

Ferret: a user-friendly tool to extract data from the 1000 Genomes Project

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Welcome to Ferret Locus Gene SNP									
Input gene(s): APOL	OR Browse No file some Input gene as: Name ID It frequencies from the Exome Sequen	selected Clear							
All Populations All All Populations (n=2,504)	Africans ✓ AFR All Africans (n=661) ☐ ACB African Caribbean (n=96) ☐ ASW African American (n=61) ☐ ESN Esan (n=99) ☐ GWD Gambian (n=113) ☐ LWK Luhya (n=99) ☐ MSL Mende (n=85) ☐ YRI Yoruba (n=108)	Americans AMR All Americans (n=347) CLM Colombian (n=94) MXL Mexican American (n=64) PEL Peruvian (n=85) PUR Puerto Rican (n=104)							
East Asians EAS All East Asians (n=504) CDX Dai Chinese (n=93) CHB Han Chinese (n=103) CHS Southern Han Chinese (n=105) JPT Japanese (n=104) KHV Kinh Vietnamese (n=99) CHD Denver Chinese (n=0)	Europeans EUR All Europeans (n=503) CEU CEPH (n=99) GBR British (n=91) FIN Finnish (n=99) IBS Spanish (n=107) TSI Tuscan (n=107)	South Asians SAS All South Asians (n=489) BEB Bengali (n=86) GIH Gujarati Indian (n=103) ITU Indian Telugu (n=102) PJL Punjabi (n=96) STU Sri Lankan Tamil (n=102)							
Browse	File Location: /Users/limousm/Des	ktop/APOL1_AFR							

Retrieve 1000 Genomes Project data (and optionally Exome Sequencing Project –ESP– data)

.map file .ped file .info file

PLINK files an be merged with

can be merged with user's dataset, etc.

HaploView files

data visualization, LD pattern, haplotypes, tagSNP design, etc.

.frq file Allele frequency file

				1	NB_1KG_	1KG_A1	ESP6500_EA	ESP6500_AA
CHR	VARIANT	POS	A1	A2	CHR	_FREQ	_A1_FREQ	_A1_FREQ
22	rs6000220	36649966	С	Τ	1322	0.8517	0.883	0.8418
22	rs182609191	36650106	Т	C	1322	1.0	0.9893	0.9986
22	chr22_36650116	36650116	TTAAAA	Τ			0.9999	0.9998
22	rs13057901	36650481	Т	C	1322	0.8464		
22	rs9610468	36650956	G	Α	1322	0.9622	0.815	0.9217
22	indel_rs136158_AT/A	36656652	AT	Α	1322	0.6354	•	

Unique advantages of Ferret

- User-friendly interface
- Accepts input query as locus, gene(s), or SNP(s)
- Handles SNPs and indels
- Outputs suitable for well-known pre-existing tools
- Computes allelic frequency for SNPs, indels and CNVs
- Retrieves allelic frequency from ESP

Future prospects:

- Minor GUI improvements
- Add a plugin with HaploView