

Supplementary Fig. 2 (online Appendix): Reconstruction (bottom panel) of the haplotypes described by Gu *et al.* (10) (top panel). We used four of our tag SNPs (in bold) and three SNPs predicted by our set of tags to reconstruct the haplotypes of Gu *et al.*: rs1832197 was predicted by test 29 ($r^2 = 0.9$), rs1999764 was predicted by test 28 ($r^2 = 1.0$) and rs2421945 was predicted by test 27 ($r^2 = 1.0$). The flanking SNP HHEX23 lies ~95 kb beyond the end of the last haplotype block, and was therefore not genotyped in our disease samples. Thus we could not resolve haplotypes H1 (frequency 28.6%) and H6 (frequency 4.4%), which were analyzed in combination in our samples. We note that haplotypes H3 and H8 cannot be distinguished with the use of the three tag SNPs by Gu *et al.* (shaded); because the G allele of rs2249960 tags haplotype H3 perfectly and its minor allele frequency is ~8% in Caucasians, we suspect that their assignment of labels H3 (frequency 11.7%) and H8 (frequency 2.7%) based on allele frequency may have been reversed. If this is the case, their allele frequencies would approximate ours closely.

ONLINE APPENDIX TABLES

Supplementary Table 1: Genotyping assays of SNPs in *IDE*

SNP	Position	Base	PCR primer 1	PCR primer 2	Extension probe	Probe direction	Assay result
rs2263638	94158777	C/T	HapMap				
rs2901587	94160831	A/C	AGCGGATAACGGTAGAAAGGCAGCTTCTAC	AGCGGATAACCTTTGTCATTGGAGGAGACC	GACCTCCTCATCCCCAGTTAT	F	Failed geno
rs11186986	94161069	A/G	AGCGGATAACTTTTTGCCATGTTGGCTAGGC	AGCGGATAACTAATCCCAACACTGTGGGAG	ACCTGAGGTCAGAAGTTC	F	Failed geno
rs7911751	94163065	C/G	AGCGGATAACTGTACAGTAAGGAGCAGACG	AGCGGATAACATGGTTGCCACGCTAATC	CTCTTTCCACTTGGCCAG	F	MONO
rs12267150	94164911	A/G	AGCGGATAACAAAGTATCTGGGTCCATGGC	AGCGGATAACGTTTTCTCCATGTTGGTCAGG	GTTGGTCAGGATGGTCTC	F	Failed geno
rs7086285	94166068	T/C	AGCGGATAACCCTGAACCTTGCACTTAGGTC	AGCGGATAACTTTGCCCAAGCCTCTGATAC	TAGGGGGCATGGTTTTAGGACTTC	F	
rs12243581	94167669	C/T	AGCGGATAACCGCAGATGGTAATAATGAAGC	AGCGGATAACGGGAGTTCGAGAAAAGGTATA	GTATAAGTATGTTCTGTTGTGTAC	R	MONO
rs2209972	94169008	C/T	HapMap				
rs967878	94169328	G/T	AGCGGATAACTCCTCATACTCCTCAGCAAG	AGCGGATAACACCCCTGCAAACCTAAGTTC	ATCCGTGGGTTACAGACAGGAAGA	R	
rs884526	94170442	G/T	AGCGGATAACTCAAAACCTTAACGGCCGC	AGCGGATAACAAAACCTCCCGAGCCAGGA	AGGAGATGAGCGGTGGA	R	
rs2094645	94170990	G/T	AGCGGATAACAAGTGGCCAACCAACTTC	AGCGGATAACTTTGAGGCTCTGTTGTTAGG	CTGTTGTTAGGTCCCTAC	R	MONO
rs1590827	94171444	G/A	AGCGGATAACGCTGCAACCCACAAATTTTG	AGCGGATAACGGCCAAAGAATTCTCAAGAG	CTCAAGAGAAATGTTAAAAAAT	R	MONO
rs11594898	94173942	T/C	AGCGGATAACGATGGTTACCGAACATTGTG	AGCGGATAACAAGTTGCAAGTAGGTTAAC	TAAAAAAATCTGGTGAGATA	F	
rs10882060	94174752	G/A	AGCGGATAACTGGCACGATCTCGGCTTACT	AGCGGATAACAAAATTAGCTGGGCGTGGTG	CGCCTGTAATCCAGCTA	R	MONO
rs12257053	94175650	C/T	AGCGGATAACTGGAATAGAATTGAGAGCCC	AGCGGATAACAACCTGAATGGTCTTGCCACC	TTGGCACCTTGTCAAAAAG	F	
rs12773353	94176753	C/T	AGCGGATAACCCCTTTAATGTATCCCTCCAG	AGCGGATAACAGCTAGGATTACAGGCATGC	TACAGGCATGCGCCACC	R	MONO
rs12266510	94177463	A/G	AGCGGATAACCTTAGTATCCAAAGTGACTC	AGCGGATAACTTGTATCATCAGTTTTGTAG	ACAGTTTTGTAGTTTTCTCA	R	MONO
rs7909013	94178323	T/C	AGCGGATAACAATAGGGATATTGCCAGGCG	AGCGGATAACTTTCACTGTATTGGCCAGGC	CCCGAAGTGCTGCGATTACAG	R	
rs7071343	94178909	A/G	HapMap				MONO
rs7071242	94179065	A/G	AGCGGATAACCATCCGAGAGTACAAAAGGG	AGCGGATAACCCAGTTTTCTAGCATAGGTG	AGGTGATGGGGTGGGTAAA	F	MONO
rs10786044	94180560	A/G	AGCGGATAACAGTGCCTTGGATAAGGCAG	AGCGGATAACAGCAGACCCCAATGAAGTTC	TTCTCCTACTTCTTAGTC	F	
rs11186993	94182794	C/T	AGCGGATAACTGGAGGGACAAGGGAAAAAG	AGCGGATAACAATCACTAAGGAGGGCTTCC	GGGCTTCCCTTCTGAATAAAAT	R	
rs12255071	94183825	C/T	AGCGGATAACATCATGCTACTGCACTCCAG	AGCGGATAACGAGTTGCTGGTATTACAGGC	AAACAGGATCTCCGTCTG	F	Failed geno
rs11186994	94184819	C/T	AGCGGATAACCTCAAAACCCATTCTCTGGC	AGCGGATAACAGCCTGGGTGACAGAATAAG	CTGGGTGACAGAATAAGACTCCGT	F	
rs10786045	94185388	A/T	HapMap				
rs10786046	94185800	A/G	AGCGGATAACGAGAAAGAATCAGATCCCGG	AGCGGATAACCCACCCAGATCTTGCTTTTC	GCTTTTCCCTCCATCTTTTC	F	Failed HW
rs12261262	94186670	G/C	AGCGGATAACTGTAATCCAGCACTTTGCG	AGCGGATAACTTTACCATGTTGGTCAGGC	CTCCTGACCTCAGATGATCCACC	R	MONO
rs10882063	94189317	G/T	AGCGGATAACGTTATTATTCTCTGCTATGG	AGCGGATAACATTTTTCAGGTTACTCTTATT	TTTCAGGTTACTCTTATTTGTAA	F	
rs12267443	94189686	C/T	AGCGGATAACTTCTAGTTTCCGTGGCATGC	AGCGGATAACAAAGCGAAAGCCTCAGAAGC	CCCTCCTGTCTCTTCCC	F	MONO
rs2771254	94190340	G/T	AGCGGATAACACAAGACACATATCATTGAC	AGCGGATAACTGACAAAAAATCATGGCAGGC	GGCCATAGTTTCCAACCT	F	MONO
rs10882064	94190749	C/T	AGCGGATAACAGGTGATTCTCCTCTCTCAG	AGCGGATAACCCCTGGCCAACATGGTAAAAC	AAAACCTGTCTCTACTAAAA	R	MONO
rs11186997	94191026	C/T	AGCGGATAACTTTGGGAGGCCAAGTGAGCG	AGCGGATAACCCACCTGAGTAGTTGGGATC	TTGGGATCACAGGCGCC	F	MONO
rs2798253	94192885	C/G	AGCGGATAACTCCACAACATAAGGTAGGG	AGCGGATAACAAGTGTAGGATTACAGGCG	CAGCCAATGAACCCGGG	F	
rs11186999	94193961	C/G	AGCGGATAACACTCCTGACTTCAGGTGATC	AGCGGATAACCCAGCTTTTTAGTTGCTAC	GGCTTACGCATGTAATCC	F	
rs4933231	94196162	C/T	AGCGGATAACTGGATGTCCTTTGGGTAAC	AGCGGATAACAGGATTATAGACGTGAGCCA	CCACTAAGCCTGGCCCTTTTGG	F	
rs11187001	94196306	C/T	AGCGGATAACACTTGTAAATCCAGCGACTC	AGCGGATAACGAGTGCAGTGGCACAATCTC	GGCACAATCTCAGCTCAC	F	Failed HW
rs10786047	94197028	A/G	AGCGGATAACAGGCTAAGGTGGTTGAATTG	AGCGGATAACCCACACCTGGCTAATTTTTG	GGCTGGTCTGAAACTCCTGG	F	

