

**Supplementary Table 1. Summary of Association Tests for SNPs with p values < 5E-04<sup>a</sup>**

rs number	Chr	Position <sup>b</sup>	Allele A <sup>c</sup>	Allele B <sup>c</sup>	ALL MAF Cases <sup>d</sup>	All MAF Controls <sup>d</sup>	ALL p-value <sup>e</sup>	OR <sup>f</sup>
rs9786944	1	5471099	A	G	0.08	0.06	4.2E-04	1.51
rs3935435	1	6494762	A	G	0.26	0.21	1.1E-04	1.32
rs671101	1	32108685	G	A	0.27	0.22	1.7E-04	1.31
rs706497	1	52887324	G	A	0.39	0.33	4.7E-05	1.30
rs6685516	1	62114818	A	G	0.18	0.23	4.8E-04	0.75
rs1260773	1	64307510	A	G	0.44	0.38	2.0E-04	1.26
rs4839556	1	111063863	A	G	0.17	0.22	3.6E-04	0.75
rs1999511	1	111123942	A	C	0.27	0.22	6.6E-05	1.33
rs4839335	1	114035394	G	A	0.30	0.25	3.2E-04	1.28
rs1230647	1	114055162	G	A	0.30	0.25	3.8E-04	1.28
rs2797409	1	114131725	G	A	0.30	0.25	2.6E-04	1.29
rs2476601	1	114179091	A	G	0.17	0.11	<b>8.2E-10</b>	1.71
rs1217407	1	114195271	A	G	0.30	0.25	2.4E-04	1.29
rs7529353	1	114221985	A	G	0.28	0.24	4.8E-04	1.28
rs2078371	1	115478706	G	A	0.15	0.11	1.8E-04	1.40
rs17362993	1	161580504	A	G	0.11	0.15	1.7E-04	0.69
rs1557121	1	171620504	A	G	0.20	0.26	7.7E-06	0.71
rs12044217	1	223969205	A	G	0.20	0.16	4.0E-04	1.32
rs728370	1	226970441	G	A	0.31	0.26	2.6E-04	1.28
rs241324	1	226983257	A	G	0.20	0.15	2.8E-04	1.34
rs644690	1	230571908	A	G	0.24	0.29	4.4E-04	0.78
rs1545255	2	24592914	A	G	0.25	0.21	3.7E-04	1.30
rs725238	2	43852686	A	G	0.34	0.29	3.7E-04	1.27
rs3762571	2	43853238	C	A	0.35	0.29	3.3E-04	1.27
rs12473962	2	44827874	A	C	0.29	0.24	3.5E-04	1.29
rs10204566	2	58853009	G	A	0.49	0.42	1.0E-05	1.32
rs6719884	2	58890420	A	C	0.48	0.40	2.7E-06	1.35
rs10865331	2	62404976	A	G	0.42	0.37	4.5E-04	1.25
rs2043092	2	73260584	A	G	0.12	0.09	1.3E-04	1.46
rs1029864	2	107150825	A	G	0.44	0.38	1.2E-04	1.27
rs2079917	2	107156923	G	A	0.41	0.35	3.6E-04	1.25
rs7421552	2	130320465	G	A	0.13	0.09	2.4E-05	1.51
rs1026290	2	173549681	A	G	0.42	0.47	4.6E-04	0.80
rs6752770	2	191681808	G	A	0.34	0.29	4.2E-04	1.27
rs1064213	2	198658485	G	A	0.45	0.51	1.6E-04	0.79
rs1389300	3	14861800	A	G	0.43	0.37	4.9E-04	1.25
rs9843745	3	24661552	A	G	0.54	0.48	1.9E-04	1.26
rs7610415	3	24666026	A	G	0.25	0.20	4.6E-04	1.29
rs9812637	3	24680225	A	G	0.54	0.48	1.9E-04	1.26
rs6550889	3	24693443	A	C	0.38	0.33	2.5E-04	1.27
rs6805565	3	119122889	A	C	0.16	0.21	1.4E-04	0.73

