

Supplemental Table 1: SNPs marginally statistically significantly associated (at genome-wide significance) with asparagus anosmia

SNP	A1	A2	Frequency A1	Marginal Beta	Marginal SE	Marginal p-value
rs6689553	T	C	0.32	0.1376	0.0099	4.26E-44
rs6678934	A	C	0.72	-0.131	0.0094	5.20E-44
rs6686797	A	G	0.28	0.1302	0.0094	5.59E-44
rs6672079	A	G	0.68	-0.1374	0.0099	5.64E-44
rs6689570	T	C	0.28	0.1307	0.0094	5.89E-44
rs4310471	A	G	0.28	0.1321	0.0095	6.70E-44
rs10788778	T	C	0.26	0.1286	0.0093	1.25E-43
rs4593862	T	G	0.74	-0.1286	0.0093	1.32E-43
rs9660769	C	G	0.74	-0.1286	0.0093	1.35E-43
rs6663817	A	G	0.26	0.1286	0.0093	1.35E-43
rs10158431	A	G	0.26	0.128	0.0092	1.37E-43
rs4481887	A	G	0.26	0.128	0.0092	1.41E-43
rs4409693	T	C	0.74	-0.1293	0.0093	1.42E-43
rs4554750	C	G	0.26	0.128	0.0092	1.43E-43
rs10749653	C	G	0.26	0.1279	0.0092	1.43E-43
rs10788782	A	C	0.74	-0.1279	0.0092	1.45E-43
rs6697863	A	G	0.74	-0.1279	0.0092	1.47E-43
rs7553333	C	G	0.26	0.1284	0.0093	1.51E-43
rs6681423	A	C	0.74	-0.1278	0.0092	1.56E-43
rs6671789	A	G	0.74	-0.1278	0.0092	1.57E-43
rs7545751	T	C	0.26	0.1288	0.0093	1.60E-43
rs4309013	T	C	0.73	-0.1268	0.0092	1.61E-43
rs6587450	A	T	0.73	-0.1268	0.0092	1.62E-43
rs4427440	A	T	0.73	-0.127	0.0092	1.63E-43
rs10888362	A	G	0.74	-0.1278	0.0092	1.64E-43
rs10788781	T	C	0.74	-0.1279	0.0092	1.65E-43
rs10158180	T	C	0.73	-0.1268	0.0092	1.66E-43
rs4916087	T	C	0.27	0.1271	0.0092	1.67E-43
rs12039929	A	G	0.73	-0.1268	0.0092	1.68E-43
rs12042602	T	C	0.73	-0.1268	0.0092	1.68E-43
rs12568122	T	C	0.74	-0.1287	0.0093	1.69E-43
rs12044126	T	C	0.27	0.1269	0.0092	1.70E-43
rs6689556	T	C	0.27	0.1315	0.0095	1.72E-43
rs4457616	A	G	0.26	0.1302	0.0094	1.74E-43
rs7515080	A	G	0.26	0.1279	0.0092	1.75E-43
rs6689193	A	T	0.73	-0.1268	0.0092	1.77E-43
rs6587452	T	C	0.74	-0.1277	0.0092	1.84E-43
rs4244187	T	C	0.27	0.1268	0.0092	1.84E-43
rs4244186	A	G	0.27	0.1268	0.0092	1.86E-43
rs9662041	A	T	0.27	0.1268	0.0092	1.90E-43
rs4369256	A	G	0.74	-0.1282	0.0093	1.92E-43
rs4279879	A	G	0.27	0.1267	0.0092	1.94E-43
rs4508046	T	C	0.26	0.1275	0.0092	1.95E-43
rs7538645	T	C	0.73	-0.1275	0.0092	1.95E-43

rs4244184	T	G	0.73	-0.1267	0.0092	1.98E-43
rs6587451	T	C	0.27	0.1267	0.0092	1.99E-43
rs11204632	A	G	0.73	-0.1275	0.0092	2.04E-43
rs11204631	A	G	0.27	0.1275	0.0092	2.04E-43
rs10888360	A	G	0.74	-0.1284	0.0093	2.05E-43
rs11204636	T	G	0.74	-0.1275	0.0092	2.07E-43
rs4551626	T	G	0.73	-0.1266	0.0092	2.13E-43
rs6681336	T	C	0.73	-0.1267	0.0092	2.15E-43
rs4350233	A	G	0.73	-0.1266	0.0092	2.16E-43
rs6681339	C	G	0.27	0.1267	0.0092	2.17E-43
rs6671702	A	G	0.73	-0.1267	0.0092	2.17E-43
rs4405158	A	C	0.27	0.1268	0.0092	2.19E-43
rs6686911	T	C	0.26	0.1295	0.0094	2.20E-43
rs6683717	A	G	0.26	0.1295	0.0094	2.20E-43
rs4537598	A	T	0.73	-0.1266	0.0092	2.21E-43
rs10788780	A	G	0.73	-0.1267	0.0092	2.22E-43
rs12042598	T	C	0.73	-0.1268	0.0092	2.22E-43
rs11204637	A	G	0.73	-0.1266	0.0092	2.23E-43
rs4534422	A	G	0.27	0.1273	0.0092	2.26E-43
rs6702113	T	C	0.27	0.1266	0.0092	2.30E-43
rs5009868	A	G	0.26	0.1313	0.0095	2.30E-43
rs12744455	A	G	0.27	0.127	0.0092	2.32E-43
rs10788779	C	G	0.27	0.1268	0.0092	2.35E-43
rs4244185	A	G	0.27	0.1266	0.0092	2.36E-43
rs7555424	A	G	0.27	0.1267	0.0092	2.50E-43
rs10157089	A	G	0.27	0.1265	0.0092	2.52E-43
rs10888364	T	G	0.27	0.1266	0.0092	2.57E-43
rs7555310	A	G	0.27	0.1266	0.0092	2.62E-43
rs10788776	T	C	0.27	0.1273	0.0092	2.62E-43
rs4409694	T	C	0.73	-0.1272	0.0092	2.65E-43
rs4244179	A	T	0.74	-0.1326	0.0096	2.67E-43
rs6686474	A	C	0.27	0.1285	0.0093	2.76E-43
rs4558008	T	C	0.73	-0.1275	0.0092	2.82E-43
rs4448547	C	G	0.73	-0.1272	0.0092	2.83E-43
rs4282853	A	G	0.27	0.129	0.0094	2.87E-43
rs4457614	A	G	0.27	0.129	0.0094	2.87E-43
rs4540687	C	G	0.27	0.1287	0.0093	2.95E-43
rs4341391	A	G	0.27	0.1287	0.0093	2.97E-43
rs4423045	T	C	0.27	0.1273	0.0092	2.97E-43
rs4307598	T	C	0.27	0.1295	0.0094	2.99E-43
rs4244181	A	G	0.26	0.132	0.0096	3.08E-43
rs4244182	A	G	0.26	0.1319	0.0096	3.09E-43
rs4244180	A	G	0.26	0.1321	0.0096	3.09E-43
rs4489592	A	T	0.26	0.1322	0.0096	3.15E-43
rs4603165	A	T	0.73	-0.1297	0.0094	3.16E-43
rs10888358	A	C	0.74	-0.1317	0.0096	3.17E-43
rs4433430	A	G	0.73	-0.1274	0.0092	3.35E-43
rs4916130	A	C	0.71	-0.1309	0.0095	3.37E-43
rs6669290	A	G	0.73	-0.1281	0.0093	3.39E-43

