Identifying optimal loci for the molecular diagnosis of microsatellite instability

Authors: Dustin R. Long, Adam Waalkes, Varun P. Panicker, Ronald J. Hause Jr., and Stephen J. Salipante

Supplemental Information

Contents:

Page 2: Supplemental Figure 1. Flowchart summarizing process for cataloging microsatellite instability events.

Page 3: Supplemental Figure 2. Relative burden of microsatellite instability events across cancer types, inferred from whole genome sequence data. Percentage of total microsatellite loci found to be mutated are reported per tumor specimen, as stratified by cancer type. Each point corresponds to an individual tumor, and its coloration indicates the corresponding MSI classification. TCGA abbreviations for cancer types are as described in the Table 1 footnote.

Pages 4-185: Supplemental Table 1. Inferred MSI diagnosis for tumors from exome sequencing.

Pages 186-203: Supplemental Table 2. Inferred MSI diagnosis for tumors from whole genome sequencing

Pages 204: Supplemental Table 3. Summary of inferred MSI diagnoses from whole genome sequencing

Pages 205-242: Supplemental Table 4. Microsatellites most informative for MSI per cancer type (p value)

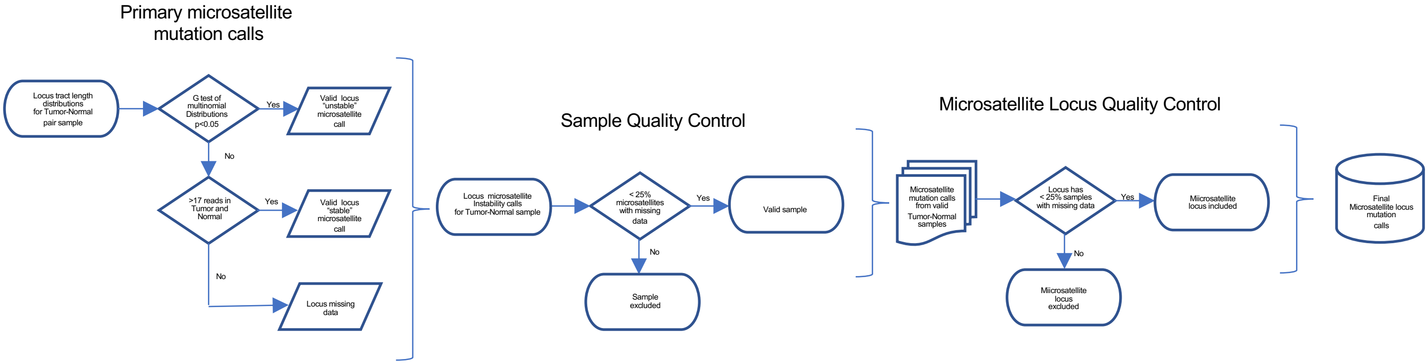
Page 243: Supplemental Table 5. Pairwise Euclidean dissimilarity matrix of tissue-specific informative microsatellite loci based on tissue-scaled p values

Page 244: Supplemental Table 6. Pairwise Cophenetic dissimilarity matrix of tissue-specific informative microsatellite loci based on tissue-scaled p values

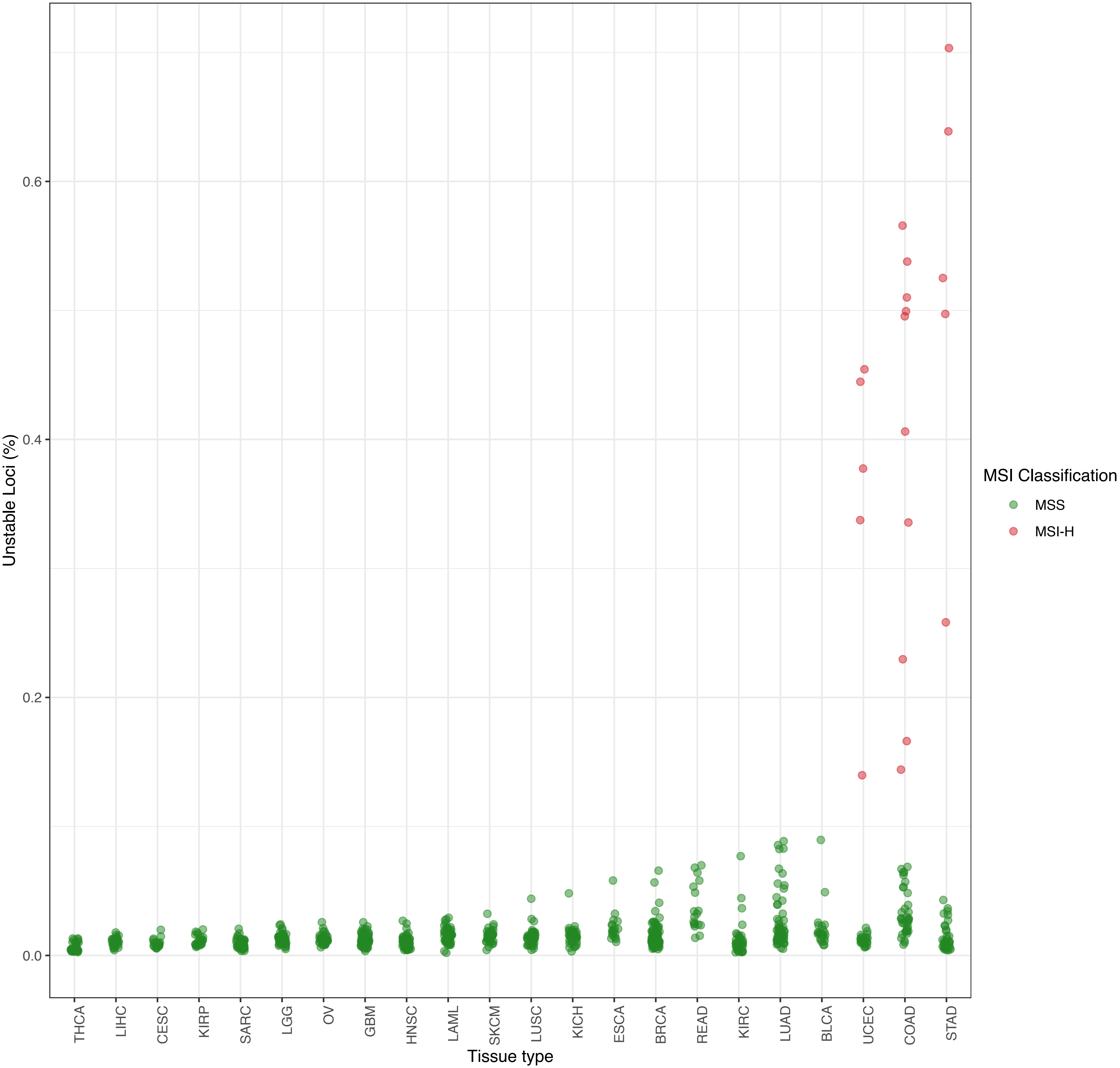
Page 245: Supplemental Table 7. Coordinates and p values of cross-informative microsatellites for diagnosing MSI in endometrial, colon, rectal, and stomach cancers

Page 246: Supplemental Table 8. Covariates associated with instability of MSI-informative microsatellites

Supplementary Figure 1



Supplementary Figure 2



Supplemental Table 1. Inferred MSI diagnosis for tumors from exome sequencing

TCGA ID	**MSI diagnosis**	**Cancer type**
TCGA-02-0003	MSS	GBM
TCGA-02-0033	MSS	GBM
TCGA-02-0047	MSS	GBM
TCGA-02-0055	MSS	GBM
TCGA-02-2466	MSS	GBM
TCGA-02-2470	MSI-H	GBM
TCGA-02-2483	MSS	GBM
TCGA-02-2485	MSS	GBM
TCGA-02-2486	MSS	GBM
TCGA-04-1331	MSS	OV
TCGA-04-1332	MSS	OV
TCGA-04-1336	MSS	OV
TCGA-04-1342	Intermediate	OV
TCGA-04-1343	MSS	OV
TCGA-04-1346	MSS	OV
TCGA-04-1347	MSS	OV
TCGA-04-1348	MSS	OV
TCGA-04-1349	MSS	OV
TCGA-04-1353	MSS	OV
TCGA-04-1356	MSS	OV
TCGA-04-1357	MSS	OV
TCGA-04-1361	MSS	OV
TCGA-04-1362	MSS	OV
TCGA-04-1367	MSS	OV
TCGA-04-1369	MSS	OV
TCGA-04-1516	MSS	OV
TCGA-04-1542	MSS	OV
TCGA-04-1638	MSS	OV
TCGA-04-1644	MSS	OV
TCGA-04-1646	Intermediate	OV
TCGA-04-1648	MSS	OV
TCGA-04-1649	MSS	OV
TCGA-04-1651	MSS	OV
TCGA-04-1652	Intermediate	OV
TCGA-04-1655	MSS	OV
TCGA-05-4244	MSS	LUAD
TCGA-05-4249	MSS	LUAD
TCGA-05-4250	MSS	LUAD
TCGA-05-4382	MSS	LUAD
TCGA-05-4384	MSS	LUAD
TCGA-05-4389	MSS	LUAD
TCGA-05-4390	MSS	LUAD
TCGA-05-4395	MSS	LUAD
TCGA-05-4396	MSS	LUAD
TCGA-05-4397	MSS	LUAD
TCGA-05-4398	MSS	LUAD
TCGA-05-4402	MSS	LUAD
TCGA-05-4403	MSS	LUAD
TCGA-05-4405	MSS	LUAD
TCGA-05-4410	MSS	LUAD

TCGA-05-4415	MSS	LUAD
TCGA-05-4417	MSS	LUAD
TCGA-05-4418	MSS	LUAD
TCGA-05-4420	MSS	LUAD
TCGA-05-4422	MSS	LUAD
TCGA-05-4424	MSS	LUAD
TCGA-05-4425	MSS	LUAD
TCGA-05-4426	MSS	LUAD
TCGA-05-4427	MSS	LUAD
TCGA-05-4430	MSS	LUAD
TCGA-05-4432	MSS	LUAD
TCGA-05-4433	MSS	LUAD
TCGA-05-4434	MSS	LUAD
TCGA-05-5420	MSS	LUAD
TCGA-05-5423	MSS	LUAD
TCGA-05-5425	MSS	LUAD
TCGA-05-5428	MSS	LUAD
TCGA-05-5429	MSS	LUAD
TCGA-05-5715	MSS	LUAD
TCGA-06-0119	MSS	GBM
TCGA-06-0122	MSS	GBM
TCGA-06-0124	MSS	GBM
TCGA-06-0125	MSI-H	GBM
TCGA-06-0125	MSS	GBM
TCGA-06-0126	MSS	GBM
TCGA-06-0128	MSS	GBM
TCGA-06-0129	MSS	GBM
TCGA-06-0130	MSS	GBM
TCGA-06-0132	MSS	GBM
TCGA-06-0137	MSS	GBM
TCGA-06-0139	MSS	GBM
TCGA-06-0140	MSS	GBM
TCGA-06-0141	MSS	GBM
TCGA-06-0142	MSS	GBM
TCGA-06-0145	MSS	GBM
TCGA-06-0151	MSS	GBM
TCGA-06-0152	MSS	GBM
TCGA-06-0154	MSS	GBM
TCGA-06-0155	MSS	GBM
TCGA-06-0156	MSS	GBM
TCGA-06-0157	MSS	GBM
TCGA-06-0158	MSS	GBM
TCGA-06-0165	MSS	GBM
TCGA-06-0166	MSS	GBM
TCGA-06-0167	MSS	GBM
TCGA-06-0168	MSS	GBM
TCGA-06-0169	MSS	GBM
TCGA-06-0171	MSI-H	GBM
TCGA-06-0171	MSS	GBM
TCGA-06-0173	MSS	GBM
TCGA-06-0174	Intermediate	GBM
TCGA-06-0176	MSS	GBM

TCGA-06-0178	MSS	GBM
TCGA-06-0184	MSS	GBM
TCGA-06-0185	MSS	GBM
TCGA-06-0187	MSI-H	GBM
TCGA-06-0188	MSS	GBM
TCGA-06-0189	MSS	GBM
TCGA-06-0190	MSS	GBM
TCGA-06-0190	MSI-H	GBM
TCGA-06-0192	MSS	GBM
TCGA-06-0195	MSS	GBM
TCGA-06-0209	MSS	GBM
TCGA-06-0210	MSS	GBM
TCGA-06-0210	MSI-H	GBM
TCGA-06-0211	MSS	GBM
TCGA-06-0213	MSS	GBM
TCGA-06-0214	MSS	GBM
TCGA-06-0216	MSS	GBM
TCGA-06-0219	MSS	GBM
TCGA-06-0221	MSI-H	GBM
TCGA-06-0221	MSS	GBM
TCGA-06-0237	MSS	GBM
TCGA-06-0238	MSS	GBM
TCGA-06-0240	MSS	GBM
TCGA-06-0241	MSS	GBM
TCGA-06-0644	MSS	GBM
TCGA-06-0645	MSS	GBM
TCGA-06-0646	MSS	GBM
TCGA-06-0648	MSS	GBM
TCGA-06-0649	MSS	GBM
TCGA-06-0650	MSS	GBM
TCGA-06-0686	MSS	GBM
TCGA-06-0743	MSS	GBM
TCGA-06-0744	MSS	GBM
TCGA-06-0745	MSS	GBM
TCGA-06-0747	MSS	GBM
TCGA-06-0749	MSS	GBM
TCGA-06-0750	MSS	GBM
TCGA-06-0875	MSS	GBM
TCGA-06-0876	MSS	GBM
TCGA-06-0877	MSS	GBM
TCGA-06-0878	MSS	GBM
TCGA-06-0879	MSS	GBM
TCGA-06-0881	MSS	GBM
TCGA-06-0882	MSS	GBM
TCGA-06-0939	MSS	GBM
TCGA-06-1084	MSS	GBM
TCGA-06-1087	MSS	GBM
TCGA-06-1800	MSS	GBM
TCGA-06-1804	MSS	GBM
TCGA-06-1806	MSS	GBM
TCGA-06-2557	MSS	GBM
TCGA-06-2558	MSS	GBM

TCGA-06-2559	MSS	GBM
TCGA-06-2561	Intermediate	GBM
TCGA-06-2562	MSS	GBM
TCGA-06-2563	MSI-H	GBM
TCGA-06-2564	MSS	GBM
TCGA-06-2565	MSS	GBM
TCGA-06-2566	MSS	GBM
TCGA-06-2567	MSS	GBM
TCGA-06-2569	MSS	GBM
TCGA-06-2570	MSS	GBM
TCGA-06-5408	MSS	GBM
TCGA-06-5410	MSS	GBM
TCGA-06-5411	MSS	GBM
TCGA-06-5412	MSS	GBM
TCGA-06-5413	MSS	GBM
TCGA-06-5414	MSS	GBM
TCGA-06-5415	MSS	GBM
TCGA-06-5416	MSS	GBM
TCGA-06-5417	MSS	GBM
TCGA-06-5418	MSS	GBM
TCGA-06-5856	MSS	GBM
TCGA-06-5858	MSS	GBM
TCGA-06-5859	MSS	GBM
TCGA-06-6388	MSS	GBM
TCGA-06-6389	MSS	GBM
TCGA-06-6390	MSS	GBM
TCGA-06-6391	MSS	GBM
TCGA-06-6693	MSS	GBM
TCGA-06-6694	MSS	GBM
TCGA-06-6695	MSS	GBM
TCGA-06-6697	MSS	GBM
TCGA-06-6698	MSS	GBM
TCGA-06-6699	MSS	GBM
TCGA-06-6700	MSS	GBM
TCGA-06-6701	MSS	GBM
TCGA-06-A5U0	MSS	GBM
TCGA-06-A5U1	MSS	GBM
TCGA-06-A6S0	MSS	GBM
TCGA-06-A6S1	MSS	GBM
TCGA-06-A7TK	MSS	GBM
TCGA-06-A7TL	MSS	GBM
TCGA-08-0386	MSS	GBM
TCGA-09-0365	MSS	OV
TCGA-09-0366	Intermediate	OV
TCGA-09-0369	MSS	OV
TCGA-09-1664	Intermediate	OV
TCGA-09-1670	MSS	OV
TCGA-09-1672	MSS	OV
TCGA-09-1673	MSS	OV
TCGA-09-1674	Intermediate	OV
TCGA-09-1675	MSS	OV
TCGA-09-2043	MSS	OV

TCGA-09-2044	MSS	OV
TCGA-09-2045	MSS	OV
TCGA-09-2049	MSS	OV
TCGA-09-2050	MSS	OV
TCGA-09-2051	MSS	OV
TCGA-09-2053	MSS	OV
TCGA-09-2055	MSS	OV
TCGA-09-2056	MSS	OV
TCGA-10-0930	MSS	OV
TCGA-10-0931	MSI-H	OV
TCGA-10-0933	MSS	OV
TCGA-10-0934	Intermediate	OV
TCGA-10-0935	Intermediate	OV
TCGA-12-0615	MSS	GBM
TCGA-12-0616	MSS	GBM
TCGA-12-0618	MSS	GBM
TCGA-12-0619	MSS	GBM
TCGA-12-0656	MSS	GBM
TCGA-12-0657	MSS	GBM
TCGA-12-0662	MSS	GBM
TCGA-12-0670	MSS	GBM
TCGA-12-0688	MSS	GBM
TCGA-12-0691	MSS	GBM
TCGA-12-0692	MSS	GBM
TCGA-12-0707	MSS	GBM
TCGA-12-0773	MSS	GBM
TCGA-12-0775	MSS	GBM
TCGA-12-0778	MSS	GBM
TCGA-12-0818	MSS	GBM
TCGA-12-0819	MSS	GBM
TCGA-12-0820	MSS	GBM
TCGA-12-0821	MSS	GBM
TCGA-12-0822	MSS	GBM
TCGA-12-0826	MSS	GBM
TCGA-12-0827	MSS	GBM
TCGA-12-0828	MSS	GBM
TCGA-12-1088	MSS	GBM
TCGA-12-1089	MSS	GBM
TCGA-12-1092	MSS	GBM
TCGA-12-1093	MSS	GBM
TCGA-12-1598	MSS	GBM
TCGA-12-1599	MSS	GBM
TCGA-12-1600	MSS	GBM
TCGA-12-1602	MSS	GBM
TCGA-12-3646	MSS	GBM
TCGA-12-3648	MSS	GBM
TCGA-12-3649	MSS	GBM
TCGA-12-3650	MSS	GBM
TCGA-12-3651	MSS	GBM
TCGA-12-3652	MSS	GBM
TCGA-12-3653	MSS	GBM
TCGA-12-5295	MSS	GBM

TCGA-12-5299	MSS	GBM
TCGA-12-5301	MSS	GBM
TCGA-13-0723	MSS	OV
TCGA-13-0724	Intermediate	OV
TCGA-13-0726	Intermediate	OV
TCGA-13-0751	Intermediate	OV
TCGA-13-0755	MSS	OV
TCGA-13-0760	MSS	OV
TCGA-13-0765	MSS	OV
TCGA-13-0791	MSS	OV
TCGA-13-0795	MSS	OV
TCGA-13-0800	MSS	OV
TCGA-13-0804	Intermediate	OV
TCGA-13-0807	MSS	OV
TCGA-13-0884	MSS	OV
TCGA-13-0885	Intermediate	OV
TCGA-13-0887	Intermediate	OV
TCGA-13-0888	MSS	OV
TCGA-13-0890	MSS	OV
TCGA-13-0893	MSS	OV
TCGA-13-0894	MSS	OV
TCGA-13-0897	MSS	OV
TCGA-13-0903	MSS	OV
TCGA-13-0905	MSS	OV
TCGA-13-0908	MSS	OV
TCGA-13-0910	MSS	OV
TCGA-13-0912	MSS	OV
TCGA-13-0920	MSS	OV
TCGA-13-0923	MSS	OV
TCGA-13-0924	Intermediate	OV
TCGA-13-1403	MSS	OV
TCGA-13-1404	MSS	OV
TCGA-13-1405	MSS	OV
TCGA-13-1409	MSS	OV
TCGA-13-1411	MSS	OV
TCGA-13-1412	MSS	OV
TCGA-13-1481	MSS	OV
TCGA-13-1482	MSS	OV
TCGA-13-1483	MSS	OV
TCGA-13-1484	MSS	OV
TCGA-13-1488	MSS	OV
TCGA-13-1491	MSS	OV
TCGA-13-1494	MSS	OV
TCGA-13-1495	MSS	OV
TCGA-13-1496	MSS	OV
TCGA-13-1497	MSS	OV
TCGA-13-1498	MSS	OV
TCGA-13-1499	MSS	OV
TCGA-13-1500	MSS	OV
TCGA-13-1501	MSS	OV
TCGA-13-1504	MSS	OV
TCGA-13-1506	MSS	OV

TCGA-13-1507	MSS	OV
TCGA-13-1509	MSS	OV
TCGA-13-1512	MSS	OV
TCGA-13-2057	MSS	OV
TCGA-13-2059	MSS	OV
TCGA-13-2060	MSS	OV
TCGA-13-2061	MSS	OV
TCGA-13-2065	MSS	OV
TCGA-13-2066	MSS	OV
TCGA-13-2071	MSS	OV
TCGA-13-A5FT	MSS	OV
TCGA-13-A5FU	MSS	OV
TCGA-14-0736	MSS	GBM
TCGA-14-0740	MSS	GBM
TCGA-14-0781	MSS	GBM
TCGA-14-0786	MSS	GBM
TCGA-14-0787	MSS	GBM
TCGA-14-0789	MSS	GBM
TCGA-14-0790	MSS	GBM
TCGA-14-0812	MSS	GBM
TCGA-14-0813	MSS	GBM
TCGA-14-0817	MSS	GBM
TCGA-14-0862	MSS	GBM
TCGA-14-0865	MSS	GBM
TCGA-14-0866	MSS	GBM
TCGA-14-0867	MSS	GBM
TCGA-14-0871	MSS	GBM
TCGA-14-1034	MSI-H	GBM
TCGA-14-1034	MSS	GBM
TCGA-14-1037	MSS	GBM
TCGA-14-1043	MSS	GBM
TCGA-14-1395	MSS	GBM
TCGA-14-1450	MSS	GBM
TCGA-14-1451	MSS	GBM
TCGA-14-1453	MSS	GBM
TCGA-14-1455	MSS	GBM
TCGA-14-1456	MSS	GBM
TCGA-14-1794	MSS	GBM
TCGA-14-1821	MSS	GBM
TCGA-14-1823	MSS	GBM
TCGA-14-1825	MSS	GBM
TCGA-14-1827	MSS	GBM
TCGA-14-1829	MSS	GBM
TCGA-14-2554	MSS	GBM
TCGA-14-3476	MSS	GBM
TCGA-14-4157	MSS	GBM
TCGA-15-0742	MSS	GBM
TCGA-15-1444	MSS	GBM
TCGA-16-0846	MSS	GBM
TCGA-16-0848	MSS	GBM
TCGA-16-0849	MSS	GBM
TCGA-16-0850	MSS	GBM

TCGA-16-0861	MSS	GBM
TCGA-16-1045	MSS	GBM
TCGA-16-1048	MSS	GBM
TCGA-16-1460	MSS	GBM
TCGA-17-Z000	MSS	LUAD
TCGA-17-Z001	MSS	LUAD
TCGA-17-Z002	MSS	LUAD
TCGA-17-Z003	MSS	LUAD
TCGA-17-Z004	MSS	LUAD
TCGA-17-Z005	MSS	LUAD
TCGA-17-Z007	Intermediate	LUAD
TCGA-17-Z009	MSS	LUAD
TCGA-17-Z010	MSS	LUAD
TCGA-17-Z011	MSS	LUAD
TCGA-17-Z013	MSS	LUAD
TCGA-17-Z014	MSS	LUAD
TCGA-17-Z015	MSS	LUAD
TCGA-17-Z016	Intermediate	LUAD
TCGA-17-Z017	MSS	LUAD
TCGA-17-Z018	MSS	LUAD
TCGA-17-Z019	MSS	LUAD
TCGA-17-Z020	MSS	LUAD
TCGA-17-Z022	MSI-H	LUAD
TCGA-17-Z023	MSS	LUAD
TCGA-17-Z025	Intermediate	LUAD
TCGA-17-Z026	MSS	LUAD
TCGA-17-Z027	MSS	LUAD
TCGA-17-Z028	MSS	LUAD
TCGA-17-Z030	MSS	LUAD
TCGA-17-Z031	MSS	LUAD
TCGA-17-Z032	Intermediate	LUAD
TCGA-17-Z033	MSS	LUAD
TCGA-17-Z036	MSI-H	LUAD
TCGA-17-Z037	MSS	LUAD
TCGA-17-Z041	MSS	LUAD
TCGA-17-Z042	MSS	LUAD
TCGA-17-Z043	MSS	LUAD
TCGA-17-Z044	MSS	LUAD
TCGA-17-Z045	MSS	LUAD
TCGA-17-Z047	MSS	LUAD
TCGA-17-Z048	MSS	LUAD
TCGA-17-Z049	MSS	LUAD
TCGA-17-Z050	MSS	LUAD
TCGA-17-Z051	MSS	LUAD
TCGA-17-Z052	MSS	LUAD
TCGA-17-Z053	MSS	LUAD
TCGA-17-Z054	MSS	LUAD
TCGA-17-Z055	MSS	LUAD
TCGA-17-Z056	MSS	LUAD
TCGA-17-Z057	MSS	LUAD
TCGA-17-Z058	MSS	LUAD
TCGA-17-Z059	MSS	LUAD

TCGA-17-Z060	MSS	LUAD
TCGA-17-Z061	MSS	LUAD
TCGA-17-Z062	MSS	LUAD
TCGA-18-3406	MSS	LUSC
TCGA-18-3407	MSS	LUSC
TCGA-18-3409	MSS	LUSC
TCGA-18-3410	MSS	LUSC
TCGA-18-3411	MSS	LUSC
TCGA-18-3412	MSS	LUSC
TCGA-18-3414	MSS	LUSC
TCGA-18-3415	MSS	LUSC
TCGA-18-3416	MSS	LUSC
TCGA-18-3417	MSS	LUSC
TCGA-18-3419	MSS	LUSC
TCGA-18-3421	MSS	LUSC
TCGA-18-4083	MSS	LUSC
TCGA-18-4086	MSS	LUSC
TCGA-18-4721	MSS	LUSC
TCGA-18-5592	MSS	LUSC
TCGA-18-5595	MSS	LUSC
TCGA-19-0957	MSS	GBM
TCGA-19-0957	MSI-H	GBM
TCGA-19-1387	MSS	GBM
TCGA-19-1389	Intermediate	GBM
TCGA-19-1786	MSS	GBM
TCGA-19-1787	Intermediate	GBM
TCGA-19-1789	MSS	GBM
TCGA-19-1790	MSS	GBM
TCGA-19-2620	MSS	GBM
TCGA-19-2624	MSS	GBM
TCGA-19-2629	MSS	GBM
TCGA-19-2631	MSS	GBM
TCGA-19-4065	MSS	GBM
TCGA-19-4068	MSS	GBM
TCGA-19-5947	MSS	GBM
TCGA-19-5950	MSS	GBM
TCGA-19-5951	MSS	GBM
TCGA-19-5952	MSS	GBM
TCGA-19-5953	MSS	GBM
TCGA-19-5954	MSS	GBM
TCGA-19-5955	MSS	GBM
TCGA-19-5956	MSS	GBM
TCGA-19-5958	MSS	GBM
TCGA-19-5959	MSS	GBM
TCGA-19-5960	MSS	GBM
TCGA-19-A60I	MSS	GBM
TCGA-19-A6J4	MSS	GBM
TCGA-19-A6J5	MSS	GBM
TCGA-20-0987	MSI-H	OV
TCGA-20-0990	MSS	OV
TCGA-20-0991	MSS	OV
TCGA-20-0996	MSS	OV

TCGA-20-1682	MSS	OV
TCGA-20-1683	MSS	OV
TCGA-20-1684	Intermediate	OV
TCGA-20-1685	MSS	OV
TCGA-20-1686	MSS	OV
TCGA-20-1687	MSS	OV
TCGA-21-1070	MSS	LUSC
TCGA-21-1071	MSS	LUSC
TCGA-21-1075	MSS	LUSC
TCGA-21-1076	MSI-H	LUSC
TCGA-21-1077	MSS	LUSC
TCGA-21-1078	MSS	LUSC
TCGA-21-1079	MSS	LUSC
TCGA-21-1080	MSI-H	LUSC
TCGA-21-1081	MSI-H	LUSC
TCGA-21-1082	MSS	LUSC
TCGA-21-1083	MSS	LUSC
TCGA-21-5782	MSS	LUSC
TCGA-21-5784	MSS	LUSC
TCGA-21-5786	MSS	LUSC
TCGA-21-5787	MSS	LUSC
TCGA-21-A5DI	MSS	LUSC
TCGA-22-0940	MSS	LUSC
TCGA-22-0944	MSS	LUSC
TCGA-22-1000	MSS	LUSC
TCGA-22-1002	MSS	LUSC
TCGA-22-1005	MSI-H	LUSC
TCGA-22-1011	MSI-H	LUSC
TCGA-22-1012	MSS	LUSC
TCGA-22-1016	MSS	LUSC
TCGA-22-4591	Intermediate	LUSC
TCGA-22-4593	MSS	LUSC
TCGA-22-4594	MSS	LUSC
TCGA-22-4595	MSS	LUSC
TCGA-22-4596	MSS	LUSC
TCGA-22-4599	MSS	LUSC
TCGA-22-4601	MSS	LUSC
TCGA-22-4604	MSS	LUSC
TCGA-22-4605	MSS	LUSC
TCGA-22-4607	MSS	LUSC
TCGA-22-4609	Intermediate	LUSC
TCGA-22-4613	MSS	LUSC
TCGA-22-5471	MSS	LUSC
TCGA-22-5472	MSS	LUSC
TCGA-22-5473	MSS	LUSC
TCGA-22-5474	MSS	LUSC
TCGA-22-5477	MSS	LUSC
TCGA-22-5478	MSS	LUSC
TCGA-22-5479	MSS	LUSC
TCGA-22-5480	MSS	LUSC
TCGA-22-5481	MSS	LUSC
TCGA-22-5482	MSS	LUSC

TCGA-22-5483	MSS	LUSC
TCGA-22-5485	MSS	LUSC
TCGA-22-5489	MSS	LUSC
TCGA-22-5491	MSS	LUSC
TCGA-22-5492	MSS	LUSC
TCGA-22-A5C4	MSS	LUSC
TCGA-23-1021	MSS	OV
TCGA-23-1022	MSS	OV
TCGA-23-1027	Intermediate	OV
TCGA-23-1029	MSS	OV
TCGA-23-1030	MSS	OV
TCGA-23-1031	MSS	OV
TCGA-23-1032	MSS	OV
TCGA-23-1110	MSS	OV
TCGA-23-1111	MSS	OV
TCGA-23-1113	MSS	OV
TCGA-23-1114	MSS	OV
TCGA-23-1116	MSS	OV
TCGA-23-1117	MSS	OV
TCGA-23-1118	MSS	OV
TCGA-23-1121	MSS	OV
TCGA-23-1122	MSS	OV
TCGA-23-1123	MSS	OV
TCGA-23-1124	MSS	OV
TCGA-23-1809	MSS	OV
TCGA-23-2072	MSS	OV
TCGA-23-2077	MSS	OV
TCGA-23-2078	MSS	OV
TCGA-23-2079	MSS	OV
TCGA-23-2081	MSI-H	OV
TCGA-23-2641	MSS	OV
TCGA-23-2643	MSS	OV
TCGA-23-2645	MSS	OV
TCGA-23-2647	MSS	OV
TCGA-23-2649	MSS	OV
TCGA-24-0966	MSS	OV
TCGA-24-0970	MSS	OV
TCGA-24-0975	MSS	OV
TCGA-24-0979	Intermediate	OV
TCGA-24-0980	Intermediate	OV
TCGA-24-0982	Intermediate	OV
TCGA-24-1103	MSS	OV
TCGA-24-1104	MSS	OV
TCGA-24-1413	MSS	OV
TCGA-24-1416	MSS	OV
TCGA-24-1417	MSS	OV
TCGA-24-1418	MSS	OV
TCGA-24-1419	MSS	OV
TCGA-24-1422	MSS	OV
TCGA-24-1423	MSS	OV
TCGA-24-1424	MSS	OV
TCGA-24-1425	MSS	OV

TCGA-24-1426	MSS	OV
TCGA-24-1427	MSS	OV
TCGA-24-1428	MSS	OV
TCGA-24-1430	MSS	OV
TCGA-24-1431	MSS	OV
TCGA-24-1434	MSS	OV
TCGA-24-1435	MSS	OV
TCGA-24-1436	MSS	OV
TCGA-24-1463	MSS	OV
TCGA-24-1464	MSS	OV
TCGA-24-1469	MSS	OV
TCGA-24-1470	MSS	OV
TCGA-24-1471	MSS	OV
TCGA-24-1474	MSS	OV
TCGA-24-1549	MSS	OV
TCGA-24-1551	MSS	OV
TCGA-24-1552	MSS	OV
TCGA-24-1562	MSS	OV
TCGA-24-1563	MSS	OV
TCGA-24-1564	MSS	OV
TCGA-24-1565	MSS	OV
TCGA-24-1603	MSS	OV
TCGA-24-1616	MSS	OV
TCGA-24-1842	MSS	OV
TCGA-24-1843	MSS	OV
TCGA-24-1844	MSS	OV
TCGA-24-1845	MSS	OV
TCGA-24-1846	MSS	OV
TCGA-24-1847	MSS	OV
TCGA-24-1849	MSS	OV
TCGA-24-1850	MSS	OV
TCGA-24-1927	MSI-H	OV
TCGA-24-2019	MSS	OV
TCGA-24-2024	Intermediate	OV
TCGA-24-2030	Intermediate	OV
TCGA-24-2033	MSS	OV
TCGA-24-2035	MSI-H	OV
TCGA-24-2038	MSS	OV
TCGA-24-2254	MSI-H	OV
TCGA-24-2260	MSS	OV
TCGA-24-2261	MSS	OV
TCGA-24-2262	MSS	OV
TCGA-24-2267	MSS	OV
TCGA-24-2271	MSS	OV
TCGA-24-2280	MSS	OV
TCGA-24-2281	MSS	OV
TCGA-24-2288	MSS	OV
TCGA-24-2289	MSS	OV
TCGA-24-2290	MSS	OV
TCGA-24-2293	MSS	OV
TCGA-24-2295	MSS	OV
TCGA-24-2298	MSS	OV

TCGA-25-1313	Intermediate	OV
TCGA-25-1314	MSS	OV
TCGA-25-1315	MSS	OV
TCGA-25-1316	MSS	OV
TCGA-25-1319	MSS	OV
TCGA-25-1320	MSI-H	OV
TCGA-25-1321	MSS	OV
TCGA-25-1322	MSS	OV
TCGA-25-1323	Intermediate	OV
TCGA-25-1326	Intermediate	OV
TCGA-25-1328	MSS	OV
TCGA-25-1329	Intermediate	OV
TCGA-25-2042	MSS	OV
TCGA-25-2391	MSS	OV
TCGA-25-2392	MSS	OV
TCGA-25-2393	MSS	OV
TCGA-25-2396	MSS	OV
TCGA-25-2397	MSS	OV
TCGA-25-2398	MSS	OV
TCGA-25-2399	MSS	OV
TCGA-25-2400	MSS	OV
TCGA-25-2401	MSS	OV
TCGA-25-2404	MSS	OV
TCGA-25-2408	MSS	OV
TCGA-25-2409	MSS	OV
TCGA-26-1439	MSS	GBM
TCGA-26-1442	MSS	GBM
TCGA-26-5132	MSS	GBM
TCGA-26-5133	MSS	GBM
TCGA-26-5134	MSS	GBM
TCGA-26-5135	MSS	GBM
TCGA-26-5136	MSS	GBM
TCGA-26-5139	MSS	GBM
TCGA-26-6173	MSS	GBM
TCGA-26-6174	MSS	GBM
TCGA-26-A7UX	MSS	GBM
TCGA-27-1830	MSS	GBM
TCGA-27-1831	MSI-H	GBM
TCGA-27-1832	MSS	GBM
TCGA-27-1833	MSS	GBM
TCGA-27-1834	MSS	GBM
TCGA-27-1835	MSS	GBM
TCGA-27-1836	MSS	GBM
TCGA-27-1837	MSS	GBM
TCGA-27-1838	MSI-H	GBM
TCGA-27-2518	MSS	GBM
TCGA-27-2519	MSS	GBM
TCGA-27-2521	MSS	GBM
TCGA-27-2523	MSS	GBM
TCGA-27-2524	MSS	GBM
TCGA-27-2526	MSS	GBM
TCGA-27-2527	MSS	GBM

TCGA-27-2528	MSS	GBM
TCGA-28-1746	MSS	GBM
TCGA-28-1747	MSS	GBM
TCGA-28-1749	MSS	GBM
TCGA-28-1752	MSS	GBM
TCGA-28-1753	MSI-H	GBM
TCGA-28-1755	MSS	GBM
TCGA-28-2499	MSS	GBM
TCGA-28-2501	MSS	GBM
TCGA-28-2502	MSS	GBM
TCGA-28-2506	MSS	GBM
TCGA-28-2509	MSS	GBM
TCGA-28-2510	MSS	GBM
TCGA-28-2513	MSI-H	GBM
TCGA-28-2514	MSS	GBM
TCGA-28-5204	MSS	GBM
TCGA-28-5207	MSS	GBM
TCGA-28-5208	MSS	GBM
TCGA-28-5209	MSS	GBM
TCGA-28-5211	MSS	GBM
TCGA-28-5213	MSS	GBM
TCGA-28-5214	MSS	GBM
TCGA-28-5215	MSS	GBM
TCGA-28-5216	MSS	GBM
TCGA-28-5218	MSS	GBM
TCGA-28-5219	MSS	GBM
TCGA-28-5220	MSS	GBM
TCGA-28-6450	MSS	GBM
TCGA-29-1688	MSI-H	OV
TCGA-29-1690	MSI-H	OV
TCGA-29-1691	MSS	OV
TCGA-29-1693	Intermediate	OV
TCGA-29-1694	MSI-H	OV
TCGA-29-1695	MSS	OV
TCGA-29-1696	MSS	OV
TCGA-29-1697	MSS	OV
TCGA-29-1698	MSS	OV
TCGA-29-1699	MSS	OV
TCGA-29-1701	MSS	OV
TCGA-29-1702	MSS	OV
TCGA-29-1703	MSS	OV
TCGA-29-1705	MSS	OV
TCGA-29-1707	MSS	OV
TCGA-29-1710	Intermediate	OV
TCGA-29-1711	MSS	OV
TCGA-29-1761	MSS	OV
TCGA-29-1762	MSS	OV
TCGA-29-1763	MSS	OV
TCGA-29-1764	MSS	OV
TCGA-29-1766	Intermediate	OV
TCGA-29-1768	MSS	OV
TCGA-29-1769	MSS	OV

