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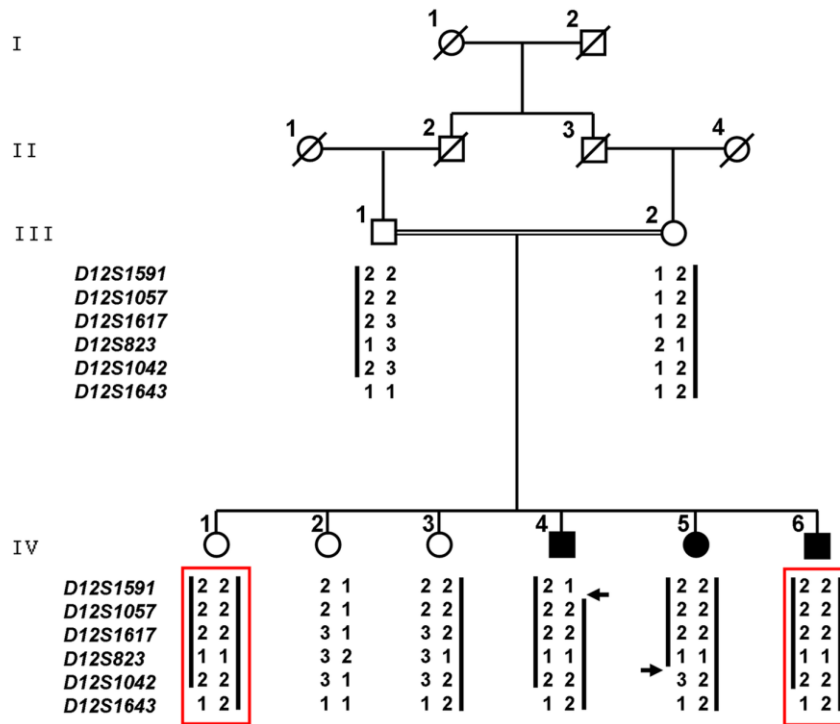
## **Supplemental Data**

### **A Mutation in *PNPT1*, Encoding**

### **Mitochondrial-RNA-Import Protein PNPase,**

### **Causes Hereditary Hearing Loss**

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**A****B**

**Figure S1. Exclusion of a Putative Locus on Chromosome 12 (A) and Overview of the Critical Region on Chromosome 2p (B)**

(A) Selected microsatellite markers covering the putative chromosome 12 locus were analysed. Haplotype reconstruction revealed that the unaffected subject IV-1 and affected subject IV-6 share identical haplotypes (red boxes). Thus, the locus was excluded as a putative candidate region.

(B) The linked region on the short arm of chromosome 2 is defined by microsatellite markers *D2S119* (telomeric) and *D2S378* (centromeric) and spans approximately 13.2 Mb. *PNPT1* is located close to the centromeric border of the linkage interval. Data was obtained from the *UCSC Genome Browser* based on Genome Reference Consortium release h37 (February 2009).