rs11187004	94199011	G/T	AGCGGATAACGAAAAGAAAGCTCCAAGCCC	AGCGGATAACCCTGGGAAAATCCACTTGG	CTTGGTCATCATGTAAGGTTG	F	
rs7910977	94199856	C/T	HapMap				
rs2251101	94201284	C/T	AGCGGATAACACAGAGCGAGACTCTGTCTC	AGCGGATAACTGATACATGGAGGGACTCAG	AGGGGACTCAGCAGGTCCCCCT	R	
rs7896688	94201876	A/G	AGCGGATAACAAATAGTACAGTGGCCAGTC	AGCGGATAACTCACTGCTTTCTGCATTATG	ACTGCTTTCTGCATTATGAACAAT	F	MONO
rs913648	94202722	A/G	HapMap				MONO
rs4646958	94204339	A/T	AGCGGATAACTCTGAATCACTTCAGGCTGC	AGCGGATAACTAGAACTGAGGTATGCTCCC	CCAGTGTCCGCCAAAAAA	R	
rs12356364	94206153	A/G	AGCGGATAACCAAGAACATGGACGGATACC	AGCGGATAACTGACCCTGCTCTTCTTTGTG	TGTGCCTAGGAAATGTTGGCAGTA	R	MONO
rs6583814	94206524	A/G	AGCGGATAACACAGAGTCTTGCTCTGTAC	AGCGGATAACACACGAGGAAGCAAGTTTGC	GCAAGTTTGCCATGTGCC	F	
rs11187009	94207018	G/A	AGCGGATAACAGAGAGCAAGCAGACTCTAG	AGCGGATAACGTAACACTGTGGTTCATCTACC	GTGGTTCATCTACCAAAAAGAGAAA	F	
rs3781239	94207777	G/C	AGCGGATAACAACTGGAGAAGGTGTTCTGC	AGCGGATAACTTCTCCATCTCTTGTACCCC	TTGTACCCCAAACCTTCATTACCC	R	MONO
rs3824738	94208177	C/T	HapMap				MONO
rs489517	94209484	C/A	AGCGGATAACGTGCAATTCCATTGCAGCAC	AGCGGATAACACACCCATCTAAATCTTCCCC	AAAATTTCCATTAGGTAGGTATAT	R	MONO
rs9420586	94209510	A/C	AGCGGATAACGTGCAATTCCATTGCAGCAC	AGCGGATAACACACCCATCTAAATCTTCCCC	TAAAAATTCTAAGAAGGATAGT	R	Failed geno
rs2247348	94209597	C/T	AGCGGATAACGCTTTAAGAGATTCACACCG	AGCGGATAACGATTTAGATGGTGTGAACCTC	TTTTTTTTTTTGAGACAGAGTCT	F	MONO
rs520711	94210625	A/T	AGCGGATAACAGGCACAGTTTCGCTCTGTC	AGCGGATAACGAGTGGAGATCATGCCACTG	TCATGCCACTGCACTCC	R	MONO
rs7098739	94211102	A/T	AGCGGATAACCTCCAAGACTCTTAAGTATCC	AGCGGATAACAATCACTTGAACCCAGGAGG	GAGTGAAACTCTGTCTCAAAAAAA	R	Failed geno
rs551266	94212604	G/A	AGCGGATAACCCACGTCCAGCCTACTTATA	AGCGGATAACTAGGTACACGGCAAATGCTC	AAATGCTCAATAAATGAGAGA	R	
rs1042444	94213696	G/A	AGCGGATAACTGGGCTATATCGTCTTCAGC	AGCGGATAACGTGGCTTTTCTGACTGGATG	TGACTGGATGATGAATCTCAAGC	R	MONO
rs1887922	94214145	T/C	HapMap				
rs10882066	94214726	A/G	HapMap				
rs2275218	94215277	T/C	AGCGGATAACGGTCTACTTAGAGAGACTTG	AGCGGATAACGTCCATAAGATAGTGATTGC	TTTTAGAAGTGGATTCTCTGT	R	
rs7893352	94216829	C/T	AGCGGATAAACCATCTCCTTTATAATGCTTG	AGCGGATAACTGCAATGAGCCATGATTGTG	GTGCCAGAGTGACAGACTGTCTC	R	MONO
rs11187014	94217818	G/C	AGCGGATAACATCCTACTTCTCCTTCCAGG	AGCGGATAACCAAGTCCAGAGGTAGATGTG	TAGATGTGATTATTTCTAGCTGG	F	MONO
rs7920976	94219726	A/T	HapMap				MONO
rs4646957	94219892	T/C	AGCGGATAACAGCAAGAGGGTTGAGTAAAC	AGCGGATAACTCCCTCTAGTCTTTCTCAAG	CCAGCATGGTGTGATAAG	R	
rs2250090	94221786	A/G	AGCGGATAACAAACAACCTCAGTGTGAGAGG	AGCGGATAACTGAAGTTCTTGCTACCCTGG	GCTGAATGATTTAGAGTCACTGAA	F	
rs2149632	94222227	T/C	HapMap				
rs2249960	94223100	A/G	AGCGGATAACCCCTCAGTGTGTATCTAATG	AGCGGATAACAAAGGGTGATACCAATCTAC	GATACCAATCTACATTTTTTTCCA	F	
rs12245118	94224735	A/T	AGCGGATAACAGTGAAAGAGACATGCGTTC	AGCGGATAACGAAAGAAGGGAAATATCCTAG	GACTTTTGAAATGATTTTTTAAAG	R	MONO
rs7073248	94227390	C/T	AGCGGATAACTGATAGGCAAGAACCTCAGC	AGCGGATAACAGTCTAGTTCCTACAGTAGG	GAAAAATGATGTGCTTGCC	R	
rs6583815	94227782	A/G	AGCGGATAACACGAGTACCCCAAAATGCTC	AGCGGATAACCCCTTTTATGGCACACATTC	GCACACATTCATCTTCACTTT	R	
rs12411941	94227902	C/T	AGCGGATAACCAAGCTTGAAACACATTC	AGCGGATAACTAGCATGCACCATTACCTAC	ACTTTATGTGTGTTTTAAATAA	R	MONO
rs5030982	94229152	G/T	AGCGGATAACTACAGTGAAGGGGTCCAC	AGCGGATAACTGTCAACATTTTCTTCCAG	CATTTTCTTCCAGCCCATT	F	MONO
rs7910605	94229773	A/G	AGCGGATAACCTGTGGTGGTTTGTGTTCTTG	AGCGGATAACAACAGCAGCCAAAAGTAGGG	AGCCAAAAGTAGGGAAAAAT	F	
rs12356508	94231074	G/A	AGCGGATAAATTCTTGGGCTCAAGTGATCC	AGCGGATAACAAATGCTACATCCAGCCTGG	GTAGTCCCAGCTACTCAG	F	MONO
rs12243214	94233186	C/T	AGCGGATAACGAGGAGGACAGAAGCAATAG	AGCGGATAACCTGCTGACTCTTGAGTATGC	CATGGGACAGCAACTCCA	R	MONO
rs2421940	94233597	A/G	AGCGGATAACATAAAAAGACACCGCGGCTTG	AGCGGATAACAGAGTTGCTTGACATGGCAG	AGGAGGGAAAGTGAAGTGA	R	
rs10882067	94234248	T/C	AGCGGATAACCCTGTAATCCCAGCACTTTG	AGCGGATAACTTTTGTGTTTTGGCCAGGC	TCTCGAACTCCTGGCCTCAAGTC	R	Failed geno
rs11595475	94234883	G/T	AGCGGATAACTGGGCAATGGAATGCGAGTC	AGCGGATAACCTGGGTAACAAGAGCGAAAC	CAAGAGCGAAAAGTCTGTC	R	MONO
IDE7	94235058	A/T	AGCGGATAACCTTATGAATAAAAAAGCAGGG	AGCGGATAACAATGGCTACCTTTGAGATTG	AATTATCAAAGAAGCAGTAAGTT	F	MONO
P539P	94236972	G/T	AGCGGATAACAGAATGAATTTATTCCTACG	AGCGGATAACCTTAATAAGAGCAGGGTATG	TATGGTGTGCCTCTTTTTCTAA	R	
rs6583817	94237227	C/T	AGCGGATAACCTACCAATCTATCGATGGG	AGCGGATAACGATGTGGAGAGGAAGAGTAG	TAGTACTAGAAAAGACTAECTCA	R	
rs11187019	94238290	G/A	AGCGGATAACTGTAATCCCAGCACTTTGGG	AGCGGATAACTCACAAATGTTGGCCAGACTG	ACTCCTGACCTCGTGATC	R	MONO