rs4336885	A	C	0.27	0.13	0.0094	3.40E-43
rs4297335	T	C	0.73	-0.13	0.0094	3.44E-43
rs4275482	T	C	0.27	0.1299	0.0094	3.45E-43
rs6678798	T	C	0.73	-0.1281	0.0093	3.45E-43
rs7524700	A	G	0.27	0.1301	0.0094	3.46E-43
rs4472780	A	G	0.73	-0.1292	0.0094	3.50E-43
rs4589143	A	G	0.26	0.1341	0.0097	3.58E-43
rs4453081	C	G	0.27	0.1287	0.0093	3.66E-43
rs4534423	C	G	0.73	-0.1289	0.0094	3.68E-43
rs4427438	C	G	0.73	-0.1287	0.0093	3.72E-43
rs4581306	A	C	0.73	-0.1285	0.0093	3.77E-43
rs10127803	A	T	0.27	0.1283	0.0093	3.78E-43
rs4376768	A	G	0.73	-0.1283	0.0093	3.81E-43
rs10788775	C	G	0.26	0.1315	0.0095	3.82E-43
rs10788774	T	C	0.26	0.1315	0.0095	3.86E-43
rs4472779	A	G	0.73	-0.1294	0.0094	3.90E-43
rs28524655	T	C	0.73	-0.1295	0.0094	3.94E-43
rs4453080	T	C	0.27	0.1294	0.0094	3.95E-43
rs12731721	A	G	0.73	-0.1295	0.0094	3.95E-43
rs4244183	A	G	0.74	-0.1317	0.0096	4.00E-43
rs4345830	C	G	0.73	-0.1295	0.0094	4.03E-43
rs4575112	A	G	0.27	0.13	0.0094	4.11E-43
rs4292985	A	T	0.73	-0.1298	0.0094	4.30E-43
rs4564179	T	C	0.27	0.1301	0.0095	4.31E-43
rs10749651	T	C	0.27	0.1299	0.0094	4.37E-43
rs4523548	T	G	0.73	-0.13	0.0094	4.39E-43
rs4390209	A	T	0.27	0.1299	0.0094	4.42E-43
rs4644528	A	T	0.73	-0.1299	0.0094	4.47E-43
rs7519334	T	C	0.73	-0.1301	0.0095	4.49E-43
rs4576683	T	C	0.27	0.1302	0.0095	4.64E-43
rs4390208	T	C	0.73	-0.1306	0.0095	5.07E-43
rs4474293	T	C	0.27	0.1336	0.0097	5.22E-43
rs4347240	C	G	0.27	0.1287	0.0094	9.61E-43
rs10788784	A	G	0.26	0.1357	0.01	5.78E-42
rs28795130	A	C	0.70	-0.1437	0.0106	6.88E-42
rs6662913	A	G	0.32	0.1493	0.011	7.53E-42
rs10888370	A	G	0.74	-0.1368	0.0101	8.74E-42
rs6699764	C	G	0.74	-0.138	0.0102	1.25E-41
rs71538191	C	G	0.59	-0.1633	0.0121	1.86E-41
rs7415807	T	G	0.68	-0.1422	0.0106	3.74E-41
rs10218489	T	G	0.71	-0.1421	0.0106	1.18E-40
rs6676064	C	G	0.72	-0.1333	0.01	2.23E-40
rs10888345	A	G	0.29	0.1363	0.0102	2.27E-40
rs6676061	C	G	0.72	-0.1333	0.01	2.39E-40
rs10888349	T	C	0.27	0.1331	0.01	3.03E-40
rs4497248	T	C	0.27	0.1328	0.01	3.03E-40
rs4278391	T	C	0.73	-0.1328	0.01	3.09E-40
rs6697456	T	C	0.63	-0.1524	0.0115	3.21E-40
rs10888343	A	G	0.27	0.1326	0.01	3.32E-40

rs10888348	C	G	0.27	0.1326	0.01	3.41E-40
rs4486480	T	C	0.74	-0.1355	0.0102	3.50E-40
rs6685871	T	C	0.70	-0.1386	0.0105	3.64E-40
rs10888347	T	C	0.27	0.1326	0.01	3.67E-40
rs7543507	T	C	0.72	-0.1331	0.01	3.82E-40
rs9651176	A	G	0.27	0.1321	0.01	3.99E-40
rs4916127	A	G	0.26	0.1331	0.01	4.51E-40
rs10888344	T	C	0.27	0.1317	0.0099	4.72E-40
rs9651175	T	G	0.73	-0.1317	0.0099	4.82E-40
rs4512685	T	C	0.73	-0.1316	0.0099	5.03E-40
rs6666903	A	T	0.73	-0.1322	0.01	5.44E-40
rs6587445	A	G	0.27	0.1311	0.0099	5.53E-40
rs6699797	T	C	0.27	0.1315	0.0099	5.77E-40
rs10888340	T	C	0.73	-0.1311	0.0099	6.20E-40
rs9651177	T	C	0.27	0.1311	0.0099	6.41E-40
rs10788765	T	C	0.73	-0.1309	0.0099	6.81E-40
rs6587444	T	C	0.27	0.1309	0.0099	7.01E-40
rs10888341	T	C	0.27	0.1311	0.0099	7.87E-40
rs11204623	A	G	0.28	0.1361	0.0103	8.08E-40
rs11204626	A	T	0.74	-0.1326	0.01	8.48E-40
rs7547808	A	T	0.28	0.1353	0.0103	8.98E-40
rs4586010	A	G	0.73	-0.1305	0.0099	9.04E-40
rs6687975	C	G	0.62	-0.156	0.0118	9.41E-40
rs10788768	A	G	0.73	-0.1326	0.01	9.66E-40
rs7513161	A	T	0.27	0.1325	0.01	9.85E-40
rs4916123	T	G	0.27	0.134	0.0102	9.92E-40
rs4244172	T	C	0.26	0.1324	0.01	1.01E-39
rs4525076	T	G	0.26	0.1327	0.0101	1.02E-39
rs10888355	A	G	0.73	-0.1326	0.0101	1.03E-39
rs4381224	A	T	0.26	0.1327	0.0101	1.04E-39
rs10736378	T	G	0.27	0.1323	0.01	1.05E-39
rs10788770	T	G	0.26	0.1327	0.0101	1.05E-39
rs12037921	T	G	0.27	0.1323	0.01	1.05E-39
rs6685754	A	C	0.72	-0.1339	0.0102	1.06E-39
rs10788769	T	C	0.73	-0.1326	0.0101	1.06E-39
rs10888352	A	G	0.74	-0.1332	0.0101	1.06E-39
rs10736379	A	T	0.27	0.1323	0.01	1.06E-39
rs6697735	C	G	0.74	-0.1322	0.01	1.09E-39
rs71538180	T	G	0.28	0.1342	0.0102	1.09E-39
rs10888356	A	G	0.26	0.1322	0.01	1.10E-39
rs4372295	T	G	0.74	-0.1322	0.01	1.10E-39
rs4916125	A	T	0.26	0.1323	0.01	1.10E-39
rs4916126	A	G	0.74	-0.1323	0.01	1.11E-39
rs7517319	A	C	0.74	-0.1323	0.01	1.11E-39
rs4916128	A	G	0.74	-0.1323	0.01	1.11E-39
rs4360553	A	G	0.26	0.1323	0.01	1.11E-39
rs6659039	T	C	0.74	-0.1323	0.01	1.12E-39
rs4344359	A	G	0.72	-0.1394	0.0106	1.12E-39
rs6663952	A	G	0.26	0.1323	0.01	1.12E-39

rs6666690	T	C	0.27	0.1323	0.01	1.14E-39
rs6656551	A	T	0.26	0.1322	0.01	1.14E-39
rs77950189	A	C	0.31	0.1396	0.0106	1.16E-39
rs80260298	A	G	0.69	-0.1396	0.0106	1.17E-39
rs4430369	A	G	0.26	0.1324	0.01	1.20E-39
rs4579792	T	C	0.26	0.1323	0.01	1.21E-39
rs10888351	A	G	0.73	-0.1322	0.01	1.23E-39
rs4244178	A	G	0.26	0.1338	0.0102	1.30E-39
rs4543835	A	T	0.27	0.1354	0.0103	1.35E-39
rs4244173	C	G	0.73	-0.1337	0.0102	1.38E-39
rs4306162	T	C	0.74	-0.1334	0.0101	1.53E-39
rs4244176	A	G	0.74	-0.1333	0.0101	1.56E-39
rs4514268	T	G	0.28	0.1302	0.0099	1.59E-39
rs7521689	T	G	0.74	-0.1305	0.0099	1.76E-39
rs4244174	A	G	0.26	0.1328	0.0101	1.78E-39
rs7525344	A	G	0.26	0.1331	0.0101	1.83E-39
rs7511706	A	G	0.74	-0.1327	0.0101	1.88E-39
rs10888353	A	T	0.28	0.1348	0.0103	1.90E-39
rs4244177	T	C	0.74	-0.1333	0.0101	1.96E-39
rs4285735	T	C	0.67	-0.1412	0.0107	1.98E-39
rs4360555	T	G	0.74	-0.1344	0.0102	1.98E-39
rs10749648	A	T	0.30	0.1347	0.0103	2.08E-39
rs7534188	T	C	0.27	0.129	0.0098	2.08E-39
rs4244175	A	G	0.74	-0.1333	0.0101	2.11E-39
rs7527822	T	C	0.26	0.1322	0.0101	2.12E-39
rs4453079	A	T	0.73	-0.1353	0.0103	2.16E-39
rs4578248	A	G	0.73	-0.1291	0.0098	2.16E-39
rs4298770	A	G	0.73	-0.1289	0.0098	2.64E-39
rs10888342	A	G	0.28	0.1294	0.0099	2.99E-39
rs4916121	T	C	0.73	-0.1288	0.0098	3.59E-39
1:248436616	A	G	0.33	0.1389	0.0106	3.59E-39
rs4460676	A	G	0.73	-0.1288	0.0098	3.61E-39
rs4517383	T	C	0.73	-0.1278	0.0098	3.70E-39
rs4295906	T	C	0.73	-0.1278	0.0098	4.30E-39
rs4916124	T	C	0.28	0.133	0.0102	4.80E-39
1:248436611	A	G	0.62	-0.1483	0.0113	4.91E-39
rs78811906	A	C	0.28	0.1278	0.0098	5.10E-39
rs10749646	T	C	0.73	-0.128	0.0098	5.42E-39
rs12046632	A	G	0.21	0.1455	0.0111	5.60E-39
rs7412034	C	G	0.72	-0.1275	0.0098	6.64E-39
rs10749647	T	C	0.68	-0.1368	0.0105	9.99E-39
rs7528645	A	T	0.72	-0.1262	0.0097	1.05E-38
rs10888337	A	G	0.72	-0.1262	0.0097	1.12E-38
rs6667171	A	C	0.73	-0.131	0.0101	1.37E-38
rs10788763	A	T	0.72	-0.1259	0.0097	2.12E-38
rs9662385	T	C	0.66	-0.1433	0.0111	3.01E-38
rs6674940	A	G	0.33	0.1403	0.0109	4.10E-38
rs10159227	C	G	0.72	-0.1307	0.0101	4.45E-38
rs7515408	T	C	0.73	-0.1265	0.0098	5.71E-38

