Part 1

SNP	CHR	Minor allele	MAF cases	MAF controls	Major allele	CHISQ	P	OR	L95	U95	Emperical P-value	Number of permutations	Gene	Functional Class
rs17197552	3	G	0.03333	0.4306	A	15.52	8.17E-05	0.04561	0.005887	0.3533	3.76E-05	797000	PPP2R3A	coding-nonsynon
rs735943	1	T	0.6	0.2917	C	8.525	0.003503	3.643	1.496	8.869	0.001078	27832	EXO1	coding-nonsynon
rs9462088	6	A	0.2	0	G	15.3	9.17E-05	n/a	n/a	n/a	0.001122	26730	FANCE	coding-nonsynon
rs1148555	12	G	0	0.2353	A	8.436	0.003678	n/a	n/a	n/a	0.003854	7784	MBD6	intron
rs4713853	6	C	0.2	0.02857	T	8.385	0.003783	8.5	1.606	45	0.005164	5808	PPARD	intron
rs1284605	12	T	0	0.2222	C	7.907	0.004924	n/a	n/a	n/a	0.005213	5754	MBD6	intron
rs1129923	1	A	0.2	0.02778	G	8.69	0.0032	8.75	1.654	46.3	0.005661	5298	DUSP23	coding-nonsynon
rs2927922	10	T	0.6333	0.3194	A	8.614	0.003336	3.68	1.507	8.985	0.00621	4830	PDSS1	intron
rs1126671	4	A	0.5	0.2273	G	6.553	0.01047	3.4	1.301	8.884	0.006308	4755	ADH4	coding-nonsynon
rs2489581	10	G	0.6333	0.3194	C	8.614	0.003336	3.68	1.507	8.985	0.006478	4630	PDSS1	intron
rs6457816	6	C	0.1333	0	T	9.992	0.001572	n/a	n/a	n/a	0.006485	4625	PPARD	intron
rs289747	16	A	0.6	0.2714	G	9.726	0.001817	4.026	1.636	9.909	0.007628	3932	CETP	3' UTR
rs1558093	5	C	0.5	0.2222	T	7.724	0.00545	3.5	1.414	8.661	0.007714	3888	SMAD5	Promoter
rs1135961	20	T	0.3	0.07143	C	9.112	0.002539	5.571	1.68	18.48	0.007754	3868	PSMA7	coding-synon,untranslated
rs697221	12	A	0	0.2	G	6.533	0.01059	n/a	n/a	n/a	0.007951	3772	DDIT3	coding-synon
rs6003071	22	C	0.7333	0.4028	T	9.256	0.002348	4.078	1.599	10.4	0.008444	3552	MT	intron
rs2040968	7	C	0.4667	0.2083	T	6.945	0.008404	3.325	1.331	8.305	0.009066	3308	HGF	intron
rs2214827	7	G	0.4667	0.2083	A	6.945	0.008404	3.325	1.331	8.305	0.009066	3308	HGF	intron
rs3093873	14	T	0.1071	0	C	7.737	0.005411	n/a	n/a	n/a	0.01076	2787	PARP2	locus
rs1800787	4	T	0.4286	0.2143	C	4.601	0.03195	2.75	1.073	7.05	0.01092	2745	FGB	locus
rs1341162	10	A	0.5714	0.3235	G	5.097	0.02397	2.788	1.128	6.889	0.011	2727	CYP2C9	intron,TagSNP:CYP2C9_8_cluster
rs2707466	7	G	0.6	0.3472	A	5.549	0.01849	2.82	1.173	6.778	0.01236	2427	WNT16	coding-nonsynon
rs743535	10	T	0.3077	0.1061	C	5.557	0.01841	3.746	1.194	11.75	0.01353	2217	CYP2E1	intron,TagSNP:CYP2E1
rs3793524	9	C	0.6	0.3056	G	7.702	0.005516	3.409	1.406	8.268	0.01371	2187	PTPN3	coding-nonsynon
rs3741927	12	G	0.07692	0	A	5.499	0.01903	n/a	n/a	n/a	0.01422	2109	DYRK4	coding-nonsynon
rs2295837	6	T	0.2	0.04167	A	6.599	0.0102	5.75	1.333	24.8	0.01598	1876	KIAA0274	coding-nonsynon
rs10977171	9	C	0.3571	0.1571	G	4.752	0.02927	2.98	1.09	8.148	0.01671	1794	PTPRD	coding-nonsynon
rs4148217	2	A	0.3667	0.1389	C	6.72	0.009534	3.589	1.322	9.745	0.01828	1640	ABCG8	coding-nonsynon
rs2295275	6	A	0.2333	0.05556	T	6.956	0.008353	5.174	1.387	19.3	0.01876	1598	TRERF1	coding-nonsynon
rs2908004	7	C	0.6	0.3611	T	4.927	0.02644	2.654	1.107	6.363	0.01954	1534	WNT16	coding-nonsynon
rs9282626	11	C	0.1	0	T	7.418	0.006457	n/a	n/a	n/a	0.02094	1432	CAT	locus