rs12219148	94238396	C/T	AGCGGATAACATTAGCCGGGTATGGTGGTG	AGCGGATAACATGATTCTCCTGCCTCAGCC	GCCTCCAAGTAGCTGA	R	Failed geno
rs11187020	94238730	G/A	AGCGGATAAAGTCCACACCAGCTAGAGATC	AGCGGATAACGGAGTAAAAAGCAACCAGCC	AGCAACCAGCCTGGACA	F	MONO
rs7093418	94239749	T/G	AGCGGATAACCCTGACTACTGATGAATGGG	AGCGGATAACTGCCTCATGTTATAGCACCG	GGAGAATTATGATTTTCAGAA	R	
rs3737225	94239962	A/G	HapMap				
rs11187021	94242628	A/G	AGCGGATAACAAATACTCTACCTGGCTGAC	AGCGGATAACTGACAGGTGAGTCATCTTGC	GAAAAGCAGATGACAAGAC	R	MONO
rs3781238	94243184	A/T	AGCGGATAACACTCTTCCATGAAACGCTTG	AGCGGATAACGTTTTCTTGTTCAGAGGGC	GTTTCAGAGGGCAAGTCCAC	F	MONO
rs3781237	94243185	C/T	HapMap				MONO
rs10882068	94243606	C/T	AGCGGATAACATGAAAGGGTATGTATGAGG	AGCGGATAACCACTCTGGTTCATAGGTATC	TGTATACTCTGTCTGTACC	R	MONO
rs1855917	94244183	C/T	AGCGGATAACCGTTGTGTTTTCTCATGTTTC	AGCGGATAACGCCAATATGGTAATGATGTG	ATGGTAATGATGTGATCCTTA	R	MONO
rs1855916	94244263	C/T	AGCGGATAACCGTTGTGTTTTCTCATGTTTC	AGCGGATAACCCTTAGAAAATGAGAGAACAGG	AGGCGAGTGGGTCACCT	R	
rs10882069	94245019	G/A	AGCGGATAACATGGCGTCTCACTCTGTTGC	AGCGGATAACTGTGCCTGTAGTCCCAGCTA	GTGGTGAGCCAAGATCG	R	Failed geno
rs7075073	94245384	A/G	AGCGGATAACACTCCTGACCTCAGGTGATC	AGCGGATAACGTGGAAGGAGAGGGTTCATC	CCTATTTAAAAATTATTGAGGC	R	Failed geno
rs11187024	94246000	G/A	AGCGGATAACCAGTCAACTTTTACTGAGTTC	AGCGGATAACTTGCTATAGGTCATGTGTCC	ATTTTGTCTTTCCAGAATTTGAC	R	MONO
rs7084090	94247198	A/T	AGCGGATAACAATCCAAGGTGCTCAAGTCC	AGCGGATAACACTTAGCTGGGATACTGCAG	AGTACCATACTACACCATT	F	
rs11187025	94247956	C/T	AGCGGATAACCACCTACTACTAGTCATGAG	AGCGGATAACTCAGGACTGTCAACTCTGAG	TGTCAACTCTGAGGTTTCA	F	
rs6583818	94247994	G/T	AGCGGATAACGTCAACTCTGAGGTTTCACG	AGCGGATAACCACCTACTACTAGTCATGAG	TACTAGTCATGAGATCTTGGATA	R	MONO
rs11187026	94249117	G/A	AGCGGATAACACTTTGGGAGACCAAAGTGG	AGCGGATAACCGTAGAGATGAGGTTTTGCC	TCTTGAACTCCTGACCTCA	F	Failed geno
rs11187028	94249288	A/G	AGCGGATAACAAATTAGCAGGGTGTGGTGG	AGCGGATAACTGATCATGGCTCACTGCAAC	CTCAAGTGATCCTTCTGCCTCA	F	Failed geno
rs10786048	94249948	C/T	AGCGGATAACATTAGCCAGACATGGTGGTG	AGCGGATAACTCACTGAAACCTCCATCTCC	ACCTCCATCTCCCAGTTTAAGC	R	MONO
rs7068618	94250507	A/G	HapMap				
rs11187031	94251771	T/G	AGCGGATAACCTTGACCTCTTGGGCTTAAG	AGCGGATAACACAGGTATAGTGGCTTGCAC	CACCCATAATCCCAGCTAC	F	
rs11187033	94252339	T/A	AGCGGATAACGGGATGGCGAGATATAGTTC	AGCGGATAACGGGAAAGTAGATTCCCTTAGG	ATGTGTATCAGTGCCATATATCAC	F	
rs1970244	94253203	A/G	AGCGGATAACCTAGGAAATACTATTAGCCAG	AGCGGATAACTAGAAATTTTAGCTGAATCC	TAGCTGAATCCTAGCATGA	F	MONO
rs11187037	94253341	T/C	AGCGGATAAACCCACCTGAACATTAGAAGAC	AGCGGATAACGCTTCATTAGCGATAATTGC	TTGCATATATAGACTTGCAC	R	
rs11187038	94254975	C/T	AGCGGATAACGGGAAAACCACGAATGTTTC	AGCGGATAACCCGCTTCCTAAATGTTTGTG	TAAAAATCCTGTAGGTGTCA	R	MONO
rs11296200	94256855	A/-	N/A				Failed design
rs1832196	94258314	C/T	AGCGGATAACAAATGGCGAAACCCCATCTC	AGCGGATAACAGTGAGATGGTGGTTGTTGG	GTGGTTGTTGGCACGCTGTTG	F	Failed geno
rs1832195	94258381	A/G	AGCGGATAACACCATCTCACTCACTAACCC	AGCGGATAACCTGGCTCTCATTTTCTCCTG	TCCTGAATAGTGTCCATG	F	
rs6583819	94259587	A/G	AGCGGATAAACAGGTGAAAATTTTGGAGG	AGCGGATAACAGGTGGGAGGATCAATTCAG	GGAGGATCAATTCAGCCAGGGA	F	
rs11187039	94259792	G/A	AGCGGATAACATTTCTGAACACCTTTTCC	AGCGGATAACCCTGTTCTATGGTAAACTAGG	CAAAAATTTATGCACTTACTTTAA	F	MONO
rs10882073	94260859	A/G	N/A				Failed design
rs11498516	94260983	C/T	AGCGGATAACACATGGTGAACCCCTGTCTC	AGCGGATAACCCAGGTTCAAGTGATTCTC	AGTAGCTGGGATTACAGG	F	Failed HW
rs17445028	94261156	C/T	AGCGGATAACGAGGAGACAGAATCAAGATG	AGCGGATAACTACAGATGTGAGCCACCATG	CCTGGCCAAAACCTGTCTTTTTA	F	
rs11187040	94262844	C/T	AGCGGATAACACAGAGTGAGACTCCATCTC	AGCGGATAACGGACTGTAGAATGTGAGTTC	ATGTGAGTTCCTAATACTATA	F	Failed geno
rs7910569	94263344	A/C	AGCGGATAAACAGCATTTTAATACCATGGG	AGCGGATAACGCACATGTTTTGTAAACAGC	ACAGCTTTTGTCTCTTTA	F	Failed geno
rs4646956	94264650	T/C	AGCGGATAACAACACTGTGAAAAAGCCAAC	AGCGGATAACGCTGTTTGTGTTTTAGGTCG	GTGTTTTAGGTCGAGGTAAGA	R	MONO
rs9633693	94265538	C/G	AGCGGATAACTAAGACACTTTTAGGCCGGG	AGCGGATAACTTCTCCATGTTGGTCAGGC	CTTGAACCTCCGACCTCAGGTGAT	F	MONO
rs7895832	94266506	A/T	AGCGGATAACGCCAAGTTACTTGTGAAAG	AGCGGATAACCTACATACATCGCTGGAGAG	AAAATAGCATTGCATCCTTTTT	R	
rs6583820	94266635	A/G	HapMap				
rs7075851	94267766	C/T	HapMap				
rs10509645	94267846	A/C	HapMap				
rs11812558	94271124	C/T	AGCGGATAACACAGAAGACAGGAACTTG	AGCGGATAACCCACCACTCCAGTCTGATAT	TTTTTTTTTACTGCACCCCT	R	
rs11187042	94271625	T/C	AGCGGATAACGAACACTAACTGGATATTTG	AGCGGATAACCATTTCCATTACCCCTTTTG	TAAATATTTAGTATATATCTCT	R	MONO