rs12487554	3	124425472	G	A	0.43	0.37	8.5E-05	1.28
rs3934729	3	124502453	G	A	0.44	0.38	2.8E-04	1.25
rs231601	3	125865366	A	G	0.41	0.47	9.6E-05	0.78
rs6808137	3	136792758	A	G	0.32	0.27	1.5E-04	1.29
rs940050	3	157585584	G	A	0.15	0.19	4.3E-04	0.74
rs10460872	3	168232433	G	A	0.38	0.32	2.3E-04	1.27
rs10936665	3	172141713	C	A	0.13	0.09	1.1E-04	1.45
rs917684	4	10961129	G	A	0.18	0.23	2.8E-04	0.75
rs1562840	4	42533105	G	A	0.51	0.45	3.8E-05	1.30
rs6850606	4	42559453	A	G	0.55	0.48	3.1E-06	1.35
rs10012449	4	42559865	A	C	0.43	0.37	5.7E-05	1.30
rs11726899	4	69680598	G	A	0.12	0.08	6.4E-05	1.49
rs2272040	4	71041636	G	A	0.11	0.15	2.9E-04	0.70
rs4235450	4	101429738	G	A	0.40	0.45	4.3E-04	0.80
rs427983	4	108047450	G	A	0.27	0.32	3.3E-04	0.78
rs4862110	4	183988023	G	A	0.23	0.18	1.7E-05	1.39
rs10075972	5	23529713	A	G	0.19	0.23	3.8E-04	0.75
rs1862573	5	37885445	A	G	0.05	0.08	1.1E-04	0.59
rs1113266	5	51773170	A	G	0.46	0.41	4.8E-04	1.25
rs37787	5	52677813	A	G	0.11	0.15	4.8E-04	0.72
rs318791	5	55460229	G	A	0.33	0.38	4.5E-04	0.80
rs1353747	5	58373238	C	A	0.07	0.10	4.5E-04	0.65
rs7727675	5	118092024	A	G	0.12	0.16	8.6E-05	0.69
rs982926	5	122382791	G	A	0.25	0.30	3.2E-04	0.78
rs156031	5	131554089	A	G	0.24	0.19	1.9E-04	1.33
rs244689	5	133450715	A	G	0.18	0.14	6.9E-05	1.39
rs756699	5	133474474	G	A	0.18	0.14	2.4E-04	1.36
rs6877546	5	133873011	G	A	0.21	0.17	4.2E-04	1.32
rs1860059	5	133875078	A	G	0.18	0.14	1.4E-04	1.37
rs2233299	5	150405660	A	G	0.31	0.26	2.1E-04	1.29
rs1422673	5	150419181	A	G	0.26	0.19	<b>6.2E-09</b>	1.53
rs2233287	5	150420290	A	G	0.14	0.09	<b>4.6E-09</b>	1.76
rs4958881	5	150430429	G	A	0.18	0.11	<b>3.2E-10</b>	1.73
rs3792785	5	150431843	G	A	0.16	0.10	<b>3.6E-08</b>	1.65
rs3792783	5	150435925	G	A	0.22	0.16	<b>1.7E-08</b>	1.56
rs13168551	5	150442831	G	A	0.49	0.42	6.0E-06	1.33
rs2431697	5	159812556	G	A	0.37	0.43	1.4E-05	0.76
rs1432910	5	168324135	G	A	0.41	0.47	3.0E-04	0.79
rs1047631	6	15631080	G	A	0.12	0.16	2.5E-05	0.67
rs1474605	6	15766191	G	A	0.17	0.22	5.4E-05	0.72
rs1235162	6	29645203	G	A	0.29	0.11	<b>1.8E-49</b>	3.30
rs2524005	6	30007656	A	G	0.41	0.19	<b>3.5E-51</b>	2.86
rs3132685	6	30053928	A	G	0.31	0.12	<b>1.0E-54</b>	3.51
rs8321	6	30140501	C	A	0.30	0.11	<b>6.5E-57</b>	3.67
rs9261290	6	30146626	G	A	0.31	0.11	<b>2.6E-58</b>	3.71
rs2523989	6	30186254	A	G	0.38	0.16	<b>1.1E-57</b>	3.26
rs2523987	6	30187972	C	A	0.37	0.15	<b>8.7E-61</b>	3.46

rs2517598	6	30188253	A	G	0.38	0.17	<b>1.4E-55</b>	3.15
rs3130380	6	30387109	A	G	0.32	0.11	<b>1.8E-62</b>	3.92
rs3130350	6	30435818	A	C	0.32	0.11	<b>3.4E-63</b>	3.96
rs3094054	6	30441484	A	C	0.32	0.12	<b>1.9E-61</b>	3.82
rs3132610	6	30652380	G	A	0.34	0.13	<b>2.8E-63</b>	3.81
rs886424	6	30889981	A	G	0.37	0.14	<b>4.1E-69</b>	4.03
rs2844659	6	30932511	A	G	0.46	0.20	<b>1.3E-68</b>	3.56
rs2844657	6	30937501	G	A	0.46	0.20	<b>3.0E-69</b>	3.57
rs4678	6	31001920	A	G	0.45	0.20	<b>4.6E-68</b>	3.58
rs3132580	6	31028103	A	G	0.38	0.14	<b>1.9E-70</b>	4.09
rs3095089	6	31041773	A	C	0.45	0.18	<b>1.8E-79</b>	4.28
rs886403	6	31065597	G	A	0.54	0.29	<b>4.6E-60</b>	3.13
rs1634718	6	31080844	G	A	0.53	0.28	<b>8.2E-61</b>	3.15
rs3130544	6	31166319	A	C	0.40	0.13	<b>1.5E-90</b>	5.64
rs2233956	6	31189184	G	A	0.43	0.18	<b>6.1E-68</b>	3.82
rs3130564	6	31209653	A	G	0.44	0.22	<b>1.6E-56</b>	3.25
rs7750641	6	31237289	A	G	0.41	0.13	<b>1.2E-92</b>	6.25
rs1265159	6	31248026	A	G	0.45	0.22	<b>1.4E-57</b>	3.22
rs887464	6	31253899	G	A	0.29	0.54	<b>2.5E-52</b>	0.34
rs3130473	6	31307187	A	G	0.48	0.25	<b>1.5E-55</b>	3.03
rs2596560	6	31463297	G	A	0.49	0.25	<b>3.1E-58</b>	3.07
rs3099844	6	31556955	A	C	0.39	0.13	<b>4.7E-85</b>	5.10
rs2855812	6	31580699	A	C	0.49	0.27	<b>4.2E-52</b>	2.91
rs2516400	6	31589084	A	G	0.58	0.33	<b>8.4E-53</b>	2.80
rs2857595	6	31676448	A	G	0.43	0.20	<b>1.0E-60</b>	3.38
rs3115663	6	31709822	G	A	0.44	0.19	<b>2.4E-67</b>	3.61
rs9267522	6	31711749	G	A	0.44	0.19	<b>3.8E-67</b>	3.61
rs3130618	6	31740113	A	C	0.44	0.19	<b>2.0E-67</b>	3.62
rs3131379	6	31829012	A	G	0.37	0.12	<b>9.7E-84</b>	5.24
rs558702	6	31978305	A	G	0.36	0.12	<b>5.2E-82</b>	5.13
rs1270942	6	32026839	G	A	0.35	0.12	<b>1.2E-79</b>	4.99
rs389884	6	32048876	G	A	0.35	0.12	<b>1.8E-79</b>	4.96
rs204990	6	32269408	A	C	0.40	0.20	<b>7.0E-49</b>	2.95
rs3131296	6	32280971	A	G	0.35	0.14	<b>7.1E-61</b>	3.78
rs7775397	6	32369230	C	A	0.34	0.12	<b>2.6E-75</b>	4.72
rs3129939	6	32444744	G	A	0.37	0.18	<b>1.1E-49</b>	3.10
rs1980493	6	32471193	G	A	0.42	0.17	<b>5.9E-70</b>	3.79
rs3129963	6	32488186	G	A	0.43	0.19	<b>2.5E-64</b>	3.49
rs3135353	6	32500855	A	G	0.41	0.16	<b>1.8E-72</b>	4.01
rs3129890	6	32522251	G	A	0.50	0.27	<b>3.4E-51</b>	2.81
rs2187668	6	32713862	A	G	0.34	0.13	<b>1.3E-67</b>	4.19
rs1794282	6	32774504	A	G	0.33	0.11	<b>1.4E-73</b>	4.68
rs7762279	6	32863268	G	A	0.28	0.10	<b>1.6E-58</b>	4.00
rs1026421	7	50291272	G	A	0.29	0.34	4.4E-04	0.79
rs10267413	7	115115076	G	A	0.12	0.09	4.4E-04	1.42
rs6466555	7	115149783	G	A	0.12	0.09	4.2E-04	1.42
rs10245192	7	115161378	G	A	0.12	0.09	4.5E-04	1.41

