

Association of *CLYD* and *NOD2* variants with susceptibility to IBD

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The data



- **n = 1,401**
- Genotyping information of **500,000 SNPs**
- Measures of age, sex, high-density lipoprotein (HDL)-cholesterol (HDL-C), low-density lipoprotein (LDL)-cholesterol, triglycerides (TGs), Coronary Artery Disease (CAD) status and Inflammatory Bowel Disease (IBD) status.
- Participant identification information
- **1,281 complete observations**
- Age of range of study participants: from **22 to 87 y/o**, with a mean of **55 y/o**
- **367 IBD positive cases.**



The trait

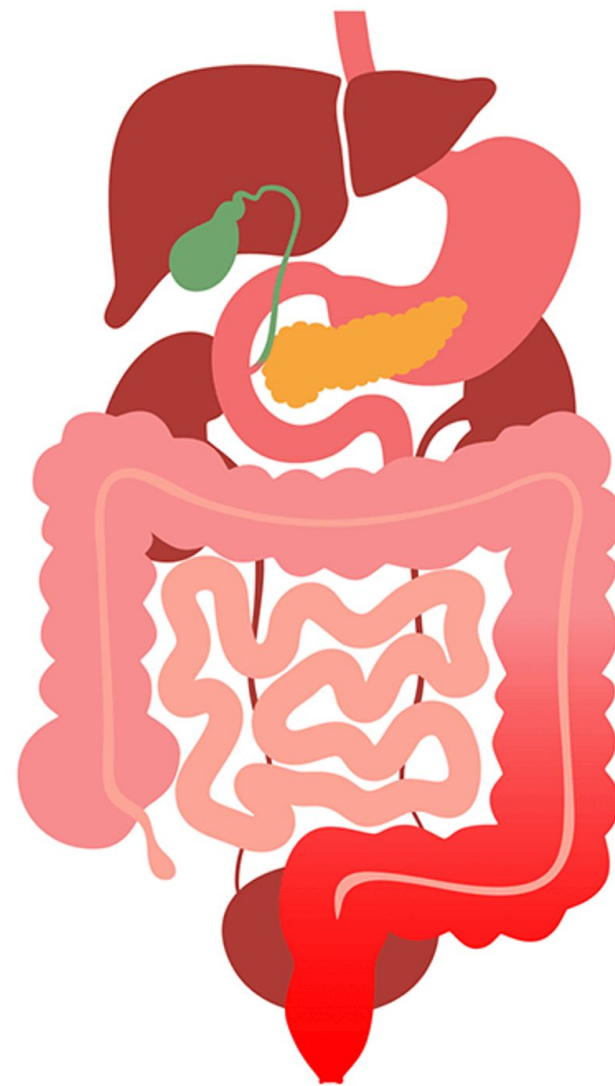


- Inflammatory Bowel Disease (IBD)
- Repetitive episodes of inflammation of the gastrointestinal tract caused by an **abnormal immune response** to gut microflora.
- Encompasses **two types of idiopathic intestinal disease** that are differentiated by their location and depth of involvement in the bowel wall.
- **Both are not curable**, and they both carry enormous morbidity. Finally, both increase the risk of colorectal cancer.
- Is estimated to affect more than 3 million people in the USA and Europe

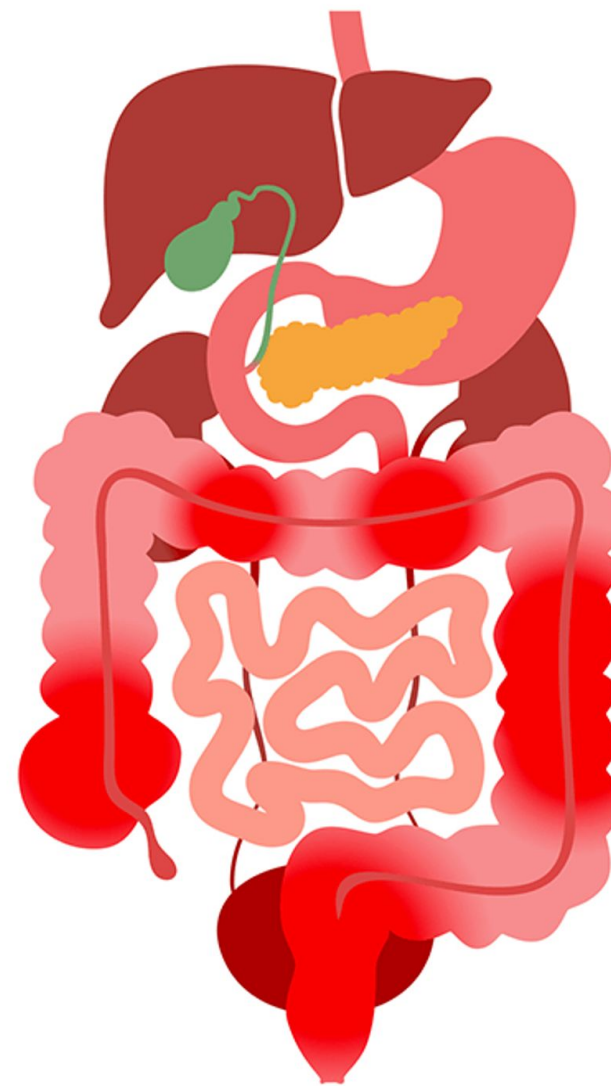


The trait

INFLAMMATORY BOWEL DISEASE (IBD)



