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A second generation human haplotype map of over 3.1 million SNPs

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1477	Toll-like receptor gene polymorphisms are associated with susceptibility to Graves' ophthalmopathy in Taiwan males. <b>2010</b> , 11, 154	39
1476	Common genetic variants on chromosome 9p21 are associated with myocardial infarction and type 2 diabetes in an Italian population. <b>2010</b> , 11, 60	16
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1474	Primate-specific evolution of noncoding element insertion into PLA2G4C and human preterm birth. <b>2010</b> , 3, 62	10
1473	ATHENA: A knowledge-based hybrid backpropagation-grammatical evolution neural network algorithm for discovering epistasis among quantitative trait Loci. <b>2010</b> , 3, 5	40
1472	Association of 17 prostate cancer susceptibility loci with prostate cancer risk in Chinese men. <b>2010</b> , 70, 425-32	47
1471	A DNA-Origami chip platform for label-free SNP genotyping using toehold-mediated strand displacement. <b>2010</b> , 6, 1854-8	115
1470	Pharmacogenomics: a systems approach. <b>2010</b> , 2, 3-22	40
1469	Our changing view of the genomic landscape of cancer. <b>2010</b> , 220, 231-43	64
1468	Linkage disequilibrium pattern in asthma candidate genes from 5q31-q33 in the Singapore Chinese population. <b>2010</b> , 74, 137-45	8
1467	Population-specific susceptibility to Crohn's disease and ulcerative colitis; dominant and recessive relative risks in the Japanese population. <b>2010</b> , 74, 126-36	32
1466	APOE is not associated with Alzheimer disease: a cautionary tale of genotype imputation. <b>2010</b> , 74, 189-94	11
1465	Identification of interacting genes in genome-wide association studies using a model-based two-stage approach. <b>2010</b> , 74, 406-15	1
1464	Discovery, evaluation and distribution of haplotypes of the wheat Ppd-D1 gene. <b>2010</b> , 185, 841-51	95

1463	A genome-wide association study identifies multiple loci associated with mathematics ability and disability. <b>2010</b> , 9, 234-47	81
1462	Association between genetic variants of the metabotropic glutamate receptor 3 (GRM3) and cognitive set shifting in healthy individuals. <b>2010</b> , 9, 459-66	14
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1459	A genome-wide association study using selective DNA pooling identifies candidate markers for fertility in Holstein cattle. <b>2010</b> , 41, 570-8	51
1458	Genetic variation in CLDN1 and susceptibility to hepatitis C virus infection. <b>2010</b> , 17, 192-200	20
1457	Endocrine autoimmune disease: genetics become complex. <b>2010</b> , 40, 1144-55	22
1456	Admixture mapping of obesity-related traits in African Americans: the Atherosclerosis Risk in Communities (ARIC) Study. <b>2010</b> , 18, 563-72	41
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1453	A genome-wide linkage scan reveals CD53 as an important regulator of innate TNF-alpha levels. <b>2010</b> , 18, 953-9	21
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1450	Risk of autoimmune diabetes in APECED: association with short alleles of the 5'insulin VNTR. <b>2010</b> , 11, 590-7	12
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1448	The CRF system, stress, depression and anxiety-insights from human genetic studies. <b>2010</b> , 15, 574-88	267
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1439	Assessing sources of inconsistencies in genotypes and their effects on genome-wide association studies with HapMap samples. <b>2010</b> , 10, 364-74		18
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1437	A genome-wide association study identifies pancreatic cancer susceptibility loci on chromosomes 13q22.1, 1q32.1 and 5p15.33. <b>2010</b> , 42, 224-8		463
1436	Genome-wide association study of hematological and biochemical traits in a Japanese population. <b>2010</b> , 42, 210-5		388
1435	Genome-wide meta-analyses identify multiple loci associated with smoking behavior. <b>2010</b> , 42, 441-7		927
1434	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. <b>2010</b> , 42, 436-40		521
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1432	Genome-wide association study identifies a sequence variant within the DAB2IP gene conferring susceptibility to abdominal aortic aneurysm. <b>2010</b> , 42, 692-7		155
1431	Genome-wide association study identifies variants in the CFH region associated with host susceptibility to meningococcal disease. <b>2010</b> , 42, 772-6		221
1430	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. <b>2010</b> , 42, 869-73		277
1429	PRDM9 variation strongly influences recombination hot-spot activity and meiotic instability in humans. <b>2010</b> , 42, 859-63		243
1428	High-throughput, pooled sequencing identifies mutations in NUBPL and FOXRED1 in human complex I deficiency. <b>2010</b> , 42, 851-8		292