TCGA-29-1770	MSS	OV
TCGA-29-1771	MSS	OV
TCGA-29-1774	MSS	OV
TCGA-29-1775	MSS	OV
TCGA-29-1776	MSS	OV
TCGA-29-1777	MSS	OV
TCGA-29-1778	MSS	OV
TCGA-29-1781	Intermediate	OV
TCGA-29-1783	MSS	OV
TCGA-29-1784	MSS	OV
TCGA-29-1785	MSS	OV
TCGA-29-2427	MSS	OV
TCGA-29-2429	MSS	OV
TCGA-29-2431	MSS	OV
TCGA-29-2432	MSS	OV
TCGA-29-2434	MSS	OV
TCGA-29-2436	MSS	OV
TCGA-29-A5NZ	MSS	OV
TCGA-2A-A8VL	MSS	PRAD
TCGA-2A-A8VO	MSS	PRAD
TCGA-2A-A8VT	MSS	PRAD
TCGA-2A-A8VV	MSS	PRAD
TCGA-2A-A8VX	MSS	PRAD
TCGA-2A-A8W1	MSS	PRAD
TCGA-2A-A8W3	MSS	PRAD
TCGA-2A-AAYF	MSS	PRAD
TCGA-2A-AAYO	MSS	PRAD
TCGA-2A-AAYU	MSS	PRAD
TCGA-2E-A9G8	MSS	UCEC
TCGA-2F-A9KO	MSS	BLCA
TCGA-2F-A9KP	MSS	BLCA
TCGA-2F-A9KQ	MSS	BLCA
TCGA-2F-A9KR	MSS	BLCA
TCGA-2F-A9KT	MSS	BLCA
TCGA-2F-A9KW	MSS	BLCA
TCGA-2G-AAEW	MSS	TGCT
TCGA-2G-AAEX	MSS	TGCT
TCGA-2G-AAF1	MSS	TGCT
TCGA-2G-AAF4	MSS	TGCT
TCGA-2G-AAF6	MSS	TGCT
TCGA-2G-AAF8	MSS	TGCT
TCGA-2G-AAFE	MSS	TGCT
TCGA-2G-AAFG	MSS	TGCT
TCGA-2G-AAFG	MSS	TGCT
TCGA-2G-AAFH	MSS	TGCT
TCGA-2G-AAFI	MSS	TGCT
TCGA-2G-AAFJ	MSS	TGCT
TCGA-2G-AAFL	MSS	TGCT
TCGA-2G-AAFM	MSS	TGCT
TCGA-2G-AAFN	MSS	TGCT
TCGA-2G-AAFO	MSS	TGCT
TCGA-2G-AAFV	MSS	TGCT

TCGA-2G-AAFY	MSS	TGCT
TCGA-2G-AAFZ	MSS	TGCT
TCGA-2G-AAG0	MSS	TGCT
TCGA-2G-AAG3	MSS	TGCT
TCGA-2G-AAG5	MSS	TGCT
TCGA-2G-AAG6	MSS	TGCT
TCGA-2G-AAG7	MSS	TGCT
TCGA-2G-AAG8	MSS	TGCT
TCGA-2G-AAG9	MSS	TGCT
TCGA-2G-AAGA	MSS	TGCT
TCGA-2G-AAGC	MSS	TGCT
TCGA-2G-AAGE	MSS	TGCT
TCGA-2G-AAGF	MSS	TGCT
TCGA-2G-AAGG	MSS	TGCT
TCGA-2G-AAGI	MSS	TGCT
TCGA-2G-AAGI	MSS	TGCT
TCGA-2G-AAGJ	MSS	TGCT
TCGA-2G-AAGK	MSS	TGCT
TCGA-2G-AAGM	MSS	TGCT
TCGA-2G-AAGN	MSS	TGCT
TCGA-2G-AAGO	MSS	TGCT
TCGA-2G-AAGP	MSS	TGCT
TCGA-2G-AAGS	MSS	TGCT
TCGA-2G-AAGT	MSS	TGCT
TCGA-2G-AAGV	MSS	TGCT
TCGA-2G-AAGW	MSS	TGCT
TCGA-2G-AAGX	MSS	TGCT
TCGA-2G-AAGY	MSS	TGCT
TCGA-2G-AAGY	MSS	TGCT
TCGA-2G-AAGZ	MSS	TGCT
TCGA-2G-AAH0	MSS	TGCT
TCGA-2G-AAH2	MSS	TGCT
TCGA-2G-AAH3	MSS	TGCT
TCGA-2G-AAH4	MSS	TGCT
TCGA-2G-AAH8	MSS	TGCT
TCGA-2G-AAHA	MSS	TGCT
TCGA-2G-AAHC	MSS	TGCT
TCGA-2G-AAHG	MSS	TGCT
TCGA-2G-AAHL	MSS	TGCT
TCGA-2G-AAHN	MSS	TGCT
TCGA-2G-AAHP	MSS	TGCT
TCGA-2G-AAHP	MSS	TGCT
TCGA-2G-AAHT	MSS	TGCT
TCGA-2G-AAKD	MSS	TGCT
TCGA-2G-AAKG	MSS	TGCT
TCGA-2G-AAKG	MSS	TGCT
TCGA-2G-AAKH	MSS	TGCT
TCGA-2G-AAKL	MSS	TGCT
TCGA-2G-AAKM	MSS	TGCT
TCGA-2G-AAKO	MSS	TGCT
TCGA-2G-AAKO	MSS	TGCT
TCGA-2G-AAL5	MSS	TGCT

TCGA-2G-AAL7	MSS	TGCT
TCGA-2G-AALF	MSS	TGCT
TCGA-2G-AALG	MSS	TGCT
TCGA-2G-AALN	MSS	TGCT
TCGA-2G-AALO	MSS	TGCT
TCGA-2G-AALP	MSS	TGCT
TCGA-2G-AALQ	MSS	TGCT
TCGA-2G-AALR	MSS	TGCT
TCGA-2G-AALS	MSS	TGCT
TCGA-2G-AALT	MSS	TGCT
TCGA-2G-AALW	MSS	TGCT
TCGA-2G-AALX	MSS	TGCT
TCGA-2G-AALY	MSS	TGCT
TCGA-2G-AALZ	MSS	TGCT
TCGA-2G-AAM2	MSS	TGCT
TCGA-2G-AAM3	MSS	TGCT
TCGA-2G-AAM4	MSS	TGCT
TCGA-2H-A9GF	MSS	ESCA
TCGA-2H-A9GH	MSS	ESCA
TCGA-2H-A9GI	MSS	ESCA
TCGA-2H-A9GJ	MSS	ESCA
TCGA-2H-A9GK	MSS	ESCA
TCGA-2H-A9GL	MSS	ESCA
TCGA-2H-A9GM	MSS	ESCA
TCGA-2H-A9GN	MSS	ESCA
TCGA-2H-A9GO	MSS	ESCA
TCGA-2H-A9GQ	MSS	ESCA
TCGA-2H-A9GR	MSS	ESCA
TCGA-2J-AAB1	MSS	PAAD
TCGA-2J-AAB4	MSS	PAAD
TCGA-2J-AAB6	MSS	PAAD
TCGA-2J-AAB8	MSS	PAAD
TCGA-2J-AAB9	MSS	PAAD
TCGA-2J-AABA	MSS	PAAD
TCGA-2J-AABE	MSS	PAAD
TCGA-2J-AABF	MSS	PAAD
TCGA-2J-AABH	MSS	PAAD
TCGA-2J-AABI	MSS	PAAD
TCGA-2J-AABK	MSS	PAAD
TCGA-2J-AABO	MSS	PAAD
TCGA-2J-AABP	MSS	PAAD
TCGA-2J-AABR	MSS	PAAD
TCGA-2J-AABT	MSS	PAAD
TCGA-2J-AABV	MSS	PAAD
TCGA-2K-A9WE	MSS	KIRP
TCGA-2L-AAQA	MSS	PAAD
TCGA-2L-AAQE	MSS	PAAD
TCGA-2L-AAQI	MSS	PAAD
TCGA-2L-AAQJ	MSS	PAAD
TCGA-2L-AAQL	MSS	PAAD
TCGA-2L-AAQM	MSS	PAAD
TCGA-2V-A95S	MSS	LIHC

TCGA-2W-A8YY	MSI-H	CESC
TCGA-2X-A9D5	MSS	TGCT
TCGA-2X-A9D6	MSS	TGCT
TCGA-2Y-A9GS	MSS	LIHC
TCGA-2Y-A9GT	MSS	LIHC
TCGA-2Y-A9GU	MSS	LIHC
TCGA-2Y-A9GV	MSS	LIHC
TCGA-2Y-A9GW	MSS	LIHC
TCGA-2Y-A9GX	MSS	LIHC
TCGA-2Y-A9GY	MSS	LIHC
TCGA-2Y-A9GZ	MSS	LIHC
TCGA-2Y-A9H0	MSS	LIHC
TCGA-2Y-A9H1	MSS	LIHC
TCGA-2Y-A9H2	MSS	LIHC
TCGA-2Y-A9H3	MSS	LIHC
TCGA-2Y-A9H4	MSS	LIHC
TCGA-2Y-A9H5	MSS	LIHC
TCGA-2Y-A9H6	MSS	LIHC
TCGA-2Y-A9H7	MSS	LIHC
TCGA-2Y-A9H8	MSS	LIHC
TCGA-2Y-A9H9	MSS	LIHC
TCGA-2Y-A9HA	MSS	LIHC
TCGA-2Y-A9HB	MSS	LIHC
TCGA-2Z-A9J1	MSS	KIRP
TCGA-2Z-A9J2	MSS	KIRP
TCGA-2Z-A9J3	MSS	KIRP
TCGA-2Z-A9J5	MSS	KIRP
TCGA-2Z-A9J6	MSS	KIRP
TCGA-2Z-A9J7	MSS	KIRP
TCGA-2Z-A9J8	MSS	KIRP
TCGA-2Z-A9J9	MSS	KIRP
TCGA-2Z-A9JD	MSS	KIRP
TCGA-2Z-A9JE	MSS	KIRP
TCGA-2Z-A9JG	MSS	KIRP
TCGA-2Z-A9JI	MSS	KIRP
TCGA-2Z-A9JJ	MSS	KIRP
TCGA-2Z-A9JK	MSS	KIRP
TCGA-2Z-A9JL	MSS	KIRP
TCGA-2Z-A9JM	MSS	KIRP
TCGA-2Z-A9JN	MSS	KIRP
TCGA-2Z-A9JO	MSS	KIRP
TCGA-2Z-A9JP	MSS	KIRP
TCGA-2Z-A9JQ	MSS	KIRP
TCGA-2Z-A9JR	MSS	KIRP
TCGA-2Z-A9JS	MSS	KIRP
TCGA-2Z-A9JT	MSS	KIRP
TCGA-30-1714	MSS	OV
TCGA-30-1718	MSS	OV
TCGA-30-1853	Intermediate	OV
TCGA-30-1855	Intermediate	OV
TCGA-30-1856	MSS	OV
TCGA-30-1857	MSS	OV

TCGA-30-1862	MSI-H	OV
TCGA-30-1891	MSS	OV
TCGA-31-1950	MSI-H	OV
TCGA-31-1953	MSI-H	OV
TCGA-31-1959	MSI-H	OV
TCGA-32-1970	MSS	GBM
TCGA-32-1976	MSS	GBM
TCGA-32-1977	MSS	GBM
TCGA-32-1979	MSS	GBM
TCGA-32-1980	MSS	GBM
TCGA-32-1982	MSS	GBM
TCGA-32-1986	MSS	GBM
TCGA-32-1991	MSS	GBM
TCGA-32-2491	MSS	GBM
TCGA-32-2494	MSS	GBM
TCGA-32-2495	MSS	GBM
TCGA-32-2615	MSS	GBM
TCGA-32-2616	MSS	GBM
TCGA-32-2634	MSS	GBM
TCGA-32-4208	MSS	GBM
TCGA-32-4209	MSS	GBM
TCGA-32-4210	MSS	GBM
TCGA-32-4211	MSS	GBM
TCGA-32-4213	MSS	GBM
TCGA-32-4719	MSS	GBM
TCGA-32-5222	MSS	GBM
TCGA-33-4532	MSS	LUSC
TCGA-33-4533	MSS	LUSC
TCGA-33-4538	MSS	LUSC
TCGA-33-4547	MSS	LUSC
TCGA-33-4566	MSS	LUSC
TCGA-33-4582	MSS	LUSC
TCGA-33-4583	MSS	LUSC
TCGA-33-4586	MSS	LUSC
TCGA-33-4587	MSS	LUSC
TCGA-33-4589	MSS	LUSC
TCGA-33-6737	MSS	LUSC
TCGA-33-6738	MSS	LUSC
TCGA-33-A4WN	MSS	LUSC
TCGA-33-A5GW	MSS	LUSC
TCGA-33-AAS8	MSS	LUSC
TCGA-33-AASB	MSS	LUSC
TCGA-33-AASD	MSS	LUSC
TCGA-33-AASI	MSS	LUSC
TCGA-33-AASJ	MSS	LUSC
TCGA-33-AASL	MSS	LUSC
TCGA-34-2596	MSI-H	LUSC
TCGA-34-2600	MSS	LUSC
TCGA-34-2604	MSS	LUSC
TCGA-34-2605	MSS	LUSC
TCGA-34-2608	MSS	LUSC
TCGA-34-5231	MSS	LUSC

TCGA-34-5232	MSS	LUSC
TCGA-34-5234	MSS	LUSC
TCGA-34-5236	MSS	LUSC
TCGA-34-5239	MSS	LUSC
TCGA-34-5240	MSS	LUSC
TCGA-34-5241	MSS	LUSC
TCGA-34-5927	MSS	LUSC
TCGA-34-5928	MSS	LUSC
TCGA-34-5929	MSS	LUSC
TCGA-34-7107	MSS	LUSC
TCGA-34-8454	MSS	LUSC
TCGA-34-8455	MSS	LUSC
TCGA-34-8456	MSS	LUSC
TCGA-34-A5IX	MSS	LUSC
TCGA-35-3615	MSS	LUAD
TCGA-35-4122	MSS	LUAD
TCGA-35-4123	MSS	LUAD
TCGA-35-5375	MSS	LUAD
TCGA-36-2530	MSS	OV
TCGA-36-2532	MSS	OV
TCGA-36-2533	MSS	OV
TCGA-36-2534	MSS	OV
TCGA-36-2537	MSS	OV
TCGA-36-2538	MSS	OV
TCGA-36-2539	MSS	OV
TCGA-36-2540	MSS	OV
TCGA-36-2542	MSS	OV
TCGA-36-2543	MSS	OV
TCGA-36-2544	MSS	OV
TCGA-36-2545	MSS	OV
TCGA-36-2547	MSS	OV
TCGA-36-2548	MSS	OV
TCGA-36-2551	MSS	OV
TCGA-36-2552	MSS	OV
TCGA-37-3783	MSS	LUSC
TCGA-37-3789	MSS	LUSC
TCGA-37-3792	MSS	LUSC
TCGA-37-4129	MSS	LUSC
TCGA-37-4130	MSS	LUSC
TCGA-37-4132	MSS	LUSC
TCGA-37-4133	MSS	LUSC
TCGA-37-4135	MSS	LUSC
TCGA-37-4141	MSS	LUSC
TCGA-37-5819	MSS	LUSC
TCGA-37-A5EL	MSS	LUSC
TCGA-37-A5EM	MSS	LUSC
TCGA-37-A5EN	MSS	LUSC
TCGA-38-4625	MSS	LUAD
TCGA-38-4626	MSS	LUAD
TCGA-38-4627	MSS	LUAD
TCGA-38-4628	MSS	LUAD
TCGA-38-4629	MSS	LUAD

TCGA-38-4630	MSS	LUAD
TCGA-38-4631	MSS	LUAD
TCGA-38-4632	MSS	LUAD
TCGA-38-6178	MSS	LUAD
TCGA-38-A44F	MSS	LUAD
TCGA-39-5011	MSS	LUSC
TCGA-39-5016	MSS	LUSC
TCGA-39-5019	MSS	LUSC
TCGA-39-5021	MSS	LUSC
TCGA-39-5022	MSS	LUSC
TCGA-39-5024	MSS	LUSC
TCGA-39-5027	MSS	LUSC
TCGA-39-5028	MSS	LUSC
TCGA-39-5029	MSS	LUSC
TCGA-39-5030	MSS	LUSC
TCGA-39-5031	MSS	LUSC
TCGA-39-5034	MSS	LUSC
TCGA-39-5035	MSS	LUSC
TCGA-39-5036	MSS	LUSC
TCGA-39-5037	MSS	LUSC
TCGA-39-5039	MSS	LUSC
TCGA-39-5040	MSS	LUSC
TCGA-3A-A9I5	MSS	PAAD
TCGA-3A-A9I7	MSS	PAAD
TCGA-3A-A9I9	MSS	PAAD
TCGA-3A-A9IB	MSS	PAAD
TCGA-3A-A9IC	MSS	PAAD
TCGA-3A-A9IH	MSS	PAAD
TCGA-3A-A9IJ	MSS	PAAD
TCGA-3A-A9IL	MSS	PAAD
TCGA-3A-A9IN	MSS	PAAD
TCGA-3A-A9IO	MSS	PAAD
TCGA-3A-A9IR	MSS	PAAD
TCGA-3A-A9IS	MSS	PAAD
TCGA-3A-A9IU	MSS	PAAD
TCGA-3A-A9IV	MSS	PAAD
TCGA-3A-A9IX	MSS	PAAD
TCGA-3A-A9IZ	MSS	PAAD
TCGA-3A-A9J0	MSS	PAAD
TCGA-3B-A9HI	MSS	SARC
TCGA-3B-A9HJ	MSS	SARC
TCGA-3B-A9HO	MSS	SARC
TCGA-3B-A9HP	MSS	SARC
TCGA-3B-A9HQ	MSS	SARC
TCGA-3B-A9HR	MSS	SARC
TCGA-3B-A9HS	MSS	SARC
TCGA-3B-A9HT	Intermediate	SARC
TCGA-3B-A9HU	MSS	SARC
TCGA-3B-A9HV	MSS	SARC
TCGA-3B-A9HX	MSS	SARC
TCGA-3B-A9HY	MSS	SARC
TCGA-3B-A9HZ	MSS	SARC

TCGA-3B-A9I0	MSS	SARC
TCGA-3B-A9I1	MSS	SARC
TCGA-3B-A9I3	MSS	SARC
TCGA-3C-AAAU	MSS	BRCA
TCGA-3C-AALI	MSS	BRCA
TCGA-3C-AALJ	MSS	BRCA
TCGA-3C-AALK	MSS	BRCA
TCGA-3E-AAAY	MSS	PAAD
TCGA-3E-AAAZ	MSS	PAAD
TCGA-3G-AB0O	MSS	THYM
TCGA-3G-AB0Q	MSS	THYM
TCGA-3G-AB0T	MSS	THYM
TCGA-3G-AB14	MSS	THYM
TCGA-3G-AB19	MSS	THYM
TCGA-3H-AB3M	MSS	MESO
TCGA-3H-AB3S	MSS	MESO
TCGA-3H-AB3T	MSS	MESO
TCGA-3K-AAZ8	MSS	LIHC
TCGA-3L-AA1B	MSS	COAD
TCGA-3M-AB46	MSS	STAD
TCGA-3M-AB47	MSS	STAD
TCGA-3N-A9WB	MSS	SKCM
TCGA-3N-A9WC	MSS	SKCM
TCGA-3N-A9WD	MSS	SKCM
TCGA-3P-A9WA	MSS	OV
TCGA-3Q-A9WF	MSS	THYM
TCGA-3R-A8YX	MSS	SARC
TCGA-3S-A8YW	MSS	THYM
TCGA-3S-AAYX	MSS	THYM
TCGA-3T-AA9L	MSS	THYM
TCGA-3U-A98D	MSS	MESO
TCGA-3U-A98G	MSS	MESO
TCGA-3U-A98I	MSS	MESO
TCGA-3X-AAV9	MSS	CHOL
TCGA-3X-AAVA	MSS	CHOL
TCGA-3X-AAVB	MSS	CHOL
TCGA-3X-AAVC	MSS	CHOL
TCGA-3X-AAVE	MSS	CHOL
TCGA-3Z-A93Z	MSS	KIRC
TCGA-41-2571	MSS	GBM
TCGA-41-2572	MSS	GBM
TCGA-41-2573	MSS	GBM
TCGA-41-3392	MSS	GBM
TCGA-41-3393	MSS	GBM
TCGA-41-3915	MSS	GBM
TCGA-41-4097	MSS	GBM
TCGA-41-5651	MSS	GBM
TCGA-41-6646	MSS	GBM
TCGA-42-2582	MSS	OV
TCGA-42-2587	MSS	OV
TCGA-42-2588	MSS	OV
TCGA-42-2590	MSS	OV

TCGA-42-2591	MSS	OV
TCGA-42-2593	MSS	OV
TCGA-43-2576	MSS	LUSC
TCGA-43-2578	MSI-H	LUSC
TCGA-43-2581	MSS	LUSC
TCGA-43-3394	MSS	LUSC
TCGA-43-3920	MSS	LUSC
TCGA-43-5668	MSS	LUSC
TCGA-43-5670	MSS	LUSC
TCGA-43-6143	MSS	LUSC
TCGA-43-6647	MSS	LUSC
TCGA-43-6770	MSS	LUSC
TCGA-43-6771	MSS	LUSC
TCGA-43-6773	MSS	LUSC
TCGA-43-7656	MSS	LUSC
TCGA-43-7657	MSS	LUSC
TCGA-43-7658	MSS	LUSC
TCGA-43-8118	MSS	LUSC
TCGA-43-A474	MSS	LUSC
TCGA-43-A475	MSS	LUSC
TCGA-43-A56U	MSS	LUSC
TCGA-43-A56V	MSS	LUSC
TCGA-44-2655	MSS	LUAD
TCGA-44-2656	MSS	LUAD
TCGA-44-2656	MSS	LUAD
TCGA-44-2657	MSS	LUAD
TCGA-44-2659	MSS	LUAD
TCGA-44-2661	MSS	LUAD
TCGA-44-2662	MSS	LUAD
TCGA-44-2662	Intermediate	LUAD
TCGA-44-2665	Intermediate	LUAD
TCGA-44-2665	MSI-H	LUAD
TCGA-44-2666	MSS	LUAD
TCGA-44-2666	MSS	LUAD
TCGA-44-2668	Intermediate	LUAD
TCGA-44-2668	MSS	LUAD
TCGA-44-3396	MSS	LUAD
TCGA-44-3398	MSS	LUAD
TCGA-44-3917	MSS	LUAD
TCGA-44-3917	MSS	LUAD
TCGA-44-3918	MSS	LUAD
TCGA-44-3918	MSS	LUAD
TCGA-44-3919	MSS	LUAD
TCGA-44-4112	MSS	LUAD
TCGA-44-4112	MSI-H	LUAD
TCGA-44-5643	MSS	LUAD
TCGA-44-5644	MSS	LUAD
TCGA-44-5645	MSS	LUAD
TCGA-44-5645	MSS	LUAD
TCGA-44-6144	MSS	LUAD
TCGA-44-6145	MSS	LUAD
TCGA-44-6146	MSS	LUAD

TCGA-44-6146	MSS	LUAD
TCGA-44-6147	MSS	LUAD
TCGA-44-6147	MSS	LUAD
TCGA-44-6148	MSS	LUAD
TCGA-44-6774	MSS	LUAD
TCGA-44-6775	MSS	LUAD
TCGA-44-6775	MSS	LUAD
TCGA-44-6776	MSS	LUAD
TCGA-44-6777	MSS	LUAD
TCGA-44-6778	MSS	LUAD
TCGA-44-6779	MSS	LUAD
TCGA-44-7659	MSS	LUAD
TCGA-44-7660	MSS	LUAD
TCGA-44-7661	MSS	LUAD
TCGA-44-7662	MSS	LUAD
TCGA-44-7667	MSS	LUAD
TCGA-44-7669	MSS	LUAD
TCGA-44-7670	MSS	LUAD
TCGA-44-7671	MSS	LUAD
TCGA-44-7672	MSS	LUAD
TCGA-44-8117	MSS	LUAD
TCGA-44-A479	MSS	LUAD
TCGA-44-A47A	MSS	LUAD
TCGA-44-A47B	MSS	LUAD
TCGA-44-A47F	MSS	LUAD
TCGA-44-A47G	MSS	LUAD
TCGA-44-A4SS	MSS	LUAD
TCGA-44-A4SU	MSS	LUAD
TCGA-46-3765	MSS	LUSC
TCGA-46-3766	MSS	LUSC
TCGA-46-3767	MSS	LUSC
TCGA-46-3768	MSS	LUSC
TCGA-46-3769	MSS	LUSC
TCGA-46-6025	MSS	LUSC
TCGA-46-6026	MSS	LUSC
TCGA-49-4486	MSS	LUAD
TCGA-49-4487	MSS	LUAD
TCGA-49-4488	MSS	LUAD
TCGA-49-4490	MSS	LUAD
TCGA-49-4494	MSS	LUAD
TCGA-49-4501	MSS	LUAD
TCGA-49-4505	MSS	LUAD
TCGA-49-4506	MSS	LUAD
TCGA-49-4507	MSS	LUAD
TCGA-49-4510	MSS	LUAD
TCGA-49-4512	MSS	LUAD
TCGA-49-4514	MSS	LUAD
TCGA-49-6742	MSS	LUAD
TCGA-49-6743	MSS	LUAD
TCGA-49-6744	MSS	LUAD
TCGA-49-6745	MSS	LUAD
TCGA-49-6761	MSS	LUAD

TCGA-49-6767	MSS	LUAD
TCGA-49-AAQV	MSS	LUAD
TCGA-49-AAR0	MSS	LUAD
TCGA-49-AAR2	MSS	LUAD
TCGA-49-AAR3	MSS	LUAD
TCGA-49-AAR4	MSS	LUAD
TCGA-49-AAR9	MSS	LUAD
TCGA-49-AARE	MSS	LUAD
TCGA-49-AARN	MSS	LUAD
TCGA-49-AARO	MSS	LUAD
TCGA-49-AARQ	MSS	LUAD
TCGA-49-AARR	MSS	LUAD
TCGA-4A-A93W	MSS	KIRP
TCGA-4A-A93X	MSS	KIRP
TCGA-4A-A93Y	MSS	KIRP
TCGA-4B-A93V	MSS	LUAD
TCGA-4C-A93U	MSS	THCA
TCGA-4E-A92E	MSS	UCEC
TCGA-4G-AAZF	MSS	CHOL
TCGA-4G-AAZG	MSS	CHOL
TCGA-4G-AAZO	MSS	CHOL
TCGA-4G-AAZR	MSS	CHOL
TCGA-4G-AAZT	MSS	CHOL
TCGA-4H-AAAK	MSS	BRCA
TCGA-4J-AA1J	MSS	CESC
TCGA-4K-AA1G	MSS	TGCT
TCGA-4K-AA1H	MSS	TGCT
TCGA-4K-AA1I	MSS	TGCT
TCGA-4K-AAAL	MSS	TGCT
TCGA-4L-AA1F	MSS	PRAD
TCGA-4N-A93T	MSS	COAD
TCGA-4P-AA8J	MSS	HNSC
TCGA-4R-AA8I	MSI-H	LIHC
TCGA-4T-AA8H	MSS	COAD
TCGA-4V-A9QI	MSS	THYM
TCGA-4V-A9QJ	MSS	THYM
TCGA-4V-A9QL	MSS	THYM
TCGA-4V-A9QM	MSS	THYM
TCGA-4V-A9QN	MSS	THYM
TCGA-4V-A9QQ	MSS	THYM
TCGA-4V-A9QR	MSS	THYM
TCGA-4V-A9QS	MSS	THYM
TCGA-4V-A9QT	MSS	THYM
TCGA-4V-A9QU	MSS	THYM
TCGA-4V-A9QW	MSS	THYM
TCGA-4V-A9QX	MSS	THYM
TCGA-4W-AA9R	MSS	GBM
TCGA-4W-AA9S	MSS	GBM
TCGA-4W-AA9T	MSS	GBM
TCGA-4X-A9F9	MSS	THYM
TCGA-4X-A9FA	MSS	THYM
TCGA-4X-A9FB	MSS	THYM

TCGA-4X-A9FC	MSS	THYM
TCGA-4X-A9FD	MSS	THYM
TCGA-4Z-AA7M	MSS	BLCA
TCGA-4Z-AA7N	MSS	BLCA
TCGA-4Z-AA7O	MSS	BLCA
TCGA-4Z-AA7Q	MSS	BLCA
TCGA-4Z-AA7R	MSS	BLCA
TCGA-4Z-AA7S	MSS	BLCA
TCGA-4Z-AA7W	MSS	BLCA
TCGA-4Z-AA7Y	MSS	BLCA
TCGA-4Z-AA80	MSS	BLCA
TCGA-4Z-AA81	MSS	BLCA
TCGA-4Z-AA82	MSS	BLCA
TCGA-4Z-AA83	MSS	BLCA
TCGA-4Z-AA84	MSS	BLCA
TCGA-4Z-AA86	MSS	BLCA
TCGA-4Z-AA87	MSS	BLCA
TCGA-4Z-AA89	MSS	BLCA
TCGA-50-5044	MSS	LUAD
TCGA-50-5045	MSS	LUAD
TCGA-50-5049	MSS	LUAD
TCGA-50-5051	MSS	LUAD
TCGA-50-5055	MSS	LUAD
TCGA-50-5066	MSS	LUAD
TCGA-50-5068	MSS	LUAD
TCGA-50-5072	MSS	LUAD
TCGA-50-5930	MSS	LUAD
TCGA-50-5931	MSS	LUAD
TCGA-50-5932	MSS	LUAD
TCGA-50-5933	MSS	LUAD
TCGA-50-5935	MSS	LUAD
TCGA-50-5936	MSS	LUAD
TCGA-50-5939	MSS	LUAD
TCGA-50-5941	MSS	LUAD
TCGA-50-5942	MSS	LUAD
TCGA-50-5944	MSS	LUAD
TCGA-50-5946	MSS	LUAD
TCGA-50-5946	MSI-H	LUAD
TCGA-50-6590	MSS	LUAD
TCGA-50-6591	MSS	LUAD
TCGA-50-6592	MSS	LUAD
TCGA-50-6593	MSS	LUAD
TCGA-50-6594	MSS	LUAD
TCGA-50-6595	MSS	LUAD
TCGA-50-6597	MSS	LUAD
TCGA-50-6673	MSS	LUAD
TCGA-50-7109	MSS	LUAD
TCGA-50-8457	MSS	LUAD
TCGA-50-8459	MSS	LUAD
TCGA-50-8460	MSS	LUAD
TCGA-51-4079	MSS	LUSC
TCGA-51-4080	MSS	LUSC

TCGA-51-4081	MSS	LUSC
TCGA-51-6867	MSS	LUSC
TCGA-52-7622	MSS	LUSC
TCGA-52-7809	MSS	LUSC
TCGA-52-7810	MSS	LUSC
TCGA-52-7811	MSS	LUSC
TCGA-52-7812	MSS	LUSC
TCGA-53-7624	MSS	LUAD
TCGA-53-7626	MSS	LUAD
TCGA-53-A4EZ	MSS	LUAD
TCGA-55-1592	MSS	LUAD
TCGA-55-1594	MSS	LUAD
TCGA-55-1595	MSS	LUAD
TCGA-55-1596	MSS	LUAD
TCGA-55-5899	MSS	LUAD
TCGA-55-6543	MSS	LUAD
TCGA-55-6642	MSS	LUAD
TCGA-55-6712	MSS	LUAD
TCGA-55-6968	MSS	LUAD
TCGA-55-6969	MSS	LUAD
TCGA-55-6970	MSS	LUAD
TCGA-55-6971	MSS	LUAD
TCGA-55-6972	MSS	LUAD
TCGA-55-6975	MSS	LUAD
TCGA-55-6978	MSS	LUAD
TCGA-55-6979	MSS	LUAD
TCGA-55-6980	MSS	LUAD
TCGA-55-6981	MSS	LUAD
TCGA-55-6982	MSS	LUAD
TCGA-55-6983	MSS	LUAD
TCGA-55-6984	MSS	LUAD
TCGA-55-6985	MSS	LUAD
TCGA-55-6986	MSS	LUAD
TCGA-55-6987	MSS	LUAD
TCGA-55-7227	MSS	LUAD
TCGA-55-7281	MSS	LUAD
TCGA-55-7283	MSS	LUAD
TCGA-55-7284	MSS	LUAD
TCGA-55-7570	MSS	LUAD
TCGA-55-7573	MSS	LUAD
TCGA-55-7574	MSS	LUAD
TCGA-55-7576	MSS	LUAD
TCGA-55-7724	MSS	LUAD
TCGA-55-7728	MSS	LUAD
TCGA-55-7815	MSS	LUAD
TCGA-55-7994	MSS	LUAD
TCGA-55-7995	MSS	LUAD
TCGA-55-8089	MSS	LUAD
TCGA-55-8091	MSS	LUAD
TCGA-55-8092	MSS	LUAD
TCGA-55-8096	MSS	LUAD
TCGA-55-8097	MSS	LUAD

TCGA-55-8204	MSS	LUAD
TCGA-55-8205	MSS	LUAD
TCGA-55-8206	MSS	LUAD
TCGA-55-8207	MSS	LUAD
TCGA-55-8299	MSS	LUAD
TCGA-55-8301	MSS	LUAD
TCGA-55-8302	MSS	LUAD
TCGA-55-8505	MSS	LUAD
TCGA-55-8506	MSI-H	LUAD
TCGA-55-8507	MSS	LUAD
TCGA-55-8508	MSS	LUAD
TCGA-55-8510	MSS	LUAD
TCGA-55-8511	MSS	LUAD
TCGA-55-8512	MSS	LUAD
TCGA-55-8513	MSS	LUAD
TCGA-55-8514	MSS	LUAD
TCGA-55-8614	MSS	LUAD
TCGA-55-8615	MSS	LUAD
TCGA-55-8616	MSS	LUAD
TCGA-55-8619	MSS	LUAD
TCGA-55-8620	MSS	LUAD
TCGA-55-8621	MSS	LUAD
TCGA-55-A48X	MSS	LUAD
TCGA-55-A48Y	MSS	LUAD
TCGA-55-A48Z	MSS	LUAD
TCGA-55-A490	MSS	LUAD
TCGA-55-A491	MSS	LUAD
TCGA-55-A492	MSS	LUAD
TCGA-55-A493	MSS	LUAD
TCGA-55-A494	MSS	LUAD
TCGA-55-A4DF	MSS	LUAD
TCGA-55-A4DG	MSS	LUAD
TCGA-55-A57B	MSS	LUAD
TCGA-56-1622	MSS	LUSC
TCGA-56-5897	MSS	LUSC
TCGA-56-5898	MSS	LUSC
TCGA-56-6545	MSS	LUSC
TCGA-56-6546	MSS	LUSC
TCGA-56-7221	MSS	LUSC
TCGA-56-7222	MSS	LUSC
TCGA-56-7223	MSS	LUSC
TCGA-56-7579	MSS	LUSC
TCGA-56-7580	MSS	LUSC
TCGA-56-7582	MSS	LUSC
TCGA-56-7730	MSS	LUSC
TCGA-56-7731	MSS	LUSC
TCGA-56-7822	MSS	LUSC
TCGA-56-8304	MSS	LUSC
TCGA-56-8305	MSS	LUSC
TCGA-56-8307	MSS	LUSC
TCGA-56-8308	MSS	LUSC
TCGA-56-8309	MSS	LUSC

TCGA-56-8503	MSS	LUSC
TCGA-56-8504	MSS	LUSC
TCGA-56-8622	MSS	LUSC
TCGA-56-8623	MSS	LUSC
TCGA-56-8624	MSS	LUSC
TCGA-56-8625	MSS	LUSC
TCGA-56-8626	MSS	LUSC
TCGA-56-8628	MSS	LUSC
TCGA-56-8629	MSS	LUSC
TCGA-56-A49D	MSS	LUSC
TCGA-56-A4BW	MSS	LUSC
TCGA-56-A4BX	MSS	LUSC
TCGA-56-A4BY	MSS	LUSC
TCGA-56-A4ZJ	MSS	LUSC
TCGA-56-A4ZK	MSS	LUSC
TCGA-56-A5DR	MSS	LUSC
TCGA-56-A5DS	MSS	LUSC
TCGA-56-A62T	MSS	LUSC
TCGA-57-1586	MSS	OV
TCGA-57-1992	Intermediate	OV
TCGA-57-1993	MSS	OV
TCGA-58-8386	MSS	LUSC
TCGA-58-8387	MSS	LUSC
TCGA-58-8388	MSS	LUSC
TCGA-58-8390	MSS	LUSC
TCGA-58-8391	MSS	LUSC
TCGA-58-8392	MSS	LUSC
TCGA-58-8393	MSS	LUSC
TCGA-58-A46J	MSS	LUSC
TCGA-58-A46K	MSS	LUSC
TCGA-58-A46L	MSS	LUSC
TCGA-58-A46M	MSS	LUSC
TCGA-58-A46N	MSS	LUSC
TCGA-59-2348	MSS	OV
TCGA-59-2349	MSI-H	OV
TCGA-59-2350	MSS	OV
TCGA-59-2351	MSS	OV
TCGA-59-2352	MSS	OV
TCGA-59-2354	MSS	OV
TCGA-59-2355	MSS	OV
TCGA-59-2363	MSS	OV
TCGA-59-2372	MSS	OV
TCGA-59-A5PD	MSS	OV
TCGA-5A-A8ZF	MSS	CHOL
TCGA-5A-A8ZG	MSS	CHOL
TCGA-5B-A90C	MSS	UCEC
TCGA-5C-A9VG	MSS	LIHC
TCGA-5C-A9VH	MSS	LIHC
TCGA-5C-AAPD	MSS	LIHC
TCGA-5G-A9ZZ	MSS	THYM
TCGA-5K-AAAP	MSS	THYM
TCGA-5L-AAT0	MSS	BRCA

TCGA-5L-AAT1	MSS	BRCA
TCGA-5M-AAT4	MSS	COAD
TCGA-5M-AAT5	MSS	COAD
TCGA-5M-AAT6	MSI-H	COAD
TCGA-5M-AATA	MSS	COAD
TCGA-5M-AATE	MSS	COAD
TCGA-5N-A9KI	MSS	BLCA
TCGA-5N-A9KM	MSS	BLCA
TCGA-5P-A9JU	MSS	KIRP
TCGA-5P-A9JV	MSS	KIRP
TCGA-5P-A9JW	MSS	KIRP
TCGA-5P-A9JY	MSS	KIRP
TCGA-5P-A9JZ	MSS	KIRP
TCGA-5P-A9K0	MSS	KIRP
TCGA-5P-A9K2	MSS	KIRP
TCGA-5P-A9K3	MSS	KIRP
TCGA-5P-A9K4	MSS	KIRP
TCGA-5P-A9K6	MSS	KIRP
TCGA-5P-A9K8	MSS	KIRP
TCGA-5P-A9K9	MSS	KIRP
TCGA-5P-A9KA	MSS	KIRP
TCGA-5P-A9KC	MSS	KIRP
TCGA-5P-A9KE	MSS	KIRP
TCGA-5P-A9KH	MSS	KIRP
TCGA-5R-AA1C	MSS	LIHC
TCGA-5R-AA1D	MSS	LIHC
TCGA-5R-AAAM	MSS	LIHC
TCGA-5S-A9Q8	MSS	UCEC
TCGA-5T-A9QA	MSS	BRCA
TCGA-5U-AB0D	MSS	THYM
TCGA-5U-AB0E	MSS	THYM
TCGA-5U-AB0F	MSS	THYM
TCGA-5V-A9RR	MSS	THYM
TCGA-5X-AA5U	MSS	OV
TCGA-60-2695	MSS	LUSC
TCGA-60-2697	MSS	LUSC
TCGA-60-2698	MSS	LUSC
TCGA-60-2703	MSS	LUSC
TCGA-60-2704	MSS	LUSC
TCGA-60-2707	MSS	LUSC
TCGA-60-2708	MSS	LUSC
TCGA-60-2709	MSS	LUSC
TCGA-60-2710	MSS	LUSC
TCGA-60-2711	MSS	LUSC
TCGA-60-2712	MSS	LUSC
TCGA-60-2713	MSS	LUSC
TCGA-60-2714	MSS	LUSC
TCGA-60-2715	MSS	LUSC
TCGA-60-2716	MSS	LUSC
TCGA-60-2719	MSI-H	LUSC
TCGA-60-2720	MSS	LUSC
TCGA-60-2721	MSS	LUSC