rs6946417	7	115162968	G	A	0.12	0.09	4.4E-04	1.41
rs4731437	7	127699802	A	G	0.15	0.12	1.0E-04	1.41
rs1466146	7	127702612	A	G	0.15	0.11	2.1E-05	1.46
rs6979784	7	127703444	A	G	0.22	0.18	2.1E-04	1.33
rs729302	7	128356196	C	A	0.27	0.33	2.3E-05	0.74
rs4728142	7	128361203	A	G	0.49	0.44	3.6E-04	1.25
rs10488631	7	128381419	G	A	0.16	0.11	4.0E-05	1.44
rs661079	7	138289386	A	G	0.31	0.26	4.0E-04	1.28
rs4725367	7	150156812	G	A	0.49	0.43	6.5E-05	1.29
rs6956432	7	150170084	G	A	0.29	0.35	2.0E-04	0.78
rs2969123	7	156401228	A	G	0.27	0.22	4.9E-05	1.33
rs7791257	7	156415603	G	A	0.27	0.21	2.7E-05	1.35
rs11989070	8	14352188	C	A	0.12	0.16	3.1E-05	0.67
rs10109853	8	39982038	G	A	0.45	0.50	3.6E-04	0.80
rs10958579	8	39986984	A	G	0.25	0.30	4.7E-04	0.78
rs17661532	8	41710431	A	G	0.21	0.26	2.0E-04	0.75
rs12679553	8	58428352	G	A	0.27	0.22	1.2E-04	1.31
rs7813241	8	60063266	G	A	0.19	0.24	3.9E-04	0.76
rs4737623	8	64060700	G	A	0.20	0.16	1.8E-04	1.34
rs1031553	8	64069382	A	G	0.20	0.16	2.2E-04	1.34
rs6990501	8	104359324	G	A	0.14	0.10	1.9E-04	1.41
rs3915792	8	125757588	A	G	0.30	0.25	1.8E-04	1.29
rs951920	8	140079282	G	A	0.38	0.33	1.1E-04	1.29
rs2382267	9	11107514	G	A	0.11	0.08	3.9E-04	1.43
rs10756426	9	12937238	A	G	0.12	0.09	3.0E-04	1.43
rs10869950	9	79446820	A	G	0.12	0.16	3.8E-04	0.72
rs1078815	9	86934630	A	G	0.49	0.44	4.6E-04	1.25
rs10868257	9	86951727	A	G	0.49	0.43	3.8E-04	1.25
rs620420	9	86968776	G	A	0.44	0.49	3.4E-04	0.80
rs2274561	9	88562610	G	A	0.18	0.14	2.2E-04	1.35
rs4978738	9	110585509	A	G	0.37	0.42	4.8E-04	0.80
rs3750340	9	130812210	A	C	0.19	0.15	3.2E-04	1.34
rs224149	10	64157079	A	G	0.52	0.46	2.7E-04	1.26
rs10761660	10	64186312	G	A	0.35	0.41	2.9E-04	0.79
rs10509279	10	68494799	A	G	0.05	0.08	4.7E-04	0.62
rs11190140	10	101281583	A	G	0.52	0.47	4.4E-04	1.25
rs10787677	10	118228407	C	A	0.10	0.07	3.7E-05	1.58
rs10787704	10	118268518	G	A	0.10	0.07	3.3E-05	1.59
rs7947162	11	98606530	G	A	0.39	0.33	3.5E-04	1.26
rs7939722	11	127771448	C	A	0.49	0.44	4.7E-04	1.25
rs7934171	11	127775054	A	C	0.49	0.43	2.0E-04	1.26
rs752450	11	128772691	A	G	0.18	0.14	2.7E-04	1.35
rs1860394	12	3309312	A	C	0.41	0.36	4.4E-04	1.26
rs10848856	12	3321534	G	A	0.41	0.36	2.7E-04	1.27
rs10849271	12	5425381	A	G	0.09	0.06	8.9E-05	1.55
rs1427271	12	39018661	A	G	0.18	0.14	1.1E-04	1.38
rs1434239	12	93813862	G	A	0.23	0.18	4.3E-05	1.36