rs6698503	A	G	0.74	-0.1287	0.01	6.03E-38
rs6695468	A	G	0.74	-0.1278	0.0099	8.63E-38
rs28399248	T	G	0.28	0.1428	0.0111	1.14E-37
rs4466692	C	G	0.28	0.1227	0.0097	6.47E-37
rs4526647	C	G	0.28	0.123	0.0097	6.56E-37
rs6686045	C	G	0.72	-0.1207	0.0096	5.92E-36
rs6703399	T	C	0.27	0.1204	0.0096	5.96E-36
rs79235483	A	C	0.31	0.123	0.0098	7.34E-36
rs10749644	A	C	0.28	0.1143	0.0092	1.07E-35
rs6587440	A	G	0.28	0.1142	0.0092	1.09E-35
rs7555217	T	G	0.28	0.1198	0.0096	1.25E-35
rs7546964	A	G	0.27	0.1145	0.0092	1.30E-35
rs6700515	A	G	0.29	0.1188	0.0095	1.34E-35
rs7414420	T	G	0.29	0.1512	0.0121	1.43E-35
rs4526648	A	T	0.72	-0.1192	0.0096	1.67E-35
rs4382760	T	G	0.72	-0.1194	0.0096	1.89E-35
rs139259149	T	C	0.67	-0.1252	0.0101	2.86E-35
rs10788762	T	C	0.70	-0.1236	0.01	3.97E-35
rs7414419	T	G	0.29	0.1502	0.0122	4.55E-35
rs141962587	A	G	0.32	0.1251	0.0101	6.18E-35
rs4559544	T	G	0.27	0.1152	0.0093	6.50E-35
rs140795021	A	C	0.66	-0.1284	0.0104	8.82E-35
rs4453078	A	G	0.72	-0.1135	0.0093	2.40E-34
rs6659585	A	T	0.69	-0.1273	0.0104	2.52E-34
rs10458557	A	C	0.44	0.1504	0.0124	7.81E-34
rs4430368	A	G	0.24	0.1056	0.0097	1.46E-27
rs11204613	A	G	0.71	-0.0958	0.009	3.01E-26
rs10888328	A	G	0.74	-0.0966	0.0092	1.01E-25
rs6695316	C	G	0.74	-0.0966	0.0093	2.38E-25
rs6697831	T	C	0.74	-0.0965	0.0093	2.46E-25
rs4916117	C	G	0.74	-0.0962	0.0093	2.72E-25
rs4916115	T	G	0.27	0.0952	0.0092	2.80E-25
rs28795805	A	T	0.49	0.1706	0.0164	2.91E-25
rs9662722	T	G	0.26	0.0961	0.0093	2.92E-25
rs28749168	A	G	0.66	-0.1404	0.0135	2.94E-25
rs71538192	A	G	0.49	0.1715	0.0165	3.18E-25
rs4390207	T	C	0.74	-0.0963	0.0093	3.46E-25
rs4474292	A	G	0.73	-0.0952	0.0092	3.74E-25
rs4309012	T	C	0.73	-0.0949	0.0092	4.00E-25
rs4347239	A	G	0.27	0.095	0.0092	4.43E-25
rs6666148	T	C	0.73	-0.095	0.0092	4.79E-25
rs7349159	T	C	0.73	-0.0945	0.0092	5.34E-25
rs28819159	T	G	0.27	0.1245	0.0121	6.20E-25
rs28883135	C	G	0.48	0.1681	0.0164	9.22E-25
rs4537599	A	G	0.74	-0.1182	0.0115	1.06E-24
rs10888329	T	C	0.27	0.0945	0.0092	1.25E-24
rs4412629	T	G	0.73	-0.0953	0.0093	1.32E-24
rs4397683	T	C	0.74	-0.0951	0.0094	3.81E-24
rs6672981	A	G	0.74	-0.0949	0.0094	4.50E-24

rs28781382	C	G	0.33	0.1288	0.0128	6.04E-24
rs28803252	A	G	0.68	-0.1508	0.015	7.33E-24
rs10788761	T	C	0.74	-0.0944	0.0094	7.76E-24
rs12757057	A	T	0.42	0.1489	0.0148	8.50E-24
rs6694598	A	G	0.27	0.0933	0.0093	9.70E-24
rs4428922	T	C	0.73	-0.0932	0.0093	1.03E-23
rs6689894	T	C	0.73	-0.0928	0.0093	1.25E-23
rs28787378	T	C	0.73	-0.115	0.0115	1.47E-23
rs10888330	A	T	0.27	0.0929	0.0093	1.51E-23
rs4642918	T	G	0.73	-0.0923	0.0092	1.62E-23
rs28579823	T	C	0.74	-0.1145	0.0115	1.62E-23
rs28581861	T	G	0.27	0.1145	0.0115	1.63E-23
rs1934544	A	G	0.73	-0.1146	0.0115	1.63E-23
rs1934543	C	G	0.27	0.1145	0.0115	1.66E-23
rs1339989	C	G	0.26	0.1135	0.0114	1.71E-23
rs1339991	T	C	0.74	-0.1134	0.0114	1.75E-23
rs28451623	A	G	0.74	-0.1134	0.0114	1.75E-23
rs1339990	T	C	0.26	0.1134	0.0114	1.75E-23
rs1339992	A	G	0.74	-0.1134	0.0114	1.75E-23
rs28782809	T	C	0.65	-0.1318	0.0133	3.30E-23
rs28883970	A	T	0.61	-0.1344	0.0136	3.88E-23
rs150452781	A	G	0.47	0.1516	0.0154	6.97E-23
rs6587439	T	C	0.75	-0.0937	0.0095	8.01E-23
rs4916113	T	C	0.75	-0.0926	0.0094	9.16E-23
rs4508045	A	G	0.75	-0.0938	0.0096	9.62E-23
rs6691024	A	G	0.25	0.0928	0.0095	1.06E-22
rs146140038	A	T	0.43	0.1518	0.0155	1.18E-22
rs7521717	A	T	0.75	-0.094	0.0096	1.18E-22
rs4328104	A	G	0.25	0.0936	0.0096	1.22E-22
rs192799404	T	C	0.54	0.178	0.0182	1.33E-22
rs4916082	T	C	0.75	-0.0937	0.0096	1.74E-22
rs4453077	T	C	0.75	-0.0946	0.0097	1.84E-22
rs7533755	A	G	0.25	0.0936	0.0096	2.41E-22
rs6587431	T	C	0.25	0.0936	0.0096	2.47E-22
rs7529247	T	C	0.75	-0.0935	0.0096	2.47E-22
rs4576682	A	T	0.25	0.0935	0.0096	2.51E-22
rs4390205	A	C	0.75	-0.0935	0.0096	2.51E-22
rs7548525	A	G	0.25	0.0935	0.0096	2.55E-22
rs183802903	A	G	0.52	-0.1487	0.0153	2.56E-22
rs4271247	T	C	0.25	0.0936	0.0096	2.62E-22
rs4546956	A	G	0.75	-0.0934	0.0096	2.72E-22
rs7529953	A	T	0.75	-0.0934	0.0096	2.78E-22
rs7522945	A	C	0.75	-0.0934	0.0096	2.79E-22
rs11204607	A	G	0.75	-0.0934	0.0096	2.79E-22
rs7544149	T	C	0.75	-0.0942	0.0097	2.80E-22
rs6587434	A	G	0.75	-0.0936	0.0096	2.80E-22
rs6587437	T	G	0.25	0.0934	0.0096	2.80E-22
rs6587438	C	G	0.75	-0.0934	0.0096	2.81E-22
rs6587433	A	G	0.75	-0.0934	0.0096	2.83E-22

