

Whole Exome Sequencing Identifies a Novel Candidate Gene in an Ashkenazi Jewish Family with Tetralogy of Fallot

JAR-YEE LIU*, AFRIDA SARA*, Jason Liu, Pritha Gupta, Judith Fan, Jessica Wang UCLA Department of Medicine - Division of Cardiology David Geffen School of Medicine at UCLA

Background

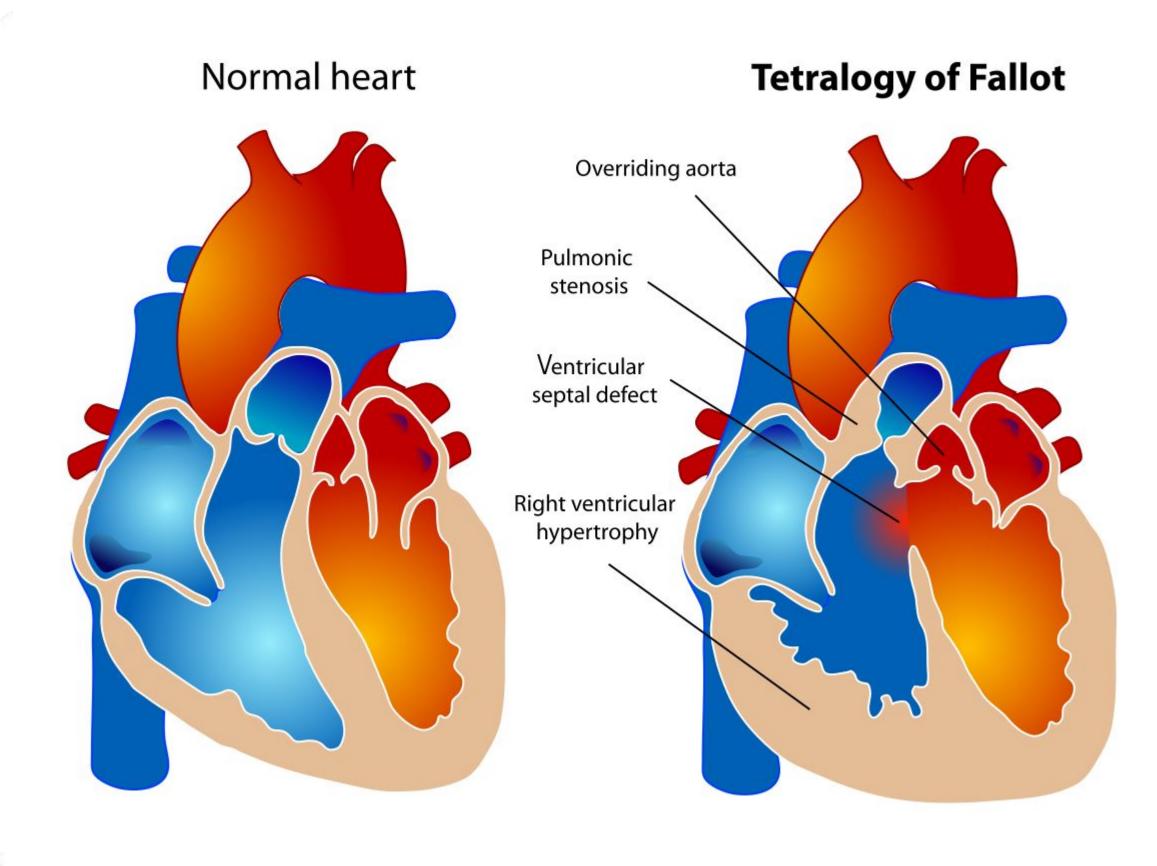


Figure 1: Diagrammatic Depiction of Tetralogy of Fallot (ToF). 70% of ToF Patients Lack of a Molecular Diagnosis

Precision Medicine



Figure 2: Precision Medicine. Delivering the right treatment, to the right person, at the right time. Removes delay, expense, and harm of trying ineffective treatments

Whole Exome Sequencing (WES)

