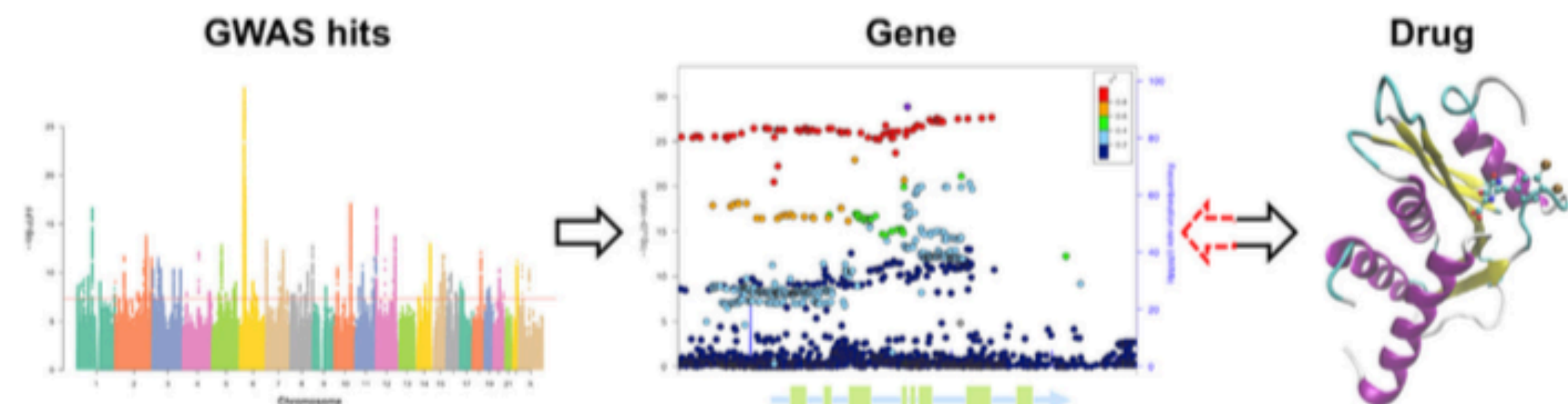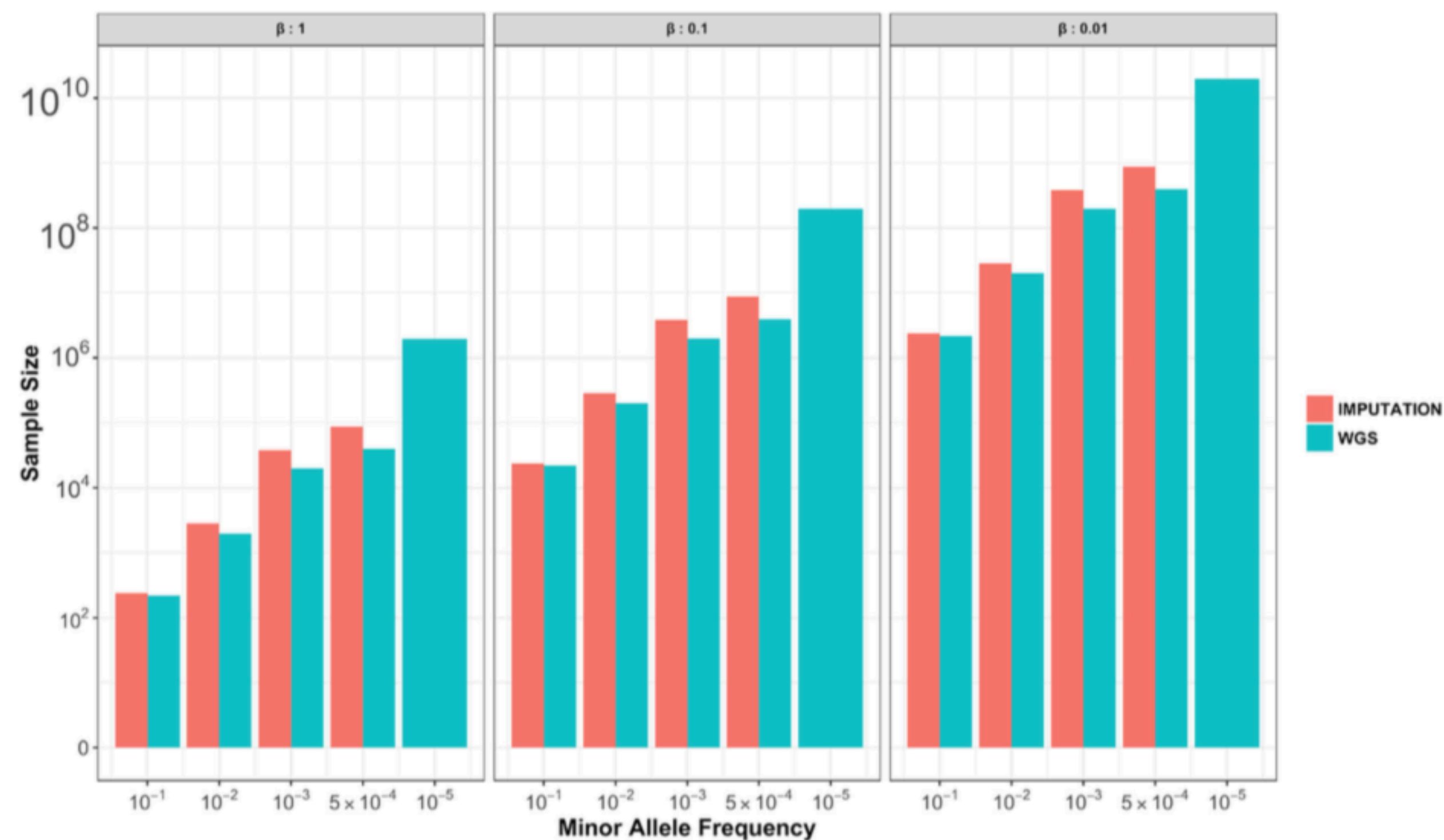- Quanto menor a associação, mais amostras necessárias.