Ulcerative colitis



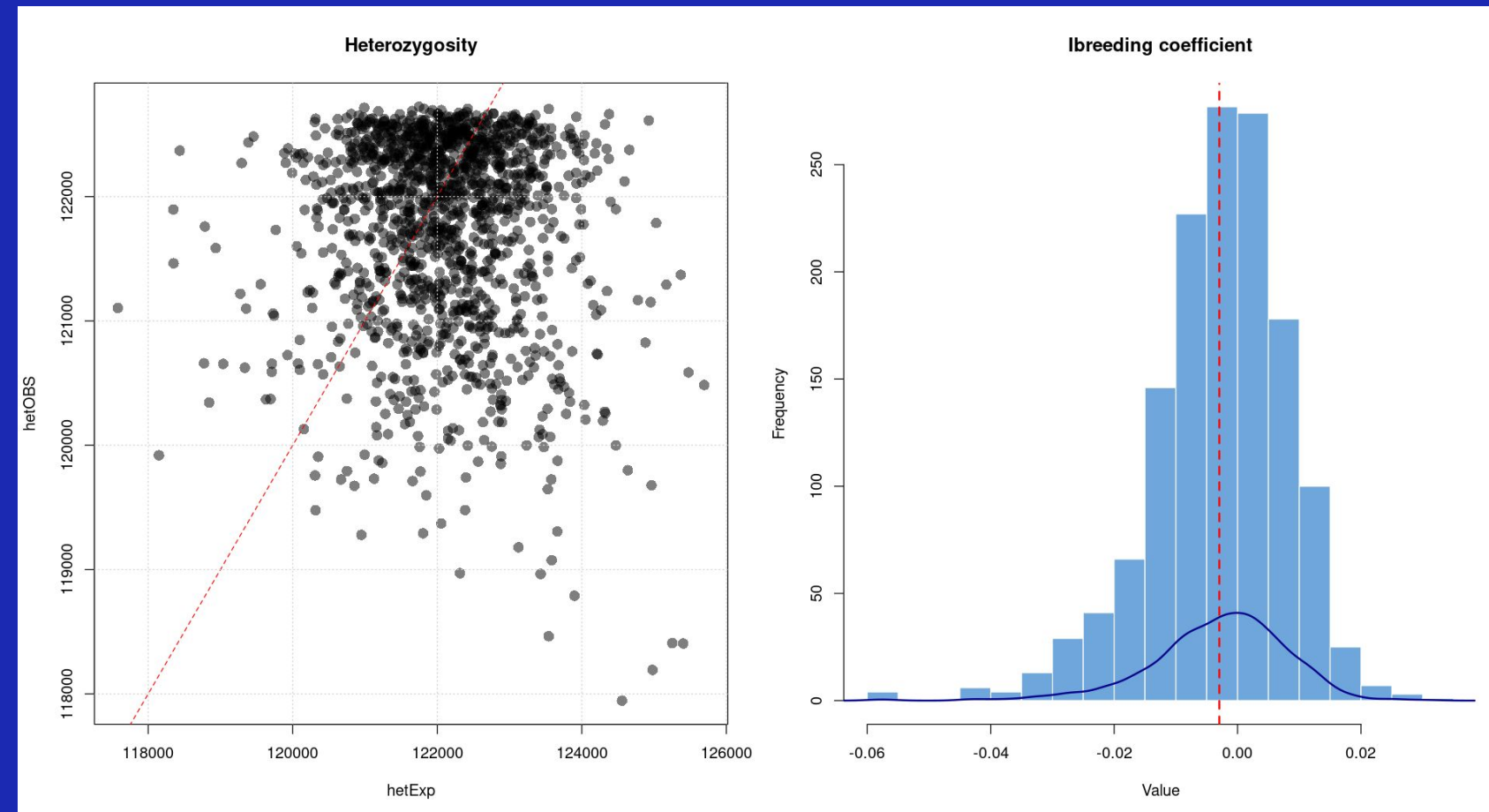
Crohn's disease



Quality control



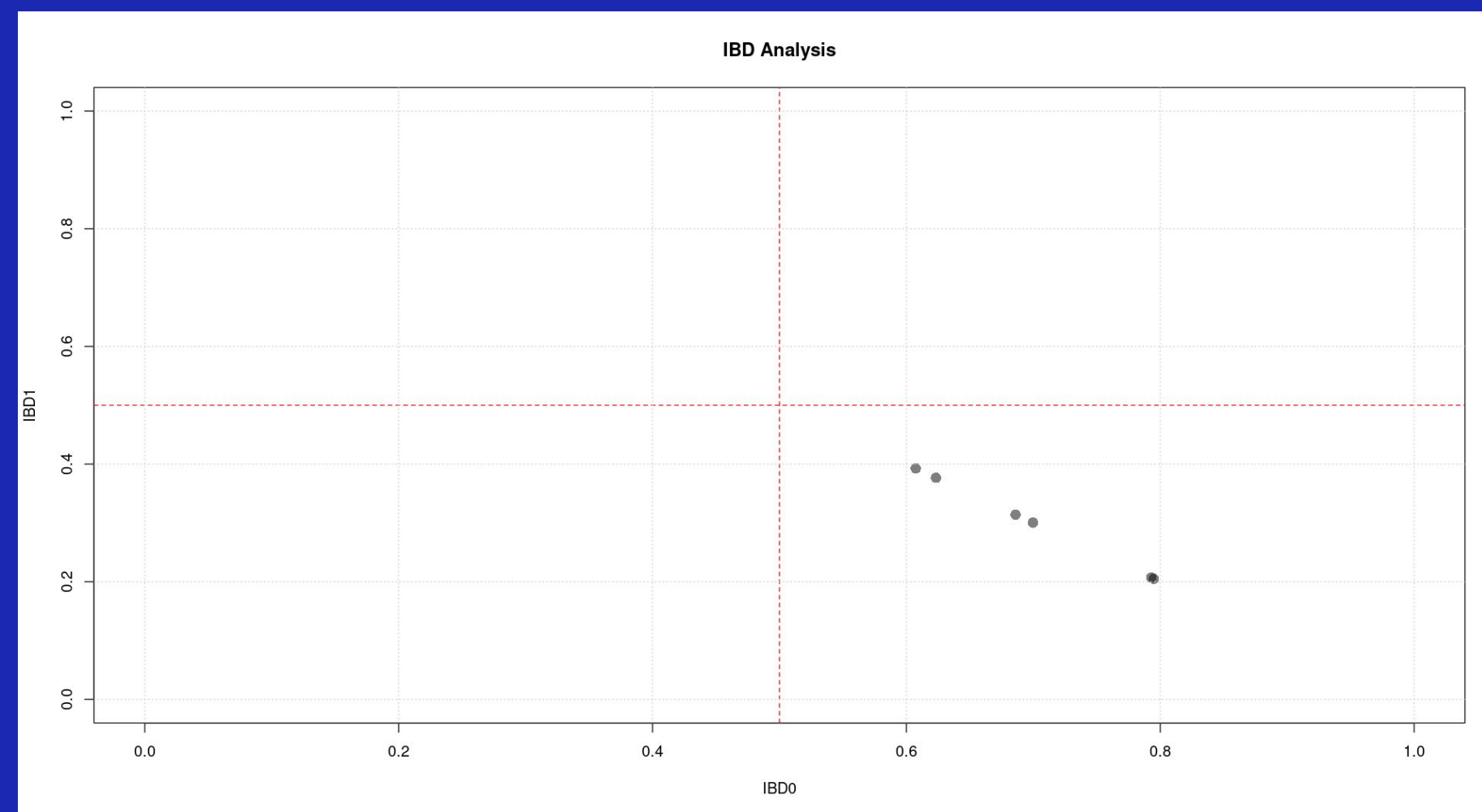
- **54,583 SNPs** removed due to **low call rate** ($CR < 95\%$, 445,417 remaining SNPS)
- **63,395 SNPs** removed due to low **MAF** ($MAF < 1\%$, 382,022 remaining SNPS)
- **4 individuals** removed due to unusual **inbreeding coefficient** (1,397 remaining individuals).



