**Proxy Search** 

Pairwise LD

**Plots** 

Map SNP IDs

ReACH

SNAP finds proxy SNPs based on linkage disequilibrium, physical distance and/or membership in selected commercial genotyping arrays. Pair-wise linkage disequilibrium is pre-calculated based on phased genotype data from the <a href="International HapMap Project">International HapMap Project</a> and the <a href="1000">1000</a> Genomes Project. Information about the genotyping arrays is based on data published by the vendors

<u>Ge</u>	nomes Project. Info ndors.	ormation about the					by t
	Query SNPs						
	Input SNPs:	File	<b>▼</b>	xample			
	File:	Choose File get_fr	eq.txt				
	SNP column:	1 He	eader li	ne: no	▼		
	Search Options						
	SNP data set:	1000 Genomes Pilot	1 ▼	r <sup>2</sup>	threshold:	1.0	▼
	Population panel:	CEU ▼		Dist	tance limit:	0	▼
	Output Options						
	Download to:	File ▼				as a proxy for it ages in output	:self
	Filter By Array	0 Illumina array(s	s) and 0 A	Affymetrix ar	ray(s) selecte	d	
Lin	nit search results to	only SNPs on the	selected	l arrays (se	elect all)		
App	Select All Illumi Illumina Human-1 Illumina HumanH Illumina HumanH Illumina Human3 Illumina HumanH Illumina HumanH Illumina HumanH Illumina HumanH Illumina HumanH Illumina GARe iSe Illumina CARe iSe Illumina OmniQua Cardio-Metabochi Illumina OmniExp Human Exome 12 Human Exome 12 OmniChip 2.5M 4 OmniChip 2.5M 4 OmniChip 5M 4 sa Omni 5 Exome (Coomni Express Exo Immuno BeadChip Immuno BeadChip Iply array filter to:	ap240S (I2) ap300 (I3) 70CNV single (IC) 70CNV quad (ICQ) ap550 (I5) ap650 (I6) ap610 quad (I6Q) M single (IM) M dual (IMD) elect (IBC) CYT) ad (OQ) p (CM) uad (IWQ) press (OE) v1 (E1) v1.1 (E11) sam (O24) sam (O24) sam (O54) 05E) p A (ICA) p B (ICB)		Affymetrix	50K Mappin 50K Human 250K Mappi 250K Mappi 5.0 (A5) 6.0 (A6) Axiom GW_ DMET plus ( 10K Mappin Axiom Exon	g XbaI (AX) g HindIII (AH) Gene Focused ng NspI (AN) ng StyI (AS)  _Hu_SNP (AxM)	10) AAE)

<ul> <li>□ D' (D prime)</li> <li>□ Genome Coordinates</li> <li>□ Array Membership</li> <li>□ Associated Gene Annotations</li> <li>✔ Include Minor Allele Frequence</li> </ul>	Recombination Rate (cM/Mb) Genetic Distance (cM) Genetic Map Position (cM) from GeneCruiser (decreases performance) cy search reset
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