TCGA-60-2722	MSS	LUSC
TCGA-60-2723	MSS	LUSC
TCGA-60-2724	MSS	LUSC
TCGA-60-2725	MSS	LUSC
TCGA-60-2726	MSS	LUSC
TCGA-61-1722	MSS	OV
TCGA-61-1725	Intermediate	OV
TCGA-61-1727	MSS	OV
TCGA-61-1728	MSI-H	OV
TCGA-61-1730	MSI-H	OV
TCGA-61-1733	MSS	OV
TCGA-61-1734	MSS	OV
TCGA-61-1736	MSS	OV
TCGA-61-1737	MSS	OV
TCGA-61-1738	MSS	OV
TCGA-61-1740	MSS	OV
TCGA-61-1741	MSS	OV
TCGA-61-1895	MSS	OV
TCGA-61-1899	MSS	OV
TCGA-61-1900	MSS	OV
TCGA-61-1901	MSS	OV
TCGA-61-1903	MSS	OV
TCGA-61-1904	MSS	OV
TCGA-61-1906	MSS	OV
TCGA-61-1907	MSS	OV
TCGA-61-1910	MSS	OV
TCGA-61-1911	MSS	OV
TCGA-61-1913	MSS	OV
TCGA-61-1914	MSS	OV
TCGA-61-1915	MSS	OV
TCGA-61-1919	MSI-H	OV
TCGA-61-1995	MSS	OV
TCGA-61-1998	MSS	OV
TCGA-61-2000	MSS	OV
TCGA-61-2002	MSS	OV
TCGA-61-2003	MSS	OV
TCGA-61-2012	MSS	OV
TCGA-61-2016	MSS	OV
TCGA-61-2018	MSS	OV
TCGA-61-2087	MSS	OV
TCGA-61-2088	MSS	OV
TCGA-61-2092	MSS	OV
TCGA-61-2094	MSS	OV
TCGA-61-2095	MSS	OV
TCGA-61-2096	MSS	OV
TCGA-61-2097	MSS	OV
TCGA-61-2101	MSS	OV
TCGA-61-2102	MSS	OV
TCGA-61-2104	MSS	OV
TCGA-61-2109	MSS	OV
TCGA-61-2110	MSS	OV
TCGA-61-2111	MSS	OV

TCGA-61-2113	MSS	OV
TCGA-61-2610	MSS	OV
TCGA-61-2611	MSS	OV
TCGA-61-2612	MSS	OV
TCGA-61-2613	MSS	OV
TCGA-61-2614	MSS	OV
TCGA-62-8394	MSS	LUAD
TCGA-62-8395	MSS	LUAD
TCGA-62-8397	MSS	LUAD
TCGA-62-8398	MSS	LUAD
TCGA-62-8399	MSS	LUAD
TCGA-62-8402	MSS	LUAD
TCGA-62-A46O	MSS	LUAD
TCGA-62-A46P	MSS	LUAD
TCGA-62-A46R	MSS	LUAD
TCGA-62-A46S	MSS	LUAD
TCGA-62-A46U	MSS	LUAD
TCGA-62-A46V	MSS	LUAD
TCGA-62-A46Y	MSS	LUAD
TCGA-62-A470	MSS	LUAD
TCGA-62-A471	MSS	LUAD
TCGA-62-A472	MSS	LUAD
TCGA-63-5128	MSS	LUSC
TCGA-63-5131	MSS	LUSC
TCGA-63-6202	MSS	LUSC
TCGA-63-7020	MSS	LUSC
TCGA-63-7021	MSS	LUSC
TCGA-63-7022	MSS	LUSC
TCGA-63-7023	MSS	LUSC
TCGA-63-A5M9	MSS	LUSC
TCGA-63-A5MB	MSS	LUSC
TCGA-63-A5MG	MSS	LUSC
TCGA-63-A5MH	MSS	LUSC
TCGA-63-A5MI	MSS	LUSC
TCGA-63-A5MJ	MSS	LUSC
TCGA-63-A5ML	MSS	LUSC
TCGA-63-A5MM	MSI-H	LUSC
TCGA-63-A5MN	MSS	LUSC
TCGA-63-A5MP	MSS	LUSC
TCGA-63-A5MR	MSS	LUSC
TCGA-63-A5MS	MSS	LUSC
TCGA-63-A5MT	MSS	LUSC
TCGA-63-A5MU	MSS	LUSC
TCGA-63-A5MV	MSS	LUSC
TCGA-63-A5MW	MSS	LUSC
TCGA-63-A5MY	MSS	LUSC
TCGA-64-1676	MSS	LUAD
TCGA-64-1677	MSS	LUAD
TCGA-64-1678	MSI-H	LUAD
TCGA-64-1679	MSS	LUAD
TCGA-64-1680	MSS	LUAD
TCGA-64-1681	MSS	LUAD

TCGA-64-5774	MSS	LUAD
TCGA-64-5775	MSS	LUAD
TCGA-64-5778	MSS	LUAD
TCGA-64-5779	MSS	LUAD
TCGA-64-5781	MSS	LUAD
TCGA-64-5815	MSS	LUAD
TCGA-66-2727	MSS	LUSC
TCGA-66-2734	MSS	LUSC
TCGA-66-2742	MSS	LUSC
TCGA-66-2744	MSS	LUSC
TCGA-66-2754	MSS	LUSC
TCGA-66-2755	MSS	LUSC
TCGA-66-2756	MSS	LUSC
TCGA-66-2757	MSS	LUSC
TCGA-66-2758	MSS	LUSC
TCGA-66-2759	MSS	LUSC
TCGA-66-2763	MSI-H	LUSC
TCGA-66-2765	MSS	LUSC
TCGA-66-2766	MSS	LUSC
TCGA-66-2767	MSS	LUSC
TCGA-66-2768	MSI-H	LUSC
TCGA-66-2769	MSS	LUSC
TCGA-66-2770	MSS	LUSC
TCGA-66-2771	MSS	LUSC
TCGA-66-2773	MSS	LUSC
TCGA-66-2777	MSS	LUSC
TCGA-66-2778	MSS	LUSC
TCGA-66-2780	MSS	LUSC
TCGA-66-2781	MSS	LUSC
TCGA-66-2782	MSS	LUSC
TCGA-66-2783	MSS	LUSC
TCGA-66-2785	MSS	LUSC
TCGA-66-2786	MSS	LUSC
TCGA-66-2787	MSS	LUSC
TCGA-66-2788	MSS	LUSC
TCGA-66-2789	MSS	LUSC
TCGA-66-2791	MSS	LUSC
TCGA-66-2792	MSS	LUSC
TCGA-66-2793	Intermediate	LUSC
TCGA-66-2794	MSS	LUSC
TCGA-66-2795	MSS	LUSC
TCGA-66-2800	MSS	LUSC
TCGA-67-3770	MSS	LUAD
TCGA-67-3771	MSI-H	LUAD
TCGA-67-3772	MSS	LUAD
TCGA-67-3773	MSS	LUAD
TCGA-67-3774	MSS	LUAD
TCGA-67-4679	MSS	LUAD
TCGA-67-6215	MSS	LUAD
TCGA-67-6216	MSS	LUAD
TCGA-67-6217	MSS	LUAD
TCGA-68-7755	MSS	LUSC

TCGA-68-7756	MSS	LUSC
TCGA-68-7757	MSS	LUSC
TCGA-68-8250	MSS	LUSC
TCGA-68-8251	MSS	LUSC
TCGA-68-A59J	MSS	LUSC
TCGA-69-7764	MSS	LUAD
TCGA-69-7973	MSS	LUAD
TCGA-69-7974	MSS	LUAD
TCGA-69-7978	MSS	LUAD
TCGA-69-7979	MSS	LUAD
TCGA-69-7980	MSS	LUAD
TCGA-69-8253	MSS	LUAD
TCGA-69-8254	MSS	LUAD
TCGA-69-8255	MSS	LUAD
TCGA-69-A59K	MSS	LUAD
TCGA-6A-AB49	MSS	LUSC
TCGA-6D-AA2E	MSS	KIRC
TCGA-70-6722	MSS	LUSC
TCGA-70-6723	MSS	LUSC
TCGA-71-6725	MSS	LUAD
TCGA-71-8520	MSS	LUAD
TCGA-73-4658	MSS	LUAD
TCGA-73-4659	MSS	LUAD
TCGA-73-4662	MSS	LUAD
TCGA-73-4666	MSS	LUAD
TCGA-73-4668	MSS	LUAD
TCGA-73-4670	MSS	LUAD
TCGA-73-4675	MSS	LUAD
TCGA-73-4676	MSS	LUAD
TCGA-73-4677	MSS	LUAD
TCGA-73-7498	MSS	LUAD
TCGA-73-7499	MSS	LUAD
TCGA-73-A9RS	MSS	LUAD
TCGA-74-6573	MSS	GBM
TCGA-74-6575	MSS	GBM
TCGA-74-6577	MSS	GBM
TCGA-74-6578	MSS	GBM
TCGA-74-6581	MSS	GBM
TCGA-74-6584	MSS	GBM
TCGA-75-5122	MSS	LUAD
TCGA-75-5125	MSS	LUAD
TCGA-75-5126	MSS	LUAD
TCGA-75-5146	MSS	LUAD
TCGA-75-5147	MSS	LUAD
TCGA-75-6203	MSS	LUAD
TCGA-75-6205	MSS	LUAD
TCGA-75-6206	MSS	LUAD
TCGA-75-6207	MSS	LUAD
TCGA-75-6211	MSS	LUAD
TCGA-75-6212	MSS	LUAD
TCGA-75-6214	MSS	LUAD
TCGA-75-7025	MSS	LUAD

TCGA-75-7027	MSS	LUAD
TCGA-75-7030	MSS	LUAD
TCGA-75-7031	MSS	LUAD
TCGA-76-4925	MSS	GBM
TCGA-76-4926	MSS	GBM
TCGA-76-4927	MSS	GBM
TCGA-76-4928	MSS	GBM
TCGA-76-4929	MSS	GBM
TCGA-76-4931	MSS	GBM
TCGA-76-4932	MSS	GBM
TCGA-76-4934	MSS	GBM
TCGA-76-4935	MSS	GBM
TCGA-76-6191	MSS	GBM
TCGA-76-6192	MSS	GBM
TCGA-76-6193	MSS	GBM
TCGA-76-6280	MSS	GBM
TCGA-76-6282	MSS	GBM
TCGA-76-6283	MSS	GBM
TCGA-76-6285	MSS	GBM
TCGA-76-6286	MSS	GBM
TCGA-76-6656	MSS	GBM
TCGA-76-6657	MSS	GBM
TCGA-76-6660	MSS	GBM
TCGA-76-6661	MSS	GBM
TCGA-76-6662	MSS	GBM
TCGA-76-6663	MSS	GBM
TCGA-76-6664	MSS	GBM
TCGA-77-6842	MSS	LUSC
TCGA-77-6843	MSS	LUSC
TCGA-77-6844	MSS	LUSC
TCGA-77-6845	MSS	LUSC
TCGA-77-7138	MSS	LUSC
TCGA-77-7139	MSS	LUSC
TCGA-77-7140	MSS	LUSC
TCGA-77-7141	MSS	LUSC
TCGA-77-7142	MSS	LUSC
TCGA-77-7335	MSS	LUSC
TCGA-77-7337	MSS	LUSC
TCGA-77-7338	Intermediate	LUSC
TCGA-77-7463	MSS	LUSC
TCGA-77-7465	MSS	LUSC
TCGA-77-8008	MSS	LUSC
TCGA-77-8009	MSS	LUSC
TCGA-77-8153	MSS	LUSC
TCGA-77-A5FZ	MSS	LUSC
TCGA-77-A5G1	MSS	LUSC
TCGA-77-A5G3	MSS	LUSC
TCGA-77-A5G6	MSS	LUSC
TCGA-77-A5G7	MSS	LUSC
TCGA-77-A5G8	MSS	LUSC
TCGA-77-A5GA	MSS	LUSC
TCGA-77-A5GB	MSS	LUSC

TCGA-77-A5GF	MSS	LUSC
TCGA-77-A5GH	MSS	LUSC
TCGA-78-7145	MSS	LUAD
TCGA-78-7146	MSS	LUAD
TCGA-78-7147	MSS	LUAD
TCGA-78-7148	MSS	LUAD
TCGA-78-7149	MSS	LUAD
TCGA-78-7150	MSS	LUAD
TCGA-78-7152	MSS	LUAD
TCGA-78-7153	MSS	LUAD
TCGA-78-7154	MSS	LUAD
TCGA-78-7155	MSS	LUAD
TCGA-78-7156	MSS	LUAD
TCGA-78-7158	MSS	LUAD
TCGA-78-7159	MSS	LUAD
TCGA-78-7160	MSS	LUAD
TCGA-78-7161	MSS	LUAD
TCGA-78-7162	MSS	LUAD
TCGA-78-7163	MSS	LUAD
TCGA-78-7166	MSS	LUAD
TCGA-78-7167	MSS	LUAD
TCGA-78-7220	MSS	LUAD
TCGA-78-7535	MSS	LUAD
TCGA-78-7536	MSS	LUAD
TCGA-78-7537	MSS	LUAD
TCGA-78-7539	MSS	LUAD
TCGA-78-7540	MSS	LUAD
TCGA-78-7542	MSS	LUAD
TCGA-78-7633	MSS	LUAD
TCGA-78-8640	MSS	LUAD
TCGA-78-8648	MSS	LUAD
TCGA-78-8655	MSS	LUAD
TCGA-78-8660	MSS	LUAD
TCGA-78-8662	MSS	LUAD
TCGA-79-5596	MSS	LUSC
TCGA-80-5607	MSS	LUAD
TCGA-80-5608	MSS	LUAD
TCGA-80-5611	MSS	LUAD
TCGA-81-5910	MSS	GBM
TCGA-81-5911	MSS	GBM
TCGA-83-5908	MSS	LUAD
TCGA-85-6175	MSS	LUSC
TCGA-85-6560	MSS	LUSC
TCGA-85-6561	MSS	LUSC
TCGA-85-6798	MSS	LUSC
TCGA-85-7696	MSS	LUSC
TCGA-85-7697	MSS	LUSC
TCGA-85-7698	MSS	LUSC
TCGA-85-7699	MSS	LUSC
TCGA-85-7710	MSS	LUSC
TCGA-85-7843	MSS	LUSC
TCGA-85-7844	MSS	LUSC

TCGA-85-8276	MSS	LUSC
TCGA-85-8277	MSS	LUSC
TCGA-85-8287	MSS	LUSC
TCGA-85-8350	MSS	LUSC
TCGA-85-8351	MSS	LUSC
TCGA-85-8352	MSS	LUSC
TCGA-85-8353	MSS	LUSC
TCGA-85-8354	MSS	LUSC
TCGA-85-8355	MSS	LUSC
TCGA-85-8479	MSS	LUSC
TCGA-85-8481	MSS	LUSC
TCGA-85-8580	MSS	LUSC
TCGA-85-8582	MSS	LUSC
TCGA-85-8584	MSS	LUSC
TCGA-85-8664	MSS	LUSC
TCGA-85-8666	MSS	LUSC
TCGA-85-A4CL	MSS	LUSC
TCGA-85-A4CN	MSS	LUSC
TCGA-85-A4JB	MSS	LUSC
TCGA-85-A4JC	MSS	LUSC
TCGA-85-A4PA	MSS	LUSC
TCGA-85-A4QQ	MSS	LUSC
TCGA-85-A4QR	MSS	LUSC
TCGA-85-A50M	MSS	LUSC
TCGA-85-A50Z	MSS	LUSC
TCGA-85-A510	MSS	LUSC
TCGA-85-A511	MSS	LUSC
TCGA-85-A512	MSS	LUSC
TCGA-85-A513	MSS	LUSC
TCGA-85-A53L	MSS	LUSC
TCGA-85-A5B5	MSS	LUSC
TCGA-86-6562	MSS	LUAD
TCGA-86-6851	MSS	LUAD
TCGA-86-7711	MSS	LUAD
TCGA-86-7713	MSS	LUAD
TCGA-86-7953	MSS	LUAD
TCGA-86-8055	MSS	LUAD
TCGA-86-8056	MSS	LUAD
TCGA-86-8076	MSS	LUAD
TCGA-86-8278	MSS	LUAD
TCGA-86-8279	MSS	LUAD
TCGA-86-8280	MSS	LUAD
TCGA-86-8281	MSS	LUAD
TCGA-86-8358	MSS	LUAD
TCGA-86-8359	MSS	LUAD
TCGA-86-8585	MSS	LUAD
TCGA-86-8668	MSS	LUAD
TCGA-86-8669	MSS	LUAD
TCGA-86-8671	MSS	LUAD
TCGA-86-8672	MSS	LUAD
TCGA-86-8673	MSS	LUAD
TCGA-86-8674	MSS	LUAD

TCGA-86-A456	MSS	LUAD
TCGA-86-A4D0	MSS	LUAD
TCGA-86-A4JF	MSI-H	LUAD
TCGA-86-A4P7	MSS	LUAD
TCGA-86-A4P8	MSS	LUAD
TCGA-87-5896	MSS	GBM
TCGA-90-6837	MSS	LUSC
TCGA-90-7766	MSS	LUSC
TCGA-90-7767	MSS	LUSC
TCGA-90-7769	MSS	LUSC
TCGA-90-7964	MSS	LUSC
TCGA-90-A4ED	MSS	LUSC
TCGA-90-A4EE	MSS	LUSC
TCGA-90-A59Q	MSS	LUSC
TCGA-91-6828	MSS	LUAD
TCGA-91-6829	MSS	LUAD
TCGA-91-6830	MSS	LUAD
TCGA-91-6831	MSS	LUAD
TCGA-91-6835	MSS	LUAD
TCGA-91-6836	MSS	LUAD
TCGA-91-6840	MSS	LUAD
TCGA-91-6847	MSS	LUAD
TCGA-91-6848	MSS	LUAD
TCGA-91-6849	MSS	LUAD
TCGA-91-7771	MSS	LUAD
TCGA-91-8496	MSS	LUAD
TCGA-91-8497	MSS	LUAD
TCGA-91-8499	MSS	LUAD
TCGA-91-A4BC	MSS	LUAD
TCGA-91-A4BD	MSS	LUAD
TCGA-92-7340	MSS	LUSC
TCGA-92-7341	MSS	LUSC
TCGA-93-7347	MSS	LUAD
TCGA-93-7348	MSS	LUAD
TCGA-93-8067	MSS	LUAD
TCGA-93-A4JN	MSS	LUAD
TCGA-93-A4JO	MSS	LUAD
TCGA-93-A4JP	MSS	LUAD
TCGA-93-A4JQ	MSS	LUAD
TCGA-94-7033	MSS	LUSC
TCGA-94-7557	MSS	LUSC
TCGA-94-7943	MSS	LUSC
TCGA-94-8490	MSI-H	LUSC
TCGA-94-8491	MSS	LUSC
TCGA-94-A4VJ	MSS	LUSC
TCGA-94-A5I4	MSS	LUSC
TCGA-94-A5I6	MSS	LUSC
TCGA-95-7039	MSS	LUAD
TCGA-95-7567	MSI-H	LUAD
TCGA-95-7944	MSS	LUAD
TCGA-95-7947	MSS	LUAD
TCGA-95-7948	MSS	LUAD

TCGA-95-8039	MSS	LUAD
TCGA-95-8494	MSS	LUAD
TCGA-95-A4VK	MSS	LUAD
TCGA-95-A4VN	MSS	LUAD
TCGA-95-A4VP	MSS	LUAD
TCGA-96-7544	MSS	LUSC
TCGA-96-7545	MSS	LUSC
TCGA-96-8169	MSS	LUSC
TCGA-96-8170	MSS	LUSC
TCGA-96-A4JK	MSS	LUSC
TCGA-96-A4JL	MSS	LUSC
TCGA-97-7546	MSS	LUAD
TCGA-97-7547	MSS	LUAD
TCGA-97-7552	MSS	LUAD
TCGA-97-7553	MSS	LUAD
TCGA-97-7554	MSS	LUAD
TCGA-97-8171	MSS	LUAD
TCGA-97-8172	MSS	LUAD
TCGA-97-8174	MSS	LUAD
TCGA-97-8175	MSS	LUAD
TCGA-97-8176	MSS	LUAD
TCGA-97-8177	MSS	LUAD
TCGA-97-8179	MSS	LUAD
TCGA-97-8547	MSS	LUAD
TCGA-97-8552	MSS	LUAD
TCGA-97-A4LX	MSS	LUAD
TCGA-97-A4M0	MSS	LUAD
TCGA-97-A4M1	MSS	LUAD
TCGA-97-A4M2	MSS	LUAD
TCGA-97-A4M3	MSS	LUAD
TCGA-97-A4M5	MSS	LUAD
TCGA-97-A4M6	MSS	LUAD
TCGA-97-A4M7	MSS	LUAD
TCGA-98-7454	MSS	LUSC
TCGA-98-A538	MSS	LUSC
TCGA-98-A539	MSS	LUSC
TCGA-98-A53A	MSS	LUSC
TCGA-98-A53B	MSS	LUSC
TCGA-98-A53C	MSS	LUSC
TCGA-98-A53H	MSS	LUSC
TCGA-98-A53I	MSS	LUSC
TCGA-98-A53J	MSS	LUSC
TCGA-99-7458	MSS	LUAD
TCGA-99-8025	MSS	LUAD
TCGA-99-8028	MSS	LUAD
TCGA-99-8032	MSS	LUAD
TCGA-99-AA5R	MSS	LUAD
TCGA-A1-A0SD	MSS	BRCA
TCGA-A1-A0SE	MSS	BRCA
TCGA-A1-A0SF	MSI-H	BRCA
TCGA-A1-A0SG	MSS	BRCA
TCGA-A1-A0SH	MSS	BRCA

TCGA-A1-A0SI	Intermediate	BRCA
TCGA-A1-A0SJ	MSS	BRCA
TCGA-A1-A0SK	MSS	BRCA
TCGA-A1-A0SM	MSS	BRCA
TCGA-A1-A0SN	MSS	BRCA
TCGA-A1-A0SO	MSS	BRCA
TCGA-A1-A0SP	Intermediate	BRCA
TCGA-A2-A04N	MSS	BRCA
TCGA-A2-A04P	MSS	BRCA
TCGA-A2-A04Q	MSS	BRCA
TCGA-A2-A04R	MSS	BRCA
TCGA-A2-A04T	MSS	BRCA
TCGA-A2-A04U	MSS	BRCA
TCGA-A2-A04V	MSS	BRCA
TCGA-A2-A04W	MSS	BRCA
TCGA-A2-A04X	MSS	BRCA
TCGA-A2-A04Y	MSS	BRCA
TCGA-A2-A0CL	MSS	BRCA
TCGA-A2-A0CM	MSS	BRCA
TCGA-A2-A0CP	MSS	BRCA
TCGA-A2-A0CQ	MSS	BRCA
TCGA-A2-A0CS	MSS	BRCA
TCGA-A2-A0CT	MSS	BRCA
TCGA-A2-A0CU	MSS	BRCA
TCGA-A2-A0CV	MSS	BRCA
TCGA-A2-A0CW	MSS	BRCA
TCGA-A2-A0CX	MSS	BRCA
TCGA-A2-A0D0	MSS	BRCA
TCGA-A2-A0D1	MSS	BRCA
TCGA-A2-A0D2	MSS	BRCA
TCGA-A2-A0D3	MSS	BRCA
TCGA-A2-A0D4	MSS	BRCA
TCGA-A2-A0EM	MSS	BRCA
TCGA-A2-A0EN	MSS	BRCA
TCGA-A2-A0EO	MSS	BRCA
TCGA-A2-A0EP	MSS	BRCA
TCGA-A2-A0EQ	MSS	BRCA
TCGA-A2-A0ER	MSS	BRCA
TCGA-A2-A0ES	MSS	BRCA
TCGA-A2-A0ET	MSS	BRCA
TCGA-A2-A0EU	MSS	BRCA
TCGA-A2-A0EV	MSS	BRCA
TCGA-A2-A0EW	MSS	BRCA
TCGA-A2-A0EX	MSS	BRCA
TCGA-A2-A0EY	MSS	BRCA
TCGA-A2-A0ST	MSS	BRCA
TCGA-A2-A0SU	MSS	BRCA
TCGA-A2-A0SV	MSS	BRCA
TCGA-A2-A0SW	MSS	BRCA
TCGA-A2-A0SX	MSS	BRCA
TCGA-A2-A0SY	MSS	BRCA
TCGA-A2-A0T0	MSS	BRCA

TCGA-A2-A0T1	MSS	BRCA
TCGA-A2-A0T2	MSS	BRCA
TCGA-A2-A0T3	MSS	BRCA
TCGA-A2-A0T4	MSS	BRCA
TCGA-A2-A0T5	MSS	BRCA
TCGA-A2-A0T6	MSS	BRCA
TCGA-A2-A0T7	MSS	BRCA
TCGA-A2-A0YC	MSS	BRCA
TCGA-A2-A0YE	MSS	BRCA
TCGA-A2-A0YF	MSS	BRCA
TCGA-A2-A0YG	MSS	BRCA
TCGA-A2-A0YH	MSS	BRCA
TCGA-A2-A0YI	MSS	BRCA
TCGA-A2-A0YJ	MSS	BRCA
TCGA-A2-A0YK	MSS	BRCA
TCGA-A2-A0YL	MSS	BRCA
TCGA-A2-A0YM	MSS	BRCA
TCGA-A2-A0YT	MSS	BRCA
TCGA-A2-A1FV	MSS	BRCA
TCGA-A2-A1FW	MSS	BRCA
TCGA-A2-A1FX	Intermediate	BRCA
TCGA-A2-A1FZ	Intermediate	BRCA
TCGA-A2-A1G0	MSS	BRCA
TCGA-A2-A1G1	MSS	BRCA
TCGA-A2-A1G4	MSS	BRCA
TCGA-A2-A1G6	MSS	BRCA
TCGA-A2-A259	Intermediate	BRCA
TCGA-A2-A25A	MSS	BRCA
TCGA-A2-A25B	MSS	BRCA
TCGA-A2-A25C	Intermediate	BRCA
TCGA-A2-A25D	MSS	BRCA
TCGA-A2-A25E	Intermediate	BRCA
TCGA-A2-A25F	MSS	BRCA
TCGA-A2-A3KD	MSS	BRCA
TCGA-A2-A3XS	MSS	BRCA
TCGA-A2-A3XT	MSS	BRCA
TCGA-A2-A3XU	MSS	BRCA
TCGA-A2-A3XV	MSS	BRCA
TCGA-A2-A3XW	MSS	BRCA
TCGA-A2-A3XX	MSS	BRCA
TCGA-A2-A3XY	MSS	BRCA
TCGA-A2-A3XZ	MSS	BRCA
TCGA-A2-A3Y0	MSS	BRCA
TCGA-A2-A4RX	MSS	BRCA
TCGA-A2-A4RY	MSS	BRCA
TCGA-A2-A4S0	MSS	BRCA
TCGA-A2-A4S1	MSS	BRCA
TCGA-A2-A4S2	MSS	BRCA
TCGA-A3-3308	MSS	KIRC
TCGA-A3-3311	MSS	KIRC
TCGA-A3-3313	MSS	KIRC
TCGA-A3-3316	MSS	KIRC

TCGA-A3-3317	MSS	KIRC
TCGA-A3-3319	MSS	KIRC
TCGA-A3-3320	MSS	KIRC
TCGA-A3-3322	MSI-H	KIRC
TCGA-A3-3323	MSS	KIRC
TCGA-A3-3326	MSS	KIRC
TCGA-A3-3331	MSS	KIRC
TCGA-A3-3346	MSS	KIRC
TCGA-A3-3357	MSS	KIRC
TCGA-A3-3358	MSS	KIRC
TCGA-A3-3363	MSI-H	KIRC
TCGA-A3-3365	MSS	KIRC
TCGA-A3-3367	MSS	KIRC
TCGA-A3-3370	Intermediate	KIRC
TCGA-A3-3372	MSS	KIRC
TCGA-A3-3373	MSS	KIRC
TCGA-A3-3374	MSS	KIRC
TCGA-A3-3376	MSS	KIRC
TCGA-A3-3378	MSS	KIRC
TCGA-A3-3380	MSS	KIRC
TCGA-A3-3382	MSS	KIRC
TCGA-A3-3383	MSS	KIRC
TCGA-A3-3385	MSS	KIRC
TCGA-A3-3387	MSS	KIRC
TCGA-A3-A6NI	MSS	KIRC
TCGA-A3-A6NJ	MSS	KIRC
TCGA-A3-A6NL	MSS	KIRC
TCGA-A3-A6NN	MSS	KIRC
TCGA-A3-A8CQ	MSS	KIRC
TCGA-A3-A8OU	MSS	KIRC
TCGA-A3-A8OV	MSS	KIRC
TCGA-A3-A8OW	MSS	KIRC
TCGA-A3-A8OX	MSS	KIRC
TCGA-A4-7286	MSS	KIRP
TCGA-A4-7287	MSS	KIRP
TCGA-A4-7288	MSS	KIRP
TCGA-A4-7583	MSS	KIRP
TCGA-A4-7584	MSS	KIRP
TCGA-A4-7585	MSS	KIRP
TCGA-A4-7732	MSS	KIRP
TCGA-A4-7734	MSS	KIRP
TCGA-A4-7828	MSS	KIRP
TCGA-A4-7915	MSS	KIRP
TCGA-A4-7996	MSS	KIRP
TCGA-A4-7997	MSS	KIRP
TCGA-A4-8098	MSS	KIRP
TCGA-A4-8310	MSS	KIRP
TCGA-A4-8311	MSS	KIRP
TCGA-A4-8312	MSS	KIRP
TCGA-A4-8515	MSS	KIRP
TCGA-A4-8517	MSS	KIRP
TCGA-A4-8518	MSS	KIRP

TCGA-A4-8630	MSS	KIRP
TCGA-A4-A5XZ	MSS	KIRP
TCGA-A4-A5Y0	MSS	KIRP
TCGA-A4-A6HP	MSS	KIRP
TCGA-A4-A772	MSS	KIRP
TCGA-A4-A7UZ	MSS	KIRP
TCGA-A5-A0G1	Intermediate	UCEC
TCGA-A5-A0G2	MSI-H	UCEC
TCGA-A5-A0G3	Intermediate	UCEC
TCGA-A5-A0G5	MSS	UCEC
TCGA-A5-A0G9	MSI-H	UCEC
TCGA-A5-A0GA	MSI-H	UCEC
TCGA-A5-A0GB	MSI-H	UCEC
TCGA-A5-A0GD	MSS	UCEC
TCGA-A5-A0GE	MSS	UCEC
TCGA-A5-A0GG	MSI-H	UCEC
TCGA-A5-A0GH	MSI-H	UCEC
TCGA-A5-A0GI	MSI-H	UCEC
TCGA-A5-A0GJ	MSS	UCEC
TCGA-A5-A0GM	MSS	UCEC
TCGA-A5-A0GN	MSS	UCEC
TCGA-A5-A0GP	MSS	UCEC
TCGA-A5-A0GQ	MSS	UCEC
TCGA-A5-A0GR	MSS	UCEC
TCGA-A5-A0GU	MSS	UCEC
TCGA-A5-A0GV	MSS	UCEC
TCGA-A5-A0GW	MSI-H	UCEC
TCGA-A5-A0GX	MSS	UCEC
TCGA-A5-A0R6	MSS	UCEC
TCGA-A5-A0R7	MSS	UCEC
TCGA-A5-A0R8	MSS	UCEC
TCGA-A5-A0R9	MSS	UCEC
TCGA-A5-A0RA	MSS	UCEC
TCGA-A5-A0VO	MSS	UCEC
TCGA-A5-A0VP	MSI-H	UCEC
TCGA-A5-A0VQ	MSI-H	UCEC
TCGA-A5-A1OF	MSI-H	UCEC
TCGA-A5-A1OG	MSS	UCEC
TCGA-A5-A1OH	MSS	UCEC
TCGA-A5-A2K2	MSS	UCEC
TCGA-A5-A2K3	MSI-H	UCEC
TCGA-A5-A2K5	MSS	UCEC
TCGA-A5-A2K7	MSI-H	UCEC
TCGA-A5-A3LO	MSS	UCEC
TCGA-A5-A7WJ	MSI-H	UCEC
TCGA-A5-A7WK	MSS	UCEC
TCGA-A5-AB3J	MSS	UCEC
TCGA-A6-2671	MSS	COAD
TCGA-A6-2672	MSI-H	COAD
TCGA-A6-2674	MSS	COAD
TCGA-A6-2674	MSS	COAD
TCGA-A6-2675	MSS	COAD

TCGA-A6-2677	MSS	COAD
TCGA-A6-2677	MSS	COAD
TCGA-A6-2679	MSS	COAD
TCGA-A6-2680	MSS	COAD
TCGA-A6-2681	MSS	COAD
TCGA-A6-2682	MSS	COAD
TCGA-A6-2684	MSS	COAD
TCGA-A6-2684	MSS	COAD
TCGA-A6-2685	MSS	COAD
TCGA-A6-2686	MSI-H	COAD
TCGA-A6-3807	MSS	COAD
TCGA-A6-3809	MSI-H	COAD
TCGA-A6-3809	MSI-H	COAD
TCGA-A6-3810	MSS	COAD
TCGA-A6-3810	MSS	COAD
TCGA-A6-4105	MSS	COAD
TCGA-A6-4107	MSS	COAD
TCGA-A6-5656	MSS	COAD
TCGA-A6-5656	MSI-H	COAD
TCGA-A6-5657	Intermediate	COAD
TCGA-A6-5659	MSS	COAD
TCGA-A6-5659	Intermediate	COAD
TCGA-A6-5660	MSS	COAD
TCGA-A6-5661	MSI-H	COAD
TCGA-A6-5662	MSS	COAD
TCGA-A6-5665	MSI-H	COAD
TCGA-A6-5665	MSI-H	COAD
TCGA-A6-5666	MSS	COAD
TCGA-A6-5667	MSS	COAD
TCGA-A6-6137	MSS	COAD
TCGA-A6-6138	MSS	COAD
TCGA-A6-6140	MSS	COAD
TCGA-A6-6141	MSS	COAD
TCGA-A6-6142	MSS	COAD
TCGA-A6-6648	MSS	COAD
TCGA-A6-6649	MSS	COAD
TCGA-A6-6650	MSS	COAD
TCGA-A6-6651	MSS	COAD
TCGA-A6-6652	MSS	COAD
TCGA-A6-6653	MSI-H	COAD
TCGA-A6-6654	MSS	COAD
TCGA-A6-6780	MSI-H	COAD
TCGA-A6-6780	MSI-H	COAD
TCGA-A6-6781	MSI-H	COAD
TCGA-A6-6781	MSI-H	COAD
TCGA-A6-A565	MSS	COAD
TCGA-A7-A0CD	MSS	BRCA
TCGA-A7-A0CE	MSS	BRCA
TCGA-A7-A0CG	MSS	BRCA
TCGA-A7-A0CJ	MSS	BRCA
TCGA-A7-A0D9	MSS	BRCA
TCGA-A7-A0DA	MSS	BRCA

TCGA-A7-A0DB	MSI-H	BRCA
TCGA-A7-A0DB	MSS	BRCA
TCGA-A7-A13D	MSS	BRCA
TCGA-A7-A13D	MSI-H	BRCA
TCGA-A7-A13E	MSS	BRCA
TCGA-A7-A13E	MSI-H	BRCA
TCGA-A7-A13F	MSS	BRCA
TCGA-A7-A13G	MSS	BRCA
TCGA-A7-A13H	MSS	BRCA
TCGA-A7-A26E	MSI-H	BRCA
TCGA-A7-A26E	MSS	BRCA
TCGA-A7-A26F	MSI-H	BRCA
TCGA-A7-A26F	Intermediate	BRCA
TCGA-A7-A26G	MSS	BRCA
TCGA-A7-A26H	MSS	BRCA
TCGA-A7-A26I	MSS	BRCA
TCGA-A7-A26I	MSS	BRCA
TCGA-A7-A26J	MSS	BRCA
TCGA-A7-A26J	MSS	BRCA
TCGA-A7-A3IY	MSS	BRCA
TCGA-A7-A3RF	MSS	BRCA
TCGA-A7-A4SA	MSS	BRCA
TCGA-A7-A4SB	MSS	BRCA
TCGA-A7-A4SC	MSS	BRCA
TCGA-A7-A4SD	MSS	BRCA
TCGA-A7-A4SE	MSS	BRCA
TCGA-A7-A5ZX	MSS	BRCA
TCGA-A7-A6VV	MSS	BRCA
TCGA-A7-A6VW	MSS	BRCA
TCGA-A7-A6VX	MSS	BRCA
TCGA-A7-A6VY	MSS	BRCA
TCGA-A8-A06O	MSS	BRCA
TCGA-A8-A06P	MSS	BRCA
TCGA-A8-A06Q	MSS	BRCA
TCGA-A8-A06R	MSS	BRCA
TCGA-A8-A06T	MSS	BRCA
TCGA-A8-A06U	MSS	BRCA
TCGA-A8-A06X	MSS	BRCA
TCGA-A8-A06Y	MSS	BRCA
TCGA-A8-A06Z	MSS	BRCA
TCGA-A8-A075	MSS	BRCA
TCGA-A8-A076	MSS	BRCA
TCGA-A8-A079	MSS	BRCA
TCGA-A8-A07B	MSS	BRCA
TCGA-A8-A07F	MSS	BRCA
TCGA-A8-A07G	MSS	BRCA
TCGA-A8-A07I	MSS	BRCA
TCGA-A8-A07J	MSS	BRCA
TCGA-A8-A07L	MSS	BRCA
TCGA-A8-A07O	MSS	BRCA
TCGA-A8-A07P	Intermediate	BRCA
TCGA-A8-A07R	MSS	BRCA

TCGA-A8-A07U	MSS	BRCA
TCGA-A8-A07W	MSS	BRCA
TCGA-A8-A07Z	MSS	BRCA
TCGA-A8-A081	MSS	BRCA
TCGA-A8-A082	MSS	BRCA
TCGA-A8-A083	MSS	BRCA
TCGA-A8-A085	MSS	BRCA
TCGA-A8-A08B	MSS	BRCA
TCGA-A8-A08C	MSS	BRCA
TCGA-A8-A08F	MSS	BRCA
TCGA-A8-A08G	MSS	BRCA
TCGA-A8-A08H	MSS	BRCA
TCGA-A8-A08J	MSS	BRCA
TCGA-A8-A08L	MSS	BRCA
TCGA-A8-A08O	MSS	BRCA
TCGA-A8-A08P	MSS	BRCA
TCGA-A8-A08R	MSS	BRCA
TCGA-A8-A08S	MSS	BRCA
TCGA-A8-A08T	MSS	BRCA
TCGA-A8-A08X	MSS	BRCA
TCGA-A8-A08Z	MSS	BRCA
TCGA-A8-A090	MSS	BRCA
TCGA-A8-A091	MSS	BRCA
TCGA-A8-A092	MSS	BRCA
TCGA-A8-A093	MSS	BRCA
TCGA-A8-A094	MSS	BRCA
TCGA-A8-A095	MSS	BRCA
TCGA-A8-A096	MSS	BRCA
TCGA-A8-A097	MSS	BRCA
TCGA-A8-A099	MSS	BRCA
TCGA-A8-A09A	MSS	BRCA
TCGA-A8-A09B	MSS	BRCA
TCGA-A8-A09C	MSS	BRCA
TCGA-A8-A09D	MSS	BRCA
TCGA-A8-A09E	MSS	BRCA
TCGA-A8-A09G	MSS	BRCA
TCGA-A8-A09I	MSS	BRCA
TCGA-A8-A09K	MSS	BRCA
TCGA-A8-A09M	MSS	BRCA
TCGA-A8-A09N	MSS	BRCA
TCGA-A8-A09Q	MSS	BRCA
TCGA-A8-A09T	MSS	BRCA
TCGA-A8-A09V	MSS	BRCA
TCGA-A8-A09W	MSS	BRCA
TCGA-A8-A09X	MSS	BRCA
TCGA-A8-A09Z	MSI-H	BRCA
TCGA-A8-A0A1	MSS	BRCA
TCGA-A8-A0A2	MSS	BRCA
TCGA-A8-A0A4	MSS	BRCA
TCGA-A8-A0A6	MSS	BRCA
TCGA-A8-A0A7	MSS	BRCA
TCGA-A8-A0A9	MSS	BRCA

