

NAMPT and NAPRT1: novel polymorphisms and distribution of variants between normal tissues and tumor samples.

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SUPPLEMENTARY FIGURES

H.sapiens MNPAABAEFNNIILAAFSNSYKVPHYC DYEPPMSKJL-SYV- C EKKKTENSKLKVIGCIEETV EXGLOVLYINSLPK EKJWV- BKTICAEKDVLWPHQDDDPENK
 P.troglodytes MNPAABAEFNNIILAAFSNSYKVPHYC DYEPPMSKJL-SYV- C EKKKTENSKLKVIGCIEETV EXGLOVLYINSLPK EKJWV- BKTICAEKDVLWPHQDDDPENK
 M.mulatta MNAAAAAEFNNIILAAFSNSYKVPHYC DYEPPMSKJL-SYV- C EKKKTENSKLKVIGCIEETV EXGLOVLYINSLPK EKJWV- BKTICAEKDVLWPHQDDDPENK
 M.musculus MNAAAAAEFNNIILAAFSNSYKVPHYC DYEPPMSKJL-SYV- C EKKKTENSKLKVIGCIEETV EXGLOVLYINSLPK EKJWV- BKTICAEKDVLWPHQDDDPENK
 R.norvegicus MNAAAAAEFNNIILAAFSNSYKVPHYC DYEPPMSKJL-SYV- C EKKKTENSKLKVIGCIEETV EXGLOVLYINSLPK EKJWV- BKTICAEKDVLWPHQDDDPENK
 B.taurus MNAAAAAEFNNIILAAFSNSYKVPHYC DYEPPMSKJL-SYV- C EKKKTENSVKRVKGIEETV EXGLOVLYINSLPK EKJWV- BKTICAEKDVLWPHQDDDPENK
 D.rerio MEK HREAAEAEFNNIILAAFSNSYKVPHYC DYEPPMSKJL-SYV- C EKKTDSKTKRKVIGCIEETV EXGLOVLYINSLPK EKJWV- BKTICAEKDVLWPHQDDDPENK
 B.floridae MDVHLLIINPSYKVPHYC DYEPPMSKJL-SYV- C EKKTDSKTKRKVIGCIEETV EXGLOVLYINSLPK EKJWV- BKTICAEKDVLWPHQDDDPENK
 S.purpuratus MAEPPTDS CFSNLMILAFNSYKVPHYC DYEPPMSKJL-SYV- C EKEPEVVFEGIQLQHVKRQH EPLVIA BKAIAEAKPRLHQS CDRHDEA
 C.teleta MANSLES TDNLLILAFNSYKVPHYC DYEPPMSKJL-SYV- C KEPFSTIPEGIQLQHVKRQH EPLVIA BKAIAEAKPRLHQS CDRHDEA
 N.vectensis MAACLE - FENITELVLSVYKVSHQYEDC LSTV- C KEPFECVFGLOVLYIKWV- BKTICAEKSILKHLHQS SELNEUE

 H.sapiens GANVLLIE-ND GDLIEIE IKAPEPGF VLP- C PECYMLTHIE T LVO- SNEV- IVAATSPERDK I LAK YLLE- LSGNMID- EPEMK LHD FGYGRGV
 P.troglodytes GANVLLIE-ND GDLIEIE IKAPEPGF VLP- C PECYMLTHIE T LVO- SNEV- IVAATSPERDK I LAK YLLE- LSGNMID- EPEMK LHD FGYGRGV
 M.mulatta GANVLLIE-ND GDLIEIE IKAPEPGS VLP- C PECYMLTHIE T LVO- SNEV- IVAATSPERDK I LAK YLLE- LSGNMID- EPEMK LHD FGYGRGV
 M.musculus GANVLLIE-ND GDLIEIE IKAPEPGS VLP- C PECYMLTHIE T LVO- SNEV- IVAATSPERDK I LAK YLLE- LSGNMID- EPEMK LHD FGYGRGV
 R.norvegicus GANVLLIE-ND GDLIEIE IKAPEPGS VLP- C PECYMLTHIE T LVO- SNEV- IVAATSPERDK I LAK YLLE- LSGNMID- EPEMK LHD FGYGRGV
 B.taurus GANVLLIE-ND GDLIEIE IKAPEPGS VLP- C PECYMLTHIE T LVO- SNEV- IVAATSPERDK I LAK YLLE- LSGNMID- EPEMK LHD FGYGRGV
 D.rerio GANVLLIE-ND GDLIEIE IKAPEPGT VLP- C PECYMLTHIE T LVO- SNEV- IVAATSPERDK I LAK YLLE- LSGNMID- EPEMK LHD FGYGRGV
 B.floridae GANVLLIE-ND GDLIEIE IKAPEPGT VLP- C PECYMLTHIE T LVO- SNEV- IVAATSPERDK I LAK YLLE- LSGNMID- EPEMK LHD FGYGRGV
 S.purpuratus GANVLLIE-ND GDLIEIE IKAPEPGT VLP- C PECYMLTHIE T LVO- SNEV- IVAATSPERDK I LAK YLLE- LSGNMID- EPEMK LHD FGYGRGV
 C.teleta GANVLLIE-ND GDLIEIE IKAPEPGT VLP- C PECYMLTHIE T LVO- SNEV- IVAATSPERDK I LAK YLLE- LSGNMID- EPEMK LHD FGYGRGV
 N.vectensis GANVLLIE-ND GDLIEIE IKAPEPGT VLP- C PECYMLTHIE T LVO- SNEV- IVAATSPERDK I LAK YLLE- LSGNMID- EPEMK LHD FGYGRGV

 H.sapiens SOETAGIGASAHHVNP- C STDTVAAGAHLI- C JNGTKDPM- C SVAEAABESTIHA- NGEDHE- DAEFHVT- SSSV- EPLVIA DSID- LYNACER INGDGDEPHL
 P.troglodytes SOETAGIGASAHHVNP- C STDTVAAGAHLI- C JNGTKDPM- C SVAEAABESTIHA- NGEDHE- DAEFHVT- SSSV- EPLVIA DSID- LYNACER INGDGDEPHL
 M.mulatta SOETAGIGASAHHVNP- C STDTVAAGAHLI- C JNGTKDPM- C SVAEAABESTIHA- NGEDHE- DAEFHVT- SSSV- EPLVIA DSID- LYNACER INGDGDEPHL
 M.musculus SOETAGIGASAHHVNP- C STDTVAAGAHLI- C JNGTKDPM- C SVAEAABESTIHA- NGEDHE- DAEFHVT- SSSV- EPLVIA DSID- LYNACER INGDGDEPHL
 R.norvegicus SOETAGIGASAHHVNP- C STDTVAAGAHLI- C JNGTKDPM- C SVAEAABESTIHA- NGEDHE- DAEFHVT- SSSV- EPLVIA DSID- LYNACER INGDGDEPHL
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 D.rerio SOETAGIGASAHHVNP- C STDTVAAGAHLI- C JNGTKDPM- C SVAEAABESTIHA- NGEDHE- DAEFHVT- SSSV- EPLVIA DSID- LYNACER INGDGDEPHL
 B.floridae AVBAAAAGAHHVNP- C STDTVAAGAHLI- C JNGTKDPM- C SVAEAABESTIHA- NGEDHE- DAEFHVT- SPSV- EPLVIA DSID- LYNACER INGDGDEPHL
 S.purpuratus SVBAGLGAAGAHVNP- C STDTVAAGAHLI- C JNGTKDPM- C SVAEAABESTIHA- NGEDHE- DAEFHVT- SPSV- EPLVIA DSID- LYNACER INGDGDEPHL
 C.teleta SVBAGLGAAGAHVNP- C STDTVAAGAHLI- C JNGTKDPM- C SVAEAABESTIHA- NGEDHE- DAEFHVT- SPSV- EPLVIA DSID- LYNACER INGDGDEPHL
 N.vectensis SVBAGLGAAGAHVNP- C STDTVAAGAHLI- C JNGTKDPM- C SVAEAABESTIHA- NGEDHE- DAEFHVT- SPSV- EPLVIA DSID- LYNACER INGDGDEPHL

