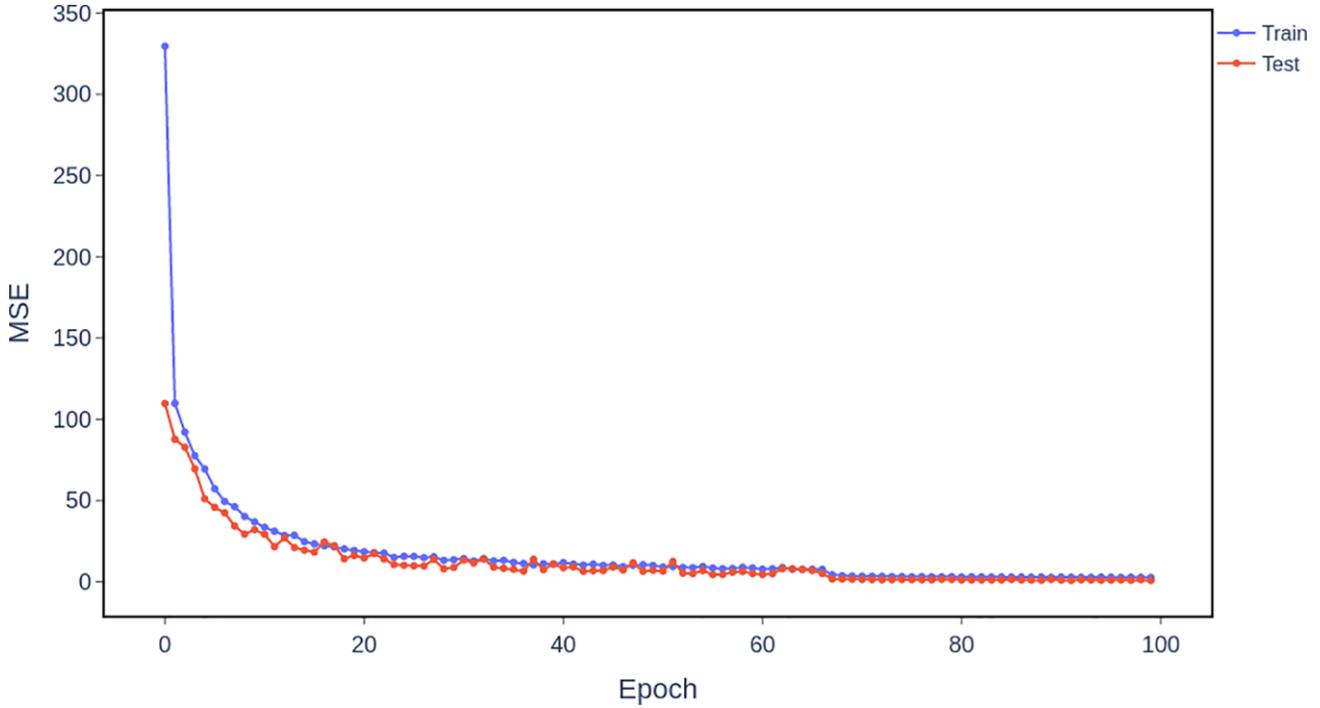


**SUPPLEMENTARY FIGURES**



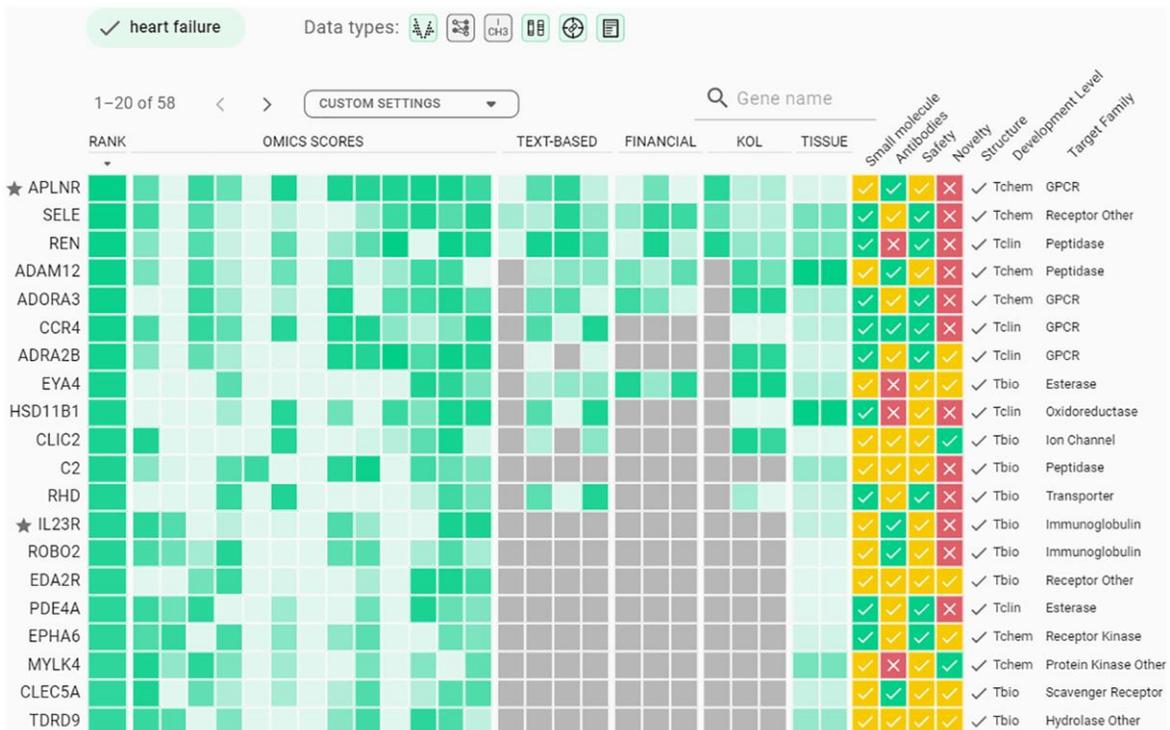
**Supplementary Figure 1. Multimodal transformer learning curves on the train and 20% hold-out test datasets.**