TCGA-A8-A0AB	MSS	BRCA
TCGA-A8-A0AD	MSS	BRCA
TCGA-AA-3488	MSS	COAD
TCGA-AA-3489	MSS	COAD
TCGA-AA-3492	MSI-H	COAD
TCGA-AA-3494	MSS	COAD
TCGA-AA-3495	MSS	COAD
TCGA-AA-3502	MSS	COAD
TCGA-AA-3506	MSS	COAD
TCGA-AA-3509	MSS	COAD
TCGA-AA-3510	MSS	COAD
TCGA-AA-3511	MSS	COAD
TCGA-AA-3530	MSS	COAD
TCGA-AA-3655	MSS	COAD
TCGA-AA-3660	MSS	COAD
TCGA-AA-3662	MSS	COAD
TCGA-AA-3663	MSI-H	COAD
TCGA-AA-3664	MSS	COAD
TCGA-AA-3666	MSS	COAD
TCGA-AA-3667	MSS	COAD
TCGA-AA-3672	MSI-H	COAD
TCGA-AA-3673	MSS	COAD
TCGA-AA-3675	MSS	COAD
TCGA-AA-3678	MSS	COAD
TCGA-AA-3679	MSS	COAD
TCGA-AA-3680	MSS	COAD
TCGA-AA-3681	MSS	COAD
TCGA-AA-3684	MSS	COAD
TCGA-AA-3685	MSS	COAD
TCGA-AA-3688	MSS	COAD
TCGA-AA-3692	MSS	COAD
TCGA-AA-3693	MSS	COAD
TCGA-AA-3695	MSS	COAD
TCGA-AA-3696	MSS	COAD
TCGA-AA-3697	MSS	COAD
TCGA-AA-3710	MSI-H	COAD
TCGA-AA-3712	MSS	COAD
TCGA-AA-3713	MSI-H	COAD
TCGA-AA-3715	MSI-H	COAD
TCGA-AA-3811	MSI-H	COAD
TCGA-AA-3812	MSS	COAD
TCGA-AA-3814	MSS	COAD
TCGA-AA-3815	MSI-H	COAD
TCGA-AA-3818	MSS	COAD
TCGA-AA-3819	MSS	COAD
TCGA-AA-3821	MSI-H	COAD
TCGA-AA-3831	MSS	COAD
TCGA-AA-3833	MSI-H	COAD
TCGA-AA-3837	MSS	COAD
TCGA-AA-3841	MSS	COAD
TCGA-AA-3842	MSS	COAD
TCGA-AA-3844	MSS	COAD

TCGA-AA-3845	MSI-H	COAD
TCGA-AA-3846	MSS	COAD
TCGA-AA-3848	MSS	COAD
TCGA-AA-3850	MSS	COAD
TCGA-AA-3851	MSS	COAD
TCGA-AA-3852	MSS	COAD
TCGA-AA-3854	MSS	COAD
TCGA-AA-3855	MSS	COAD
TCGA-AA-3856	MSS	COAD
TCGA-AA-3858	MSS	COAD
TCGA-AA-3860	MSS	COAD
TCGA-AA-3864	MSI-H	COAD
TCGA-AA-3866	MSS	COAD
TCGA-AA-3867	MSS	COAD
TCGA-AA-3869	MSS	COAD
TCGA-AA-3870	MSS	COAD
TCGA-AA-3872	MSS	COAD
TCGA-AA-3875	MSS	COAD
TCGA-AA-3877	MSI-H	COAD
TCGA-AA-3930	MSS	COAD
TCGA-AA-3939	MSS	COAD
TCGA-AA-3941	MSS	COAD
TCGA-AA-3947	MSI-H	COAD
TCGA-AA-3949	MSI-H	COAD
TCGA-AA-3950	MSI-H	COAD
TCGA-AA-3952	MSS	COAD
TCGA-AA-3955	MSS	COAD
TCGA-AA-3956	MSS	COAD
TCGA-AA-3966	MSI-H	COAD
TCGA-AA-3967	MSS	COAD
TCGA-AA-3968	MSS	COAD
TCGA-AA-3971	MSS	COAD
TCGA-AA-3973	MSS	COAD
TCGA-AA-3975	MSS	COAD
TCGA-AA-3976	MSS	COAD
TCGA-AA-3980	MSS	COAD
TCGA-AA-3982	MSS	COAD
TCGA-AA-3984	MSS	COAD
TCGA-AA-3986	MSS	COAD
TCGA-AA-3989	MSS	COAD
TCGA-AA-3994	MSS	COAD
TCGA-AA-A004	MSS	COAD
TCGA-AA-A00N	MSS	COAD
TCGA-AA-A00O	MSS	COAD
TCGA-AA-A010	MSI-H	COAD
TCGA-AA-A017	MSS	COAD
TCGA-AA-A01C	MSS	COAD
TCGA-AA-A01D	MSS	COAD
TCGA-AA-A01I	MSS	COAD
TCGA-AA-A01K	MSS	COAD
TCGA-AA-A01P	MSI-H	COAD
TCGA-AA-A01R	MSI-H	COAD

TCGA-AA-A01S	MSS	COAD
TCGA-AA-A01T	MSS	COAD
TCGA-AA-A01V	MSS	COAD
TCGA-AA-A01X	MSS	COAD
TCGA-AA-A01Z	MSS	COAD
TCGA-AA-A022	MSI-H	COAD
TCGA-AA-A024	Intermediate	COAD
TCGA-AA-A029	MSS	COAD
TCGA-AA-A02E	MSS	COAD
TCGA-AA-A02F	MSS	COAD
TCGA-AA-A02H	MSS	COAD
TCGA-AA-A02J	Intermediate	COAD
TCGA-AA-A02K	MSS	COAD
TCGA-AA-A02O	MSS	COAD
TCGA-AA-A02R	MSI-H	COAD
TCGA-AA-A02W	MSS	COAD
TCGA-AA-A02Y	MSS	COAD
TCGA-AA-A03F	MSS	COAD
TCGA-AA-A03J	MSS	COAD
TCGA-AB-2802	MSS	LAML
TCGA-AB-2803	MSS	LAML
TCGA-AB-2804	MSS	LAML
TCGA-AB-2805	MSS	LAML
TCGA-AB-2806	MSS	LAML
TCGA-AB-2807	MSS	LAML
TCGA-AB-2807	MSS	LAML
TCGA-AB-2808	MSS	LAML
TCGA-AB-2808	MSI-H	LAML
TCGA-AB-2809	MSS	LAML
TCGA-AB-2810	MSS	LAML
TCGA-AB-2811	MSS	LAML
TCGA-AB-2812	MSS	LAML
TCGA-AB-2813	MSS	LAML
TCGA-AB-2814	MSS	LAML
TCGA-AB-2815	MSS	LAML
TCGA-AB-2816	MSS	LAML
TCGA-AB-2817	MSS	LAML
TCGA-AB-2818	MSS	LAML
TCGA-AB-2819	MSS	LAML
TCGA-AB-2820	MSS	LAML
TCGA-AB-2821	MSS	LAML
TCGA-AB-2822	MSS	LAML
TCGA-AB-2823	MSS	LAML
TCGA-AB-2824	MSS	LAML
TCGA-AB-2825	MSS	LAML
TCGA-AB-2825	MSS	LAML
TCGA-AB-2826	MSS	LAML
TCGA-AB-2827	MSS	LAML
TCGA-AB-2828	MSS	LAML
TCGA-AB-2830	MSS	LAML
TCGA-AB-2831	MSS	LAML
TCGA-AB-2832	MSS	LAML

TCGA-AB-2833	MSS	LAML
TCGA-AB-2835	MSS	LAML
TCGA-AB-2836	MSS	LAML
TCGA-AB-2838	MSS	LAML
TCGA-AB-2839	MSS	LAML
TCGA-AB-2840	Intermediate	LAML
TCGA-AB-2840	MSS	LAML
TCGA-AB-2842	MSS	LAML
TCGA-AB-2843	MSS	LAML
TCGA-AB-2844	MSS	LAML
TCGA-AB-2845	MSS	LAML
TCGA-AB-2850	MSS	LAML
TCGA-AB-2851	MSS	LAML
TCGA-AB-2853	MSS	LAML
TCGA-AB-2854	MSS	LAML
TCGA-AB-2856	MSS	LAML
TCGA-AB-2857	MSS	LAML
TCGA-AB-2858	MSS	LAML
TCGA-AB-2859	MSS	LAML
TCGA-AB-2860	MSS	LAML
TCGA-AB-2861	MSS	LAML
TCGA-AB-2863	MSS	LAML
TCGA-AB-2864	MSS	LAML
TCGA-AB-2864	Intermediate	LAML
TCGA-AB-2865	MSS	LAML
TCGA-AB-2866	MSS	LAML
TCGA-AB-2867	MSS	LAML
TCGA-AB-2868	MSS	LAML
TCGA-AB-2869	MSS	LAML
TCGA-AB-2870	MSS	LAML
TCGA-AB-2871	MSS	LAML
TCGA-AB-2872	MSS	LAML
TCGA-AB-2873	MSS	LAML
TCGA-AB-2874	MSS	LAML
TCGA-AB-2875	MSS	LAML
TCGA-AB-2876	MSS	LAML
TCGA-AB-2877	MSS	LAML
TCGA-AB-2878	MSS	LAML
TCGA-AB-2879	MSS	LAML
TCGA-AB-2880	MSS	LAML
TCGA-AB-2881	MSS	LAML
TCGA-AB-2882	MSS	LAML
TCGA-AB-2887	MSS	LAML
TCGA-AB-2888	MSS	LAML
TCGA-AB-2889	MSS	LAML
TCGA-AB-2890	MSS	LAML
TCGA-AB-2895	MSS	LAML
TCGA-AB-2896	MSS	LAML
TCGA-AB-2898	MSS	LAML
TCGA-AB-2899	MSS	LAML
TCGA-AB-2900	MSS	LAML
TCGA-AB-2901	MSS	LAML

TCGA-AB-2903	MSS	LAML
TCGA-AB-2908	MSS	LAML
TCGA-AB-2909	MSS	LAML
TCGA-AB-2910	MSS	LAML
TCGA-AB-2915	MSS	LAML
TCGA-AB-2918	Intermediate	LAML
TCGA-AB-2919	MSS	LAML
TCGA-AB-2921	MSS	LAML
TCGA-AB-2922	MSS	LAML
TCGA-AB-2923	MSS	LAML
TCGA-AB-2924	MSS	LAML
TCGA-AB-2925	MSS	LAML
TCGA-AB-2926	MSS	LAML
TCGA-AB-2927	MSS	LAML
TCGA-AB-2928	MSS	LAML
TCGA-AB-2930	MSS	LAML
TCGA-AB-2931	MSS	LAML
TCGA-AB-2932	MSI-H	LAML
TCGA-AB-2933	MSS	LAML
TCGA-AB-2934	Intermediate	LAML
TCGA-AB-2935	Intermediate	LAML
TCGA-AB-2936	MSS	LAML
TCGA-AB-2937	MSS	LAML
TCGA-AB-2938	MSS	LAML
TCGA-AB-2939	Intermediate	LAML
TCGA-AB-2941	Intermediate	LAML
TCGA-AB-2943	Intermediate	LAML
TCGA-AB-2945	MSS	LAML
TCGA-AB-2946	MSS	LAML
TCGA-AB-2947	MSS	LAML
TCGA-AB-2948	MSS	LAML
TCGA-AB-2949	MSS	LAML
TCGA-AB-2950	MSS	LAML
TCGA-AB-2954	MSS	LAML
TCGA-AB-2955	MSS	LAML
TCGA-AB-2956	MSS	LAML
TCGA-AB-2957	MSS	LAML
TCGA-AB-2959	MSS	LAML
TCGA-AC-A23C	MSS	BRCA
TCGA-AC-A23E	MSS	BRCA
TCGA-AC-A23G	MSS	BRCA
TCGA-AC-A23H	MSS	BRCA
TCGA-AC-A2B8	MSS	BRCA
TCGA-AC-A2BM	MSS	BRCA
TCGA-AC-A2FB	MSS	BRCA
TCGA-AC-A2FF	MSS	BRCA
TCGA-AC-A2FG	Intermediate	BRCA
TCGA-AC-A2FK	MSS	BRCA
TCGA-AC-A2FM	MSS	BRCA
TCGA-AC-A2FO	MSS	BRCA
TCGA-AC-A2QH	MSS	BRCA
TCGA-AC-A2QH	MSS	BRCA

TCGA-AC-A2QI	MSS	BRCA
TCGA-AC-A2QJ	MSS	BRCA
TCGA-AC-A3BB	MSS	BRCA
TCGA-AC-A3OD	MSS	BRCA
TCGA-AC-A3OD	MSS	BRCA
TCGA-AC-A3QQ	Intermediate	BRCA
TCGA-AC-A3QQ	MSS	BRCA
TCGA-AC-A3W5	MSS	BRCA
TCGA-AC-A3W6	MSS	BRCA
TCGA-AC-A3W7	MSS	BRCA
TCGA-AC-A3YJ	MSS	BRCA
TCGA-AC-A4ZE	MSS	BRCA
TCGA-AC-A5XS	MSS	BRCA
TCGA-AC-A62V	MSS	BRCA
TCGA-AC-A62Y	MSS	BRCA
TCGA-AC-A6IV	MSS	BRCA
TCGA-AC-A6IW	MSS	BRCA
TCGA-AC-A6IX	MSS	BRCA
TCGA-AC-A6IX	MSS	BRCA
TCGA-AC-A6NO	MSS	BRCA
TCGA-AC-A7VB	MSS	BRCA
TCGA-AC-A7VC	MSS	BRCA
TCGA-AC-A8OP	MSS	BRCA
TCGA-AC-A8OQ	MSS	BRCA
TCGA-AC-A8OR	MSS	BRCA
TCGA-AC-A8OS	MSS	BRCA
TCGA-AD-5900	MSI-H	COAD
TCGA-AD-6888	MSS	COAD
TCGA-AD-6889	MSI-H	COAD
TCGA-AD-6890	MSS	COAD
TCGA-AD-6895	MSI-H	COAD
TCGA-AD-6899	MSS	COAD
TCGA-AD-6901	MSS	COAD
TCGA-AD-6963	MSS	COAD
TCGA-AD-6964	MSI-H	COAD
TCGA-AD-6965	MSS	COAD
TCGA-AD-A5EJ	MSI-H	COAD
TCGA-AF-2687	MSS	READ
TCGA-AF-2690	MSS	READ
TCGA-AF-2693	MSS	READ
TCGA-AF-3911	MSS	READ
TCGA-AF-3913	MSS	READ
TCGA-AF-3914	MSS	READ
TCGA-AF-4110	MSS	READ
TCGA-AF-5654	MSS	READ
TCGA-AF-6136	MSS	READ
TCGA-AF-6655	MSS	READ
TCGA-AF-6672	MSS	READ
TCGA-AF-A56K	MSS	READ
TCGA-AF-A56L	MSS	READ
TCGA-AF-A56N	MSS	READ
TCGA-AG-3591	MSS	READ

TCGA-AG-3592	MSS	READ
TCGA-AG-3725	MSS	READ
TCGA-AG-3726	MSS	READ
TCGA-AG-3727	MSS	READ
TCGA-AG-3728	MSS	READ
TCGA-AG-3731	MSS	READ
TCGA-AG-3732	MSS	READ
TCGA-AG-3742	MSS	READ
TCGA-AG-3878	MSS	READ
TCGA-AG-3881	MSS	READ
TCGA-AG-3882	MSS	READ
TCGA-AG-3883	MSS	READ
TCGA-AG-3885	MSS	READ
TCGA-AG-3887	MSS	READ
TCGA-AG-3890	MSS	READ
TCGA-AG-3891	MSI-H	READ
TCGA-AG-3892	MSS	READ
TCGA-AG-3893	MSS	READ
TCGA-AG-3894	MSS	READ
TCGA-AG-3896	MSS	READ
TCGA-AG-3898	MSS	READ
TCGA-AG-3901	MSS	READ
TCGA-AG-3902	MSS	READ
TCGA-AG-3906	MSI-H	READ
TCGA-AG-3909	MSS	READ
TCGA-AG-3999	Intermediate	READ
TCGA-AG-4001	MSI-H	READ
TCGA-AG-4005	MSS	READ
TCGA-AG-4007	MSS	READ
TCGA-AG-4008	MSS	READ
TCGA-AG-4009	MSS	READ
TCGA-AG-4015	Intermediate	READ
TCGA-AG-4021	MSS	READ
TCGA-AG-4022	MSS	READ
TCGA-AG-A002	MSI-H	READ
TCGA-AG-A008	MSS	READ
TCGA-AG-A00C	MSS	READ
TCGA-AG-A00H	MSS	READ
TCGA-AG-A00Y	MSS	READ
TCGA-AG-A011	MSS	READ
TCGA-AG-A014	MSS	READ
TCGA-AG-A015	MSS	READ
TCGA-AG-A016	MSS	READ
TCGA-AG-A01J	MSS	READ
TCGA-AG-A01L	MSS	READ
TCGA-AG-A01N	MSS	READ
TCGA-AG-A01W	MSS	READ
TCGA-AG-A01Y	MSS	READ
TCGA-AG-A020	MSS	READ
TCGA-AG-A023	MSS	READ
TCGA-AG-A025	MSS	READ
TCGA-AG-A026	MSS	READ

TCGA-AG-A02G	MSS	READ
TCGA-AG-A02N	MSI-H	READ
TCGA-AG-A02X	MSS	READ
TCGA-AG-A032	MSS	READ
TCGA-AG-A036	MSS	READ
TCGA-AH-6544	MSS	READ
TCGA-AH-6547	MSS	READ
TCGA-AH-6549	MSS	READ
TCGA-AH-6643	MSS	READ
TCGA-AH-6644	MSS	READ
TCGA-AH-6897	MSS	READ
TCGA-AH-6903	MSS	READ
TCGA-AJ-A23M	MSS	UCEC
TCGA-AJ-A23N	MSS	UCEC
TCGA-AJ-A23O	MSI-H	UCEC
TCGA-AJ-A2QL	MSS	UCEC
TCGA-AJ-A2QM	MSS	UCEC
TCGA-AJ-A2QN	MSS	UCEC
TCGA-AJ-A2QO	MSI-H	UCEC
TCGA-AJ-A3BD	MSS	UCEC
TCGA-AJ-A3BF	MSS	UCEC
TCGA-AJ-A3BG	MSI-H	UCEC
TCGA-AJ-A3BH	MSI-H	UCEC
TCGA-AJ-A3BK	MSS	UCEC
TCGA-AJ-A3EJ	MSS	UCEC
TCGA-AJ-A3EK	MSI-H	UCEC
TCGA-AJ-A3EL	MSI-H	UCEC
TCGA-AJ-A3IA	MSS	UCEC
TCGA-AJ-A3NC	MSS	UCEC
TCGA-AJ-A3NE	MSI-H	UCEC
TCGA-AJ-A3NG	MSS	UCEC
TCGA-AJ-A3OJ	MSI-H	UCEC
TCGA-AJ-A3OK	MSI-H	UCEC
TCGA-AJ-A3QS	MSS	UCEC
TCGA-AJ-A3TW	MSS	UCEC
TCGA-AJ-A5DV	MSS	UCEC
TCGA-AJ-A5DW	MSS	UCEC
TCGA-AJ-A6NU	MSS	UCEC
TCGA-AJ-A8CT	MSI-H	UCEC
TCGA-AJ-A8CV	MSI-H	UCEC
TCGA-AJ-A8CW	MSI-H	UCEC
TCGA-AK-3427	MSI-H	KIRC
TCGA-AK-3440	MSS	KIRC
TCGA-AK-3443	MSS	KIRC
TCGA-AK-3444	MSS	KIRC
TCGA-AK-3447	MSS	KIRC
TCGA-AK-3453	MSS	KIRC
TCGA-AK-3455	MSS	KIRC
TCGA-AK-3465	MSS	KIRC
TCGA-AL-3466	MSS	KIRP
TCGA-AL-3467	MSS	KIRP
TCGA-AL-3468	MSS	KIRP

TCGA-AL-3472	MSS	KIRP
TCGA-AL-3473	MSS	KIRP
TCGA-AL-7173	MSS	KIRP
TCGA-AM-5820	MSS	COAD
TCGA-AM-5821	MSI-H	COAD
TCGA-AN-A03X	MSS	BRCA
TCGA-AN-A03Y	MSS	BRCA
TCGA-AN-A041	MSS	BRCA
TCGA-AN-A046	MSS	BRCA
TCGA-AN-A049	MSS	BRCA
TCGA-AN-A04A	MSS	BRCA
TCGA-AN-A04C	MSS	BRCA
TCGA-AN-A04D	MSS	BRCA
TCGA-AN-A0AJ	MSS	BRCA
TCGA-AN-A0AK	MSI-H	BRCA
TCGA-AN-A0AL	MSS	BRCA
TCGA-AN-A0AM	MSS	BRCA
TCGA-AN-A0AR	MSS	BRCA
TCGA-AN-A0AS	MSS	BRCA
TCGA-AN-A0AT	MSS	BRCA
TCGA-AN-A0FD	MSS	BRCA
TCGA-AN-A0FF	MSS	BRCA
TCGA-AN-A0FJ	MSS	BRCA
TCGA-AN-A0FK	MSS	BRCA
TCGA-AN-A0FL	MSS	BRCA
TCGA-AN-A0FN	MSS	BRCA
TCGA-AN-A0FS	MSS	BRCA
TCGA-AN-A0FT	MSS	BRCA
TCGA-AN-A0FV	MSS	BRCA
TCGA-AN-A0FW	MSS	BRCA
TCGA-AN-A0FX	MSS	BRCA
TCGA-AN-A0FY	MSS	BRCA
TCGA-AN-A0FZ	MSS	BRCA
TCGA-AN-A0G0	MSS	BRCA
TCGA-AN-A0XN	MSS	BRCA
TCGA-AN-A0XP	MSS	BRCA
TCGA-AN-A0XR	MSS	BRCA
TCGA-AN-A0XS	MSS	BRCA
TCGA-AN-A0XT	MSS	BRCA
TCGA-AN-A0XU	MSS	BRCA
TCGA-AN-A0XV	MSS	BRCA
TCGA-AN-A0XW	MSS	BRCA
TCGA-AO-A03L	MSS	BRCA
TCGA-AO-A03O	MSS	BRCA
TCGA-AO-A03P	MSS	BRCA
TCGA-AO-A03R	MSS	BRCA
TCGA-AO-A03T	MSS	BRCA
TCGA-AO-A03V	MSS	BRCA
TCGA-AO-A0J2	MSS	BRCA
TCGA-AO-A0J3	MSS	BRCA
TCGA-AO-A0J4	MSS	BRCA
TCGA-AO-A0J5	MSS	BRCA

TCGA-AO-A0J6	MSS	BRCA
TCGA-AO-A0J7	MSS	BRCA
TCGA-AO-A0J8	MSS	BRCA
TCGA-AO-A0J9	MSS	BRCA
TCGA-AO-A0JA	MSS	BRCA
TCGA-AO-A0JB	MSS	BRCA
TCGA-AO-A0JC	MSS	BRCA
TCGA-AO-A0JD	MSS	BRCA
TCGA-AO-A0JE	MSS	BRCA
TCGA-AO-A0JF	MSS	BRCA
TCGA-AO-A0JG	MSS	BRCA
TCGA-AO-A0JI	MSS	BRCA
TCGA-AO-A0JJ	MSS	BRCA
TCGA-AO-A0JM	MSS	BRCA
TCGA-AO-A124	MSS	BRCA
TCGA-AO-A12A	MSS	BRCA
TCGA-AO-A12D	MSS	BRCA
TCGA-AO-A12F	MSS	BRCA
TCGA-AO-A12H	MSS	BRCA
TCGA-AO-A1KO	MSS	BRCA
TCGA-AO-A1KP	MSS	BRCA
TCGA-AO-A1KR	MSS	BRCA
TCGA-AO-A1KS	MSS	BRCA
TCGA-AO-A1KT	MSI-H	BRCA
TCGA-AP-A051	MSI-H	UCEC
TCGA-AP-A052	MSS	UCEC
TCGA-AP-A053	MSS	UCEC
TCGA-AP-A054	MSI-H	UCEC
TCGA-AP-A056	Intermediate	UCEC
TCGA-AP-A059	MSI-H	UCEC
TCGA-AP-A05A	MSS	UCEC
TCGA-AP-A05D	MSS	UCEC
TCGA-AP-A05H	MSS	UCEC
TCGA-AP-A05J	MSS	UCEC
TCGA-AP-A05N	MSI-H	UCEC
TCGA-AP-A05O	MSI-H	UCEC
TCGA-AP-A05P	MSS	UCEC
TCGA-AP-A0L8	MSS	UCEC
TCGA-AP-A0L9	MSS	UCEC
TCGA-AP-A0LD	MSI-H	UCEC
TCGA-AP-A0LE	MSI-H	UCEC
TCGA-AP-A0LF	MSS	UCEC
TCGA-AP-A0LG	MSI-H	UCEC
TCGA-AP-A0LH	MSS	UCEC
TCGA-AP-A0LI	MSS	UCEC
TCGA-AP-A0LJ	MSS	UCEC
TCGA-AP-A0LL	MSS	UCEC
TCGA-AP-A0LM	MSI-H	UCEC
TCGA-AP-A0LN	MSS	UCEC
TCGA-AP-A0LO	MSS	UCEC
TCGA-AP-A0LP	MSI-H	UCEC
TCGA-AP-A0LQ	MSS	UCEC

TCGA-AP-A0LS	MSI-H	UCEC
TCGA-AP-A0LT	MSI-H	UCEC
TCGA-AP-A0LV	MSS	UCEC
TCGA-AP-A1DK	MSI-H	UCEC
TCGA-AP-A1DM	MSI-H	UCEC
TCGA-AP-A1DO	MSI-H	UCEC
TCGA-AP-A1DP	MSI-H	UCEC
TCGA-AP-A1DQ	MSS	UCEC
TCGA-AP-A1DR	MSI-H	UCEC
TCGA-AP-A1E4	MSS	UCEC
TCGA-AP-A3K1	MSS	UCEC
TCGA-AP-A5FX	Intermediate	UCEC
TCGA-AQ-A04H	MSS	BRCA
TCGA-AQ-A04J	MSS	BRCA
TCGA-AQ-A1H2	MSS	BRCA
TCGA-AQ-A1H3	Intermediate	BRCA
TCGA-AQ-A7U7	MSS	BRCA
TCGA-AR-A0TP	MSS	BRCA
TCGA-AR-A0TQ	MSS	BRCA
TCGA-AR-A0TR	MSS	BRCA
TCGA-AR-A0TS	MSS	BRCA
TCGA-AR-A0TT	MSS	BRCA
TCGA-AR-A0TU	MSS	BRCA
TCGA-AR-A0TV	MSS	BRCA
TCGA-AR-A0TW	MSS	BRCA
TCGA-AR-A0TX	MSS	BRCA
TCGA-AR-A0TY	MSI-H	BRCA
TCGA-AR-A0TZ	MSS	BRCA
TCGA-AR-A0U0	MSS	BRCA
TCGA-AR-A0U1	MSS	BRCA
TCGA-AR-A0U2	MSS	BRCA
TCGA-AR-A0U3	MSS	BRCA
TCGA-AR-A1AH	MSS	BRCA
TCGA-AR-A1AI	Intermediate	BRCA
TCGA-AR-A1AJ	MSS	BRCA
TCGA-AR-A1AK	MSS	BRCA
TCGA-AR-A1AL	MSS	BRCA
TCGA-AR-A1AN	MSS	BRCA
TCGA-AR-A1AO	MSS	BRCA
TCGA-AR-A1AP	MSS	BRCA
TCGA-AR-A1AQ	MSS	BRCA
TCGA-AR-A1AR	MSS	BRCA
TCGA-AR-A1AS	MSS	BRCA
TCGA-AR-A1AT	MSS	BRCA
TCGA-AR-A1AU	MSS	BRCA
TCGA-AR-A1AV	MSS	BRCA
TCGA-AR-A1AW	MSS	BRCA
TCGA-AR-A1AX	MSS	BRCA
TCGA-AR-A1AY	MSS	BRCA
TCGA-AR-A24H	Intermediate	BRCA
TCGA-AR-A24K	MSS	BRCA
TCGA-AR-A24L	MSS	BRCA

TCGA-AR-A24M	MSS	BRCA
TCGA-AR-A24N	MSS	BRCA
TCGA-AR-A24O	MSS	BRCA
TCGA-AR-A24P	MSS	BRCA
TCGA-AR-A24Q	MSS	BRCA
TCGA-AR-A24R	MSS	BRCA
TCGA-AR-A24S	MSS	BRCA
TCGA-AR-A24T	MSS	BRCA
TCGA-AR-A24U	Intermediate	BRCA
TCGA-AR-A24V	Intermediate	BRCA
TCGA-AR-A24W	MSS	BRCA
TCGA-AR-A24X	MSS	BRCA
TCGA-AR-A24Z	MSS	BRCA
TCGA-AR-A250	MSS	BRCA
TCGA-AR-A251	Intermediate	BRCA
TCGA-AR-A252	MSS	BRCA
TCGA-AR-A254	Intermediate	BRCA
TCGA-AR-A255	MSI-H	BRCA
TCGA-AR-A256	MSI-H	BRCA
TCGA-AR-A2LE	MSS	BRCA
TCGA-AR-A2LH	MSS	BRCA
TCGA-AR-A2LK	MSS	BRCA
TCGA-AR-A2LL	MSS	BRCA
TCGA-AR-A2LM	MSS	BRCA
TCGA-AR-A2LN	MSS	BRCA
TCGA-AR-A2LO	MSS	BRCA
TCGA-AR-A2LQ	MSS	BRCA
TCGA-AR-A2LR	MSS	BRCA
TCGA-AR-A5QP	MSS	BRCA
TCGA-AR-A5QQ	MSS	BRCA
TCGA-AS-3777	MSS	KIRC
TCGA-AS-3778	MSS	KIRC
TCGA-AU-3779	MSS	COAD
TCGA-AU-6004	MSI-H	COAD
TCGA-AX-A05S	MSI-H	UCEC
TCGA-AX-A05T	MSS	UCEC
TCGA-AX-A05U	MSS	UCEC
TCGA-AX-A05W	MSS	UCEC
TCGA-AX-A05Y	MSI-H	UCEC
TCGA-AX-A05Z	MSS	UCEC
TCGA-AX-A062	MSS	UCEC
TCGA-AX-A063	MSI-H	UCEC
TCGA-AX-A064	MSI-H	UCEC
TCGA-AX-A06B	MSS	UCEC
TCGA-AX-A06D	MSI-H	UCEC
TCGA-AX-A06F	Intermediate	UCEC
TCGA-AX-A06H	MSI-H	UCEC
TCGA-AX-A06J	MSS	UCEC
TCGA-AX-A06L	MSS	UCEC
TCGA-AX-A0IS	MSS	UCEC
TCGA-AX-A0IU	MSS	UCEC
TCGA-AX-A0IW	MSS	UCEC

TCGA-AX-A0IZ	MSI-H	UCEC
TCGA-AX-A0J0	Intermediate	UCEC
TCGA-AX-A0J1	MSI-H	UCEC
TCGA-AX-A1C4	MSI-H	UCEC
TCGA-AX-A1C5	MSI-H	UCEC
TCGA-AX-A1C7	MSS	UCEC
TCGA-AX-A1C8	MSS	UCEC
TCGA-AX-A1C9	MSI-H	UCEC
TCGA-AX-A1CA	MSI-H	UCEC
TCGA-AX-A1CC	MSI-H	UCEC
TCGA-AX-A1CE	MSI-H	UCEC
TCGA-AX-A1CF	MSS	UCEC
TCGA-AX-A1CI	MSI-H	UCEC
TCGA-AX-A1CK	MSS	UCEC
TCGA-AX-A1CP	MSS	UCEC
TCGA-AX-A1CR	MSS	UCEC
TCGA-AX-A2H5	MSS	UCEC
TCGA-AX-A2H7	MSS	UCEC
TCGA-AX-A2HA	MSI-H	UCEC
TCGA-AX-A2HC	MSI-H	UCEC
TCGA-AX-A2HD	MSI-H	UCEC
TCGA-AX-A2HF	MSS	UCEC
TCGA-AX-A2HG	MSI-H	UCEC
TCGA-AX-A2HJ	MSI-H	UCEC
TCGA-AX-A2IO	MSS	UCEC
TCGA-AX-A3FS	MSI-H	UCEC
TCGA-AX-A3FT	MSI-H	UCEC
TCGA-AX-A3FW	MSS	UCEC
TCGA-AX-A3FX	MSS	UCEC
TCGA-AX-A3FZ	MSS	UCEC
TCGA-AX-A3G4	MSS	UCEC
TCGA-AX-A3G7	MSS	UCEC
TCGA-AX-A3G8	MSI-H	UCEC
TCGA-AX-A3G9	MSI-H	UCEC
TCGA-AX-A3GB	MSS	UCEC
TCGA-AY-4070	MSS	COAD
TCGA-AY-4071	MSS	COAD
TCGA-AY-5543	MSS	COAD
TCGA-AY-6196	MSS	COAD
TCGA-AY-6197	MSI-H	COAD
TCGA-AY-6386	MSS	COAD
TCGA-AY-A69D	MSS	COAD
TCGA-AY-A71X	MSS	COAD
TCGA-AY-A8YK	MSS	COAD
TCGA-AZ-4308	Intermediate	COAD
TCGA-AZ-4313	MSI-H	COAD
TCGA-AZ-4315	Intermediate	COAD
TCGA-AZ-4614	Intermediate	COAD
TCGA-AZ-4615	MSI-H	COAD
TCGA-AZ-4681	MSS	COAD
TCGA-AZ-4682	MSS	COAD
TCGA-AZ-4684	MSS	COAD

TCGA-AZ-5403	MSS	COAD
TCGA-AZ-5407	MSS	COAD
TCGA-AZ-6598	MSI-H	COAD
TCGA-AZ-6599	MSS	COAD
TCGA-AZ-6600	MSS	COAD
TCGA-AZ-6601	MSI-H	COAD
TCGA-AZ-6606	MSS	COAD
TCGA-AZ-6607	MSS	COAD
TCGA-AZ-6608	MSS	COAD
TCGA-B0-4700	MSS	KIRC
TCGA-B0-4823	MSS	KIRC
TCGA-B0-4827	MSS	KIRC
TCGA-B0-4842	MSS	KIRC
TCGA-B0-4945	MSS	KIRC
TCGA-B0-5075	MSS	KIRC
TCGA-B0-5077	MSS	KIRC
TCGA-B0-5081	MSS	KIRC
TCGA-B0-5083	MSS	KIRC
TCGA-B0-5084	MSS	KIRC
TCGA-B0-5085	MSS	KIRC
TCGA-B0-5088	MSS	KIRC
TCGA-B0-5092	MSS	KIRC
TCGA-B0-5094	MSS	KIRC
TCGA-B0-5095	MSS	KIRC
TCGA-B0-5096	MSS	KIRC
TCGA-B0-5097	MSS	KIRC
TCGA-B0-5098	MSI-H	KIRC
TCGA-B0-5099	MSS	KIRC
TCGA-B0-5100	MSS	KIRC
TCGA-B0-5102	MSS	KIRC
TCGA-B0-5104	MSS	KIRC
TCGA-B0-5106	MSS	KIRC
TCGA-B0-5107	MSS	KIRC
TCGA-B0-5108	MSS	KIRC
TCGA-B0-5109	MSS	KIRC
TCGA-B0-5110	MSS	KIRC
TCGA-B0-5113	MSS	KIRC
TCGA-B0-5115	MSS	KIRC
TCGA-B0-5116	MSS	KIRC
TCGA-B0-5117	MSS	KIRC
TCGA-B0-5119	MSS	KIRC
TCGA-B0-5120	MSS	KIRC
TCGA-B0-5121	MSS	KIRC
TCGA-B0-5399	MSS	KIRC
TCGA-B0-5400	MSS	KIRC
TCGA-B0-5402	MSS	KIRC
TCGA-B0-5690	MSS	KIRC
TCGA-B0-5691	MSS	KIRC
TCGA-B0-5692	MSS	KIRC
TCGA-B0-5693	MSS	KIRC
TCGA-B0-5694	MSS	KIRC
TCGA-B0-5695	MSS	KIRC

TCGA-B0-5696	MSS	KIRC
TCGA-B0-5697	MSS	KIRC
TCGA-B0-5698	MSS	KIRC
TCGA-B0-5699	MSS	KIRC
TCGA-B0-5700	MSS	KIRC
TCGA-B0-5701	MSS	KIRC
TCGA-B0-5702	MSS	KIRC
TCGA-B0-5703	MSS	KIRC
TCGA-B0-5705	MSS	KIRC
TCGA-B0-5706	MSS	KIRC
TCGA-B0-5707	MSS	KIRC
TCGA-B0-5709	MSS	KIRC
TCGA-B0-5710	MSS	KIRC
TCGA-B0-5711	MSS	KIRC
TCGA-B0-5712	MSS	KIRC
TCGA-B0-5713	MSS	KIRC
TCGA-B0-5812	MSS	KIRC
TCGA-B1-5398	MSS	KIRP
TCGA-B1-7332	MSS	KIRP
TCGA-B1-A654	MSS	KIRP
TCGA-B1-A655	MSS	KIRP
TCGA-B1-A656	MSS	KIRP
TCGA-B1-A657	MSS	KIRP
TCGA-B2-4101	MSS	KIRC
TCGA-B2-4102	MSS	KIRC
TCGA-B2-5633	MSS	KIRC
TCGA-B2-5633	MSS	KIRC
TCGA-B2-5635	MSS	KIRC
TCGA-B2-5636	MSS	KIRC
TCGA-B2-5639	MSS	KIRC
TCGA-B2-5641	MSS	KIRC
TCGA-B2-A4SR	MSS	KIRC
TCGA-B3-3925	MSS	KIRP
TCGA-B3-3926	MSS	KIRP
TCGA-B3-4103	MSS	KIRP
TCGA-B3-4104	MSS	KIRP
TCGA-B3-8121	MSS	KIRP
TCGA-B3-A6W5	MSS	KIRP
TCGA-B4-5377	MSS	KIRC
TCGA-B4-5378	MSS	KIRC
TCGA-B4-5832	MSS	KIRC
TCGA-B4-5834	MSS	KIRC
TCGA-B4-5835	MSS	KIRC
TCGA-B4-5836	MSS	KIRC
TCGA-B4-5838	MSS	KIRC
TCGA-B4-5843	MSS	KIRC
TCGA-B4-5844	MSS	KIRC
TCGA-B5-A0JN	MSS	UCEC
TCGA-B5-A0JR	MSI-H	UCEC
TCGA-B5-A0JS	MSS	UCEC
TCGA-B5-A0JT	MSS	UCEC
TCGA-B5-A0JU	MSI-H	UCEC

