

Online Appendix A. Brief Linkage Rationale

During gamete formation the segregation of the alleles of one allelic pair is independent of the segregation of the alleles of another allelic pair but only if they are not linked. Typically, in diploid creatures such as humans, each organism's genetic heritage comes in the form of homologous pairs of chromosomes, with one provided by the mother and one by the father. These pairs reside together in most cells of our body but during the construction of gametes change is possible. In diploid organisms, preparation for the reproductive process requires the creation of haploid cells (so that the merging of the sperm and egg will yield a diploid offspring). This is accomplished through a process known as meiosis. Usually this process entails the selection of either the chromosome originally provided by the mother or the chromosome originally provided by the father, but sometimes during meiosis, instead of pulling apart into the same discrete maternal and paternal individual chromosomes, portions of one homologous chromosome "cross-over" such that the chromosome in the gamete is a combination of material originally on the maternal chromosome and material originally on the paternal homologous chromosome. The analytical value of these recombination events is that, by simple laws of probability, genes close to each other on a chromosome are less likely to be separated by a recombination event than are those at opposite ends of the chromosome. With enough cases and enough time, this process makes it possible to map the relative location of genes and, ultimately, to establish the approximate location of a gene relevant to a trait of interest. For those interested in a more detailed exploration of linkage methodology, the Queensland Institute of Medical Research offers instructional material at <http://www.qimr.edu.au/davidD/Course/index.html>.

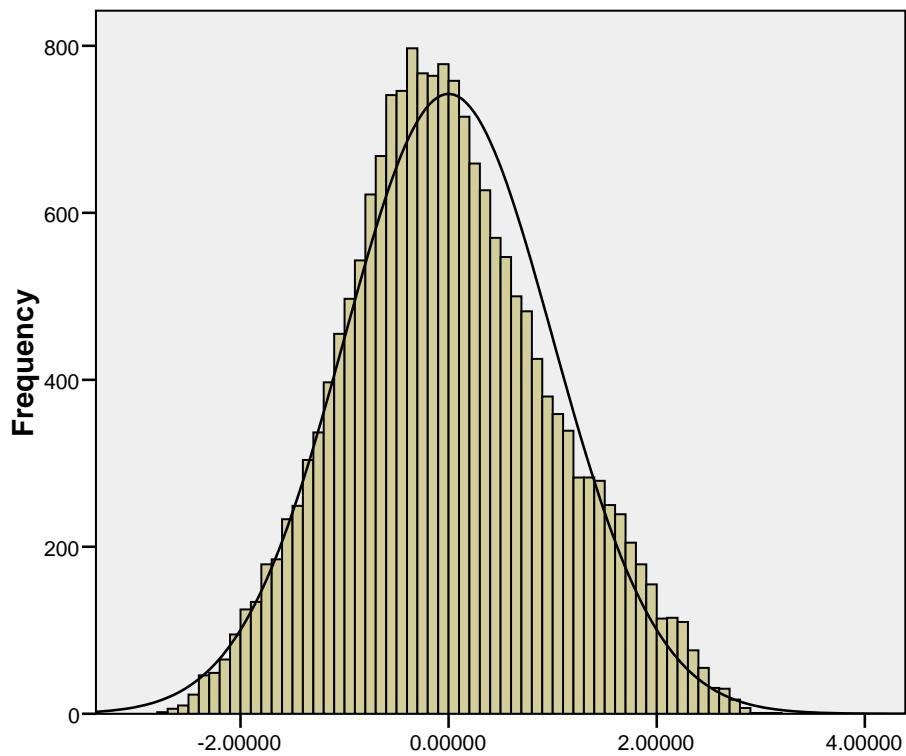
Online Appendix B. Attitudes in the 1990 Australian Conservatism-Liberalism Factor

ATTITUDES

56. Here is a list of various topics. For each one please indicate whether or not you agree with it by CIRCLING "YES" or "NO" as appropriate. If you are uncertain please circle "?". It's just your first reaction we want so please do not spend too long on any one topic.

1. Death penalty	Yes	?	No	26. Multiculturalism	Yes	?	No
2. Casual sex	Yes	?	No	27. Chastity	Yes	?	No
3. Privatisation	Yes	?	No	28. Fluoridation	Yes	?	No
4. Medicare	Yes	?	No	29. Royalty	Yes	?	No
5. Stiffer jail terms	Yes	?	No	30. Women judges	Yes	?	No
6. Trade unions	Yes	?	No	31. Strict rules	Yes	?	No
7. Patriotism	Yes	?	No	32. Test-tube babies	Yes	?	No
8. Voluntary euthanasia	Yes	?	No	33. Apartheid	Yes	?	No
9. Nuclear power	Yes	?	No	34. Asian immigration	Yes	?	No
10. Working mothers	Yes	?	No	35. Church authority	Yes	?	No
11. Bible truth	Yes	?	No	36. Disarmament	Yes	?	No
12. Gay rights	Yes	?	No	37. Censorship	Yes	?	No
13. Inborn conscience	Yes	?	No	38. White lies	Yes	?	No
14. Government welfare	Yes	?	No	39. Caning	Yes	?	No
15. Divine law	Yes	?	No	40. Teenage dole	Yes	?	No
16. Socialism	Yes	?	No	41. Private schools	Yes	?	No
17. White superiority	Yes	?	No	42. Chiropractors	Yes	?	No
18. Herbal remedies	Yes	?	No	43. Defence spending	Yes	?	No
19. Charity work	Yes	?	No	44. Divorce	Yes	?	No
20. Suicide	Yes	?	No	45. Foreign ownership	Yes	?	No
21. Conservationists	Yes	?	No	46. Surrogate mothers	Yes	?	No
22. Licensing laws	Yes	?	No	47. Legalised abortion	Yes	?	No
23. Birth control	Yes	?	No	48. Modern art	Yes	?	No
24. Evolution theory	Yes	?	No	49. Condom machines	Yes	?	No
25. Sabbath observance	Yes	?	No	50. Legalised prostitution	Yes	?	No

Online Appendix C. Distribution of Conservatism-Liberalism Attitude Factor



Online Appendix D. Gene-Dropping Simulations

With genome-wide linkage, knowing how many peaks of similar height are expected by chance, conditional on the Conservatism-Liberalism phenotype and the available set of genetic markers specific to the population, minimizes the probability of attributing greater significance to linkage findings. This approach, not yet commonly used, offers a more conservative test than the widely accepted LOD score of 3 for statistical significance (Lander and Kruglyak 1995). We added this measure by using gene dropping simulations, which replaces the observed genotyped data with simulated chromosomes conditional on family structure, actual marker spacing, allele frequencies, and missing data patterns under the null hypothesis of no linkage.¹ The original phenotypic data is unchanged. Stricter genome wide empirical p-values can then be obtained by calculating how often the observed results occur by chance within the simulated data.