rs6538566	12	93820689	A	C	0.25	0.20	1.2E-04	1.33
rs10746129	12	107615218	G	A	0.41	0.47	1.6E-04	0.79
rs1946295	12	113286744	A	G	0.23	0.27	4.4E-04	0.77
rs780876	12	114672478	A	G	0.34	0.28	2.0E-05	1.33
rs9515742	13	89883355	A	G	0.38	0.33	1.9E-04	1.28
rs2210054	14	33091890	G	A	0.46	0.41	3.7E-04	1.26
rs7146515	14	43109124	A	G	0.15	0.11	2.9E-05	1.45
rs2038532	14	43248804	A	G	0.14	0.10	1.0E-04	1.44
rs9323081	14	43263007	A	G	0.14	0.10	1.3E-04	1.43
rs17309078	14	43277325	A	G	0.14	0.10	2.8E-04	1.41
rs7148865	14	97858159	A	C	0.21	0.17	1.4E-04	1.34
rs7152787	14	97885039	G	A	0.47	0.41	4.8E-05	1.29
rs8008676	14	102304315	A	G	0.24	0.20	4.1E-04	1.30
rs7143963	14	102374178	A	G	0.21	0.17	1.7E-04	1.34
rs1131877	14	102411802	G	A	0.27	0.22	2.1E-04	1.30
rs4906269	14	102431770	C	A	0.21	0.16	2.2E-05	1.39
rs10133111	14	102447074	A	G	0.20	0.16	1.7E-04	1.34
rs7169523	15	29250670	A	G	0.28	0.22	1.9E-06	1.40
rs11636101	15	30061449	A	C	0.35	0.30	3.0E-04	1.27
rs2063722	15	30083665	C	A	0.45	0.39	1.2E-04	1.28
rs16954263	15	32688722	A	G	0.27	0.32	3.5E-04	0.78
rs10518693	15	38487314	A	G	0.36	0.41	1.9E-04	0.79
rs2034650	15	38504594	G	A	0.53	0.47	3.2E-04	1.25
rs2290430	15	58579246	C	A	0.07	0.10	4.3E-04	0.65
rs10519096	15	59077236	A	G	0.18	0.14	9.2E-05	1.38
rs10519097	15	59077480	A	G	0.19	0.14	4.7E-05	1.39
rs4776292	15	64300867	A	G	0.27	0.32	1.3E-04	0.77
rs3812945	15	73076775	G	A	0.43	0.49	4.6E-04	0.80
rs12148488	15	73169595	A	C	0.54	0.48	3.8E-04	1.25
rs4420499	15	75102029	A	C	0.18	0.14	3.6E-04	1.35
rs4985147	16	15076261	A	G	0.45	0.40	2.4E-04	1.26
rs2271047	16	69376260	G	A	0.48	0.43	4.8E-04	1.24
rs6540278	16	84178403	G	A	0.10	0.14	2.9E-04	0.69
rs9925302	16	85223804	A	G	0.15	0.11	3.6E-04	1.37
rs1877031	17	35067606	G	A	0.28	0.34	3.0E-04	0.78
rs2271308	17	35071008	A	G	0.23	0.28	2.9E-04	0.77
rs931992	17	35074961	C	A	0.28	0.33	4.9E-04	0.79
rs907092	17	35175785	A	G	0.53	0.48	4.4E-04	1.25
rs9303277	17	35229995	G	A	0.42	0.48	1.5E-05	0.76
rs11557467	17	35282160	C	A	0.42	0.49	6.0E-05	0.78
rs8067378	17	35304874	A	G	0.42	0.48	2.7E-05	0.77
rs2290400	17	35319766	A	G	0.43	0.49	3.8E-05	0.77
rs7216389	17	35323475	A	G	0.43	0.49	1.2E-04	0.79
rs7502006	17	68414311	G	A	0.53	0.47	4.5E-04	1.24
rs6501581	17	68427194	G	A	0.38	0.44	3.1E-04	0.79
rs3745004	18	41914398	A	C	0.08	0.12	7.2E-05	0.65
rs323092	18	47545959	G	A	0.17	0.14	3.5E-04	1.35