TCGA-B5-A0JV	MSI-H	UCEC
TCGA-B5-A0JY	Intermediate	UCEC
TCGA-B5-A0JZ	MSI-H	UCEC
TCGA-B5-A0K0	MSS	UCEC
TCGA-B5-A0K1	MSS	UCEC
TCGA-B5-A0K2	MSI-H	UCEC
TCGA-B5-A0K3	MSS	UCEC
TCGA-B5-A0K4	MSS	UCEC
TCGA-B5-A0K6	MSI-H	UCEC
TCGA-B5-A0K7	MSS	UCEC
TCGA-B5-A0K8	MSS	UCEC
TCGA-B5-A0K9	MSI-H	UCEC
TCGA-B5-A11E	MSI-H	UCEC
TCGA-B5-A11F	MSS	UCEC
TCGA-B5-A11G	MSI-H	UCEC
TCGA-B5-A11H	MSI-H	UCEC
TCGA-B5-A11I	Intermediate	UCEC
TCGA-B5-A11J	MSI-H	UCEC
TCGA-B5-A11M	MSS	UCEC
TCGA-B5-A11N	MSS	UCEC
TCGA-B5-A11O	MSS	UCEC
TCGA-B5-A11Q	MSS	UCEC
TCGA-B5-A11R	MSS	UCEC
TCGA-B5-A11S	MSS	UCEC
TCGA-B5-A11U	MSI-H	UCEC
TCGA-B5-A11V	MSS	UCEC
TCGA-B5-A11W	MSS	UCEC
TCGA-B5-A11X	MSS	UCEC
TCGA-B5-A11Y	MSI-H	UCEC
TCGA-B5-A11Z	MSS	UCEC
TCGA-B5-A121	MSS	UCEC
TCGA-B5-A1MR	MSS	UCEC
TCGA-B5-A1MS	MSS	UCEC
TCGA-B5-A1MU	MSS	UCEC
TCGA-B5-A1MV	MSS	UCEC
TCGA-B5-A1MW	MSI-H	UCEC
TCGA-B5-A1MX	MSI-H	UCEC
TCGA-B5-A1MY	MSS	UCEC
TCGA-B5-A1N2	MSI-H	UCEC
TCGA-B5-A3F9	MSS	UCEC
TCGA-B5-A3FA	MSI-H	UCEC
TCGA-B5-A3FC	MSI-H	UCEC
TCGA-B5-A5OC	MSI-H	UCEC
TCGA-B5-A5OD	MSS	UCEC
TCGA-B5-A5OE	MSS	UCEC
TCGA-B6-A0I1	MSS	BRCA
TCGA-B6-A0I2	MSS	BRCA
TCGA-B6-A0I5	MSS	BRCA
TCGA-B6-A0I6	MSS	BRCA
TCGA-B6-A0I6	MSS	BRCA
TCGA-B6-A0I8	MSS	BRCA
TCGA-B6-A0I9	MSS	BRCA

TCGA-B6-A0IA	MSS	BRCA
TCGA-B6-A0IB	MSS	BRCA
TCGA-B6-A0IC	MSS	BRCA
TCGA-B6-A0IE	MSS	BRCA
TCGA-B6-A0IH	MSS	BRCA
TCGA-B6-A0IJ	MSS	BRCA
TCGA-B6-A0IK	MSS	BRCA
TCGA-B6-A0IM	MSS	BRCA
TCGA-B6-A0IN	MSS	BRCA
TCGA-B6-A0RE	MSS	BRCA
TCGA-B6-A0RG	MSS	BRCA
TCGA-B6-A0RH	MSS	BRCA
TCGA-B6-A0RI	MSS	BRCA
TCGA-B6-A0RL	MSS	BRCA
TCGA-B6-A0RM	MSS	BRCA
TCGA-B6-A0RN	MSS	BRCA
TCGA-B6-A0RO	MSS	BRCA
TCGA-B6-A0RP	MSS	BRCA
TCGA-B6-A0RQ	MSS	BRCA
TCGA-B6-A0RS	MSS	BRCA
TCGA-B6-A0RT	MSS	BRCA
TCGA-B6-A0RU	MSS	BRCA
TCGA-B6-A0RV	MSS	BRCA
TCGA-B6-A0WS	MSS	BRCA
TCGA-B6-A0WT	MSS	BRCA
TCGA-B6-A0WV	MSS	BRCA
TCGA-B6-A0WW	MSS	BRCA
TCGA-B6-A0WX	MSS	BRCA
TCGA-B6-A0WY	MSS	BRCA
TCGA-B6-A0WZ	MSS	BRCA
TCGA-B6-A0X0	MSS	BRCA
TCGA-B6-A0X1	MSS	BRCA
TCGA-B6-A0X4	MSS	BRCA
TCGA-B6-A0X5	MSS	BRCA
TCGA-B6-A1KC	MSS	BRCA
TCGA-B6-A1KF	MSS	BRCA
TCGA-B6-A1KI	MSS	BRCA
TCGA-B6-A1KN	MSS	BRCA
TCGA-B6-A2IU	MSS	BRCA
TCGA-B6-A400	MSS	BRCA
TCGA-B6-A401	MSS	BRCA
TCGA-B6-A402	MSS	BRCA
TCGA-B6-A409	MSS	BRCA
TCGA-B6-A40B	MSS	BRCA
TCGA-B7-5816	MSI-H	STAD
TCGA-B7-5818	MSS	STAD
TCGA-B7-A5TI	MSI-H	STAD
TCGA-B7-A5TJ	MSS	STAD
TCGA-B7-A5TK	MSS	STAD
TCGA-B7-A5TN	MSS	STAD
TCGA-B8-4143	MSS	KIRC
TCGA-B8-4146	MSS	KIRC

TCGA-B8-4148	MSS	KIRC
TCGA-B8-4151	MSS	KIRC
TCGA-B8-4153	MSS	KIRC
TCGA-B8-4621	MSS	KIRC
TCGA-B8-4622	MSS	KIRC
TCGA-B8-5158	MSS	KIRC
TCGA-B8-5159	MSS	KIRC
TCGA-B8-5162	MSS	KIRC
TCGA-B8-5163	MSS	KIRC
TCGA-B8-5164	MSS	KIRC
TCGA-B8-5165	MSS	KIRC
TCGA-B8-5545	MSS	KIRC
TCGA-B8-5546	MSS	KIRC
TCGA-B8-5549	MSS	KIRC
TCGA-B8-5550	MSS	KIRC
TCGA-B8-5551	MSS	KIRC
TCGA-B8-5552	MSS	KIRC
TCGA-B8-5553	MSS	KIRC
TCGA-B8-A54H	MSS	KIRC
TCGA-B8-A54I	MSS	KIRC
TCGA-B8-A54J	MSS	KIRC
TCGA-B8-A54K	MSS	KIRC
TCGA-B8-A7U6	MSS	KIRC
TCGA-B8-A8YJ	MSS	KIRC
TCGA-B9-4113	MSS	KIRP
TCGA-B9-4114	MSS	KIRP
TCGA-B9-4115	MSS	KIRP
TCGA-B9-4116	MSS	KIRP
TCGA-B9-4117	MSS	KIRP
TCGA-B9-4617	MSS	KIRP
TCGA-B9-5155	MSS	KIRP
TCGA-B9-5156	MSS	KIRP
TCGA-B9-7268	MSS	KIRP
TCGA-B9-A5W7	MSS	KIRP
TCGA-B9-A69E	MSS	KIRP
TCGA-B9-A8YH	MSS	KIRP
TCGA-B9-A8YI	MSS	KIRP
TCGA-BA-4074	MSS	HNSC
TCGA-BA-4075	MSS	HNSC
TCGA-BA-4076	MSS	HNSC
TCGA-BA-4077	MSS	HNSC
TCGA-BA-4078	MSS	HNSC
TCGA-BA-5149	MSS	HNSC
TCGA-BA-5151	MSS	HNSC
TCGA-BA-5152	MSS	HNSC
TCGA-BA-5153	MSS	HNSC
TCGA-BA-5555	MSS	HNSC
TCGA-BA-5556	MSS	HNSC
TCGA-BA-5557	MSS	HNSC
TCGA-BA-5558	MSS	HNSC
TCGA-BA-5559	MSS	HNSC
TCGA-BA-6868	MSS	HNSC

TCGA-BA-6869	MSS	HNSC
TCGA-BA-6870	MSS	HNSC
TCGA-BA-6871	MSS	HNSC
TCGA-BA-6872	MSS	HNSC
TCGA-BA-6873	MSS	HNSC
TCGA-BA-7269	MSS	HNSC
TCGA-BA-A4IF	MSS	HNSC
TCGA-BA-A4IG	MSS	HNSC
TCGA-BA-A4IH	MSS	HNSC
TCGA-BA-A4II	MSS	HNSC
TCGA-BA-A6D8	MSS	HNSC
TCGA-BA-A6DA	MSS	HNSC
TCGA-BA-A6DB	MSS	HNSC
TCGA-BA-A6DD	MSS	HNSC
TCGA-BA-A6DE	MSS	HNSC
TCGA-BA-A6DF	MSS	HNSC
TCGA-BA-A6DG	MSS	HNSC
TCGA-BA-A6DI	MSS	HNSC
TCGA-BA-A6DJ	MSS	HNSC
TCGA-BA-A6DL	MSS	HNSC
TCGA-BA-A8YP	MSS	HNSC
TCGA-BB-4217	MSS	HNSC
TCGA-BB-4223	MSS	HNSC
TCGA-BB-4224	MSS	HNSC
TCGA-BB-4225	MSS	HNSC
TCGA-BB-4227	MSS	HNSC
TCGA-BB-4228	MSS	HNSC
TCGA-BB-7870	MSS	HNSC
TCGA-BB-8596	MSS	HNSC
TCGA-BB-8601	MSS	HNSC
TCGA-BB-A5HU	MSS	HNSC
TCGA-BB-A5HY	MSS	HNSC
TCGA-BB-A5HZ	MSS	HNSC
TCGA-BB-A6UM	MSS	HNSC
TCGA-BB-A6UO	MSS	HNSC
TCGA-BC-4073	MSS	LIHC
TCGA-BC-A10Q	MSS	LIHC
TCGA-BC-A10R	MSS	LIHC
TCGA-BC-A10S	MSS	LIHC
TCGA-BC-A10T	MSS	LIHC
TCGA-BC-A10U	MSS	LIHC
TCGA-BC-A10W	MSS	LIHC
TCGA-BC-A10X	MSS	LIHC
TCGA-BC-A10Y	MSS	LIHC
TCGA-BC-A10Z	MSS	LIHC
TCGA-BC-A110	MSS	LIHC
TCGA-BC-A112	MSI-H	LIHC
TCGA-BC-A216	MSS	LIHC
TCGA-BC-A217	MSS	LIHC
TCGA-BC-A3KG	MSS	LIHC
TCGA-BC-A69H	MSS	LIHC
TCGA-BC-A69I	MSS	LIHC

TCGA-BC-A8YO	MSS	LIHC
TCGA-BD-A3EP	MSS	LIHC
TCGA-BD-A3ER	MSS	LIHC
TCGA-BF-A1PU	MSS	SKCM
TCGA-BF-A1PX	MSS	SKCM
TCGA-BF-A1PZ	MSS	SKCM
TCGA-BF-A1Q0	MSS	SKCM
TCGA-BF-A3DL	MSS	SKCM
TCGA-BF-A5EO	MSS	SKCM
TCGA-BF-A5EP	MSS	SKCM
TCGA-BF-A5EQ	MSS	SKCM
TCGA-BF-A5ER	MSS	SKCM
TCGA-BF-A5ES	MSS	SKCM
TCGA-BF-A9VF	MSS	SKCM
TCGA-BF-AAOU	MSS	SKCM
TCGA-BF-AAOX	MSS	SKCM
TCGA-BF-AAP0	MSS	SKCM
TCGA-BF-AAP1	MSS	SKCM
TCGA-BF-AAP2	MSS	SKCM
TCGA-BF-AAP4	MSS	SKCM
TCGA-BF-AAP6	MSS	SKCM
TCGA-BF-AAP7	MSS	SKCM
TCGA-BF-AAP8	MSS	SKCM
TCGA-BG-A0LW	MSS	UCEC
TCGA-BG-A0LX	MSI-H	UCEC
TCGA-BG-A0M0	MSI-H	UCEC
TCGA-BG-A0M2	MSS	UCEC
TCGA-BG-A0M3	MSS	UCEC
TCGA-BG-A0M4	MSI-H	UCEC
TCGA-BG-A0M6	Intermediate	UCEC
TCGA-BG-A0M7	MSS	UCEC
TCGA-BG-A0M8	MSS	UCEC
TCGA-BG-A0M9	MSS	UCEC
TCGA-BG-A0MC	MSS	UCEC
TCGA-BG-A0MG	MSS	UCEC
TCGA-BG-A0MI	MSS	UCEC
TCGA-BG-A0MK	MSS	UCEC
TCGA-BG-A0MO	MSS	UCEC
TCGA-BG-A0MQ	MSI-H	UCEC
TCGA-BG-A0MS	Intermediate	UCEC
TCGA-BG-A0MT	MSS	UCEC
TCGA-BG-A0MU	MSS	UCEC
TCGA-BG-A0RY	MSS	UCEC
TCGA-BG-A0VT	MSS	UCEC
TCGA-BG-A0VV	MSS	UCEC
TCGA-BG-A0VW	MSI-H	UCEC
TCGA-BG-A0VX	MSS	UCEC
TCGA-BG-A0VZ	MSI-H	UCEC
TCGA-BG-A0W1	MSS	UCEC
TCGA-BG-A0W2	MSS	UCEC
TCGA-BG-A0YU	MSS	UCEC
TCGA-BG-A0YV	MSS	UCEC

TCGA-BG-A186	MSS	UCEC
TCGA-BG-A187	MSS	UCEC
TCGA-BG-A18A	MSS	UCEC
TCGA-BG-A18B	MSI-H	UCEC
TCGA-BG-A18C	MSS	UCEC
TCGA-BG-A220	MSI-H	UCEC
TCGA-BG-A221	MSI-H	UCEC
TCGA-BG-A222	MSI-H	UCEC
TCGA-BG-A2AE	MSS	UCEC
TCGA-BG-A2L7	MSI-H	UCEC
TCGA-BG-A3EW	MSI-H	UCEC
TCGA-BH-A0AU	MSS	BRCA
TCGA-BH-A0AV	MSS	BRCA
TCGA-BH-A0AW	MSS	BRCA
TCGA-BH-A0AY	MSS	BRCA
TCGA-BH-A0AZ	MSS	BRCA
TCGA-BH-A0B0	MSS	BRCA
TCGA-BH-A0B3	MSS	BRCA
TCGA-BH-A0B4	MSS	BRCA
TCGA-BH-A0B5	MSS	BRCA
TCGA-BH-A0B6	MSS	BRCA
TCGA-BH-A0B7	MSS	BRCA
TCGA-BH-A0B8	MSS	BRCA
TCGA-BH-A0B9	MSS	BRCA
TCGA-BH-A0BA	MSS	BRCA
TCGA-BH-A0BC	MSS	BRCA
TCGA-BH-A0BD	MSS	BRCA
TCGA-BH-A0BF	MSS	BRCA
TCGA-BH-A0BG	MSS	BRCA
TCGA-BH-A0BJ	MSS	BRCA
TCGA-BH-A0BL	MSS	BRCA
TCGA-BH-A0BM	MSS	BRCA
TCGA-BH-A0BO	MSS	BRCA
TCGA-BH-A0BP	MSS	BRCA
TCGA-BH-A0BQ	MSS	BRCA
TCGA-BH-A0BR	MSS	BRCA
TCGA-BH-A0BS	MSS	BRCA
TCGA-BH-A0BT	MSS	BRCA
TCGA-BH-A0BV	MSS	BRCA
TCGA-BH-A0BW	MSS	BRCA
TCGA-BH-A0BZ	MSS	BRCA
TCGA-BH-A0C0	MSS	BRCA
TCGA-BH-A0C1	MSS	BRCA
TCGA-BH-A0C3	MSS	BRCA
TCGA-BH-A0C7	MSS	BRCA
TCGA-BH-A0DD	MSS	BRCA
TCGA-BH-A0DE	MSS	BRCA
TCGA-BH-A0DG	MSS	BRCA
TCGA-BH-A0DH	MSS	BRCA
TCGA-BH-A0DI	MSS	BRCA
TCGA-BH-A0DK	MSS	BRCA
TCGA-BH-A0DL	MSS	BRCA

TCGA-BH-A0DO	MSS	BRCA
TCGA-BH-A0DP	MSS	BRCA
TCGA-BH-A0DQ	MSS	BRCA
TCGA-BH-A0DS	MSS	BRCA
TCGA-BH-A0DT	MSS	BRCA
TCGA-BH-A0DV	MSS	BRCA
TCGA-BH-A0DX	MSS	BRCA
TCGA-BH-A0DZ	MSS	BRCA
TCGA-BH-A0E0	MSS	BRCA
TCGA-BH-A0E1	MSS	BRCA
TCGA-BH-A0E2	MSS	BRCA
TCGA-BH-A0E7	MSS	BRCA
TCGA-BH-A0E9	MSS	BRCA
TCGA-BH-A0EA	MSS	BRCA
TCGA-BH-A0EB	MSS	BRCA
TCGA-BH-A0EE	MSS	BRCA
TCGA-BH-A0EI	MSS	BRCA
TCGA-BH-A0GY	MSS	BRCA
TCGA-BH-A0GZ	MSS	BRCA
TCGA-BH-A0H0	MSS	BRCA
TCGA-BH-A0H3	MSS	BRCA
TCGA-BH-A0H5	MSS	BRCA
TCGA-BH-A0H6	MSS	BRCA
TCGA-BH-A0H7	MSS	BRCA
TCGA-BH-A0H9	MSS	BRCA
TCGA-BH-A0HA	MSI-H	BRCA
TCGA-BH-A0HB	MSS	BRCA
TCGA-BH-A0HF	MSS	BRCA
TCGA-BH-A0HI	MSS	BRCA
TCGA-BH-A0HK	MSS	BRCA
TCGA-BH-A0HL	MSS	BRCA
TCGA-BH-A0HN	MSS	BRCA
TCGA-BH-A0HO	MSS	BRCA
TCGA-BH-A0HP	MSS	BRCA
TCGA-BH-A0HQ	MSS	BRCA
TCGA-BH-A0HU	MSS	BRCA
TCGA-BH-A0HW	MSS	BRCA
TCGA-BH-A0HX	MSS	BRCA
TCGA-BH-A0HY	MSS	BRCA
TCGA-BH-A0RX	MSS	BRCA
TCGA-BH-A0W3	MSS	BRCA
TCGA-BH-A0W4	MSS	BRCA
TCGA-BH-A0W5	MSS	BRCA
TCGA-BH-A0W7	MSS	BRCA
TCGA-BH-A0WA	MSS	BRCA
TCGA-BH-A18F	MSS	BRCA
TCGA-BH-A18G	MSI-H	BRCA
TCGA-BH-A18H	MSS	BRCA
TCGA-BH-A18I	MSS	BRCA
TCGA-BH-A18J	MSS	BRCA
TCGA-BH-A18K	MSS	BRCA
TCGA-BH-A18L	MSS	BRCA

TCGA-BH-A18M	MSS	BRCA
TCGA-BH-A18N	MSS	BRCA
TCGA-BH-A18P	MSS	BRCA
TCGA-BH-A18Q	MSS	BRCA
TCGA-BH-A18R	MSS	BRCA
TCGA-BH-A18S	MSS	BRCA
TCGA-BH-A18T	MSS	BRCA
TCGA-BH-A18U	MSS	BRCA
TCGA-BH-A18V	MSS	BRCA
TCGA-BH-A18V	MSS	BRCA
TCGA-BH-A1EN	MSS	BRCA
TCGA-BH-A1EO	MSS	BRCA
TCGA-BH-A1ES	MSS	BRCA
TCGA-BH-A1ES	Intermediate	BRCA
TCGA-BH-A1ET	MSS	BRCA
TCGA-BH-A1EU	MSS	BRCA
TCGA-BH-A1EV	MSS	BRCA
TCGA-BH-A1EW	MSS	BRCA
TCGA-BH-A1EX	MSS	BRCA
TCGA-BH-A1EY	MSS	BRCA
TCGA-BH-A1F0	MSS	BRCA
TCGA-BH-A1F2	MSS	BRCA
TCGA-BH-A1F5	MSS	BRCA
TCGA-BH-A1F6	Intermediate	BRCA
TCGA-BH-A1F8	MSS	BRCA
TCGA-BH-A1FC	Intermediate	BRCA
TCGA-BH-A1FE	MSS	BRCA
TCGA-BH-A1FE	MSS	BRCA
TCGA-BH-A1FG	MSS	BRCA
TCGA-BH-A1FH	MSS	BRCA
TCGA-BH-A1FJ	MSI-H	BRCA
TCGA-BH-A1FL	MSS	BRCA
TCGA-BH-A1FM	MSI-H	BRCA
TCGA-BH-A1FN	MSS	BRCA
TCGA-BH-A1FR	MSS	BRCA
TCGA-BH-A1FU	MSS	BRCA
TCGA-BH-A201	MSS	BRCA
TCGA-BH-A202	MSS	BRCA
TCGA-BH-A203	MSS	BRCA
TCGA-BH-A204	MSS	BRCA
TCGA-BH-A208	Intermediate	BRCA
TCGA-BH-A209	MSS	BRCA
TCGA-BH-A28O	MSS	BRCA
TCGA-BH-A28Q	MSS	BRCA
TCGA-BH-A2L8	MSS	BRCA
TCGA-BH-A5J0	MSS	BRCA
TCGA-BH-A6R8	MSS	BRCA
TCGA-BH-A6R9	MSS	BRCA
TCGA-BH-A8FY	MSS	BRCA
TCGA-BH-A8FZ	MSS	BRCA
TCGA-BH-A8G0	MSS	BRCA
TCGA-BH-AB28	MSS	BRCA

TCGA-BI-A0VR	MSS	CESC
TCGA-BI-A0VS	MSS	CESC
TCGA-BJ-A0YZ	MSS	THCA
TCGA-BJ-A0Z0	MSS	THCA
TCGA-BJ-A0Z2	MSS	THCA
TCGA-BJ-A0Z3	MSS	THCA
TCGA-BJ-A0Z9	MSS	THCA
TCGA-BJ-A0ZA	MSS	THCA
TCGA-BJ-A0ZB	MSS	THCA
TCGA-BJ-A0ZC	MSS	THCA
TCGA-BJ-A0ZE	MSS	THCA
TCGA-BJ-A0ZF	MSS	THCA
TCGA-BJ-A0ZG	MSS	THCA
TCGA-BJ-A0ZH	MSS	THCA
TCGA-BJ-A0ZJ	MSS	THCA
TCGA-BJ-A18Y	MSS	THCA
TCGA-BJ-A18Z	MSS	THCA
TCGA-BJ-A191	MSS	THCA
TCGA-BJ-A192	MSS	THCA
TCGA-BJ-A28R	MSS	THCA
TCGA-BJ-A28S	MSS	THCA
TCGA-BJ-A28T	MSS	THCA
TCGA-BJ-A28V	MSS	THCA
TCGA-BJ-A28Z	MSS	THCA
TCGA-BJ-A290	MSS	THCA
TCGA-BJ-A2N7	MSS	THCA
TCGA-BJ-A2N8	MSS	THCA
TCGA-BJ-A2N9	MSS	THCA
TCGA-BJ-A2NA	MSS	THCA
TCGA-BJ-A2P4	MSS	THCA
TCGA-BJ-A3EZ	MSS	THCA
TCGA-BJ-A3F0	MSS	THCA
TCGA-BJ-A3PR	MSS	THCA
TCGA-BJ-A3PT	MSS	THCA
TCGA-BJ-A3PU	MSS	THCA
TCGA-BJ-A45D	MSS	THCA
TCGA-BJ-A45G	MSS	THCA
TCGA-BJ-A45H	MSS	THCA
TCGA-BJ-A45I	MSS	THCA
TCGA-BJ-A45J	MSS	THCA
TCGA-BJ-A4O8	MSS	THCA
TCGA-BK-A0C9	MSI-H	UCEC
TCGA-BK-A0CA	MSS	UCEC
TCGA-BK-A0CA	MSI-H	UCEC
TCGA-BK-A0CB	MSS	UCEC
TCGA-BK-A0CC	MSS	UCEC
TCGA-BK-A0CC	MSI-H	UCEC
TCGA-BK-A139	MSI-H	UCEC
TCGA-BK-A139	MSI-H	UCEC
TCGA-BK-A139	MSI-H	UCEC
TCGA-BK-A13B	MSI-H	UCEC
TCGA-BK-A13C	MSS	UCEC

TCGA-BK-A26L	MSS	UCEC
TCGA-BK-A26L	MSI-H	UCEC
TCGA-BK-A6W3	MSS	UCEC
TCGA-BK-A6W4	MSS	UCEC
TCGA-BL-A0C8	MSS	BLCA
TCGA-BL-A0C8	Intermediate	BLCA
TCGA-BL-A13I	MSS	BLCA
TCGA-BL-A13I	MSS	BLCA
TCGA-BL-A13J	MSS	BLCA
TCGA-BL-A13J	MSS	BLCA
TCGA-BL-A5ZZ	MSS	BLCA
TCGA-BM-6198	MSS	READ
TCGA-BP-4177	MSS	KIRC
TCGA-BP-4760	MSS	KIRC
TCGA-BP-4770	MSS	KIRC
TCGA-BP-4782	MSS	KIRC
TCGA-BP-4795	MSS	KIRC
TCGA-BP-4801	MSS	KIRC
TCGA-BP-4960	MSS	KIRC
TCGA-BP-4961	MSS	KIRC
TCGA-BP-4962	MSS	KIRC
TCGA-BP-4963	MSS	KIRC
TCGA-BP-4964	MSS	KIRC
TCGA-BP-4965	MSS	KIRC
TCGA-BP-4967	MSS	KIRC
TCGA-BP-4968	MSS	KIRC
TCGA-BP-4970	MSS	KIRC
TCGA-BP-4971	MSS	KIRC
TCGA-BP-4972	MSS	KIRC
TCGA-BP-4973	MSS	KIRC
TCGA-BP-4974	MSS	KIRC
TCGA-BP-4975	MSS	KIRC
TCGA-BP-4976	MSS	KIRC
TCGA-BP-4977	Intermediate	KIRC
TCGA-BP-4981	MSS	KIRC
TCGA-BP-4982	MSS	KIRC
TCGA-BP-4983	MSS	KIRC
TCGA-BP-4985	MSS	KIRC
TCGA-BP-4986	MSS	KIRC
TCGA-BP-4987	MSS	KIRC
TCGA-BP-4988	MSS	KIRC
TCGA-BP-4989	MSS	KIRC
TCGA-BP-4991	MSS	KIRC
TCGA-BP-4992	MSS	KIRC
TCGA-BP-4993	MSS	KIRC
TCGA-BP-4995	MSS	KIRC
TCGA-BP-4998	MSS	KIRC
TCGA-BP-4999	MSS	KIRC
TCGA-BP-5000	MSS	KIRC
TCGA-BP-5001	MSS	KIRC
TCGA-BP-5004	MSS	KIRC
TCGA-BP-5006	MSS	KIRC

TCGA-BP-5007	MSS	KIRC
TCGA-BP-5008	MSS	KIRC
TCGA-BP-5009	MSS	KIRC
TCGA-BP-5010	MSS	KIRC
TCGA-BP-5168	MSS	KIRC
TCGA-BP-5169	MSS	KIRC
TCGA-BP-5170	MSS	KIRC
TCGA-BP-5173	Intermediate	KIRC
TCGA-BP-5174	MSS	KIRC
TCGA-BP-5175	MSS	KIRC
TCGA-BP-5176	Intermediate	KIRC
TCGA-BP-5177	MSS	KIRC
TCGA-BP-5178	MSS	KIRC
TCGA-BP-5180	MSS	KIRC
TCGA-BP-5181	MSS	KIRC
TCGA-BP-5182	MSS	KIRC
TCGA-BP-5183	MSS	KIRC
TCGA-BP-5184	MSS	KIRC
TCGA-BP-5185	MSS	KIRC
TCGA-BP-5186	MSS	KIRC
TCGA-BP-5187	MSS	KIRC
TCGA-BP-5189	MSS	KIRC
TCGA-BP-5190	MSS	KIRC
TCGA-BP-5191	MSS	KIRC
TCGA-BP-5192	MSS	KIRC
TCGA-BP-5194	MSS	KIRC
TCGA-BP-5195	MSS	KIRC
TCGA-BP-5196	MSS	KIRC
TCGA-BP-5198	MSS	KIRC
TCGA-BP-5199	MSS	KIRC
TCGA-BP-5200	MSS	KIRC
TCGA-BP-5201	MSS	KIRC
TCGA-BP-5202	MSS	KIRC
TCGA-BQ-5875	MSS	KIRP
TCGA-BQ-5876	MSS	KIRP
TCGA-BQ-5877	MSS	KIRP
TCGA-BQ-5878	MSS	KIRP
TCGA-BQ-5879	MSS	KIRP
TCGA-BQ-5880	MSS	KIRP
TCGA-BQ-5881	MSS	KIRP
TCGA-BQ-5882	MSS	KIRP
TCGA-BQ-5883	MSS	KIRP
TCGA-BQ-5884	MSS	KIRP
TCGA-BQ-5885	MSS	KIRP
TCGA-BQ-5886	MSS	KIRP
TCGA-BQ-5887	MSS	KIRP
TCGA-BQ-5888	MSS	KIRP
TCGA-BQ-5889	MSS	KIRP
TCGA-BQ-5890	MSS	KIRP
TCGA-BQ-5891	MSS	KIRP
TCGA-BQ-5892	MSS	KIRP
TCGA-BQ-5893	MSS	KIRP

TCGA-BQ-5894	MSS	KIRP
TCGA-BQ-7044	MSS	KIRP
TCGA-BQ-7045	MSS	KIRP
TCGA-BQ-7046	MSS	KIRP
TCGA-BQ-7048	MSS	KIRP
TCGA-BQ-7049	MSS	KIRP
TCGA-BQ-7050	MSS	KIRP
TCGA-BQ-7051	MSS	KIRP
TCGA-BQ-7053	MSS	KIRP
TCGA-BQ-7055	MSS	KIRP
TCGA-BQ-7056	MSS	KIRP
TCGA-BQ-7058	MSS	KIRP
TCGA-BQ-7059	MSS	KIRP
TCGA-BQ-7060	MSS	KIRP
TCGA-BQ-7061	MSS	KIRP
TCGA-BQ-7062	MSS	KIRP
TCGA-BR-4183	MSS	STAD
TCGA-BR-4184	MSI-H	STAD
TCGA-BR-4187	MSS	STAD
TCGA-BR-4188	MSS	STAD
TCGA-BR-4191	MSS	STAD
TCGA-BR-4201	MSI-H	STAD
TCGA-BR-4253	MSS	STAD
TCGA-BR-4255	MSS	STAD
TCGA-BR-4256	MSI-H	STAD
TCGA-BR-4257	MSI-H	STAD
TCGA-BR-4267	MSS	STAD
TCGA-BR-4279	MSS	STAD
TCGA-BR-4280	MSI-H	STAD
TCGA-BR-4292	MSI-H	STAD
TCGA-BR-4294	MSS	STAD
TCGA-BR-4357	MSS	STAD
TCGA-BR-4361	MSI-H	STAD
TCGA-BR-4362	MSI-H	STAD
TCGA-BR-4363	MSI-H	STAD
TCGA-BR-4366	MSS	STAD
TCGA-BR-4368	MSI-H	STAD
TCGA-BR-4369	MSS	STAD
TCGA-BR-4370	MSI-H	STAD
TCGA-BR-4371	MSS	STAD
TCGA-BR-6452	MSI-H	STAD
TCGA-BR-6453	MSS	STAD
TCGA-BR-6454	MSS	STAD
TCGA-BR-6455	MSS	STAD
TCGA-BR-6456	MSS	STAD
TCGA-BR-6457	MSS	STAD
TCGA-BR-6458	MSS	STAD
TCGA-BR-6563	MSS	STAD
TCGA-BR-6564	MSS	STAD
TCGA-BR-6565	MSS	STAD
TCGA-BR-6566	MSI-H	STAD
TCGA-BR-6705	MSS	STAD

TCGA-BR-6706	MSS	STAD
TCGA-BR-6707	MSS	STAD
TCGA-BR-6709	MSS	STAD
TCGA-BR-6710	MSS	STAD
TCGA-BR-6801	MSS	STAD
TCGA-BR-6802	MSI-H	STAD
TCGA-BR-6803	MSS	STAD
TCGA-BR-6852	MSI-H	STAD
TCGA-BR-7196	MSS	STAD
TCGA-BR-7197	MSI-H	STAD
TCGA-BR-7703	MSI-H	STAD
TCGA-BR-7704	MSS	STAD
TCGA-BR-7707	MSI-H	STAD
TCGA-BR-7722	MSS	STAD
TCGA-BR-7851	MSI-H	STAD
TCGA-BR-7901	MSS	STAD
TCGA-BR-7958	MSS	STAD
TCGA-BR-7959	MSS	STAD
TCGA-BR-8059	MSI-H	STAD
TCGA-BR-8060	MSS	STAD
TCGA-BR-8077	MSS	STAD
TCGA-BR-8078	MSI-H	STAD
TCGA-BR-8080	MSS	STAD
TCGA-BR-8081	MSI-H	STAD
TCGA-BR-8284	MSI-H	STAD
TCGA-BR-8285	MSS	STAD
TCGA-BR-8286	MSS	STAD
TCGA-BR-8289	MSS	STAD
TCGA-BR-8295	MSS	STAD
TCGA-BR-8296	MSS	STAD
TCGA-BR-8360	MSI-H	STAD
TCGA-BR-8361	MSI-H	STAD
TCGA-BR-8362	MSS	STAD
TCGA-BR-8363	MSI-H	STAD
TCGA-BR-8365	MSS	STAD
TCGA-BR-8366	MSS	STAD
TCGA-BR-8367	MSS	STAD
TCGA-BR-8368	MSI-H	STAD
TCGA-BR-8369	MSS	STAD
TCGA-BR-8370	MSS	STAD
TCGA-BR-8371	MSS	STAD
TCGA-BR-8372	MSI-H	STAD
TCGA-BR-8373	MSS	STAD
TCGA-BR-8381	MSS	STAD
TCGA-BR-8382	MSI-H	STAD
TCGA-BR-8384	MSS	STAD
TCGA-BR-8483	MSS	STAD
TCGA-BR-8484	MSS	STAD
TCGA-BR-8485	MSS	STAD
TCGA-BR-8486	MSS	STAD
TCGA-BR-8487	MSI-H	STAD
TCGA-BR-8588	MSS	STAD

TCGA-BR-8589	MSS	STAD
TCGA-BR-8590	MSS	STAD
TCGA-BR-8591	MSI-H	STAD
TCGA-BR-8676	MSS	STAD
TCGA-BR-8677	MSS	STAD
TCGA-BR-8678	MSS	STAD
TCGA-BR-8679	MSS	STAD
TCGA-BR-8680	MSS	STAD
TCGA-BR-8682	MSS	STAD
TCGA-BR-8683	MSS	STAD
TCGA-BR-8687	MSS	STAD
TCGA-BR-8690	MSS	STAD
TCGA-BR-A44T	MSS	STAD
TCGA-BR-A44U	MSS	STAD
TCGA-BR-A452	MSS	STAD
TCGA-BR-A453	MSS	STAD
TCGA-BR-A4CQ	MSS	STAD
TCGA-BR-A4CR	MSS	STAD
TCGA-BR-A4CS	MSS	STAD
TCGA-BR-A4IV	MSS	STAD
TCGA-BR-A4IY	MSS	STAD
TCGA-BR-A4IZ	MSS	STAD
TCGA-BR-A4J1	MSS	STAD
TCGA-BR-A4J2	MSS	STAD
TCGA-BR-A4J4	MSS	STAD
TCGA-BR-A4J5	MSS	STAD
TCGA-BR-A4J6	MSS	STAD
TCGA-BR-A4J7	MSS	STAD
TCGA-BR-A4J8	MSS	STAD
TCGA-BR-A4J9	MSS	STAD
TCGA-BR-A4PD	MSS	STAD
TCGA-BR-A4PE	MSS	STAD
TCGA-BR-A4PF	MSS	STAD
TCGA-BR-A4QI	MSS	STAD
TCGA-BR-A4QL	MSI-H	STAD
TCGA-BS-A0T9	MSS	UCEC
TCGA-BS-A0TA	MSI-H	UCEC
TCGA-BS-A0TC	Intermediate	UCEC
TCGA-BS-A0TD	MSS	UCEC
TCGA-BS-A0TE	MSI-H	UCEC
TCGA-BS-A0TG	MSS	UCEC
TCGA-BS-A0TI	MSS	UCEC
TCGA-BS-A0TJ	MSI-H	UCEC
TCGA-BS-A0U5	MSS	UCEC
TCGA-BS-A0U7	MSI-H	UCEC
TCGA-BS-A0U8	MSI-H	UCEC
TCGA-BS-A0UA	MSI-H	UCEC
TCGA-BS-A0UF	Intermediate	UCEC
TCGA-BS-A0UJ	MSI-H	UCEC
TCGA-BS-A0UL	MSI-H	UCEC
TCGA-BS-A0UM	MSI-H	UCEC
TCGA-BS-A0UT	MSS	UCEC

TCGA-BS-A0UV	Intermediate	UCEC
TCGA-BS-A0V6	MSS	UCEC
TCGA-BS-A0V7	MSS	UCEC
TCGA-BS-A0V8	MSS	UCEC
TCGA-BS-A0VI	MSI-H	UCEC
TCGA-BS-A0WQ	MSS	UCEC
TCGA-BT-A0S7	MSS	BLCA
TCGA-BT-A0YX	MSS	BLCA
TCGA-BT-A20J	MSS	BLCA
TCGA-BT-A20N	MSS	BLCA
TCGA-BT-A20O	MSS	BLCA
TCGA-BT-A20P	MSS	BLCA
TCGA-BT-A20Q	MSS	BLCA
TCGA-BT-A20R	MSS	BLCA
TCGA-BT-A20T	MSS	BLCA
TCGA-BT-A20U	MSS	BLCA
TCGA-BT-A20V	MSS	BLCA
TCGA-BT-A20W	MSS	BLCA
TCGA-BT-A20X	MSS	BLCA
TCGA-BT-A2LA	MSS	BLCA
TCGA-BT-A2LB	MSS	BLCA
TCGA-BT-A2LD	MSS	BLCA
TCGA-BT-A3PH	MSS	BLCA
TCGA-BT-A3PJ	MSS	BLCA
TCGA-BT-A3PK	MSS	BLCA
TCGA-BT-A42B	MSS	BLCA
TCGA-BT-A42C	MSS	BLCA
TCGA-BT-A42E	MSS	BLCA
TCGA-BT-A42F	MSS	BLCA
TCGA-C4-A0EZ	MSS	BLCA
TCGA-C4-A0F0	MSS	BLCA
TCGA-C4-A0F1	MSS	BLCA
TCGA-C4-A0F6	MSS	BLCA
TCGA-C4-A0F7	MSS	BLCA
TCGA-C5-A0TN	MSS	CESC
TCGA-C5-A1BE	MSS	CESC
TCGA-C5-A1BF	MSS	CESC
TCGA-C5-A1BI	MSS	CESC
TCGA-C5-A1BJ	MSS	CESC
TCGA-C5-A1BK	MSS	CESC
TCGA-C5-A1BL	MSS	CESC
TCGA-C5-A1BM	MSS	CESC
TCGA-C5-A1BN	MSS	CESC
TCGA-C5-A1BQ	MSS	CESC
TCGA-C5-A1M5	MSS	CESC
TCGA-C5-A1M6	MSS	CESC
TCGA-C5-A1M7	MSS	CESC
TCGA-C5-A1M8	MSS	CESC
TCGA-C5-A1M9	MSS	CESC
TCGA-C5-A1ME	MSS	CESC
TCGA-C5-A1MF	MSS	CESC
TCGA-C5-A1MH	MSS	CESC

