Introduction
The mechanism underlying the phenotypic and symptomatologic variation of β-talassemias is still unclear. Metabolic composition of the human placenta could be affected by the presence of pathological states such as β-thalassemia. The aim of our study was to describe metabolic changes in chorionic villi samples (CVS) of fetuses affected by β-thalassemia compared to a control group by applying a metabolomics approach.

Methods
3 groups were identified based on the CVS result: Group 1, Control (n=27); Group 2, heterozygous (n=7); Group 3, homozygous (n=7). Samples have been analyzed using Gas chromatography-mass spectrometry (GC-MS). Subsequently, multivariate and univariate statistical analysis were performed.

Results:
Supervised multivariate models were used to compare the samples from the three groups. The strongest model was given by the comparison between Groups 1 and 3. (R2X=0.49, R2Y=0.92, Q2=0.66, p<0.0001). Discriminant metabolites were identified, fingerprint for homozygotes allowing the identification of the main altered pathways: pentose phosphate pathway (PPP), arachidonic acid metabolism, glutamic acid metabolism, glycolysis and gluconeogenesis, suggesting an energetic shift and the presence of oxidative stress.

Conclusion
By metabolomic investigation we were able to highlight a specific metabolic pattern in chorionic villi of patients with β-talassemia, underlining how some alterations characteristic of this pathology can be evaluated in early phases of the pregnancy directly from the placenta.