Quality control

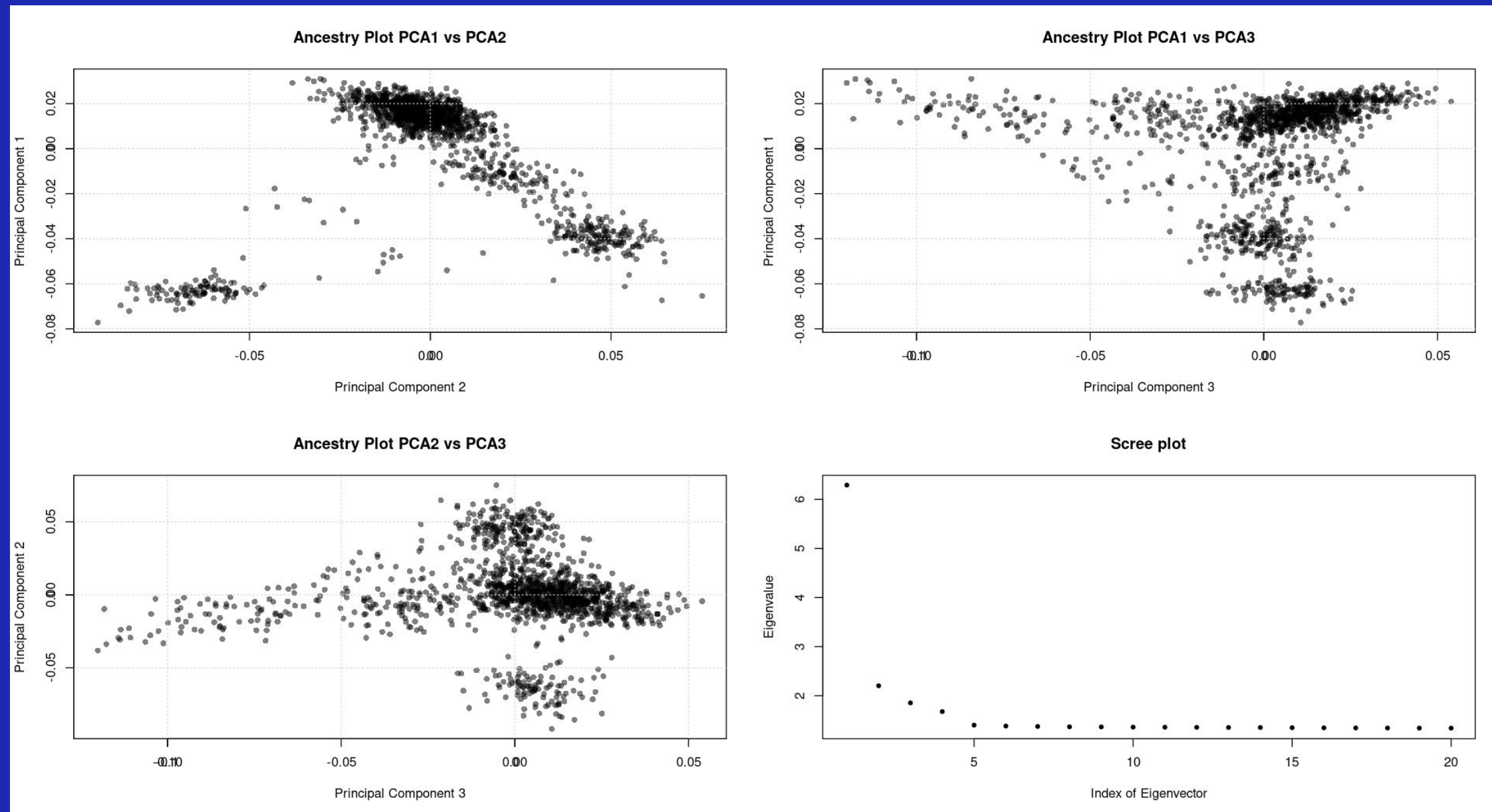


- **1,187 SNPs** removed due to high **HWE** (380,835 remaining SNPs).
- 380,369 SNPs used in IBD analysis.
- **5 similar samples** removed due to **correlation coefficient** ≥ 0.05