TCGA-C5-A1MI	MSS	CESC
TCGA-C5-A1MJ	MSS	CESC
TCGA-C5-A1MK	MSS	CESC
TCGA-C5-A1ML	MSS	CESC
TCGA-C5-A1MN	MSS	CESC
TCGA-C5-A1MP	MSS	CESC
TCGA-C5-A1MQ	MSS	CESC
TCGA-C5-A2LS	MSS	CESC
TCGA-C5-A2LZ	MSS	CESC
TCGA-C5-A3HD	MSS	CESC
TCGA-C5-A3HE	MSS	CESC
TCGA-C5-A3HF	MSS	CESC
TCGA-C5-A3HL	MSS	CESC
TCGA-C5-A7CG	MSS	CESC
TCGA-C5-A7CH	MSS	CESC
TCGA-C5-A7CJ	MSS	CESC
TCGA-C5-A7CK	MSS	CESC
TCGA-C5-A7CL	MSS	CESC
TCGA-C5-A7CM	MSS	CESC
TCGA-C5-A7CO	MSS	CESC
TCGA-C5-A7UC	MSS	CESC
TCGA-C5-A7UE	MSS	CESC
TCGA-C5-A7UH	MSS	CESC
TCGA-C5-A7UI	MSS	CESC
TCGA-C5-A7X3	MSS	CESC
TCGA-C5-A7X5	MSS	CESC
TCGA-C5-A7X8	MSS	CESC
TCGA-C5-A8XH	MSS	CESC
TCGA-C5-A8XI	MSS	CESC
TCGA-C5-A8XJ	MSS	CESC
TCGA-C5-A8XK	MSS	CESC
TCGA-C5-A8YQ	MSS	CESC
TCGA-C5-A8YR	MSS	CESC
TCGA-C5-A8YT	MSS	CESC
TCGA-C5-A8ZZ	MSS	CESC
TCGA-C5-A901	MSS	CESC
TCGA-C5-A902	MSS	CESC
TCGA-C5-A905	MSS	CESC
TCGA-C5-A907	MSS	CESC
TCGA-C8-A12K	MSS	BRCA
TCGA-C8-A12L	MSS	BRCA
TCGA-C8-A12M	MSS	BRCA
TCGA-C8-A12N	MSS	BRCA
TCGA-C8-A12O	MSS	BRCA
TCGA-C8-A12P	MSS	BRCA
TCGA-C8-A12Q	MSS	BRCA
TCGA-C8-A12T	MSS	BRCA
TCGA-C8-A12U	MSS	BRCA
TCGA-C8-A12V	MSS	BRCA
TCGA-C8-A12W	MSS	BRCA
TCGA-C8-A12X	MSS	BRCA
TCGA-C8-A12Y	MSS	BRCA

TCGA-C8-A12Z	MSS	BRCA
TCGA-C8-A130	MSS	BRCA
TCGA-C8-A131	MSS	BRCA
TCGA-C8-A132	MSS	BRCA
TCGA-C8-A133	MSS	BRCA
TCGA-C8-A134	MSS	BRCA
TCGA-C8-A135	MSS	BRCA
TCGA-C8-A137	MSS	BRCA
TCGA-C8-A138	MSS	BRCA
TCGA-C8-A1HE	Intermediate	BRCA
TCGA-C8-A1HF	MSS	BRCA
TCGA-C8-A1HG	MSS	BRCA
TCGA-C8-A1HJ	MSI-H	BRCA
TCGA-C8-A1HK	Intermediate	BRCA
TCGA-C8-A1HL	MSS	BRCA
TCGA-C8-A1HM	MSS	BRCA
TCGA-C8-A1HN	MSS	BRCA
TCGA-C8-A1HO	Intermediate	BRCA
TCGA-C8-A26V	MSS	BRCA
TCGA-C8-A26W	MSS	BRCA
TCGA-C8-A26X	MSS	BRCA
TCGA-C8-A26Y	MSS	BRCA
TCGA-C8-A26Z	MSS	BRCA
TCGA-C8-A273	MSS	BRCA
TCGA-C8-A274	MSS	BRCA
TCGA-C8-A275	MSS	BRCA
TCGA-C8-A278	MSS	BRCA
TCGA-C8-A27A	MSS	BRCA
TCGA-C8-A27B	MSI-H	BRCA
TCGA-C8-A8HP	MSS	BRCA
TCGA-C8-A8HQ	MSS	BRCA
TCGA-C8-A8HR	MSS	BRCA
TCGA-C8-A9FZ	MSS	BRCA
TCGA-C9-A47Z	MSS	HNSC
TCGA-C9-A480	MSS	HNSC
TCGA-CA-5254	MSS	COAD
TCGA-CA-5255	MSS	COAD
TCGA-CA-5256	MSS	COAD
TCGA-CA-5796	MSS	COAD
TCGA-CA-5797	MSS	COAD
TCGA-CA-6715	MSS	COAD
TCGA-CA-6716	MSS	COAD
TCGA-CA-6717	MSS	COAD
TCGA-CA-6718	MSS	COAD
TCGA-CA-6719	MSS	COAD
TCGA-CC-5258	MSS	LIHC
TCGA-CC-5259	MSS	LIHC
TCGA-CC-5260	MSS	LIHC
TCGA-CC-5261	MSS	LIHC
TCGA-CC-5262	MSS	LIHC
TCGA-CC-5263	MSS	LIHC
TCGA-CC-5264	MSS	LIHC

TCGA-CC-A123	MSS	LIHC
TCGA-CC-A1HT	MSS	LIHC
TCGA-CC-A3M9	MSS	LIHC
TCGA-CC-A3MA	MSS	LIHC
TCGA-CC-A3MC	MSS	LIHC
TCGA-CC-A7IE	MSS	LIHC
TCGA-CC-A7IF	MSS	LIHC
TCGA-CC-A7IG	MSS	LIHC
TCGA-CC-A7IH	MSS	LIHC
TCGA-CC-A7II	MSS	LIHC
TCGA-CC-A7IJ	MSS	LIHC
TCGA-CC-A7IK	MSS	LIHC
TCGA-CC-A7IL	MSS	LIHC
TCGA-CC-A8HS	MSS	LIHC
TCGA-CC-A8HT	MSS	LIHC
TCGA-CC-A8HU	MSS	LIHC
TCGA-CC-A8HV	MSS	LIHC
TCGA-CC-A9FS	MSS	LIHC
TCGA-CC-A9FU	MSS	LIHC
TCGA-CC-A9FV	MSS	LIHC
TCGA-CC-A9FW	MSS	LIHC
TCGA-CD-5798	MSS	STAD
TCGA-CD-5799	MSS	STAD
TCGA-CD-5800	MSS	STAD
TCGA-CD-5801	MSS	STAD
TCGA-CD-5802	MSS	STAD
TCGA-CD-5803	MSS	STAD
TCGA-CD-5813	MSS	STAD
TCGA-CD-8524	MSS	STAD
TCGA-CD-8525	MSS	STAD
TCGA-CD-8526	MSS	STAD
TCGA-CD-8527	Intermediate	STAD
TCGA-CD-8528	MSS	STAD
TCGA-CD-8529	MSS	STAD
TCGA-CD-8530	MSS	STAD
TCGA-CD-8531	MSS	STAD
TCGA-CD-8532	MSS	STAD
TCGA-CD-8534	MSS	STAD
TCGA-CD-8535	MSS	STAD
TCGA-CD-8536	MSI-H	STAD
TCGA-CD-A486	MSS	STAD
TCGA-CD-A487	MSS	STAD
TCGA-CD-A489	MSS	STAD
TCGA-CD-A48A	MSS	STAD
TCGA-CD-A48C	MSS	STAD
TCGA-CD-A4MG	MSI-H	STAD
TCGA-CD-A4MH	MSS	STAD
TCGA-CD-A4MI	MSI-H	STAD
TCGA-CD-A4MJ	MSI-H	STAD
TCGA-CE-A13K	MSS	THCA
TCGA-CE-A27D	MSS	THCA
TCGA-CE-A3MD	MSS	THCA

TCGA-CE-A3ME	MSS	THCA
TCGA-CE-A482	MSS	THCA
TCGA-CE-A483	MSS	THCA
TCGA-CE-A484	MSS	THCA
TCGA-CF-A1HR	MSS	BLCA
TCGA-CF-A1HS	MSS	BLCA
TCGA-CF-A27C	MSS	BLCA
TCGA-CF-A3MH	MSS	BLCA
TCGA-CF-A47S	MSS	BLCA
TCGA-CF-A47T	MSS	BLCA
TCGA-CF-A47V	MSS	BLCA
TCGA-CF-A47W	MSS	BLCA
TCGA-CF-A47X	MSS	BLCA
TCGA-CF-A47Y	MSS	BLCA
TCGA-CF-A5U8	MSS	BLCA
TCGA-CF-A5UA	MSS	BLCA
TCGA-CF-A7I0	MSS	BLCA
TCGA-CF-A8HX	MSS	BLCA
TCGA-CF-A8HY	MSS	BLCA
TCGA-CF-A9FF	MSS	BLCA
TCGA-CF-A9FH	MSS	BLCA
TCGA-CF-A9FL	MSS	BLCA
TCGA-CF-A9FM	MSS	BLCA
TCGA-CG-4300	MSS	STAD
TCGA-CG-4301	MSS	STAD
TCGA-CG-4304	MSS	STAD
TCGA-CG-4305	MSI-H	STAD
TCGA-CG-4306	MSI-H	STAD
TCGA-CG-4436	MSS	STAD
TCGA-CG-4437	MSS	STAD
TCGA-CG-4438	MSS	STAD
TCGA-CG-4440	MSS	STAD
TCGA-CG-4441	MSS	STAD
TCGA-CG-4442	MSI-H	STAD
TCGA-CG-4443	MSS	STAD
TCGA-CG-4444	MSS	STAD
TCGA-CG-4449	MSS	STAD
TCGA-CG-4455	MSS	STAD
TCGA-CG-4460	MSI-H	STAD
TCGA-CG-4462	MSS	STAD
TCGA-CG-4465	MSI-H	STAD
TCGA-CG-4466	MSS	STAD
TCGA-CG-4469	MSS	STAD
TCGA-CG-4474	Intermediate	STAD
TCGA-CG-4475	MSS	STAD
TCGA-CG-4476	MSS	STAD
TCGA-CG-4477	MSS	STAD
TCGA-CG-5716	MSS	STAD
TCGA-CG-5717	MSS	STAD
TCGA-CG-5718	MSS	STAD
TCGA-CG-5719	MSS	STAD
TCGA-CG-5720	MSS	STAD

TCGA-CG-5721	MSI-H	STAD
TCGA-CG-5722	MSS	STAD
TCGA-CG-5723	MSI-H	STAD
TCGA-CG-5724	MSS	STAD
TCGA-CG-5725	MSS	STAD
TCGA-CG-5726	MSI-H	STAD
TCGA-CG-5727	MSS	STAD
TCGA-CG-5728	MSI-H	STAD
TCGA-CG-5730	MSS	STAD
TCGA-CG-5732	MSS	STAD
TCGA-CG-5733	MSI-H	STAD
TCGA-CG-5734	MSS	STAD
TCGA-CH-5737	MSS	PRAD
TCGA-CH-5738	MSS	PRAD
TCGA-CH-5739	MSS	PRAD
TCGA-CH-5740	MSS	PRAD
TCGA-CH-5741	MSS	PRAD
TCGA-CH-5743	MSS	PRAD
TCGA-CH-5744	MSS	PRAD
TCGA-CH-5745	MSS	PRAD
TCGA-CH-5746	MSS	PRAD
TCGA-CH-5748	MSS	PRAD
TCGA-CH-5750	MSS	PRAD
TCGA-CH-5751	MSS	PRAD
TCGA-CH-5752	MSS	PRAD
TCGA-CH-5753	MSS	PRAD
TCGA-CH-5754	MSS	PRAD
TCGA-CH-5761	MSS	PRAD
TCGA-CH-5762	MSS	PRAD
TCGA-CH-5763	MSS	PRAD
TCGA-CH-5764	MSS	PRAD
TCGA-CH-5765	MSS	PRAD
TCGA-CH-5766	MSS	PRAD
TCGA-CH-5767	MSS	PRAD
TCGA-CH-5768	MSS	PRAD
TCGA-CH-5769	MSS	PRAD
TCGA-CH-5771	MSS	PRAD
TCGA-CH-5772	MSS	PRAD
TCGA-CH-5788	MSS	PRAD
TCGA-CH-5789	MSS	PRAD
TCGA-CH-5790	MSS	PRAD
TCGA-CH-5791	MSS	PRAD
TCGA-CH-5792	MSS	PRAD
TCGA-CH-5794	MSS	PRAD
TCGA-CI-6619	MSS	READ
TCGA-CI-6620	MSS	READ
TCGA-CI-6621	MSS	READ
TCGA-CI-6622	MSS	READ
TCGA-CI-6623	MSS	READ
TCGA-CI-6624	MSS	READ
TCGA-CJ-4869	MSS	KIRC
TCGA-CJ-4882	MSS	KIRC

TCGA-CJ-4899	MSS	KIRC
TCGA-CJ-4900	MSS	KIRC
TCGA-CJ-4901	MSS	KIRC
TCGA-CJ-4902	MSS	KIRC
TCGA-CJ-4903	MSS	KIRC
TCGA-CJ-4904	MSS	KIRC
TCGA-CJ-4905	MSS	KIRC
TCGA-CJ-4907	MSS	KIRC
TCGA-CJ-4908	MSS	KIRC
TCGA-CJ-4912	MSS	KIRC
TCGA-CJ-4913	MSS	KIRC
TCGA-CJ-4916	MSS	KIRC
TCGA-CJ-4918	MSS	KIRC
TCGA-CJ-4920	MSS	KIRC
TCGA-CJ-4923	MSS	KIRC
TCGA-CJ-5671	MSS	KIRC
TCGA-CJ-5672	MSS	KIRC
TCGA-CJ-5675	MSS	KIRC
TCGA-CJ-5676	MSS	KIRC
TCGA-CJ-5677	MSS	KIRC
TCGA-CJ-5678	MSS	KIRC
TCGA-CJ-5679	MSS	KIRC
TCGA-CJ-5680	MSS	KIRC
TCGA-CJ-5681	MSS	KIRC
TCGA-CJ-5682	MSS	KIRC
TCGA-CJ-5683	MSS	KIRC
TCGA-CJ-5684	MSS	KIRC
TCGA-CJ-5686	MSS	KIRC
TCGA-CJ-5689	MSS	KIRC
TCGA-CJ-6027	MSS	KIRC
TCGA-CJ-6028	MSS	KIRC
TCGA-CJ-6030	MSS	KIRC
TCGA-CJ-6031	MSS	KIRC
TCGA-CJ-6032	MSS	KIRC
TCGA-CJ-6033	MSS	KIRC
TCGA-CK-4947	MSS	COAD
TCGA-CK-4948	MSS	COAD
TCGA-CK-4950	MSS	COAD
TCGA-CK-4951	MSI-H	COAD
TCGA-CK-4952	MSS	COAD
TCGA-CK-5912	MSS	COAD
TCGA-CK-5913	MSI-H	COAD
TCGA-CK-5914	MSS	COAD
TCGA-CK-5915	MSS	COAD
TCGA-CK-5916	MSI-H	COAD
TCGA-CK-6746	MSI-H	COAD
TCGA-CK-6747	MSS	COAD
TCGA-CK-6748	MSS	COAD
TCGA-CK-6751	MSS	COAD
TCGA-CL-4957	MSS	READ
TCGA-CL-5917	MSS	READ
TCGA-CL-5918	MSS	READ

TCGA-CM-4743	MSI-H	COAD
TCGA-CM-4744	MSS	COAD
TCGA-CM-4746	MSI-H	COAD
TCGA-CM-4747	MSS	COAD
TCGA-CM-4748	MSS	COAD
TCGA-CM-4750	MSS	COAD
TCGA-CM-4751	MSS	COAD
TCGA-CM-4752	MSS	COAD
TCGA-CM-5341	MSS	COAD
TCGA-CM-5344	MSS	COAD
TCGA-CM-5348	MSS	COAD
TCGA-CM-5349	MSS	COAD
TCGA-CM-5860	MSS	COAD
TCGA-CM-5861	MSI-H	COAD
TCGA-CM-5862	MSS	COAD
TCGA-CM-5863	MSS	COAD
TCGA-CM-5864	MSS	COAD
TCGA-CM-6161	MSS	COAD
TCGA-CM-6162	MSI-H	COAD
TCGA-CM-6163	MSS	COAD
TCGA-CM-6164	MSS	COAD
TCGA-CM-6165	MSS	COAD
TCGA-CM-6166	MSS	COAD
TCGA-CM-6167	MSS	COAD
TCGA-CM-6168	MSS	COAD
TCGA-CM-6169	MSS	COAD
TCGA-CM-6170	MSS	COAD
TCGA-CM-6171	MSI-H	COAD
TCGA-CM-6172	MSS	COAD
TCGA-CM-6674	MSI-H	COAD
TCGA-CM-6675	MSS	COAD
TCGA-CM-6676	MSS	COAD
TCGA-CM-6677	MSS	COAD
TCGA-CM-6678	MSS	COAD
TCGA-CN-4723	MSS	HNSC
TCGA-CN-4725	MSS	HNSC
TCGA-CN-4726	MSS	HNSC
TCGA-CN-4727	MSS	HNSC
TCGA-CN-4728	MSS	HNSC
TCGA-CN-4729	MSS	HNSC
TCGA-CN-4730	MSS	HNSC
TCGA-CN-4731	MSS	HNSC
TCGA-CN-4733	MSS	HNSC
TCGA-CN-4734	MSS	HNSC
TCGA-CN-4735	MSS	HNSC
TCGA-CN-4736	MSS	HNSC
TCGA-CN-4737	MSS	HNSC
TCGA-CN-4738	MSS	HNSC
TCGA-CN-4739	MSS	HNSC
TCGA-CN-4740	MSS	HNSC
TCGA-CN-4741	MSS	HNSC
TCGA-CN-4742	MSS	HNSC

TCGA-CN-5355	MSS	HNSC
TCGA-CN-5356	MSS	HNSC
TCGA-CN-5358	MSS	HNSC
TCGA-CN-5359	MSS	HNSC
TCGA-CN-5360	MSS	HNSC
TCGA-CN-5361	MSS	HNSC
TCGA-CN-5363	MSS	HNSC
TCGA-CN-5364	MSS	HNSC
TCGA-CN-5365	Intermediate	HNSC
TCGA-CN-5366	MSS	HNSC
TCGA-CN-5367	MSS	HNSC
TCGA-CN-5369	MSI-H	HNSC
TCGA-CN-5370	MSS	HNSC
TCGA-CN-5373	MSS	HNSC
TCGA-CN-5374	MSS	HNSC
TCGA-CN-6010	MSS	HNSC
TCGA-CN-6011	MSS	HNSC
TCGA-CN-6012	MSS	HNSC
TCGA-CN-6013	MSS	HNSC
TCGA-CN-6016	MSS	HNSC
TCGA-CN-6017	MSS	HNSC
TCGA-CN-6018	MSS	HNSC
TCGA-CN-6019	MSS	HNSC
TCGA-CN-6020	MSS	HNSC
TCGA-CN-6021	MSS	HNSC
TCGA-CN-6022	MSS	HNSC
TCGA-CN-6023	MSS	HNSC
TCGA-CN-6024	MSS	HNSC
TCGA-CN-6988	MSS	HNSC
TCGA-CN-6989	MSS	HNSC
TCGA-CN-6992	MSS	HNSC
TCGA-CN-6994	MSS	HNSC
TCGA-CN-6995	MSS	HNSC
TCGA-CN-6996	MSS	HNSC
TCGA-CN-6997	MSS	HNSC
TCGA-CN-6998	MSS	HNSC
TCGA-CN-A497	MSS	HNSC
TCGA-CN-A498	MSS	HNSC
TCGA-CN-A499	MSS	HNSC
TCGA-CN-A49A	MSS	HNSC
TCGA-CN-A49B	MSS	HNSC
TCGA-CN-A49C	MSS	HNSC
TCGA-CN-A63T	MSS	HNSC
TCGA-CN-A63U	MSS	HNSC
TCGA-CN-A63V	MSS	HNSC
TCGA-CN-A63W	MSS	HNSC
TCGA-CN-A63Y	MSS	HNSC
TCGA-CN-A640	MSS	HNSC
TCGA-CN-A641	MSS	HNSC
TCGA-CN-A642	MSS	HNSC
TCGA-CN-A6UY	MSS	HNSC
TCGA-CN-A6V1	MSS	HNSC

TCGA-CN-A6V3	MSS	HNSC
TCGA-CN-A6V6	MSS	HNSC
TCGA-CN-A6V7	MSS	HNSC
TCGA-CQ-5323	MSS	HNSC
TCGA-CQ-5324	MSS	HNSC
TCGA-CQ-5325	MSS	HNSC
TCGA-CQ-5326	MSS	HNSC
TCGA-CQ-5327	MSS	HNSC
TCGA-CQ-5329	MSS	HNSC
TCGA-CQ-5330	MSS	HNSC
TCGA-CQ-5331	MSS	HNSC
TCGA-CQ-5332	MSS	HNSC
TCGA-CQ-5333	MSS	HNSC
TCGA-CQ-5334	MSS	HNSC
TCGA-CQ-6218	MSS	HNSC
TCGA-CQ-6219	MSS	HNSC
TCGA-CQ-6220	MSS	HNSC
TCGA-CQ-6221	MSS	HNSC
TCGA-CQ-6222	MSS	HNSC
TCGA-CQ-6223	MSS	HNSC
TCGA-CQ-6224	MSS	HNSC
TCGA-CQ-6225	MSS	HNSC
TCGA-CQ-6227	MSS	HNSC
TCGA-CQ-6228	MSS	HNSC
TCGA-CQ-6229	MSS	HNSC
TCGA-CQ-7063	MSS	HNSC
TCGA-CQ-7064	MSS	HNSC
TCGA-CQ-7065	MSS	HNSC
TCGA-CQ-7068	MSS	HNSC
TCGA-CQ-7069	MSS	HNSC
TCGA-CQ-7071	MSS	HNSC
TCGA-CQ-7072	MSS	HNSC
TCGA-CQ-A4C6	MSS	HNSC
TCGA-CQ-A4C7	MSS	HNSC
TCGA-CQ-A4C9	MSS	HNSC
TCGA-CQ-A4CA	MSS	HNSC
TCGA-CQ-A4CB	MSS	HNSC
TCGA-CQ-A4CD	MSS	HNSC
TCGA-CQ-A4CE	MSS	HNSC
TCGA-CQ-A4CG	MSS	HNSC
TCGA-CQ-A4CH	MSS	HNSC
TCGA-CQ-A4CI	MSS	HNSC
TCGA-CR-5243	MSS	HNSC
TCGA-CR-5247	MSS	HNSC
TCGA-CR-5248	MSS	HNSC
TCGA-CR-5249	MSS	HNSC
TCGA-CR-5250	MSS	HNSC
TCGA-CR-6467	MSS	HNSC
TCGA-CR-6470	MSS	HNSC
TCGA-CR-6471	MSS	HNSC
TCGA-CR-6472	MSS	HNSC
TCGA-CR-6473	MSS	HNSC

TCGA-CR-6474	MSS	HNSC
TCGA-CR-6477	MSS	HNSC
TCGA-CR-6478	MSS	HNSC
TCGA-CR-6480	MSS	HNSC
TCGA-CR-6481	MSS	HNSC
TCGA-CR-6482	MSS	HNSC
TCGA-CR-6484	MSS	HNSC
TCGA-CR-6487	MSS	HNSC
TCGA-CR-6488	MSS	HNSC
TCGA-CR-6491	MSS	HNSC
TCGA-CR-6492	MSS	HNSC
TCGA-CR-6493	MSS	HNSC
TCGA-CR-7364	MSS	HNSC
TCGA-CR-7365	MSS	HNSC
TCGA-CR-7367	MSS	HNSC
TCGA-CR-7368	MSS	HNSC
TCGA-CR-7369	MSS	HNSC
TCGA-CR-7370	MSS	HNSC
TCGA-CR-7371	MSS	HNSC
TCGA-CR-7372	MSS	HNSC
TCGA-CR-7373	MSS	HNSC
TCGA-CR-7374	MSS	HNSC
TCGA-CR-7376	MSS	HNSC
TCGA-CR-7377	MSS	HNSC
TCGA-CR-7379	MSS	HNSC
TCGA-CR-7380	MSS	HNSC
TCGA-CR-7382	MSS	HNSC
TCGA-CR-7383	MSS	HNSC
TCGA-CR-7385	MSS	HNSC
TCGA-CR-7386	MSS	HNSC
TCGA-CR-7388	MSS	HNSC
TCGA-CR-7389	MSS	HNSC
TCGA-CR-7390	MSS	HNSC
TCGA-CR-7391	MSS	HNSC
TCGA-CR-7392	MSS	HNSC
TCGA-CR-7393	MSS	HNSC
TCGA-CR-7394	MSS	HNSC
TCGA-CR-7395	MSS	HNSC
TCGA-CR-7397	MSS	HNSC
TCGA-CR-7398	MSS	HNSC
TCGA-CR-7399	MSS	HNSC
TCGA-CR-7401	MSS	HNSC
TCGA-CR-7402	MSS	HNSC
TCGA-CR-7404	MSS	HNSC
TCGA-CS-4938	MSS	LGG
TCGA-CS-4941	MSS	LGG
TCGA-CS-4942	MSS	LGG
TCGA-CS-4943	MSS	LGG
TCGA-CS-4944	MSS	LGG
TCGA-CS-5390	MSS	LGG
TCGA-CS-5393	MSS	LGG
TCGA-CS-5394	MSS	LGG

TCGA-CS-5395	MSS	LGG
TCGA-CS-5396	MSS	LGG
TCGA-CS-5397	MSS	LGG
TCGA-CS-6186	MSS	LGG
TCGA-CS-6188	MSS	LGG
TCGA-CS-6290	MSS	LGG
TCGA-CS-6665	MSS	LGG
TCGA-CS-6666	MSS	LGG
TCGA-CS-6667	MSS	LGG
TCGA-CS-6668	MSS	LGG
TCGA-CS-6669	MSS	LGG
TCGA-CS-6670	MSS	LGG
TCGA-CU-A0YN	MSS	BLCA
TCGA-CU-A0YO	MSS	BLCA
TCGA-CU-A0YR	MSS	BLCA
TCGA-CU-A3QU	MSS	BLCA
TCGA-CU-A3YL	MSS	BLCA
TCGA-CU-A5W6	MSS	BLCA
TCGA-CU-A72E	MSS	BLCA
TCGA-CV-5430	MSS	HNSC
TCGA-CV-5432	MSS	HNSC
TCGA-CV-5434	MSS	HNSC
TCGA-CV-5435	MSS	HNSC
TCGA-CV-5436	MSS	HNSC
TCGA-CV-5439	MSS	HNSC
TCGA-CV-5440	Intermediate	HNSC
TCGA-CV-5441	MSS	HNSC
TCGA-CV-5442	MSS	HNSC
TCGA-CV-5443	MSS	HNSC
TCGA-CV-5444	MSS	HNSC
TCGA-CV-5966	MSS	HNSC
TCGA-CV-5970	MSS	HNSC
TCGA-CV-5971	MSS	HNSC
TCGA-CV-5973	MSS	HNSC
TCGA-CV-5976	MSS	HNSC
TCGA-CV-5977	MSS	HNSC
TCGA-CV-5978	MSS	HNSC
TCGA-CV-5979	MSS	HNSC
TCGA-CV-6003	MSS	HNSC
TCGA-CV-6433	MSS	HNSC
TCGA-CV-6436	MSS	HNSC
TCGA-CV-6441	MSS	HNSC
TCGA-CV-6933	MSS	HNSC
TCGA-CV-6934	MSS	HNSC
TCGA-CV-6935	MSS	HNSC
TCGA-CV-6936	MSS	HNSC
TCGA-CV-6937	MSS	HNSC
TCGA-CV-6938	MSS	HNSC
TCGA-CV-6939	MSS	HNSC
TCGA-CV-6940	MSS	HNSC
TCGA-CV-6941	MSS	HNSC
TCGA-CV-6942	MSS	HNSC

TCGA-CV-6943	MSS	HNSC
TCGA-CV-6945	MSS	HNSC
TCGA-CV-6948	MSS	HNSC
TCGA-CV-6950	MSS	HNSC
TCGA-CV-6951	MSS	HNSC
TCGA-CV-6952	MSS	HNSC
TCGA-CV-6953	MSS	HNSC
TCGA-CV-6954	MSS	HNSC
TCGA-CV-6955	MSS	HNSC
TCGA-CV-6956	MSS	HNSC
TCGA-CV-6959	MSS	HNSC
TCGA-CV-6960	MSS	HNSC
TCGA-CV-6961	MSS	HNSC
TCGA-CV-6962	MSS	HNSC
TCGA-CV-7089	MSS	HNSC
TCGA-CV-7090	MSS	HNSC
TCGA-CV-7091	MSS	HNSC
TCGA-CV-7095	MSS	HNSC
TCGA-CV-7097	MSS	HNSC
TCGA-CV-7099	MSS	HNSC
TCGA-CV-7100	MSS	HNSC
TCGA-CV-7101	MSS	HNSC
TCGA-CV-7102	MSS	HNSC
TCGA-CV-7103	MSS	HNSC
TCGA-CV-7104	MSS	HNSC
TCGA-CV-7177	MSS	HNSC
TCGA-CV-7178	MSS	HNSC
TCGA-CV-7180	MSS	HNSC
TCGA-CV-7183	MSS	HNSC
TCGA-CV-7235	MSS	HNSC
TCGA-CV-7236	MSS	HNSC
TCGA-CV-7238	MSS	HNSC
TCGA-CV-7242	MSS	HNSC
TCGA-CV-7243	MSS	HNSC
TCGA-CV-7245	MSS	HNSC
TCGA-CV-7247	MSS	HNSC
TCGA-CV-7248	MSS	HNSC
TCGA-CV-7250	MSS	HNSC
TCGA-CV-7252	MSS	HNSC
TCGA-CV-7253	MSS	HNSC
TCGA-CV-7254	MSS	HNSC
TCGA-CV-7255	MSS	HNSC
TCGA-CV-7261	MSS	HNSC
TCGA-CV-7263	MSS	HNSC
TCGA-CV-7406	MSS	HNSC
TCGA-CV-7407	MSS	HNSC
TCGA-CV-7410	MSS	HNSC
TCGA-CV-7411	MSS	HNSC
TCGA-CV-7413	MSS	HNSC
TCGA-CV-7414	MSS	HNSC
TCGA-CV-7415	MSS	HNSC
TCGA-CV-7416	MSS	HNSC

TCGA-CV-7418	MSS	HNSC
TCGA-CV-7421	MSS	HNSC
TCGA-CV-7422	MSS	HNSC
TCGA-CV-7423	MSS	HNSC
TCGA-CV-7424	MSS	HNSC
TCGA-CV-7425	MSS	HNSC
TCGA-CV-7427	MSS	HNSC
TCGA-CV-7429	MSS	HNSC
TCGA-CV-7430	MSS	HNSC
TCGA-CV-7432	MSS	HNSC
TCGA-CV-7433	MSS	HNSC
TCGA-CV-7434	MSS	HNSC
TCGA-CV-7435	MSS	HNSC
TCGA-CV-7437	MSS	HNSC
TCGA-CV-7438	MSS	HNSC
TCGA-CV-7440	MSS	HNSC
TCGA-CV-7446	MSS	HNSC
TCGA-CV-7568	MSS	HNSC
TCGA-CV-A45O	MSS	HNSC
TCGA-CV-A45P	MSS	HNSC
TCGA-CV-A45Q	MSS	HNSC
TCGA-CV-A45R	MSS	HNSC
TCGA-CV-A45T	MSS	HNSC
TCGA-CV-A45U	MSS	HNSC
TCGA-CV-A45V	MSS	HNSC
TCGA-CV-A45W	MSS	HNSC
TCGA-CV-A45X	MSS	HNSC
TCGA-CV-A45Y	MSS	HNSC
TCGA-CV-A45Z	MSS	HNSC
TCGA-CV-A460	MSS	HNSC
TCGA-CV-A461	MSS	HNSC
TCGA-CV-A463	MSS	HNSC
TCGA-CV-A464	MSS	HNSC
TCGA-CV-A465	MSS	HNSC
TCGA-CV-A468	MSS	HNSC
TCGA-CV-A6JD	MSS	HNSC
TCGA-CV-A6JE	MSS	HNSC
TCGA-CV-A6JM	MSS	HNSC
TCGA-CV-A6JN	MSS	HNSC
TCGA-CV-A6JO	MSS	HNSC
TCGA-CV-A6JT	MSS	HNSC
TCGA-CV-A6JU	MSS	HNSC
TCGA-CV-A6JY	MSS	HNSC
TCGA-CV-A6JZ	MSS	HNSC
TCGA-CV-A6K0	MSS	HNSC
TCGA-CV-A6K1	MSI-H	HNSC
TCGA-CV-A6K2	MSS	HNSC
TCGA-CW-5580	MSS	KIRC
TCGA-CW-5581	MSS	KIRC
TCGA-CW-5583	MSS	KIRC
TCGA-CW-5584	MSS	KIRC
TCGA-CW-5585	MSS	KIRC

TCGA-CW-5587	MSS	KIRC
TCGA-CW-5588	MSS	KIRC
TCGA-CW-5589	Intermediate	KIRC
TCGA-CW-5591	MSS	KIRC
TCGA-CW-6087	MSI-H	KIRC
TCGA-CW-6090	MSS	KIRC
TCGA-CW-6093	MSS	KIRC
TCGA-CW-6097	MSS	KIRC
TCGA-CX-7082	MSS	HNSC
TCGA-CX-7085	MSS	HNSC
TCGA-CX-7086	MSS	HNSC
TCGA-CX-7219	MSS	HNSC
TCGA-CX-A4AQ	MSS	HNSC
TCGA-CZ-4853	MSS	KIRC
TCGA-CZ-4856	MSS	KIRC
TCGA-CZ-4859	MSS	KIRC
TCGA-CZ-4863	MSS	KIRC
TCGA-CZ-4864	MSS	KIRC
TCGA-CZ-4865	MSS	KIRC
TCGA-CZ-4866	MSS	KIRC
TCGA-CZ-5451	MSS	KIRC
TCGA-CZ-5452	MSS	KIRC
TCGA-CZ-5453	MSS	KIRC
TCGA-CZ-5454	MSS	KIRC
TCGA-CZ-5455	MSS	KIRC
TCGA-CZ-5456	MSS	KIRC
TCGA-CZ-5457	MSS	KIRC
TCGA-CZ-5458	MSS	KIRC
TCGA-CZ-5459	MSS	KIRC
TCGA-CZ-5460	MSS	KIRC
TCGA-CZ-5461	MSS	KIRC
TCGA-CZ-5462	MSS	KIRC
TCGA-CZ-5463	MSS	KIRC
TCGA-CZ-5464	MSS	KIRC
TCGA-CZ-5465	MSS	KIRC
TCGA-CZ-5466	MSS	KIRC
TCGA-CZ-5467	MSS	KIRC
TCGA-CZ-5468	MSS	KIRC
TCGA-CZ-5469	MSS	KIRC
TCGA-CZ-5470	MSS	KIRC
TCGA-CZ-5982	MSS	KIRC
TCGA-CZ-5984	MSS	KIRC
TCGA-CZ-5985	MSS	KIRC
TCGA-CZ-5986	MSS	KIRC
TCGA-CZ-5987	MSS	KIRC
TCGA-CZ-5988	MSS	KIRC
TCGA-CZ-5989	MSS	KIRC
TCGA-D1-A0ZN	MSS	UCEC
TCGA-D1-A0ZO	MSI-H	UCEC
TCGA-D1-A0ZP	MSS	UCEC
TCGA-D1-A0ZQ	MSS	UCEC
TCGA-D1-A0ZR	MSS	UCEC

TCGA-D1-A0ZS	MSI-H	UCEC
TCGA-D1-A0ZU	MSS	UCEC
TCGA-D1-A0ZV	MSS	UCEC
TCGA-D1-A0ZZ	MSS	UCEC
TCGA-D1-A101	MSI-H	UCEC
TCGA-D1-A102	MSS	UCEC
TCGA-D1-A103	MSI-H	UCEC
TCGA-D1-A15V	MSS	UCEC
TCGA-D1-A15W	MSS	UCEC
TCGA-D1-A15X	MSI-H	UCEC
TCGA-D1-A15Z	MSS	UCEC
TCGA-D1-A160	MSI-H	UCEC
TCGA-D1-A161	MSS	UCEC
TCGA-D1-A163	MSI-H	UCEC
TCGA-D1-A165	MSS	UCEC
TCGA-D1-A167	MSI-H	UCEC
TCGA-D1-A168	MSS	UCEC
TCGA-D1-A169	MSS	UCEC
TCGA-D1-A16B	MSS	UCEC
TCGA-D1-A16D	MSS	UCEC
TCGA-D1-A16E	MSS	UCEC
TCGA-D1-A16F	MSI-H	UCEC
TCGA-D1-A16G	MSS	UCEC
TCGA-D1-A16I	MSS	UCEC
TCGA-D1-A16J	MSS	UCEC
TCGA-D1-A16N	Intermediate	UCEC
TCGA-D1-A16O	MSS	UCEC
TCGA-D1-A16Q	MSS	UCEC
TCGA-D1-A16R	MSS	UCEC
TCGA-D1-A16S	MSS	UCEC
TCGA-D1-A16V	MSS	UCEC
TCGA-D1-A16X	MSS	UCEC
TCGA-D1-A16Y	MSS	UCEC
TCGA-D1-A174	MSI-H	UCEC
TCGA-D1-A175	MSI-H	UCEC
TCGA-D1-A176	MSI-H	UCEC
TCGA-D1-A177	MSI-H	UCEC
TCGA-D1-A179	MSS	UCEC
TCGA-D1-A17A	MSI-H	UCEC
TCGA-D1-A17B	MSI-H	UCEC
TCGA-D1-A17C	MSS	UCEC
TCGA-D1-A17D	MSI-H	UCEC
TCGA-D1-A17F	MSI-H	UCEC
TCGA-D1-A17H	MSI-H	UCEC
TCGA-D1-A17K	MSS	UCEC
TCGA-D1-A17L	MSS	UCEC
TCGA-D1-A17M	MSI-H	UCEC
TCGA-D1-A17N	MSS	UCEC
TCGA-D1-A17Q	MSS	UCEC
TCGA-D1-A17R	MSI-H	UCEC
TCGA-D1-A17S	MSS	UCEC
TCGA-D1-A17T	MSS	UCEC

TCGA-D1-A17U	MSI-H	UCEC
TCGA-D1-A1NS	MSI-H	UCEC
TCGA-D1-A1NU	MSS	UCEC
TCGA-D1-A1NW	MSS	UCEC
TCGA-D1-A1NX	MSS	UCEC
TCGA-D1-A1NY	MSI-H	UCEC
TCGA-D1-A1NZ	MSI-H	UCEC
TCGA-D1-A1O0	MSS	UCEC
TCGA-D1-A1O7	MSI-H	UCEC
TCGA-D1-A2G0	MSI-H	UCEC
TCGA-D1-A2G5	Intermediate	UCEC
TCGA-D1-A3DA	MSS	UCEC
TCGA-D1-A3DG	MSS	UCEC
TCGA-D1-A3DH	MSS	UCEC
TCGA-D1-A3JQ	MSS	UCEC
TCGA-D3-A1Q1	MSS	SKCM
TCGA-D3-A1Q7	MSS	SKCM
TCGA-D3-A1Q8	MSS	SKCM
TCGA-D3-A1QA	MSS	SKCM
TCGA-D3-A1QB	MSS	SKCM
TCGA-D3-A2J6	MSS	SKCM
TCGA-D3-A2J7	MSS	SKCM
TCGA-D3-A2J8	MSS	SKCM
TCGA-D3-A2JA	MSS	SKCM
TCGA-D3-A2JC	MSS	SKCM
TCGA-D3-A2JD	MSS	SKCM
TCGA-D3-A2JE	MSS	SKCM
TCGA-D3-A2JF	MSS	SKCM
TCGA-D3-A2JG	MSS	SKCM
TCGA-D3-A2JH	MSS	SKCM
TCGA-D3-A2JK	MSS	SKCM
TCGA-D3-A2JL	MSS	SKCM
TCGA-D3-A2JN	MSS	SKCM
TCGA-D3-A2JO	MSS	SKCM
TCGA-D3-A2JP	MSS	SKCM
TCGA-D3-A3BZ	MSS	SKCM
TCGA-D3-A3C1	MSS	SKCM
TCGA-D3-A3C3	MSS	SKCM
TCGA-D3-A3C6	MSS	SKCM
TCGA-D3-A3C7	MSS	SKCM
TCGA-D3-A3C8	MSS	SKCM
TCGA-D3-A3CB	MSS	SKCM
TCGA-D3-A3CC	MSS	SKCM
TCGA-D3-A3CE	MSS	SKCM
TCGA-D3-A3CF	MSS	SKCM
TCGA-D3-A3MO	MSS	SKCM
TCGA-D3-A3MR	MSS	SKCM
TCGA-D3-A3MU	MSS	SKCM
TCGA-D3-A51E	MSS	SKCM
TCGA-D3-A51G	MSS	SKCM
TCGA-D3-A51H	MSS	SKCM
TCGA-D3-A51J	MSS	SKCM

