1796C>G c.1858C>T c.1898A>G c.1954A>C c.1954A>C c.1954A>C c.1953C>A c.1953C>A |
| R C I I I S S S C I I I I S S S C I I I I | Y V V T T T N N R T T M M E E K K A A P N K K T T T T T T T T T T T T T T T T T | 509 515 532 541 542 564 576 587 588 590 590 620 633 634 652 653 665 665 666 665 665 | | -0.697 -0.371 -0.708 -1.271 -1.983 -0.702 -0.303 -1.234 -0.269 -0.309 -0.412 -0.557 -0.757 -0.026 -0.363 -0.115 -0.584 -0.906 -0.612 -0.629 -0.0629 -0.0629 -0.0629 -0.0629 -0.0629 | 20.341 6.634 3.775 15.026 16.356 12.55 15.447 22.181 22.181 23.998 16.899 23.914 27.347 26.65 24.831 24.831 18.778 20.288 17.859 11.47 | -0.005 0.083 -0.02 -0.448 -0.047 -0.345 -0.029 -0.234 -0.109 -0.372 -0.062 -0.073 -0.016 -0.066 -0.201 0.191 -0.022 -0.132 0.097 | 1 1 1 1 2 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 | gnomad | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 153247259 153247207 153247181 1532451717 153245501 15324544 15324542 15324542 15324542 15324542 15324542 15324429 15324429 15324420 15324419 15324419 15324419 15324419 15324419 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 rs1429385222 rs1269436440 rs751435265 - rs1290448722 rs766088325 rs1395643251 rs758163453 rs1199177582 rs1176237757 rs775781675 | C G T T T G G G G G G C T T T T T G G G C T T T T | T A A C C C C C C G T A T T C C C C C C C C C C C C C C C C | gnomAD Exomes gnomAD Genomes gnomAD Genomes gnomAD Exomes | p.Thr532lle p.Thr541Ser p.Asn542Ser p.Asn542Ser p.Arg564Cys p.Thr576Met p.Met587lle p.Glu588Asp p.Lys590Glu p.Lys590Glu p.Lys590Arg p.Ala599Gly p.Pro620Ser p.Asn633Ser p.Lys652Gln p.Thr653Lys p.Thr653Lys p.Thr653Met p.Pre656Tyr p.Arg658Gln p.Thr662Ala p.Ser665lle p.Ile675Val | C.1595C>T C.1621A>T C.1625A>G C.1690C>T C.1727C>T C.1761G>A C.1764A>T C.1768A>G C.1768A>G C.1768A>G C.1768A>G C.1768A>G C.1768A>G C.1769A>G C.1768A>G C.1769A>G C.1858C>T C.1858C>A C.1954A>C C.1957SA C.1957SA C.1937A>G C.1937A>G C.1934A>G |
| T R C S S C M T D E R G S S R Q K M Y Q Q A A A A A A A A A A A A A A A A A | Y V T T T T N N R T T M M E K K K A A P N K K T T T T T T T T T T T T T T T T T | 509 515 532 541 542 564 576 587 588 590 590 620 633 634 652 653 653 656 658 666 665 675 | | -0.697 -0.371 -0.708 -1.271 -1.983 -1.234 -0.269 -0.309 -0.412 -0.557 -0.757 -0.026 -0.136 -0.136 -0.115 -0.584 -0.906 -0.612 -0.629 -0.612 -0.629 | 20.341 6.634 3.775 15.026 16.356 12.55 15.447 22.181 3.998 16.899 23.914 27.347 26.65 24.831 24.831 18.778 20.288 17.859 11.47 14.286 20.339 | -0.005 0.083 -0.02 -0.448 -0.047 -0.345 0.029 -0.234 -0.109 -0.372 -0.062 -0.073 -0.05 0.13 -0.116 0.066 -0.201 -0.022 -0.132 -0.032 | 1 1 1 1 1 2 1 2 1 1 1 1 1 1 3 3 1 1 1 1 | gnomad | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 153247259 153247207 153247181 153247181 153245501 153245464 153245430 153245427 153245422 153245422 153245425 153244259 153244259 15324426 153244199 153244199 153244194 153244163 