Table 1. Loci in which inferred selection is identified in all populations (PLG, CEU, CHB, JPT, and YRI) . HP: Host-Pathogen. RP: Reproduction. DM: DNA Metabolism. CC: Cell-Cycle. PM: Protein Metabolism. NF: Neuronal Function.

Gene	HP	RP	DM	CC	PM	NF	Description
IL1RAPL2	X					X	The protein encoded by this gene is a member of the interleukin 1 receptor family. This protein is similar to the interleukin 1 accessory proteins, and is most closely related to interleukin 1 receptor accessory protein-like 1 (IL1RAPL1). This gene and IL1RAPL1 are located at a region on chromosome X that is associated with X-linked non-syndromic mental retardation.
FOLH1		X			X	X	This gene encodes a type II transmembrane glycoprotein belonging to the M28 peptidase family. Three functionally distinct proteins are encoded, including folylpoly-gamma-glutamate carboxypeptidase in the intestine, N-acetylated alpha-linked acidic dipeptidase 1 in the brain, and prostate-specific membrane antigen in the prostate. A mutation in the intestinal form may be associated with impaired intestinal absorption of dietary folates, resulting in low blood folate levels and consequent hyperhomocysteinemia. The form expressed in the brain may be involved in a number of pathological conditions associated with glutamate excitotoxicity. The prostate form is up-regulated in cancerous cells and is used as an effective diagnostic and prognostic indicator of prostate cancer. This gene likely arose from a duplication event of a nearby chromosomal region. Alternative splicing gives rise to multiple transcript variants.
KIAA1463					X	X	Next to MAP1A and CKMT1: creatine kinase, mitochondrial 1 (ubiquitous)
PRRG1					X	X	gla residues are produced after subsequent posttranslational modifications of glutamate by a vitamin k-dependent gamma-carboxylase. Tissue Specificity: highly expressed in the spinal cord
S66645/TYR					X	X	This is a copper-containing oxidase that functions in the formation of pigments such as melanins and other polyphenolic compounds. Catalyzes the rate-limiting conversions of tyrosine to DOPA, DOPA to DOPA-quinone and possibly 5,6-dihydroxyindole to indole-5,6 quinone.
TTBK2					X	X	tau tubulin kinase 2
AK096379				X		X	Close to MAGED4
BC034574				X		X	calmodulin-binding protein which may function as scaffolding or signaling protein and may play a role in dendritic ca(2+) signaling
AUTS2						X	
BX537851						X	67% normalized expression in amygdala
COH1						X	This protein may play a role in the development and the function of the eye, hematological system, and central nervous system. Mutations in this gene have been associated with Cohen syndrome. No Mouse/Rat/Zebrafish/Fly/C elegans/yeast homolog
COL4A6						X	Basement membrane abnormalities causes eye problem and renal problem. Responsible for Alport Syndrome; head to head with COL4A5;
CSEN						X	This gene encodes a member of the family of voltage-gated potassium (Kv) channel-interacting proteins (KCNIPs), which belong to the recoverin branch of the EF-hand superfamily. Members of the KCNIP family are small calcium binding proteins. They all have EF-hand-like domains, and differ from each other in the N-terminus. They are integral subunit components of native Kv4 channel complexes. They may regulate A-type currents, and hence neuronal excitability, in response to changes in intracellular calcium. The protein encoded by this gene is also shown to function as a calcium-regulated transcriptional repressor, and to interact with presenilins. Mutations in the presenilin genes have been implicated in Alzheimer's disease. Due to utilization of an alternate in-frame translation start codon, this gene encodes two isoforms with different sizes.
GALK2						X	This gene encodes a highly efficient N-acetylgalactosamine (GalNAc) kinase, which has galactokinase activity when galactose is present at high concentrations. Two alternatively spliced transcript variants encoding different isoforms have been found for this gene.
GLRA2						X	the glycine receptor is a neurotransmitter-gated ion channel. binding of glycine to its receptor increases the chloride conductance and thus produces hyperpolarization (inhibition of neuronal firing).