Characterizing the false-positive rate in terms of an empirical distribution of p-values is implemented in MERLIN.² These p-values are based on the relative rank in the empiric list and are calculated as $(r+1)/(n+1)$ where n is the number of simulations performed and r is the number of null tests that generated more significant results than the actual data.³ To be clear, the simulation does not replace the LOD score criteria, but does offer an alternative statistical test.

¹Hansell, N. K., S. E. Medland, M. A. Ferreira, G. M. Geffen, G. Zhu, G. W. Montgomery, et al. 2006. "Linkage Analyses of Event-Related Potential Slow Wave Phenotypes Recorded in a Working Memory Task." *Behav Genet* 36: 29–44;

Medland, S. E., D.Z. Loesch, B. Mdzewski, G. Zhu, G. W. Montgomery, and N. G. Martin 2007. "Linkage Analysis of a Model Quantitative Trait in Humans: Finger Ridge Count Shows Significant Multivariate Linkage to 5q14.1." *PLoS Genet* 3: 1736–44

² Abecasis, G.R., S.S. Cherny, W.O. Cookson, and L.R. Cardon. 2002. "Merlin-Rapid Analysis of Dense Genetic Maps Using Sparse Gene Flow Trees." *Nature Genetics* 30: 97–101.

³ North, B. V., D. Curtis, and P.C. Sham. 2002. "A Note on the Calculation of Empirical P Values from Monte Carlo Procedures." *Am J Hum Genet* 71: 439–41.

Online Appendix E. Genes within the Significant Region on Chromosome 4 (95% Confidence Interval)

LOD Score	Start Location	End Location	Genetic Marker	Description
2.76	138369212	138375931	RPS23	Ribosomal protein S23
2.85	138369559	138377037	LOC653658	Similar to hCG1990955
2.85	138438316	138453668	PCDH18	Protocadherin 18
2.85	139075470	139163572	SLC7A11	Solute carrier family 7, cationic amino acid transporter
2.85	139390190	139412278	ARMC1	Armadillo repeat containing 1
2.85	139481805	139518027	NOB1	NIN1/RPN12 binding protein 1 homolog (<i>S. cerevisiae</i>)
2.85	139936632	139968801	CCRN4L	CCR4 carbon catabolite repression 4-like (<i>S. cerevisiae</i>)
2.85	139949266	140098372	ELF2	E74-like factor 2 (ets domain transcription factor)
2.85	139965296	139965614	CCRN4L	CCR4 carbon catabolite repression 4-like (<i>S. cerevisiae</i>)
2.85	140035798	140036536	PPP1R14B	Protein phosphatase 1 regulatory (inhibitor) subunit14B
3.38	140187316	140201609	OSAP	Ovary-specific acidic protein
3.38	140188034	140223705	NDUFC1	NADH dehydrogenase (ubiquinone) 1, 6kDa
3.38	140219229	140341217	NARG1	NMDA receptor regulated 1
3.38	140291706	140292401	MRNA	sequence
3.38	140374961	140397072	RAB33B	RAB33B, member RAS oncogene family
3.38	140522026	140527530	SETD7	SET domain containing (lysine methyltransferase) 7
3.38	140539290	140544386	Homo sapiens, clone IMAGE:5243978, mRNA	
3.38	140560059	140661971	MGST2	Microsomal glutathione S-transferase 2
3.38	140593909	140644361	H3F3A	Similar to histone
3.38	140609618	140619464	DACH1	Dachshund homolog 1 (<i>Drosophila</i>)
3.38	140618818	140631041	H3F3A	H3 histone, family 3A
3.38	140619365	140619581	LOC100132361	Similar to histone
3.38	140637545	141075338	MAML3	Mastermind-like 3 (<i>Drosophila</i>)
3.38	140652766	140654081	Homo sapiens, clone IMAGE:5194204, mRNA	
3.38	140675992	140679413	MRNA;	cDNA DKFZp434M063 (from clone DKFZp434M063)
3.38	140809538	140817703	LOC100128457	Similar to hCG2026341
3.38	141042380	141072856	BUB3	BUB3 budding uninhibited by benzimidazoles 3
3.38	141178440	141336194	SCOC	Short coiled-coil protein
3.38	141257849	141296313	RPL14	Ribosomal protein L14
3.38	141287354	141287945	LOC730747	Similar to 60S ribosomal protein L14 (CAG-ISL 7)
3.38	141291024	141349122	CLGN	Calmegin
3.38	141363791	141422484	LOC152586	Similar to RIKEN cDNA 4933434I20
3.38	141445259	141474930	ELMOD2	ELMO/CED-12 domain containing 2
3.38	141480863	141489959	UCP1	Uncoupling protein 1 (mitochondrial, proton carrier)
3.38	141541625	141677471	TBC1D9	TBC1 domain family, member 9 (with GRAM domain)
3.38	141546566	141564234	LOC644962	Trinucleotide repeat containing 18 pseudogene
3.38	141563251	141563737	TNRC18	Trinucleotide repeat containing 18
3.38	141786708	142054616	RNF150	Ring finger protein 150
3.44	141936097	141937832	CDNA	FLJ11592 fis, clone HEMBA1003799
3.44	142142024	142155854	ZNF330	Zinc finger protein 330
3.26	142557303	142655057	IL15	Interleukin 15
3.26	142931810	143768592	INPP4B	Inositol polyphosphate-4-phosphatase, type II, 105kDa
2.83	143766690	143769122	FLJ44477	FLJ44477 protein

Notes: LOD Peak is enclosed by border. Genetic markers of interest are in bold font.