- Quanto menor a MAF (Minor Alelle Frequency), mais amostras necessárias.

- Permite identificar genes alvo.

- Desenvolvimento de drogas.

Trait	Gene with GWAS hits	Known or candidate drug
Type 2 Diabetes	SLC30A8/KCNJ11	ZnT-8 antagonists/Glyburide
Rheumatoid Arthritis	PADI4/IL6R	BB-Cl-amidine/Tocilizumab
Ankylosing Spondylitis(AS)	TNFR1/PTGER4/TYK2	TNF-inhibitors/NSAIDs/fostamatinib
Psoriasis(Ps)	IL23A	Risankizumab
Osteoporosis	RANKL/ESR1	Denosumab/Raloxifene and HRT
Schizophrenia	DRD2	Anti-psychotics
LDL cholesterol	HMGCR	Pravastatin
AS, Ps, Psoriatic Arthritis	IL12B	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
[a] Imputed based public GWAS discovery meta-analysis (NuGENE + GERA cohort, 7,522 cases and 50,446 controls)
[b] Transancestry DIAGRAM Consortium (26,488 cases and 83,964 controls) [c] Meta P-value estimated using a weighted Z-score method due to unavailable SE information from Stage 2 replication cohorts [d] T2D Diabetes Genetic Portal (Exome-Chip + Exome Sequencing, 35,789 cases and 56,738 controls) [e] Full imputed based public GWAS meta-analysis (NuGENE + GERA cohort + GENEVA + FUSION + WTCCC, 12,931 cases and 57,196 controls)
[f] 70KforT2D Men Cohort (GERA cohort + GENEVA + FUSION, 5,277 cases and 15,702 controls older than 55 years)
[g] Replication 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)