HCN1						X	Hyperpolarization-activated cation channels of the HCN gene family, such as HCN1, contribute to spontaneous rhythmic activity in both heart and brain.[supplied by OMIM].
OPHN1						X	Oligophrenin 1 has 25 exons and encodes a Rho-GTPase-activating protein. The Rho proteins are important mediators of intracellular signal transduction, which affects cell migration and cell morphogenesis. Mutations in this gene are responsible for non-specific X-linked mental retardation
OR4A5						X	Olfactory receptors interact with odorant molecules in the nose, to initiate a neuronal response that triggers the perception of a smell. The olfactory receptor proteins are members of a large family of G-protein-coupled receptors (GPCR) arising from single coding-exon genes. Olfactory receptors share a 7-transmembrane domain structure with many neurotransmitter and hormone receptors and are responsible for the recognition and G protein-mediated transduction of odorant signals. The olfactory receptor gene family is the largest in the genome. The nomenclature assigned to the olfactory receptor genes and proteins for this organism is independent of other organisms.
OR4C13						X	
OR4X1						X	
OR5AS1						X	
OR8I2						X	
OR8K1						X	
PROM2						X	defects in prom1 are the cause of an autosomal recessive form of retinal degeneration [mim:604365]. the disease is characterized by night blindness and loss of peripheral vision from childhood with progression to profound visual impairment and extinguished electroretinograms by the third decade. a single nucleotide deletion yields a truncated protein lacking half of the second extracellular loop, the final membrane-spanning domain and the cytoplasmic c-terminus.
RAPSN						X	This protein belongs to a family of proteins that are receptor associated proteins of the synapse. It contains a conserved cAMP-dependent protein kinase phosphorylation site. It is believed to play some role in anchoring or stabilizing the nicotinic acetylcholine receptor at synaptic sites. It may link the receptor to the underlying postsynaptic cytoskeleton, possibly by direct association with actin or spectrin. Two splice variants have been identified for this gene.
RTN1						X	This gene belongs to the family of reticulon encoding genes. Reticulons are associated with the endoplasmic reticulum, and are involved in neuroendocrine secretion or in membrane trafficking in neuroendocrine cells. Alternatively spliced transcript variants encoding different isoforms have been identified. Multiple promoters rather than alternative splicing of internal exons seem to be involved in this diversity.
SNTG1						X	The protein encoded by this gene is a member of the syntrophin family. Syntrophins are cytoplasmic peripheral membrane proteins that typically contain 2 pleckstrin homology (PH) domains, a PDZ domain that bisects the first PH domain, and a C-terminal domain that mediates dystrophin binding. This gene is specifically expressed in the brain. Transcript variants for this gene have been described, but their full-length nature has not been determined.

PSMC3	X				X		The 26S proteasome is a multicatalytic proteinase complex with a highly ordered structure composed of 2 complexes, a 20S core and a 19S regulator. The 20S core is composed of 4 rings of 28 non-identical subunits; 2 rings are composed of 7 alpha subunits and 2 rings are composed of 7 beta subunits. The 19S regulator is composed of a base, which contains 6 ATPase subunits and 2 non-ATPase subunits, and a lid, which contains up to 10 non-ATPase subunits. Proteasomes are distributed throughout eukaryotic cells at a high concentration and cleave peptides in an ATP/ubiquitin-dependent process in a non-lysosomal pathway. An essential function of a modified proteasome, the immunoproteasome, is the processing of class I MHC peptides. This gene encodes one of the ATPase subunits, a member of the triple-A family of ATPases which have a chaperone-like activity. This subunit may compete with PSMC2 for binding to the HIV tat protein to regulate the interaction between the viral protein and the transcription complex. A pseudogene has been identified on chromosome 9. FUNCTION: Interacts with the human
SERPINC1	X				X		Most important serine protease inhibitor in plasma that regulates the blood coagulation cascade. AT-III inhibits thrombin as well as factors IXa, Xa and XIa. Its inhibitory activity is greatly enhanced in the presence of heparin.