Online Appendix F. Genes within the 90% Confidence Interval of the LOD Peak on Chromosome 9

LOD Score	Start Location	End Location	Genetic Marker	Description
2.16	136080666	136084628	OBP2B	odorant binding protein 2B
2.16	136130563	136150630	ABO	ABO blood group
2.16	136184440	136185304	LCN1L2	lipocalin 1-like 2
2.16	136205827	136206299	RPL21P81	ribosomal protein L21 pseudogene 81
2.16	136207744	136214972	MED22	mediator complex subunit 22
2.16	136215069	136218280	RPL7A	ribosomal protein L7a
2.16	136216251	136216325	SNORD	small nucleolar RNA, C/D box 24, 36B, 36A, 36C
2.16	136271186	136283164	REXO4	REX4, RNA exonuclease 4 homolog (S. cerevisiae)
2.16	136279459	136324508	ADAMTS13	ADAM metallopeptidase with thrombospondin type
2.16	136336216	136344276	SLC2A6	solute carrier (facilitated glucose transporter)
2.16	136397286	136440641	ADAMTSL2	ADAMTS-like 2
2.16	136444144	136445345	FAM163B	family with sequence similarity 163, member B
2.28	136501485	136524466	DBH	dopamine beta-hydroxylase (beta-monooxygenase)
2.28	136528682	136605077	SARDH	sarcosine dehydrogenase
2.28	136627016	136857446	VAV2	vav 2 guanine nucleotide exchange factor
2.28	136890589	136893220	NCRNA00094	non-protein coding RNA 94
2.28	136895427	136933141	BRD3	bromodomain containing 3
2.28	136943753	136944869	ARF4P	ADP-ribosylation factor 4 pseudogene
2.28	137001210	137025094	WDR5	WD repeat domain 5
2.28	137029562	137029686	RNU6ATAC	RNA, U6atac small nuclear (U12-dependent splicing)
2.28	137218316	137332431	RXRA	retinoid X receptor, alpha
2.55	137533652	137736689	COL5A1	collagen, type V, alpha 1
2.55	137772658	137779366	FCN2	ficolin (collagen/fibrinogen domain containing lectin)
2.55	137801432	137809809	FCN1	ficolin (collagen/fibrinogen domain containing) 1
2.55	137967089	138013030	OLFM1	olfactomedin 1
2.55	138371648	138380739	KIAA0649	KIAA0649
2.55	138392483	138396519	MRPS2	mitochondrial ribosomal protein S2
2.55	138413286	138418378	LCN1	lipocalin 1 (tear prealbumin)
2.55	138437985	138441815	OBP2A	odorant binding protein 2A
2.55	138453604	138458622	PAEP	progesterone-associated endometrial protein
2.55	138515502	138531386	GLT6D1	glycosyltransferase 6 domain containing 1
2.55	138555168	138557949	LCN9	lipocalin 9
2.55	138585253	138591374	SOHLH1	spermatogenesis and oogenesis specific basic helix-loop
2.55	138594038	138684992	KCNT1	potassium channel, subfamily T, member 1
2.55	138700333	138799005	CAMSAP1	
2.55	138824815	138853226	UBAC1	UBA domain containing 1
2.76	138903202	138987131	NACC2	NACC family member 2, BEN and BTB (POZ) domain
2.76	139088096	139096955	LHX3	LIM homeobox 3
2.76	139098179	139137687	QSOX2	quiescin Q6 sulfhydryl oxidase 2

2.76	139221932	139254057	GPSM1	G-protein signaling modulator 1 (AGS3-like, C. elegans)
2.76	139256352	139258241	DNLZ	DNL-type zinc finger
2.76	139258408	139268133	CARD9	caspase recruitment domain family, member 9
2.76	139270029	139292889	SNAPC4	small nuclear RNA activating complex, polypeptide 4
2.76	139296374	139305054	SDCCAG3	serologically defined colon cancer antigen 3
2.76	139305116	139318213	PMPCA	peptidase (mitochondrial processing) alpha
2.76	139323071	139334256	INPP5E	inositol polyphosphate-5-phosphatase, 72 kDa
2.76	139334548	139377507	SEC16A	SEC16 homolog A (S. cerevisiae)
2.76	139388896	139440238	NOTCH1	Notch homolog 1, translocation-associated (Drosophila)
2.76	139557377	139567130	EGFL7	EGF-like-domain, multiple 7
2.76	139567595	139581911	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2
2.76	139607030	139618489	FAM69B	family with sequence similarity 69, member B
2.78	139619046	139622636	SNHG7	small nucleolar RNA host gene 7 (non-protein coding)
2.78	139620556	139620689	SNORA	small nucleolar RNA, H/ACA box17, 43
2.78	139632619	139637411	LCN10	lipocalin 10
2.78	139638469	139642980	LCN6	lipocalin 6
2.78	139648840	139652731	LCN8	lipocalin 8
2.78	139654086	139658965	LCN15	lipocalin 15
2.78	139685777	139687769	TMEM141	transmembrane protein 141
2.78	139690802	139702193	KIAA1984	KIAA1984
2.78	139743256	139745490	PHPT1	phosphohistidine phosphatase 1
2.78	139746819	139755251	MAMDC4	MAM domain containing 4
2.78	139756571	139760738	EDF1	endothelial differentiation-related factor 1
2.78	139780965	139821067	TRAF2	TNF receptor-associated factor 2
2.78	139834887	139839173	FBXW5	F-box and WD repeat domain containing 5
2.78	139839698	139841426	C8G	complement component 8, gamma polypeptide
2.78	139846768	139849949	LCN12	lipocalin 12
2.78	139871956	139876194	PTGDS	prostaglandin D2 synthase 21kDa (brain)
2.78	139877445	139880210	LCNL1	lipocalin-like 1
2.78	139889060	139891024	CLIC3	chloride intracellular channel 3
2.78	139901686	139923374	ABCA2	ATP-binding cassette, sub-family A (ABC1), member 2
2.78	139924626	139927292	FUT7	fucosyltransferase 7 (alpha (1,3) fucosyltransferase)
2.78	139933909	139940676	NPDC1	neural proliferation, differentiation and control, 1
2.78	139942553	139948505	ENTPD2	ectonucleoside triphosphate diphosphohydrolase 2
2.78	139971953	139978990	UAP1L1	UDP-N-acetylglucosamine pyrophosphorylase 1-like 1
2.78	139981417	140003639	MAN1B1	mannosidase, alpha, class 1B, member 1
2.78	140004992	140009195	DPP7	dipeptidyl-peptidase 7
2.78	140033609	140063208	GRIN1	glutamate receptor, ionotropic, NMDA 1
2.78	140063210	140064491	LRRC26	leucine rich repeat containing 26
2.78	140069236	140083057	ANAPC2	anaphase promoting complex subunit 2
2.78	140083054	140084822	SSNA1	Sjogren syndrome nuclear autoantigen 1
2.78	140098534	140100090	TMEM203	transmembrane protein 203
2.78	140100119	140113813	NDOR1	NADPH dependent diflavin oxidoreductase 1