 H.sapiens VSR-STOAALIIIRPDGSNMPD TLVVKLVDI- C L3-KKK- C FPTVTE- C NSKGW- DLPYR LOG DGDW INTLIEVEGMQOKKMS IEVNSFESGSD- C ILOR- LTRDPLLNC
 P.troglodytes VSR-STOAALIIIRPDGSNMPD TLVVKLVDI- C L3-KKK- C FPTVTE- C NSKGW- DLPYR LOG DGDW INTLIEVEGMQOKKMS IEVNSFESGSD- C ILOR- LTRDPLLNC
 M.mulatta VSR-STEAALIIIRPDGSNMPD TLVVKLVDI- C L3-KKK- C FPTVTE- C NSKGW- DLPYR LOG DGDW INTLIEVEGMQOKKMS IEVNSFESGSD- C ILOR- LTRDPLLNC
 M.musculus VSR-STEAALIIIRPDGSNMPD TLVVKLVDI- C L3-KKK- C FPTVTE- C NSKGW- DLPYR LOG DGDW INTLIEVEGMQOKKMS IEVNSFESGSD- C ILOR- LTRDPLLNC
 R.norvegicus VSR-STEAALIIIRPDGSNMPD TLVVKLVDI- C L3-KKK- C FPTVTE- C NSKGW- DLPYR LOG DGDW INTLIEVEGMQOKKMS IEVNSFESGSD- C ILOR- LTRDPLLNC
 B.taurus VSR-STEAALIIIRPDGSNMPD TLVVKLVDI- C L3-KKK- C FPTVTE- C NSKGW- DLPYR LOG DGDW INTLIEVEGMQOKKMS IEVNSFESGSD- C ILOR- LTRDPLLNC
 D.rerio VSR-STEAALIIIRPDGSNMPD TLVVKLVDI- C L3-KKK- C FPTVTE- C NSKGW- DLPYR LOG DGDW INTLIEVEGMQOKKMS IEVNSFESGSD- C ILOR- LTRDPLLNC
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 C.teleta VSR-STEAALIIIRPDGSNMPD TLVVKLVDI- C L3-KKK- C FPTVTE- C NSKGW- DLPYR LOG DGDW INTLIEVEGMQOKKMS IEVNSFESGSD- C ILOR- LTRDPLLNC
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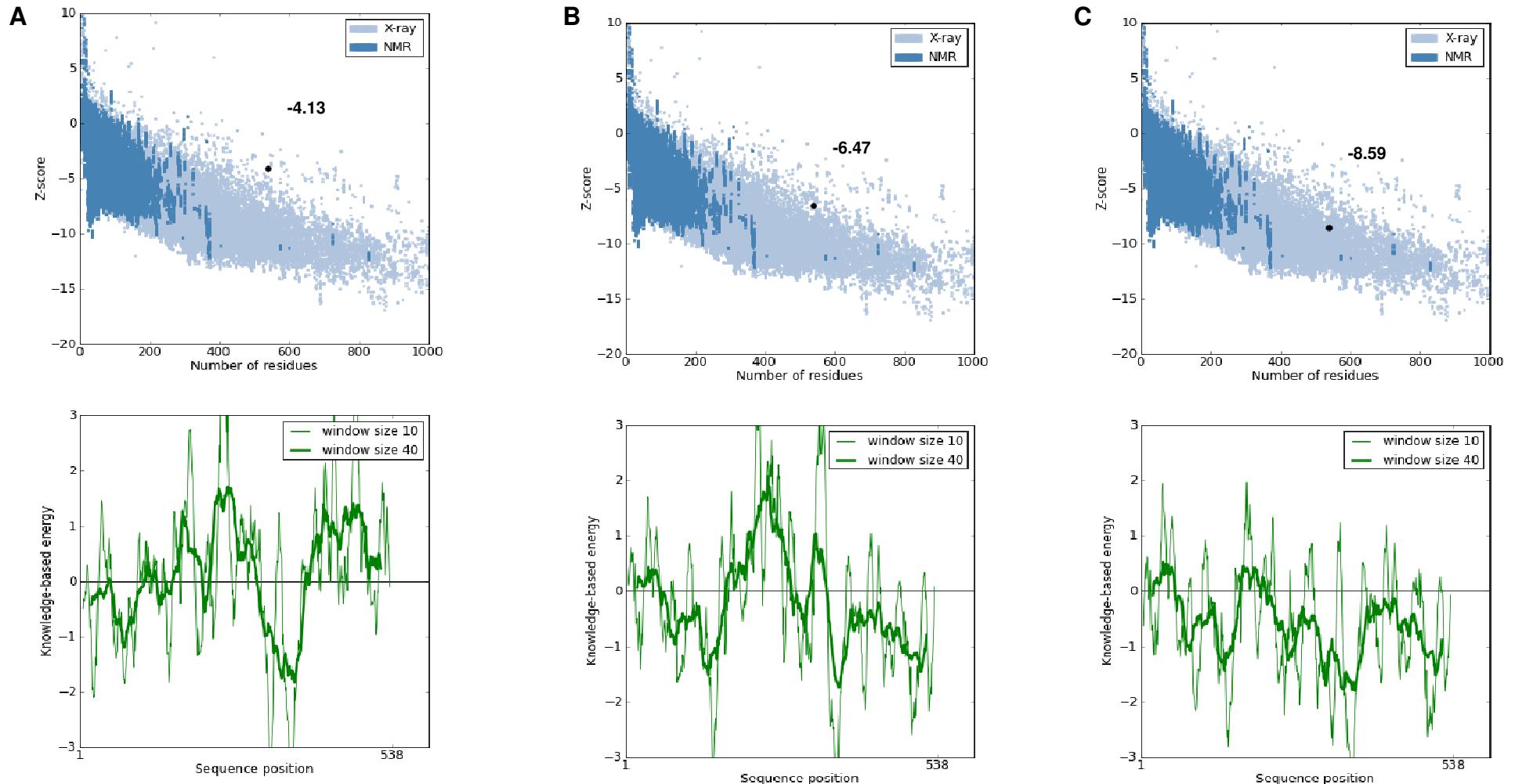
 H.sapiens FKCSYVWVINGLGIVNED- C DEVAADPNKRSKKG- C LS- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 P.troglodytes FKCSYVWVINGLGIVNED- C DEVAADPNKRSKKG- C LS- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 M.mulatta FKCSYVWVINGLGIVNED- C DEVAADPNKRSKKG- C LS- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
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 B.taurus FKCSYVWVINGLGIVNED- C DEVAADPNKRSKKG- C LS- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C MEQDVAHP
 D.rerio FKCSYVWVINGLGIVNED- C DEVAADPNKRSKKG- C LS- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 B.floridae FKCSYVWVINGLGIVNED- C DEVAADPNKRSKKG- C LS- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 S.purpuratus FKCSYVWVINGLGIVNED- C DEVAADPNKRSKKG- C LS- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 C.teleta FKCSYVWVINGLGIVNED- C DEVAADPNKRSKKG- C LS- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 N.vectensis FKCSYVWVINGLGIVNED- C DEVAADPNKRSKKG- C LS- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH

 H.sapiens YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 P.troglodytes YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 M.mulatta YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 M.musculus YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 R.norvegicus YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 B.taurus YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 D.rerio YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 B.floridae YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 S.purpuratus YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 C.teleta YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 N.vectensis YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH

 H.sapiens YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 P.troglodytes YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 M.mulatta YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 M.musculus YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 R.norvegicus YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
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 D.rerio YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
 B.floridae YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH
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 N.vectensis YKCSWVWVINGLGIVNED- C CESTDLGKSKKG- C LS- EQDV- C S- IV- C TLEEECKGDL- EPLVTE- C NGKVIKSY- SFD- EPLKNAQIN- C IELEAAHH