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5' -tcattggcggcgagctgtgtgcatgtgtgagagccgtgatggatga
1 atgaatgtgtgtgtatgtgagagctgaggatgatgaagagtgtgagatgatgaagatg
1 M N V C V C E R L R M M K S V R M M K M
1 atgatgaagactcgcctctgtggtggcggtgtgtggtcaggggattcagcagcac
61 M M K T R L C W A R V C A V R G I Q Q H
21 agcggcccggtcacactaggagacaggaagttggagatctccactgggaaactggccgc
121 S A T V T L G D R K L E I S T G K L A R
41 ttctctgacggctgtgagctggtcaagtcgggtgagacgtcagtgatggtgacagcggtc
181 F S D G C A V V K S G E T S V M V T A V
61 agtaagagcagaccggccgctcagttcatgccgcttgggtggattacagacagaag
241 S K S R P A A A Q F M P L V V D Y R Q K
81 gcagcagcggctggggaatccccactaacctctgagacgagagctgggaccactgac
301 A A A A G R I P T N H L R R E L G T T D
101 accgagatcctgaccagcagactcatcgatcgatccattaggccgctgttctctgctgga
361 T E I L T S R L I D R S I R P L F P A G
121 tacttctacgacacacaggtgatgtgaacatactggcgctgatggagtcaacgatcct
421 Y F Y D T Q V M C N I L A A D G V N D P
141 gacgttctggccattaatggagcgtctgcagctctgactctctctgatattccctggaac
481 D V L A I N G A S A A L T L S D I P W N
161 ggccccatcggagcgggtgctgtgggtctgctggacggggagtctctcattaaccctgcc
541 G P I G A V R V G L L D G E F L I N P S
181 cgctctgagatgaaccgcagctccctgaacctcgtgacgcgcgcgcgcgcgcgcgcgcgc
601 R S E M N R S S L N L V I A A A P S S H
201 gtggtgatgatagaggcagcagcagagaacatcctccagcaggacttctgtcacgcggtg
661 V V M I E A A A E N I L Q Q D F C H A V
221 aagctgggagtgaacacacacagcagatcatccagagcctgcagcagatcagcagagac
721 K L G V K H T Q Q I I Q S L Q Q I S R D
241 atgaagatcagcaagaggagcagcagactgtacaccgctgcagcagacatcagcagcac
781 M K I S K R S S R L Y T A A A D M Q E H
261 acacgcctgctggcgtctgacaggtctacgctgtgtttacagactcaccatgacaag
841 T R L L A S D R I Y A V F T D F T H D K
281 attctagagacagggcagatcaataagatccgtctggaggcaggagagaagatcagagag
901 I S R D E A I N K I R L E A E E K I R E
301 aagttccacatgcagagccgttcaggtgatggaggccttcaacagcgtctccaaaggag
961 K F P H A E P F E V M E A F N S V S K E
321 atctcaggaagctggtgctgcagcaggtacagcgggtgagcggcagagatctgaccgct
1021 I F R K L V L Q E Y R R C D G R D L T A
341 ctccgcaacatctcctgaggtggcgtgttcaaacgcgtgcagcggctccgcaactgttc
1081 L R N I S C E V D V F K P L H G S A L F
361 cagaggggtcaaacacaggtgctgtgtcagtgactttgactctctggagtccagtttg
1141 Q R G Q T Q V L C S V T F D S L E S S L
381 aagacagcgtgatcacctcagcgtcagtgaggatcaagacaagaactctcgtctgac
1201 K T D V I T S A L S G V K D K N F L L H
401 tatgagtttccctcactacgcaactaacagatcggcagaaccggggagccaaaccgcaga
1261 Y E F P P Y A T N E I G R T G G A N R R
421 gagctgggcccagcagcgtcagcggagaagctctgagacccgctcaccctccagtttc
1321 E L G H G A L A E K A L R P V I P S S F
441 cccttaccatccgctcacctcagcagtgctggagtctaacggctcgtctcgtgagcc
1381 P F T I R V T S V L E S N G S S S M A
461 tcagtggtggagcagctctggcactgatggagcaggtgtgcccagatctcctctcagta
1441 S V C G G S L A L M D A G V P I S S P V
481 gcggagtgggccatcggcctgatctcagagctcatcctgacagcggcgtcggagatcgag
1501 A G V A I G L I S E A H P D R P S E I E
501 agctaccgctgctgacggacatcctgggaatagaggactacaatggagacatggacttc
1561 S Y R L L T D I L G I E D Y N G D M D F
521 aagatggcgggcagcagcaaggcatcactgctctgcagcggatgtcaagataccagga
1621 K M A G S S K G I T A L Q A D V K I P G
541 ctctcctcgaagatcgtgatggagccatacagcagggccacagtgcccaagcagagagatt
1681 L P L K I V M E A I Q Q A T V A K R E I
561 ctgggcatcatgggtcagtgcatctccgacccggagttccaggaagggagaaaggccct
1741 L G I M G Q C I S R P R S S R K E N G P
581 gttgtggagaacatcacagtcggcttatccagaagagcgtgttcatcggccgggagggc
1801 V V E N I T V P L S R R A L F I G P G G
601 ataaactgcgcagactgcaggtcagacgggtgtgaccatcagtcaggtagacgagcag
1861 I N L R R L Q A Q T G V T I S Q V D E Q
621 acgttctcagtgctcgtccacacctgcagccatgagtgagcagcagagatcaca
1921 T F S V F A P T P A A M S E A Q E I I K
641 gacacctgcagagacgatcaggagcagcagctggagttcggcgcatttacacagccacc
1981 D T C R D D Q E Q Q L E F G A I Y T A T
661 atcactgagatcaggatgtgggtgtgatggtgaagctgtatcccaacatgagtcgggtt
2041 I T E I R D V G V M V K L Y P N M S P V
681 ctgctgcacaactcacagctggaccacaaggattcagcaccaccagcgtctcggcctg
2101 L L H N S Q L D H K R I Q H P S A L G L
701 gatgtgggtcagcagatacaggtgaagtattcggcgtgacccgacagacggcaggtg
2161 D V G Q Q I Q V K Y F G R D P T D G R M
721 aggetctccggagggtgctgctccccgacggccacgctggccaagagctcagagcag
2221 R L S R K V L L S P T A T L A K S L S E
741 agacacagcatctctggtggatcctccagccagaacccccggcagccctgagagccctgca
2281 R H S I S V G S S S Q N P A D P *
761 tgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt-3'
2341