TCGA-D3-A51K	MSS	SKCM
TCGA-D3-A51N	MSS	SKCM
TCGA-D3-A51T	MSS	SKCM
TCGA-D3-A5GL	MSS	SKCM
TCGA-D3-A5GN	MSS	SKCM
TCGA-D3-A5GO	MSS	SKCM
TCGA-D3-A5GR	MSS	SKCM
TCGA-D3-A5GS	MSS	SKCM
TCGA-D3-A5GT	MSS	SKCM
TCGA-D3-A5GU	MSS	SKCM
TCGA-D3-A8GB	MSS	SKCM
TCGA-D3-A8GC	MSS	SKCM
TCGA-D3-A8GD	MSS	SKCM
TCGA-D3-A8GE	MSS	SKCM
TCGA-D3-A8GI	MSS	SKCM
TCGA-D3-A8GJ	MSS	SKCM
TCGA-D3-A8GK	MSS	SKCM
TCGA-D3-A8GL	MSS	SKCM
TCGA-D3-A8GM	MSI-H	SKCM
TCGA-D3-A8GN	MSS	SKCM
TCGA-D3-A8GO	MSS	SKCM
TCGA-D3-A8GP	MSS	SKCM
TCGA-D3-A8GQ	MSS	SKCM
TCGA-D3-A8GR	MSS	SKCM
TCGA-D3-A8GS	MSS	SKCM
TCGA-D3-A8GV	MSS	SKCM
TCGA-D5-5537	MSS	COAD
TCGA-D5-5538	MSS	COAD
TCGA-D5-5539	MSS	COAD
TCGA-D5-5540	MSS	COAD
TCGA-D5-5541	MSS	COAD
TCGA-D5-6529	MSS	COAD
TCGA-D5-6530	MSI-H	COAD
TCGA-D5-6531	MSS	COAD
TCGA-D5-6532	MSS	COAD
TCGA-D5-6533	MSS	COAD
TCGA-D5-6534	MSS	COAD
TCGA-D5-6535	MSS	COAD
TCGA-D5-6537	MSS	COAD
TCGA-D5-6538	MSS	COAD
TCGA-D5-6539	MSS	COAD
TCGA-D5-6540	MSI-H	COAD
TCGA-D5-6541	MSS	COAD
TCGA-D5-6898	MSS	COAD
TCGA-D5-6920	MSS	COAD
TCGA-D5-6922	MSS	COAD
TCGA-D5-6923	MSS	COAD
TCGA-D5-6924	MSS	COAD
TCGA-D5-6926	MSS	COAD
TCGA-D5-6927	MSI-H	COAD
TCGA-D5-6928	MSI-H	COAD
TCGA-D5-6929	MSS	COAD

TCGA-D5-6930	MSI-H	COAD
TCGA-D5-6931	MSS	COAD
TCGA-D5-6932	MSS	COAD
TCGA-D5-7000	MSS	COAD
TCGA-D6-6515	MSS	HNSC
TCGA-D6-6516	MSS	HNSC
TCGA-D6-6517	MSS	HNSC
TCGA-D6-6823	MSS	HNSC
TCGA-D6-6824	MSS	HNSC
TCGA-D6-6825	MSS	HNSC
TCGA-D6-6826	MSS	HNSC
TCGA-D6-6827	MSS	HNSC
TCGA-D6-8568	MSS	HNSC
TCGA-D6-8569	MSS	HNSC
TCGA-D6-A4Z9	MSS	HNSC
TCGA-D6-A4ZB	MSS	HNSC
TCGA-D6-A6EK	MSS	HNSC
TCGA-D6-A6EM	MSS	HNSC
TCGA-D6-A6EN	MSS	HNSC
TCGA-D6-A6EO	MSS	HNSC
TCGA-D6-A6EP	MSS	HNSC
TCGA-D6-A6EQ	MSS	HNSC
TCGA-D6-A6ES	MSS	HNSC
TCGA-D6-A74Q	MSS	HNSC
TCGA-D7-5577	MSS	STAD
TCGA-D7-5578	MSS	STAD
TCGA-D7-5579	MSS	STAD
TCGA-D7-6518	MSS	STAD
TCGA-D7-6519	MSS	STAD
TCGA-D7-6520	MSS	STAD
TCGA-D7-6521	MSS	STAD
TCGA-D7-6522	MSS	STAD
TCGA-D7-6524	MSS	STAD
TCGA-D7-6525	MSS	STAD
TCGA-D7-6526	MSS	STAD
TCGA-D7-6527	MSS	STAD
TCGA-D7-6528	MSS	STAD
TCGA-D7-6815	MSS	STAD
TCGA-D7-6817	MSS	STAD
TCGA-D7-6818	MSS	STAD
TCGA-D7-6820	MSS	STAD
TCGA-D7-6822	MSS	STAD
TCGA-D7-8570	MSS	STAD
TCGA-D7-8572	MSS	STAD
TCGA-D7-8573	MSS	STAD
TCGA-D7-8574	MSS	STAD
TCGA-D7-8575	MSS	STAD
TCGA-D7-8576	MSS	STAD
TCGA-D7-8578	MSS	STAD
TCGA-D7-8579	MSS	STAD
TCGA-D7-A4YT	MSS	STAD
TCGA-D7-A4YU	MSS	STAD

TCGA-D7-A4YV	MSI-H	STAD
TCGA-D7-A4YX	MSS	STAD
TCGA-D7-A4YY	MSI-H	STAD
TCGA-D7-A4Z0	MSS	STAD
TCGA-D7-A6ET	MSS	STAD
TCGA-D7-A6EV	MSS	STAD
TCGA-D7-A6EX	MSS	STAD
TCGA-D7-A6EY	MSI-H	STAD
TCGA-D7-A6EZ	MSS	STAD
TCGA-D7-A6F0	MSS	STAD
TCGA-D7-A6F2	MSS	STAD
TCGA-D7-A747	MSS	STAD
TCGA-D7-A748	MSS	STAD
TCGA-D7-A74A	MSS	STAD
TCGA-D7-A74B	MSS	STAD
TCGA-D8-A13Y	MSS	BRCA
TCGA-D8-A13Z	MSS	BRCA
TCGA-D8-A140	MSS	BRCA
TCGA-D8-A141	MSS	BRCA
TCGA-D8-A142	MSS	BRCA
TCGA-D8-A143	MSS	BRCA
TCGA-D8-A145	MSS	BRCA
TCGA-D8-A146	MSS	BRCA
TCGA-D8-A147	MSS	BRCA
TCGA-D8-A1J8	MSI-H	BRCA
TCGA-D8-A1J9	MSS	BRCA
TCGA-D8-A1JA	MSS	BRCA
TCGA-D8-A1JB	MSS	BRCA
TCGA-D8-A1JC	MSS	BRCA
TCGA-D8-A1JD	MSS	BRCA
TCGA-D8-A1JE	MSI-H	BRCA
TCGA-D8-A1JF	MSS	BRCA
TCGA-D8-A1JG	MSS	BRCA
TCGA-D8-A1JH	MSS	BRCA
TCGA-D8-A1JI	MSS	BRCA
TCGA-D8-A1JJ	MSS	BRCA
TCGA-D8-A1JK	MSS	BRCA
TCGA-D8-A1JL	MSS	BRCA
TCGA-D8-A1JM	Intermediate	BRCA
TCGA-D8-A1JN	MSS	BRCA
TCGA-D8-A1JP	MSS	BRCA
TCGA-D8-A1JS	MSS	BRCA
TCGA-D8-A1JT	MSS	BRCA
TCGA-D8-A1JU	MSI-H	BRCA
TCGA-D8-A1X5	MSS	BRCA
TCGA-D8-A1X7	MSS	BRCA
TCGA-D8-A1X8	MSS	BRCA
TCGA-D8-A1X9	MSI-H	BRCA
TCGA-D8-A1XA	MSS	BRCA
TCGA-D8-A1XB	MSS	BRCA
TCGA-D8-A1XC	MSS	BRCA
TCGA-D8-A1XF	MSS	BRCA

TCGA-D8-A1XG	MSI-H	BRCA
TCGA-D8-A1XJ	MSS	BRCA
TCGA-D8-A1XK	MSI-H	BRCA
TCGA-D8-A1XL	MSS	BRCA
TCGA-D8-A1XM	MSS	BRCA
TCGA-D8-A1XO	MSS	BRCA
TCGA-D8-A1XQ	MSI-H	BRCA
TCGA-D8-A1XR	MSS	BRCA
TCGA-D8-A1XS	MSS	BRCA
TCGA-D8-A1XT	MSS	BRCA
TCGA-D8-A1XU	MSS	BRCA
TCGA-D8-A1XV	MSS	BRCA
TCGA-D8-A1XW	MSS	BRCA
TCGA-D8-A1XY	MSS	BRCA
TCGA-D8-A1XZ	MSS	BRCA
TCGA-D8-A1Y0	MSI-H	BRCA
TCGA-D8-A1Y1	MSI-H	BRCA
TCGA-D8-A1Y2	MSI-H	BRCA
TCGA-D8-A1Y3	MSS	BRCA
TCGA-D8-A27E	MSS	BRCA
TCGA-D8-A27F	MSS	BRCA
TCGA-D8-A27G	MSS	BRCA
TCGA-D8-A27I	MSS	BRCA
TCGA-D8-A27K	MSS	BRCA
TCGA-D8-A27L	MSS	BRCA
TCGA-D8-A27M	MSS	BRCA
TCGA-D8-A27N	MSS	BRCA
TCGA-D8-A27P	MSS	BRCA
TCGA-D8-A27R	MSS	BRCA
TCGA-D8-A27T	MSS	BRCA
TCGA-D8-A27V	MSS	BRCA
TCGA-D8-A27W	MSS	BRCA
TCGA-D8-A73U	MSS	BRCA
TCGA-D8-A73W	MSS	BRCA
TCGA-D8-A73X	MSS	BRCA
TCGA-D9-A148	MSS	SKCM
TCGA-D9-A149	MSS	SKCM
TCGA-D9-A1JW	MSS	SKCM
TCGA-D9-A1JX	MSS	SKCM
TCGA-D9-A1X3	MSS	SKCM
TCGA-D9-A3Z1	MSS	SKCM
TCGA-D9-A3Z3	MSS	SKCM
TCGA-D9-A3Z4	MSS	SKCM
TCGA-D9-A4Z2	MSS	SKCM
TCGA-D9-A4Z3	MSS	SKCM
TCGA-D9-A4Z5	MSS	SKCM
TCGA-D9-A4Z6	MSS	SKCM
TCGA-D9-A6E9	MSS	SKCM
TCGA-D9-A6EA	MSS	SKCM
TCGA-D9-A6EC	MSS	SKCM
TCGA-D9-A6EG	MSS	SKCM
TCGA-DA-A1HV	MSS	SKCM

TCGA-DA-A1HW	MSS	SKCM
TCGA-DA-A1HY	MSS	SKCM
TCGA-DA-A1I0	MSS	SKCM
TCGA-DA-A1I1	MSS	SKCM
TCGA-DA-A1I2	MSS	SKCM
TCGA-DA-A1I4	MSS	SKCM
TCGA-DA-A1I5	MSS	SKCM
TCGA-DA-A1I7	MSS	SKCM
TCGA-DA-A1I8	MSS	SKCM
TCGA-DA-A1IA	MSS	SKCM
TCGA-DA-A1IB	MSS	SKCM
TCGA-DA-A1IC	MSS	SKCM
TCGA-DA-A3F2	MSS	SKCM
TCGA-DA-A3F5	MSS	SKCM
TCGA-DA-A3F8	MSS	SKCM
TCGA-DA-A95V	MSS	SKCM
TCGA-DA-A95W	MSS	SKCM
TCGA-DA-A95X	MSS	SKCM
TCGA-DA-A95Y	MSS	SKCM
TCGA-DA-A95Z	MSS	SKCM
TCGA-DA-A960	MSS	SKCM
TCGA-DB-5270	MSS	LGG
TCGA-DB-5273	MSS	LGG
TCGA-DB-5274	MSS	LGG
TCGA-DB-5275	MSS	LGG
TCGA-DB-5276	MSS	LGG
TCGA-DB-5277	MSS	LGG
TCGA-DB-5278	MSS	LGG
TCGA-DB-5279	MSS	LGG
TCGA-DB-5280	MSS	LGG
TCGA-DB-5281	MSS	LGG
TCGA-DB-A4XD	MSS	LGG
TCGA-DB-A4XE	MSS	LGG
TCGA-DB-A4XF	MSS	LGG
TCGA-DB-A4XG	MSS	LGG
TCGA-DB-A4XH	MSS	LGG
TCGA-DB-A64L	MSS	LGG
TCGA-DB-A64O	MSS	LGG
TCGA-DB-A64P	MSS	LGG
TCGA-DB-A64Q	MSS	LGG
TCGA-DB-A64R	MSS	LGG
TCGA-DB-A64S	MSS	LGG
TCGA-DB-A64U	MSS	LGG
TCGA-DB-A64V	MSS	LGG
TCGA-DB-A64W	MSS	LGG
TCGA-DB-A64X	MSS	LGG
TCGA-DB-A75K	MSS	LGG
TCGA-DB-A75L	MSS	LGG
TCGA-DB-A75M	MSS	LGG
TCGA-DB-A75O	MSS	LGG
TCGA-DB-A75P	MSS	LGG
TCGA-DC-4745	MSS	READ

TCGA-DC-4749	MSS	READ
TCGA-DC-5337	MSS	READ
TCGA-DC-5869	MSS	READ
TCGA-DC-6155	MSS	READ
TCGA-DC-6157	MSS	READ
TCGA-DC-6158	MSS	READ
TCGA-DC-6160	MSS	READ
TCGA-DC-6681	MSS	READ
TCGA-DC-6682	MSS	READ
TCGA-DC-6683	MSS	READ
TCGA-DD-A113	MSS	LIHC
TCGA-DD-A114	MSS	LIHC
TCGA-DD-A115	MSS	LIHC
TCGA-DD-A116	MSS	LIHC
TCGA-DD-A118	MSS	LIHC
TCGA-DD-A119	MSS	LIHC
TCGA-DD-A11A	MSS	LIHC
TCGA-DD-A11B	MSS	LIHC
TCGA-DD-A11C	MSS	LIHC
TCGA-DD-A11D	MSS	LIHC
TCGA-DD-A1E9	MSS	LIHC
TCGA-DD-A1EA	MSS	LIHC
TCGA-DD-A1EB	MSS	LIHC
TCGA-DD-A1EC	MSS	LIHC
TCGA-DD-A1ED	MSS	LIHC
TCGA-DD-A1EE	MSS	LIHC
TCGA-DD-A1EF	MSS	LIHC
TCGA-DD-A1EG	MSS	LIHC
TCGA-DD-A1EH	MSS	LIHC
TCGA-DD-A1EI	MSS	LIHC
TCGA-DD-A1EJ	MSS	LIHC
TCGA-DD-A1EK	MSS	LIHC
TCGA-DD-A1EL	MSS	LIHC
TCGA-DD-A39V	MSS	LIHC
TCGA-DD-A39W	MSS	LIHC
TCGA-DD-A39X	MSS	LIHC
TCGA-DD-A39Y	MSS	LIHC
TCGA-DD-A39Z	MSS	LIHC
TCGA-DD-A3A0	Intermediate	LIHC
TCGA-DD-A3A1	MSS	LIHC
TCGA-DD-A3A2	MSS	LIHC
TCGA-DD-A3A3	MSS	LIHC
TCGA-DD-A3A4	MSS	LIHC
TCGA-DD-A3A5	MSS	LIHC
TCGA-DD-A3A6	MSS	LIHC
TCGA-DD-A3A7	MSS	LIHC
TCGA-DD-A3A8	MSS	LIHC
TCGA-DD-A3A9	MSS	LIHC
TCGA-DD-A4NB	MSS	LIHC
TCGA-DD-A4ND	MSS	LIHC
TCGA-DD-A4NR	MSS	LIHC
TCGA-DD-A4NS	MSS	LIHC

TCGA-DD-A4NV	MSS	LIHC
TCGA-DD-A73A	MSS	LIHC
TCGA-DD-A73B	MSS	LIHC
TCGA-DD-A73C	MSS	LIHC
TCGA-DD-A73D	MSS	LIHC
TCGA-DD-A73E	MSS	LIHC
TCGA-DD-A73F	MSS	LIHC
TCGA-DD-A73G	MSS	LIHC
TCGA-DD-AA3A	MSS	LIHC
TCGA-DD-AAC8	MSS	LIHC
TCGA-DD-AAC9	MSS	LIHC
TCGA-DD-AACA	MSS	LIHC
TCGA-DD-AACA	MSS	LIHC
TCGA-DD-AACA	MSS	LIHC
TCGA-DD-AACB	MSS	LIHC
TCGA-DD-AACC	MSS	LIHC
TCGA-DD-AACD	MSS	LIHC
TCGA-DD-AACE	MSS	LIHC
TCGA-DD-AACF	MSS	LIHC
TCGA-DD-AACG	MSS	LIHC
TCGA-DD-AACH	MSS	LIHC
TCGA-DD-AACI	MSS	LIHC
TCGA-DD-AACJ	MSS	LIHC
TCGA-DD-AACK	MSS	LIHC
TCGA-DD-AACL	MSS	LIHC
TCGA-DD-AACM	MSS	LIHC
TCGA-DD-AACN	MSS	LIHC
TCGA-DD-AACO	MSS	LIHC
TCGA-DD-AACP	MSS	LIHC
TCGA-DD-AACQ	MSS	LIHC
TCGA-DD-AACS	MSS	LIHC
TCGA-DD-AACT	MSS	LIHC
TCGA-DD-AACU	MSS	LIHC
TCGA-DD-AACV	MSS	LIHC
TCGA-DD-AACW	MSS	LIHC
TCGA-DD-AACX	MSS	LIHC
TCGA-DD-AACY	MSS	LIHC
TCGA-DD-AACZ	MSS	LIHC
TCGA-DD-AAD0	MSS	LIHC
TCGA-DD-AAD1	MSS	LIHC
TCGA-DD-AAD2	MSS	LIHC
TCGA-DD-AAD3	MSS	LIHC
TCGA-DD-AAD5	MSS	LIHC
TCGA-DD-AAD6	MSS	LIHC
TCGA-DD-AAD8	MSS	LIHC
TCGA-DD-AADA	MSS	LIHC
TCGA-DD-AADB	MSS	LIHC
TCGA-DD-AADC	MSS	LIHC
TCGA-DD-AADD	MSS	LIHC
TCGA-DD-AADE	MSS	LIHC
TCGA-DD-AADF	MSS	LIHC
TCGA-DD-AADG	MSS	LIHC

TCGA-DD-AADI	MSS	LIHC
TCGA-DD-AADJ	MSS	LIHC
TCGA-DD-AADK	MSS	LIHC
TCGA-DD-AADL	MSS	LIHC
TCGA-DD-AADM	MSS	LIHC
TCGA-DD-AADN	MSS	LIHC
TCGA-DD-AADO	MSS	LIHC
TCGA-DD-AADP	MSS	LIHC
TCGA-DD-AADQ	MSS	LIHC
TCGA-DD-AADR	MSS	LIHC
TCGA-DD-AADS	MSS	LIHC
TCGA-DD-AADU	MSS	LIHC
TCGA-DD-AADV	MSS	LIHC
TCGA-DD-AADW	MSS	LIHC
TCGA-DD-AADY	MSS	LIHC
TCGA-DD-AAE0	MSS	LIHC
TCGA-DD-AAE1	MSS	LIHC
TCGA-DD-AAE2	MSS	LIHC
TCGA-DD-AAE3	MSS	LIHC
TCGA-DD-AAE4	MSS	LIHC
TCGA-DD-AAE6	MSS	LIHC
TCGA-DD-AAE7	MSS	LIHC
TCGA-DD-AAE8	MSS	LIHC
TCGA-DD-AAE9	MSS	LIHC
TCGA-DD-AAEA	MSS	LIHC
TCGA-DD-AAEB	MSS	LIHC
TCGA-DD-AAED	MSS	LIHC
TCGA-DD-AAEE	MSS	LIHC
TCGA-DD-AAEG	MSS	LIHC
TCGA-DD-AAEH	MSS	LIHC
TCGA-DD-AAEI	MSS	LIHC
TCGA-DD-AAEK	MSS	LIHC
TCGA-DD-AAVP	MSS	LIHC
TCGA-DD-AAVQ	MSS	LIHC
TCGA-DD-AAVR	MSS	LIHC
TCGA-DD-AAVS	MSS	LIHC
TCGA-DD-AAVU	MSS	LIHC
TCGA-DD-AAVV	MSS	LIHC
TCGA-DD-AAVW	MSS	LIHC
TCGA-DD-AAVX	MSS	LIHC
TCGA-DD-AAVY	MSS	LIHC
TCGA-DD-AAVZ	MSS	LIHC
TCGA-DD-AAW0	MSS	LIHC
TCGA-DD-AAW1	MSS	LIHC
TCGA-DD-AAW2	MSS	LIHC
TCGA-DD-AAW3	MSS	LIHC
TCGA-DE-A0XZ	MSS	THCA
TCGA-DE-A0Y2	MSS	THCA
TCGA-DE-A0Y3	MSS	THCA
TCGA-DE-A2OL	MSS	THCA
TCGA-DE-A3KN	MSS	THCA
TCGA-DE-A4M8	MSS	THCA

TCGA-DE-A4M9	MSS	THCA
TCGA-DE-A4MA	MSS	THCA
TCGA-DE-A4MB	MSS	THCA
TCGA-DE-A4MC	MSS	THCA
TCGA-DE-A4MD	MSS	THCA
TCGA-DE-A4MD	MSS	THCA
TCGA-DE-A69J	MSS	THCA
TCGA-DE-A69K	MSS	THCA
TCGA-DE-A7U5	MSS	THCA
TCGA-DF-A2KN	MSI-H	UCEC
TCGA-DF-A2KY	MSI-H	UCEC
TCGA-DF-A2KZ	MSI-H	UCEC
TCGA-DH-5140	MSS	LGG
TCGA-DH-5141	MSS	LGG
TCGA-DH-5142	MSS	LGG
TCGA-DH-5143	MSS	LGG
TCGA-DH-5144	MSS	LGG
TCGA-DH-A669	MSS	LGG
TCGA-DH-A669	MSS	LGG
TCGA-DH-A66B	MSS	LGG
TCGA-DH-A66D	MSS	LGG
TCGA-DH-A66F	MSS	LGG
TCGA-DH-A66G	MSS	LGG
TCGA-DH-A7UR	MSS	LGG
TCGA-DH-A7US	MSS	LGG
TCGA-DH-A7UT	MSS	LGG
TCGA-DH-A7UU	MSS	LGG
TCGA-DH-A7UV	MSS	LGG
TCGA-DI-A0WH	MSI-H	UCEC
TCGA-DI-A1BU	MSI-H	UCEC
TCGA-DI-A1BY	MSS	UCEC
TCGA-DI-A1C3	MSS	UCEC
TCGA-DI-A1NN	MSS	UCEC
TCGA-DI-A1NO	MSS	UCEC
TCGA-DI-A2QT	MSS	UCEC
TCGA-DJ-A13L	MSS	THCA
TCGA-DJ-A13M	MSS	THCA
TCGA-DJ-A13O	MSS	THCA
TCGA-DJ-A13P	MSS	THCA
TCGA-DJ-A13R	MSS	THCA
TCGA-DJ-A13S	MSS	THCA
TCGA-DJ-A13T	MSS	THCA
TCGA-DJ-A13U	MSS	THCA
TCGA-DJ-A13V	MSS	THCA
TCGA-DJ-A13W	MSS	THCA
TCGA-DJ-A13X	MSS	THCA
TCGA-DJ-A1QD	MSS	THCA
TCGA-DJ-A1QE	MSS	THCA
TCGA-DJ-A1QF	MSS	THCA
TCGA-DJ-A1QG	MSS	THCA
TCGA-DJ-A1QH	MSS	THCA
TCGA-DJ-A1QI	MSS	THCA

TCGA-DJ-A1QL	MSS	THCA
TCGA-DJ-A1QM	MSS	THCA
TCGA-DJ-A1QN	MSS	THCA
TCGA-DJ-A1QO	MSS	THCA
TCGA-DJ-A1QQ	MSS	THCA
TCGA-DJ-A2PN	MSS	THCA
TCGA-DJ-A2PO	MSS	THCA
TCGA-DJ-A2PP	MSS	THCA
TCGA-DJ-A2PQ	MSS	THCA
TCGA-DJ-A2PR	MSS	THCA
TCGA-DJ-A2PS	MSS	THCA
TCGA-DJ-A2PT	MSS	THCA
TCGA-DJ-A2PU	MSS	THCA
TCGA-DJ-A2PV	MSS	THCA
TCGA-DJ-A2PW	MSS	THCA
TCGA-DJ-A2PX	MSS	THCA
TCGA-DJ-A2PY	MSS	THCA
TCGA-DJ-A2PZ	MSS	THCA
TCGA-DJ-A2Q0	MSS	THCA
TCGA-DJ-A2Q1	MSS	THCA
TCGA-DJ-A2Q2	MSS	THCA
TCGA-DJ-A2Q3	MSS	THCA
TCGA-DJ-A2Q4	MSS	THCA
TCGA-DJ-A2Q5	MSS	THCA
TCGA-DJ-A2Q6	MSS	THCA
TCGA-DJ-A2Q7	MSS	THCA
TCGA-DJ-A2Q8	MSS	THCA
TCGA-DJ-A2Q9	MSS	THCA
TCGA-DJ-A2QA	MSS	THCA
TCGA-DJ-A2QB	MSS	THCA
TCGA-DJ-A2QC	MSS	THCA
TCGA-DJ-A3UK	MSS	THCA
TCGA-DJ-A3UM	MSS	THCA
TCGA-DJ-A3UN	MSS	THCA
TCGA-DJ-A3UP	MSS	THCA
TCGA-DJ-A3UR	MSS	THCA
TCGA-DJ-A3US	MSS	THCA
TCGA-DJ-A3UT	MSS	THCA
TCGA-DJ-A3UU	MSS	THCA
TCGA-DJ-A3UW	MSS	THCA
TCGA-DJ-A3UX	MSS	THCA
TCGA-DJ-A3UZ	MSS	THCA
TCGA-DJ-A3V0	MSS	THCA
TCGA-DJ-A3V2	MSS	THCA
TCGA-DJ-A3V4	MSS	THCA
TCGA-DJ-A3V5	MSS	THCA
TCGA-DJ-A3V6	MSS	THCA
TCGA-DJ-A3V7	MSS	THCA
TCGA-DJ-A3V8	MSS	THCA
TCGA-DJ-A3V9	MSS	THCA
TCGA-DJ-A3VA	MSS	THCA
TCGA-DJ-A3VB	MSS	THCA

TCGA-DJ-A3VD	MSS	THCA
TCGA-DJ-A3VE	MSS	THCA
TCGA-DJ-A3VF	MSS	THCA
TCGA-DJ-A3VG	MSS	THCA
TCGA-DJ-A3VI	MSS	THCA
TCGA-DJ-A3VJ	MSS	THCA
TCGA-DJ-A3VK	MSS	THCA
TCGA-DJ-A3VL	MSS	THCA
TCGA-DJ-A3VM	MSS	THCA
TCGA-DJ-A4UL	MSS	THCA
TCGA-DJ-A4UP	MSS	THCA
TCGA-DJ-A4UQ	MSS	THCA
TCGA-DJ-A4UR	MSS	THCA
TCGA-DJ-A4UT	MSS	THCA
TCGA-DJ-A4UW	MSS	THCA
TCGA-DJ-A4V0	MSS	THCA
TCGA-DJ-A4V2	MSS	THCA
TCGA-DJ-A4V4	MSS	THCA
TCGA-DJ-A4V5	MSS	THCA
TCGA-DK-A1A3	MSS	BLCA
TCGA-DK-A1A5	MSS	BLCA
TCGA-DK-A1A6	Intermediate	BLCA
TCGA-DK-A1A6	MSS	BLCA
TCGA-DK-A1A7	MSS	BLCA
TCGA-DK-A1AA	MSS	BLCA
TCGA-DK-A1AB	MSS	BLCA
TCGA-DK-A1AC	MSS	BLCA
TCGA-DK-A1AD	MSS	BLCA
TCGA-DK-A1AE	MSS	BLCA
TCGA-DK-A1AF	MSS	BLCA
TCGA-DK-A1AG	MSS	BLCA
TCGA-DK-A2HX	MSS	BLCA
TCGA-DK-A2I1	MSS	BLCA
TCGA-DK-A2I2	MSS	BLCA
TCGA-DK-A2I6	MSS	BLCA
TCGA-DK-A3IM	MSS	BLCA
TCGA-DK-A3IN	MSS	BLCA
TCGA-DK-A3IT	MSS	BLCA
TCGA-DK-A3IU	MSS	BLCA
TCGA-DK-A3WW	MSS	BLCA
TCGA-DK-A3WX	MSS	BLCA
TCGA-DK-A3WY	MSS	BLCA
TCGA-DK-A3X1	MSS	BLCA
TCGA-DK-A3X2	MSS	BLCA
TCGA-DK-A6AV	MSS	BLCA
TCGA-DK-A6AW	MSS	BLCA
TCGA-DK-A6B0	MSS	BLCA
TCGA-DK-A6B1	MSS	BLCA
TCGA-DK-A6B2	MSS	BLCA
TCGA-DK-A6B5	MSS	BLCA
TCGA-DK-A6B6	MSS	BLCA
TCGA-DK-AA6L	MSS	BLCA

TCGA-DK-AA6M	MSS	BLCA
TCGA-DK-AA6P	MSS	BLCA
TCGA-DK-AA6Q	MSS	BLCA
TCGA-DK-AA6R	MSS	BLCA
TCGA-DK-AA6S	MSS	BLCA
TCGA-DK-AA6T	MSS	BLCA
TCGA-DK-AA6U	MSS	BLCA
TCGA-DK-AA6W	MSS	BLCA
TCGA-DK-AA6X	MSS	BLCA
TCGA-DK-AA71	MSS	BLCA
TCGA-DK-AA74	MSS	BLCA
TCGA-DK-AA75	MSS	BLCA
TCGA-DK-AA76	MSS	BLCA
TCGA-DK-AA77	MSS	BLCA
TCGA-DM-A0X9	MSS	COAD
TCGA-DM-A0XD	MSS	COAD
TCGA-DM-A0XF	MSS	COAD
TCGA-DM-A1D0	MSS	COAD
TCGA-DM-A1D4	MSS	COAD
TCGA-DM-A1D6	MSS	COAD
TCGA-DM-A1D7	MSS	COAD
TCGA-DM-A1D8	MSS	COAD
TCGA-DM-A1D9	MSS	COAD
TCGA-DM-A1DA	MSS	COAD
TCGA-DM-A1DB	MSS	COAD
TCGA-DM-A1HA	MSS	COAD
TCGA-DM-A1HB	MSI-H	COAD
TCGA-DM-A280	MSS	COAD
TCGA-DM-A282	MSS	COAD
TCGA-DM-A285	MSS	COAD
TCGA-DM-A288	MSS	COAD
TCGA-DM-A28A	MSS	COAD
TCGA-DM-A28C	MSS	COAD
TCGA-DM-A28E	MSS	COAD
TCGA-DM-A28F	MSS	COAD
TCGA-DM-A28G	MSS	COAD
TCGA-DM-A28H	MSS	COAD
TCGA-DM-A28K	MSS	COAD
TCGA-DM-A28M	MSS	COAD
TCGA-DO-A1JZ	MSS	THCA
TCGA-DO-A1K0	MSS	THCA
TCGA-DQ-5624	MSS	HNSC
TCGA-DQ-5625	MSS	HNSC
TCGA-DQ-5629	MSS	HNSC
TCGA-DQ-5630	MSS	HNSC
TCGA-DQ-5631	MSS	HNSC
TCGA-DQ-7588	MSS	HNSC
TCGA-DQ-7591	MSS	HNSC
TCGA-DQ-7592	MSS	HNSC
TCGA-DQ-7593	MSS	HNSC
TCGA-DQ-7596	MSS	HNSC
TCGA-DR-A0ZL	MSS	CESC

TCGA-DR-A0ZM	MSS	CESC
TCGA-DS-A0VK	MSS	CESC
TCGA-DS-A0VL	MSS	CESC
TCGA-DS-A0VM	MSS	CESC
TCGA-DS-A0VN	MSS	CESC
TCGA-DS-A1OB	MSS	CESC
TCGA-DS-A1OC	MSS	CESC
TCGA-DS-A1OD	MSS	CESC
TCGA-DS-A7WF	MSS	CESC
TCGA-DS-A7WH	MSS	CESC
TCGA-DS-A7WI	MSS	CESC
TCGA-DT-5265	MSS	READ
TCGA-DU-5847	MSS	LGG
TCGA-DU-5849	MSS	LGG
TCGA-DU-5851	MSS	LGG
TCGA-DU-5852	MSS	LGG
TCGA-DU-5853	MSS	LGG
TCGA-DU-5854	MSS	LGG
TCGA-DU-5855	MSS	LGG
TCGA-DU-5870	MSS	LGG
TCGA-DU-5870	MSS	LGG
TCGA-DU-5871	MSS	LGG
TCGA-DU-5872	MSS	LGG
TCGA-DU-5872	MSS	LGG
TCGA-DU-5874	MSS	LGG
TCGA-DU-6392	MSI-H	LGG
TCGA-DU-6393	MSS	LGG
TCGA-DU-6394	MSS	LGG
TCGA-DU-6395	MSS	LGG
TCGA-DU-6396	MSS	LGG
TCGA-DU-6397	MSS	LGG
TCGA-DU-6397	MSS	LGG
TCGA-DU-6399	MSS	LGG
TCGA-DU-6400	MSS	LGG
TCGA-DU-6401	MSS	LGG
TCGA-DU-6402	MSS	LGG
TCGA-DU-6403	MSS	LGG
TCGA-DU-6404	MSS	LGG
TCGA-DU-6404	MSS	LGG
TCGA-DU-6404	MSS	LGG
TCGA-DU-6405	MSS	LGG
TCGA-DU-6406	MSS	LGG
TCGA-DU-6407	MSS	LGG
TCGA-DU-6407	MSS	LGG
TCGA-DU-6407	MSS	LGG
TCGA-DU-6408	MSS	LGG
TCGA-DU-6410	MSS	LGG
TCGA-DU-6542	MSS	LGG
TCGA-DU-7006	MSS	LGG
TCGA-DU-7007	MSS	LGG
TCGA-DU-7008	MSS	LGG
TCGA-DU-7009	MSS	LGG

TCGA-DU-7010	MSS	LGG
TCGA-DU-7011	MSS	LGG
TCGA-DU-7012	MSS	LGG
TCGA-DU-7013	MSS	LGG
TCGA-DU-7014	MSS	LGG
TCGA-DU-7015	MSS	LGG
TCGA-DU-7018	MSS	LGG
TCGA-DU-7019	MSS	LGG
TCGA-DU-7290	MSS	LGG
TCGA-DU-7292	MSS	LGG
TCGA-DU-7294	MSS	LGG
TCGA-DU-7298	MSS	LGG
TCGA-DU-7299	MSS	LGG
TCGA-DU-7300	MSS	LGG
TCGA-DU-7301	MSS	LGG
TCGA-DU-7302	MSS	LGG
TCGA-DU-7304	MSS	LGG
TCGA-DU-7304	MSS	LGG
TCGA-DU-7306	MSS	LGG
TCGA-DU-7309	MSS	LGG
TCGA-DU-8158	MSS	LGG
TCGA-DU-8161	MSS	LGG
TCGA-DU-8166	MSS	LGG
TCGA-DU-8167	MSS	LGG
TCGA-DU-8168	MSS	LGG
TCGA-DU-A5TP	MSS	LGG
TCGA-DU-A5TR	MSS	LGG
TCGA-DU-A5TS	MSS	LGG
TCGA-DU-A5TT	MSS	LGG
TCGA-DU-A5TU	MSS	LGG
TCGA-DU-A5TW	MSS	LGG
TCGA-DU-A5TY	MSS	LGG
TCGA-DU-A6S2	MSS	LGG
TCGA-DU-A6S3	MSS	LGG
TCGA-DU-A6S6	MSS	LGG
TCGA-DU-A6S7	MSS	LGG
TCGA-DU-A6S8	MSS	LGG
TCGA-DU-A76K	MSS	LGG
TCGA-DU-A76L	MSS	LGG
TCGA-DU-A76R	MSS	LGG
TCGA-DU-A7T6	MSS	LGG
TCGA-DU-A7T8	MSS	LGG
TCGA-DU-A7TA	MSS	LGG
TCGA-DU-A7TB	MSS	LGG
TCGA-DU-A7TC	MSS	LGG
TCGA-DU-A7TD	MSS	LGG
TCGA-DU-A7TG	MSS	LGG
TCGA-DU-A7TI	MSS	LGG
TCGA-DU-A7TJ	MSS	LGG
TCGA-DV-5565	MSS	KIRC
TCGA-DV-5566	MSS	KIRC
TCGA-DV-5567	MSS	KIRC

TCGA-DV-5568	MSS	KIRC
TCGA-DV-5569	MSS	KIRC
TCGA-DV-5573	MSS	KIRC
TCGA-DV-5574	MSS	KIRC
TCGA-DV-5575	MSS	KIRC
TCGA-DV-5576	MSS	KIRC
TCGA-DV-A4VZ	MSS	KIRC
TCGA-DW-5560	MSS	KIRP
TCGA-DW-5561	MSS	KIRP
TCGA-DW-7834	MSS	KIRP
TCGA-DW-7836	Intermediate	KIRP
TCGA-DW-7837	MSS	KIRP
TCGA-DW-7838	MSS	KIRP
TCGA-DW-7839	MSS	KIRP
TCGA-DW-7840	MSS	KIRP
TCGA-DW-7841	MSS	KIRP
TCGA-DW-7842	MSS	KIRP
TCGA-DX-A1KX	MSS	SARC
TCGA-DX-A1KY	MSS	SARC
TCGA-DX-A1L3	MSS	SARC
TCGA-DX-A23U	MSS	SARC
TCGA-DX-A3M2	MSS	SARC
TCGA-DX-A3U6	MSS	SARC
TCGA-DX-A3U9	MSS	SARC
TCGA-DX-A3UA	MSS	SARC
TCGA-DX-A3UB	MSS	SARC
TCGA-DX-A3UC	MSS	SARC
TCGA-DX-A3UD	MSS	SARC
TCGA-DX-A3UE	MSS	SARC
TCGA-DX-A3UF	MSS	SARC
TCGA-DX-A48J	MSS	SARC
TCGA-DX-A48K	MSS	SARC
TCGA-DX-A48L	MSS	SARC
TCGA-DX-A48N	MSS	SARC
TCGA-DX-A48O	MSS	SARC
TCGA-DX-A48P	MSS	SARC
TCGA-DX-A48R	MSS	SARC
TCGA-DX-A48U	MSS	SARC
TCGA-DX-A48V	MSS	SARC
TCGA-DX-A6B7	MSS	SARC
TCGA-DX-A6B8	MSS	SARC
TCGA-DX-A6B9	MSS	SARC
TCGA-DX-A6BA	MSS	SARC
TCGA-DX-A6BB	MSS	SARC
TCGA-DX-A6BE	MSS	SARC
TCGA-DX-A6BF	MSS	SARC
TCGA-DX-A6BG	MSS	SARC
TCGA-DX-A6BH	MSS	SARC
TCGA-DX-A6BK	MSS	SARC
TCGA-DX-A6YQ	MSS	SARC
TCGA-DX-A6YR	MSS	SARC
TCGA-DX-A6YS	MSS	SARC

