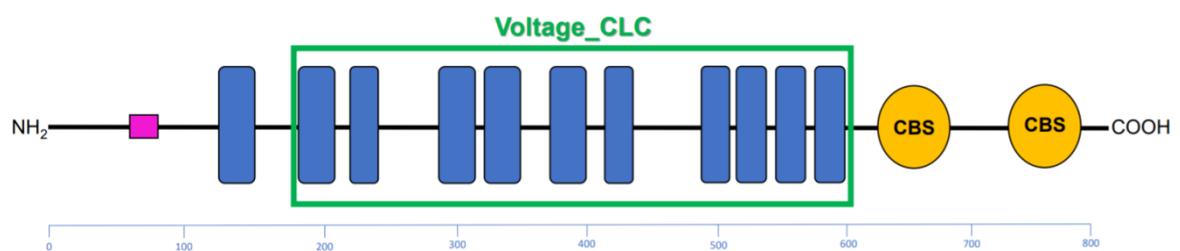


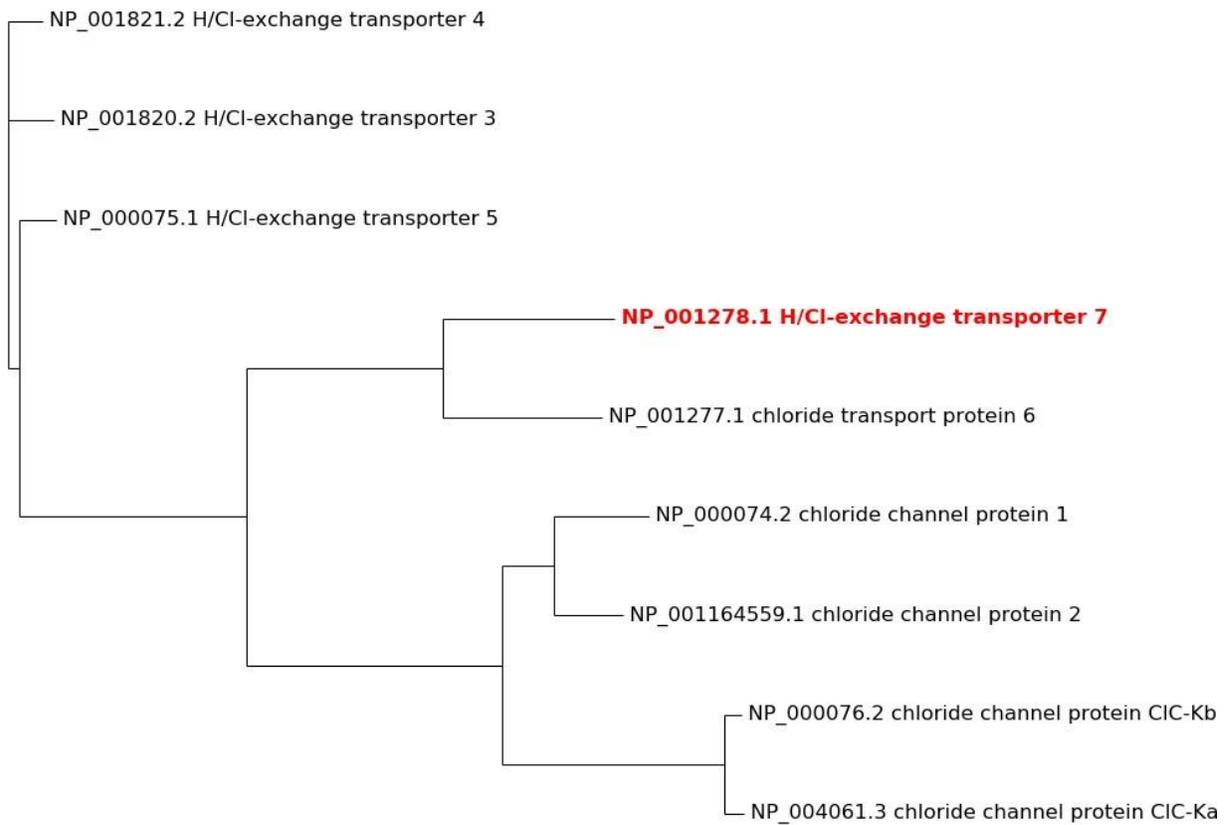
## Supplementary Material

# Identification and characterization of a novel *CLCN7* variant associated with osteopetrosis

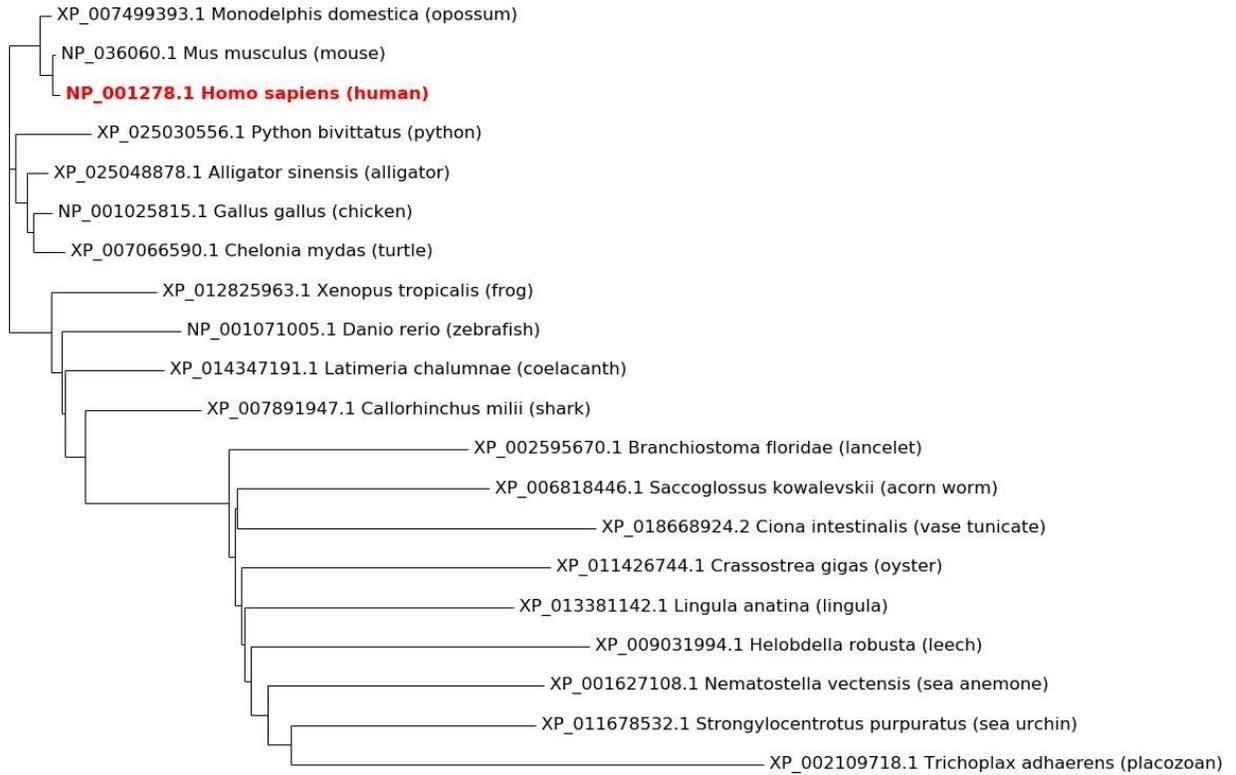
Dmitrii S. Bug<sup>1</sup>, Ildar M. Barkhatov<sup>2</sup>, Yana V. Gudozhnikova<sup>3</sup>, Artem V. Tishkov<sup>1</sup>,  