153244163 153244163 153244163 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 rs1429385222 rs1269436440 rs751435265 - rs1290448722 rs766088325 rs1375643251 rs758163453 rs1199177582 rs1182453513 rs775781675 rs1776781675 rs176781675 rs1767874517 rs75981675 rs1446303596 rs981679859 | C G G C T T T G G G G G A C C T T T C G G G C T T T T T T T T T T | T A A C C C C C C G T T C C C C T T T T T C C T T T T | gnomAD Exomes gnomAD Genomes gnomAD Exomes | p.Thr532lle p.Thr541Ser p.Asn542Ser p.Asn542Ser p.Asn542Ser p.Arg564Cys p.Thr576Met p.MetS87lle p.Glu588Asp p.Lys590Glu p.Lys590Glu p.Lys590Glu p.Pro620Ser p.Asn633Ser p.Lys634Arg p.Lys632Gln p.Thr653Lys p.Thr653Hys p.Thr653Met p.Phe656Tyr p.Arg658Gln p.Thr662Ala p.Ser665lle p.lle675Val p.Ala677Thr | C.1595C>T C.1621A>T C.1621A>T C.1625A>G C.1690C>T C.1727C>T C.1764A>T C.1768A>G C.1764A>T C.1768A>G C.1769A>G C.1769C>G C.1858C>T C.1858C>T C.1954A>C C.1954A>C C.1958C>A C.1958C>A C.1958C>T C.1958 |
| R C C II I S S S C C M II D E R G S S R Q K M Y Q Q A A II / | Y V V T T T N N R T T M M E E K K A A P N K K T T T T T T T T T T T T T T T T T | 509 515 532 541 542 564 576 587 588 590 590 620 633 634 652 653 665 665 666 665 665 | | -0.697 -0.371 -0.708 -1.271 -1.983 -0.702 -0.303 -1.234 -0.269 -0.309 -0.412 -0.557 -0.757 -0.026 -0.363 -0.115 -0.584 -0.906 -0.612 -0.629 -0.0629 -0.0629 -0.0629 -0.0629 -0.0629 | 20.341 6.634 3.775 15.026 16.356 12.55 15.447 22.181 22.181 23.998 16.899 23.914 27.347 26.65 24.831 24.831 18.778 20.288 17.859 11.47 | -0.005 0.083 -0.02 -0.448 -0.047 -0.345 -0.029 -0.234 -0.109 -0.372 -0.062 -0.073 -0.016 -0.066 -0.201 0.191 -0.022 -0.132 0.097 | 1 1 1 1 2 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 | gnomad | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 153247259 153247207 153247181 1532451717 153245501 15324544 15324542 15324542 15324542 15324542 15324542 15324429 15324429 15324420 15324419 15324419 15324419 15324419 15324419 | rs757683191 rs1179476070 rs1184403966 rs1462861861 rs1024060344 rs1429385222 rs1269436440 rs751435265 - rs1290448722 rs766088325 rs1395643251 rs758163453 rs1199177582 rs1176237757 rs775781675 | C G T T T G G G G G G C T T T T T G G G C T T T T | T A A C C C C C G G T T A T C C A A | gnomAD Exomes gnomAD Genomes gnomAD Genomes gnomAD Exomes | p.Thr532lle p.Thr541Ser p.Asn542Ser p.Asn542Ser p.Arg564Cys p.Thr576Met p.Met587lle p.Glu588Asp p.Lys590Glu p.Lys590Glu p.Lys590Arg p.Ala599Gly p.Pro620Ser p.Asn633Ser p.Lys652Gln p.Thr653Lys p.Thr653Lys p.Thr653Met p.Pre656Tyr p.Arg658Gln p.Thr662Ala p.Ser665lle p.Ile675Val | C.1595C>T C.1621A>T C.1622A>G C.1690C>T C.1727C>T C.1761G>A C.1764A>T C.1768A>G C.1769A>G C.1769A>G C.1769A>G C.1769A>G C.1788C>T C.1858C>T C.1858C>T C.1858C>T C.1954A>G C.1954A>C |

*residue affected in both clincal cohort and gnomAD. Mutation Cutoff Scanning Matrix (mCSM); Protein–protein interactions (PPI).