

Data No.	Species	Description	Individuals	Markers	Format	Link
3	maize		282	50K	hapmap	https://www.panzea.org/genotypes
4	human		179	14.8M	hapmap	ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/pilot_data/paper_data_sets/a_map_of_human_variation/low_coverage/snps/
6	rice		235	30K	hapmap	http://tropgenedb.cirad.fr/tropgene/JSP/interface.jsp?module=RICE
7	soybean		20080	42K	VCF	https://soybase.org/snps/
8	arabidopsis		150	250K	hapmap	https://github.com/Gregor-Mendel-Institute/atpolydb/wiki
9	easyGWAS					https://easygwas.biochem.mpg.de/
10	Arabidopsis thaliana	F1-Hybrids (Seymour et al. 2016, PNAS)	372	204753		https://easygwas.ethz.ch/download/dataset/download/42/
11	Pristionchus pacificus	Linking genotype and phenotype in P. pacificus (McGaughran et al.)	149	2135350		https://easygwas.ethz.ch/download/dataset/download/5/
12	Drosophila melanogaster	Drosophila Genetic Reference Panel (DGRP, Mackay et al.)	172	2476799		https://easygwas.ethz.ch/download/dataset/download/3/
13	Arabidopsis thaliana	AtPolyDB (call method 75, Horton et al.)	1307	214051		https://easygwas.ethz.ch/download/dataset/download/1/
14	DRYAD					http://datadryad.org/discover?query=gwas&submit=Go
15	Parus major	Recent natural selection causes adaptive evolution of an avian polygenic trait. (Bosse et al. 2017, Science)	3,015	485,122	Plink	http://datadryad.org/resource/doi:10.5061/dryad.p03j0
16	Mice	Genome-wide association study of behavioral, physiological and gene expression traits in outbred CFW mice. (Parker et al. 2016, Nature Genetics)	1,161	92,734		http://datadryad.org/resource/doi:10.5061/dryad.2rs41
17	Parus major	Genomic dissection of variation in clutch size and egg mass in a wild great tit (Parus major) population. (Santure et al. 2013, Molecular Ecology)	2,497	5,591	Plink	http://datadryad.org/resource/doi:10.5061/dryad.ck1rq
18	Blue mussel	Linking genotype to phenotype in a changing ocean: inferring the genomic architecture of a blue mussel stress response with genome-wide association. (Kingston, et al. 2018, Journal of Evolutionary Biology)	322	over 170,000	vcf	http://datadryad.org/resource/doi:10.5061/dryad.2d8b5
19	Sorghum	Dissecting genome-wide association signals for loss-of-function phenotypes in sorghum flavonoid pigmentation traits. (Morris et al. 2013, G3)	263	265,487	hapmap	http://datadryad.org/resource/doi:10.5061/dryad.620cq
20	Maize	Insights into the maize pan-genome and pan-transcriptome. (Hirsch et al. 2014, The Plant Cell)	503	485,179		http://datadryad.org/resource/doi:10.5061/dryad.r73c5
21	Maize	TASSEL demo data				http://www.maizegenetics.net/tassel
23	yaks	Identification of genetic loci associated with growth traits at weaning in yak through a genome-wide association study	354	92K	plink	https://osf.io/23kg5/?view_only=5e1d91d8c1364488bd5d122da0377714
24	human	YRI (release 23, 90 individuals, 3.88 million SNPs)	2390	3.88M	hapmap	https://zzz.bwh.harvard.edu/plink/dist/hapmap_YRI_r23a.zip
25	Human	CEU founders (release 22, 60 individuals, filtered 2.2 million SNPs)	2260	2.2M	hapmap	https://zzz.bwh.harvard.edu/plink/dist/hapmap-ceu.zip
26	mice			138K		https://data.broadinstitute.org/mouse/hapmap/hapmapseqs.txt.gz
27	pig	Genome-Wide Association Study Reveals Candidate Genes for Growth Relevant Traits in Pigs	3200	50K	Plink	https://figshare.com/articles/dataset/pig-growth-data_zip/7533020
28	pig					https://www.animalgenome.org/cgi-bin/QLTdb/SS/index
29	peach	Genome-wide association study of 12 agronomic traits in peach	129	34K		https://figshare.com/articles/dataset/Peach_SNP_database/3486737
30	peach	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm	1580	9K		https://www.rosaceae.org/sites/default/files/files/mcl_template_genotype_May_2019_Rubus_SNPArray.zip