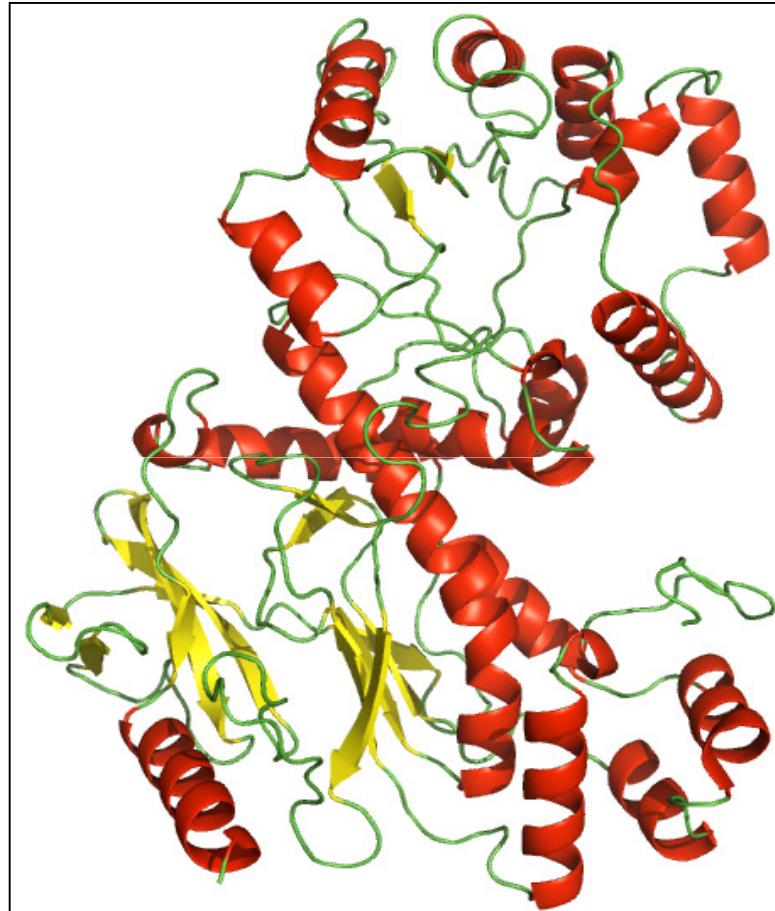
Supplementary Fig. S1. Amino acid sequences alignment of NAMPT in different species.

