

c.355C>T; p.R119C

# Figure EV1. Identification of the p.R119C mutation of THPO. A Family pedigree indicating the genotype and phenotype of the family members. "+" and "-" indicate the wild-type and the mutant (c.355C>T; p.R119C) allele, respectively. Different symbols indicate the presence of severe thrombocytopenia, anemia, neutropenia, or infections, as shown in the figure.

B Electropherogram showing the homozygous c.355C>T mutation in the proband.

## Α

THPO		R119		
Hs	106	CLSSLLGQLSGQV <b>R</b> L <b>L</b> LGA <b>L</b> QS <b>L</b> L <b>G</b> T <b>Q</b>	132	
Bt	106	CLSSLLVQLSGQV <b>R</b> L <b>L</b> LGA <b>L</b> QG <b>L</b> L <b>G</b> T <b>Q</b>	132	
Oa	106	CLSSLLVQLSGQV <b>R</b> L <b>L</b> LGA <b>L</b> QG <b>L</b> L <b>G</b> T <b>Q</b>	132	
Cl	106	CLSSLLGQLSGQV <mark>R</mark> L <b>L</b> LGA <b>L</b> QG <b>L</b> L <b>G</b> T <b>Q</b>	132	
Fc	106	CLSSLLGQLSGQV <mark>R</mark> L <b>L</b> LGA <b>L</b> QG <b>L</b> L <b>G</b> T <b>Q</b>	132	
Мm	106	CLSSLLGQLSGQV <mark>R</mark> L <b>L</b> LGA <b>L</b> QG <b>L</b> L <b>G</b> T <b>Q</b>	132	
Rn	106	CLSSLLGQLSGQV <mark>R</mark> L <b>L</b> LGA <b>L</b> QG <b>L</b> L <b>G</b> T <b>Q</b>	132	



### С

EPO	R103	
Hs	90 plolhvdkavsgi <mark>r</mark> s <b>l</b> ttl <b>l</b> ra <b>l-gaq</b> 1	15
Bt	90 ALRLHVDKAVSGI <mark>r</mark> sltsllral-Gaq 1	
Oa	90 ALRLHVDKAVSGI <mark>r</mark> sltsllral-Gaq 1	
Cl	90 TPQLHVDKAVSSI <mark>r</mark> sltsl <b>l</b> ra <b>l-Gaq</b> 1	15
Fc	90 TLQLHVDKAVSSI <mark>r</mark> sltsl <b>l</b> ra <b>l-Gaq</b> 1	
Мm	90 TLQLHIDKAISGI <mark>r</mark> sltsllrvl-GaQ 1	
Rn	90 SLQLHIDKAISGI <mark>r</mark> s <b>l</b> tsl <b>l</b> rv <b>l-G</b> a <b>q</b> 1	15

D

В

#### Figure EV2. R119 is highly conserved, and the p.R119C is expected to affect THPO binding to its receptor.

- A Multiple-sequence alignment analysis of THPO orthologs from different species. *Hs, Homo sapiens* (NP\_000451.1); *Bt, Bos taurus* (NP\_001159512.1); *Oa, Ovis aries* (XP\_011984347.1); *Cl, Canis lupus familiaris* (XP\_005639837.1); *Fc, Felis catus* (NP\_001157128.1); *Mm, Mus musculus* (NP\_033405.1); *Rn, Rattus norvegicus* (NP\_112395.1). Residues in bold are conserved among both THPO and EPO orthologs. Residues in gray are not conserved within THPO or EPO.
- B Cartoon representation of the structure of the receptor binding domain of THPO (in sky blue) in complex with a neutralizing antibody fragment (in magenta) (PDB 1V7M) (Feese *et al*, 2004). The inset shows a zoom of the interaction involving R119 (in red) with the D31 of the antibody fragment (in green).
- C Multiple-sequence alignment analysis of EPO orthologs from different species. *Hs, Homo sapiens* (NP\_000790.2); *Bt, Bos taurus* (NP\_776334.1); *Oa, Ovis aries* (NP\_001019908.1); *Cl, Canis lupus familiaris* (NP\_001006647.1); *Fc, Felis catus* (NP\_001009269.1); *Mm, Mus musculus* (NP\_031968.1); *Rn, Rattus norvegicus* (NP\_058697.1). Residues in bold are conserved among both THPO and EPO orthologs. Residues in gray are not conserved within THPO or EPO.
- D Cartoon representation of the structure of the receptor binding domain of EPO (in violet) in complex with its receptor (in green) (PDB 1EER) (Syed *et al*, 1998). The inset shows a zoom of the cluster salt bridge interactions involving R103 (in red), the analogous of R119 in THPO.