2.78	140114707	140115775	RNF208	ring finger protein 208
2.78	140125385	140131006	SLC34A3	solute carrier family 34 (sodium phosphate), member 3
2.78	140135711	140138159	TUBB2C	tubulin, beta 2C
2.78	140138037	140142222	FAM166A	family with sequence similarity 166, member A
2.78	140149759	140168000	COBRA1	cofactor of BRCA1
2.78	140194083	140196703	NRARP	NOTCH-regulated ankyrin repeat protein
2.78	140201348	140317714	EXD3	exonuclease 3'-5' domain containing 3
2.78	140317847	140328858	NOXA1	NADPH oxidase activator 1
2.78	140328816	140335901	ENTPD8	ectonucleoside triphosphate diphosphohydrolase 8
2.78	140342022	140353786	NELF	nasal embryonic LHRH factor
2.78	140354405	140444986	PNPLA7	patatin-like phospholipase domain containing 7
2.78	140446309	140447007	MRPL41	mitochondrial ribosomal protein L41
2.78	140449361	140473387	WDR85	WD repeat domain 85
2.78	140476531	140484937	ZMYND19	zinc finger, MYND-type containing 19
2.78	140500096	140509812	ARRDC1	arrestin domain containing 1
2.78	140605417	140730579	EHMT1	euchromatic histone-lysine N-methyltransferase 1
2.78	140732871	140732968	MIR602	
2.78	140772241	141019076	CACNA1B	calcium channel, voltage-dependent, N type, alpha 1B
2.78	141069494	141071716	TUBBP5	tubulin, beta pseudogene 5

Notes: Genetic markers of interest in the suggestive region are in bold font.

Online Appendix G. Genes within the Significant Region on Chromosome 2 (95% Confidence Interval)

LOD Score	Start Location	End Location	Genetic Marker	Description
2.16	133014539	133014653	MIR663B	microRNA 663B
2.16	133018761	133020670	LOC647696	similar to cell division cycle protein 27
2.16	133066882	133076309	ZNF806	zinc finger protein 806
2.16	133089314	133090325	AZFP	AML-associated zinc finger protein
2.18	133174147	133404169	GPR39	G protein-coupled receptor 39
2.18	133402337	133429070	LYPD1	LY6/PLAUR domain containing 1
2.18	133429372	134326031	NAP5	Nck-associated protein 5
2.18	135011830	135206468	MGAT5	mannosyl (alpha-1,6)-glycoprotein beta-1
2.18	135076967	135077773	FAM12CP	family with sequence similarity 12, member C
2.18	135213330	135476571	TMEM163	transmembrane protein 163
2.18	135596186	135659604	ACMSD	aminocarboxymuconatesemialdehydedecarboxylase
2.18	135676393	135714584	CCNT2	cyclin T2
2.18	135722273	135782248	YSK4	YSK4 Sps1/Ste20-related kinase homolog
2.18	135809853	135927559	RAB3GAP1	RAB3 GTPase activating protein subunit 1
2.18	135957571	136288806	ZRANB3	zinc finger, RAN-binding domain containing 3
2.58	136289083	136482839	R3HDM1	R3H domain containing 1
2.58	136422967	136423048	MIR128-1	microRNA 128-1
2.58	136499189	136542633	UBXN4	UBX domain protein 4
2.58	136545415	136594750	LCT	lactase
2.58	136597196	136634011	MCM6	minichromosome maintenance complex component
2.58	136655519	136664130	LOC391448	similar to mannosidase, endo-alpha-like
2.58	136664254	136743222	DARS	aspartyl-tRNA synthetase
2.58	136871919	136875725	CXCR4	chemokine (C-X-C motif) receptor 4
2.58	136956684	136958073	LOC389053	similar to heterogeneous nuclear ribonucleoprotein
2.58	137086870	137087572	UBBP1	ubiquitin B pseudogene 1
2.58	137748462	138435287	THSD7B	thrombospondin, type I, domain containing 7B
2.58	138721808	138773934	HNMT	histamine N-methyltransferase
2.58	139036108	139037021	RPL15P5	ribosomal protein L15 pseudogene 5
2.58	139044689	139046450	LOC440917	Mitochondrial import stimulation factor L MSF
2.58	139064889	139065546	LOC647002	similar to isopentenyl-diphosphate delta isomerase
2.58	139169636	139171099	LOC100129375	similar to ring finger protein 14
2.58	139259350	139330805	SPOPL	speckle-type POZ protein-like
2.58	139426727	139537811	NXPH2	neurexophilin 2
2.58	139654896	139656744	LOC647012	similar to YY1 transcription factor
2.58	139659003	139660317	LOC129560	similar to S-adenosylhomocysteine hydrolase
2.58	140426104	140426879	MRPS18BP2	mitochondrial ribosomal protein S18B pseudogene
2.58	140490277	140490857	RPL9P13	ribosomal protein L9 pseudogene 13
2.78	140988996	142889270	LRP1B	low density lipoprotein-related protein 1B