Quality control

- **Three PCAs** retained



- **1,392 samples & 380,835 SNPs** included in analysis

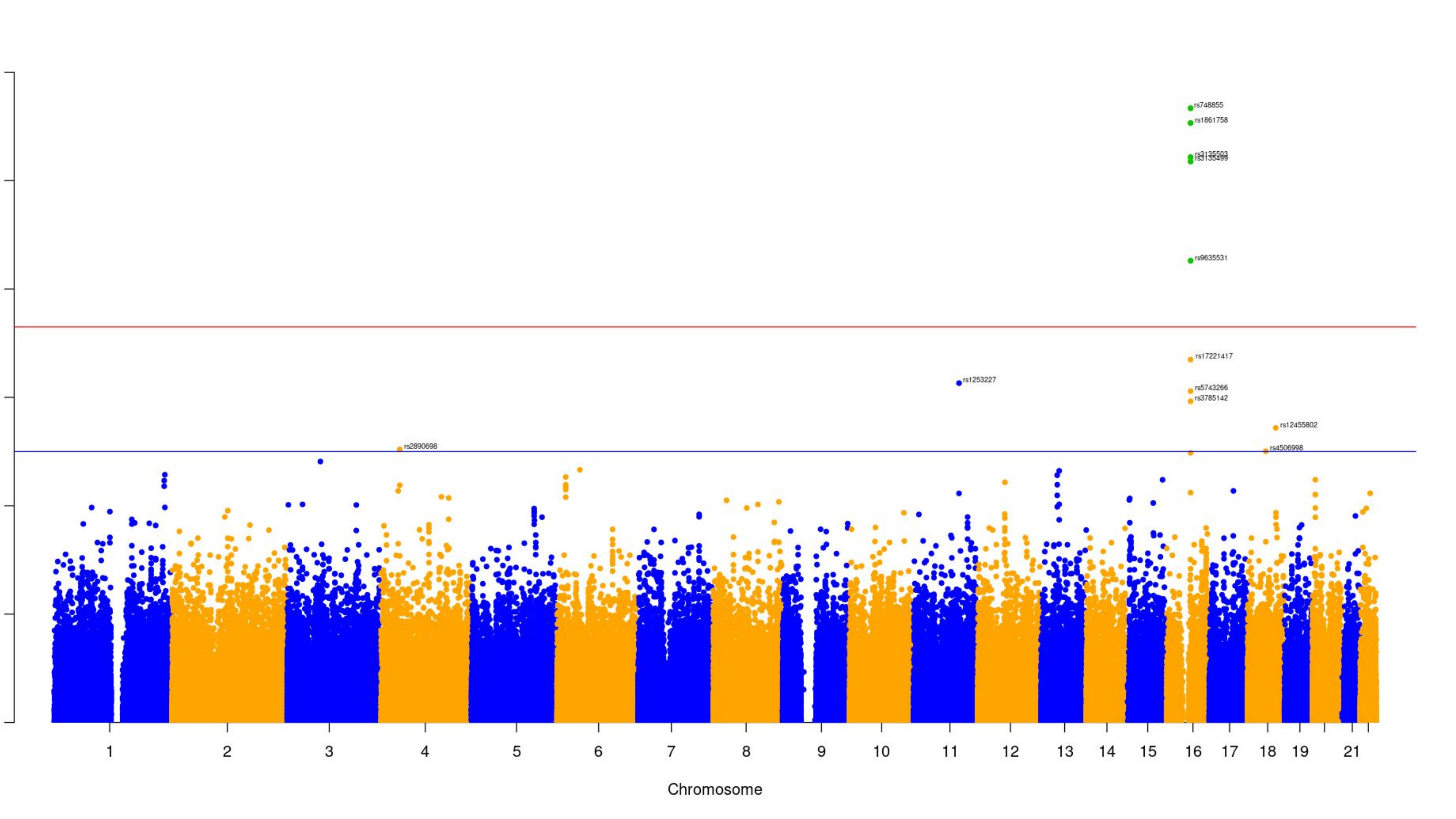
The model



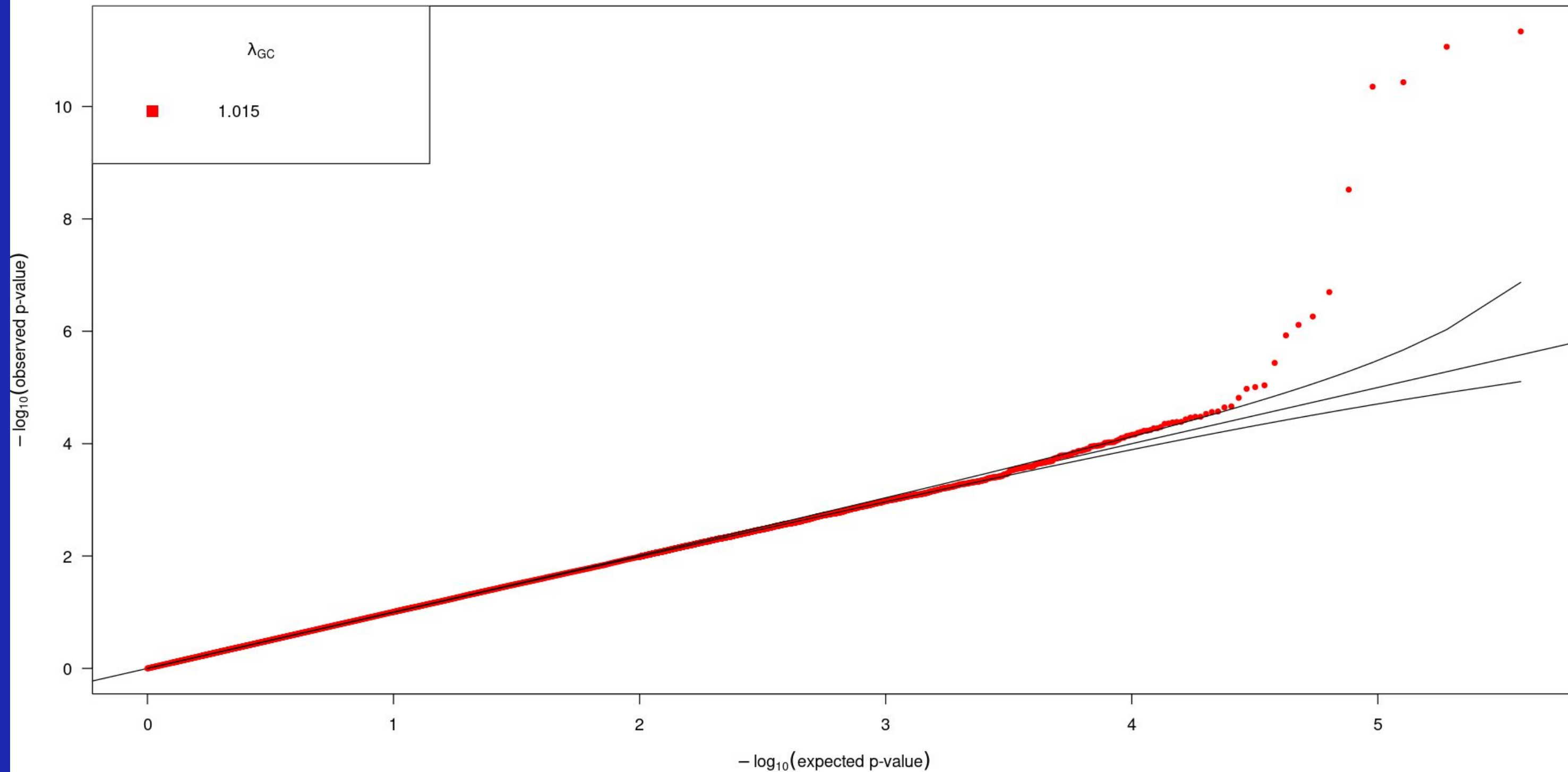
$$Y = \alpha * SNP + \text{age} + \text{CAD} + \text{sex} + \text{tg} + \text{hdl} + \text{ldl} + \text{PC1} + \text{PC2} + \text{PC3}$$

```
result <- summary(glm(phenotype ~ . - FamID, family = binomial, data = cbind(phenodata, snp = genoNum[, snp.name])))
```

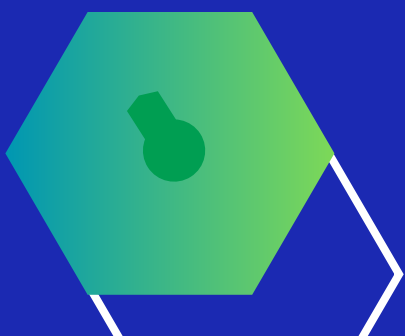




Genomic control



Preliminary hits



Aa SNP	# P-value	# Chromosome	≡ Gene	# Position	≡ A1	≡ A2	📄 Clinical Significance	📄 GWAS catalog status
📄 rs748855	0.0000000000005	16	<i>NOD2</i>	50751398	C	T	Possible	Not reported
📄 rs1861758	0.0000000000009	16	<i>NOD2</i>	50751787	T	C	Possible	Not reported
📄 rs3135503	0.000000000004	16	<i>CYLD</i>	50791250	G	T	Not reported	Not reported
📄 rs3135499	0.000000000004	16	<i>NOD2, LOC124903774</i>	50766127	G	T	More possible	Not reported
📄 rs9635531	0.0000000003	16	<i>LINC02168</i>	50841795	A	G	Not reported	Not reported
📄 rs17221417	0.00000002	16	<i>NOD2</i>	50739582	C	G	Possible	Reported
📄 rs1253227	0.00000005	11	<i>MAML2</i>	96029482	G	A	Not reported	Not reported
📄 rs5743266	0.00000008	16	<i>NOD2</i>	50731096	T	C		
📄 rs3785142	0.00000118211857916311	16	<i>CLYD</i>	50787147	G	A	Not reported	Not reported
📄 rs12455802	0.00000365675300118725	18	<i>PIGN</i>	59582470	C	G	Not reported	Not reported
📄 rs2890698	0.00000915661334099731	4	<i>SMIM14, UGDH-AS1</i>	39586775	T	G	Not reported	Not reported
📄 rs4506998	0.00000983751181627577	18		38643072	A	G	Not reported	Not reported