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1425 Genome-wide association study identifies a psoriasis susceptibility locus at TRAF3IP2. <b>2010</b> , 42, 991-5	283
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1404	Fertile soil or no man land:. 165-173	11
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1395	Protein Bioinformatics Infrastructure for the Integration and Analysis of Multiple High-Throughput "omics" Data. <b>2010</b> , 423589	15
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1393	The characterization of twenty sequenced human genomes. <b>2010</b> , 6, e1001111	133
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1382 1381	Domain altering SNPs in the human proteome and their impact on signaling pathways. <b>2010</b> , 5, e12890  Genome-wide data-mining of candidate human splice translational efficiency polymorphisms (STEPs) and an online database. <b>2010</b> , 5, e13340	5
1381	Genome-wide data-mining of candidate human splice translational efficiency polymorphisms	
1381	Genome-wide data-mining of candidate human splice translational efficiency polymorphisms (STEPs) and an online database. <b>2010</b> , 5, e13340	4
1381	Genome-wide data-mining of candidate human splice translational efficiency polymorphisms (STEPs) and an online database. <b>2010</b> , 5, e13340  Genomic runs of homozygosity record population history and consanguinity. <b>2010</b> , 5, e13996	281
1381 1380 1379	Genome-wide data-mining of candidate human splice translational efficiency polymorphisms (STEPs) and an online database. <b>2010</b> , 5, e13340  Genomic runs of homozygosity record population history and consanguinity. <b>2010</b> , 5, e13996  Presymptomatic risk assessment for chronic non-communicable diseases. <b>2010</b> , 5, e14338  Development of two multiplex mini-sequencing panels of ancestry informative SNPs for studies in	4 281 11
1381 1380 1379 1378	Genome-wide data-mining of candidate human splice translational efficiency polymorphisms (STEPs) and an online database. 2010, 5, e13340  Genomic runs of homozygosity record population history and consanguinity. 2010, 5, e13996  Presymptomatic risk assessment for chronic non-communicable diseases. 2010, 5, e14338  Development of two multiplex mini-sequencing panels of ancestry informative SNPs for studies in Latin Americans: an application to populations of the State of Minas Gerais (Brazil). 2010, 9, 2069-85	4 281 11
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1365 Search for cance	er risk factors with microarray-based genome-wide association studies. <b>2010</b> , 9, 107-21	7
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-	eling of complex disease by random forests. <b>2010</b> , 72, 73-99  ositive selection apparent in a small sample of human exomes. <b>2010</b> , 20, 1327-34	26 18
1363 Signatures of po		
1363 Signatures of po	ositive selection apparent in a small sample of human exomes. <b>2010</b> , 20, 1327-34	18
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1340	CYP2C19*2 and CYP2C9*3 alleles are associated with stent thrombosis: a case-control study. <b>2010</b> , 31, 3046-53	118
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1336	Refining the prostate cancer genetic association within the JAZF1 gene on chromosome 7p15.2. <b>2010</b> , 19, 1349-55	21
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1333	Candidate gene association resource (CARe): design, methods, and proof of concept. <b>2010</b> , 3, 267-75	125
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1323	A Bayesian approach using covariance of single nucleotide polymorphism data to detect differences in linkage disequilibrium patterns between groups of individuals. <b>2010</b> , 26, 1999-2003	5
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1318	Genome-wide association study of height and body mass index in Australian twin families. <b>2010</b> , 13, 179-93	51
1317	Personalized healthcare in clotting disorders. <b>2010</b> , 7, 65-73	
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1315	Current concepts of pharmacogenetics, pharmacogenomics, and the druggable genome. 2010, 205-223	
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1305	Genetic polymorphism of inosine-triphosphate-pyrophosphatase influences mercaptopurine metabolism and toxicity during treatment of acute lymphoblastic leukemia individualized for thiopurine-S-methyl-transferase status. <b>2010</b> , 9, 23-37	48
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1303	Evolving molecular diagnostics for familial cardiomyopathies: at the heart of it all. <b>2010</b> , 10, 329-51	22
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1296	Progress in the genetics of common obesity and type 2 diabetes. <b>2010</b> , 12, e7	67
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1294	Variant of TYR and autoimmunity susceptibility loci in generalized vitiligo. <b>2010</b> , 362, 1686-97	281
1293	Colloquium paper: genome-wide patterns of population structure and admixture among Hispanic/Latino populations. <b>2010</b> , 107 Suppl 2, 8954-61	293
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1288	Impact of replication timing on non-CpG and CpG substitution rates in mammalian genomes. <b>2010</b> , 20, 447-57	151
1287	Germline genetic markers for urinary bladder cancer risk, prognosis and treatment response. <b>2010</b> , 6, 1433-60	14
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