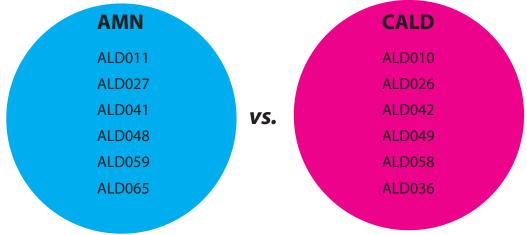
First Approach

Find variants in all CALD, absent from all AMN, and vice versa



Variants can be: Het/HomoAlt in one group, and HomoRef in the other HomoAlt in one group, and Het/HomoRef in the other

Result: Too strict. Issues with genotyping and lack of consensus hurts this approach

Second Approach

Find variants in some (4/6 or 5/6) CALD, absent from most (4/6 or 5/6)AMN, and vice versa

AMN		CALD
ALD011		ALD010
ALD027		ALD026
ALD041	vs.	ALD042
ALD048		ALD049
ALD059		ALD058
ALD065		ALD036

Result: Too loose at 4/6, and assumptions for shared SAME VARIANT modifiers across cohort hurts this approach.

Third Approach

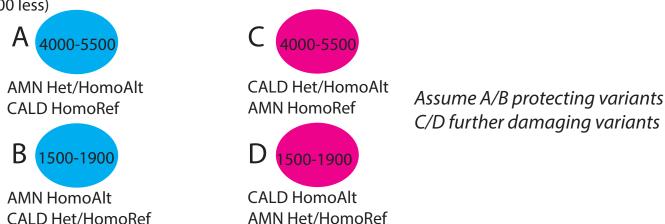
Find family-wise discriminating variants (HIGH/MED impact) **AMN CALD** VS. **ALD011** ALD010 VS. ALD027 ALD026 VS. ALD042 **ALD041** VS. **ALD049** ALD048 VS. **ALD059** ALD058 ALD036 ALD065 VS.

Variants can be:

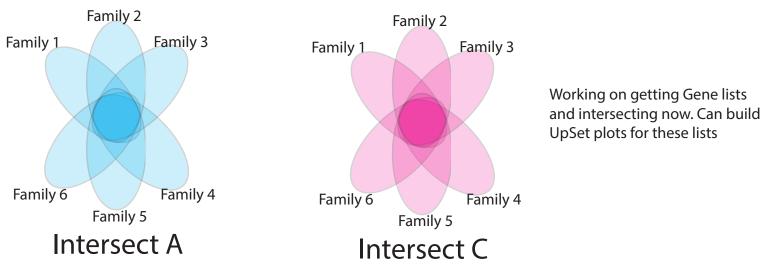
Het/HomoAlt in one group, and HomoRef in the other HomoAlt in one group, and Het/HomoRef in the other

Results:

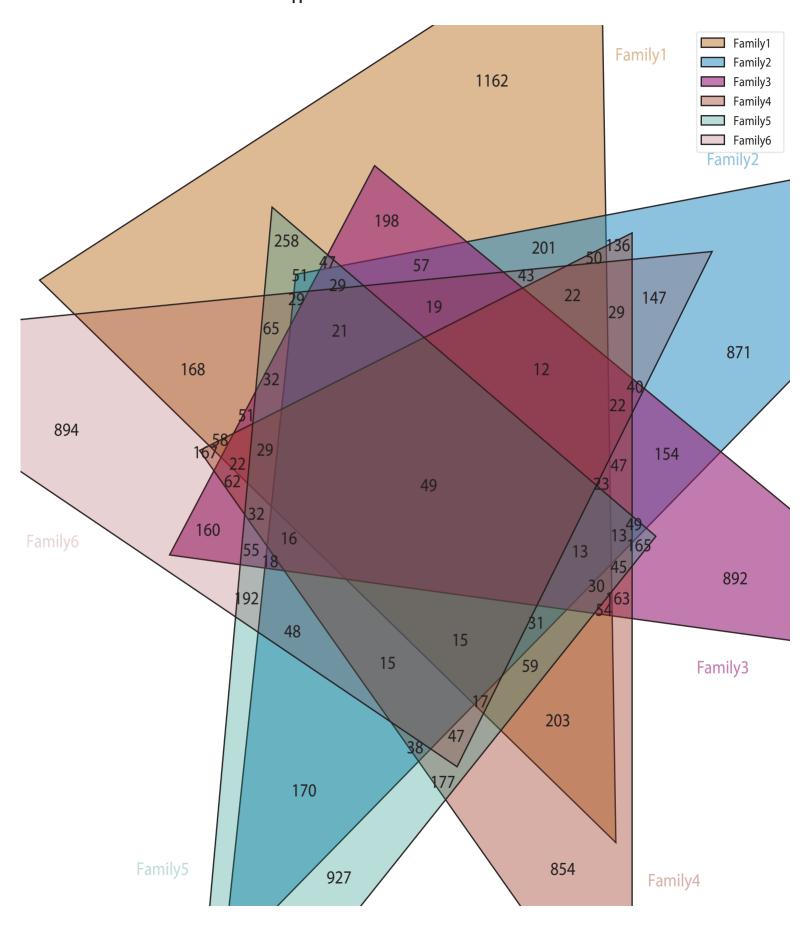
For each family 1-6, about 4000-5500 variants in the Het/HomoAlt vs. HomoRef, And 1500-1900 variants in the HomoAlt vs. Het/HomoRef. Roughly same number of genes affected (~500-1000 less)