H.sapiens	MAAEQDP-----	EAAAAAEPEIINIIIAAANALGYNPAGRARDAAEELFFP ¹ CPFGGAFAIAAGHRDCVP ² PAF	
P.troglodytes	MAAEQDP-----	EAAAAAEPEIINIIIAAANALGYNPAGRARDAAEELFFP ¹ CPFGGAFAIAAGHRDCVP ² PAF	
M.mulatta	MAAEQDP-----	EGRAAAEPFIINIIIAAANALGYNPAGRARDAAEELFFP ¹ CPFGGAFAIAAGHRDCVP ² PAF	
M.musculus	MEMELDS-----	EGRMVPEPFIINIIIAAANALGYNPAGRACEAAEELFFP ¹ CPFGGSFALSAGHQDCMPEP ² PAF	
R.norvegicus	MEMELDD-----	QGRMVPEPFIINIIIAAANALGYNPAGRACEAAEELFFP ¹ CPFGGSFALTAGHQDCIPEP ² PAF	
B.taurus	MAAEQDP-----	EGRAAAEPFIINIIIAAANALGYNPAGRAODQAEELFFP ¹ CPFGGAFAIAAGHRDCVP ² PAF	
D.rerio	MATSNEAG-----	SVLNRPVEPIINIIIAAANALGYNPAGRNNEPAVEELFFP ¹ CPFGGAFAIAAGHRDCVP ² PAF	
B.floridae	MATPPFQGSFND-----	HISHKNNQN----GIVOSIPIINIIIAAANALGYNPAGRNNEPAVEELFFP ¹ CPFGGAFAIAAGHRDCVP ² PAF	
C.intestinalis	MSAGDANEINTSLNNSSSKSDKVAMNGPSAELRAAASYPYGLVQP-----	AYAYDNCSGEMEDDAVEELFFP ¹ NPKKGPEAIFAGCISBCLKFNNSPF	
S.purpuratus	MSWHP-----	MSPTNDSAVEP ² FFFP ¹ NPKDGETIFAGCISBCLKFNQNP	
C.teleta	MSBP-----	MSKRSIDD ² WYHAAVETN-FPDVTYTCKTNB-SQLTNNKEBAINW ¹ KPQFSY ² GNLP	
N.vectensis	MSWHP-----	VIQFPIINIIIAAANALGYNPAGRNNEPAVEELFFP ¹ NPKGGPESLFAAGCISDCLIFQNP	
S.cerevisiae	MSBP-----	VIKSLSIDD ² WYHAAVETN-FPDVTYTCKTNB-SQLTNNKEBAINW ¹ KPQFSY ² GNLP	
H.sapiens	LRDADWQJIASV-----	LDPEHFRALDCESETVRADEEGS ¹ PLQVSPLVQD ² ETLLCDV ³ MSLJA ⁴ TNAARLP ⁵ IAGPEKRL ⁶ HEMG ⁷ LRPA	
P.troglodytes	LRDADWQJIASV-----	LDPEHFRALDCESETVRADEEGS ¹ PLQVSPLVQD ² ETLLCDV ³ MSLJA ⁴ TNAARLP ⁵ IAGPEKRL ⁶ HEMG ⁷ LRPA	
M.mulatta	LRDADWQJIASV-----	LDPEHFRALDCESETVRADEEGS ¹ PLQVSPLVQD ² ETLLCDV ³ MSLJA ⁴ TNAARLP ⁵ IAGPEKRL ⁶ HEMG ⁷ LRPA	
M.musculus	LRDADWQJIASV-----	LDPEHFRALDCESETVRADEEGS ¹ PLQVSPLVQD ² ETLLCDV ³ MSLJA ⁴ TNAARLP ⁵ IAGPEKRL ⁶ HEMG ⁷ LRPA	
R.norvegicus	LRDADWQJIASV-----	LDPEHFRALDCESETVRADEEGS ¹ PLQVSPLVQD ² ETLLCDV ³ MSLJA ⁴ TNAARLP ⁵ IAGPEKRL ⁶ HEMG ⁷ LRPA	
B.taurus	LDPEHFRALDCESETVRADEEGS ¹ PLQVSPLVQD ² ETLLCDV ³ MSLJA ⁴ TNAARLP ⁵ IAGPEKRL ⁶ HEMG ⁷ LRPA	LDPEHFRALDCESETVRADEEGS ¹ PLQVSPLVQD ² ETLLCDV ³ MSLJA ⁴ TNAARLP ⁵ IAGPEKRL ⁶ HEMG ⁷ LRPA	
D.rerio	FSSEDINYYPTTIEPSVEEEFDYD ¹ GSLSDEBVSILAYEV ² WV ³ HEVLEPGP ⁴ PLAVW ⁵ ETETLLCDV ⁶ MSLJA ⁷ TNAARLP ⁸ IAGPDK ⁹ DEG ¹⁰ GLRPA	FSSEDINYYPTTIEPSVEEEFDYD ¹ GSLSDEBVSILAYEV ² WV ³ HEVLEPGP ⁴ PLAVW ⁵ ETETLLCDV ⁶ MSLJA ⁷ TNAARLP ⁸ IAGPDK ⁹ DEG ¹⁰ GLRPA	
B.floridae	FSESDINYYPTTIEPSVEEEFDYD ¹ GSLSDEBVSILAYEV ² WV ³ HEVLEPGP ⁴ PLAVW ⁵ ETETLLCDV ⁶ MSLJA ⁷ TNAARLP ⁸ IAGPDK ⁹ DEG ¹⁰ GLRPA	FSESDINYYPTTIEPSVEEEFDYD ¹ GSLSDEBVSILAYEV ² WV ³ HEVLEPGP ⁴ PLAVW ⁵ ETETLLCDV ⁶ MSLJA ⁷ TNAARLP ⁸ IAGPDK ⁹ DEG ¹⁰ GLRPA	
C.intestinalis	PSDSDIAYV-----	PSDSDIAYV ¹ TTTCA ² ASTEGE ³ REY ⁴ CTLD ⁵ CSNIIVY ⁶ IE ⁷ EGSW ⁸ W ⁹ PRM ¹⁰ HLLEG ¹¹ PL ¹² ETETLLCDV ¹³ MSLJA ¹⁴ TNAARLP ¹⁵ IAGKEV ¹⁶ DEG ¹⁷ GLRPA	PSDSDIAYV ¹ TTTCA ² ASTEGE ³ REY ⁴ CTLD ⁵ CSNIIVY ⁶ IE ⁷ EGSW ⁸ W ⁹ PRM ¹⁰ HLLEG ¹¹ PL ¹² ETETLLCDV ¹³ MSLJA ¹⁴ TNAARLP ¹⁵ IAGKEV ¹⁶ DEG ¹⁷ GLRPA
S.purpuratus	PSDSDIAYV-----	PSDSDIAYV ¹ TTTCA ² ASTEGE ³ REY ⁴ CTLD ⁵ CSNIIVY ⁶ IE ⁷ EGSW ⁸ W ⁹ PRM ¹⁰ HLLEG ¹¹ PL ¹² ETETLLCDV ¹³ MSLJA ¹⁴ TNAARLP ¹⁵ IAGKEV ¹⁶ DEG ¹⁷ GLRPA	PSDSDIAYV ¹ TTTCA ² ASTEGE ³ REY ⁴ CTLD ⁵ CSNIIVY ⁶ IE ⁷ EGSW ⁸ W ⁹ PRM ¹⁰ HLLEG ¹¹ PL ¹² ETETLLCDV ¹³ MSLJA ¹⁴ TNAARLP ¹⁵ IAGKEV ¹⁶ DEG ¹⁷ GLRPA
C.teleta	PSDSDIAYV-----	PSDSDIAYV ¹ TTTCA ² ASTEGE ³ REY ⁴ CTLD ⁵ CSNIIVY ⁶ IE ⁷ EGSW ⁸ W ⁹ PRM ¹⁰ HLLEG ¹¹ PL ¹² ETETLLCDV ¹³ MSLJA ¹⁴ TNAARLP ¹⁵ IAGKEV ¹⁶ DEG ¹⁷ GLRPA	PSDSDIAYV ¹ TTTCA ² ASTEGE ³ REY ⁴ CTLD ⁵ CSNIIVY ⁶ IE ⁷ EGSW ⁸ W ⁹ PRM ¹⁰ HLLEG ¹¹ PL ¹² ETETLLCDV ¹³ MSLJA ¹⁴ TNAARLP ¹⁵ IAGKEV ¹⁶ DEG ¹⁷ GLRPA
N.vectensis	PSDSDIAYV-----	PSDSDIAYV ¹ TTTCA ² ASTEGE ³ REY ⁴ CTLD ⁵ CSNIIVY ⁶ IE ⁷ EGSW ⁸ W ⁹ PRM ¹⁰ HLLEG ¹¹ PL ¹² ETETLLCDV ¹³ MSLJA ¹⁴ TNAARLP ¹⁵ IAGKEV ¹⁶ DEG ¹⁷ GLRPA	PSDSDIAYV ¹ TTTCA ² ASTEGE ³ REY ⁴ CTLD ⁵ CSNIIVY ⁶ IE ⁷ EGSW ⁸ W ⁹ PRM ¹⁰ HLLEG ¹¹ PL ¹² ETETLLCDV ¹³ MSLJA ¹⁴ TNAARLP ¹⁵ IAGKEV ¹⁶ DEG ¹⁷ GLRPA
S.cerevisiae	PSDSDIAYV-----	PSDSDIAYV ¹ TTTCA ² ASTEGE ³ REY ⁴ CTLD ⁵ CSNIIVY ⁶ IE ⁷ EGSW ⁸ W ⁹ PRM ¹⁰ HLLEG ¹¹ PL ¹² ETETLLCDV ¹³ MSLJA ¹⁴ TNAARLP ¹⁵ IAGKEV ¹⁶ DEG ¹⁷ GLRPA	PSDSDIAYV ¹ TTTCA ² ASTEGE ³ REY ⁴ CTLD ⁵ CSNIIVY ⁶ IE ⁷ EGSW ⁸ W ⁹ PRM ¹⁰ HLLEG ¹¹ PL ¹² ETETLLCDV ¹³ MSLJA ¹⁴ TNAARLP ¹⁵ IAGKEV ¹⁶ DEG ¹⁷ GLRPA