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**Figure S2. Identification of *pnpt1* in Zebrafish by RACE-PCR and RT-PCR**

To identify the putative *PNPT1* ortholog in zebrafish, which was not yet annotated in common databases, we performed RACE-PCR (rapid amplification of cDNA ends, 5'/3' RACE 2<sup>nd</sup> generation kit, Roche, Mannheim, Germany) and RT-PCR (OneStep RT-PCR kit, Qiagen, Hilden, Germany) using RNA from zebrafish embryos 48 hours post fertilization (RNA isolation performed with TRIzol reagent, Invitrogen, Darmstadt, Germany). Obtained fragments were analysed by Sanger sequencing and assembled using Seqman software (DNASTAR, Madison, USA). The assembled cDNA sequence contains an open reading frame of 2328 bp and codes for a protein of 776 amino acids (human PNPT1: 783 amino acids). The triplet coding for the crucial glutamic acid is highlighted in red. The zebrafish *pnpt1* sequence is available under GenBank accession number JN381023.

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human      MAACRYCCSCLRLRPLSDGPFLLPRRDRALTQLQVRALWSSAGSRAVAVDLGNRKLEISS 60
zebrafish  ---MNVVCERLRMMKSVMMKMMKTRLCWARVCAVRG-IQQHSATVTLGDRKLEIST 55
          * * *** :. . : : . * : * : . . : : * ** : * * * * * :

human      GKLARFADGSAAVQSGDTAVMVTAVSKTKPSQFMPPLVVDYRQKAAAAGRIPTNYLRRE 120
zebrafish  GKLARFSDGCAVVKSGETSVMVTAVSKSRPAAQFMPPLVVDYRQKAAAAGRIPTNHLRRE 115
          * * * * * : * . * * * : * * : * : * * * * * * * * * * * * * * * * : * * * *

human      IGTSKDKEILTSRIIDRSIRPLFPAGYFYDTQVLCNLLAVDGVNEPDVLAINGASVALSLS 180
zebrafish  LGTTDTEILTSRLIDRSIRPLFPAGYFYDTQVMCNILAADGVNDPDVLAINGASAALTLS 175
          : * * : * . * * * * * : * * * * * * * * * * * * * * * * * * * * * * * * * *

human      DIPWNGPVGAVRIGIIDGEYVVPTRKEMSSSTLNLVVAGAPKSOIVMLEASAENILQQD 240
zebrafish  DIPWNGPIGAVRVGLLDGEFLINPSRSEMTRSSLNLVIAAAPSSHVVMIEAAAENILQQD 235
          * * * * * : * * * * * : * : * * * : : * * : * * : * : * * * * * : * * * * * * * * * *

human      FCHAIKVGVKYEQIIQGIQQLVKETGVTKRTPQKLFTPSPEIVKYTHKLAMERLYAVFT 300
zebrafish  FCHAVKLVKHTQIIQSLQQISRDMMKISKRS-SRLYTAADMQEHTRLASDRIYAVFT 294
          * * * * * : * * * * * : * * * * * : : * * : : * * : : * * : * * : * * : * * * * *