2.78	141965651	141966004	RPS16P3	ribosomal protein S16 pseudogene 3
3.01	143635195	143799885	KYNU	kynureinase (L-kynureanine hydrolase)
3.01	143886899	144525921	ARHGAP15	Rho GTPase activating protein 15
2.88	144703581	145061211	GTDC1	glycosyltransferase-like domain containing 1
2.62	145145583	145277916	ZEB2	zinc finger E-box binding homeobox 2
2.62	145512076	145513709	SGCEP	sarcoglycan, epsilon, pseudogene
2.62	146094801	146095631	RPL6P5	ribosomal protein L6 pseudogene 5
2.62	146583104	146585410	LOC727713	methionyl aminopeptidase 2 pseudogene
2.62	146902625	146902885	RNU7-2P	RNA, U7 small nuclear 2 pseudogene
2.62	146951864	146952389	RPL17P12	ribosomal protein L17 pseudogene 12
2.38	147344625	147348558	PABPCP2	poly(A) binding protein, cytoplasmic, pseudogene
2.38	148559416	148568133	RPL26P14	ribosomal protein L26 pseudogene 14
2.38	148602570	148688393	ACVR2A	activin A receptor, type IIA
2.38	148691732	148779136	ORC4L	origin recognition complex, subunit 4-like (yeast)
2.18	149053125	149055399	LOC100130682	similar to ubiquitin-specific protease 12-like 1
2.18	149088855	149089707	LOC641381	ADP-ribosylation factor-like 5A pseudogene
2.18	149216038	149271046	MBD5	methyl-CpG binding domain protein 5
2.18	149352697	149352984	RPS29P8	ribosomal protein S29 pseudogene 8
2.18	149402560	149545136	EPC2	enhancer of polycomb homolog 2 (Drosophila)
2.18	149620995	149621370	UBBP3	ubiquitin B pseudogene 3
2.18	149627550	149628075	RPS20P13	ribosomal protein S20 pseudogene 13
2.18	149632819	149686923	KIF5C	kinesin family member 5C
2.18	149639365	149639417	MIR1978	microRNA 1978
2.18	149793795	149883269	KIF5C	kinesin family member 5C
2.18	149894981	150071772	LYPD6B	LY6/PLAUR domain containing 6B
2.06	149924982	149925441	LOC151276	thioredoxin 1 pseudogene 1
2.06	150174907	150181365	FAM8A3P	family sequence similarity 8, A3 pseudogene
2.06	150187113	150330138	LYPD6	LY6/PLAUR domain containing 6
2.06	150296411	150296941	RPL17P13	ribosomal protein L17 pseudogene 13
2.06	150426147	150444330	MMADHC	methylmalonic aciduria(cobalamin deficiency)cblD
1.91	151219277	151219349	TRNAE38P	transfer RNA glutamic acid 38 anticodon CUC
1.91	151324709	151344180	RND3	Rho family GTPase 3
1.91	152042675	152043305	FABP5L10	fatty acid binding protein 5-like 10
1.91	152104728	152118389	RBM43	RNA binding motif protein 43
1.91	152126982	152146430	NMI	N-myc (and STAT) interactor

Notes: LOD Peak is enclosed by border. Genetic markers of interest are in bold font.

Online Appendix H. Genes within the Suggestive Region on Chromosome 6 (95% Confidence Interval)

LOD Score	Start Location	End Location	Genetic Marker	Description
1.88	78171948	78173120	HTR1B	5-hydroxytryptamine (serotonin) receptor 1B
1.88	78201312	78206460	RPS6P7	ribosomal protein S6 pseudogene 7
1.88	79577189	79608320	IRAK1BP1	interleukin-1 receptor-associated kinase 1 binding protein 1
1.88	79644136	79788011	PHIP	pleckstrin homology domain interacting protein
1.88	79668010	79668082	TRNAF13P	transfer RNA phenylalanine 13 (anticodon GAA) pseudogene
1.88	79910962	79944455	HMGN3	high mobility group nucleosomal binding domain 3
1.88	80036248	80045765	LOC100131959	similar to DnaJ (Hsp40) homolog, subfamily B, member 6
1.88	80146408	80146941	DBIL2	diazepam binding inhibitor-like 2 (pseudogene)
1.88	80194708	80247147	LCA5	Leber congenital amaurosis 5
1.88	80256938	80262967	LOC100130012	similar to Thiamine transporter 2
1.88	80341000	80413369	SH3BGRL2	SH3 domain binding glutamic acid-rich protein like 2
1.88	80624529	80657315	ELOVL4	elongation of very long chain fatty acids (FEN1/Elo2,SUR4/Elo3)
1.88	80662668	80663727	GAPDHL8	glyceraldehyde-3-phosphate dehydrogenase-like 8
1.88	80673932	80674239	RPL35AP18	ribosomal protein L35a pseudogene 18
1.88	80714359	80752239	TTK	TTK protein kinase
1.88	80773213	80780300	LOC643562	Rho GTPase activating protein 21 pseudogene
1.88	80816344	81055987	BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide
1.88	81083696	81084321	RPL17P25	ribosomal protein L17 pseudogene 25
1.88	81265939	81266708	LOC648934	similar to citrate synthase
2.06	82455447	82462428	FAM46A	family with sequence similarity 46, member A
2.06	82879956	82957448	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase
2.06	82973727	82974691	LOC100132659	similar to single-stranded DNA binding protein 2
2.06	83073539	83076628	TPBG	trophoblast glycoprotein
2.06	83602186	83775545	UBE2CBP	ubiquitin-conjugating enzyme E2C binding protein
2.06	83777385	83878127	DOPEY1	dopey family member 1
2.06	83878628	83902935	PGM3	phosphoglucomutase 3
2.06	83903032	83906256	RWDD2A	RWD domain containing 2A
2.06	83920108	84140779	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic
2.06	84101825	84103340	GAPDHL5	glyceraldehyde-3-phosphate dehydrogenase-like 5
2.06	84222271	84235423	PRSS35	protease, serine, 35
2.06	84262604	84419127	SNAP91	synaptosomal-associated protein, 91kDa homolog
2.06	84562985	84567234	RIPPLY2	ripply2 homolog (zebrafish)
2.06	84569370	84670146	CYB5R4	cytochrome b5 reductase 4
2.06	84672790	84676105	LOC100132652	similar to hCG2038304
2.06	84743420	84800606	MRAP2	melanocortin 2 receptor accessory protein 2
2.06	84833960	84937335	KIAA1009	KIAA1009
2.16	85139299	85140519	LOC442233	SWI/SNF related, actin dependent regulator of chromatin
2.16	85444157	85473899	TBX18	T-box 18
2.16	85967006	85967459	RPL31P32	ribosomal protein L31 pseudogene 32