rs1619323	18	48215948	G	A	0.24	0.20	3.9E-04	1.30
rs1790588	18	65686164	G	A	0.54	0.48	4.9E-04	1.24
rs9956473	18	73065628	G	A	0.18	0.14	2.1E-04	1.36
rs12456229	18	73247400	A	C	0.27	0.33	5.5E-05	0.75
rs6565965	18	73256562	G	A	0.40	0.46	1.2E-04	0.78
rs8099113	18	75367142	A	G	0.10	0.07	4.2E-04	1.46
rs11668429	19	10477303	C	A	0.31	0.36	4.0E-04	0.79
rs8111895	19	22865045	A	G	0.16	0.12	2.1E-04	1.38
rs4801321	19	61662562	A	G	0.10	0.15	1.4E-04	0.69
rs3760848	19	61673194	G	A	0.12	0.16	4.3E-04	0.72
rs1548866	19	61837246	G	A	0.36	0.41	4.8E-04	0.80
rs4813669	20	4040860	G	A	0.28	0.33	1.1E-04	0.77
rs2422979	20	4712682	A	G	0.39	0.45	1.6E-04	0.79
rs11698138	20	17539579	G	A	0.13	0.09	1.6E-05	1.50
rs6028806	20	38094753	A	G	0.18	0.24	4.5E-05	0.72
rs6066968	20	47160748	G	A	0.36	0.41	3.5E-04	0.80
rs572159	22	26060109	G	A	0.37	0.43	9.1E-05	0.78
rs470049	22	33089241	G	A	0.34	0.28	4.8E-05	1.32
rs5963897	23	40677339	A	G	0.22	0.27	4.4E-04	0.75
rs5936708	23	68760973	G	A	0.21	0.26	3.1E-04	0.75
rs1327347	23	68773178	G	A	0.34	0.39	3.6E-04	0.78
rs5921691	23	100049724	C	A	0.39	0.46	1.1E-05	0.74
rs1204413	23	100075191	A	G	0.22	0.27	2.3E-04	0.74
rs845188	23	140204554	G	A	0.39	0.33	1.4E-04	1.30
rs497220	23	149426932	G	A	0.09	0.13	1.9E-04	0.65

- For the MHC region on chromosome 6 only the 50 SNPs with the best p-values are included.
- Base-pair position based on NCBI build 36, HG18.
- Minor allele (Allele A) and alternative allele (Allele B).
- MAF are the Case and control minor allele frequencies.
- Combined p value adjusting for ancestry and gender covariates (see methods).
- Odds ratio (OR) and 95% confidence intervals [lower (L96); upper (U95)] and are based on :
- Discovery p value adjusting for ancestry and gender covariates (see methods).
- Replication set p values adjusting for ancestry and gender covariates (see methods).

L95 <sup>f</sup>	U95 <sup>f</sup>	DISC p-value <sup>g</sup>	Rep p-value <sup>h</sup>	CMH P-value
1.20	1.90	1.4E-02	9.6E-03	3.2E-04
1.15	1.51	3.0E-05	4.8E-01	5.9E-05
1.14	1.51	3.7E-03	1.4E-02	2.2E-04
1.15	1.47	1.7E-05	2.1E-01	3.9E-05
0.64	0.88	1.1E-02	1.2E-02	7.1E-04
1.12	1.43	8.3E-03	1.4E-02	1.5E-04
0.64	0.88	3.3E-03	5.8E-02	4.8E-04
1.16	1.53	2.3E-03	1.4E-02	8.9E-05
1.12	1.47	1.7E-03	6.3E-02	2.8E-04
1.12	1.47	1.7E-03	7.1E-02	3.3E-04
1.12	1.47	1.2E-03	7.2E-02	2.2E-04
1.44	2.02	6.5E-09	6.2E-03	3.7E-10
1.13	1.48	1.1E-03	6.6E-02	2.0E-04
1.11	1.47	1.5E-03	1.0E-01	4.2E-04
1.17	1.67	1.8E-02	4.3E-03	1.6E-04
0.57	0.84	9.9E-02	1.9E-04	1.2E-04
0.61	0.83	2.1E-03	1.0E-03	5.4E-06
1.13	1.54	1.0E-02	1.7E-02	5.0E-04
1.12	1.47	5.0E-03	1.2E-02	1.6E-04
1.15	1.58	6.9E-03	1.2E-02	1.8E-04
0.67	0.89	1.2E-02	7.7E-03	4.7E-04
1.12	1.50	7.2E-03	2.9E-02	3.7E-04
1.11	1.45	2.6E-04	2.3E-01	3.9E-04
1.11	1.44	1.9E-04	2.8E-01	3.2E-04
1.12	1.48	9.1E-03	1.6E-02	2.9E-04
1.17	1.50	4.6E-02	6.7E-06	8.1E-06
1.19	1.52	1.3E-02	1.4E-05	2.2E-06
1.10	1.41	4.6E-03	4.7E-02	3.4E-04
1.20	1.77	1.7E-02	1.9E-03	1.3E-04
1.12	1.44	1.7E-02	2.1E-03	8.3E-05
1.11	1.41	5.1E-02	1.8E-03	2.6E-04
1.25	1.82	4.4E-02	6.1E-05	2.8E-05
0.71	0.91	3.3E-03	8.0E-02	4.7E-04
1.11	1.44	1.3E-02	6.4E-03	5.2E-04
0.70	0.89	2.5E-03	2.8E-02	1.8E-04
1.10	1.41	1.8E-04	4.5E-01	4.1E-04
1.12	1.43	2.2E-04	2.3E-01	1.6E-04
1.12	1.49	6.0E-05	5.3E-01	3.9E-04
1.12	1.42	2.2E-04	2.4E-01	1.6E-04
1.12	1.45	2.4E-04	2.3E-01	2.1E-04
0.62	0.86	1.1E-02	2.6E-03	2.0E-04