human      DYEHDKVSDEAVNKIRLDTTEEQLKEKFPPEADPYEIESFNVAKEVFRSIVLNEYKRC 360
zebrafish  DFTHDKISRDEAINKIRLEAEKIREKFPHAEPPFEVMEAFNSVSKEIFRKLVLQYRRC 354
          * : * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * *

human      GRDLTSLRNVSCVDMFKTLHGSALEFQRGQTQVLCVTFDSLESGIKSDQVITAINGIK 420
zebrafish  GRDLTALRNISCEVDVFKPLHGSALEFQRGQTQVLCVTFDSLESLKTDVITSALSGVK 414
          * * * * * : * * * * * : * * * * * * * * * * * * * * * * * * * * * * * * * *

human      KNFMLHYEFPYPATNEIGKVTGLNRRELGHGALAEKALYPVIPRDFPFTIRVTSVLES 480
zebrafish  KNFLHYEFPYPATNEIGRTGGANRRELGHGALAEKALRPVIPSFPFTIRVTSVLES 474
          * * * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

human      GSSSMASACGSLALMDSGVPISSAVAGVAIGLVTKTDPEK-GEIEDYRLLTDILGIEDY 539
zebrafish  GSSSMASVCGSLALMDAGVPISSPVAGVAIGLISEAHPDRPSEIESYRLLTDILGIEDY 534
          * * * * * . * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

human      NGDMDFKIAGTNKGITALQADIKLPGIPIKIVMEAIQQASVAKKEILQIMNKTISKPRAS 599
zebrafish  NGDMDFKMAGSSKGITALQADV KIPGLPLKIVMEAIQHATVAKREILGIMGQCISRPRS 594
          * * * * * : * * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

human      RKENGPVVEVTVQVPLSKRAKRVGPGGYNLKKLQAETGVTISQVDEETFSVFAPTPSAMHE 659
zebrafish  RNENGPVVENITVPLSRRALFIGPGGINLRRLQAQTGVTISQVDEQTFVVFAPTPAAMSE 654
          * : * * * * * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

human      ARDFITEICKDDQEQLEFGAVYTATITEIRDTGVMVKLYPNMTAVLLHNTQLDQRKIKH 719
zebrafish  AQEIIKDTCRDDQEQLEFGAIYTATITEIRDVGMVKLYPNMSPVLLHNSQLDHKRIQH 714
          * : : * * : * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

human      PTALGLEVGQEIQVKYFGRDPADGRMRLSRKVLQSPATTVVRTLNDRSSIVMGEPISQSS 779
zebrafish  PSALGLYVGGQIQVKYFGRDPTDGKMLSRKVLVLSPTATLAKSLSERHSISVGGSS----- 769
          * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

human      SNSQ 783
zebrafish  ----

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**Figure S3. Alignment of Human and Zebrafish PNPase**

The alignment illustrates the high conservation of PNPase amino acid sequence between human and zebrafish. In zebrafish PNPase, the critical glutamic acid (highlighted in red) is conserved and found at position 469 as compared to position 475 in human PNPase. \* indicates fully conserved amino acids, : indicates conservation between residues with strongly similar properties, and . indicates conservation between residues with weakly similar properties.



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Human      1  MAA.....CRYCCSCLRLRPLSDGPFLLPRDRALTLQVLRALWSSAGSRAVAVD...LGNRKLETSSGKLARLAFDGSAVVQSGDTAVMVTA.VSKTKPSPSQEMPLVVDYRKA
Drosophila 1  MAMIFTRKSLKLLNRYLKLCLSLSPGGR.....RGIQSSNGEAPSVEVNFNSNGRNMTFSSGRLARFANGTAVCQMGDTAVMVTA.VAKAKPNPQCEMPLVVDYRKN
M.tuberculosis 1  MSA.....AEIDEGVFETTATIDNGSFGTRTIREFTGRLALQAA GAVVAYLDDNMLLSATTASKNPKHFDFPLTVDVEERM
B.subtilis 1  MGQ.....EKHVFTID...WAGRTLLIVETGQLAKQANGAVMTRYGDTAVLSTA.TASKEPKK.LDFFPLTVNYEERL
E.coli     1  MLN.....PIVRKFO...YGOHTVTLLETGMMARQAATAAVMVSMDDTAVFVTV.VCQKRAKPGQDFPLTVNYQERT