2.16	85987143	85995378	KRT18P30	keratin 18 pseudogene 30
2.16	86136351	86137681	LOC643870	similar to tumor protein, translationally-controlled 1
2.16	86159302	86205498	NT5E	5'-nucleotidase, ecto (CD73)
2.16	86215214	86303629	SNX14	sorting nexin 14
2.16	86323939	86353027	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein
2.36	86369696	86441776	LOC100127917	similar to HSP90AB1 protein
2.36	86386725	86388451	SNHG5	small nucleolar RNA host gene 5 (non-protein coding)
2.36	86387012	86387086	SNORD50A	small nucleolar RNA, C/D box 50A
2.36	86387307	86387377	SNORD50B	small nucleolar RNA, C/D box 50B
2.36	86578662	86579193	LOC100133102	similar to ras-related C3 botulinum toxin substrate 1
2.36	86796067	86796893	RPL7P27	ribosomal protein L7 pseudogene 27
2.36	86880165	86883630	LOC643916	similar to RAB1A, member RAS oncogene family
2.36	87141965	87142427	LOC643926	similar to hCG1652647
2.36	87606836	87607450	LOC100289653	similar to heat shock 70kD protein binding protein
2.36	87647024	87726397	HTR1E	5-hydroxytryptamine (serotonin) receptor 1E
2.36	87680152	87680976	RPL7P29	ribosomal protein L7 pseudogene 29
2.36	87795222	87804824	CGA	glycoprotein hormones, alpha polypeptide
2.36	87831411	87832406	LOC442234	similar to reticulocalbin 1
2.36	87865269	87973406	ZNF292	zinc finger protein 292
2.36	87992697	88038996	GJB7	gap junction protein, beta 7, 25kDa
2.36	88008490	88010180	LOC644016	similar to chaperonin
2.36	88135358	88135779	TAF13P	TAF13 RNA polymerase II, TATA box binding protein (TBP)
2.36	88182643	88222057	SLC35A1	solute carrier family 35 (CMP-sialic acid transporter), member A1
2.36	88224096	88299735	RARS2	arginyl-tRNA synthetase 2, mitochondrial
2.36	88299843	88377169	ORC3L	origin recognition complex, subunit 3-like (yeast)
2.36	88384578	88411985	AKIRIN2	akirin 2
2.36	88410020	88410933	NCRNA00120	non-protein coding RNA 120
2.36	88757507	88776550	SPACA1	sperm acrosome associated 1
2.36	88849583	88855056	CNR1	cannabinoid receptor 1 (brain)
2.36	88974892	88975304	RPS14P9	ribosomal protein S14 pseudogene 9
2.36	88985179	88986792	ACTBP8	actin, beta pseudogene 8
2.36	89319989	89673348	RNGTT	RNA guanylyltransferase and 5'-phosphatase
2.36	89378294	89380624	LOC100130179	similar to env protein
2.36	89712449	89712619	CYCSP16	cytochrome c, somatic pseudogene 16
2.36	89769353	89769783	LOC100131124	similar to adaptor-related protein complex 4, sigma 1 subunit
2.36	89790429	89794879	PNRC1	proline-rich nuclear receptor coactivator 1
2.48	89805678	89827800	SRrp35	serine-arginine repressor protein (35 kDa)
2.48	89855769	89875284	PM20D2	peptidase M20 domain containing 2
2.48	89887223	89927496	GABRR1	gamma-aminobutyric acid (GABA) receptor, rho 1
2.48	89967239	90024967	GABRR2	gamma-aminobutyric acid (GABA) receptor, rho 2
2.48	90036344	90062619	UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)
2.48	90074335	90121995	RRAGD	Ras-related GTP binding D
2.48	90131818	90182639	LOC100128021	similar to nascent polypeptide-associated complex alpha subunit

2.48	90142897	90343403	ANKRD6	ankyrin repeat domain 6
2.52	90341943	90348474	LYRM2	LYR motif containing 2
2.52	90353231	90529442	MDN1	MDN1, midasin homolog (yeast)
2.52	90539619	90584155	CASP8AP2	caspase 8 associated protein 2
2.52	90586230	90586597	RPL22P14	ribosomal protein L22 pseudogene 14
2.52	90595334	90597574	LOC644269	similar to Gps1
2.52	90604188	90605819	GJA10	gap junction protein, alpha 10, 62kDa
2.52	90636247	91006562	BACH2	BTB & CNC homology 1 basic leucine zipper transcription factor
2.52	90659817	90661708	LOC100129711	similar to mCG1050952
2.52	91225353	91296907	MAP3K7	mitogen-activated protein kinase 7
2.52	92525558	92526131	LOC100129847	similar to ras homolog gene family, member A
2.52	92723552	92724356	RPL5P19	ribosomal protein L5 pseudogene 19
2.55	93596985	93597776	LOC100128159	similar to activating transcription factor 1
2.55	93801543	93802701	COPS5P	COP9 constitutive photomorphogenic homolog subunit 5
2.55	93949738	94129300	EPHA7	EPH receptor A7
2.43	94416801	94486199	TSG1	tumor suppressor TSG1
2.43	95151747	95156547	LOC100132830	similar to zinc finger CCCH-type containing 14
2.43	95952058	95952372	CYCSP17	cytochrome c, somatic pseudogene 17
2.43	96025413	96057326	MANEA	mannosidase, endo-alpha
2.43	96438948	96440277	KRT18P50	keratin 18 pseudogene 50
2.43	96463845	96663488	FUT9	fucosyltransferase 9 (alpha (1,3) fucosyltransferase)
2.43	96969702	97003152	KIAA0776	KIAA0776
2.43	97010435	97064512	FHL5	four and a half LIM domains 5
2.43	97096331	97096983	RPS7P8	ribosomal protein S7 pseudogene 8
2.43	97245888	97285353	GPR63	G protein-coupled receptor 63
2.43	97338140	97345767	NDUFAF4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,4
2.43	97372496	97588630	KLHL32	kelch-like 32 (Drosophila)
2.43	98472407	98472497	MIR2113	microRNA 2113
2.43	98626536	98627716	LOC100190924	eukaryotic translation initiation factor 4E binding protein
2.2	99282580	99286666	POU3F2	POU class 3 homeobox 2
2.2	99321601	99395849	FBXL4	F-box and leucine-rich repeat protein 4
2.2	99622547	99625446	BDH2P1	3-hydroxybutyrate dehydrogenase, type 2 pseudogene 1
2.2	99817348	99842082	COQ3	coenzyme Q3 homolog, methyltransferase (<i>S. cerevisiae</i>)
2.2	99847840	99873207	SFRS18	splicing factor, arginine-serine-rich 18
2.2	99880182	99963252	USP45	ubiquitin specific peptidase 45
2.2	99973955	99979790	LOC100130890	similar to hCG2030844
2.2	99990263	100016690	CCNC	cyclin C
1.89	100023558	100024408	RPS3P5	ribosomal protein S3 pseudogene 5
1.89	100054650	100063454	PRDM13	PR domain containing 13
1.89	100367786	100442114	MCHR2	melanin-concentrating hormone receptor 2
1.89	100498248	100499141	LOC100128985	similar to nucleophosmin 1
1.89	100583940	100584539	LOC442239	similar to peroxiredoxin 2
1.89	100610754	100626052	LOC100129854	similar to arginase 2