Final hits



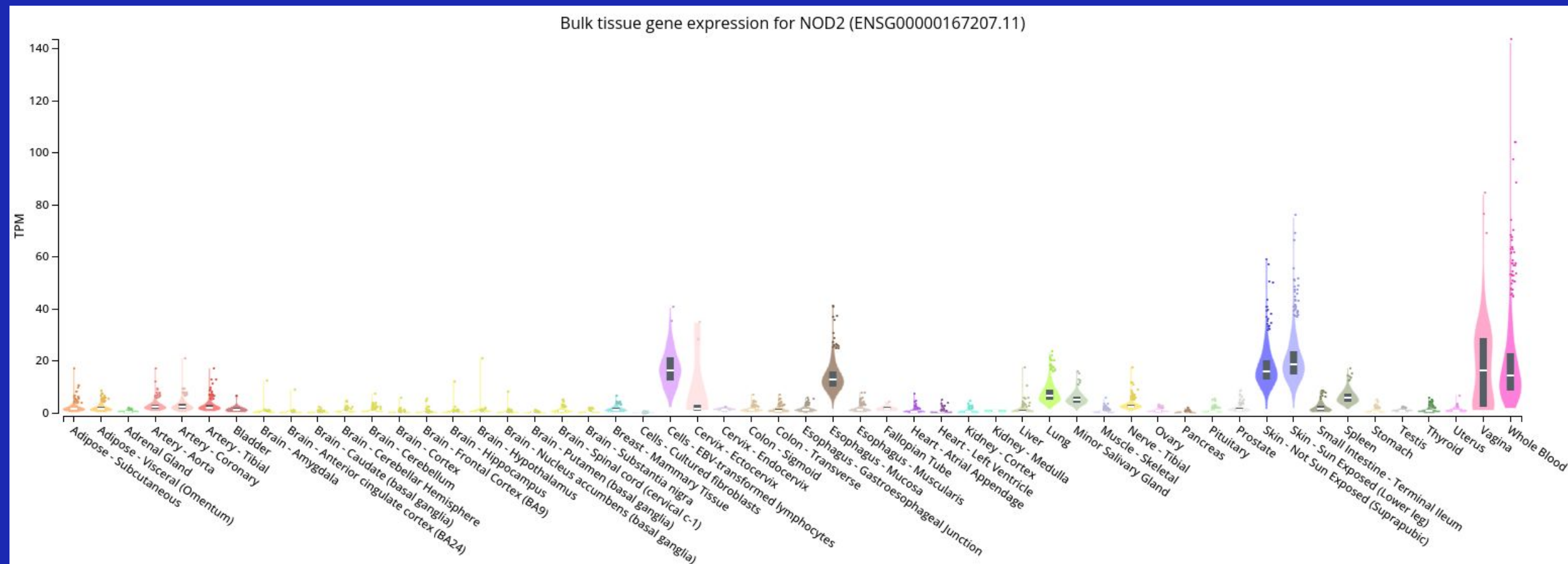
Aa SNP	# P-value	# Chromosome	≡ Gene	# Position	≡ A1	≡ A2	⌵ Clinical Significance	⌵ GWAS catalog status
 rs748855	0.0000000000005	16	NOD2	50751398	C	T	Possible	Not reported
 rs1861758	0.0000000000009	16	NOD2	50751787	T	C	Possible	Not reported
 rs3135503	0.0000000000004	16	CYLD	50791250	G	T	Not reported	Not reported
 rs17221417	0.00000002	16	NOD2	50739582	C	G	Possible	Reported
 rs3785142	0.00000118211857916311	16	CLYD	50787147	G	A	Not reported	Not reported

The following databases were researched: **Bravo**, **ClinVar** (if the registry existed), **dbSNP**, **GWAS catalog**, **GnomAD**