Human      107 AAGRIPTNYIRREIGTSDKEILLRSLIDRSIRPLEPAGFYDITOVLCNLLAVDGVNEPDVLAINGASVALSLSDIPWNGPVGAVRIGIIDGEVNVNPTRKESSSTLNLVVAG.....
Drosophila 104 AASGRIPMNFMRRELGPSEKEILSARLIDRSIRPLEHFKDRTETQOLVCNMLAMPVHSPDVLAINAASMAISLSDIPWNGPIGAVRVGLDGEVLIINPTRELOTQSOLDLVVSA.....
M.tuberculosis 80 YAAGRIPGSEFRREGRPSDDAILLQRLIDRPLRPSFVDGIRNETQIVVTTLSLDPGDLVDVLAINAASASTQLGGLPFGPIGAVRVALIDGTVVGGPPTVDQTERAVFDMVVAGRIVEGD
B.subtilis 68 YAVGKIPGSEFKREGRPSEKAVLASRLIDRPIRPLEADGERNEQVISIVMSVQNCSSSEMAAMFGSSIALSVSDIPFEGPIAGVTVGRTDDQFLINPTVDQLEKSDINLVVAG.....
E.coli     68 YAAGRIPGSEFRREGRPSEKETLIRLIDRPIRPLEPEGEVNEVQVIATVVSVPQVNPDIIVAMIGASAAISLSCIPFNGPIGAAAVRVYINDQVVLNPTQDELKESKLDLVVAG.....

Human      221 .....APKSOIVMLEASAENLQQDFCHAIKVGKVKYTOOIIQGIQOLVKETGVTKRTPQKLETP...SPEIVKYVTHKLAMERLYAVFTDYEHDKVSRDFAVNKIRLDTDEEQKPK
Drosophila 218 .....TKQNLVVMLECKGNVYLQQDLKAIKQGTREAOFTIHEIERLQKANGROKREVEVAAEV...DPELGKAVRSMCEMRLREIEQDSTHDKMSRDNAVNEVRSNVTDKVVSS
M.tuberculosis 200 VAIMMVEAETENVVELVEGGAQAPTESVVAAGLEAAKPFIAAICTAQOELADAAKSGSKPT.VDFPVPFDYGEDVYYSVSSVATDELAALALT..IGGKAERDQRIDEIKTQVVRQADT
B.subtilis 182 .....TKDAINMVEAGADEVEEINLEAMFGHEEIKRIIAFOEELVAAVGKESSEIKLEELI...DEELNEVKALAEEDLLKAIQ..VHEKHAREDAINEVKNVAVAKFEDE
E.coli     182 .....TEAAVLMVSEAOQLSEDOQLGAVVFGHEQQQVVIQNIINELVREAGKPRWDW.QPEPI...NEALNARVAALAEARLSDAYR..ITDKOERYAQVDVIKSETIATLLAE

Human      328 FPEADP.YEIIIESFNVAKEVFRSIVLNEYKRCOGRDLTSLRNVSCEVDVFKTIHGSALFQRGTOVLCTVTFDSLESCKISDOVITAIN.GIKDKNFMHHEFPPPYATNEIKAVTGLNR
Drosophila 325 FPDTEP.SLITEQFNQTSRTIFRELIIFERGLRCDGRDYDQLRNI SCQVDYKPLHGSALFQRGTOVQVETVSLDSQESAMKLDLSAALDSGGLKAKNFMHHEFPPPYATGEVGRIGPVGR
M.tuberculosis 317 YEGRE..KEVGAAIRALTKKIVRORILTDHFRIDGRGITLIRALSAEVAVVPRAHGSALFERGETOILGVTTLLDMIKMAQQIDSIG....PESKRFMHHEYFPPFSTGETGRVGSKRR
B.subtilis 285 EHDDETIKQVKQILSKIVKNEVRRLITEKVRPDRGRGVDQIRPLSSEVGLLPRHGSGLFTRGTOCALSVCTLGAIGDVOILDGLG....VEBSKRFMHHEYFPPFQESVGETGEMRGRGR
E.coli     285 DETTDE.NELGEILHAIEKNVVRSRVLAGEPRIDGREKDMIRGLDVRTGVLPRTHGSALFTRGTOCALVYATLGTARDAQVLDLDM....CERTDTFLHHEYFPPYSVGETGMVGSKRR