rs10882074	94271665	T/G	AGCGGATAACCATTTCCATTCACCCTTTTG	AGCGGATAACGAACACTAACTGGATATTTG	ATATTTATGAGCAAAATGATATC	F	
rs11187043	94271861	T/G	AGCGGATAACCTCCTGATCCTGTGGTAAAC	AGCGGATAACAAATAAGGGTGGGAGGGAAG	GGAGGGAAGAGAGAAAAAAG	F	MONO
rs11187044	94272258	T/G	AGCGGATAAECTCTCTCCTCTCTGTACTC	AGCGGATAACAAGGAAGAGCCATTCAAGGG	GGGAAAAAGAAAAGGAACTA	R	MONO
rs7915971	94272698	T/C	AGCGGATAACGTGTCATTGCACTCAAGGTG	AGCGGATAACACACTCAGTGAAATCCTGGG	ATCCTGGGTTTGCCTTGCT	F	MONO
rs4933233	94273091	C/T	AGCGGATAAECTGTAGTGAGCCGAGATCATG	AGCGGATAAECTGTGCCAGCAAGTAAAAG	GGGTTTCTTCTGTCAATTCA	R	MONO
rs11187045	94273349	A/T	AGCGGATAACCTTTCTTTCACTTGCTGGG	AGCGGATAACGTATTTTAGGTGTGCGTGAC	CCTCCTAGGTTTAAAGTGGT	R	MONO
rs11187046	94273981	A/G	AGCGGATAAECTGAGGCAGAACTGCTTGAAC	AGCGGATAACAGTCTCACTCTGTCCACCAAG	CACAATCTCAGCTTACCG	R	MONO
rs4641376	94275508	A/C	AGCGGATAAECTGCCAACAGTGAACAATCTG	AGCGGATAACGAGGGCTTTTTTGTGTGTG	ATAAATGGGATTGCTTTCTTG	R	
rs11187055	94276174	C/T	AGCGGATAACAGATTGTGCATATGAAGCCC	AGCGGATAAECTTTTTCAGAACTCTACTGTCC	AGAATCCTACTGTCTTTTCACAG	F	MONO
rs10882077	94276465	C/T	AGCGGATAAECTAGCTGAGTGTGGTAGTGTG	AGCGGATAAECTTTGGCACTCTGTAACTC	CCAGCCTCCCAAGTAGCTGA	R	MONO
rs2421942	94277360	C/G	AGCGGATAACCAATTACAGGAAAATGCTGG	AGCGGATAACGGCATTCTTTTATATCCATTAC	TATATCCATTACATATTTCTTG	F	
rs7078413	94280464	A/C	HapMap				
rs17107709	94282086	G/T	AGCGGATAACGCAGGTCATAGTTTTTAGGC	AGCGGATAAECTTTGTCTAAGGTGCCTGAG	AGGTGCCTGAGTCTAAGTGAA	R	
rs4646955	94284271	A/G	AGCGGATAACATGAAGCCATCTCTGTGGAA	AGCGGATAACACAGGTAATGCAGAATACCC	ATTATCCAACTTTGTGTACTTA	R	
rs7077418	94285778	A/G	AGCGGATAACCAACAGAGTGAGACTCTGTC	AGCGGATAACCATGGGCACATTTCTTACAC	CAGGTTGCTTCTTTTTTTTTTT	R	Failed geno
rs2275221	94286967	C/T	AGCGGATAACCTGAAACAACCTGCAGTTTACC	AGCGGATAACACTCAATAGTTACCGTTCC	ACCTTATTTTATACCAGAACCCCTC	R	MONO
rs1832197	94288311	A/G	HapMap				
rs12416180	94290376	A/T	AGCGGATAAACACAGTTGTGGTTTGGACAG	AGCGGATAAECTTTCTCTGTGGTGCCTGAC	GAGTTTGACTTAGGTAACCAAAA	F	
rs10882078	94292030	T/C	AGCGGATAAACTATAGCCTCAACATCCCG	AGCGGATAACAAATTAGCTGGGTACGGTGG	CGGTGGTGAGTGCCTAT	R	
rs11815736	94292741	T/C	AGCGGATAACGTGACCTTTTCACTCTTCTC	AGCGGATAACGTGAGTAGGAAGCAAAAAGC	AAAGCAAAAGTAAAATTTCCCA	R	MONO
rs11187060	94294112	C/T	AGCGGATAACCTTAAGTGGTGGGTCGTAAC	AGCGGATAAECTATGCAAGCACTGACTGAGC	GAGTTGAAGAGGATGACTGC	R	MONO
rs7915349	94294428	A/G	HapMap				
rs11187061	94295389	T/C	AGCGGATAAACCATGCTTGCCCTAAGCAAAG	AGCGGATAAECTCACACCAACTTCATGCCAC	GCCACCACTGAAGCCTCAAT	R	
rs11187062	94296406	T/C	AGCGGATAAECTTGCCACAAGAAATAGGAG	AGCGGATAACGTAATGAGTAAAGTCCTGAG	AACTTAGTTGACTGATGCTGT	R	MONO
rs10218994	94296563	A/G	AGCGGATAACGTTGAGGGGAGAATTTATTC	AGCGGATAACAACCTTGACACTTCCAGTAAC	ACTTCCAGTAACTAATAGCTAA	F	MONO
rs11187064	94298233	T/C	AGCGGATAAECTGCATCACACTCAGACAACC	AGCGGATAAECTACCAGGAACTATGCCTTGG	GGAACATATGCCTTGGTGAAGTTT	R	
rs10219017	94298446	G/A	AGCGGATAAECTACCTGGTTTCTAATAGTC	AGCGGATAAECTTCTGAGGTCAAAAAC	CTGGAGGTCAAAAACATTCATTA	F	MONO
rs7909636	94299843	C/T	AGCGGATAACGCAGGAGAATCTCTTGAACC	AGCGGATAACAGTTTTTGTAGTGGCCAGG	ATGGCGTGATCTCAGCTTGCTGC	R	
rs10882079	94300414	G/C	AGCGGATAACAGAGATAGCGCCACTACACT	AGCGGATAACAGAAACGGGGTTTACCATG	GTTTACCATGTTGGCCA	R	Failed HW
rs2421943	94301795	A/G	AGCGGATAAECTGTTACATATTCTTTATCAC	AGCGGATAACGTTGTTAGGTTAGTTTGTAG	TGTTAGAATATTGATTGTTTCTCA	R	Failed HW
rs11187065	94301904	C/T	AGCGGATAAACACATTGAAGGAGTGTAAAAG	AGCGGATAACGTAGTTCTTTTTCTTTAGGC	CTTAGGCTTTATTGTATCCAGTCA	R	
rs4406744	94302165	T/A	AGCGGATAACCGGAGAAGGCTACAATTGTGG	AGCGGATAAECTGGACAGCCACATATACAG	ATTTCTATGTCTTTTTGTATATA	R	MONO
rs1987122	94303116	A/G	AGCGGATAACACAGAGTCTCACTCTGTTGC	AGCGGATAAECTTGTGTAACCTTGGGAGGC	TTGCAGTGAGCCAAGACT	F	Failed geno
rs6583821	94304548	T/C	AGCGGATAACAATTGCTTGAACCTGGGAGG	AGCGGATAAECTTGTGCTCAGGCTAGAGTG	AGGCTAGAGTGCAAGAGT	R	Failed geno
rs10882080	94304589	T/C	AGCGGATAAECTGCATGTGGCATCTGAAAGC	AGCGGATAAECTTAGCCTGAGCAACAAGAG	GCAACAAGAGCAAAATTTCCA	F	MONO
rs7908111	94304784	A/G	AGCGGATAACACCTCCATTGTGTACTTCAG	AGCGGATAACGGCTTTCAGCTTTTCACTGC	GTTTGCTTGTCTTCCATGGC	R	
rs10882081	94305004	A/G	AGCGGATAAECTTTCACCATGTTGGTCAAGC	AGCGGATAACAATCACACTAAAGAGGCCGG	AACACTTTGGGAGCTGAG	F	Failed geno
rs7917163	94306808	C/A	AGCGGATAACGTTTCATGGATGGGAAGACAG	AGCGGATAACGGTCTCTGCATTTCCAAAC	TGTCATTTCTGCAAAAAGGAG	R	
rs7394234	94307486	G/A	AGCGGATAAECTGGCGAAGATGGTGAACAC	AGCGGATAAECTCCGCCTCCAGGTTTAAAC	AGGTGTTGGCCACCATG	R	
rs11187066	94307851	A/G	AGCGGATAAECTTTTGTCTTGTGCCCAGG	AGCGGATAACACAGGAGAATCGCTTGAACC	GGACGTTGCGGTGAGCTGAGATCA	R	Failed geno
rs7098744	94308049	C/T	AGCGGATAAECTCTCAAACCTGACCTCAG	AGCGGATAAECTTATTGGCCAGGCATGGTG	CTGTAATCCTAGCACTTTG	R	MONO
rs11187067	94309312	T/C	AGCGGATAACATGAATGGTCCAGAACAGGC	AGCGGATAACCACTCTATTCCACTCTTCCC	GCAGCCACTCATCTTTCTTTCT	R	
rs1999763	94309972	A/G	HapMap				