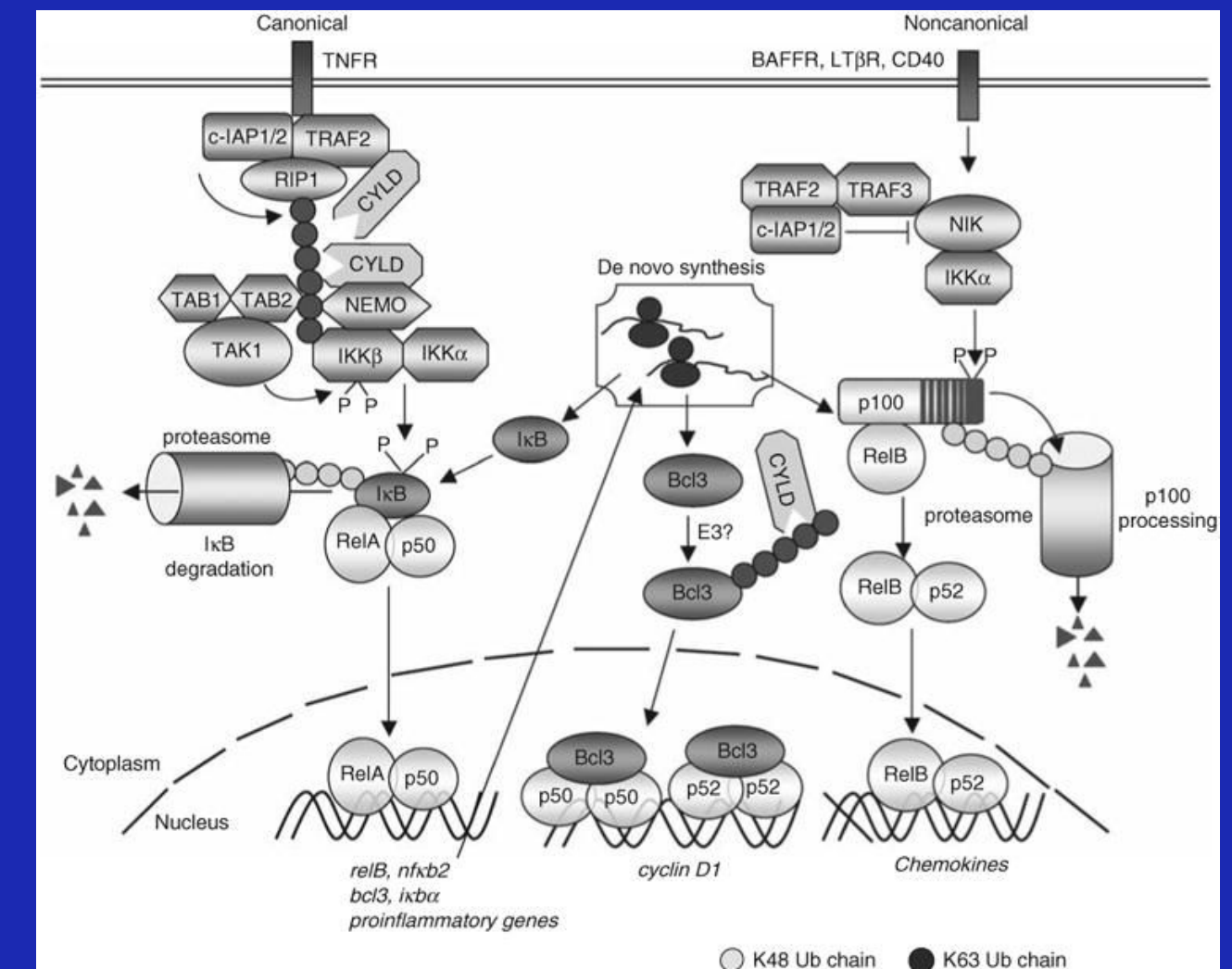
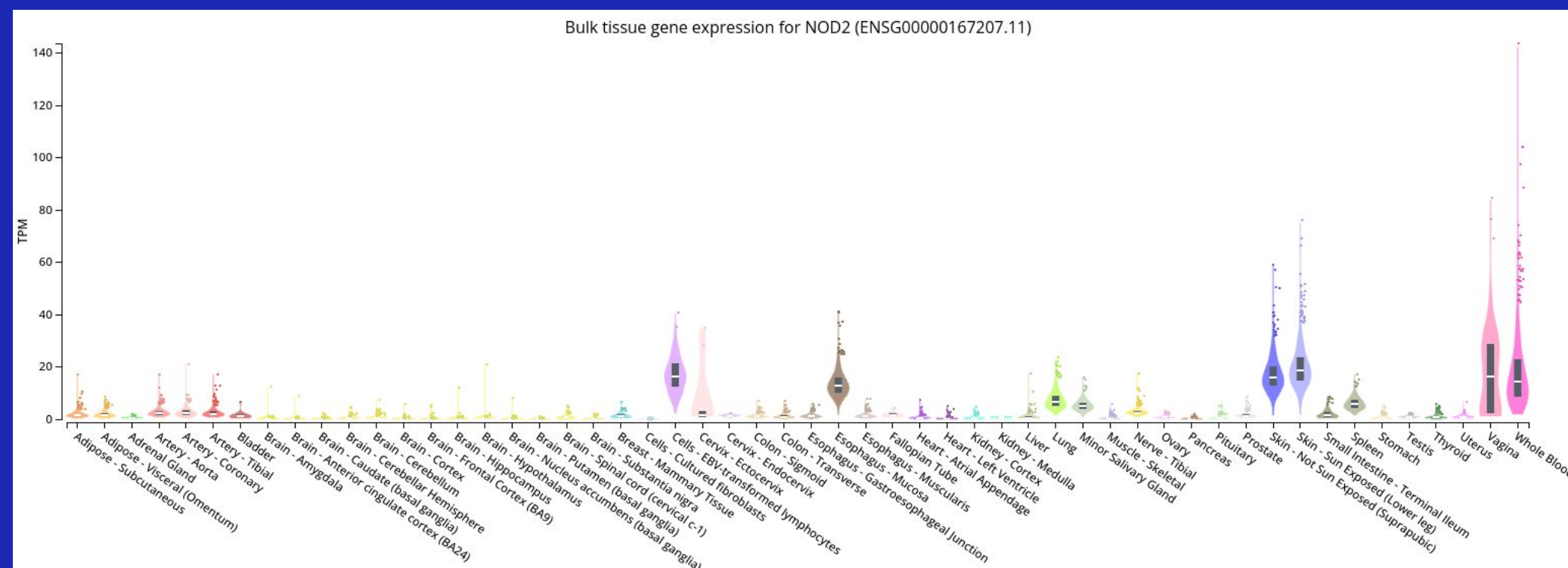
NOD2

- Involved in **recognizing certain bacteria and stimulating the immune system to respond** appropriately.
- When triggered by specific substances produced by bacteria, the NOD2 protein **turns on** a protein complex called **nuclear factor-kappa-B**.
 - This protein complex regulates the activity of multiple genes, including genes that control immune responses and inflammatory reactions.
- Its variation is associated with Crohn's disease risk



CYLD

- Deubiquitinating enzyme that removes lys63-linked ubiquitin chains and acts as a negative regulator of NF-kappa-B signaling.
- *CYLD* deubiquitinates several NF-kappa-B regulators, including TRAF2, TRAF6, and NEMO.
- Down regulated in IBD.
- Anti-inflammatory role.