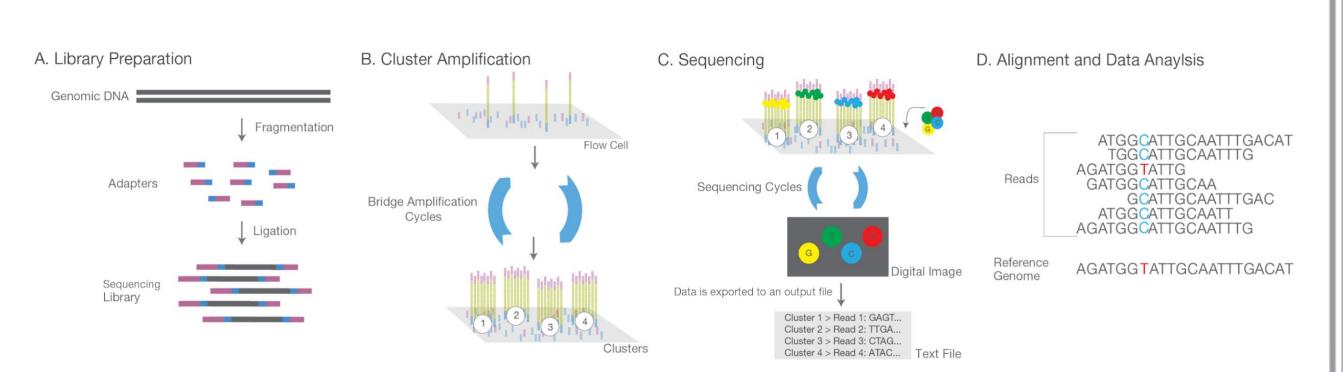
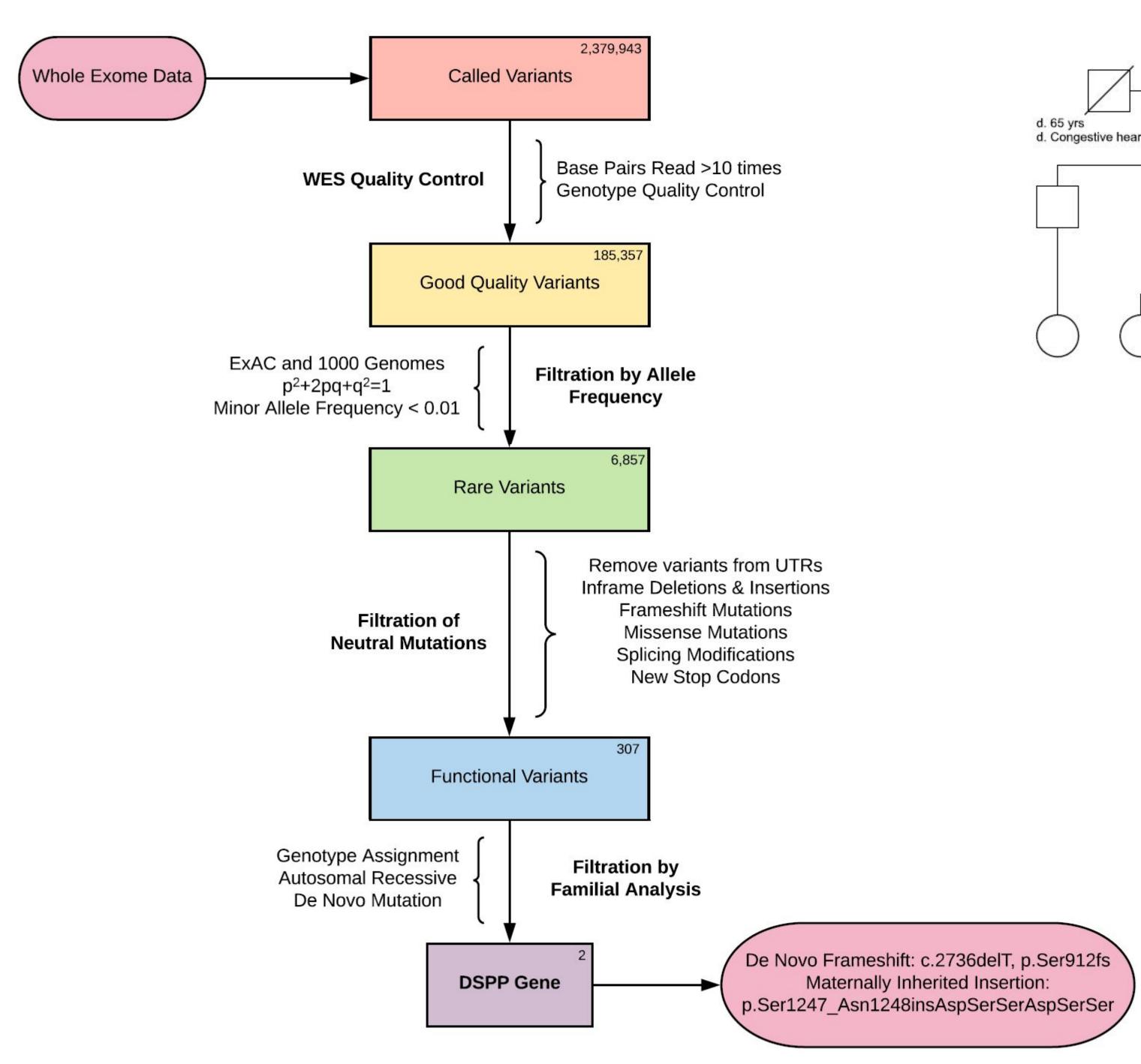