rs1999764	94310119	T/C	AGCGGATAACAGCCATCTTGCTCCAAAAGG	AGCGGATAACAGAGAGGGAGAAAAGAGAGC	GAGTGTAAATGTAACAAGGTAGGG	R	
rs11187069	94310846	C/T	AGCGGATAACGAGACCAGCTTGCCCAACAT	AGCGGATAACTGCCATCTCGGCTTACTGCA	CCACCACCGTGCCCGCT	R	Failed geno
rs10882083	94311953	C/G	AGCGGATAACGACCGACTATAAATGAGGTC	AGCGGATAACGCAAAACATATCCACATGCC	TATCCACATGCCACATCC	F	
rs4933729	94313002	A/C	AGCGGATAACAAGAGCAAACTCCACCTCG	AGCGGATAACTAAGGAGCTGGAACACTACAGG	GATGGGGGTTTCCACATG	R	
rs11187071	94314015	C/T	AGCGGATAACGAGACTATCCTTCAGGACAC	AGCGGATAACGGCAACCATTCTGTAGCAAG	TGTAGCAAGCCTGGAGAAAA	F	MONO
rs11187072	94314389	C/T	AGCGGATAAATTGCAGTAAGCCGAGACTGC	AGCGGATAACCCCACTTGATCTTATGGTCC	GAGACAGTCTCGCTTTATC	R	Failed HW
rs11187073	94314708	T/C	AGCGGATAAACTCAGGTGATCAACCCACCTC	AGCGGATAACGCTGGGCATAACAAAGCAAC	GATCAAGAAATAACAGTAGCCAGG	F	Failed geno
rs7076966	94315491	C/T	AGCGGATAACAATGCTTCTGCAGATCTCC	AGCGGATAACGGGACGTTAAAACAGGGAG	TCTGAAGTGATTACTGGATA	R	
rs2421944	94316150	A/T	N/A				Failed design
rs7100623	94317136	C/T	HapMap				
rs12355977	94317963	G/C	AGCGGATAAAGTCAAGTATGCCCTGGTATC	AGCGGATAACCCTGAAATTTGAGGGAGAGG	GGGAGAGGTTCTGGCTA	F	
rs7915220	94318582	C/T	AGCGGATAACACAAGGGCAGACTCTTTCTC	AGCGGATAACTTATAACTCTGCTCCTCCCC	CTGCTCCTCCCCTGTAAGGTATT	R	
rs10882084	94319093	A/G	AGCGGATAAAGTTCAGCCTTCTGTCTCC	AGCGGATAACCCACTGGTGATATTTAGGCG	CGAGACAACAGCTTGGG	F	MONO
rs7097014	94320200	A/C	AGCGGATAACATATGTTAGGTTCTGGAGCC	AGCGGATAACGTGATCACTACAGAGTAGAC	GAAAACAGACTGAAGACAAGCCAA	F	
rs4304670	94321119	C/T	HapMap				
rs2421945	94321321	G/A	AGCGGATAACCCTTGTCTGTGTTTCAGCTG	AGCGGATAACGGGAATGGGCTATTATCTCC	CTATTATCTCCAGGTGCCCA	F	
rs10736067	94321742	G/C	AGCGGATAACATGAGCCAGCTAGAAAGCTC	AGCGGATAACCTAATCCCTTTGGTTGGACC	TCTCAAAGCCTCACTCACT	F	MONO
rs7909487	94322696	A/G	AGCGGATAACTATGTGTCTGCCTTCCAAGG	AGCGGATAACCACACCCCTTGAGCTATCTC	CCCAATCCGCTCCAATC	F	MONO
rs12783634	94323222	A/G	AGCGGATAACTAAAGGAATCCGGCGACTTC	AGCGGATAACACTCAGTGCCCGGAGAAAAG	AGGGCTGAGGGCAAGGT	F	
rs4646954	94323807	G/A	AGCGGATAACAAAACCCGGAGCAGCTACCTC	AGCGGATAACATCACCGCAAACGCTTCCCTG	CAAACGCTTCTGCTTGCCTTC	F	Failed geno
rs4646953	94323935	A/G	AGCGGATAACAAAACCCCTGTCCCTCCAGTC	AGCGGATAACTTTGCTGAGCCGGATGG	GCAGGCGAGGACGGTGA	F	
rs3758505	94324758	T/G	AGCGGATAACGGAACCCCTCCTACTGAATTC	AGCGGATAACACAGACGATCAAGACTGCAG	AAAAACGGGTGCTCTTAGTCCA	R	
rs7099761	94325779	A/G	AGCGGATAACGAAGGAGCCATGTACAATGC	AGCGGATAACAAGAGGAGGTGGATGGAAGG	GGTGGATGGAAGAAAAGTA	F	
rs3758503	94326684	C/T	AGCGGATAACGGAAGGAACCTACAGCACAG	AGCGGATAACTGCTGAAGTCATTCTTTGCC	CATTCTTGCCTTAGATAGGAAA	R	
rs7921325	94328632	T/A	AGCGGATAAAGTACAGAGTGCAGTCTGTC	AGCGGATAACGAACAGCTGAGGAACATTGG	GTCTCAAAGACATTTTTTTTT	F	Failed geno
rs7905037	94328678	A/G	AGCGGATAACAGAGGTTGCAGTGAGCCAAG	AGCGGATAACGAACAGCTGAGGAACATTGG	CCCAGGCTGGAGTGCAATG	F	Failed geno
rs11187077	94330087	G/T	AGCGGATAACATGCCTGTAATCCCAGCTAC	AGCGGATAACAATCTCAGCTCACTGCACTC	AAGCAATTCTCCTGCCTCAG	R	MONO
rs11187078	94330685	C/G	AGCGGATAACGATCCTGATTTGAACAAAACCC	AGCGGATAACATCCACAGGCACTAACATAC	CCTGAGTGTTCCCACTTT	F	
rs11187079	94331572	C/T	AGCGGATAACGCTAACACAGTGAACAAAACCC	AGCGGATAAAGTCCGATTCCCTGGTTAAGC	GGTTTAAGCAATTCTGTCTCAAC	F	
rs11187080	94333545	C/T	AGCGGATAACAAGTCTGTAATCTGGGAGG	AGCGGATAAAGTCTGCTTGTGCCCAGG	GCTGGAGTGCAATGCCA	F	Failed geno
rs6583823	94334395	C/T	HapMap				
rs2421941	94335889	G/A	AGCGGATAACATCCTCTCTGCATTTCTTC	AGCGGATAACGAAATGCTCAGCTATGAACAG	CAGCTATGAACAGACATAAT	R	
rs11187081	94337053	C/T	AGCGGATAAAGTACAGGTATGAGCTGCCATG	AGCGGATAACCGTGTGTTGCTCTGGCATTTC	CTTTCAGGAGTATATGTACTTCTC	R	MONO
rs6583826	94337810	G/A	AGCGGATAACAGGCTGAGTAGTTTGACAAC	AGCGGATAACGGCCCATGTAAGTGTGTTTG	ACTAAGCAGTCCCTGAAATGT	R	
rs7911019	94338815	A/T	AGCGGATAACAAGAGAAAAGGAAAGACGGCC	AGCGGATAACATAGGCACAAGCCACCAGAC	AGCCACCAGACCTGGCT	R	MONO
rs1889894	94340487	A/G	AGCGGATAACGACCTATCTCCACCCTAATC	AGCGGATAACTCAACAGGACTCCACTACAC	CACGTGGAGGAATCAAAG	F	MONO
rs12355158	94340661	G/A	AGCGGATAACAGAAGGAGCTGTAGATGCAG	AGCGGATAACTTCTCCACTTGCTAATCCC	CCCCTACATGCGCCCCC	R	
rs11595187	94341915	C/T	AGCGGATAACAGGAGTTTGAGACCAGTCTG	AGCGGATAACTAGATGGGACAAAAGGCAC	ACACCAGGCTATTTTTTCCC	F	Failed geno
rs2297743	94342803	C/G	HapMap				
rs3824736	94344062	C/T	HapMap				MONO
rs11187085	94344692	A/G	AGCGGATAAAGTGGTGCCTGTCATTAAGC	AGCGGATAACAAAAGGCTTACCAACCCCTG	GAGGACCTCGCAACTCATAAGT	R	
rs11187086	94344951	A/C	AGCGGATAAAGTTCCTCCACTTCAGCCTCTC	AGCGGATAAAGTGGTAAACCCCATCTCTAC	AAAATACAAAATTAGCCAGGCAT	R	Failed geno
rs11817798	94345504	G/A	AGCGGATAACGCTAAGTGGAAATGAGCAAG	AGCGGATAAAGTTCCTCTCCATCAACC	CATCAACCCGACACCTACCATT	F	