ADK	X						This gene encodes adenosine kinase, an abundant enzyme in mammalian tissues. The enzyme catalyzes the transfer of the gamma-phosphate from ATP to adenosine, thereby serving as a regulator of concentrations of both extracellular adenosine and intracellular adenine nucleotides. Adenosine has widespread effects on the cardiovascular, nervous, respiratory, and immune systems and inhibitors of the enzyme could play an important pharmacological role in increasing intravascular adenosine concentrations and acting as anti-inflammatory agents. Alternative splicing results in two transcript variants encoding different isoforms. Both isoforms of the enzyme phosphorylate adenosine with identical kinetics and both require Mg2+ for activity.
AF035029	X						
AF035035	X						
AP3M1	X						
CSMD3	X						ca(2+)-dependent receptor for myeloid cells that binds to carbohydrates on neutrophils and monocytes. mediates the interaction of activated endothelial cells or platelets with leukocytes. the ligand recognized is sialyl-lewis x.
D63480	X						CEBPD overlap
F8	X						Defects in this gene results in hemophilia A, a common recessive X-linked coagulation disorder.
FLJ42925	X						LANCL3: LanC lantibiotic synthetase component C-like 3 (bacterial)
LRBA	X						Patients with Chediak-Higashi syndrome (CHS1; MIM 214500) suffer from a systemic immunodeficiency involving defects in polarized trafficking of vesicles in a number of immune system cell types. In mouse, this syndrome is reproduced in strains with a mutation in the 'beige' gene that results in proteins lacking the BEACH (beige and CHS1) domain and C-terminal WD repeats. LRBA contains key features of both beige/CHS1 and A kinase anchor proteins (AKAPs; see MIM 602449).[supplied by OMIM].
SCAP1	X						The protein encoded by this gene belongs to the src family kinases. It is a cytoplasmic protein which is preferentially expressed in T-lymphocytes where it interacts with the protein-tyrosine kinase p59fyn. The presence of a PH domain and a SH3 domain suggests that this encoded protein is capable of interacting with several other intracellular proteins.
SPI1	X						binds to the pu-box, a purine-rich dna sequence (5'- gaggaa-3') that can act as a lymphoid-specific enhancer. this protein is a transcriptional activator that may be specifically involved in the differentiation or activation of macrophages or b- cells.
SUPT3H	X		X	X			Transcription initiation protein SPT3 homolog (SPT3-like protein).
NCOA6		X	X		X		The protein encoded by this gene is a transcriptional coactivator that can interact with nuclear hormone receptors to enhance their transcriptional activator functions. The encoded protein has been shown to be involved in the hormone-dependent coactivation of several receptors, including prostanoid, retinoid, vitamin D3, thyroid hormone, and steroid receptors. The encoded protein may also act as a general coactivator since it has been shown to interact with some basal transcription factors, histone acetyltransferases, and methyltransferases.
AK091585		X	X				Zinc Finger Transcription Factor predominantly in Testis
AK131264		X	X				Zinc Finger Transcription Factor predominantly in Testis
AK131417		X	X				Zinc Finger Transcription Factor predominantly in Testis
AK097440		X					
AK131413		X					
ECM2		X					expressed predominantly in adipose tissue as well as female-specific organs such as mammary gland, ovary, and uterus.
POTE8		X					Prostate, ovary, testis expressed protein on chromosome 8
RNF18		X					The protein encoded by this gene contains a RING zinc finger, a motif known to be involved in protein-protein interactions. This gene has been found to be preferentially expressed in testis.
STS		X					The protein encoded by this gene catalyzes the conversion of sulfated steroid precursors to estrogens during pregnancy. The encoded protein is found in the endoplasmic reticulum, where it acts as a homodimer. Mutations in this gene are known to cause X-linked ichthyosis (XLI).