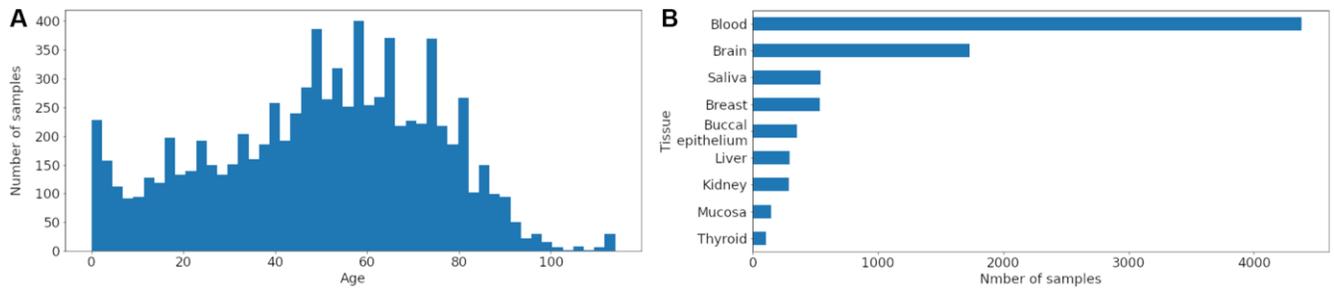
**Supplementary Figure 2. Example of target ID output for idiopathic pulmonary fibrosis.** Top-200 genes from expression classifiers were applied as a gene list in PandaOmics corresponding project for idiopathic pulmonary fibrosis, and a filter for small molecules was applied to identify druggable targets. Twenty genes highly ranked by PandaOmics are shown.



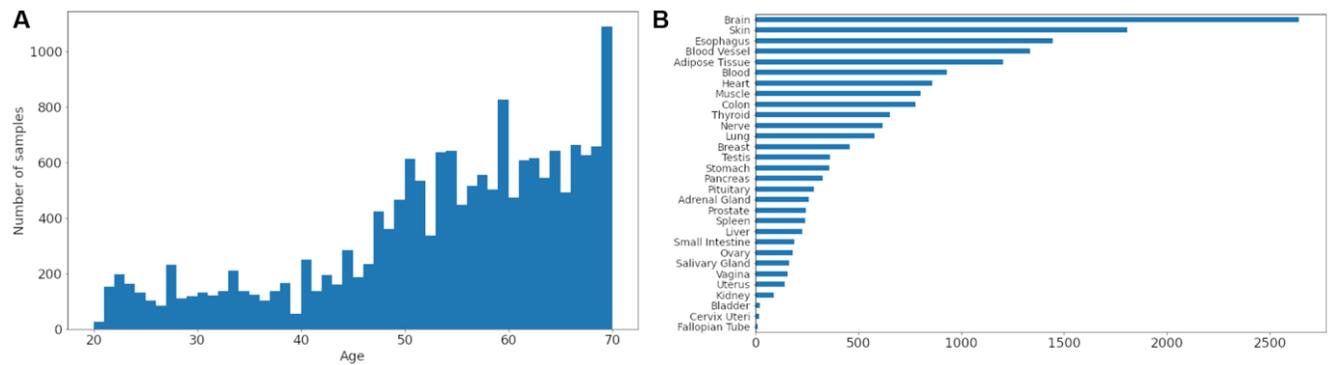
**Supplementary Figure 3. Example of target ID output for Parkinson’s disease.** Top-200 genes from expression classifiers were applied as a gene list in PandaOmics corresponding project for PD, and a filter for small molecules was applied to identify druggable targets. Twenty genes highly ranked by PandaOmics are shown.



**Supplementary Figure 4. Example of target ID output for heart failure.** Top-200 genes from expression classifiers were applied as a gene list in PandaOmics corresponding project for heart failure, and a filter for small molecules was applied to identify druggable targets. Twenty genes highly ranked by PandaOmics are shown.



**Supplementary Figure 5.** Distribution by age (A) and tissues (B) for DNAm samples. Data was obtained from CNCB EWAS data hub. Ages distributed from 0 to 110 years. Most of the samples are blood samples.



**Supplementary Figure 6.** Distribution by age (A) and tissues (B) for RNA-seq samples. Data are obtained from the GTEx project. Ages are distributed between 20 and 70 years. Brain and Skin samples comprise a bigger part of the dataset.