1.13	1.45	1.2E-05	4.8E-01	7.0E-05
1.11	1.42	4.7E-05	5.3E-01	2.1E-04
0.69	0.88	2.0E-03	2.2E-02	1.0E-04
1.13	1.47	7.5E-03	3.5E-03	1.4E-04
0.62	0.87	1.6E-02	8.8E-03	4.7E-04
1.12	1.44	1.7E-02	1.7E-03	2.2E-04
1.20	1.75	3.3E-03	2.0E-02	7.4E-05
0.64	0.88	1.4E-03	7.1E-02	2.4E-04
1.15	1.47	1.3E-05	2.9E-01	4.0E-05
1.19	1.53	1.7E-06	1.6E-01	3.4E-06
1.14	1.47	2.0E-04	6.5E-02	6.0E-05
1.23	1.82	1.8E-06	8.7E-01	7.9E-05
0.58	0.85	1.3E-02	6.7E-03	2.4E-04
0.70	0.91	3.0E-02	3.1E-03	6.9E-04
0.68	0.89	8.0E-03	1.4E-02	3.0E-04
1.19	1.61	3.1E-01	2.7E-07	1.4E-05
0.65	0.88	9.4E-03	2.3E-02	3.4E-04
0.45	0.77	3.0E-02	7.7E-04	1.0E-04
1.10	1.41	5.5E-03	6.1E-02	5.8E-04
0.59	0.86	7.5E-03	2.4E-02	5.4E-04
0.70	0.90	1.4E-03	8.8E-02	3.5E-04
0.51	0.83	1.5E-02	8.8E-03	4.5E-04
0.57	0.83	4.0E-05	3.2E-01	9.3E-05
0.68	0.89	3.1E-03	6.2E-02	2.5E-04
1.14	1.54	1.6E-03	4.8E-02	1.8E-04
1.18	1.64	1.8E-03	1.2E-02	6.6E-05
1.15	1.60	2.8E-02	1.7E-03	2.1E-04
1.13	1.54	2.1E-03	1.0E-01	5.2E-04
1.17	1.61	1.3E-03	4.3E-02	1.6E-04
1.13	1.48	8.6E-02	2.1E-04	2.8E-04
1.32	1.76	1.7E-05	8.1E-05	1.8E-09
1.46	2.12	4.4E-06	3.9E-04	3.5E-09
1.46	2.06	1.2E-05	7.7E-06	2.6E-10
1.38	1.97	2.1E-05	1.0E-03	3.1E-08
1.33	1.81	3.7E-04	7.0E-06	1.4E-08
1.18	1.50	5.1E-03	1.5E-04	6.1E-06
0.67	0.86	4.0E-04	1.2E-02	1.4E-05
0.70	0.90	1.1E-04	3.5E-01	2.8E-04
0.56	0.81	1.6E-03	5.1E-03	2.0E-05
0.61	0.84	2.8E-03	6.8E-03	4.4E-05
2.82	3.87	1.6E-27	1.4E-23	4.5E-57
2.49	3.27	1.1E-27	2.4E-25	4.3E-59
2.99	4.11	1.4E-30	1.3E-25	1.5E-62
3.13	4.31	7.0E-33	1.5E-25	2.0E-66
3.17	4.36	2.0E-32	1.7E-27	8.3E-68
2.82	3.77	5.9E-33	1.1E-26	4.6E-67
2.98	4.01	4.1E-35	9.2E-28	3.4E-71