1.89	100836750	100911551	SIM1	single-minded homolog 1 (Drosophila)
1.89	100956608	101329224	ASCC3	activating signal cointegrator 1 complex subunit 3
1.89	100978037	100979105	LOC153893	similar to RP42 homolog
1.89	101337479	101338216	LOC728098	similar to MAPK-interacting and spindle-stabilizing protein
1.89	101846905	102517958	GRIK2	glutamate receptor, ionotropic, kainate 2
1.89	102901203	102942944	LOC100132919	similar to hCG1642312
1.77	104240543	104242231	FLJ10088	similar to hypothetical protein (L1H 3 region)
1.77	104465502	104469868	LOC100129694	similar to R3H domain containing 2
1.77	104472802	104474734	NPM1P10	nucleophosmin 1 (nucleolar phosphoprotein B23, numatrin)
1.77	105175968	105307794	HACE1	HECT domain and ankyrin repeat, E3 ubiquitin protein ligase 1
1.77	105404923	105531206	LIN28B	lin-28 homolog B (C. elegans)
1.77	105544697	105584543	BVES	blood vessel epicardial substance
1.77	105605775	105627858	POPDC3	popeye domain containing 3
1.77	105725506	105850969	PREP	prolyl endopeptidase
1.77	105746016	105746821	RPL7AP35	ribosomal protein L7a pseudogene 35
1.77	105750295	105750734	RPL35P3	ribosomal protein L35 pseudogene 3
1.52	106114201	106115873	LOC100130683	similar to chromatin assembly factor 1 subunit B
1.52	106534195	106557814	PRDM1	PR domain containing 1, with ZNF domain
1.52	106632352	106773695	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)
1.52	106959730	107018335	AIM1	absent in melanoma 1
1.63	107018903	107077373	RTN4IP1	reticulon 4 interacting protein 1
1.63	107077441	107116292	QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1
1.63	107090295	107090834	RPL21P65	ribosomal protein L21 pseudogene 65
1.63	107232000	107232095	MIR587	microRNA 587
1.63	107386385	107420489	BEND3	BEN domain containing 3
1.63	107473761	107780779	PDSS2	prenyl (decaprenyl) diphosphate synthase, subunit 2
1.63	107550963	107551356	RPS24P12	ribosomal protein S24 pseudogene 12
1.63	107811317	107982513	SOBP	sine oculis binding protein homolog (Drosophila)
1.63	108023364	108145521	SCML4	sex comb on midleg-like 4 (Drosophila)
1.63	108188960	108279482	SEC63	SEC63 homolog (S. cerevisiae)
1.63	108253004	108253458	RPL23AP50	ribosomal protein L23a pseudogene 50
1.63	108325506	108326798	RPL3P7	ribosomal protein L3 pseudogene 7
1.63	108362613	108395941	OSTM1	osteopetrosis associated transmembrane protein 1
1.63	108477081	108480596	LOC100287366	similar to hCG2038817
1.78	108487215	108510013	NR2E1	nuclear receptor subfamily 2, group E, member 1
1.78	108532717	108582464	SNX3	sorting nexin 3
1.78	108616098	108844258	LACE1	lactation elevated 1
1.78	108639256	108639658	RPL36AP24	ribosomal protein L36a pseudogene 24
1.78	108881026	109005971	FOXO3	forkhead box O3
1.78	109106692	109108262	ZNF259P	zinc finger protein 259, pseudogene
1.78	109138883	109139129	RPL37AP3	ribosomal protein L37a pseudogene 3
1.78	109169619	109295352	ARMC2	armadillo repeat containing 2
1.78	109177556	109177940	RPS12P13	ribosomal protein S12 pseudogene 13