rs12025218	A	G	0.25	0.0934	0.0096	2.84E-22
rs11204611	T	C	0.25	0.0933	0.0096	2.84E-22
rs12117067	A	G	0.25	0.0933	0.0096	2.85E-22
rs7541625	C	G	0.75	-0.0933	0.0096	2.89E-22
rs7512756	T	C	0.25	0.0933	0.0096	2.90E-22
rs7550630	T	C	0.75	-0.0933	0.0096	2.90E-22
rs11204610	T	C	0.75	-0.0933	0.0096	2.91E-22
rs6587432	T	C	0.75	-0.0935	0.0096	2.92E-22
rs4916107	A	G	0.75	-0.0933	0.0096	3.07E-22
rs140803038	C	G	0.46	0.1462	0.0151	3.21E-22
rs10888323	T	C	0.75	-0.0932	0.0096	3.26E-22
rs4916109	A	G	0.75	-0.0932	0.0096	3.27E-22
rs11204608	T	C	0.75	-0.0932	0.0096	3.28E-22
rs4916108	A	G	0.75	-0.0932	0.0096	3.28E-22
rs10888324	A	G	0.75	-0.0932	0.0096	3.83E-22
rs4916110	T	C	0.25	0.0931	0.0096	4.37E-22
rs7530153	T	C	0.28	0.0959	0.01	6.84E-22
rs6587430	T	G	0.28	0.0976	0.0102	1.06E-21
rs7516704	A	T	0.72	-0.0967	0.0101	1.17E-21
rs6587436	A	G	0.28	0.0955	0.01	1.17E-21
rs7518603	A	T	0.25	0.0927	0.0097	1.34E-21
rs10788783	A	C	0.58	-0.0819	0.0086	2.01E-21
rs4364913	A	C	0.69	-0.1056	0.0111	2.57E-21
rs4916106	A	G	0.75	-0.0911	0.0096	2.58E-21
rs6677282	A	T	0.58	-0.0854	0.009	3.25E-21
rs4415607	T	C	0.42	0.0836	0.0089	4.70E-21
rs4415610	T	C	0.56	-0.0825	0.0088	4.72E-21
rs11204639	T	C	0.58	-0.0836	0.0089	4.72E-21
rs4589144	T	C	0.42	0.0839	0.0089	5.79E-21
rs4477316	T	C	0.42	0.0841	0.009	6.68E-21
rs28857255	T	C	0.49	0.1	0.0107	6.95E-21
rs11485478	T	C	0.22	0.1509	0.0161	8.80E-21
rs28590733	T	C	0.32	0.1029	0.0111	1.49E-20
rs10888367	A	G	0.42	0.0846	0.0091	1.52E-20
rs28680862	T	C	0.32	0.1024	0.0111	1.97E-20
rs4639798	A	G	0.32	0.1023	0.011	2.03E-20
rs6665904	T	C	0.47	0.0939	0.0102	2.29E-20
rs1538703	T	G	0.31	0.1019	0.011	2.73E-20
rs10888371	T	G	0.58	-0.0848	0.0092	2.74E-20
rs28706835	A	G	0.31	0.1028	0.0111	2.86E-20
rs11204641	A	G	0.41	0.0858	0.0093	3.13E-20
rs28572435	A	G	0.44	0.1304	0.0142	3.17E-20
rs6665424	T	G	0.42	0.0856	0.0093	3.23E-20
rs28607212	T	C	0.31	0.1018	0.0111	3.34E-20
rs6657694	T	C	0.58	-0.0858	0.0093	3.37E-20
rs10888368	T	C	0.56	-0.0846	0.0092	3.74E-20
rs10749656	T	C	0.58	-0.0843	0.0092	4.17E-20
rs6680993	T	C	0.42	0.0842	0.0092	4.39E-20
rs28565101	T	C	0.69	-0.1015	0.0111	6.94E-20

rs11204642	A	G	0.57	-0.0862	0.0094	6.97E-20
rs28444488	A	C	0.70	-0.1004	0.011	8.49E-20
rs28616194	A	T	0.70	-0.1004	0.011	8.50E-20
rs6587458	A	T	0.70	-0.1004	0.011	8.50E-20
rs6688853	A	G	0.69	-0.1007	0.0111	8.58E-20
rs6682953	T	C	0.30	0.1004	0.011	8.66E-20
rs6682957	T	G	0.30	0.1004	0.011	8.67E-20
rs6587462	A	G	0.30	0.1005	0.011	8.91E-20
rs6674078	A	G	0.70	-0.1007	0.0111	9.11E-20
rs6696691	T	C	0.30	0.1004	0.011	9.30E-20
rs6681758	A	T	0.70	-0.1004	0.011	9.36E-20
rs7540715	T	C	0.70	-0.1006	0.0111	9.57E-20
rs6587463	C	G	0.70	-0.1006	0.0111	9.63E-20
rs6421453	A	G	0.31	0.1012	0.0111	9.69E-20
rs1361413	C	G	0.30	0.0999	0.011	1.25E-19
rs6691314	A	G	0.69	-0.0995	0.011	1.41E-19
rs7519867	T	C	0.50	-0.0854	0.0095	1.72E-19
rs11488133	T	C	0.31	0.0992	0.011	1.79E-19
rs28546934	A	G	0.30	0.1	0.0111	1.82E-19
rs946761	T	C	0.30	0.0993	0.011	1.87E-19
rs11488132	A	G	0.19	0.1208	0.0134	2.14E-19
rs946764	A	C	0.30	0.0989	0.011	2.18E-19
rs28719164	T	G	0.32	0.0999	0.0111	2.40E-19
rs1538704	A	G	0.70	-0.0983	0.011	3.49E-19
rs12749362	A	G	0.51	-0.0837	0.0094	3.81E-19
rs1544177	C	G	0.30	0.0982	0.011	3.92E-19
rs7524978	A	T	0.30	0.0981	0.011	4.31E-19
rs7520659	A	C	0.70	-0.0981	0.011	4.37E-19
rs7527991	A	T	0.70	-0.098	0.011	4.39E-19
rs7511986	A	G	0.70	-0.098	0.011	4.41E-19
rs28421649	C	G	0.68	-0.0983	0.011	4.64E-19
rs141353932	A	G	0.41	-0.1598	0.0179	5.08E-19
rs55741505	A	G	0.69	-0.0989	0.0111	5.76E-19
rs7417519	A	G	0.30	0.0974	0.011	6.32E-19
rs6587467	T	G	0.31	0.0974	0.011	6.53E-19
rs4360554	T	C	0.69	-0.0973	0.011	7.52E-19
rs28818253	A	G	0.46	-0.0951	0.0107	7.82E-19
rs28684663	T	C	0.31	0.0972	0.011	8.00E-19
rs11204634	C	G	0.48	0.078	0.0088	9.73E-19
rs6587471	A	G	0.69	-0.0968	0.011	1.02E-18
rs4297336	A	G	0.52	-0.081	0.0092	1.24E-18
rs28869306	C	G	0.41	0.1104	0.0126	1.66E-18
rs4916129	T	C	0.50	-0.0802	0.0091	1.70E-18
rs138556316	A	G	0.69	-0.0965	0.011	1.71E-18
rs28468416	T	G	0.69	-0.0971	0.0111	2.09E-18
rs4559542	T	C	0.53	-0.0762	0.0087	2.16E-18
rs28858103	T	G	0.51	-0.0849	0.0097	2.30E-18
rs28763387	T	C	0.30	0.0956	0.011	2.96E-18
rs11488135	A	G	0.69	-0.0966	0.0111	4.36E-18

rs28729425	T	C	0.30	0.0956	0.0111	5.72E-18
rs28589987	T	C	0.31	0.0955	0.0111	6.79E-18
rs34542972	T	C	0.52	-0.0816	0.0095	6.96E-18
rs75349579	A	C	0.37	0.1038	0.0121	7.92E-18
rs141135906	T	C	0.52	-0.0829	0.0097	9.52E-18
rs11485458	A	G	0.31	0.0954	0.0111	1.12E-17
rs7411614	T	C	0.47	0.0759	0.0092	1.26E-16
rs28769405	A	G	0.24	0.1671	0.0203	2.10E-16
rs1538702	A	T	0.41	0.0926	0.0113	2.62E-16
rs10888339	T	C	0.46	0.075	0.0092	3.64E-16
rs11204620	T	C	0.46	0.0741	0.0091	3.90E-16
rs10788764	A	G	0.47	0.0744	0.0092	6.01E-16
rs12034050	T	C	0.50	-0.0796	0.0099	6.80E-16
rs6695780	A	G	0.79	-0.1056	0.0132	1.14E-15
rs6656862	T	C	0.45	0.0722	0.0091	2.16E-15
rs75983624	T	C	0.07	0.2533	0.032	2.37E-15
rs12723512	A	G	0.48	0.0736	0.0093	2.41E-15
1:248458571	A	T	0.52	-0.0729	0.0093	4.09E-15
rs77795510	T	C	0.62	0.132	0.0169	5.99E-15
rs28642279	C	G	0.21	0.0961	0.013	1.39E-13
rs56162116	A	G	0.38	-0.1183	0.0162	3.11E-13
rs28515652	A	G	0.63	-0.1107	0.0154	5.97E-13
rs28813072	A	G	0.48	-0.092	0.0129	9.54E-13
rs7414182	A	G	0.58	-0.0745	0.0104	9.58E-13
rs111453957	A	G	0.92	-0.1282	0.0181	1.36E-12
rs6657960	A	G	0.52	-0.0797	0.0113	1.44E-12
rs6668460	C	G	0.46	0.0793	0.0112	1.70E-12
rs28571812	C	G	0.52	-0.0792	0.0113	2.06E-12
rs28465434	C	G	0.48	0.0789	0.0112	2.06E-12
rs6662468	A	G	0.55	0.0925	0.0132	2.15E-12
rs6667849	T	C	0.55	-0.0753	0.0107	2.17E-12
rs6667858	T	C	0.56	-0.0747	0.0106	2.32E-12
rs1538710	T	G	0.43	0.0726	0.0104	2.49E-12
rs28769991	T	C	0.44	0.0721	0.0103	2.86E-12
rs4354569	A	G	0.57	-0.0724	0.0104	2.89E-12
rs28576448	T	C	0.56	-0.0716	0.0103	3.14E-12
rs28790302	A	G	0.44	0.0721	0.0103	3.22E-12
rs3949391	A	G	0.43	0.0722	0.0104	3.26E-12
rs28873533	T	G	0.44	0.0718	0.0103	3.30E-12
rs1934545	A	G	0.56	-0.0717	0.0103	3.31E-12
rs28754930	A	T	0.44	0.0717	0.0103	3.32E-12
rs28816758	T	C	0.55	-0.0727	0.0104	3.36E-12
rs4916131	A	G	0.44	0.0716	0.0103	3.36E-12
rs28631494	A	C	0.43	0.0719	0.0103	3.37E-12
rs28431379	A	T	0.45	0.0723	0.0104	3.38E-12
rs28704053	C	G	0.44	0.072	0.0103	3.41E-12
rs28469841	T	C	0.43	0.071	0.0102	3.43E-12
rs28607995	A	G	0.57	-0.0717	0.0103	3.47E-12
rs4576685	T	G	0.56	-0.0711	0.0102	3.48E-12