Human      446 RELHGICALAEKALYVPVIP..RDFPPTIRVISEVLESNGSSSMASACGGSLALMDSGVPISSAVAGVAIGLVTK.TDPEKGEI....EDYRILLTDILGEDYNGDMDFKLAGTKGITAL
Drosophila 444 REMHGICALAERSLLEPLP..NDYPTVRLISEVLESNGSSSMASVCGGSLALMDAGVPISSAVAGVAIGLVTKFENDDTKHL....QDYRILLTDILGEDYNGDMDFKLAGTKGITAL
M.tuberculosis 430 REIHGICALAERALVPVLPVVEFPYAIRQVSEALCSNGSISMGSVCASLALLNAGVPIKAPVAGIAMGLVSD.DIQVEGAVDGVVERREVTLLTDILGAEADFGDMDFKVAGTADFVTAL
B.subtilis 400 REIHGICALGERALEPVIPSEKDFPYTVRIVSEVLESNGSISQASICASLALMDAGVPIKAPVAGIAMGLVKS.G.....EHYTVLTDIQGMEDALGDMDFKVAGTEKGVITAL
E.coli     399 REIHGRRLAKRGVLAVMPDMDKFPYTVRIVSEITEVLESNGSSSMASVCGGSLALMDAGVPIKAPVAGIAMGLVKE.G.....DNYVVLSDIILGEDHLDGDMDFVAGSERDGISAL

Human      558 QADIKLPGIPIKIVMEAIQOASVAKKEILLQIMNKTIISKPRASRKENCPVVEVTVQVPLSKRAKFGVGGYLNKKIQAETGVTTISQVDEEITFSVFAPTPSMHEARDFITTEICKDDQEQ..
Drosophila 557 QADIKLPGIPIKIVMEAIQOASVAKKEILLQIMNKTIISKPRASRKENCPVVEVTVQVPLSKRAKFGVGGYLNKKIQAETGVTTISQVDEEITFSVFAPTPSMHEARDFITTEICKDDQEQ..
M.tuberculosis 549 OLDIKLDGIESQVLAGALQAKDARLITILEVMBAIDRPLDEMSBYAPRVITIKVVPDKI GEVIGPKGVINAIIEETCAQTSIEDDGTVEVGCATDGPQAQAIDKINAI.....ANPQL
B.subtilis 507 QMDIKIEGLSREILAEALQOAKKGRMEILNSMLATLSESRKELSRYPKILMTINPDKIRDVIGESGKQINKIIEETGVKIDTEODGTFISSTDESQNKAKKIIIEDL....VRE..
E.coli     506 QMDIKIEGITKEILQVALNOAKGARLHILCVMEQAINAPRGDISSEFAPRLHTIKLNPKIKKDVIGKGGSVIRALTEETCTTIEIEDDGTVEVGCATDGEKAKHAIIRRIEETI....TAE..

Human      676 IEFCAVYTAITTEIRDTGVMVKLYNMTAVLLHNTQLDQ.RKIKHPTALGLEVGQEIQVRYFGRDPADGRMRLSRKVLQSPATTVVRTLNDRSSIVMCEPISQSSNSQ
Drosophila 675 IEFGCIYTAKITTEIRDTGVMVILYPSMPPALLHNSQLDQ.RKIAHPSALNLEVGQEIQVRYFGRDPVSGFMRLSRKVLQGPALGIPRSLNKSAG.....ESGT
M.tuberculosis 663 PTVGERELGIVVKITDFGAFVSLPGRDGLVHISKLKCKRIAKVEDVIVNVGDKLRVETIADIDK.RKISILLVA.....DEDSTAAATDAATVTS...
B.subtilis 620 VEVGQIYLGVKRIEKFGAFVEIISGKDG.LVHISELAL.ERVGKVEDVIVKIGDEILVKVTEIDK.QGRVNLRSKAV.....LREKEKEEQS.....
E.coli     619 IEVGRVYTGKVRTIVDFGAFVAIGGKKEG.LVHISQIAD.KRVKVTDY.LQMGQEVVVKVLEVDR.QGRIRLSIKEA.....TEQSQPAAPEAPAAEQGE

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**Figure S5. Multiple Species Alignment of PNPase Protein Sequences**

Multiple alignment of representative PNPase protein sequences was generated by the L-INS-I algorithm of the MAFFT package (Kotah et al., *Nucleic acids research* 30:3059-3066, 2002). Residues invariant or conservatively substituted in at least 50% of the sequences are rendered on black and grey background, respectively. The altered Glu475 residue is highlighted in red, the Arg/Lys residue that is predicted to form an inter-subunit salt bridge with Glu475 is highlighted in blue.