H.sapiens	QGPDGGLTAS ¹ TYS ² MLG ³ EDPSS ⁴ SVN ⁵ LAG ⁶ LG ⁷ PGV ⁸ AGV ⁹ T ¹⁰ PLA ¹¹ G ¹² W ¹³ Q ¹⁴ W ¹⁵ U ¹⁶ V ¹⁷ Y ¹⁸ U ¹⁹ W ²⁰ Y ²¹ Y ²² Y ²³ Y ²⁴ Y ²⁵ Y ²⁶ Y ²⁷ Y ²⁸ Y ²⁹ Y ³⁰ Y ³¹ Y ³² Y ³³ Y ³⁴ Y ³⁵ Y ³⁶ Y ³⁷ Y ³⁸ Y ³⁹ Y ⁴⁰ Y ⁴¹ Y ⁴² Y ⁴³ Y ⁴⁴ Y ⁴⁵ Y ⁴⁶ Y ⁴⁷ Y ⁴⁸ Y ⁴⁹ Y ⁵⁰ Y ⁵¹ Y ⁵² Y ⁵³ Y ⁵⁴ Y ⁵⁵ Y ⁵⁶ Y ⁵⁷ Y ⁵⁸ Y ⁵⁹ Y ⁶⁰ Y ⁶¹ Y ⁶² Y ⁶³ Y ⁶⁴ Y ⁶⁵ Y ⁶⁶ Y ⁶⁷ Y ⁶⁸ Y ⁶⁹ Y ⁷⁰ Y ⁷¹ Y ⁷² Y ⁷³ Y ⁷⁴ Y ⁷⁵ Y ⁷⁶ Y ⁷⁷ Y ⁷⁸ Y ⁷⁹ Y ⁸⁰ Y ⁸¹ Y ⁸² Y ⁸³ Y ⁸⁴ Y ⁸⁵ Y ⁸⁶ Y ⁸⁷ Y ⁸⁸ Y ⁸⁹ Y ⁹⁰ Y ⁹¹ Y ⁹² Y ⁹³ Y ⁹⁴ Y ⁹⁵ Y ⁹⁶ Y ⁹⁷ Y ⁹⁸ Y ⁹⁹ Y ¹⁰⁰ Y ¹⁰¹ Y ¹⁰² Y ¹⁰³ Y ¹⁰⁴ Y ¹⁰⁵ Y ¹⁰⁶ Y ¹⁰⁷ Y ¹⁰⁸ Y ¹⁰⁹ Y ¹¹⁰ Y ¹¹¹ Y ¹¹² Y ¹¹³ Y ¹¹⁴ Y ¹¹⁵ Y ¹¹⁶ Y ¹¹⁷ Y ¹¹⁸ Y ¹¹⁹ Y ¹²⁰ Y ¹²¹ Y ¹²² Y ¹²³ Y ¹²⁴ Y ¹²⁵ Y ¹²⁶ Y ¹²⁷ Y ¹²⁸ Y ¹²⁹ Y ¹³⁰ Y ¹³¹ Y ¹³² Y ¹³³ Y ¹³⁴ Y ¹³⁵ Y ¹³⁶ Y ¹³⁷ Y ¹³⁸ Y ¹³⁹ Y ¹⁴⁰ Y ¹⁴¹ Y ¹⁴² Y ¹⁴³ Y ¹⁴⁴ Y ¹⁴⁵ Y ¹⁴⁶ Y ¹⁴⁷ Y ¹⁴⁸ Y ¹⁴⁹ Y ¹⁵⁰ Y ¹⁵¹ Y ¹⁵² Y ¹⁵³ Y ¹⁵⁴ Y ¹⁵⁵ Y ¹⁵⁶ Y ¹⁵⁷ Y ¹⁵⁸ Y ¹⁵⁹ Y ¹⁶⁰ Y ¹⁶¹ Y ¹⁶² Y ¹⁶³ Y ¹⁶⁴ Y ¹⁶⁵ Y ¹⁶⁶ Y ¹⁶⁷ Y ¹⁶⁸ Y ¹⁶⁹ Y ¹⁷⁰ Y ¹⁷¹ Y ¹⁷² Y ¹⁷³ Y ¹⁷⁴ Y ¹⁷⁵ Y ¹⁷⁶ Y ¹⁷⁷ Y ¹⁷⁸ Y ¹⁷⁹ Y ¹⁸⁰ Y ¹⁸¹ Y ¹⁸² Y ¹⁸³ Y ¹⁸⁴ Y ¹⁸⁵ Y ¹⁸⁶ Y ¹⁸⁷ Y ¹⁸⁸ Y ¹⁸⁹ Y ¹⁹⁰ Y ¹⁹¹ Y ¹⁹² Y ¹⁹³ Y ¹⁹⁴ Y ¹⁹⁵ Y ¹⁹⁶ Y ¹⁹⁷ Y ¹⁹⁸ Y ¹⁹⁹ Y ²⁰⁰ Y ²⁰¹ Y ²⁰² Y ²⁰³ Y ²⁰⁴ Y ²⁰⁵ Y ²⁰⁶ Y ²⁰⁷ Y ²⁰⁸ Y ²⁰⁹ Y ²¹⁰ Y ²¹¹ Y ²¹² Y ²¹³ Y ²¹⁴ Y ²¹⁵ Y ²¹⁶ Y ²¹⁷ Y ²¹⁸ Y ²¹⁹ Y ²²⁰ Y ²²¹ Y ²²² Y ²²³ Y ²²⁴ Y ²²⁵ Y ²²⁶ Y ²²⁷ Y ²²⁸ Y ²²⁹ Y ²³⁰ Y ²³¹ Y ²³² Y ²³³ Y ²³⁴ Y ²³⁵ Y ²³⁶ Y ²³⁷ Y ²³⁸ Y ²³⁹ Y ²⁴⁰ Y ²⁴¹ Y ²⁴² Y ²⁴³ Y ²⁴⁴ Y ²⁴⁵ Y ²⁴⁶ Y ²⁴⁷ Y ²⁴⁸ Y ²⁴⁹ Y ²⁵⁰ Y ²⁵¹ Y ²⁵² Y ²⁵³ Y ²⁵⁴ Y ²⁵⁵ Y ²⁵⁶ Y ²⁵⁷ Y ²⁵⁸ Y ²⁵⁹ Y ²⁶⁰ Y ²⁶¹ Y ²⁶² Y ²⁶³ Y ²⁶⁴ Y ²⁶⁵ Y ²⁶⁶ Y ²⁶⁷ Y ²⁶⁸ Y ²⁶⁹ Y ²⁷⁰ Y ²⁷¹ Y ²⁷² Y ²⁷³ Y ²⁷⁴ Y ²⁷⁵ Y ²⁷⁶ Y ²⁷⁷ Y ²⁷⁸ Y ²⁷⁹ Y ²⁸⁰ Y ²⁸¹ Y ²⁸² Y ²⁸³ Y ²⁸⁴ Y ²⁸⁵ Y ²⁸⁶ Y ²⁸⁷ Y ²⁸⁸ Y ²⁸⁹ Y ²⁹⁰ Y ²⁹¹ Y ²⁹² Y ²⁹³ Y ²⁹⁴ Y ²⁹⁵ Y ²⁹⁶ Y ²⁹⁷ Y ²⁹⁸ Y ²⁹⁹ Y ³⁰⁰ Y ³⁰¹ Y ³⁰² Y ³⁰³ Y ³⁰⁴ Y ³⁰⁵ Y ³⁰⁶ Y ³⁰⁷ Y ³⁰⁸ Y ³⁰⁹ Y ³¹⁰ Y ³¹¹ Y ³¹² Y ³¹³ Y ³¹⁴ Y ³¹⁵ Y ³¹⁶ Y ³¹⁷ Y ³¹⁸ Y ³¹⁹ Y ³²⁰ Y ³²¹ Y ³²² Y ³²³ Y ³²⁴ Y ³²⁵ Y ³²⁶ Y ³²⁷ Y ³²⁸ Y ³²⁹ Y ³³⁰ Y ³³¹ Y ³³² Y ³³³ Y ³³⁴ Y ³³⁵ Y ³³⁶ Y ³³⁷ Y ³³⁸ Y ³³⁹ Y ³⁴⁰ Y ³⁴¹ Y ³⁴² Y ³⁴³ Y ³⁴⁴ Y ³⁴⁵ Y ³⁴⁶ Y ³⁴⁷ Y ³⁴⁸ Y ³⁴⁹ Y ³⁵⁰ Y ³⁵¹ Y ³⁵² Y ³⁵³ Y ³⁵⁴ Y ³⁵⁵ Y ³⁵⁶ Y ³⁵⁷ Y ³⁵⁸ Y ³⁵⁹ Y ³⁶⁰ Y ³⁶¹ Y ³⁶² Y ³⁶³ Y ³⁶⁴ Y ³⁶⁵ Y ³⁶⁶ Y ³⁶⁷ Y ³⁶⁸ Y ³⁶⁹ Y ³⁷⁰ Y ³⁷¹ Y ³⁷² Y ³⁷³ Y ³⁷⁴ Y ³⁷⁵ Y ³⁷⁶ Y ³⁷⁷ Y ³⁷⁸ Y ³⁷⁹ Y ³⁸⁰ Y ³⁸¹ Y ³⁸² Y ³⁸³ Y ³⁸⁴ Y ³⁸⁵ Y ³⁸⁶ Y ³⁸⁷ Y ³⁸⁸ Y ³⁸⁹ Y ³⁹⁰ Y ³⁹¹ Y ³⁹² Y ³⁹³ Y ³⁹⁴ Y ³⁹⁵ Y ³⁹⁶ Y ³⁹⁷ Y ³⁹⁸ Y ³⁹⁹ Y ⁴⁰⁰ Y ⁴⁰¹ Y ⁴⁰² Y ⁴⁰³ Y ⁴⁰⁴ Y ⁴⁰⁵ Y ⁴⁰⁶ Y ⁴⁰⁷ Y ⁴⁰⁸ Y ⁴⁰⁹ Y ⁴¹⁰ Y ⁴¹¹ Y ⁴¹² Y ⁴¹³ Y ⁴¹⁴ Y ⁴¹⁵ Y ⁴¹⁶ Y ⁴¹⁷ Y ⁴¹⁸ Y ⁴¹⁹ Y ⁴²⁰ Y ⁴²¹ Y ⁴²² Y ⁴²³ Y ⁴²⁴ Y ⁴²⁵ Y ⁴²⁶ Y ⁴²⁷ Y ⁴²⁸ Y ⁴²⁹ Y ⁴³⁰ Y ⁴³¹ Y ⁴³² Y ⁴³³ Y ⁴³⁴ Y ⁴³⁵ Y ⁴³⁶ Y ⁴³⁷ Y ⁴³⁸ Y ⁴³⁹ Y ⁴⁴⁰ Y ⁴⁴¹ Y ⁴⁴² Y ⁴⁴³ Y ⁴⁴⁴ Y ⁴⁴⁵ Y ⁴⁴⁶ Y ⁴⁴⁷ Y ⁴⁴⁸ Y ⁴⁴⁹ Y ⁴⁵⁰ Y ⁴⁵¹ Y ⁴⁵² Y ⁴⁵³ Y ⁴⁵⁴ Y ⁴⁵⁵ Y ⁴⁵⁶ Y ⁴⁵⁷ Y ⁴⁵⁸ Y ⁴⁵⁹ Y ⁴⁶⁰ Y ⁴⁶¹ Y ⁴⁶² Y ⁴⁶³ Y ⁴⁶⁴ Y ⁴⁶⁵ Y ⁴⁶⁶ Y ⁴⁶⁷ Y ⁴⁶⁸ Y ⁴⁶⁹ Y ⁴⁷⁰ Y ⁴⁷¹ Y ⁴⁷² Y ⁴⁷³ Y ⁴⁷⁴ Y ⁴⁷⁵ Y ⁴⁷⁶ Y ⁴⁷⁷ Y ⁴⁷⁸ Y ⁴⁷⁹ Y ⁴⁸⁰ Y ⁴⁸¹ Y ⁴⁸² Y ⁴⁸³ Y ⁴⁸⁴ Y ⁴⁸⁵ Y ⁴⁸⁶ Y ⁴⁸⁷ Y ⁴⁸⁸ Y ⁴⁸⁹ Y ⁴⁹⁰ Y ⁴⁹¹ Y ⁴⁹² Y ⁴⁹³ Y ⁴⁹⁴ Y ⁴⁹⁵ Y ⁴⁹⁶ Y ⁴⁹⁷ Y ⁴⁹⁸ Y ⁴⁹⁹ Y ⁵⁰⁰ Y ⁵⁰¹ Y ⁵⁰² Y ⁵⁰³ Y ⁵⁰⁴ Y ⁵⁰⁵ Y ⁵⁰⁶ Y ⁵⁰⁷ Y ⁵⁰⁸ Y ⁵⁰⁹ Y ⁵¹⁰ Y ⁵¹¹ Y ⁵¹² Y ⁵¹³ Y ⁵¹⁴ Y ⁵¹⁵ Y ⁵¹⁶ Y ⁵¹⁷ Y ⁵¹⁸ Y ⁵¹⁹ Y ⁵²⁰ Y ⁵²¹ Y ⁵²² Y ⁵²³ Y ⁵²⁴ Y ⁵²⁵ Y ⁵²⁶ Y ⁵²⁷ Y ⁵²⁸ Y ⁵²⁹ Y ⁵³⁰ Y ⁵³¹ Y ⁵³² Y ⁵³³ Y ⁵³⁴ Y ⁵³⁵ Y ⁵³⁶ Y ⁵³⁷ Y ⁵³⁸ Y ⁵³⁹ Y ⁵⁴⁰ Y ⁵⁴¹ Y ⁵⁴² Y ⁵⁴³ Y ⁵⁴⁴ Y ⁵⁴⁵ Y ⁵⁴⁶ Y ⁵⁴⁷ Y ⁵⁴⁸ Y ⁵⁴⁹ Y ⁵⁵⁰ Y ⁵⁵¹ Y ⁵⁵² Y ⁵⁵³ Y ⁵⁵⁴ Y ⁵⁵⁵ Y ⁵⁵⁶ Y ⁵⁵⁷ Y ⁵⁵⁸ Y ⁵⁵⁹ Y ⁵⁶⁰ Y ⁵⁶¹ Y ⁵⁶² Y ⁵⁶³ Y ⁵⁶⁴ Y ⁵⁶⁵ Y ⁵⁶⁶ Y ⁵⁶⁷ Y ⁵⁶⁸ Y ⁵⁶⁹ Y ⁵⁷⁰ Y ⁵⁷¹ Y ⁵⁷² Y ⁵⁷³ Y ⁵⁷⁴ Y ⁵⁷⁵ Y ⁵⁷⁶ Y ⁵⁷⁷ Y ⁵⁷⁸ Y ⁵⁷⁹ Y ⁵⁸⁰ Y ⁵⁸¹ Y ⁵⁸² Y ⁵⁸³ Y ⁵⁸⁴ Y ⁵⁸⁵ Y ⁵⁸⁶ Y ⁵⁸⁷ Y ⁵⁸⁸ Y ⁵⁸⁹ Y ⁵⁹⁰ Y ⁵⁹¹ Y ⁵⁹² Y ⁵⁹³ Y ⁵⁹⁴ Y ⁵⁹⁵ Y ⁵⁹⁶ Y ⁵⁹⁷ Y ⁵⁹⁸ Y ⁵⁹⁹ Y ⁶⁰⁰ Y ⁶⁰¹ Y ⁶⁰² Y ⁶⁰³ Y ⁶⁰⁴ Y ⁶⁰⁵ Y ⁶⁰⁶ Y ⁶⁰⁷ Y ⁶⁰⁸ Y ⁶⁰⁹ Y ⁶¹⁰ Y ⁶¹¹ Y ⁶¹² Y ⁶¹³ Y ⁶¹⁴ Y ⁶¹⁵ Y ⁶¹⁶ Y ⁶¹⁷ Y ⁶¹⁸ Y ⁶¹⁹ Y ⁶²⁰ Y ⁶²¹ Y ⁶²² Y ⁶²³ Y ⁶²⁴ Y ⁶²⁵ Y ⁶²⁶ Y ⁶²⁷ Y ⁶²⁸ Y ⁶²⁹ Y ⁶³⁰ Y ⁶³¹ Y ⁶³² Y ⁶³³ Y ⁶³⁴ Y ⁶³⁵ Y ⁶³⁶ Y ⁶³⁷ Y ⁶³⁸ Y ⁶³⁹ Y ⁶⁴⁰ Y ⁶⁴¹ Y ⁶⁴² Y ⁶⁴³ Y ⁶⁴⁴ Y ⁶⁴⁵ Y ⁶⁴⁶ Y ⁶⁴⁷ Y ⁶⁴⁸ Y ⁶⁴⁹ Y ⁶⁵⁰ Y ⁶⁵¹ Y ⁶⁵² Y ⁶⁵³ Y ⁶⁵⁴ Y ⁶⁵⁵ Y ⁶⁵⁶ Y ⁶⁵⁷ Y ⁶⁵⁸ Y ⁶⁵⁹ Y ⁶⁶⁰ Y ⁶⁶¹ Y ⁶⁶² Y ⁶⁶³ Y ⁶⁶⁴ Y ⁶⁶⁵ Y ⁶⁶⁶ Y ⁶⁶⁷ Y ⁶⁶⁸ Y ⁶⁶⁹ Y ⁶⁷⁰ Y ⁶⁷¹ Y ⁶⁷² Y ⁶⁷³ Y ⁶⁷⁴ Y ⁶⁷⁵ Y ⁶⁷⁶ Y ⁶⁷⁷ Y ⁶⁷⁸ Y ⁶⁷⁹ Y<		