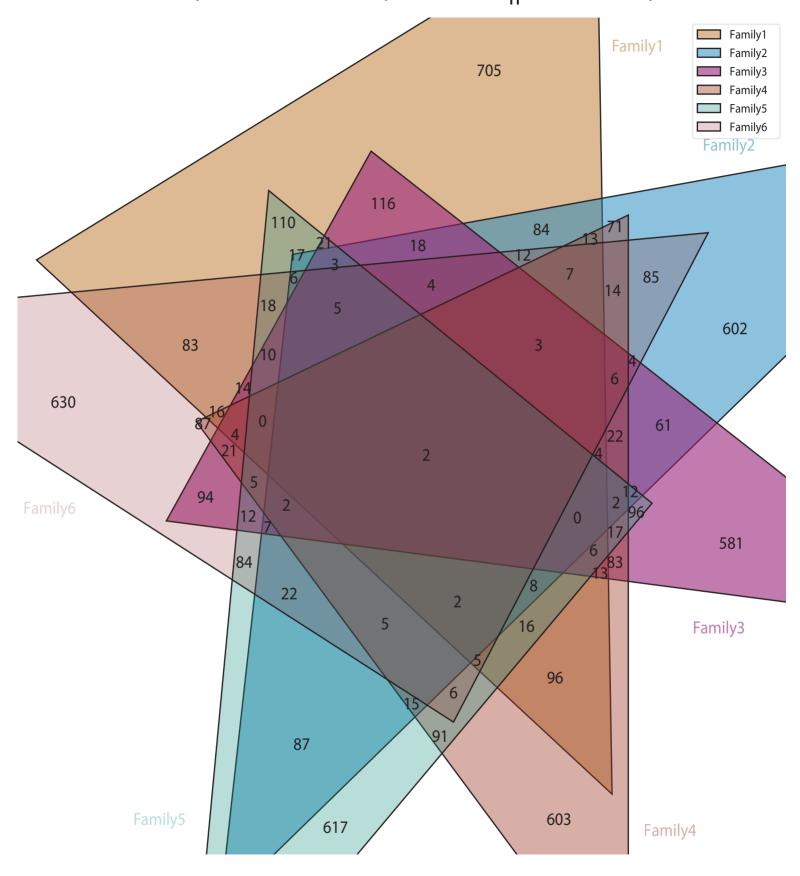
Ideas now: Look for overlap gene-wise for these sets across each family (A, B, C, D) A and C Shown below:

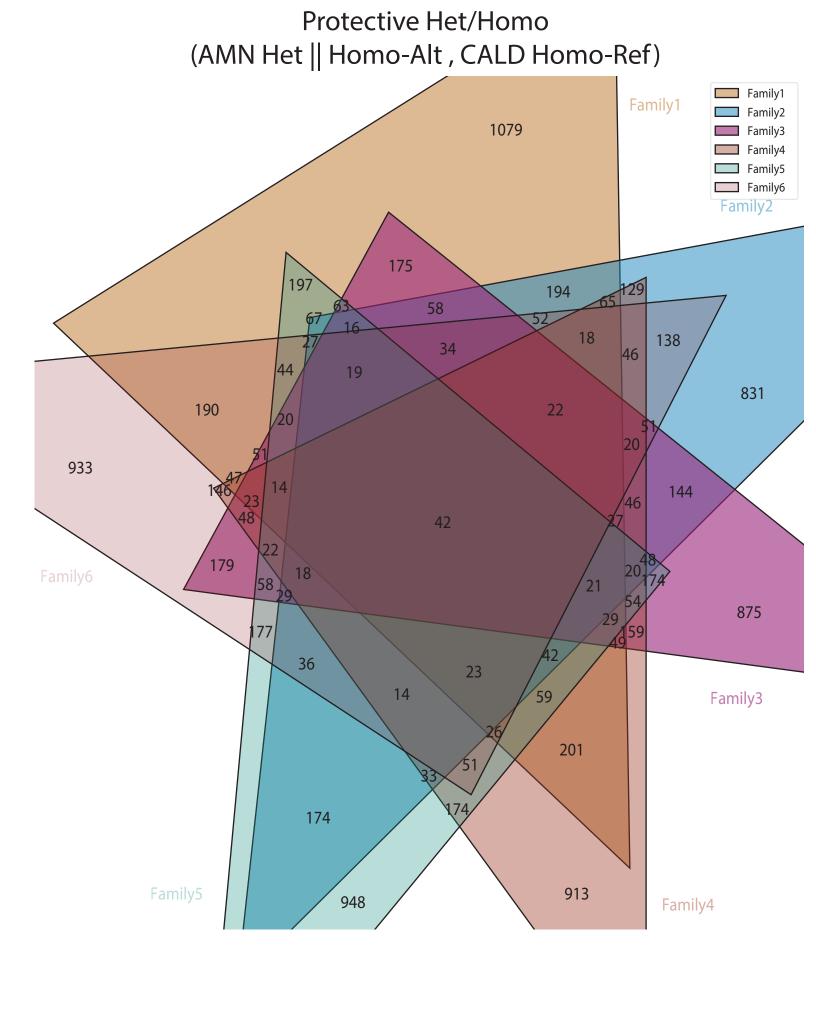


Damaging Het/Homo (CALD Het || Homo-Alt , AMN Homo-Ref)

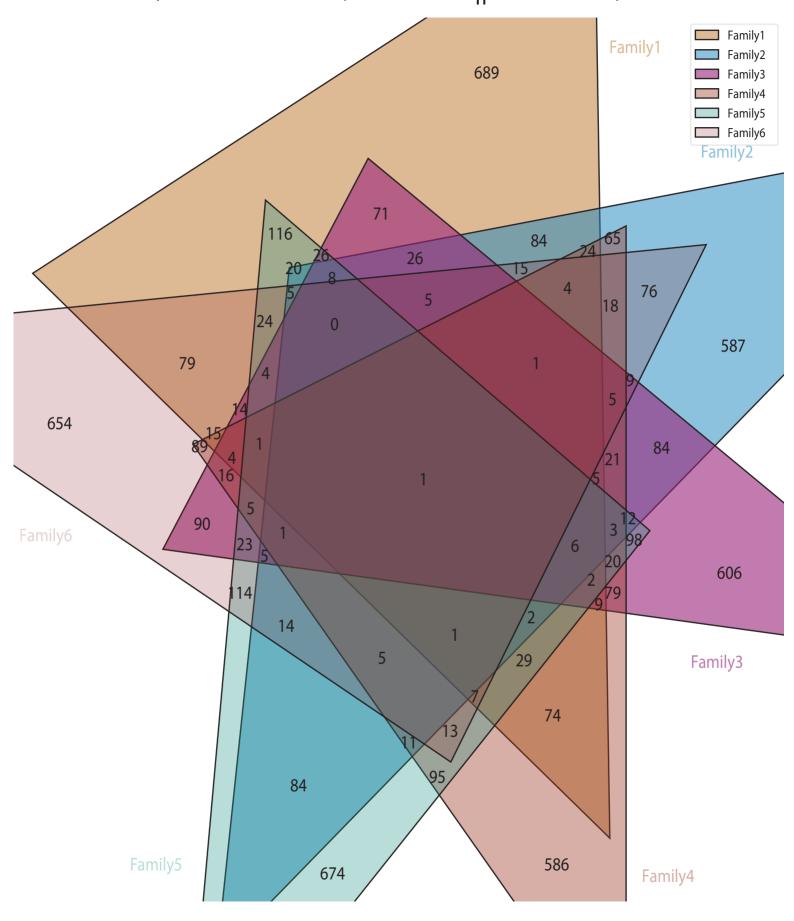


Damaging Homozygous (CALD Homo-Alt, AMN Het || Homo-Ref)