SLC39A13			X		X		Zinc is an essential cofactor for hundreds of enzymes. It is involved in protein, nucleic acid, carbohydrate, and lipid metabolism, as well as in the control of gene transcription, growth, development, and differentiation. SLC39A13 belongs to a subfamily of proteins that show structural characteristics of zinc transporters (Taylor and Nicholson, 2003).[supplied by OMIM].
ZBTB37			X		X		Zinc finger and BTB domain containing 37
ZNF192			X		X		May be involved in transcriptional regulation.
ZNF193			X		X		May be involved in transcriptional regulation.
BRODL			X	X			Predominantly Expressed in Larynx(46.68%) and Thymus(14.4%)
CSE1L			X	X			Proteins that carry a nuclear localization signal (NLS) are transported into the nucleus by the importin-alpha/beta heterodimer. Importin-alpha binds the NLS, while importin-beta mediates translocation through the nuclear pore complex. After translocation, RanGTP binds importin-beta and displaces importin-alpha. Importin-alpha must then be returned to the cytoplasm, leaving the NLS protein behind. The protein encoded by this gene binds strongly to NLS-free importin-alpha, and this binding is released in the cytoplasm by the combined action of RANBP1 and RANGAP1. In addition, the encoded protein may play a role both in apoptosis and in cell proliferation. Multiple transcript variants encoding several different isoforms have been described for this gene.
FANCC			X	X			The protein encoded by this gene delays the onset of apoptosis and promotes homologous recombination repair of damaged DNA. Mutations in this gene result in Fanconi anemia.
PARP4			X	X			This gene encodes poly(ADP-ribosyl)transferase-like 1 protein, which contains a catalytic domain and is capable of catalyzing a poly(ADP-ribosyl)ation reaction. This protein has a catalytic domain which is homologous to that of poly (ADP-ribosyl) transferase, but lacks an N-terminal DNA binding domain which activates the C-terminal catalytic domain of poly (ADP-ribosyl) transferase. Since this protein is not capable of binding DNA directly, its transferase activity may be activated by other factors such as protein-protein interaction mediated by the extensive carboxyl terminus.
PNUTL2			X	X			This gene is a member of the septin gene family of nucleotide binding proteins, originally described in yeast as cell division cycle regulatory proteins. Septins are highly conserved in yeast, Drosophila, and mouse and appear to regulate cytoskeletal organization. The protein encoded by this gene is thought to be part of a complex involved in cytokinesis. Alternate splicing of this gene results in four transcript variants which encode different isoforms.
TP53INP2			X	X			
AF318371			X				Zinc Finger Transcription Factor

BC046415			X				Zinc Finger Transcription Factor
CPEB3			X				
DJ467N11.1			X				
HGNT-IV-H			X				UDP-N-acetylglucosamine:alpha-1,3-D-mannoside beta-1,4-N- acetylglucosaminyltransferase IV-homologue. FUNCTION: Binds specifically to U7 snRNA (By similarity).
HKR1			X				Krueppel-related zinc finger protein 1
KHDRBS2			X				KH domain-containing, RNA-binding, signal transduction-associated protein 2.
MGC46496			X				binds to g-rich structures in 28s rrna and in mrnas. plays a regulatory role in the translation apparatus; inhibits cell-free translation of mrnas.
NT5C2			X				Purine 5-prime-nucleotidase (EC 3.1.3.5) preferentially hydrolyzes inosine 5-prime-monophosphate (IMP) and other purine nucleotides, and is allosterically activated by various compounds, including ATP. The enzyme is exclusively located in the cytoplasmic matrix of cells and may have a critical role in the maintenance of a constant composition of intracellular purine/pyrimidine nucleotides in cooperation with other nucleotidases.[supplied by OMIM].