Igor B. Zhulin<sup>1,4\*</sup> and Natalia V. Petukhova<sup>1\*</sup>



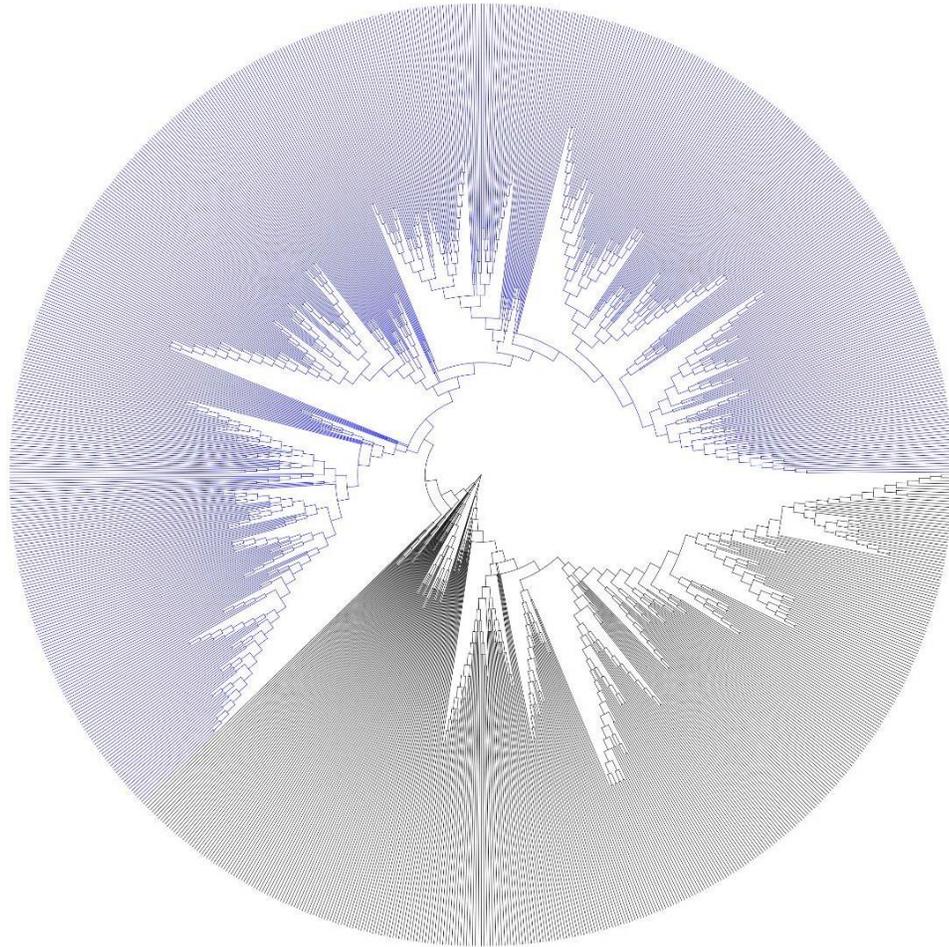
**Supplemental Figure 1:** Predicted domain architecture. Low complexity region colored in pink; transmembrane regions are indicated by blue boxes; CBS - cystathionine beta synthase domain; green box shows Voltage-gated chloride channels superfamily.