1.78	109228680	109229098	ATP5J2P2	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, F2
1.78	109307645	109415277	SESN1	sestrin 1
1.78	109648378	109649096	RPL7P28	ribosomal protein L7 pseudogene 28
1.78	109687717	109703762	CD164	CD164 molecule, sialomucin
1.78	109711418	109761847	PPIL6	peptidylprolyl isomerase (cyclophilin)-like 6
1.78	109761931	109765122	SMPD2	sphingomyelin phosphodiesterase 2, neutral membrane
1.78	109765265	109777190	MICAL1	microtubule associated monooxygenase, calponin and LIM domain
1.78	109783719	109804440	ZBTB24	zinc finger and BTB domain containing 24
1.78	109870887	110012415	AKD2	adenylate kinase domain containing 2
1.78	110012424	110146634	FIG4	FIG4 homolog (S. cerevisiae)
1.78	110300298	110301923	GPR6	G protein-coupled receptor 6
1.78	110421022	110501207	WASF1	WAS protein family, member 1
1.78	110501624	110553423	CDC40	cell division cycle 40 homolog (S. cerevisiae)
1.78	110713383	110736753	DDO	D-aspartate oxidase
1.78	110745906	110797844	SLC22A16	solute carrier family 22 (organic cation/carnitine transporter),
1.78	110883378	110890566	RPS19P5	ribosomal protein S19 pseudogene 5
1.78	110931181	111136412	CDC2L6	cell division cycle 2-like 6 (CDK8-like)
1.78	110966965	110967761	LOC100129155	similar to phosphatase, orphan 1
1.78	111021643	111022126	RPS20P18	ribosomal protein S20 pseudogene 18
1.78	111179442	111180350	LOC441166	similar to hCG33896
1.78	111195987	111216913	AMD1	adenosylmethionine decarboxylase 1
1.78	111244769	111245314	LOC442244	similar to PDGFA associated protein 1
1.78	111279763	111289091	GTF3C6	general transcription factor IIIC, polypeptide 6, alpha 35kDa
1.78	111303291	111346794	BXDC1	brix domain containing 1
1.78	111368071	111368724	LOC442245	glutathione S-transferase M1 pseudogene
1.78	111408781	111544608	SLC16A10	solute carrier family 16, member 10 (aromatic amino acid)
1.78	111580482	111590263	KIAA1919	KIAA1919
1.78	111620234	111804414	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)
1.78	111880143	111927321	TRAF3IP2	TRAF3 interacting protein 2
1.78	111982485	112194627	FYN	FYN oncogene related to SRC, FGR, YES
1.78	112375278	112390889	WISP3	WNT1 inducible signaling pathway protein 3
1.78	112391860	112408751	TUBE1	tubulin, epsilon 1
1.78	112429134	112575828	LAMA4	laminin, alpha 4
1.78	112619624	112647951	LOC100128588	similar to hCG34808
1.78	112668532	112672498	RFPL4B	ret finger protein-like 4B
1.78	112676954	112677995	RPSAP45	ribosomal protein SA pseudogene 45
1.78	112682639	112684118	LOC442249	similar to keratin 18
1.78	112686922	112688646	LOC643859	similar to fem-1 homolog a
1.78	112937031	112939232	PA2G4P5	proliferation-associated 2G4 pseudogene 5
1.78	113543368	113545274	LOC643884	similar to suppressor of cytokine signaling 5
1.78	113902665	113903201	RPS27AP11	ribosomal protein S27a pseudogene 11
1.78	114151025	114155968	RPL30P8	ribosomal protein L30 pseudogene 8
1.78	114178527	114184652	MARCKS	myristoylated alanine-rich protein kinase C substrate

1.78	114257326	114292354	HDAC2	histone deacetylase 2
1.78	114376750	114384041	HS3ST5	heparan sulfate (glucosamine) 3-O-sulfotransferase 5
1.78	114405363	114405956	RPSAP43	ribosomal protein SA pseudogene 43
1.78	114551305	114560363	LOC441167	hCG1820801
1.78	114670647	114677328	LOC728614	similar to Dnaj (Hsp40) homolog, subfamily A, member 1
1.78	116262693	116381921	FRK	fyn-related kinase
1.78	116359919	116360993	LOC728402	triosephosphate isomerase 1 pseudogene
1.78	116421999	116566853	NT5DC1	5'-nucleotidase domain containing 1
1.78	116440085	116447296	COL10A1	collagen, type X, alpha 1
1.78	116571127	116575261	TSPYL4	TSPY-like 4
1.78	116579604	116580397	LOC100287430	similar to ribosomal protein S5
1.78	116579608	116580350	RPS5P1	ribosomal protein S5 pseudogene 1
1.78	116597744	116601280	TSPYL1	TSPY-like 1
1.78	116601283	116759442	DSE	dermatan sulfate epimerase
1.78	116773956	116774728	LOC644101	similar to chromobox homolog 3
1.78	116778486	116779768	KRT18P22	keratin 18 pseudogene 22
1.78	116782556	116784934	FAM26F	family with sequence similarity 26, member F
1.78	116817752	116866773	BET3L	BET3 like (<i>S. cerevisiae</i>)
1.78	116832808	116839709	FAM26E	family with sequence similarity 26, member E
1.78	116850195	116880031	FAM26D	family with sequence similarity 26, member D
1.83	116892583	116914438	RWDD1	RWD domain containing 1
1.83	116937650	116954141	RSPH4A	radial spoke head 4 homolog A (<i>Chlamydomonas</i>)
1.83	116956781	116989957	ZUFSP	zinc finger with UFM1-specific peptidase domain
1.83	117002367	117063030	KPNA5	karyopherin alpha 5 (importin alpha 6)
1.83	117073360	117086886	FAM162B	family with sequence similarity 162, member B
1.83	117113248	117150198	GPRC6A	G protein-coupled receptor, family C, group 6, member A
1.83	117198376	117253314	RFX6	regulatory factor X, 6
1.83	117369833	117370004	RPS29P13	ribosomal protein S29 pseudogene 13
1.83	117586721	117594728	VGLL2	vestigial like 2 (<i>Drosophila</i>)
1.83	117609530	117747018	ROS1	c-ros oncogene 1 , receptor tyrosine kinase
1.83	117752754	117753198	LOC100132917	similar to RAP1B, member of RAS oncogene family
1.83	117803820	117891021	DCBLD1	discoidin, CUB and LCCL domain containing 1
1.83	117881432	117923681	GOPC	golgi associated PDZ and coiled-coil motif containing
1.83	117924091	117966250	LOC442253	NEPN pseudogene
1.83	117996617	118031890	NUS1	nuclear undecaprenyl pyrophosphate synthase 1 homolog
1.83	118228689	118638839	SLC35F1	solute carrier family 35, member F1
1.83	118320091	118320749	RPL29P4	ribosomal protein L29 pseudogene 4

Notes: LOD Peak in suggestive region is enclosed by border. Genetic markers of interest are in bold font.