### Main Result

- **220 loci** (chromosome regions and genes) associated with CO in seven species
- **182 human orthologs**, identification of genomic overlaps with chromosome mutations
- **12 pathways** identified, five already discovered on a rat model, most significant muscle contraction pathway
- A cohort of novel 43 CO network-predicted candidate genes
- Literature-collected and network-predicted genes share common significant pathways
- **225 genes; 182** literature-collected + 43 network-predicted
- **50 genes (175 genes filtered out)**
- Two main groups of clusters
- PPIN of 50 genes
- CO candidate genes within multiple reports, multiple pathways and genomic overlaps

### Procedure

1. **Collection of CO-associated loci from the literature**
2. Development of the CO database and genomic view, identification of human orthologs
3. **Pathway identification and network-based data mining discovery**
   - Pathway identification related to the gene list
   - Network-based prediction of 182 CO candidate genes by identifying first neighbours
   - Union of the CO related genes
   - Selection of the genes present in at least two of the pathways
   - Pathway analysis to evaluate the importance of 43 novel candidate genes
   - Hierarchical bi-clustering of the matrix of 50 genes and 12 columns (representing pathways)
4. **Candidate gene prioritization and genetic variability of stronger candidate genes**

### Results, associated to RASopathies

- **12 enriched pathways**, including pathways related to muscle contraction and cardiomyopathy
- Muscle contraction and cardiomyopathy pathways confirmed
- Evidence for genomic connections between cryptorchidism and cardiomyopathy pathways in RASopathies