**Table S1. Protein-Coding Genes within the Linked Region on Chromosome 2**

Gene Name (HGNC)	Protein-Coding Exons	Position on Chromosome 2
<i>LRPPRC</i>	38	44,113,363-44,223,144
<i>PPM1B</i>	5	44,396,000-44,461,741
<i>SLC3A1</i>	10	44,502,597-44,547,959
<i>PREPL</i>	13	44,545,903-44,586,889
<i>C2orf34</i>	11	44,589,043-44,999,729
<i>SIX3</i>	2	45,169,037-45,172,390
<i>SIX2</i>	2	45,232,325-45,236,542
<i>SRBD1</i>	20	45,615,820-45,838,433
<i>PRKCE</i>	15	45,879,043-46,415,128
<i>EPAS1</i>	16	46,524,563-46,613,835
<i>ATP6V1E2</i>	1	46,738,988-46,747,096
<i>RHOQ</i>	5	46,769,867-46,811,825
<i>PIGF</i>	5	46,808,414-46,844,251
<i>CRIP1</i>	5	46,844,325-46,852,880
<i>SOCS5</i>	1	46,926,099-46,989,926
<i>MCFD2</i>	3	47,129,017-47,142,949
<i>TTC7A</i>	20	47,168,313-47,303,274
<i>CALM2</i>	6	47,387,221-47,403,740
<i>EPCAM</i>	9	47,596,287-47,614,165
<i>MSH2</i>	16	47,630,263-47,710,360
<i>KCNK12</i>	2	47,747,917-47,797,470
<i>MSH6</i>	10	48,010,221-48,034,084
<i>FBXO11</i>	23	48,039,990-48,132,814
<i>FOXN2</i>	5	48,541,795-48,606,434
<i>KLRAQ1</i>	21	48,667,908-48,742,524
<i>STON1</i>	3	48,807,763-48,826,025
<i>GTF2A1L</i>	9	48,844,948-48,960,284
<i>LHCGR</i>	11	48,913,921-48,982,880
<i>FSHR</i>	10	49,189,653-49,381,630
<i>NRXN1</i>	21	50,145,644-51,259,674
<i>ASB3</i>	9	53,897,118-54,014,079
<i>CHAC2</i>	3	53,994,929-54,002,287
<i>ERLEC1</i>	14	54,014,068-54,046,495
<i>GPR75</i>	1	54,080,050-54,087,126
<i>PSME4</i>	46	54,091,204-54,197,977
<i>ACYP2</i>	4	54,342,410-54,532,433
<i>C2orf73</i>	5	54,558,071-54,588,714
<i>SPTBN1</i>	35	54,683,454-54,898,582
<i>EML6</i>	41	54,952,149-55,199,154
<i>RTN4</i>	9	55,199,329-55,277,734
<i>C2orf63</i>	12	55,399,687-55,459,449
<i>RPS27A</i>	5	55,459,635-55,462,748
<i>MTIF2</i>	13	55,463,758-55,496,384
<i>CCDC88A</i>	31	55,514,978-55,647,057
<i>CCDC104</i>	10	55,746,740-55,772,216
<i>SMEK2</i>	15	55,775,515-55,844,796
<i>PNPT1</i>	28	55,861,198-55,921,011
<i>EFEMP1</i>	10	56,093,103-56,150,356
<i>CCDC85A</i>	6	56,411,258-56,613,308

Table lists all known protein coding *RefSeq* Genes between *D2S119* and *D2S378*. Data was taken from *UCSC Genome Browser* based on Genome Reference Consortium release h37 (February 2009). All protein coding exons and at least 50 bp of flanking sequence were analyzed. Primer sequences are available upon request.