rs4336886	T	C	0.44	0.0711	0.0102	3.48E-12
rs28396562	T	C	0.44	0.0717	0.0103	3.51E-12
rs28712553	C	G	0.57	-0.0718	0.0103	3.51E-12
rs28728105	T	C	0.57	-0.0711	0.0102	3.53E-12
rs28545014	T	G	0.57	-0.0717	0.0103	3.53E-12
rs28377739	A	G	0.57	-0.0717	0.0103	3.54E-12
rs28372410	T	G	0.43	0.0711	0.0102	3.54E-12
rs28419186	T	G	0.57	-0.0711	0.0102	3.54E-12
rs28657383	A	T	0.43	0.0717	0.0103	3.55E-12
rs28481429	C	G	0.57	-0.0717	0.0103	3.55E-12
rs28609049	T	C	0.43	0.0717	0.0103	3.55E-12
rs2039824	T	C	0.57	-0.0717	0.0103	3.55E-12
rs28680702	A	G	0.57	-0.0717	0.0103	3.57E-12
rs1339988	A	G	0.57	-0.0708	0.0102	3.64E-12
rs28430581	A	T	0.56	-0.0713	0.0103	3.68E-12
rs28693517	T	C	0.56	-0.0723	0.0104	4.04E-12
rs28539363	A	C	0.56	-0.0723	0.0104	4.07E-12
rs28589611	A	G	0.44	0.0723	0.0104	4.09E-12
rs12354081	A	G	0.55	-0.061	0.0088	4.76E-12
rs4509607	A	C	0.55	-0.0609	0.0088	5.32E-12
rs11204614	A	C	0.55	-0.061	0.0089	5.82E-12
rs6660381	T	C	0.61	-0.0594	0.0086	6.29E-12
rs56344892	A	G	0.63	0.1087	0.0158	6.41E-12
rs71538193	A	G	0.37	-0.1088	0.0159	6.99E-12
rs10888322	A	G	0.61	-0.0591	0.0086	7.42E-12
rs7522840	C	G	0.39	0.0591	0.0086	7.76E-12
rs61832942	A	C	0.30	-0.1366	0.0201	1.00E-11
rs10888375	A	G	0.29	-0.1356	0.02	1.09E-11
rs12133646	A	G	0.51	-0.0646	0.0095	1.09E-11
rs11204612	A	G	0.40	0.06	0.0088	1.10E-11
rs7514239	T	C	0.60	-0.0597	0.0088	1.30E-11
rs3927687	T	C	0.48	0.0696	0.0103	1.32E-11
rs4626922	T	C	0.42	0.0607	0.009	1.45E-11
rs4494168	T	C	0.58	-0.0607	0.009	1.45E-11
rs7516127	A	G	0.48	0.0693	0.0103	1.58E-11
rs7513570	A	G	0.45	0.0688	0.0102	1.58E-11
rs28701914	T	C	0.48	0.0688	0.0103	1.95E-11
rs35489390	T	G	0.52	-0.0688	0.0103	1.96E-11
rs12063997	A	C	0.39	0.0587	0.0088	2.02E-11
rs6688371	C	G	0.51	-0.0691	0.0103	2.03E-11
rs34850199	A	G	0.51	-0.069	0.0103	2.07E-11
rs1538701	A	G	0.52	-0.0687	0.0103	2.09E-11
rs28574687	T	G	0.49	0.0691	0.0103	2.10E-11
rs61832889	A	G	0.39	-0.1013	0.0151	2.12E-11
rs4326658	A	C	0.60	-0.0579	0.0087	2.17E-11
rs6702640	A	G	0.49	0.0689	0.0103	2.21E-11
rs6697835	T	C	0.51	-0.0689	0.0103	2.22E-11
rs6702777	A	G	0.49	0.0687	0.0103	2.24E-11
rs28547518	T	G	0.47	0.0685	0.0102	2.24E-11

rs28496519	A	C	0.46	0.0687	0.0103	2.26E-11
rs6702450	A	G	0.49	0.0687	0.0103	2.27E-11
rs6688663	T	G	0.51	-0.0688	0.0103	2.29E-11
rs6698060	T	C	0.51	-0.0691	0.0103	2.29E-11
rs28692768	A	G	0.52	-0.069	0.0103	2.31E-11
rs28683073	A	C	0.54	-0.0687	0.0103	2.35E-11
rs28590551	A	G	0.49	0.0687	0.0103	2.40E-11
rs7544362	A	G	0.50	-0.0728	0.0109	2.40E-11
rs6673454	A	G	0.06	0.1629	0.0244	2.41E-11
rs11488124	A	C	0.59	-0.059	0.0088	2.41E-11
rs1934542	T	C	0.49	0.0689	0.0103	2.42E-11
rs35274032	A	G	0.48	0.0689	0.0103	2.42E-11
rs28708457	T	C	0.51	-0.0687	0.0103	2.43E-11
rs34389617	T	G	0.51	-0.0689	0.0103	2.44E-11
rs1544176	A	G	0.54	-0.068	0.0102	2.45E-11
rs7515376	T	C	0.50	0.0728	0.0109	2.47E-11
rs1538709	T	C	0.51	-0.0688	0.0103	2.48E-11
rs1934541	T	C	0.49	0.0687	0.0103	2.51E-11
rs28819183	T	C	0.45	0.0772	0.0116	2.52E-11
rs4366353	T	C	0.51	-0.0691	0.0104	2.52E-11
rs1544175	A	G	0.54	-0.0682	0.0102	2.54E-11
rs28582047	A	G	0.51	-0.0691	0.0104	2.57E-11
rs28408294	T	G	0.46	0.0679	0.0102	2.58E-11
rs28545558	A	G	0.54	-0.0678	0.0102	2.58E-11
rs28583925	A	G	0.49	0.0688	0.0103	2.60E-11
rs4916111	A	G	0.40	0.0581	0.0087	2.60E-11
rs7520424	T	C	0.54	-0.0679	0.0102	2.61E-11
rs4916112	A	G	0.60	-0.0582	0.0087	2.63E-11
rs28525318	A	G	0.51	-0.0686	0.0103	2.69E-11
rs10888325	A	G	0.40	0.0579	0.0087	2.74E-11
rs6587460	T	C	0.45	0.068	0.0102	2.84E-11
rs12022706	T	C	0.58	-0.0594	0.0089	2.93E-11
rs7550643	T	C	0.60	-0.0578	0.0087	2.99E-11
rs28627313	T	C	0.45	0.068	0.0102	3.04E-11
rs7523228	C	G	0.45	0.068	0.0102	3.09E-11
rs6587457	A	G	0.55	-0.0676	0.0102	3.10E-11
rs6696565	A	G	0.55	-0.0677	0.0102	3.12E-11
rs4412631	T	G	0.61	-0.0568	0.0086	3.14E-11
rs4412630	T	G	0.61	-0.0568	0.0086	3.15E-11
rs12022705	T	C	0.58	-0.0595	0.009	3.23E-11
rs61832688	T	G	0.59	-0.0586	0.0088	3.35E-11
rs1339987	T	C	0.55	-0.0676	0.0102	3.60E-11
rs6678999	A	G	0.45	0.0677	0.0102	3.60E-11
rs28555620	T	C	0.54	-0.0676	0.0102	3.72E-11
rs28514998	T	G	0.46	0.0676	0.0102	3.74E-11
rs28738670	T	C	0.54	-0.0676	0.0102	3.76E-11
rs10788757	A	G	0.61	-0.0563	0.0085	3.93E-11
rs12088869	C	G	0.61	-0.0562	0.0085	4.10E-11
rs28523425	A	T	0.44	0.0697	0.0106	4.88E-11