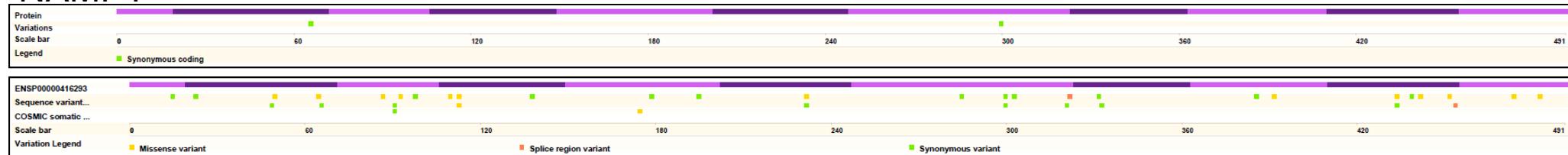
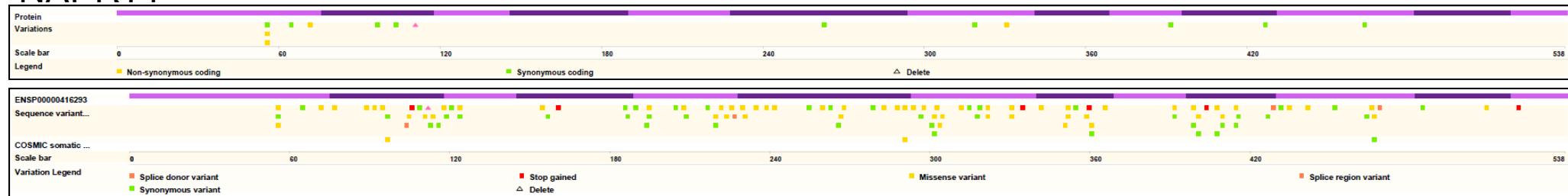
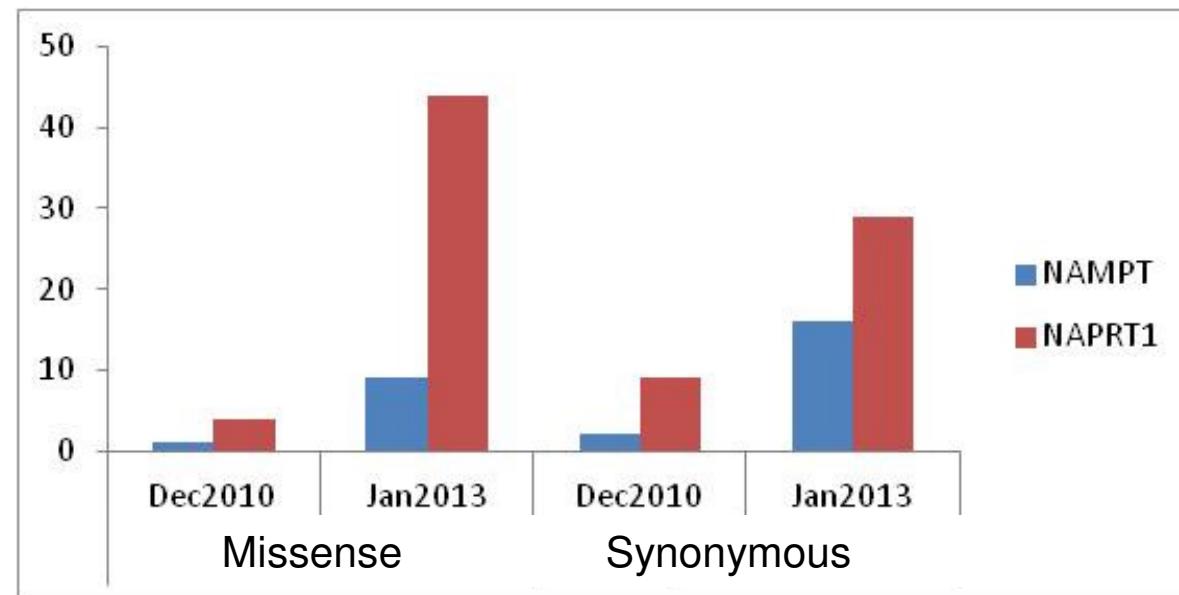
Supplementary Fig. S3. Quality evaluation of the modeled structures of the human NAPRT1 protein.