RAD51C			X				This gene is a member of the RAD51 family of related genes, which encode strand-transfer proteins thought to be involved in recombinational repair of damaged DNA and in meiotic recombination. This gene product interacts with two other DNA repair proteins, encoded by RAD51B and XRCC3, but not with itself. The protein copurifies with XRCC3 protein in a complex, reflecting their endogenous association and suggesting a cooperative role during recombinational repair. This gene is one of four localized to a region of chromosome 17q23 where amplification occurs frequently in breast tumors. Overexpression of the four genes during amplification has been observed and suggests a possible role in tumor progression. Alternative splicing has been observed for this gene and three variants encoding different isoforms have been identified.
ZCWCC2			X				zinc finger, CW type with coiled-coil domain 2
ZNF2			X				
ZNF322A			X				it may play a role in renal development and may also be involved in the repair of the kidney after ischemia-reperfusion or folic acid administration.
ZNF37A			X				May be involved in transcriptional regulation.
ZNF514			X				May be involved in transcriptional regulation.
ZNF569			X				
ZNF570			X				
C15orf16				X	X		Has deubiquitinating activity that is directed towards Lys-48 or Lys-63-linked polyubiquitin chains. Hydrolyzes both linear and branched forms of polyubiquitin (By similarity)
C6.1A				X	X		This gene encodes a subunit of the BRCA1-BRCA2-containing complex (BRCC), which is an E3 ubiquitin ligase. This protein is also thought to be involved in the cellular response to ionizing radiation and progression through the G2/M checkpoint
MAST2				X	X		protein kinase that seems to play a role in the regulation of cell morphogenesis and proliferation.
PPM1E				X	X		The protein encoded by this gene is a member of the PP2C family of Ser/Thr protein phosphatases. PP2C family members are known to be negative regulators of cell stress response pathways. This phosphatase was identified as an interacting protein of Rho guanine nucleotide exchange factors (PIX). PIX proteins are regulators of p21/Cdc42/Rac1-activated kinase 1 (PAK1), a protein kinase mediating biological effects downstream of Rho GTPases. This phosphatase has been shown to block the effects of PAK, and thus inhibit actin stress fiber breakdown and morphological changes driven by cell division cycle 42 (CDC42).
UBR1				X	X		recognition component of the n-end rule pathway. binds to proteins bearing amino-terminal residues that are destabilizing according to the n-end rule, but does not bind to otherwise identical proteins bearing stabilizing amino-terminal residues.
AB037807/CCM1					X	X	cerebral cavernous malformations 1
FLJ14442					X		
HDHD1A					X		haloacid dehalogenase-like hydrolase domain containing 1A
IMMP2L					X		IMP2 inner mitochondrial membrane protease-like (S. cerevisiae)
LOC220594					X		belongs to the peptidase c19 family.
MTMR4					X		dual-specificity phosphatase that acts on both phosphotyrosine and phosphoserine. could be involved in a signal transduction pathway necessary for late myogenesis, although its ubiquitous expression suggests a wider function.
TEX14					X		Protein Kinase Activity
AF318346				X			Bone Ossification?
AKAP9				X		X	Binds to type II regulatory subunits of protein kinase A. Scaffolding protein that assembles several protein kinases and phosphatases on centrosome and Golgi apparatus where physiological events can be regulated by phosphorylation state of protein substrates. Isoform 4/Yotiao is associated with the N-methyl-D- aspartate receptor and is specifically found in the neuromuscular junction (NMJ) as well as in neuronal synapses explaining that its role may be to organize postsynaptic specializations.
CDC91L1				X			The protein encoded by this gene shares similarity with Saccharomyces cerevisiae Cdc91, a predicted integral membrane protein that may function in cell division control. The protein encoded by this gene is the fifth subunit of GPI transamidase that attaches GPI-anchors to proteins
FUNDC2				X			FUN14 domain containing 2 (Cervical cancer oncogene 3) (Hypothetical protein PD03104) (Hepatitis C virus core-binding protein 6).