rs28729893	A	G	0.45	0.0674	0.0102	4.97E-11
rs11204598	A	T	0.40	0.056	0.0085	5.08E-11
rs12049453	T	C	0.60	-0.0561	0.0085	5.19E-11
rs7520734	T	C	0.36	0.0562	0.0086	5.40E-11
rs28390128	A	G	0.49	0.0686	0.0105	5.40E-11
rs4615870	T	C	0.64	-0.0562	0.0086	5.42E-11
rs884544	T	C	0.53	-0.0668	0.0102	5.46E-11
rs946762	T	C	0.47	0.0668	0.0102	5.59E-11
rs4475789	T	G	0.36	0.0562	0.0086	6.16E-11
rs7515550	A	G	0.35	0.056	0.0086	6.20E-11
rs147267541	T	C	0.08	0.1265	0.0194	6.55E-11
rs2153388	T	C	0.48	0.066	0.0101	7.25E-11
rs12022610	T	C	0.60	-0.0566	0.0087	7.33E-11
rs946766	T	C	0.52	-0.066	0.0101	7.52E-11
rs946767	A	T	0.48	0.0659	0.0101	7.69E-11
rs28719833	A	T	0.52	-0.0658	0.0101	7.78E-11
rs946765	T	C	0.52	-0.066	0.0102	7.85E-11
rs946763	A	G	0.48	0.066	0.0101	7.88E-11
rs1556967	T	C	0.52	-0.0658	0.0101	8.04E-11
rs1339986	A	G	0.54	-0.0663	0.0102	8.40E-11
rs28893010	A	T	0.54	-0.0666	0.0103	8.42E-11
rs7364694	A	G	0.24	0.1038	0.016	8.57E-11
rs10888320	A	T	0.36	0.0565	0.0087	9.25E-11
rs28523915	A	G	0.46	0.0669	0.0104	1.07E-10
rs7551888	T	C	0.64	-0.0554	0.0086	1.14E-10
rs10888318	C	G	0.64	-0.0552	0.0086	1.17E-10
rs9435920	T	C	0.36	0.0553	0.0086	1.26E-10
rs28503806	A	G	0.67	-0.1172	0.0182	1.29E-10
rs28599722	A	G	0.45	0.0679	0.0106	1.31E-10
rs6587429	A	T	0.64	-0.0551	0.0086	1.31E-10
rs4916181	A	G	0.90	-0.1341	0.0209	1.32E-10
rs11204604	A	G	0.64	-0.0567	0.0088	1.45E-10
rs12048030	A	G	0.55	-0.0604	0.0094	1.46E-10
rs12024915	T	C	0.45	0.0603	0.0094	1.46E-10
rs28404051	A	T	0.23	0.1015	0.0159	1.59E-10
rs11485460	A	G	0.25	0.1045	0.0163	1.60E-10
rs11204605	A	G	0.55	-0.0598	0.0094	1.84E-10
rs2185358	A	T	0.78	-0.0916	0.0144	1.89E-10
rs12044201	A	G	0.64	-0.0552	0.0087	1.91E-10
rs4417104	T	C	0.58	-0.057	0.009	1.92E-10
rs2095952	A	G	0.24	0.091	0.0143	1.98E-10
rs4504921	T	C	0.23	0.0889	0.014	2.02E-10
rs4475788	A	G	0.36	0.0544	0.0086	2.05E-10
rs4309011	A	C	0.36	0.0544	0.0086	2.07E-10
rs10788759	A	G	0.36	0.0542	0.0085	2.11E-10
rs10788758	A	G	0.64	-0.0542	0.0085	2.12E-10
rs113871675	A	G	0.93	-0.1208	0.0191	2.40E-10
rs4309010	A	G	0.64	-0.0542	0.0086	2.40E-10
rs28534600	A	T	0.54	-0.0655	0.0104	2.45E-10

rs10888316	A	C	0.36	0.0544	0.0086	2.46E-10
rs10888319	C	G	0.36	0.054	0.0085	2.66E-10
rs4244171	C	G	0.42	0.0589	0.0093	2.71E-10
rs6700218	T	C	0.36	0.0539	0.0085	2.76E-10
rs6692295	T	C	0.64	-0.0539	0.0085	2.78E-10
rs6692096	C	G	0.36	0.0539	0.0085	2.82E-10
rs12094919	A	G	0.36	0.0539	0.0085	2.83E-10
rs7518270	T	C	0.36	0.0538	0.0085	2.84E-10
rs7513567	T	C	0.64	-0.0538	0.0085	2.88E-10
rs7521431	T	G	0.36	0.0538	0.0085	3.02E-10
rs116660969	T	G	0.05	0.1228	0.0195	3.05E-10
rs146005063	C	G	0.95	-0.1228	0.0195	3.05E-10
rs28444499	A	C	0.78	-0.1045	0.0166	3.08E-10
rs6697190	A	G	0.36	0.054	0.0086	3.09E-10
rs28661952	A	G	0.46	0.065	0.0103	3.15E-10
rs72763235	T	G	0.06	0.1187	0.0189	3.23E-10
rs6587475	T	C	0.77	-0.0759	0.0121	3.24E-10
rs56965727	A	G	0.94	-0.1212	0.0193	3.44E-10
rs72763236	T	C	0.06	0.1171	0.0187	3.74E-10
rs4436422	T	G	0.64	-0.0535	0.0085	3.83E-10
rs4592280	A	G	0.46	0.0648	0.0104	3.92E-10
rs72763234	C	G	0.94	-0.1163	0.0186	3.98E-10
rs13373863	A	G	0.07	0.1165	0.0186	4.11E-10
rs72763233	A	G	0.94	-0.1155	0.0185	4.32E-10
rs4571999	A	C	0.36	0.0533	0.0085	4.34E-10
rs78865120	A	G	0.94	-0.1211	0.0194	4.34E-10
rs7417968	T	C	0.64	-0.0533	0.0085	4.34E-10
rs12756779	A	T	0.36	0.0533	0.0085	4.35E-10
rs72763220	C	G	0.93	-0.1238	0.0198	4.39E-10
rs3001305	T	C	0.36	0.0533	0.0085	4.41E-10
rs4430367	A	G	0.64	-0.0533	0.0085	4.41E-10
rs7549018	C	G	0.36	0.0533	0.0085	4.42E-10
rs4430366	A	G	0.64	-0.0533	0.0085	4.44E-10
rs3010202	C	G	0.36	0.0533	0.0085	4.45E-10
rs72763229	T	C	0.06	0.1178	0.0189	4.54E-10
rs1538705	A	T	0.47	0.0644	0.0103	4.54E-10
rs12733732	T	C	0.43	0.0553	0.0089	4.56E-10
rs9435892	A	T	0.64	-0.0532	0.0085	4.60E-10
rs9435921	T	G	0.36	0.0532	0.0085	4.62E-10
rs9435891	T	C	0.36	0.0533	0.0085	4.63E-10
rs4916105	T	C	0.64	-0.0533	0.0086	4.65E-10
rs10788753	A	T	0.94	-0.1145	0.0184	4.75E-10
rs4628537	T	C	0.64	-0.0532	0.0085	4.76E-10
rs72763237	A	G	0.06	0.1164	0.0187	4.86E-10
rs61832672	T	G	0.45	0.0616	0.0099	4.87E-10
rs7512072	T	C	0.94	-0.1146	0.0184	4.88E-10
rs6657389	T	G	0.05	0.1175	0.0189	4.93E-10
rs10888317	A	G	0.37	0.0532	0.0086	5.00E-10
rs72763240	A	G	0.94	-0.1168	0.0188	5.07E-10

