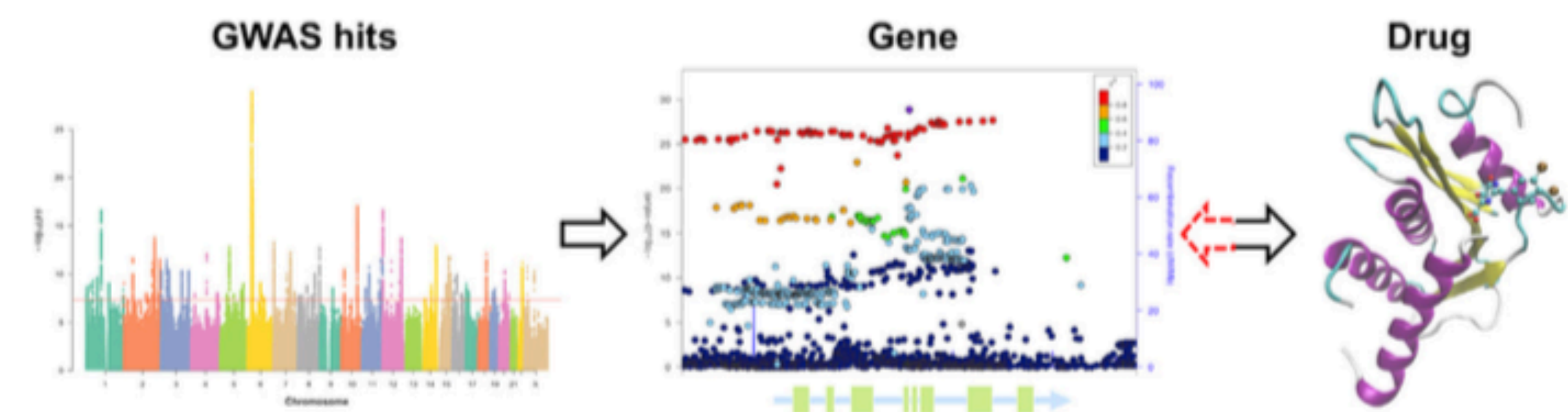
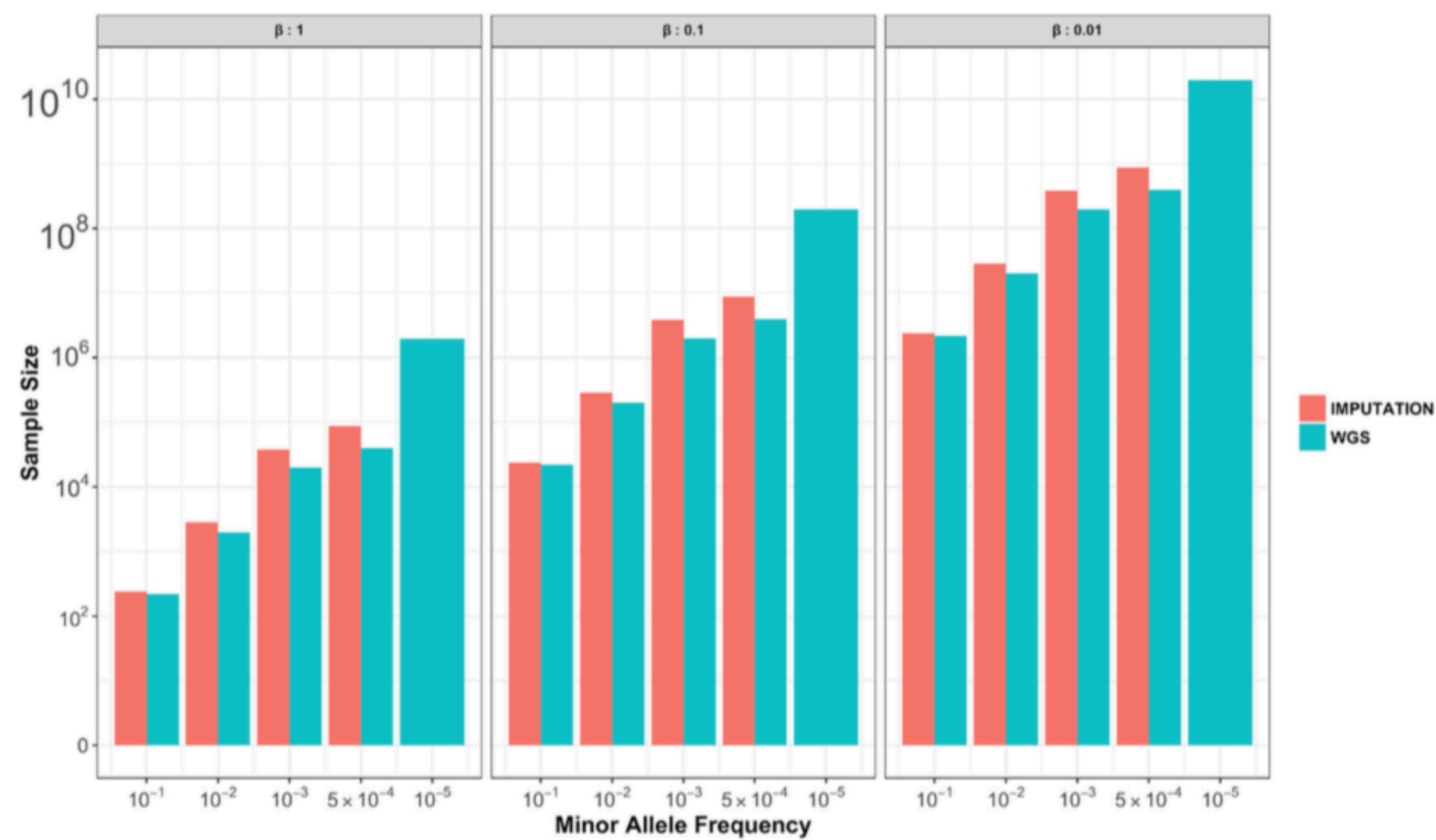