rs11187087	94346261	G/A	AGCGGATAACACCCAATGGATGGCTACTTG	AGCGGATAACCAACAGTGCATAAGGGTTCC	TCTCCACATCCTCACCAAC	F	
rs4604791	94346892	C/T	AGCGGATAACCAGGGTTTCTTCTGCTTTGG	AGCGGATAACACATTGTGTCAGATCCTTTGGC	CCTTTGGCATCAGGAGAA	R	
rs6583827	94348003	A/T	AGCGGATAACGTTGGACCCTTATCTAACAC	AGCGGATAACTCCATTGTGAAGCTTTTGCC	TTTTTGATCCATTTTGAGTTAAT	F	
rs11187089	94349194	G/A	AGCGGATAACAGGAGAATCGCTTGAACCTG	AGCGGATAACACAGAGTCTCACTCTGTTGC	TGGCTCACCACAACCTC	R	MONO
rs12218324	94349700	A/T	AGCGGATAACAATAAACAGAAAGTTCAATAG	AGCGGATAACCAAGTTCTGGGATTACAGC	TGCCTGGCTTTTTTTTTTTTTT	F	Failed geno
rs12411873	94350841	C/T	AGCGGATAACAAAGGTTGAGGGCCAAGAGC	AGCGGATAACCTTGAACCTGACCTCGTG	CTCCTGACCTCGTGATCCATC	F	
rs7096101	94352908	G/A	AGCGGATAACGGTGAAGATAGTTGGTTGC	AGCGGATAACTGGCTCCCTTGCTTTTTAGG	TCTGCTTAAATATCACCTGC	F	
rs4933731	94353973	C/T	HapMap				
rs10882086	94355005	T/C	AGCGGATAACAGTGTAGACCTTCTGTGTC	AGCGGATAACTGTCCACACAACACTGTGAG	CAACACTGTGAGGTTGGTAAT	R	
rs10786050	94357210	A/G	AGCGGATAACTCAATGGAAGAGGAAGGACC	AGCGGATAACTCTGCTCCAACCTTCTGTC	CCATTCTGTCATAAATAGAC	R	
rs10882088	94358568	T/C	AGCGGATAACAATGCTCAGGGATGAAGATG	AGCGGATAACTACAACAGTCTGTTCTACAG	CAGTCTGTTCTACAGTAGTCTTC	R	
rs11599330	94360614	A/G	AGCGGATAACAGATCATGGAATTTTGGATG	AGCGGATAACTTCCATTTTATTGGAAAGCC	TTGGAAAGCCATTAAGTGAAAAT	R	
rs2275219	94362922	A/G	AGCGGATAACAAGCTAATCACCCAGTGACC	AGCGGATAACGAAGTGGTAAGCATCCACC	CTCTTAAACACCTTATAGAGCAGC	R	
rs10882091	94364357	C/T	AGCGGATAAAGTGTAGGTTGGTGTATG	AGCGGATAACTTCTAAGCAGCCTCTACC	ACCACACTAGCGAGCATTCACTTG	R	
rs12252836	94366308	C/A	AGCGGATAACTATCCTAAGGGTCGAGACTC	AGCGGATAACTAAGACCACTATGCCCAACC	CCCAACCTTTAAAAAGGAAGTT	R	
rs11187100	94367517	A/C	AGCGGATAACTGCACTGAGTCAAGATCGTG	AGCGGATAACAAAATGGTACTTCACTACGG	TGAGATGAAGTCTCGCTCTTTCA	F	
rs11187101	94367754	C/A	AGCGGATAACAAAACCATATTGGGGCCAGG	AGCGGATAACTCCTGACCTCGTAATCTG	AAATGCTGGGATCACAGG	F	Failed geno
rs10882092	94369203	G/A	AGCGGATAACCTTGGGCAATTATCCCAGAG	AGCGGATAACGTCCATGGTGAGTATGTACC	AACTGCTATTGACATTCATTTATA	F	
rs12260688	94369694	C/T	HapMap				
rs12781567	94369814	C/T	AGCGGATAACAGCGAGACTCCGTCTCAAAA	AGCGGATAACAAGCAGTAGTGTCTTCTTCC	ATGTAATGTCTGGTCTTTG	F	MONO
rs7084441	94370112	C/T	AGCGGATAACCAAAGTGTCTGGGATTACAGG	AGCGGATAACAAGCATGTGTCCTGCCTTTC	CCTATAAGAACTATACCTCTGGCC	R	Failed geno
rs11187102	94371489	A/C	AGCGGATAACCAAGTAGCTGGGATTATAGG	AGCGGATAACAACAAAATAGAAGCCTAGGC	AATTAGCAGGGTGTGGTG	R	Failed geno
rs7914814	94372930	C/T	HapMap				
rs7898506	94372946	A/G	HapMap				
rs10082524	94373182	T/C	AGCGGATAACGCTTCTGGTTATTATTAGGTC	AGCGGATAACCCTGATTGTGTTTATCCTTG	AGATATTAGGAAGCAAGACTT	F	
rs10882093	94374055	C/T	AGCGGATAACTATAGTGGTGTGATCTCGGC	AGCGGATAACTTGTAAATCCCAGCTACTCGG	AGAATCACTGAACCTGGGAG	R	MONO
rs11187106	94375670	C/G	AGCGGATAACCTTCTTATCCATGAGCATGG	AGCGGATAACTGAAGGATCTCTACGGTAAG	GAAAGAAATCAGAGTTGACA	F	MONO
rs1573051	94377314	A/G	AGCGGATAACCATCCCTGTCTCTCTTTTG	AGCGGATAACTGACAGATATCACACAGGG	AAGATCCCAAAGGAAAGAAAA	F	
rs10882094	94377656	A/T	HapMap				
rs12244924	94378087	G/T	AGCGGATAACAGGTATCTTAGAAGGAAGG	AGCGGATAACAGTGGTGTGTTGTGCGTGTG	GTCTCAGTTTTTAACCCCTAA	F	
rs7068540	94379401	A/G	AGCGGATAACGCCACCCTCATATTAATACC	AGCGGATAACTGAGGCTGCAGTAAGATATG	TATGATTACACCACTGCAC	R	
rs9731595	94381028	C/T	AGCGGATAACCTTTCATCATCAGAACATAC	AGCGGATAACTGCAGTGAACCGAGATCATG	GTAACAGAGCAAGACTCTGT	F	Failed geno
rs2275217	94382267	A/G	HapMap				MONO
rs11818705	94382708	C/T	HapMap				

Genotyping assays for 243 SNPs in *IDE*, showing the sequences of the PCR primers and the extension probe, its direction (forward or reverse) and reasons for assay failure. Position is according to the NCBI 35 release. HapMap, SNPs and genotypes obtained from the HapMap website (www.hapmap.org). Failed design, failed assay design on Sequenom platform; failed HW, failed Hardy-Weinberg equilibrium in the CEPH reference panel; failed geno, genotyping rate <75% or >1 Mendel errors; MONO, monomorphic SNP in the CEPH reference panel.

