

A

studies	genotyping_techs	countries_of_recruitment
<ul style="list-style-type: none"> study_id reported_trait initial_sample_size replication_sample_size gxe gxc snp_count qualifier imputed pooled study_design_comment full_pvalue_set user_requested 	<ul style="list-style-type: none"> study_id genotyping technology 	<ul style="list-style-type: none"> study_id ancestry_id country_name major_area region
platforms	ancestries	countries_of_origin
<ul style="list-style-type: none"> study_id manufacturer 	<ul style="list-style-type: none"> study_id ancestry_id country_name major_area region 	<ul style="list-style-type: none"> study_id ancestry_id country_name major_area region
ancestral_groups	publications	
<ul style="list-style-type: none"> study_id ancestry_id ancestral_group 	<ul style="list-style-type: none"> study_id pubmed_id publication_date publication title author_fullname author_orcid 	

C

variants	genomic_contexts	ensembl_ids
<ul style="list-style-type: none"> variant_id merged functional_class chromosome_name chromosome_position chromosome_region last_update_date 	<ul style="list-style-type: none"> variant_id gene_name chromosome_name chromosome_position distance is_closest_gene is_intergenic is_upstream is_downstream source mapping_method 	<ul style="list-style-type: none"> variant_id gene_name ensembl_id
	entrez_ids	
	<ul style="list-style-type: none"> variant_id gene_name entrez_id 	

B

associations	loci	genes
<ul style="list-style-type: none"> association_id pvalue pvalue_description pvalue_mantissa pvalue_exponent multiple_snp_haplotype snp_interaction snp_type standard_error range or_per_copy_number beta_number beta_unit beta_direction beta_description last_mapping_date last_update_date 	<ul style="list-style-type: none"> association_id locus_id haplotype_snp_count description 	<ul style="list-style-type: none"> association_id locus_id gene_name
	risk_alleles	ensembl_ids
	<ul style="list-style-type: none"> association_id locus_id variant_id risk_allele risk_frequency genome_wide limited_list 	<ul style="list-style-type: none"> association_id locus_id gene_name ensembl_id
		entrez_ids
		<ul style="list-style-type: none"> association_id locus_id gene_name entrez_id

D

traits
<ul style="list-style-type: none"> efo_id trait uri

Figure S1 | S4 representation of studies, associations, variants and traits. **(A)** S4 studies object, comprising 8 slots, i.e., 8 tables: studies, genotyping_techs, platforms, ancestries, ancestral_groups, countries_of_recruitment, countries_of_origin and publications. All tables share the primary key study_id. **(B)** S4 associations object, comprising 6 slots, i.e., 6 tables: associations, loci, risk_alleles, genes, ensembl_ids and entrez_ids. All tables share the primary key association_id. **(C)** S4 variants object, comprising 4 slots, i.e., 4 tables: variants, genomic_contexts, ensembl_ids and entrez_ids. All tables share the primary key variant_id. **(D)** S4 traits object, with one slot, i.e., one single tables: traits. The traits has the primary key efo_id.