Evaluation of model quality for the predicted 3D structures of human NAPRT1, both overall (top) and locally (bottom) as estimated in ProSA-web. The models were predicted by MODELLER based on the *S. cerevisiae* Npt1 (**A**), the *E. faecalis* putative NAPRT1 protein (**B**), or predicted by I-TASSER (**C**), and the best z-score value was obtained in the latter.



Supplementary Fig. S4. Predicted tertiary structure of human NAPRT1.

The model was obtained using the I-TASSER server. α -Helices are in red, β -sheets are in yellow and loops are in green.

A**NAMPT****NAPRT1****B****Supplementary Fig. S5. NAMPT and NAPRT1 variation data retrieved from Ensembl Genome Browser.****A.** Comparison between 2010 and 2013 shows the increasing number of mutations reported for both genes.**B.** Missense and synonymous variants underline that *NAPRT1* has a higher genetic diversity than *NAMPT*.

Supplementary Tables

Supplementary Table S1. Oligonucleotide sequences used for amplification of NAMPT and NAPRT1 genes.

Gene	Location	Primer forward (5'-3')	Primer reverse (5'-3')	Annealing temperature (°C)	Product size (bp)
NAMPT	Intron 1 - Intron 2	CTTCAAGCCTTTCTGTTGTG	CTTAGAACATCAAACACACACC	60	424
	Intron 3 - Intron 4	AGCACGTGGCAGCATTAAAC	GATGAGGAAATTGAAGCCTGG	58	502
	Exon 7 - Intron 7	CATAACAGCTTGGGGAAAG	CTCTCTCTGGGCTGCAACT	58	362
	Intron 8 -Intron 9	CAGTCTTGGATGCTTCATTC	CTCCCTTCTTCCTTGTTCTG	58	402
NAPRT1	Exon 1 - Intron 1	ACCTCTACCAGGCCACCATG	GGTAACTGCCTGAGACCAG	64	310
	Intron 1 - Intron 3	CTGGTCTCAGCGCAGTTACC	CAGCCCACCTGGCGTAGC	60	425
	Exon 6 - Intron 7	CTACAGCGTGTGGAGGTGAG	CACCTGTGCTCACCTTCTGC	60	404

Supplementary Table S2. Sequences of NAMPT and NAPRT1 protein orthologues.

The table lists the species and the associated protein identifier and source used in the protein alignment.

Species	NAMPT			NAPRT1		
	ID	source	size (aa)	ID	source	size (aa)
<i>Homo sapiens</i>	NP_005737	NCBI	491	NP_660202	NCBI	538
<i>Pan troglodytes</i>	JAA31706	NCBI	491	JAA00578	NCBI	538
<i>Macaca mulatta</i>	AFI35917	NCBI	491	XP_001097478.2	NCBI	481
<i>Mus musculus</i>	NP_067499	NCBI	491	NP_766195	NCBI	538
<i>Rattus norvegicus</i>	NP_808789	NCBI	491	NP_997492	NCBI	538
<i>Bos taurus</i>	NP_001231070	NCBI	491	NP_001092327	NCBI	533
<i>Danio rerio</i>	CU928083.1	Ensembl	493	NP_957184	NCBI	548
<i>Branchiostoma floridae</i>	288618	JGI	475	278419	JGI	497
<i>Ciona intestinalis</i>	-	-	-	211042	JGI	524
<i>Strongylocentrotus purpuratus</i>	XP_782393	NCBI	480	XP_787773.3	NCBI	584
<i>Capitella teleta</i>	162451	JGI	482	175488	JGI	540
<i>Nematostella vectensis</i>	135670	JGI	476	89511	JGI	547
<i>Saccharomyces cerevisiae</i>	-	-	-	NP_014852	NCBI	429

Supplementary Table S3. Bootstrap analyses between allele frequencies of the *NAPRT1* variants obtained in our study versus allele frequencies from the 1000 Genomes Project. The method used for the construction of the bootstrap confidence intervals (95%) was the accelerated bias-correction available in MATLAB (R2011a, MathWorks, Natick, MA, USA).

		Bootstrap CI		1000Genomes		InsideCIBootstrap?
		left	right			
rs2015562	Control	0,097	0,174	EUR_AF	0,09	no
	Tumor	0,294	0,444	ASN_AF	0,36	yes
rs896953	Control	0,618	0,725	EUR_AF	0,7	yes
	Tumor	0,625	0,763	ASN_AF	0,73	yes
rs896954	Control	0,107	0,191	EUR_AF	0,19	yes
	Tumor	0,075	0,181	ASN_AF	0,11	yes
rs145565666	Control	0,000	0,017	EUR_AF	0,004	yes
	Tumor	-	-	ASN_AF	n/a	-
rs2305496	Control	0,091	0,168	EUR_AF	0,09	no
	Tumor	0,263	0,406	ASN_AF	0,38	yes
rs744650	Control	0,003	0,030	EUR_AF	0,04	no
	Tumor	-	-	ASN_AF	n/a	-
rs872935	Control	0,567	0,688	EUR_AF	0,63	yes
	Tumor	0,200	0,331	ASN_AF	0,35	no
rs35975875	Control	0,000	0,023	EUR_AF	0,01	yes
	Tumor	-	-	ASN_AF	n/a	-
rs114291348	Control	0,013	0,063	EUR_AF	0,03	yes
	Tumor	0,000	0,039	ASN_AF	n/a	-

Supplementary Table S4. Predicted impact of all dbSNP missense variants for the human *NAMPT* and *NAPRT1 genes*, according to SIFT and PolyPhen calculations. Variants were retrieved from Ensembl (release 75 - February 2014), considering the reference transcripts ENST00000222553 and ENST00000449291, respectively.

Gene	ID	Chr:bp	Alleles	Global MAF	AA	AA coord	SIFT	PolyPhen
<i>NAMPT</i>	rs202025145	7:1058915547:105891554	A/G	0.001(G)	I/T	484	tolerated	0,42
	rs140819103	7:1058915817:105891581	T/G	-	E/A	475	tolerated	0,15
	rs376047293	7:1058934707:105893470	T/C	-	Y/C	453	tolerated	0,17
	rs138426703	7:1058935007:105893500	A/G	-	L/P	443	deleterious	0,03
	rs146170636	7:1058935247:105893524	G/A	0.001(A)	T/M	435	tolerated	0,1
	rs61738828	7:1058948617:105894861	A/C	-	D/E	393	deleterious	0
	rs148806435	7:1059089557:105908955	G/A	-	T/M	233	tolerated	0,19
	rs61746104	7:1059130827:105913082	A/G	-	I/T	114	deleterious	0,01
	rs142386213	7:1059130837:105913083	T/C	-	I/V	114	tolerated	0,93
	rs370987898	7:1059130917:105913091	T/C	-	H/R	111	tolerated	0,42
	rs370874972	7:1059154297:105915429	T/C	-	D/G	94	tolerated	0,22
	rs373913615	7:1059154477:105915447	T/C	-	K/R	88	tolerated	0,51
	rs368481844	7:1059174877:105917487	G/C	-	L/V	66	deleterious	0,05
	rs139282739	7:1059175317:105917531	T/C	-	K/R	51	tolerated	0,06
<i>NAPRT1</i>	rs199590650	8:1446571828:144657182	G/A	-	R/W	510	deleterious	0
	rs368170412	8:1446573848:144657384	G/A	-	R/W	475	deleterious	0
	rs199833066	8:1446573988:144657398	A/C	-	V/G	470	deleterious	0
	rs149178575	8:1446574058:144657405	C/T	-	A/T	468	tolerated	0,28
	rs201086959	8:1446574078:144657407	G/A	-	P/L	467	deleterious	0
	rs141565399	8:1446574808:144657480	C/G	0.000 (G)	E/Q	443	deleterious	0
	rs147123886	8:1446575008:144657500	T/A	-	D/V	436	deleterious	0
	rs147154210	8:1446576378:144657637	G/A/T	-	T/M	416	deleterious	0
	rs147154210	8:1446576378:144657637	G/A/T	-	T/K	416	deleterious	0
	rs139521261	8:1446576538:144657653	C/T	0.001 (T)	D/N	411	deleterious	0
	rs144545750	8:1446576588:144657658	G/A	-	T/I	409	deleterious	0
	rs369842187	8:1446576798:144657679	C/T	-	G/D	402	tolerated	0,08
	rs148462517	8:1446576868:144657686	C/T	-	V/M	400	deleterious	0,01
	rs369189989	8:1446578038:144657803	C/T	-	G/S	393	deleterious	0,02