2.73	3.63	2.3E-31	2.6E-26	2.5E-64
3.34	4.61	8.6E-36	2.2E-28	3.7E-73
3.37	4.65	7.2E-36	5.4E-29	1.9E-74
3.26	4.48	1.7E-35	1.2E-27	3.0E-71
3.26	4.46	2.1E-37	1.3E-27	4.2E-73
3.45	4.71	7.0E-40	9.7E-31	2.2E-81
3.09	4.11	2.3E-38	9.3E-32	1.5E-81
3.10	4.11	8.6E-40	5.2E-31	1.8E-82
3.10	4.13	1.0E-39	6.6E-30	9.3E-81
3.50	4.78	6.8E-40	7.2E-32	4.2E-82
3.68	4.98	8.9E-44	7.1E-37	1.2E-96
2.73	3.59	8.9E-30	2.1E-32	7.8E-67
2.75	3.62	1.9E-31	1.8E-31	3.0E-68
4.77	6.67	8.0E-54	3.3E-38	2.6E-110
3.28	4.44	2.6E-41	5.6E-28	1.2E-76
2.81	3.77	8.0E-38	2.0E-20	9.8E-60
4.89	6.85	9.6E-56	2.4E-38	1.7E-114
2.79	3.72	6.4E-32	5.2E-27	9.3E-63
0.30	0.39	4.3E-32	4.6E-22	7.1E-58
2.64	3.48	2.3E-32	7.6E-25	2.2E-61
2.68	3.51	2.6E-38	2.6E-21	2.3E-65
4.33	6.00	8.0E-53	7.5E-34	7.2E-104
2.53	3.33	4.1E-31	4.0E-22	2.8E-55
2.45	3.19	3.9E-30	3.3E-24	6.7E-59
2.93	3.91	1.2E-40	7.8E-22	1.1E-66
3.13	4.18	9.2E-41	1.6E-27	4.5E-78
3.12	4.17	1.8E-40	1.4E-27	1.1E-77
3.13	4.18	8.3E-41	1.6E-27	3.2E-78
4.43	6.19	2.1E-49	6.3E-36	4.2E-100
4.34	6.06	3.0E-48	1.5E-35	7.2E-97
4.22	5.89	1.5E-46	7.5E-35	4.3E-93
4.20	5.86	3.9E-47	4.2E-34	1.8E-93
2.56	3.41	2.7E-28	4.9E-22	3.2E-52
3.22	4.42	7.3E-34	2.0E-28	3.9E-68
4.00	5.58	7.6E-44	3.1E-33	3.0E-87
2.67	3.60	2.6E-28	7.0E-23	6.5E-52
3.27	4.39	8.7E-39	1.2E-32	2.1E-83
3.02	4.04	6.6E-35	8.9E-31	3.9E-73
3.45	4.66	2.5E-40	1.3E-33	7.1E-86
2.45	3.21	1.0E-27	1.6E-24	8.1E-56
3.57	4.93	8.0E-42	2.7E-27	4.9E-76
3.96	5.53	2.6E-43	7.6E-32	1.2E-83
3.38	4.74	8.4E-32	2.9E-28	1.4E-64
0.69	0.90	4.6E-03	4.7E-02	3.5E-04
1.17	1.72	1.4E-02	1.0E-02	3.7E-04
1.17	1.72	9.1E-03	1.6E-02	3.7E-04
1.17	1.72	8.8E-03	1.7E-02	3.8E-04

1.17	1.72	9.3E-03	1.6E-02	3.9E-04
1.18	1.67	6.3E-03	8.9E-03	1.1E-04
1.23	1.74	3.1E-03	2.9E-03	2.0E-05
1.14	1.54	5.5E-03	2.4E-02	2.4E-04
0.65	0.85	1.2E-03	5.2E-03	2.4E-05
1.11	1.41	2.3E-03	5.1E-02	4.3E-04
1.21	1.71	6.3E-06	3.3E-01	3.9E-05
1.12	1.46	6.9E-05	4.2E-01	5.8E-04
1.14	1.46	3.6E-02	1.0E-04	7.8E-05
0.68	0.89	1.2E-01	4.4E-05	1.6E-04
1.16	1.53	6.9E-04	3.0E-02	3.9E-05
1.17	1.55	7.6E-04	1.4E-02	2.2E-05
0.56	0.81	3.4E-04	2.6E-02	3.6E-05
0.71	0.90	6.4E-03	2.4E-02	3.7E-04
0.68	0.90	1.0E-01	3.8E-04	3.1E-04
0.65	0.87	3.7E-03	3.0E-02	2.4E-04
1.14	1.51	2.2E-03	2.1E-02	1.4E-04
0.65	0.88	1.3E-03	1.4E-01	5.5E-04
1.15	1.57	1.2E-01	1.3E-04	1.4E-04
1.15	1.56	1.5E-01	1.1E-04	1.8E-04
1.18	1.69	2.7E-02	1.5E-03	1.8E-04
1.13	1.48	5.1E-02	5.7E-04	2.0E-04
1.13	1.46	1.8E-04	1.5E-01	1.2E-04
1.18	1.75	1.4E-03	1.3E-01	3.3E-04
1.18	1.73	8.0E-02	4.8E-04	2.7E-04
0.59	0.86	4.4E-03	3.9E-02	3.8E-04
1.10	1.41	4.4E-04	1.8E-01	7.0E-04
1.11	1.42	4.2E-04	1.6E-01	5.8E-04
0.70	0.90	5.0E-03	1.8E-02	4.4E-04
1.15	1.59	7.1E-03	2.1E-02	1.7E-04
0.70	0.91	5.0E-03	4.9E-02	7.9E-04
1.14	1.58	1.7E-03	5.5E-02	3.0E-04
1.11	1.42	1.6E-01	4.1E-05	2.8E-04
0.70	0.90	2.5E-02	1.8E-03	2.0E-04
0.48	0.81	1.6E-02	8.9E-03	5.0E-04
1.10	1.41	7.9E-04	1.9E-01	4.6E-04
1.27	1.96	2.8E-04	2.3E-02	5.5E-05
1.28	1.97	3.8E-04	1.6E-02	5.0E-05
1.11	1.43	2.5E-02	4.0E-03	2.9E-04
1.10	1.41	3.7E-02	2.2E-03	3.8E-04
1.12	1.43	3.5E-02	7.1E-04	1.9E-04
1.15	1.58	2.9E-02	1.6E-03	2.8E-04
1.11	1.43	1.5E-02	8.4E-03	5.5E-04
1.12	1.44	4.4E-03	2.8E-02	3.7E-04
1.25	1.93	9.2E-04	3.7E-02	1.1E-04
1.17	1.62	1.8E-03	2.1E-02	8.7E-05
1.18	1.58	1.5E-03	9.7E-03	4.2E-05