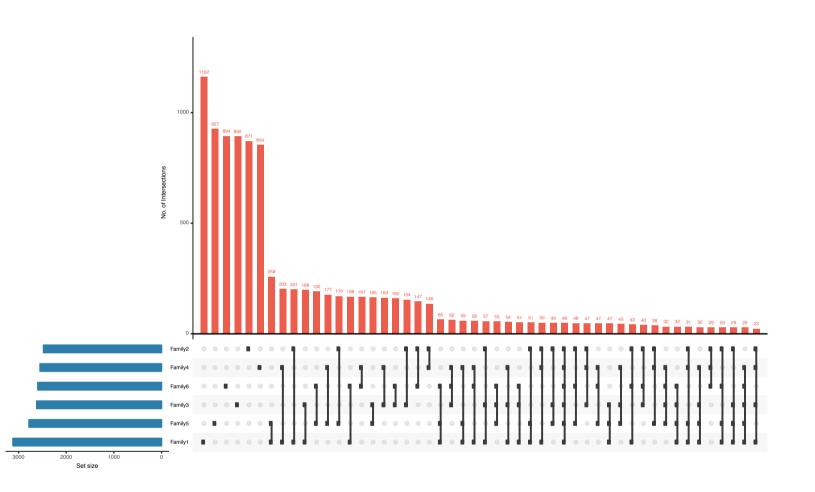




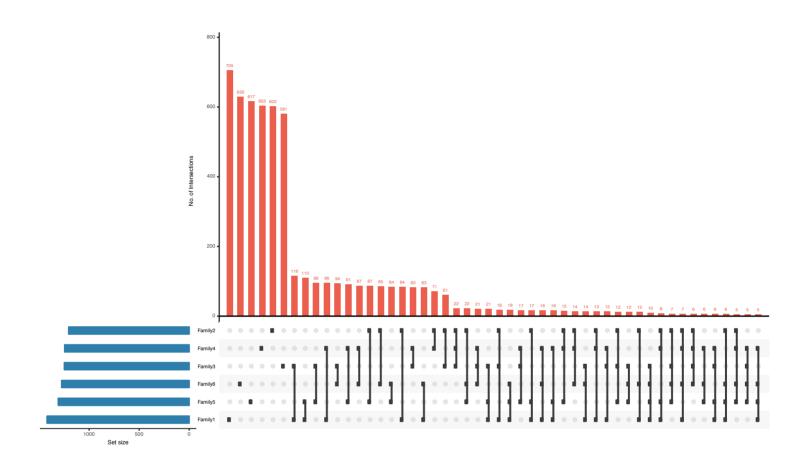
Protective Homo (AMN Homo-Alt , CALD Het || Homo-Ref)



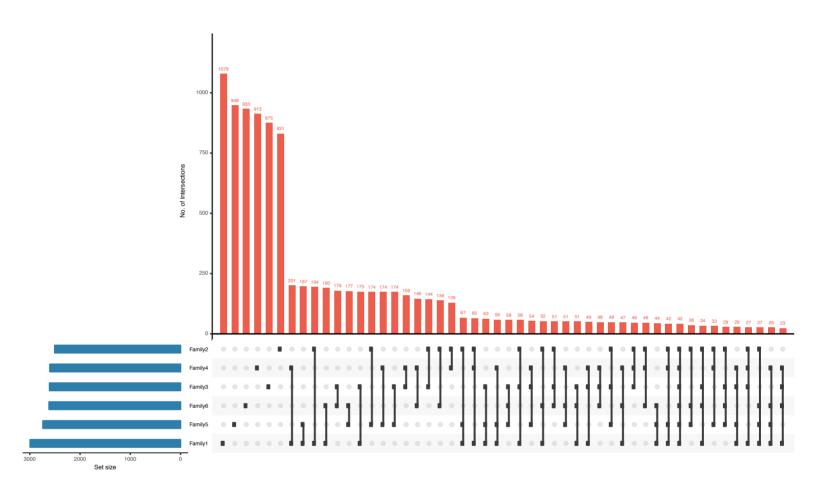
Damaging Het/Homo (CALD Het || Homo-Alt , AMN Homo-Ref)



Damaging Homozygous (CALD Homo-Alt, AMN Het || Homo-Ref)



Protective Het/Homo (AMN Het || Homo-Alt , CALD Homo-Ref)



Protective Homo (AMN Homo-Alt , CALD Het || Homo-Ref)