CYLD

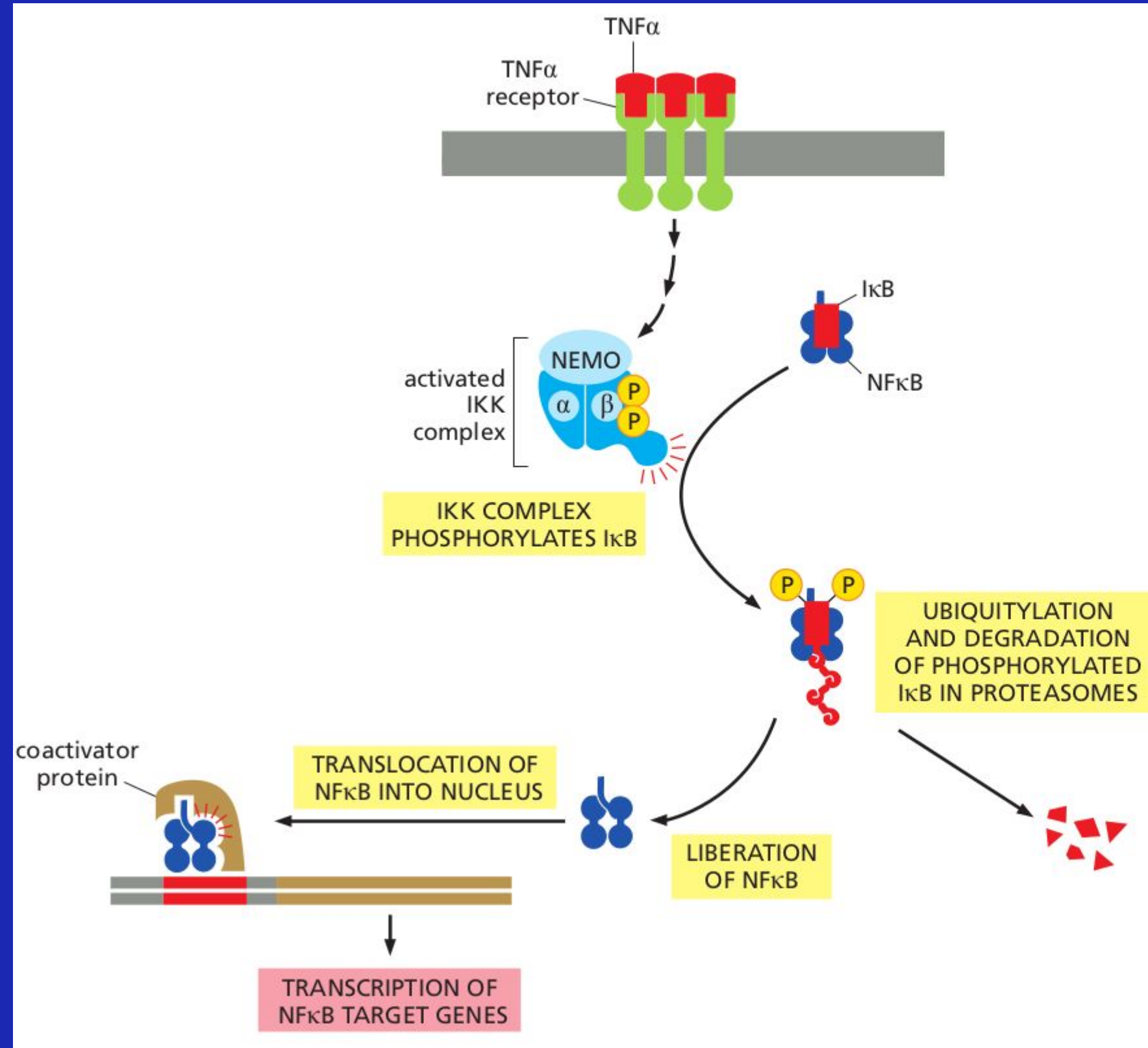


Figure 15–62 The activation of the NFκB pathway by TNFα. Both TNFα and its receptors are trimers. The binding of TNFα causes a rearrangement of the clustered cytosolic tails of the receptors, which now recruit various signaling proteins, resulting in the activation of a protein kinase that phosphorylates and activates IκB kinase kinase (IKK). IKK is a heterotrimer composed of two kinase subunits (IKKα and IKKβ) and a regulatory subunit called NEMO. IKKβ then phosphorylates IκB on two serines, which marks the protein for ubiquitylation and degradation in proteasomes. The released NFκB translocates into the nucleus, where, in collaboration with coactivator proteins, it stimulates the transcription of its target genes.

Conclusions



The susceptibility to IBD appears to be linked to various variations in the *NOD2* gene.

In the course of this study of association, there were identified three variants that had been reported previously.

Additionally, there were detected variants in the *CLYD* gene, previously unrecognized as pathogenic, suggesting their potential involvement in the development of IBD.

This investigation postulates that variants within the *CLYD* gene may contribute to the onset of inflammatory bowel disease.



Resources



- Biology Lectures (Director). (2019). NOD like receptor signaling pathway (NOD1/NOD2 signaling pathway). https://www.youtube.com/watch?v=_y9F8C_wXVg
- Hussain Biology (Director). (2019, February 18). NF- κ B Pathway | Cell Survival Pathway. <https://www.youtube.com/watch?v=8HWVhdSRvng>
- Inflammatory Bowel Disease (IBD). (2022, May 16). <https://www.hopkinsmedicine.org/health/conditions-and-diseases/inflammatory-bowel-disease>
- McDowell, C., Farooq, U., & Haseeb, M. (2023). Inflammatory Bowel Disease. In StatPearls. StatPearls Publishing. <http://www.ncbi.nlm.nih.gov/books/NBK470312/>
- NOD2 gene: MedlinePlus Genetics. (n.d.). Retrieved November 28, 2023, from <https://medlineplus.gov/genetics/gene/nod2/>
- Roda, G., Chien Ng, S., Kotze, P. G., Argollo, M., Panaccione, R., Spinelli, A., Kaser, A., Peyrin-Biroulet, L., & Danese, S. (2020). Crohn's disease. Nature Reviews Disease Primers, 6(1), Article 1. <https://doi.org/10.1038/s41572-020-0156-2>
- Seyedian, S. S., Nokhostin, F., & Malamir, M. D. (2019). A review of the diagnosis, prevention, and treatment methods of inflammatory bowel disease. Journal of Medicine and Life, 12(2), 113–122. <https://doi.org/10.25122/jml-2018-0075>
- Sun, S.-C. (2010). CYLD: A tumor suppressor deubiquitinase regulating NF- κ B activation and diverse biological processes. Cell Death and Differentiation, 17(1), 25–34. <https://doi.org/10.1038/cdd.2009.43>