rs201030598	8:1446582568:144658256	C/T	0,002 (T)	A/T	367	tolerated	0,07	benign	0,07
rs200059887	8:1446582708:144658270	G/A	0,001 (A)	A/V	362	tolerated	0,38	benign	0,009
rs369217099	8:1446582778:144658277	C/T	-	E/K	360	deleterious	0	probably damaging	0,997
rs373535032	8:1446582978:144658297	A/G	-	V/A	353	tolerated	0,43	benign	0,006
rs144202509	8:1446582988:144658298	C/T	0,001 (T)	V/I	353	tolerated	0,11	benign	0,228
rs373926829	8:1446583008:144658300	A/T	-	I/N	352	deleterious	0	probably damaging	1
rs377542827	8:1446583278:144658327	T/C	-	Q/R	343	tolerated	0,45	benign	0,046
rs184059139	8:1446586298:144658629	C/T	0,001 (T)	R/H	332	deleterious	0,02	possibly damaging	0,868
rs35975875	8:1446586308:144658630	G/A	0,003 (A)	R/C	332	deleterious	0	probably damaging	0,999
rs372036233	8:1446586378:144658637	C/A	-	Q/H	329	tolerated	0,59	benign	0,013
rs201149658	8:1446586558:144658655	G/T	0,000 (T)	D/E	323	deleterious	0	probably damaging	0,995
rs188697057	8:1446586568:144658656	T/C	0,000 (C)	D/G	323	deleterious	0	probably damaging	0,996
rs374121375	8:1446586878:144658687	G/A	-	R/W	313	deleterious	0	probably damaging	0,946
rs145806784	8:1446587078:144658707	G/A	-	A/V	306	deleterious	0,04	probably damaging	0,923
rs872935	8:1446587118:144658711	G/A/C	0,449 (A)	L/V	305	deleterious	0,04	probably damaging	0,999
rs367982076	8:1446587148:144658714	C/T	-	A/T	304	tolerated	0,06	probably damaging	0,939
rs147107119	8:1446587168:144658716	A/G	-	V/A	303	deleterious	0	probably damaging	0,999
rs370157447	8:1446587288:144658728	T/G	-	N/T	299	deleterious	0	probably damaging	0,997
rs372583646	8:1446587418:144658741	T/C	-	S/G	295	deleterious	0	probably damaging	1
rs199622906	8:1446588238:144658823	C/A	-	V/L	292	deleterious	0,02	possibly damaging	0,519
rs143378632	8:1446588318:144658831	G/A	-	T/I	289	deleterious	0	possibly damaging	0,799
rs145759182	8:1446588468:144658846	T/C	-	Q/R	284	deleterious	0	benign	0,142
rs267601812	8:1446588598:144658859	G/A	-	P/S	280	deleterious	0	probably damaging	1
rs148205878	8:1446588918:144658891	C/T	-	R/Q	269	deleterious	0,01	benign	0,011
rs374205789	8:1446588958:144658895	C/T	-	E/K	268	deleterious	0	probably damaging	0,988
rs199672137	8:1446589168:144658916	C/A	0,000 (A)	V/L	261	tolerated	0,65	benign	0,001
rs373667786	8:1446589198:144658919	C/G	-	G/R	260	tolerated	0,58	benign	0,005
rs199843319	8:1446589698:144658969	G/A	-	A/V	243	tolerated	1	benign	0,004
rs150754257	8:1446589798:144658979	C/T	-	V/M	240	tolerated	0,27	benign	0,094
rs139128977	8:1446589918:144658991	C/T	-	E/K	236	tolerated	0,89	benign	0,001
rs368314681	8:1446590028:144659002	G/A	-	P/L	232	tolerated	0,24	benign	0,272
rs201161077	8:1446590058:144659005	G/A	-	A/V	231	tolerated	0,32	benign	0,017
rs200176063	8:1446592378:144659237	C/T	0,002 (T)	D/N	227	tolerated	0,33	benign	0,003

rs146015422	8:1446592428:144659242	G/A	-	P/L	225	tolerated	0,52	benign	0,043
rs373219862	8:1446592498:144659249	C/T	-	E/K	223	tolerated	0,11	possibly damaging	0,821
rs139975718	8:1446592548:144659254	C/T	-	G/D	221	tolerated	0,13	probably damaging	0,955
rs144223221	8:1446592918:144659291	C/T	-	G/R	209	deleterious	0	probably damaging	0,999
rs142312560	8:1446593308:144659330	T/G	-	N/H	196	deleterious	0	probably damaging	1
rs111826960	8:1446595418:144659541	G/A	-	R/C	156	deleterious	0	probably damaging	0,991
rs376323296	8:1446598918:144659891	A/C	-	S/A	125	tolerated	0,1	benign	0,009
rs111763816	8:1446599088:144659908	A/G	-	V/A	119	deleterious	0,01	probably damaging	0,998
rs369745388	8:1446599978:144659997	C/T	-	A/T	115	deleterious	0,01	possibly damaging	0,713
rs373884377	8:1446600068:144660006	C/T	-	G/S	112	deleterious	0	probably damaging	1
rs200364051	8:1446600248:144660024	C/T	-	V/M	106	tolerated	0,16	benign	0,153
rs186257137	8:1446600548:144660054	G/A	0.000 (A)	L/F	96	deleterious	0	probably damaging	0,973
rs201407810	8:1446600638:144660063	A/G	0.000 (G)	F/L	93	tolerated	0,06	benign	0,053
rs376515994	8:1446600728:144660072	G/T	-	P/T	90	tolerated	0,23	possibly damaging	0,811
rs200997239	8:1446601068:144660106	C/G	0.001 (G)	Q/H	78	deleterious	0,05	possibly damaging	0,62
rs11990768	8:1446602718:144660271	C/T	-	R/Q	73	tolerated	0,07	benign	0,002
rs35914195	8:1446603188:144660318-14	GG/TA	-	A/V	57	deleterious	0,01	benign	0,08
rs896950	8:1446603198:144660319	G/A	0.014 (A)	A/V	57	deleterious	0,01	benign	0,08

Supplementary Table S5. Predicted impact of the *NAMPT* and *NAPRT1* variants found in our study. Variants were retrieved from 1000 Genomes Browser and scored according to the CADD server (<http://cadd.gs.washington.edu/score>).

Gene	ID	Chr	Position	Variant type		Cscore	Splice annotation
<i>NAMPT</i>	rs41430346	7	105913155	Non-coding	-	2,069	NA
	rs375379216	7	105913141	Non-coding	-	-	-
	rs112487390	7	105912865	Non-coding	-	11,33	NA
	rs2302559	7	105903904	Silent	Ser301Ser	7,273	NA
	rs144888107	7	105903789	Non-coding	-	4,783	NA
<i>NAPRT1</i>	rs2015562	8	144660257	Non-coding	-	1,111	DONOR
	rs896953	8	144660189	Non-coding	-	0,123	NA
	rs896954	8	144660046	Silent	Ala98Ala	11,6	NA
	rs200364051	8	144660024	Missense	Val106Met	-	-
	rs145565666	8	144659998	Silent	Leu114Leu	13,01	DONOR
	rs2305496	8	144659949	Non-coding	-	4,955	NA
	-	8	144659838	Silent	Val142Val	-	-
	rs12678314	8	144659608	Non-coding	-	5,774	NA
	rs744650	8	144658730	Silent	Pro298Pro	3,054	ACCEPTOR
	rs872935	8	144658711	Silent	Leu305Leu	1,158	NA
	rs35975875	8	144658630	Missense	Arg332Cys	20,9	NA
	rs114291348	8	144658505	Non-coding	-	3,723	NA
	-	8	144658501	Non-coding	-	-	-
	rs896955	8	144658370	Non-coding	-	6,296	NA
	-	8	144657972	Non-coding	-	-	-
	rs2290417	8	144657269	Non-coding	-	14,31	ACCEPTOR
	rs77951814	8	144657152	Non-coding	-	16,73	DONOR