**Supplemental Figure 2:** Neighbor-joining phylogenetic tree of CLCN7 paralogs identified in the human genome. The product of *CLCN7* gene is shown in red.



**Supplemental Figure 3:** Neighbor-joining phylogenetic tree of CLCN7 orthologs from representative metazoan genomes.



**Supplemental Figure 4:** Separation of CLCN7 orthologs from the closely related paralogs. The neighbor-joining phylogenetic tree contains 1000 CLCN6 and CLCN7 protein sequences from the RefSeq database (limited to Metazoa). The CLCN7 clade (shown in blue) is separated from the rest of the tree by the longest branch.

**Supplemental Table 1:** Clinical features of the proband.

| <b>Clinical Features</b>                            | <b>Comment</b>   |
|---|--|
| Osteosclerosis, diffuse symmetrical                 | Bone density studies showed increasing of Z-score in lumbar vertebrae from 9.2 to 10.6, as well as symmetrical widening of diaphyses and metaphyses of femur, fibula, tibia and humerus. |
| Increased long bone fracture rate (75% of patients) | Not observed.  |
| Multiple fractures                                  | More than ten.   |
| Bone marrow failure                                 | Bone marrow biopsy showed erythroid hyperplasia (>50% of cells), and signs of diserythropoiesis: deformed erythroblasts nuclei, the presence of binucleated cells and megaloblasts.      |
| Onset in childhood                                  | Proband diagnosed at the age of four.  |
| Hepatomegaly  | Maximum liver dimension is 16.6.   |
| Splenomegaly  | Enlarged spleen occupies half of the abdominal cavity. Splenic vein diameter increased up to 1.4 cm.   |
| Anemia  | Hemoglobin level decreased to 46 g/l.  |
| Reticulocytosis                                     | Reticulocyte count is 9.83 %.  |
| Thrombocytopenia                                    | Platelet count is 17 109/l.  |
| Failure to thrive                                   | Proband weighed 45 kg.   |
| Hydrocephalus                                       | Not observed.  |
| Splayed metaphyses                                  | Bone scintigraphy showed splayed metaphyses  |
| Low serum calcium                                   | 2.16 mmol/l.   |
| Elevated serum alkaline phosphatase                 | 161.6 U/l.   |
| Valgus deformity                                    | Not observed.  |
| Dental anomalies                                    | Malocclusion.  |
| Elevated serum lactate                              | 631.6 U/l.   |

|                               |   |
|-------------------------------|---|
| dehydrogenase                 |   |
| Lymphocytosis                 | Lymphocyte count is $5.6 \times 10^9/l$ . |
| Skeletal defects              | Right leg is shortened by 2 cm.           |
| Right thoracolumbar scoliosis | Not observed.                             |
| Low hairline                  | Not observed.                             |
| Double xiphoid process        | Not observed.                             |

**Supplemental Table 2:** Functional effect of mutation L614R by different SNP predictors.

| <b>SNP predictor</b> | <b>Functional effect</b>                       | <b>Prediction score</b> |
|----------------------|--|-------------------------|
| PolyPhen2            | Probably damaging                              | 1.000                   |
| SIFT                 | Affect protein function<br>(probably damaging) | 0.00                    |
| PROVEAN              | Deleterious                                    | -5.794                  |
| PANTHER              | Disease causing variant                        | 0.845                   |
| PhD-NP               | Disease causing variant                        | 0.910                   |
| Meta-SNP             | Disease causing variant                        | 0.850                   |
| PredictSNP           | Deleterious                                    | 0.79                    |
| SNAP                 | Affect protein function (deleterious)          | 69                      |