rs7553421	A	T	0.36	0.0532	0.0086	5.16E-10
rs72763239	T	G	0.94	-0.1166	0.0188	5.18E-10
rs79752829	T	G	0.94	-0.1166	0.0188	5.50E-10
rs4916104	T	C	0.42	0.0581	0.0094	5.69E-10
rs28667896	A	G	0.46	0.0644	0.0104	5.80E-10
rs72763243	T	C	0.06	0.1163	0.0188	5.97E-10
rs6685509	T	C	0.05	0.1149	0.0186	6.22E-10
rs10888312	A	C	0.06	0.1141	0.0184	6.24E-10
rs7532628	T	G	0.05	0.1149	0.0186	6.29E-10
rs4424545	A	G	0.64	-0.0527	0.0085	6.31E-10
rs72763230	A	T	0.94	-0.1168	0.0189	6.51E-10
rs6701653	T	C	0.95	-0.1147	0.0186	6.53E-10
rs6692201	T	C	0.05	0.1147	0.0186	6.55E-10
rs11204600	T	C	0.36	0.0526	0.0085	6.65E-10
rs4415609	A	G	0.36	0.0527	0.0085	6.69E-10
rs4559543	T	C	0.64	-0.0527	0.0085	6.72E-10
rs5015666	C	G	0.95	-0.1146	0.0186	6.72E-10
rs72763224	T	C	0.06	0.1205	0.0195	6.77E-10
rs5015664	T	C	0.05	0.1146	0.0186	6.78E-10
rs5015668	T	C	0.95	-0.1146	0.0186	6.81E-10
rs115276215	T	G	0.05	0.1148	0.0186	6.82E-10
rs11204601	A	G	0.36	0.0526	0.0085	6.82E-10
rs4313428	A	G	0.05	0.1145	0.0186	6.85E-10
rs5015665	C	G	0.05	0.1146	0.0186	6.90E-10
rs10888315	A	G	0.64	-0.0526	0.0085	6.90E-10
rs11204602	T	C	0.36	0.0526	0.0085	7.10E-10
rs12756781	A	G	0.37	0.0529	0.0086	7.20E-10
rs6587420	T	C	0.05	0.1146	0.0186	7.24E-10
rs7544991	T	C	0.95	-0.1145	0.0186	7.25E-10
rs12037329	T	C	0.05	0.114	0.0185	7.36E-10
rs73145287	T	C	0.05	0.1142	0.0186	7.38E-10
rs4916114	A	G	0.57	-0.0543	0.0088	7.39E-10
rs11204597	T	G	0.36	0.0572	0.0093	7.56E-10
rs112229130	A	G	0.06	0.1202	0.0196	7.86E-10
rs35675628	T	C	0.41	0.0687	0.0112	7.90E-10
rs12034548	A	T	0.05	0.114	0.0186	8.13E-10
rs12037761	T	C	0.95	-0.1155	0.0188	8.57E-10
rs72763222	A	C	0.06	0.1207	0.0197	8.61E-10
rs12033551	C	G	0.05	0.114	0.0186	8.63E-10
rs9435919	T	C	0.62	-0.0545	0.0089	8.72E-10
rs112526160	T	C	0.95	-0.1157	0.0189	8.78E-10
rs72763248	T	C	0.95	-0.115	0.0188	8.81E-10
rs12029827	A	C	0.05	0.1141	0.0186	8.87E-10
rs6665846	A	G	0.95	-0.1326	0.0216	8.89E-10
rs4471301	A	G	0.95	-0.1174	0.0192	8.89E-10
rs111755774	C	G	0.05	0.1144	0.0187	8.91E-10
rs144861534	A	C	0.05	0.1144	0.0187	8.91E-10
rs6658256	T	C	0.12	0.0867	0.0141	8.97E-10
rs140264447	A	C	0.05	0.1144	0.0187	9.14E-10

rs4636501	C	G	0.95	-0.1143	0.0187	9.25E-10
rs12028988	A	G	0.05	0.1142	0.0186	9.28E-10
rs12028959	T	G	0.05	0.1141	0.0186	9.31E-10
rs12036678	T	C	0.95	-0.1143	0.0187	9.63E-10
rs12034675	A	G	0.95	-0.1143	0.0187	9.66E-10
rs6682718	T	C	0.95	-0.1142	0.0187	9.80E-10
rs192107511	A	T	0.05	0.1141	0.0187	9.83E-10
rs61216800	A	G	0.05	0.1142	0.0187	9.84E-10
rs72763219	C	G	0.07	0.1236	0.0202	9.87E-10
rs12033903	T	G	0.05	0.1142	0.0187	9.89E-10
rs73129409	T	C	0.95	-0.1142	0.0187	9.93E-10
rs73145245	T	G	0.95	-0.1157	0.0189	9.93E-10
rs6682869	C	G	0.05	0.114	0.0187	9.94E-10
rs140784417	A	T	0.95	-0.1143	0.0187	9.95E-10
rs73147262	T	C	0.05	0.114	0.0187	9.97E-10
rs73147263	A	T	0.05	0.114	0.0187	9.97E-10
rs147639902	T	C	0.05	0.114	0.0187	1.00E-09
rs12038708	A	G	0.95	-0.1141	0.0187	1.01E-09
rs12022488	T	G	0.94	-0.115	0.0188	1.01E-09
rs6691972	T	C	0.05	0.114	0.0187	1.01E-09
rs12032973	A	G	0.95	-0.1138	0.0186	1.02E-09
rs61273564	A	G	0.05	0.1138	0.0186	1.02E-09
rs12035965	T	G	0.95	-0.1139	0.0187	1.03E-09
rs73141294	T	C	0.06	0.1287	0.0211	1.03E-09
rs7520873	A	G	0.94	-0.1285	0.0211	1.04E-09
rs73145260	A	C	0.05	0.1153	0.0189	1.05E-09
rs138789716	A	G	0.95	-0.1143	0.0187	1.08E-09
rs6692816	A	G	0.06	0.1263	0.0207	1.08E-09
rs60425460	A	G	0.94	-0.121	0.0199	1.10E-09
rs73141301	A	G	0.06	0.1334	0.0219	1.20E-09
rs11204589	A	G	0.15	0.0726	0.0119	1.22E-09
rs73141297	C	G	0.94	-0.1331	0.0219	1.24E-09
rs12026307	T	C	0.05	0.114	0.0188	1.27E-09
rs7535770	A	C	0.05	0.1135	0.0188	1.47E-09
rs4474291	A	G	0.05	0.1134	0.0188	1.47E-09
rs12028480	A	G	0.94	-0.1178	0.0195	1.49E-09
rs73141286	T	C	0.95	-0.124	0.0205	1.53E-09
rs12033940	T	C	0.95	-0.1132	0.0187	1.54E-09
rs57237504	A	C	0.06	0.1244	0.0206	1.58E-09
rs73141283	A	G	0.95	-0.1236	0.0205	1.60E-09
rs73129418	A	G	0.06	0.1115	0.0185	1.65E-09
rs12026297	A	T	0.06	0.1172	0.0194	1.66E-09
rs6587419	T	G	0.14	0.0717	0.0119	1.71E-09
rs73141281	T	C	0.05	0.1231	0.0204	1.72E-09
rs10788751	A	G	0.16	0.0727	0.0121	1.77E-09
rs11204588	A	T	0.86	-0.0716	0.0119	1.78E-09
rs12043363	A	G	0.06	0.1163	0.0193	1.78E-09
rs11204587	A	C	0.14	0.0716	0.0119	1.79E-09
rs10788752	C	G	0.16	0.0726	0.0121	1.80E-09

rs12047499	A	G	0.06	0.116	0.0193	1.84E-09
rs74798649	T	C	0.05	0.1225	0.0204	1.86E-09
rs73141272	C	G	0.95	-0.122	0.0203	1.91E-09
rs10888311	C	G	0.14	0.0716	0.0119	1.99E-09
rs57684757	T	C	0.14	0.0724	0.0121	2.07E-09
rs75149475	A	G	0.95	-0.1232	0.0206	2.08E-09
rs41295946	A	G	0.06	0.1151	0.0192	2.13E-09
rs10788750	T	C	0.86	-0.0707	0.0118	2.26E-09
rs7527770	A	C	0.14	0.0702	0.0118	2.33E-09
rs73141225	T	C	0.06	0.1138	0.0191	2.49E-09
rs55937620	A	G	0.85	-0.0729	0.0122	2.60E-09
rs76530775	A	T	0.05	0.1136	0.0191	2.67E-09
rs12042804	A	C	0.05	0.1134	0.0191	2.69E-09
rs12562434	A	G	0.86	-0.0723	0.0121	2.69E-09
rs61856413	T	C	0.86	-0.0717	0.0121	2.77E-09
rs11204586	C	G	0.84	-0.0713	0.012	2.81E-09
rs73145253	T	C	0.14	0.0721	0.0121	2.85E-09
rs6658227	T	C	0.14	0.0717	0.0121	2.94E-09
rs12035071	T	G	0.05	0.1125	0.019	2.95E-09
rs59385443	A	G	0.86	-0.0718	0.0121	2.96E-09
rs74824567	A	G	0.95	-0.127	0.0214	2.98E-09
rs12035070	A	G	0.05	0.1123	0.0189	3.06E-09
rs12040091	T	C	0.95	-0.1123	0.0189	3.06E-09
rs111538251	C	G	0.05	0.1122	0.0189	3.10E-09
rs78951761	A	T	0.05	0.1267	0.0214	3.12E-09
rs10888313	C	G	0.95	-0.1121	0.0189	3.16E-09
rs6666048	T	C	0.86	-0.0716	0.0121	3.25E-09
rs12032193	T	C	0.05	0.1102	0.0186	3.35E-09
rs28687288	A	G	0.53	-0.0618	0.0105	3.47E-09
rs76289694	A	T	0.86	-0.0715	0.0121	3.77E-09
rs6703679	T	C	0.94	-0.1076	0.0183	3.87E-09
rs12029352	T	G	0.05	0.1102	0.0187	4.00E-09
rs12034735	T	C	0.05	0.1153	0.0196	4.02E-09
rs55893924	T	C	0.85	-0.0701	0.0119	4.28E-09
rs4146708	A	T	0.05	0.1099	0.0188	4.68E-09
rs28376879	A	T	0.53	-0.0609	0.0104	5.42E-09
rs4511156	T	C	0.15	0.0696	0.012	6.09E-09
rs149316915	A	G	0.86	-0.0749	0.0129	6.96E-09
rs115484985	T	C	0.04	0.1316	0.0228	7.70E-09
rs4614295	T	C	0.15	0.069	0.012	8.76E-09
rs188697725	T	C	0.05	0.1173	0.0204	9.06E-09
rs193191589	A	C	0.95	-0.1173	0.0204	9.08E-09
rs72763221	A	G	0.95	-0.1262	0.022	9.39E-09
rs4517381	A	T	0.88	-0.079	0.0138	1.11E-08
rs4501866	T	C	0.08	0.0893	0.0157	1.15E-08
rs6669478	A	G	0.08	0.0893	0.0157	1.15E-08
rs140976623	A	C	0.95	-0.1201	0.0211	1.23E-08
rs9435910	T	C	0.12	0.0791	0.0139	1.28E-08
rs6587415	T	C	0.86	-0.0702	0.0123	1.30E-08