- Quanto menor a associação, mais amostras necessárias.
- Quanto menor a MAF (Minor Allele Frequency), mais amostras necessárias.
- Permite identificar genes alvo.
- Desenvolvimento de drogas.



| Trait | Gene with GWAS hits | Known or candidate drug |
|-----------------------------|--------------------------|------------------------------------|
| Type 2 Diabetes | <i>SLC30A8/KCNJ11</i> | ZnT-8 antagonists/Glyburide |
| Rheumatoid Arthritis | <i>PADI4/IL6R</i> | BB-CI-amidine/Tocilizumab |
| Ankylosing Spondylitis(AS) | <i>TNFR1/PTGER4/TYK2</i> | TNF-inhibitors/NSAIDs/fostamatinib |
| Psoriasis(Ps) | <i>IL23A</i> | Risankizumab |
| Osteoporosis | <i>RANKL/ESR1</i> | Denosumab/Raloxifene and HRT |
| Schizophrenia | <i>DRD2</i> | Anti-psychotics |
| LDL cholesterol | <i>HMGCR</i> | Pravastatin |
| AS, Ps, Psoriatic Arthritis | <i>IL12B</i> | Ustekinumab |

Diabetes tipo II

- Background genético
- Influência ambiental e comportamental.

| Table 1 Novel T2D-associated loci | | | | | | |
|-------------------------------------------|-----|-------------------|-----------------------------------------------|--------------------------------------------------|------------------------------------------------|-------|
| Novel Locus | Chr | rsID--Risk Allele | OR (95% CI) P-value | | | MAF |
| | | | Stage1 Discovery Meta-analysis | Stage2 Replication Meta-analysis | Stage1 + Stage2 Combined Meta-analysis | |
| LYPLAL1/ZC3H11B (1q41) | 1 | rs2820443-T | 1.08 (1.04-1.13) 2.94 × 10 ⁻⁴ a | 1.06 (1.03-1.09) 2.10 × 10 ⁻⁵ b | 1.07 (1.04-1.09) 2.56 × 10 ⁻⁸ c | 0.28 |
| EHMT2 (6p21.33-p21.32) | 6 | rs115884658-A | 1.34 (1.18-1.53) 1.00 × 10 ⁻⁵ a | 1.17 (1.09-1.26) 2.90 × 10 ⁻⁶ c, d | 1.21 (1.14-1.29) 3.00 × 10 ⁻¹⁰ c | 0.02 |
| ABO (9q34.2) | 9 | rs505922-C | 1.07 (1.03-1.11) 6.93 × 10 ⁻⁴ a | 1.06 (1.03-1.09) 1.90 × 10 ⁻⁵ b | 1.06 (1.04-1.09) 4.94 × 10 ⁻⁸ c | 0.34 |
| NEUROG3 (10q22.1) | 10 | rs2642587-G | 1.12 (1.08-1.16) 8.45 × 10 ⁻⁹ e | - | - | 0.22 |
| CAMKK2 (12q24.31) | 12 | rs3794205-G | 1.09 (1.05-1.14) 4.18 × 10 ⁻⁵ a | 1.06 (1.03-1.09) 1.60 × 10 ⁻⁴ b | 1.07 (1.04-1.10) 4.11 × 10 ⁻⁸ c | 0.32 |
| CALCOCO2/ATP5G1/UBE2Z/SNF8/GIP (17q21.32) | 17 | rs12453394-A | 1.08 (1.04-1.12) 7.86 × 10 ⁻⁵ a | 1.07 (1.03-1.11) 9.60 × 10 ⁻⁵ b | 1.07 (1.05-1.10) 3.23 × 10 ⁻⁸ c | 0.47 |
| AGTR2 (Xq23) | X | rs146662075-T | 3.09 (2.06-4.60) 3.24 × 10 ⁻⁸ f | 1.57 (1.19-2.07) 1.42 × 10 ⁻³ g | 1.95 (1.56-2.45) 7.85 × 10 ⁻⁹ | 0.008 |

Chr chromosome, OR odds ratio, MAF minor allele frequency

^aImputed based public GWAS discovery meta-analysis (NuGENE + GERA cohort, 7,522 cases and 50,446 controls)

^bTransancestry DIAGRAM Consortium (26,488 cases and 83,964 controls)^cMeta P-value estimated using a weighted Z-score method due to unavailable SE information from Stage 2 replication cohorts^dT2D Diabetes Genetic Portal (Exome-Chip + Exome Sequencing, 35,789 cases and 56,738 controls)^eFull imputed based public GWAS meta-analysis (NuGENE + GERA cohort + GENEVA + FUSION + WTCCC, 12,931 cases and 57,196 controls)

^f70KforT2D Men Cohort (GERA cohort + GENEVA + FUSION, 5,277 cases and 15,702 controls older than 55 years)

^gReplication Men Cohort SIGMA UK10K imputation + InterAct + Danish Cohort (case control and follow-up) + Partners Biobank + UK Biobank (18,370 cases and 88,283 controls older than 55 years and OGTT > 7.8 mmol l⁻¹, when available)