1.15	1.53	1.3E-03	3.0E-02	9.6E-05
0.70	0.89	2.0E-03	3.3E-02	1.5E-04
0.67	0.89	8.1E-04	1.7E-01	5.2E-04
1.17	1.52	1.8E-03	3.4E-03	2.4E-05
1.12	1.45	2.2E-03	3.4E-02	2.5E-04
1.11	1.42	1.7E-04	3.1E-01	4.2E-04
1.22	1.73	3.4E-03	2.1E-03	1.4E-05
1.20	1.74	6.6E-04	4.8E-02	6.9E-05
1.19	1.73	8.5E-04	5.0E-02	9.5E-05
1.17	1.69	1.9E-03	5.2E-02	1.8E-04
1.15	1.56	2.3E-03	2.4E-02	1.6E-04
1.14	1.46	5.3E-04	3.0E-02	4.9E-05
1.13	1.51	2.9E-04	3.1E-01	4.4E-04
1.15	1.56	3.6E-04	1.4E-01	1.1E-04
1.13	1.49	9.8E-04	8.7E-02	1.7E-04
1.19	1.61	1.3E-04	5.6E-02	1.3E-05
1.15	1.56	2.4E-04	1.6E-01	1.2E-04
1.22	1.60	7.5E-04	5.9E-04	1.5E-06
1.12	1.44	7.6E-03	2.1E-02	2.6E-04
1.13	1.45	1.1E-03	5.8E-02	1.3E-04
0.68	0.89	2.4E-03	6.7E-02	3.8E-04
0.70	0.89	1.9E-02	2.7E-03	1.3E-04
1.11	1.40	2.2E-02	3.4E-03	1.9E-04
0.52	0.83	2.6E-03	6.8E-02	3.7E-04
1.17	1.62	3.4E-03	1.8E-02	1.2E-04
1.19	1.63	2.5E-03	1.3E-02	6.6E-05
0.67	0.88	2.5E-03	1.6E-02	1.2E-04
0.71	0.91	1.4E-03	9.9E-02	3.2E-04
1.11	1.41	4.2E-04	2.2E-01	3.0E-04
1.14	1.59	3.0E-03	3.4E-02	3.5E-04
1.12	1.43	2.2E-03	4.9E-02	2.8E-04
1.10	1.41	1.6E-01	8.5E-05	3.7E-04
0.57	0.84	1.2E-02	1.3E-02	4.0E-04
1.15	1.64	2.0E-01	5.8E-05	3.0E-04
0.68	0.89	6.4E-03	2.1E-02	2.9E-04
0.66	0.89	2.9E-03	5.5E-02	3.2E-04
0.69	0.90	9.9E-03	2.2E-02	4.6E-04
1.10	1.41	1.3E-01	4.1E-04	5.4E-04
0.67	0.86	3.4E-02	4.1E-05	1.2E-05
0.69	0.88	8.5E-02	5.0E-05	5.4E-05
0.68	0.87	4.7E-02	6.1E-05	2.4E-05
0.68	0.87	5.0E-02	9.2E-05	3.7E-05
0.69	0.89	1.2E-01	6.8E-05	1.3E-04
1.10	1.40	2.6E-04	3.8E-01	5.3E-04
0.70	0.90	3.2E-04	2.2E-01	4.0E-04
0.52	0.80	3.2E-05	2.1E-01	4.8E-05
1.15	1.59	8.4E-02	4.0E-04	3.5E-04

1.13	1.50	1.5E-04	2.7E-01	3.4E-04
1.10	1.40	7.1E-04	2.0E-01	4.0E-04
1.16	1.60	3.7E-03	2.6E-02	2.0E-04
0.66	0.87	1.8E-03	1.8E-02	4.3E-05
0.69	0.89	2.6E-03	2.7E-02	8.5E-05
1.18	1.81	9.5E-02	1.0E-03	3.6E-04
0.69	0.90	2.3E-02	6.7E-03	4.9E-04
1.16	1.64	5.3E-03	2.0E-02	2.2E-04
0.57	0.83	4.0E-03	8.6E-03	8.6E-05
0.60	0.86	2.5E-02	3.2E-03	2.5E-04
0.70	0.91	3.2E-05	7.6E-01	5.4E-04
0.67	0.88	3.5E-02	6.9E-04	1.4E-04
0.69	0.89	8.5E-04	4.9E-02	1.7E-04
1.25	1.81	7.9E-05	7.7E-02	1.1E-05
0.62	0.84	3.1E-03	7.6E-03	4.6E-05
0.70	0.90	1.0E-05	9.6E-01	3.6E-04
0.68	0.88	3.5E-02	2.0E-04	1.1E-04
1.15	1.51	6.1E-04	4.6E-02	6.0E-05
0.64	0.88	3.4E-02	2.9E-03	5.9E-04
0.64	0.87	7.3E-04	1.3E-01	1.6E-04
0.68	0.89	3.7E-03	3.9E-02	3.9E-04
0.65	0.85	5.4E-04	7.8E-03	4.9E-05
0.64	0.87	4.3E-03	1.4E-02	2.8E-04
1.14	1.50	1.8E-04	1.3E-01	1.8E-04
0.52	0.82	3.2E-03	1.8E-02	4.5E-04

d.

an additive model.