Part 2

SNP	CHR	Minor allele	MAF cases	MAF controls	Major allele	CHISQ	P	OR	L95	U95	Emperical P-value	Number of permutations	Gene	Functional Class
rs10018239	4	G	0.1333	0.3571	A	5.109	0.0238	0.2769	0.08675	0.884	0.02108	1422	PPARGC1A	intron,TAG ERROR
rs667565	1	G	0.2333	0.4444	A	3.996	0.0456	0.3804	0.1449	0.9989	0.02126	1410	DPYD	intron,TagSNP:DPYD
rs1126670	4	G	0.4	0.1714	T	6.015	0.01418	3.222	1.235	8.408	0.02132	1406	ADH4	coding-synon
rs827500	1	T	0.5667	0.3472	G	4.21	0.04018	2.458	1.03	5.868	0.02198	1364	DPYD	intron,TagSNP:DPYD
rs2227869	13	C	0.1	0	G	7.418	0.006457	n/a	n/a	n/a	0.02204	1360	ERCC5	coding-nonsynon
rs4646285	14	A	0.2	0.04167	G	6.599	0.0102	5.75	1.333	24.8	0.02274	1318	SLC10A1	coding-synon
rs183484	11	T	0.3	0.5429	G	4.972	0.02576	0.3609	0.145	0.898	0.02364	1268	RRM1	coding-synon
rs17607	17	A	0.1333	0.01389	G	6.481	0.0109	10.92	1.166	102.3	0.02402	1248	CD68	coding-nonsynon
rs17722293	5	T	0.1	0	C	7.418	0.006457	n/a	n/a	n/a	0.02425	1236	SH3TC2	coding-nonsynon
rs6901410	6	C	0.1333	0.01389	T	6.481	0.0109	10.92	1.166	102.3	0.02527	1186	PPARD	intron
rs6902123	6	C	0.1333	0.01389	T	6.481	0.0109	10.92	1.166	102.3	0.02527	1186	PPARD	intron
rs7739752	6	T	0.1333	0.01389	C	6.481	0.0109	10.92	1.166	102.3	0.02527	1186	PPARD	intron
rs7903344	10	C	0.3	0.5714	T	6.191	0.01284	0.3214	0.129	0.8011	0.02681	1118	CHUK	coding-nonsynon
rs4135113	12	A	0.1333	0.01389	G	6.481	0.0109	10.92	1.166	102.3	0.0276	1086	TDG	coding-nonsynon
rs3258	8	C	0.5667	0.3194	T	5.43	0.0198	2.786	1.161	6.688	0.02796	1072	FDFT1	untranslated
rs4947324	6	T	0.1	0	C	7.015	0.008084	n/a	n/a	n/a	0.02938	1020	TNF	locus, TagSNP:TNF
rs1029871	3	G	0.5667	0.3429	C	4.349	0.03704	2.506	1.045	6.011	0.02962	1012	NEK4	coding-nonsynon
rs2257212	3	A	0.6	0.3571	G	5.053	0.02458	2.7	1.121	6.503	0.02978	1040	SLC15A2	coding-nonsynon
rs1040090	1	A	0.4333	0.2206	G	4.617	0.03166	2.702	1.075	6.793	0.03043	985	DPYD	intron,TagSNP:DPYD
rs13815	22	C	0.2	0.4583	G	5.984	0.01443	0.2955	0.1079	0.8092	0.03099	967	MT	coding-nonsynon
rs504122	13	T	0.4667	0.2206	C	6.05	0.01391	3.092	1.234	7.744	0.03175	944	SPRY2	coding-nonsynon
rs3752988	10	C	0.6	0.3472	T	5.549	0.01849	2.82	1.173	6.778	0.03185	941	CYP2C9	intron,TagSNP:CYP2C9_8_cluster
rs1051061	2	G	0.2143	0.4444	A	4.533	0.03325	0.3409	0.1235	0.941	0.03247	923	VRK2	coding-nonsynon
rs1799801	16	C	0.1333	0.3611	T	5.292	0.02142	0.2722	0.08556	0.8659	0.03796	763	ERCC4	coding-synon
rs483536	6	T	0.5	0.2571	A	5.602	0.01794	2.889	1.181	7.064	0.0394	735	NFKBIE	locus, TagSNP:HSPCB
rs3803390	15	A	0.07143	0	G	5.104	0.02387	n/a	n/a	n/a	0.03962	731	SLC28A1	coding-synon
rs6998760	8	A	0.5357	0.2813	C	5.483	0.0192	2.949	1.174	7.408	0.04108	705	PSKH2	coding-nonsynon
rs882709	9	G	0.1667	0.04167	C	4.578	0.03239	4.6	1.024	20.67	0.04155	697	SETX	coding-nonsynon
rs877518	1	A	0.2667	0.08333	G	6.011	0.01422	4	1.25	12.8	0.04589	631	ID3	Promoter
rs338599	19	C	0.1667	0.04167	G	4.578	0.03239	4.6	1.024	20.67	0.04841	598	CYP2S1	coding-synon
rs2283512	16	T	0.4333	0.2361	G	3.967	0.04639	2.474	1.002	6.11	0.04858	596	ABCC1	intron,TagSNP:ABCC1
rs5361	1	C	0.2	0.04167	A	6.599	0.0102	5.75	1.333	24.8	0.0489	592	SELE	coding-nonsynon
rs2246176	5	C	0.06667	0.25	T	4.515	0.03359	0.2143	0.04638	0.9901	0.0494	586	RAD50	intron,TagSNP:RAD50
rs1130371	17	T	0.3333	0.1528	C	4.223	0.03989	2.773	1.026	7.493	0.04966	583	CCL3	coding-synon