rs7553764	A	C	0.88	-0.0789	0.0139	1.31E-08
rs145052285	T	C	0.05	0.12	0.0211	1.31E-08
rs12041993	T	G	0.92	-0.0891	0.0157	1.39E-08
rs73141280	T	C	0.12	0.0789	0.0139	1.39E-08
rs58722933	T	C	0.08	0.0889	0.0157	1.41E-08
rs6675835	A	C	0.92	-0.0888	0.0157	1.47E-08
rs28749860	A	G	0.12	0.0791	0.014	1.49E-08
rs3010199	T	C	0.09	0.0888	0.0157	1.50E-08
rs41295944	T	C	0.08	0.0881	0.0156	1.65E-08
rs10788756	A	G	0.85	-0.0683	0.0121	1.72E-08
rs7545169	A	T	0.08	0.0886	0.0157	1.80E-08
rs28837817	A	T	0.88	-0.0787	0.014	1.80E-08
rs7553029	A	T	0.91	-0.0892	0.0158	1.82E-08
rs3001301	A	G	0.85	-0.0681	0.0121	1.83E-08
rs12040974	A	C	0.08	0.0893	0.0159	1.85E-08
rs12042271	A	T	0.92	-0.0893	0.0159	1.86E-08
rs12038290	A	G	0.08	0.0893	0.0159	1.88E-08
rs12093163	A	G	0.86	-0.0694	0.0123	1.90E-08
rs116291302	T	C	0.92	-0.089	0.0159	2.03E-08
rs12037196	T	G	0.08	0.0893	0.0159	2.05E-08
rs6699753	C	G	0.85	-0.0683	0.0122	2.05E-08
rs9435907	A	G	0.15	0.0685	0.0122	2.05E-08
rs9435899	T	G	0.15	0.0676	0.0121	2.17E-08
rs12040557	A	G	0.92	-0.0889	0.0159	2.36E-08
rs12023592	T	C	0.95	-0.1336	0.0239	2.43E-08
rs59447628	A	G	0.08	0.089	0.016	2.56E-08
rs142728151	A	G	0.02	0.1854	0.0334	2.92E-08
rs10749643	T	C	0.82	-0.0683	0.0123	3.03E-08
rs61856398	T	C	0.87	-0.0688	0.0124	3.14E-08
rs6587416	A	G	0.87	-0.0687	0.0124	3.15E-08
rs61856399	A	G	0.13	0.0686	0.0124	3.41E-08
rs9435877	T	C	0.85	-0.0698	0.0126	3.47E-08
rs6684616	A	T	0.15	0.0693	0.0126	3.52E-08
rs6659253	T	C	0.85	-0.0698	0.0127	4.18E-08
rs9435912	T	G	0.85	-0.0694	0.0127	4.50E-08
rs6699713	T	C	0.15	0.0694	0.0127	4.74E-08
rs6655937	A	C	0.85	-0.0694	0.0127	4.78E-08
rs9435884	C	G	0.15	0.0704	0.0129	4.79E-08
rs11804999	A	C	0.14	0.0693	0.0127	4.80E-08
rs61856443	T	C	0.85	-0.0693	0.0127	4.90E-08
rs61856444	T	G	0.85	-0.0693	0.0127	4.91E-08
rs61856445	T	G	0.85	-0.0693	0.0127	4.91E-08
rs9435883	T	C	0.15	0.0693	0.0127	4.96E-08

Supplemental Table 2. Results of stepwise conditional analysis: SNPs that remain independently statistically significantly associated with asparagus anosmia after mutual adjustment

SNP	Locus	Reference Allele	Alt Allele	Frequency of Reference Allele	Marginal Beta	Marginal SE	Conditional Beta	Conditional SE	Number of SNPs in LD group**	Heterogeneity chi-square***	Heterogeneity p-value***
rs13373863	247994384	A	G	0.07	0.12	0.02	0.14	0.02	63	0.85	0.36
rs71538191	248306916	C	G	0.60	-0.16	0.01	-0.10	0.01	0	5.928	0.01
rs6689553	248313953	T	C	0.32	0.14	0.01	0.10	0.01	9	3.642	0.06

LD = linkage disequilibrium

*OR = Odds Ratio

**SNPs with $r^2 > 0.8$

***Cochran's Q for heterogeneity

Supplemental Table 3. Percentages of those who can and cannot smell the odor across genotypes for each of the three independent variants.

SNP	Genotype	Anosmic	Can Smell
rs13373863	AA	0.17	0.36
	AG	9.09	13.65
	GG	90.75	85.98
rs71538191	CC	53.39	38.62
	CG	41.01	50.56
	GG	5.60	10.81
rs6689553	TT	5.31	8.30
	TC	35.05	45.90
	CC	59.64	43.61

Supplemental Table 4. Missense SNPs associated with asparagus anosmia at genome-wide significance ($p < 5 \times 10^{-8}$)

SNP	Gene	Possible impact	Polyphen score	Reference Allele	Alt Allele	Marginal Beta	Marginal SE	Marginal p-value	Lead SNP and r^2
rs6658227	<i>OR2L3</i>	Probably damaging	0.97	T	C	0.07	0.01	2.94e-9	rs13373863 $r^2 = 0.29$
rs28545014	<i>OR14C36</i>	Probably damaging	1	T	G	-0.07	0.01	3.53e-12	rs71538191 $r^2 = 0.25$
rs7555310	<i>OR2M7</i>	Probably damaging	0.97	A	G	0.13	0.009	2.62 e-43	rs6689553 $r^2 = 0.80$
rs7555424	<i>OR2M7</i>	Possibly damaging	0.85	A	G	0.13	0.009	2.50 e-43	rs6689553 $r^2 = 0.80$

Supplemental Table 5: Genome-wide significant missense SNPs, VEP and Polyphen scores, and LD with the three lead SNPs identified in conditional analyses

SNP	A1	A2	b	se	p	VEP Score	Polyphen Score	LD rs13373863 (r ²)	LD rs71538191 (r ²)	LD rs6689553 (r ²)
rs28377739	A	G	-0.0717	0.0103	3.54E-12	benign(0)	0.002	0.0002	0.25	0.31
rs28545014	T	G	-0.0717	0.0103	3.53E-12	probably_damaging(0.95)	1.00	0.0002	0.25	0.31
rs28599722	A	G	0.0679	0.0106	1.31E-10	benign(0.001)	0	0.006	0.15	0.19
rs4244171	C	G	0.0589	0.0093	2.71E-10	benign(0.06)	0	0.04	0.08	0.08
rs4916104	T	C	0.0581	0.0094	5.69E-10	benign(0)	0	0.003	0.08	0.08
rs4916129	T	C	-0.0802	0.0091	1.70E-18	benign(0.232)	0.041	0.007	0.23	0.29
rs4916130	A	C	-0.1309	0.0095	3.37E-43	benign(0)	0	0.01	0.44	0.7
rs55937620	A	G	-0.0729	0.0122	2.60E-09	benign(0)	0	0.26	0.008	0.001
rs56834114	A	G	-0.0815	0.015	5.50E-08	benign(0.001)	----	0.17	0.01	0.006
rs6587467	T	G	0.0974	0.011	6.53E-19	benign(0)	0	0.0003	0.26	0.38
rs6658227	T	C	0.0717	0.0121	2.94E-09	probably_damaging(0.928)	0.969	0.29	0.007	0.0005
rs6658256	T	C	0.0867	0.0141	8.97E-10	benign(0)	0	0.25	0.004	0.0006
rs6666048	T	C	-0.0716	0.0121	3.25E-09	benign(0.001)	0	0.29	0.007	0.0003
rs6667171	A	C	-0.131	0.0101	1.37E-38	benign(0.092)	0.01	0.009	0.54	0.74
rs73141283	A	G	-0.1236	0.0205	1.60E-09	benign(0.077)	----	0.77	6.95E-05	0.005
rs7555310	A	G	0.1266	0.0092	2.62E-43	possibly_damaging(0.566)	0.969	0.01	0.53	0.8
rs7555424	A	G	0.1267	0.0092	2.50E-43	possibly_damaging(0.481)	0.85	0.01	0.52	0.8