Figure 3: Whole Exome Sequencing & Analysis Workflow

Goal

To identify a genetic basis for development of Tetralogy of Fallot (ToF) within an affected family

Methods & Tertiary Analysis



d. 65 yrs
d. Colon cancer
Colon or rectal cancer, 85 yrs
d. Natural Causes
Skin cancer (melanoma)

46 yrs
White
Ashkenazi Jewish
Anerican
Ashrenazi Jewish
Anerican
Ashrenazi Jewish
Anerican
Ashrenazi Jewish
Ash

Figure 4: Familial Pedigree. Two affected sisters (red) with no pertinent family history.

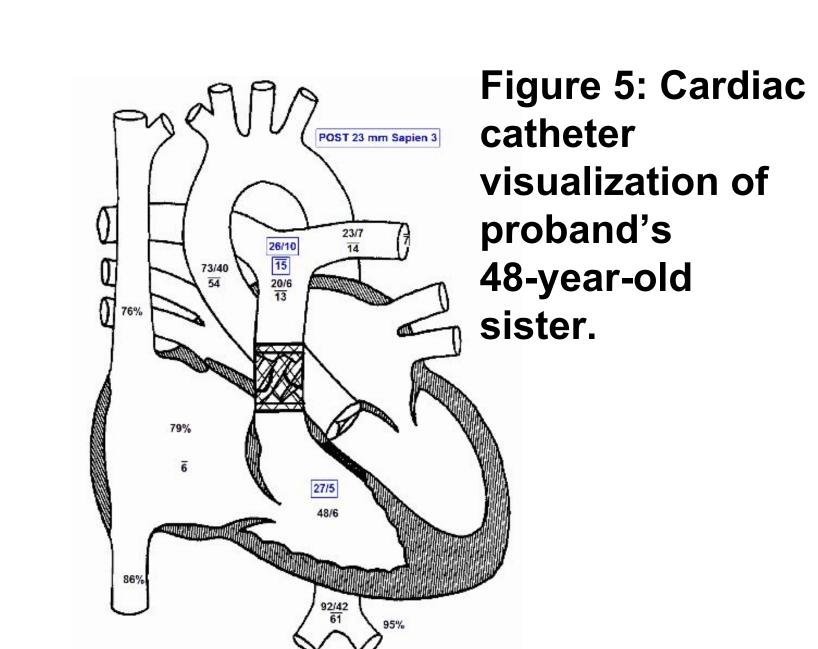
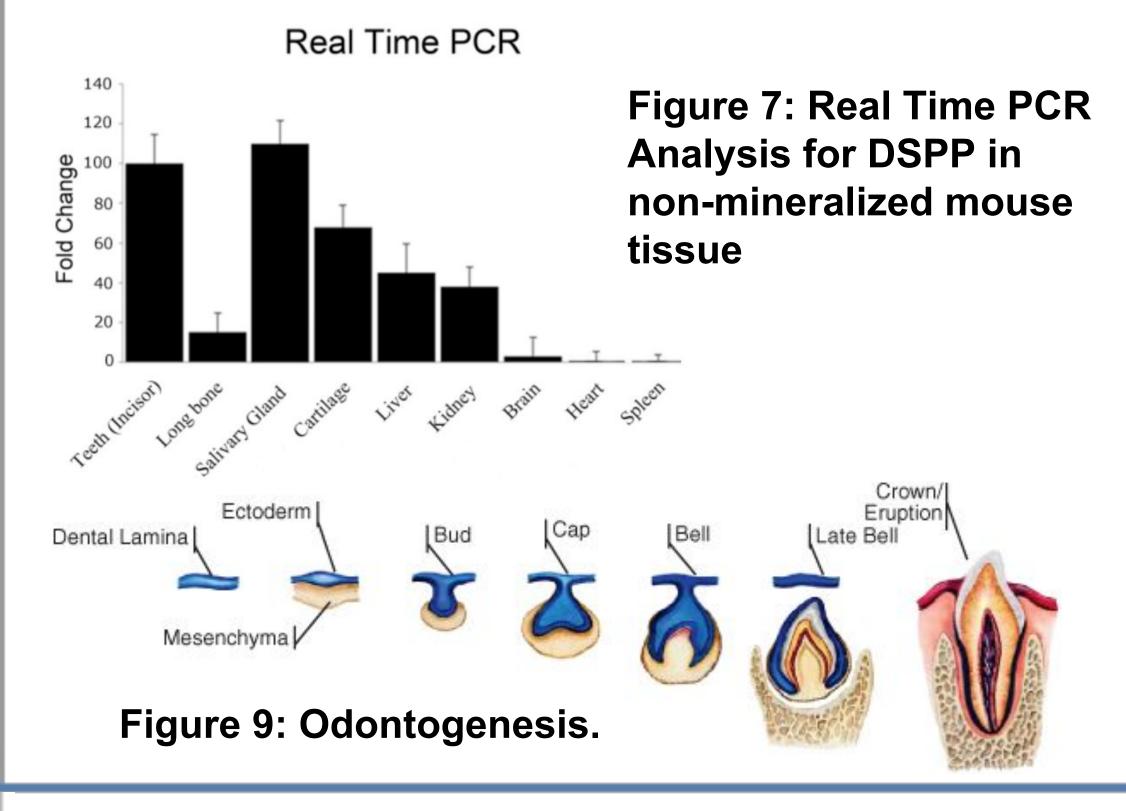


Figure 6: Computational Exome Analysis Workflow

Discussion



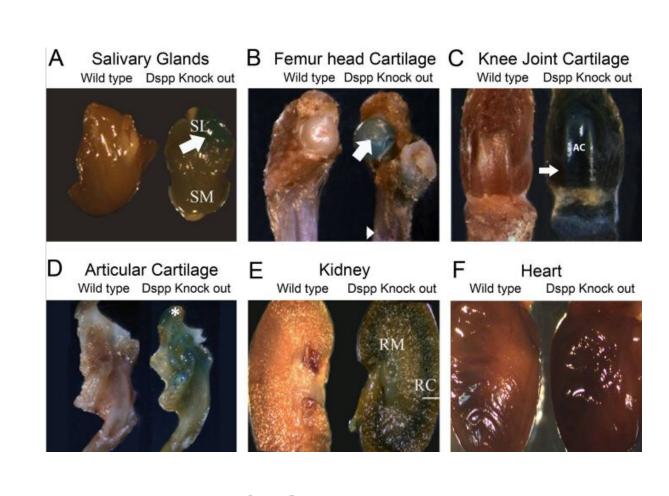


Figure 8: β-Galactosidase
Assays for DSPP in
non-mineralized mouse tissue

Future Directions

- Immunohistochemistry for DSPP visualization in developing embryonic mice
- Molecular cloning for gene expression in cell culture

Acknowledgements