Supplementary Table 2: Genotype counts of individual SNPs in *IDE*

Allele counts for each of the 21 single-marker (top) and 13 multi-marker (bottom) tests in our diabetic subsamples; within each SNP, the major allele is presented first. The components of the multi-marker tags (bottom panel) are numbered as in the top panel, and correspond to those in Table 2.

Multi-marker haplotypes were assigned [frequency](#) probabilities according to an expectation-maximization algorithm, and are compared versus all other possibilities at those loci (see text for details). T, transmitted; U, untransmitted; C/C, case/control.

Test Tag	Alleles	Scandinavian trios		Canadian C/C		Scandinavian C/C		Sweden C/C		Scandinavian sib pairs (cases)		
		T	U	Cases	Controls	Cases	Controls	Cases	Controls	Excess allele 1	Excess allele 2	
1	rs2263638	C/T	124	108	153 / 73	140 / 86	621 / 323	623 / 321	644 / 348	648 / 328	69	69
2	rs2209972	C/T	96	107	160 / 64	162 / 64	663 / 291	652 / 290	644 / 304	628 / 294	71	76
3	rs967878	C/A	124	117	132 / 90	132 / 92	548 / 390	492 / 430	480 / 414	497 / 375	82	67
4	rs884526	G/T	108	125	164 / 64	165 / 61	662 / 290	654 / 292	682 / 320	665 / 319	74	74
5	rs12257053	T/C	48	27	197 / 27	199 / 27	846 / 78	822 / 102	865 / 111	875 / 81	36	25
6	rs11186994	C/T	125	138	163 / 65	165 / 63	651 / 299	657 / 291	675 / 329	660 / 328	73	79
7	rs10882063	G/T	112	100	137 / 83	141 / 81	564 / 356	518 / 396	561 / 389	574 / 366	79	68
8	rs2251101	T/C	86	108	151 / 73	149 / 75	717 / 219	725 / 217	746 / 244	725 / 241	64	70
9	rs4646958	T/A	54	44	196 / 32	199 / 27	859 / 93	861 / 87	894 / 112	914 / 76	34	19
10	rs1887922	T/C	33	42	179 / 47	180 / 46	776 / 176	776 / 168	799 / 147	773 / 153	48	52
11	rs2275218	T/C	23	17	221 / 7	221 / 5	866 / 58	849 / 61	870 / 38	897 / 29	13	15
12	rs2250090	G/A	16	12	202 / 26	197 / 25	923 / 15	903 / 23	892 / 24	910 / 30	2	8
13	rs2249960	A/G	15	11	198 / 20	179 / 25	836 / 76	838 / 80	820 / 86	809 / 87	22	28
14	rs11187031	T/G	104	81	177 / 49	168 / 46	691 / 265	712 / 234	721 / 251	694 / 276	81	58
15	rs4641376	C/A	91	93	183 / 45	179 / 41	785 / 165	779 / 171	833 / 161	823 / 149	57	36
16	rs10882083	C/G	156	153	136 / 92	122 / 102	577 / 379	570 / 378	579 / 421	562 / 420	60	76
17	rs12355977	G/C	67	40	208 / 18	193 / 21	854 / 102	850 / 96	877 / 97	862 / 102	31	41
18	rs4646953	A/G	91	78	180 / 46	185 / 43	721 / 225	734 / 198	786 / 200	737 / 241	64	48
19	rs10882086	T/C	56	43	198 / 28	191 / 23	867 / 87	854 / 90	888 / 88	904 / 64	33	22
20	rs12252836	C/A	32	31	204 / 24	192 / 30	859 / 41	863 / 43	716 / 30	710 / 26	18	21
21	rs12260688	C/T	7	17	223 / 3	207 / 5	930 / 18	914 / 28	934 / 38	936 / 30	5	6
22	21,20,11	C,C,T	46.8	48.5	194 / 34	186.9 / 41.1	834 / 122	814.7 / 137.3	883.4 / 120.6	891.6 / 98.4	37	45
23	20,8	A,C	16.5	23.4	21.1 / 206.9	27.1 / 198.9	42.2 / 913.8	42 / 908	38 / 962	32.9 / 955.1	16	15
24	18,10	A,T	85.8	89	135.2 / 92.8	140.2 / 87.8	552.1 / 403.9	576.9 / 371.1	635.1 / 356.9	580.7 / 405.3	85	75
25	18,15	G,A	35.7	27.6	13.7 / 214.3	12.4 / 215.6	78.7 / 877.3	76.5 / 875.5	65.7 / 940.3	80.6 / 907.4	24	31
26	16,8	G,T	109.8	109.9	67.5 / 160.5	74.3 / 153.7	330.3 / 625.7	329.5 / 622.5	344.7 / 659.3	352 / 636	93	77
27	16,10	C,T	115.4	119.1	88.8 / 139.2	78.1 / 147.9	400.1 / 555.9	401.5 / 548.5	421.6 / 578.4	400.9 / 587.1	66	86
28	15,9	A,A	34	35.4	31 / 197	27 / 201	83.5 / 872.5	85.9 / 866.1	101.9 / 904.1	65.4 / 926.6	21	33
29	15,14,11	C,T,T	113.4	112.5	141.5 / 86.5	145.3 / 82.7	540.8 / 415.2	556 / 396	610.4 / 395.6	608.1 / 383.9	101	76
30	15,14	C,T	101	98.6	147.5 / 80.5	146.8 / 79.2	600.8 / 355.2	619.9 / 332.1	652.4 / 353.6	640.1 / 351.9	99	71
31	11,9	T,T	55.9	55.5	190.5 / 37.5	198 / 30	804.5 / 149.5	802.4 / 149.6	856.4 / 149.6	888.5 / 103.5	47	35
32	10,7	C,G	45.9	38.7	39.5 / 188.5	36.6 / 191.4	162 / 792	153.4 / 798.6	140.3 / 857.7	147.9 / 836.1	56	54
33	7,2	T,T	90.2	75.8	57.7 / 168.3	53.7 / 174.3	257 / 699	271.7 / 680.3	274.8 / 723.2	270.2 / 715.8	70	72
34	6,2	C,C	87	99	160 / 68	164 / 64	653 / 303	658 / 292	670.7 / 335.3	659.7 / 330.3	80	85

Supplementary Table 3: Correlation of *IDE* SNPs to tagging tests selected by *Tagger*

SNP ID	Position	MAF	Allele captured	Tagging test	Number	Genotype	r^2
rs2263638	94158777	0.30	C	rs2263638	1	C	1.00
rs7086285	94166068	0.41	T	rs967878	3	C	1.00
rs2209972	94169008	0.31	C	rs2209972	2	C	1.00
rs967878	94169328	0.41	C	rs967878	3	C	1.00
rs884526	94170442	0.30	G	rs884526	4	G	1.00
rs11594898	94173942	0.01	T	Not captured	N/A	N/A	0.00
rs12257053	94175650	0.07	T	rs12257053	5	T	1.00
rs7909013	94178323	0.33	T	rs2209972	2	C	0.89
rs10786044	94180560	0.33	A	rs11186994,rs2209972	34	C,C	0.96
rs11186993	94182794	0.28	C	rs11186994	6	C	0.92
rs11186994	94184819	0.28	C	rs11186994	6	C	1.00
rs10786045	94185388	0.28	T	rs10882063,rs2209972	33	T,T	0.92
rs10882063	94189317	0.37	G	rs10882063	7	G	1.00
rs2798253	94192885	0.36	G	rs10882083,rs2251101	26	G,T	0.93
rs11186999	94193961	0.08	G	rs4641376,rs4646958	28	A,A	1.00
rs4933231	94196162	0.15	T	rs2275218,rs4646958	31	T,T	1.00
rs10786047	94197028	0.15	A	rs2275218,rs4646958	31	T,T	1.00
rs11187004	94199011	0.15	T	rs2275218,rs4646958	31	T,T	1.00
rs7910977	94199856	0.15	C	rs2275218,rs4646958	31	T,T	1.00
rs2251101	94201284	0.22	T	rs2251101	8	T	1.00
rs4646958	94204339	0.10	T	rs4646958	9	T	1.00
rs6583814	94206524	0.18	A	rs2275218,rs4646958	31	T,T	0.83
rs11187009	94207018	0.30	G	rs11187031	14	T	0.96
rs551266	94212604	0.16	A	rs1887922	10	T	1.00
rs1887922	94214145	0.16	T	rs1887922	10	T	1.00
rs10882066	94214726	0.08	G	rs4641376,rs4646958	28	A,A	1.00
rs2275218	94215277	0.08	T	rs2275218	11	T	1.00
rs4646957	94219892	0.43	T	rs10882083,rs1887922	27	C,T	0.97
rs2250090	94221786	0.02	G	rs2250090	12	G	1.00
rs2149632	94222227	0.35	C	rs10882083,rs2251101	26	G,T	0.96
rs2249960	94223100	0.08	A	rs2249960	13	A	1.00
rs7073248	94227390	0.16	T	rs1887922	10	T	1.00
rs6583815	94227782	0.15	A	rs2275218,rs4646958	31	T,T	1.00
rs7910605	94229773	0.15	A	rs2275218,rs4646958	31	T,T	1.00
rs2421940	94233597	0.08	G	rs4641376,rs4646958	28	A,A	1.00
P539P	94236972	0.03	G	rs12260688	21	C	0.36
rs6583817	94237227	0.15	C	rs2275218,rs4646958	31	T,T	1.00
rs7093418	94239749	0.16	G	rs1887922	10	T	1.00
rs3737225	94239962	0.08	G	rs2275218	11	T	0.89
rs1855916	94244263	0.16	C	rs1887922	10	T	1.00
rs7084090	94247198	0.16	T	rs1887922	10	T	1.00
rs11187025	94247956	0.26	C	rs4646953	18	A	1.00
rs7068618	94250507	0.08	A	rs4641376,rs4646958	28	A,A	1.00
rs11187031	94251771	0.29	T	rs11187031	14	T	1.00