MAGED1				X			This gene is a member of the melanoma antigen gene (MAGE) family. Most of the genes of this family encode tumor specific antigens that are not expressed in normal adult tissues except testis. Although the protein encoded by this gene shares strong homology with members of the MAGE family, it is expressed in almost all normal adult tissues. This gene has been demonstrated to be involved in the p75 neurotrophin receptor mediated programmed cell death pathway. Three transcript variants encoding two different isoforms have been found for this gene.
SFI1				X			Sfi1 homolog, spindle assembly associated (yeast)
AB058732							
AF116680							
AK090675							51% similarity to Mus Retrovirus-related Pol polyprotein LINE-1
AK125992							
ASCC3							
BC027488							48% similarity to Mus Retrovirus-related Pol polyprotein LINE-1
C10orf68							Myosin heavy chain, nonmuscle type A
CPNE8							may function in membrane trafficking. exhibits calcium- dependent phospholipid binding properties (by similarity
FAM46D							
FAM47A							
FLJ32191							it may play a role in renal development and may also be involved in the repair of the kidney after ischemia-reperfusion or folic acid administration.
FLJ33979							Next to KIF18A, stomach cancer antigen

FLJ46156							may play a key role in embryonic cellularization by interacting with both the cytoskeleton and other cellular components. alternatively, it may play a structural role in indirect flight muscle. vital for embryonic development.
GBA							defects in gba are the cause of gaucher disease (gd) [mim:230800, 230900, 231000]. gd is the most prevalent lysosomal storage disease. the defect leads to accumulation of glucosylceramide within the cells of the reticuloendothelial system. gaucher disease has been classified into three phenotypes. type 1 (adult, nonneuronopathic) is characterized by hepatosplenomegaly (consequent anemia and thrombopenia), and bone involvement, but the central nervous system is not involved. type 2 (acute neuronopathic), is the most severe form and is universally progressive and fatal. it manifests soon after birth, with death generally occurring before patients reach two years of age. type 3 (subacute, neuronopathic) have central nervous manifestations. another classification is based on the absence (type 1) or presence and severity of primary cns involvement.
GPR23							not detected in the brain regions thalamus, putamen, caudate, frontal cortex, pons, hypothalamus and hippocampus.
HPSE2							heparanase 2, cell surface coating carbohydrate metabolism
KIAA0377							
LOC492307							Muscle Specific, no Mouse/Rat/Zebrafish/Fly/C.elegans/Yeast Homolog
LOC51057							Next to MDH1: malate dehydrogenase 1, NAD (soluble); Malate dehydrogenase catalyzes the reversible oxidation of malate to oxaloacetate, utilizing the NAD/NADH cofactor system in the citric acid cycle. The protein encoded by this gene is localized to the cytoplasm and may play pivotal roles in the malate-aspartate shuttle that operates in the metabolic coordination between cytosol and mitochondria.
MAGEB6							This gene is a member of the MAGEB gene family. The members of this family have their entire coding sequences located in the last exon, and the encoded proteins show 50 to 68% sequence identity to each other. The promoters and first exons of the MAGEB genes show considerable variability, suggesting that the existence of this gene family enables the same function to be expressed under different transcriptional controls. This gene is expressed in testis, and in a significant fraction of tumors of various histological types. The MAGEB genes are clustered on chromosome Xp22-p21.
MGC12197							
MGC35232							it may play a role in renal development and may also be involved in the repair of the kidney after ischemia-reperfusion or folic acid administration.
MTCH2							mitochondrial carrier homolog 2 (C. elegans)
OCIAD1							Ovarian immunoreactive antigen
RABGAP1L							RAB GTPase-ACTIVATING PROTEIN 1-LIKE
SH3BGRL							SH3 domain binding glutamic acid-rich protein like
VCL							Vinculin is a cytoskeletal protein associated with cell-cell and cell-matrix junctions, where it is thought to function as one of several interacting proteins involved in anchoring F-actin to the membrane. Multiple alternatively spliced transcript variants have been found for this gene, but the biological validity of some variants has not been determined. Human vinculin protein exhibits a greater than 95% sequence identity to the chicken vinculin protein.