rs11187033	94252339	0.35	A	rs10882083,rs2251101	26	G,T	0.96
rs11187037	94253341	0.08	C	rs4641376,rs4646958	28	A,A	1.00
rs1832195	94258381	0.03	A	rs12260688	21	C	0.49
rs6583819	94259587	0.16	G	rs1887922	10	T	1.00
rs17445028	94261156	0.26	T	rs4646953	18	A	1.00
rs7895832	94266506	0.08	T	rs4641376,rs4646958	28	A,A	1.00
rs6583820	94266635	0.08	G	rs4641376,rs4646958	28	A,A	1.00
rs7075851	94267766	0.08	T	rs4641376,rs4646958	28	A,A	1.00
rs10509645	94267846	0.35	A	rs10882083,rs2251101	26	G,T	0.96
rs11812558	94271124	0.05	C	rs12252836,rs2251101	23	A,C	0.85
rs10882074	94271665	0.35	G	rs10882083,rs2251101	26	G,T	0.96
rs4641376	94275508	0.19	C	rs4641376	15	C	1.00
rs2421942	94277360	0.07	C	rs2275218	11	T	0.88
rs7078413	94280464	0.38	A	rs4641376,rs11187031	30	C,T	0.93
rs17107709	94282086	0.02	T	rs2250090	12	G	1.00
rs4646955	94284271	0.31	A	rs11187031	14	T	0.92
rs1832197	94288311	0.47	G	rs4641376,rs11187031,rs2275218	29	C,T,T	0.90
rs12416180	94290376	0.08	T	rs4641376,rs4646958	28	A,A	1.00
rs10882078	94292030	0.08	C	rs4641376,rs4646958	28	A,A	1.00
rs11187060	94294112	0.41	T	rs10882083,rs2251101	26	G,T	0.87
rs11187061	94295389	0.16	C	rs1887922	10	T	1.00
rs11187064	94298233	0.31	T	rs11187031	14	T	0.92
rs7909636	94299843	0.16	T	rs1887922	10	T	1.00
rs11187065	94301904	0.26	T	rs4646953	18	A	1.00
rs7908111	94304784	0.16	G	rs1887922	10	T	1.00
rs7917163	94306808	0.13	C	rs1887922,rs10882063	32	C,G	1.00
rs7394234	94307486	0.08	A	rs4641376,rs4646958	28	A,A	1.00
rs11187067	94309312	0.26	T	rs4646953	18	A	1.00
rs1999763	94309972	0.08	A	rs4641376,rs4646958	28	A,A	1.00
rs1999764	94310119	0.08	C	rs4641376,rs4646958	28	A,A	1.00
rs10882083	94311953	0.42	C	rs10882083	16	C	1.00
rs4933729	94313002	0.15	A	rs1887922	10	T	0.94
rs7076966	94315491	0.42	C	rs10882083	16	C	1.00
rs7100623	94317136	0.16	C	rs1887922	10	T	1.00
rs12355977	94317963	0.12	G	rs12355977	17	G	1.00
rs7915220	94318582	0.08	T	rs4641376,rs4646958	28	A,A	1.00
rs7097014	94320200	0.15	C	rs1887922	10	T	0.94
rs4304670	94321119	0.43	C	rs10882083,rs1887922	27	C,T	1.00
rs2421945	94321321	0.43	A	rs10882083,rs1887922	27	C,T	1.00
rs12783634	94323222	0.13	A	rs4646953,rs4641376	25	G,A	0.93
rs4646953	94323935	0.26	A	rs4646953	18	A	1.00
rs3758505	94324758	0.08	G	rs4641376,rs4646958	28	A,A	1.00
rs7099761	94325779	0.44	A	rs10882083	16	C	0.90
rs3758503	94326684	0.07	C	rs4641376,rs4646958	28	A,A	0.88
rs11187078	94330685	0.33	G	rs10882083,rs2251101	26	G,T	0.90
rs11187079	94331572	0.08	T	rs4641376,rs4646958	28	A,A	1.00
rs6583823	94334395	0.44	C	rs10882083	16	C	0.90
rs2421941	94335889	0.39	T	rs4646953,rs1887922	24	A,T	0.90

rs6583826	94337810	0.49	G	rs10882083	16	C	0.74
rs12355158	94340661	0.36	A	rs10882083,rs2251101	26	G,T	0.93
rs2297743	94342803	0.07	G	rs10882086	19	T	1.00
rs11187085	94344692	0.18	A	rs12260688,rs12252836,rs2275218	22	C,C,T	1.00
rs11817798	94345504	0.05	G	rs12260688	21	C	1.00
rs11187087	94346261	0.05	G	rs12260688	21	C	1.00
rs4604791	94346892	0.05	C	rs12260688	21	C	1.00
rs6583827	94348003	0.40	T	rs4646953,rs1887922	24	A,T	0.81
rs12411873	94350841	0.06	C	rs10882086	19	T	0.87
rs7096101	94352908	0.39	A	rs4646953,rs1887922	24	A,T	0.84
rs4933731	94353973	0.07	C	rs10882086	19	T	1.00
rs10882086	94355005	0.07	T	rs10882086	19	T	1.00
rs10786050	94357210	0.40	G	rs4646953,rs1887922	24	A,T	0.81
rs10882088	94358568	0.07	T	rs10882086	19	T	1.00
rs11599330	94360614	0.03	A	rs10882086	19	T	0.36
rs2275219	94362922	0.07	A	rs10882086	19	T	1.00
rs10882091	94364357	0.39	T	rs4646953,rs1887922	24	A,T	0.84
rs12252836	94366308	0.07	C	rs12252836	20	C	1.00
rs11187100	94367517	0.05	C	rs12260688	21	C	1.00
rs10882092	94369203	0.36	A	rs10882083,rs2251101	26	G,T	0.93
rs12260688	94369694	0.05	C	rs12260688	21	C	1.00
rs7914814	94372930	0.39	C	rs4646953,rs1887922	24	A,T	0.84
rs7898506	94372946	0.05	G	rs12260688	21	C	1.00
rs10082524	94373182	0.07	T	rs12252836	20	C	1.00
rs1573051	94377314	0.36	G	rs10882083,rs2251101	26	G,T	0.93
rs10882094	94377656	0.39	A	rs4646953,rs1887922	24	A,T	0.84
rs12244924	94378087	0.05	T	rs12260688	21	C	1.00
rs7068540	94379401	0.03	A	rs12260688	21	C	0.49
rs11818705	94382708	0.05	C	rs12260688	21	C	1.00

The *Tagger* algorithm (<http://www.broad.mit.edu/mpg/tagger>) was used to select single and multi-marker tests to capture all SNPs of minor allele frequency (MAF) $\geq 5\%$ with an $r^2 \geq 0.8$ (see text for details). SNPs previously associated with type 2 diabetes or related phenotypes (8-10) were forced in as tags and are shown in bold. Five SNPs that are less well captured at $r^2 < 0.8$ have MAF $< 5\%$; a sixth SNP (rs6583826) which had been selected as a tag but failed genotyping in the disease samples was captured by rs10882083 with $r^2 = 0.74$.