TCGA-DX-A6YU	MSS	SARC
TCGA-DX-A6YV	MSS	SARC
TCGA-DX-A6YX	MSS	SARC
TCGA-DX-A6YZ	MSS	SARC
TCGA-DX-A6Z0	MSS	SARC
TCGA-DX-A6Z2	MSS	SARC
TCGA-DX-A7EF	MSS	SARC
TCGA-DX-A7EI	MSS	SARC
TCGA-DX-A7EL	MSS	SARC
TCGA-DX-A7EM	MSS	SARC
TCGA-DX-A7EN	MSS	SARC
TCGA-DX-A7EO	MSS	SARC
TCGA-DX-A7EQ	MSS	SARC
TCGA-DX-A7ER	MSS	SARC
TCGA-DX-A7ES	MSS	SARC
TCGA-DX-A7ET	MSS	SARC
TCGA-DX-A7EU	MSS	SARC
TCGA-DX-A8BG	MSS	SARC
TCGA-DX-A8BJ	MSS	SARC
TCGA-DX-A8BL	MSS	SARC
TCGA-DX-A8BM	MSS	SARC
TCGA-DX-A8BN	MSS	SARC
TCGA-DX-A8BO	MSS	SARC
TCGA-DX-A8BP	MSS	SARC
TCGA-DX-A8BR	MSS	SARC
TCGA-DX-A8BT	MSS	SARC
TCGA-DX-A8BU	MSS	SARC
TCGA-DX-A8BV	MSS	SARC
TCGA-DX-A8BX	MSS	SARC
TCGA-DX-A8BZ	MSS	SARC
TCGA-DX-AATS	MSS	SARC
TCGA-DX-AB2E	MSS	SARC
TCGA-DX-AB2F	MSS	SARC
TCGA-DX-AB2G	MSS	SARC
TCGA-DX-AB2H	MSS	SARC
TCGA-DX-AB2J	MSS	SARC
TCGA-DX-AB2L	MSS	SARC
TCGA-DX-AB2O	MSS	SARC
TCGA-DX-AB2P	MSS	SARC
TCGA-DX-AB2Q	MSS	SARC
TCGA-DX-AB2S	MSS	SARC
TCGA-DX-AB2T	MSS	SARC
TCGA-DX-AB2V	MSS	SARC
TCGA-DX-AB2W	MSS	SARC
TCGA-DX-AB2X	MSS	SARC
TCGA-DX-AB2Z	MSS	SARC
TCGA-DX-AB30	MSS	SARC
TCGA-DX-AB32	MSS	SARC
TCGA-DX-AB35	MSS	SARC
TCGA-DX-AB36	MSS	SARC
TCGA-DX-AB37	MSS	SARC
TCGA-DX-AB3A	MSS	SARC

TCGA-DX-AB3B	MSS	SARC
TCGA-DX-AB3C	MSS	SARC
TCGA-DY-A0XA	MSS	READ
TCGA-DY-A1DC	MSS	READ
TCGA-DY-A1DD	MSS	READ
TCGA-DY-A1DF	MSS	READ
TCGA-DY-A1DG	MSS	READ
TCGA-DY-A1H8	MSS	READ
TCGA-DZ-6131	MSS	KIRP
TCGA-DZ-6132	MSS	KIRP
TCGA-DZ-6133	MSS	KIRP
TCGA-DZ-6134	MSS	KIRP
TCGA-DZ-6135	MSS	KIRP
TCGA-E1-5302	MSS	LGG
TCGA-E1-5303	MSS	LGG
TCGA-E1-5304	MSS	LGG
TCGA-E1-5305	MSS	LGG
TCGA-E1-5307	MSS	LGG
TCGA-E1-5311	MSS	LGG
TCGA-E1-5318	MSS	LGG
TCGA-E1-5319	MSS	LGG
TCGA-E1-5322	MSS	LGG
TCGA-E1-A7YD	MSS	LGG
TCGA-E1-A7YE	MSS	LGG
TCGA-E1-A7YH	MSS	LGG
TCGA-E1-A7YI	MSS	LGG
TCGA-E1-A7YJ	MSS	LGG
TCGA-E1-A7YK	MSS	LGG
TCGA-E1-A7YL	MSS	LGG
TCGA-E1-A7YM	MSS	LGG
TCGA-E1-A7YN	MSS	LGG
TCGA-E1-A7YO	MSS	LGG
TCGA-E1-A7YQ	MSS	LGG
TCGA-E1-A7YS	MSS	LGG
TCGA-E1-A7YU	MSS	LGG
TCGA-E1-A7YV	MSS	LGG
TCGA-E1-A7YW	MSS	LGG
TCGA-E1-A7YY	MSS	LGG
TCGA-E1-A7Z2	MSS	LGG
TCGA-E1-A7Z3	MSS	LGG
TCGA-E1-A7Z4	MSS	LGG
TCGA-E1-A7Z6	MSS	LGG
TCGA-E2-A10A	MSS	BRCA
TCGA-E2-A10C	MSS	BRCA
TCGA-E2-A14N	MSS	BRCA
TCGA-E2-A14P	MSS	BRCA
TCGA-E2-A14Q	MSS	BRCA
TCGA-E2-A14R	MSS	BRCA
TCGA-E2-A14S	MSS	BRCA
TCGA-E2-A14T	MSS	BRCA
TCGA-E2-A14V	MSS	BRCA
TCGA-E2-A14W	MSS	BRCA

TCGA-E2-A14X	MSS	BRCA
TCGA-E2-A14Y	MSS	BRCA
TCGA-E2-A14Z	MSS	BRCA
TCGA-E2-A150	MSS	BRCA
TCGA-E2-A152	MSS	BRCA
TCGA-E2-A153	MSS	BRCA
TCGA-E2-A154	MSS	BRCA
TCGA-E2-A155	MSS	BRCA
TCGA-E2-A156	MSS	BRCA
TCGA-E2-A158	MSS	BRCA
TCGA-E2-A159	MSS	BRCA
TCGA-E2-A15A	MSS	BRCA
TCGA-E2-A15A	MSS	BRCA
TCGA-E2-A15C	MSS	BRCA
TCGA-E2-A15D	MSS	BRCA
TCGA-E2-A15E	MSS	BRCA
TCGA-E2-A15E	MSS	BRCA
TCGA-E2-A15G	MSS	BRCA
TCGA-E2-A15H	MSS	BRCA
TCGA-E2-A15I	MSS	BRCA
TCGA-E2-A15J	MSS	BRCA
TCGA-E2-A15K	MSS	BRCA
TCGA-E2-A15K	MSS	BRCA
TCGA-E2-A15L	MSS	BRCA
TCGA-E2-A15M	MSS	BRCA
TCGA-E2-A15O	MSS	BRCA
TCGA-E2-A15P	MSS	BRCA
TCGA-E2-A15R	MSS	BRCA
TCGA-E2-A15S	Intermediate	BRCA
TCGA-E2-A15T	MSS	BRCA
TCGA-E2-A1AZ	MSS	BRCA
TCGA-E2-A1B0	MSS	BRCA
TCGA-E2-A1B1	MSS	BRCA
TCGA-E2-A1B4	MSS	BRCA
TCGA-E2-A1B5	MSS	BRCA
TCGA-E2-A1B6	MSS	BRCA
TCGA-E2-A1BC	MSS	BRCA
TCGA-E2-A1BD	MSS	BRCA
TCGA-E2-A1IE	MSS	BRCA
TCGA-E2-A1IF	Intermediate	BRCA
TCGA-E2-A1IG	MSS	BRCA
TCGA-E2-A1IH	MSS	BRCA
TCGA-E2-A1II	MSI-H	BRCA
TCGA-E2-A1IJ	MSI-H	BRCA
TCGA-E2-A1IK	MSS	BRCA
TCGA-E2-A1IL	MSI-H	BRCA
TCGA-E2-A1IN	MSI-H	BRCA
TCGA-E2-A1IO	MSI-H	BRCA
TCGA-E2-A1IU	MSI-H	BRCA
TCGA-E2-A1L6	MSS	BRCA
TCGA-E2-A1L7	MSS	BRCA
TCGA-E2-A1L8	MSS	BRCA

TCGA-E2-A1L9	MSI-H	BRCA
TCGA-E2-A1LB	Intermediate	BRCA
TCGA-E2-A1LG	MSS	BRCA
TCGA-E2-A1LH	MSS	BRCA
TCGA-E2-A1LI	Intermediate	BRCA
TCGA-E2-A1LK	MSI-H	BRCA
TCGA-E2-A1LL	Intermediate	BRCA
TCGA-E2-A1LS	MSI-H	BRCA
TCGA-E2-A56Z	MSS	BRCA
TCGA-E2-A570	MSS	BRCA
TCGA-E2-A572	MSS	BRCA
TCGA-E2-A573	MSS	BRCA
TCGA-E2-A576	MSS	BRCA
TCGA-E2-A9RU	MSS	BRCA
TCGA-E3-A3DY	MSS	THCA
TCGA-E3-A3DZ	MSS	THCA
TCGA-E3-A3E0	MSS	THCA
TCGA-E3-A3E1	MSS	THCA
TCGA-E3-A3E5	MSS	THCA
TCGA-E5-A2PC	MSS	BLCA
TCGA-E5-A4TZ	MSS	BLCA
TCGA-E5-A4U1	MSS	BLCA
TCGA-E6-A1LX	Intermediate	UCEC
TCGA-E6-A1LZ	MSS	UCEC
TCGA-E6-A2P8	MSI-H	UCEC
TCGA-E6-A2P9	MSI-H	UCEC
TCGA-E6-A8L9	MSS	UCEC
TCGA-E7-A3X6	MSS	BLCA
TCGA-E7-A3Y1	MSS	BLCA
TCGA-E7-A4XJ	MSS	BLCA
TCGA-E7-A5KE	MSS	BLCA
TCGA-E7-A5KF	MSS	BLCA
TCGA-E7-A677	MSS	BLCA
TCGA-E7-A678	MSS	BLCA
TCGA-E7-A6MD	MSS	BLCA
TCGA-E7-A6ME	MSS	BLCA
TCGA-E7-A6MF	MSS	BLCA
TCGA-E7-A7DU	MSS	BLCA
TCGA-E7-A7DV	MSS	BLCA
TCGA-E7-A7PW	MSS	BLCA
TCGA-E7-A7XN	MSS	BLCA
TCGA-E7-A85H	MSS	BLCA
TCGA-E7-A8O7	MSS	BLCA
TCGA-E7-A8O8	MSS	BLCA
TCGA-E7-A97P	MSS	BLCA
TCGA-E7-A97Q	MSS	BLCA
TCGA-E8-A242	MSS	THCA
TCGA-E8-A2EA	MSS	THCA
TCGA-E8-A2JQ	MSS	THCA
TCGA-E8-A3X7	MSS	THCA
TCGA-E8-A413	MSS	THCA
TCGA-E8-A414	MSS	THCA

TCGA-E8-A415	MSS	THCA
TCGA-E8-A416	MSS	THCA
TCGA-E8-A417	MSS	THCA
TCGA-E8-A418	MSS	THCA
TCGA-E8-A419	MSS	THCA
TCGA-E8-A432	MSS	THCA
TCGA-E8-A433	MSS	THCA
TCGA-E8-A434	MSS	THCA
TCGA-E8-A44K	MSS	THCA
TCGA-E8-A44M	MSS	THCA
TCGA-E9-A1N3	MSS	BRCA
TCGA-E9-A1N4	MSS	BRCA
TCGA-E9-A1N5	Intermediate	BRCA
TCGA-E9-A1N8	MSI-H	BRCA
TCGA-E9-A1N9	MSS	BRCA
TCGA-E9-A1NA	MSI-H	BRCA
TCGA-E9-A1NC	MSS	BRCA
TCGA-E9-A1ND	MSS	BRCA
TCGA-E9-A1NE	MSS	BRCA
TCGA-E9-A1NF	MSI-H	BRCA
TCGA-E9-A1NG	MSS	BRCA
TCGA-E9-A1NH	MSS	BRCA
TCGA-E9-A1NI	MSI-H	BRCA
TCGA-E9-A1QZ	MSS	BRCA
TCGA-E9-A1R0	MSS	BRCA
TCGA-E9-A1R2	MSS	BRCA
TCGA-E9-A1R3	MSS	BRCA
TCGA-E9-A1R4	MSS	BRCA
TCGA-E9-A1R5	MSS	BRCA
TCGA-E9-A1R6	MSS	BRCA
TCGA-E9-A1R7	MSI-H	BRCA
TCGA-E9-A1RA	MSS	BRCA
TCGA-E9-A1RB	MSS	BRCA
TCGA-E9-A1RC	MSS	BRCA
TCGA-E9-A1RD	MSS	BRCA
TCGA-E9-A1RE	MSI-H	BRCA
TCGA-E9-A1RF	Intermediate	BRCA
TCGA-E9-A1RG	MSS	BRCA
TCGA-E9-A1RH	MSS	BRCA
TCGA-E9-A1RI	MSS	BRCA
TCGA-E9-A226	MSS	BRCA
TCGA-E9-A227	MSS	BRCA
TCGA-E9-A228	Intermediate	BRCA
TCGA-E9-A229	MSS	BRCA
TCGA-E9-A22A	MSS	BRCA
TCGA-E9-A22B	MSS	BRCA
TCGA-E9-A22D	MSS	BRCA
TCGA-E9-A22E	MSI-H	BRCA
TCGA-E9-A22G	MSS	BRCA
TCGA-E9-A22H	MSS	BRCA
TCGA-E9-A243	MSS	BRCA
TCGA-E9-A244	Intermediate	BRCA

TCGA-E9-A245	MSS	BRCA
TCGA-E9-A247	MSI-H	BRCA
TCGA-E9-A248	MSS	BRCA
TCGA-E9-A249	Intermediate	BRCA
TCGA-E9-A24A	MSS	BRCA
TCGA-E9-A295	MSS	BRCA
TCGA-E9-A2JS	MSS	BRCA
TCGA-E9-A2JT	MSS	BRCA
TCGA-E9-A3Q9	MSS	BRCA
TCGA-E9-A3X8	MSS	BRCA
TCGA-E9-A5FL	MSS	BRCA
TCGA-E9-A6HE	MSS	BRCA
TCGA-EA-A1QS	MSS	CESC
TCGA-EA-A1QT	MSS	CESC
TCGA-EA-A3Y4	MSS	CESC
TCGA-EA-A410	MSI-H	CESC
TCGA-EA-A44S	MSS	CESC
TCGA-EA-A556	MSS	CESC
TCGA-EA-A6QX	MSS	CESC
TCGA-EA-A78R	MSS	CESC
TCGA-EA-A97N	MSS	CESC
TCGA-EB-A1NK	MSS	SKCM
TCGA-EB-A24C	MSS	SKCM
TCGA-EB-A24D	MSS	SKCM
TCGA-EB-A299	MSS	SKCM
TCGA-EB-A3HV	MSS	SKCM
TCGA-EB-A3XB	MSS	SKCM
TCGA-EB-A3XC	MSS	SKCM
TCGA-EB-A3XD	MSS	SKCM
TCGA-EB-A3XE	MSS	SKCM
TCGA-EB-A3XF	MSS	SKCM
TCGA-EB-A3Y6	MSS	SKCM
TCGA-EB-A3Y7	MSS	SKCM
TCGA-EB-A41A	MSS	SKCM
TCGA-EB-A41B	MSS	SKCM
TCGA-EB-A42Y	MSS	SKCM
TCGA-EB-A42Z	MSS	SKCM
TCGA-EB-A430	MSS	SKCM
TCGA-EB-A431	MSS	SKCM
TCGA-EB-A44N	MSS	SKCM
TCGA-EB-A44O	MSS	SKCM
TCGA-EB-A44P	Intermediate	SKCM
TCGA-EB-A44Q	MSS	SKCM
TCGA-EB-A4IQ	MSS	SKCM
TCGA-EB-A4IS	MSS	SKCM
TCGA-EB-A4OY	MSS	SKCM
TCGA-EB-A4P0	MSS	SKCM
TCGA-EB-A4XL	MSS	SKCM
TCGA-EB-A51B	MSS	SKCM
TCGA-EB-A550	MSS	SKCM
TCGA-EB-A551	MSS	SKCM
TCGA-EB-A553	MSS	SKCM

TCGA-EB-A57M	MSS	SKCM
TCGA-EB-A5FP	MSS	SKCM
TCGA-EB-A5KH	MSS	SKCM
TCGA-EB-A5SE	MSS	SKCM
TCGA-EB-A5SF	MSS	SKCM
TCGA-EB-A5SG	MSS	SKCM
TCGA-EB-A5SH	MSS	SKCM
TCGA-EB-A5UL	MSS	SKCM
TCGA-EB-A5UM	MSS	SKCM
TCGA-EB-A5UN	MSS	SKCM
TCGA-EB-A5VU	MSS	SKCM
TCGA-EB-A5VV	MSS	SKCM
TCGA-EB-A6L9	MSS	SKCM
TCGA-EB-A6QY	MSS	SKCM
TCGA-EB-A6QZ	MSS	SKCM
TCGA-EB-A6R0	MSS	SKCM
TCGA-EB-A82B	MSS	SKCM
TCGA-EB-A82C	MSS	SKCM
TCGA-EB-A85I	MSS	SKCM
TCGA-EB-A85J	MSS	SKCM
TCGA-EB-A97M	MSS	SKCM
TCGA-EC-A1QX	MSI-H	UCEC
TCGA-EC-A24G	MSI-H	UCEC
TCGA-ED-A627	MSS	LIHC
TCGA-ED-A66X	MSS	LIHC
TCGA-ED-A66Y	MSS	LIHC
TCGA-ED-A7PX	MSS	LIHC
TCGA-ED-A7PY	MSS	LIHC
TCGA-ED-A7PZ	MSS	LIHC
TCGA-ED-A7XO	MSS	LIHC
TCGA-ED-A7XP	MSS	LIHC
TCGA-ED-A82E	MSS	LIHC
TCGA-ED-A8O5	MSS	LIHC
TCGA-ED-A8O6	MSS	LIHC
TCGA-ED-A97K	MSS	LIHC
TCGA-EE-A17X	MSS	SKCM
TCGA-EE-A17Y	MSS	SKCM
TCGA-EE-A17Z	MSS	SKCM
TCGA-EE-A180	MSS	SKCM
TCGA-EE-A181	MSS	SKCM
TCGA-EE-A182	MSS	SKCM
TCGA-EE-A183	MSS	SKCM
TCGA-EE-A184	MSS	SKCM
TCGA-EE-A185	MSS	SKCM
TCGA-EE-A20B	MSS	SKCM
TCGA-EE-A20C	MSS	SKCM
TCGA-EE-A20F	MSS	SKCM
TCGA-EE-A20H	MSS	SKCM
TCGA-EE-A20I	MSS	SKCM
TCGA-EE-A29A	MSS	SKCM
TCGA-EE-A29B	MSS	SKCM
TCGA-EE-A29C	MSS	SKCM

TCGA-EE-A29D	MSS	SKCM
TCGA-EE-A29E	MSS	SKCM
TCGA-EE-A29G	MSS	SKCM
TCGA-EE-A29H	MSS	SKCM
TCGA-EE-A29L	MSS	SKCM
TCGA-EE-A29M	MSS	SKCM
TCGA-EE-A29N	MSS	SKCM
TCGA-EE-A29P	MSS	SKCM
TCGA-EE-A29Q	MSS	SKCM
TCGA-EE-A29R	MSS	SKCM
TCGA-EE-A29S	MSS	SKCM
TCGA-EE-A29T	MSS	SKCM
TCGA-EE-A29V	MSS	SKCM
TCGA-EE-A29W	MSS	SKCM
TCGA-EE-A29X	MSS	SKCM
TCGA-EE-A2A0	MSS	SKCM
TCGA-EE-A2A1	MSS	SKCM
TCGA-EE-A2A2	MSS	SKCM
TCGA-EE-A2A5	MSS	SKCM
TCGA-EE-A2A6	MSS	SKCM
TCGA-EE-A2GB	MSS	SKCM
TCGA-EE-A2GC	MSS	SKCM
TCGA-EE-A2GD	MSS	SKCM
TCGA-EE-A2GE	MSS	SKCM
TCGA-EE-A2GH	MSS	SKCM
TCGA-EE-A2GI	MSS	SKCM
TCGA-EE-A2GJ	MSS	SKCM
TCGA-EE-A2GK	MSS	SKCM
TCGA-EE-A2GL	MSS	SKCM
TCGA-EE-A2GM	MSS	SKCM
TCGA-EE-A2GN	MSS	SKCM
TCGA-EE-A2GO	MSS	SKCM
TCGA-EE-A2GP	MSS	SKCM
TCGA-EE-A2GR	MSS	SKCM
TCGA-EE-A2GS	MSS	SKCM
TCGA-EE-A2GT	MSS	SKCM
TCGA-EE-A2GU	MSS	SKCM
TCGA-EE-A2M5	MSS	SKCM
TCGA-EE-A2M6	MSS	SKCM
TCGA-EE-A2M7	MSS	SKCM
TCGA-EE-A2M8	MSS	SKCM
TCGA-EE-A2MC	MSS	SKCM
TCGA-EE-A2MD	MSS	SKCM
TCGA-EE-A2ME	MSS	SKCM
TCGA-EE-A2MG	MSS	SKCM
TCGA-EE-A2MH	MSS	SKCM
TCGA-EE-A2MJ	MSS	SKCM
TCGA-EE-A2MK	MSS	SKCM
TCGA-EE-A2ML	MSS	SKCM
TCGA-EE-A2MM	MSS	SKCM
TCGA-EE-A2MN	MSS	SKCM
TCGA-EE-A2MP	MSS	SKCM

TCGA-EE-A2MQ	MSS	SKCM
TCGA-EE-A2MS	MSS	SKCM
TCGA-EE-A2MT	MSS	SKCM
TCGA-EE-A2MU	MSS	SKCM
TCGA-EE-A3AA	MSS	SKCM
TCGA-EE-A3AB	MSS	SKCM
TCGA-EE-A3AC	MSS	SKCM
TCGA-EE-A3AD	MSS	SKCM
TCGA-EE-A3AE	MSS	SKCM
TCGA-EE-A3AF	MSS	SKCM
TCGA-EE-A3AH	MSS	SKCM
TCGA-EE-A3J3	MSS	SKCM
TCGA-EE-A3J4	MSS	SKCM
TCGA-EE-A3J5	MSS	SKCM
TCGA-EE-A3J8	MSS	SKCM
TCGA-EE-A3JB	MSS	SKCM
TCGA-EE-A3JD	MSS	SKCM
TCGA-EE-A3JE	MSS	SKCM
TCGA-EE-A3JI	MSS	SKCM
TCGA-EF-5830	MSS	READ
TCGA-EI-6506	MSS	READ
TCGA-EI-6507	MSI-H	READ
TCGA-EI-6508	MSS	READ
TCGA-EI-6509	MSS	READ
TCGA-EI-6510	MSS	READ
TCGA-EI-6511	MSS	READ
TCGA-EI-6512	MSS	READ
TCGA-EI-6513	MSS	READ
TCGA-EI-6514	MSS	READ
TCGA-EI-6881	MSS	READ
TCGA-EI-6882	MSI-H	READ
TCGA-EI-6883	MSS	READ
TCGA-EI-6884	MSS	READ
TCGA-EI-6885	MSS	READ
TCGA-EI-6917	MSS	READ
TCGA-EI-7002	MSS	READ
TCGA-EI-7004	MSS	READ
TCGA-EJ-5494	MSS	PRAD
TCGA-EJ-5495	MSS	PRAD
TCGA-EJ-5496	MSS	PRAD
TCGA-EJ-5497	MSS	PRAD
TCGA-EJ-5498	MSS	PRAD
TCGA-EJ-5499	MSS	PRAD
TCGA-EJ-5501	MSS	PRAD
TCGA-EJ-5502	MSS	PRAD
TCGA-EJ-5503	MSS	PRAD
TCGA-EJ-5504	MSS	PRAD
TCGA-EJ-5505	MSS	PRAD
TCGA-EJ-5506	MSS	PRAD
TCGA-EJ-5507	MSS	PRAD
TCGA-EJ-5508	MSS	PRAD
TCGA-EJ-5509	MSS	PRAD

TCGA-EJ-5510	MSS	PRAD
TCGA-EJ-5511	MSS	PRAD
TCGA-EJ-5512	MSS	PRAD
TCGA-EJ-5514	MSS	PRAD
TCGA-EJ-5515	MSS	PRAD
TCGA-EJ-5516	MSS	PRAD
TCGA-EJ-5517	MSS	PRAD
TCGA-EJ-5518	MSS	PRAD
TCGA-EJ-5519	MSS	PRAD
TCGA-EJ-5521	MSS	PRAD
TCGA-EJ-5522	MSS	PRAD
TCGA-EJ-5524	MSS	PRAD
TCGA-EJ-5525	MSS	PRAD
TCGA-EJ-5526	MSS	PRAD
TCGA-EJ-5527	MSS	PRAD
TCGA-EJ-5530	MSS	PRAD
TCGA-EJ-5531	MSS	PRAD
TCGA-EJ-5532	MSS	PRAD
TCGA-EJ-5542	MSS	PRAD
TCGA-EJ-7115	MSS	PRAD
TCGA-EJ-7123	MSS	PRAD
TCGA-EJ-7125	MSS	PRAD
TCGA-EJ-7218	MSS	PRAD
TCGA-EJ-7312	MSS	PRAD
TCGA-EJ-7314	MSS	PRAD
TCGA-EJ-7315	MSS	PRAD
TCGA-EJ-7318	MSS	PRAD
TCGA-EJ-7325	MSS	PRAD
TCGA-EJ-7327	MSS	PRAD
TCGA-EJ-7328	MSS	PRAD
TCGA-EJ-7330	MSS	PRAD
TCGA-EJ-7331	MSS	PRAD
TCGA-EJ-7781	MSS	PRAD
TCGA-EJ-7782	MSI-H	PRAD
TCGA-EJ-7783	MSS	PRAD
TCGA-EJ-7784	MSS	PRAD
TCGA-EJ-7785	MSS	PRAD
TCGA-EJ-7786	MSS	PRAD
TCGA-EJ-7789	MSS	PRAD
TCGA-EJ-7791	MSS	PRAD
TCGA-EJ-7792	MSS	PRAD
TCGA-EJ-8468	MSS	PRAD
TCGA-EJ-8469	MSS	PRAD
TCGA-EJ-8470	MSS	PRAD
TCGA-EJ-8472	MSS	PRAD
TCGA-EJ-8474	MSS	PRAD
TCGA-EJ-A46B	MSS	PRAD
TCGA-EJ-A46D	MSS	PRAD
TCGA-EJ-A46E	MSS	PRAD
TCGA-EJ-A46F	MSS	PRAD
TCGA-EJ-A65B	MSS	PRAD
TCGA-EJ-A65D	MSS	PRAD

TCGA-EJ-A65E	MSS	PRAD
TCGA-EJ-A65F	MSS	PRAD
TCGA-EJ-A65G	MSS	PRAD
TCGA-EJ-A65J	MSS	PRAD
TCGA-EJ-A65M	MSS	PRAD
TCGA-EJ-A6RA	MSS	PRAD
TCGA-EJ-A6RC	MSS	PRAD
TCGA-EJ-A7NF	MSS	PRAD
TCGA-EJ-A7NG	MSS	PRAD
TCGA-EJ-A7NH	MSS	PRAD
TCGA-EJ-A7NJ	MSS	PRAD
TCGA-EJ-A7NK	MSS	PRAD
TCGA-EJ-A7NM	MSS	PRAD
TCGA-EJ-A7NN	MSS	PRAD
TCGA-EJ-A8FN	MSS	PRAD
TCGA-EJ-A8FO	MSS	PRAD
TCGA-EJ-A8FP	MSS	PRAD
TCGA-EJ-A8FS	MSS	PRAD
TCGA-EJ-A8FU	MSS	PRAD
TCGA-EJ-AB20	MSS	PRAD
TCGA-EJ-AB27	MSS	PRAD
TCGA-EK-A2H1	MSS	CESC
TCGA-EK-A2RC	MSS	CESC
TCGA-EK-A2RM	MSS	CESC
TCGA-EL-A3CL	MSS	THCA
TCGA-EL-A3CM	MSS	THCA
TCGA-EL-A3CN	MSS	THCA
TCGA-EL-A3CO	MSS	THCA
TCGA-EL-A3CP	MSS	THCA
TCGA-EL-A3CR	MSS	THCA
TCGA-EL-A3CS	MSS	THCA
TCGA-EL-A3CT	MSS	THCA
TCGA-EL-A3CU	MSS	THCA
TCGA-EL-A3CV	MSS	THCA
TCGA-EL-A3CW	MSS	THCA
TCGA-EL-A3CX	MSS	THCA
TCGA-EL-A3CY	MSS	THCA
TCGA-EL-A3CZ	MSS	THCA
TCGA-EL-A3D0	MSS	THCA
TCGA-EL-A3D1	MSS	THCA
TCGA-EL-A3D4	MSS	THCA
TCGA-EL-A3D5	MSS	THCA
TCGA-EL-A3D6	MSS	THCA
TCGA-EL-A3GO	MSS	THCA
TCGA-EL-A3GP	MSS	THCA
TCGA-EL-A3GQ	MSS	THCA
TCGA-EL-A3GR	MSS	THCA
TCGA-EL-A3GS	MSS	THCA
TCGA-EL-A3GW	MSS	THCA
TCGA-EL-A3GX	MSS	THCA
TCGA-EL-A3GY	MSS	THCA
TCGA-EL-A3GZ	MSS	THCA

TCGA-EL-A3H2	MSS	THCA
TCGA-EL-A3H3	MSS	THCA
TCGA-EL-A3H4	MSS	THCA
TCGA-EL-A3H5	MSS	THCA
TCGA-EL-A3H7	MSS	THCA
TCGA-EL-A3H8	MSS	THCA
TCGA-EL-A3MW	MSS	THCA
TCGA-EL-A3N3	MSS	THCA
TCGA-EL-A3T0	MSS	THCA
TCGA-EL-A3T1	MSS	THCA
TCGA-EL-A3T3	MSS	THCA
TCGA-EL-A3T6	MSS	THCA
TCGA-EL-A3T7	MSS	THCA
TCGA-EL-A3T8	MSS	THCA
TCGA-EL-A3T9	MSS	THCA
TCGA-EL-A3TB	MSS	THCA
TCGA-EL-A3ZG	MSS	THCA
TCGA-EL-A3ZH	MSS	THCA
TCGA-EL-A3ZK	MSS	THCA
TCGA-EL-A3ZL	MSS	THCA
TCGA-EL-A3ZM	MSS	THCA
TCGA-EL-A3ZN	MSS	THCA
TCGA-EL-A3ZO	MSS	THCA
TCGA-EL-A3ZP	MSS	THCA
TCGA-EL-A3ZQ	MSS	THCA
TCGA-EL-A3ZR	MSS	THCA
TCGA-EL-A3ZS	MSS	THCA
TCGA-EL-A3ZT	MSS	THCA
TCGA-EL-A4JV	MSS	THCA
TCGA-EL-A4JW	MSS	THCA
TCGA-EL-A4JX	MSS	THCA
TCGA-EL-A4JZ	MSS	THCA
TCGA-EL-A4K0	MSS	THCA
TCGA-EL-A4K1	MSS	THCA
TCGA-EL-A4K2	MSS	THCA
TCGA-EL-A4K4	MSS	THCA
TCGA-EL-A4K6	MSS	THCA
TCGA-EL-A4K7	MSS	THCA
TCGA-EL-A4K9	MSS	THCA
TCGA-EL-A4KD	MSS	THCA
TCGA-EL-A4KG	MSS	THCA
TCGA-EL-A4KH	MSS	THCA
TCGA-EL-A4KI	MSS	THCA
TCGA-EM-A1CS	MSS	THCA
TCGA-EM-A1CT	MSS	THCA
TCGA-EM-A1CU	MSS	THCA
TCGA-EM-A1CV	MSS	THCA
TCGA-EM-A1CW	MSS	THCA
TCGA-EM-A1YA	MSS	THCA
TCGA-EM-A1YB	MSS	THCA
TCGA-EM-A1YC	MSS	THCA
TCGA-EM-A1YD	MSS	THCA

TCGA-EM-A1YE	MSS	THCA
TCGA-EM-A22I	MSS	THCA
TCGA-EM-A22J	MSS	THCA
TCGA-EM-A22K	MSS	THCA
TCGA-EM-A22L	MSS	THCA
TCGA-EM-A22M	MSS	THCA
TCGA-EM-A22N	MSS	THCA
TCGA-EM-A22O	MSS	THCA
TCGA-EM-A22P	MSS	THCA
TCGA-EM-A22Q	MSS	THCA
TCGA-EM-A2CJ	MSS	THCA
TCGA-EM-A2CK	MSS	THCA
TCGA-EM-A2CL	MSS	THCA
TCGA-EM-A2CM	MSS	THCA
TCGA-EM-A2CN	MSS	THCA
TCGA-EM-A2CO	MSS	THCA
TCGA-EM-A2CP	MSS	THCA
TCGA-EM-A2CQ	MSS	THCA
TCGA-EM-A2CR	MSS	THCA
TCGA-EM-A2CS	MSS	THCA
TCGA-EM-A2CS	MSS	THCA
TCGA-EM-A2CT	MSS	THCA
TCGA-EM-A2CU	MSS	THCA
TCGA-EM-A2OV	MSS	THCA
TCGA-EM-A2OW	MSS	THCA
TCGA-EM-A2OX	MSS	THCA
TCGA-EM-A2OY	MSS	THCA
TCGA-EM-A2OZ	MSS	THCA
TCGA-EM-A2P0	MSS	THCA
TCGA-EM-A2P1	MSS	THCA
TCGA-EM-A2P1	MSS	THCA
TCGA-EM-A2P2	MSS	THCA
TCGA-EM-A2P3	MSS	THCA
TCGA-EM-A3AI	MSS	THCA
TCGA-EM-A3AJ	MSS	THCA
TCGA-EM-A3AK	MSS	THCA
TCGA-EM-A3AL	MSS	THCA
TCGA-EM-A3AN	MSS	THCA
TCGA-EM-A3AO	MSS	THCA
TCGA-EM-A3AQ	MSS	THCA
TCGA-EM-A3AR	MSS	THCA
TCGA-EM-A3FR	MSS	THCA
TCGA-EM-A3O3	MSS	THCA
TCGA-EM-A3O6	MSS	THCA
TCGA-EM-A3O7	MSS	THCA
TCGA-EM-A3O8	MSS	THCA
TCGA-EM-A3O9	MSS	THCA
TCGA-EM-A3OA	MSS	THCA
TCGA-EM-A3OB	MSS	THCA
TCGA-EM-A3ST	MSS	THCA
TCGA-EM-A3SU	MSS	THCA
TCGA-EM-A3SU	MSS	THCA

TCGA-EM-A3SX	MSS	THCA
TCGA-EM-A3SY	MSS	THCA
TCGA-EM-A3SZ	MSS	THCA
TCGA-EM-A4FF	MSS	THCA
TCGA-EM-A4FH	MSS	THCA
TCGA-EM-A4FK	MSS	THCA
TCGA-EM-A4FM	MSS	THCA
TCGA-EM-A4FN	MSS	THCA
TCGA-EM-A4FO	MSS	THCA
TCGA-EM-A4FQ	MSS	THCA
TCGA-EM-A4FR	MSS	THCA
TCGA-EM-A4FU	MSS	THCA
TCGA-EM-A4FV	MSS	THCA
TCGA-EM-A4G1	MSS	THCA
TCGA-EO-A1Y5	MSS	UCEC
TCGA-EO-A1Y7	MSS	UCEC
TCGA-EO-A1Y8	MSS	UCEC
TCGA-EO-A22R	MSI-H	UCEC
TCGA-EO-A22S	MSI-H	UCEC
TCGA-EO-A22T	MSI-H	UCEC
TCGA-EO-A2CG	MSS	UCEC
TCGA-EO-A3AU	MSI-H	UCEC
TCGA-EO-A3AV	MSS	UCEC
TCGA-EO-A3AY	MSS	UCEC
TCGA-EO-A3AZ	MSI-H	UCEC
TCGA-EO-A3B1	MSS	UCEC
TCGA-EO-A3KU	MSS	UCEC
TCGA-EO-A3KX	MSI-H	UCEC
TCGA-EP-A12J	MSS	LIHC
TCGA-EP-A26S	MSS	LIHC
TCGA-EP-A2KA	MSS	LIHC
TCGA-EP-A2KB	MSS	LIHC
TCGA-EP-A3RK	MSS	LIHC
TCGA-EQ-5647	MSS	STAD
TCGA-EQ-8122	MSS	STAD
TCGA-EQ-A4SO	MSS	STAD
TCGA-ER-A193	MSS	SKCM
TCGA-ER-A194	MSS	SKCM
TCGA-ER-A195	MSS	SKCM
TCGA-ER-A196	MSS	SKCM
TCGA-ER-A197	MSS	SKCM
TCGA-ER-A198	MSS	SKCM
TCGA-ER-A199	MSS	SKCM
TCGA-ER-A19A	MSS	SKCM
TCGA-ER-A19B	MSS	SKCM
TCGA-ER-A19C	MSS	SKCM
TCGA-ER-A19D	MSS	SKCM
TCGA-ER-A19E	MSS	SKCM
TCGA-ER-A19F	MSS	SKCM
TCGA-ER-A19G	MSS	SKCM
TCGA-ER-A19H	MSS	SKCM
TCGA-ER-A19K	MSS	SKCM

TCGA-ER-A19L	MSS	SKCM
TCGA-ER-A19M	MSS	SKCM
TCGA-ER-A19N	MSS	SKCM
TCGA-ER-A19O	MSS	SKCM
TCGA-ER-A19P	MSS	SKCM
TCGA-ER-A19Q	MSS	SKCM
TCGA-ER-A19S	MSS	SKCM
TCGA-ER-A19T	MSS	SKCM
TCGA-ER-A19T	MSS	SKCM
TCGA-ER-A19W	MSS	SKCM
TCGA-ER-A1A1	MSS	SKCM
TCGA-ER-A2NB	MSS	SKCM
TCGA-ER-A2NC	MSS	SKCM
TCGA-ER-A2ND	MSS	SKCM
TCGA-ER-A2NE	MSS	SKCM
TCGA-ER-A2NF	MSS	SKCM
TCGA-ER-A2NF	MSS	SKCM
TCGA-ER-A2NG	MSS	SKCM
TCGA-ER-A2NH	MSS	SKCM
TCGA-ER-A3ES	MSS	SKCM
TCGA-ER-A3ET	MSS	SKCM
TCGA-ER-A3EV	MSS	SKCM
TCGA-ER-A3PL	MSS	SKCM
TCGA-ER-A42H	MSS	SKCM
TCGA-ER-A42K	MSS	SKCM
TCGA-ER-A42L	MSS	SKCM
TCGA-ES-A2HS	MSS	LIHC
TCGA-ES-A2HT	MSS	LIHC
TCGA-ET-A25G	MSS	THCA
TCGA-ET-A25I	MSS	THCA
TCGA-ET-A25J	MSS	THCA
TCGA-ET-A25K	MSS	THCA
TCGA-ET-A25O	MSS	THCA
TCGA-ET-A25R	MSS	THCA
TCGA-ET-A2MX	MSS	THCA
TCGA-ET-A2MY	MSS	THCA
TCGA-ET-A2MZ	MSS	THCA
TCGA-ET-A2N0	MSS	THCA
TCGA-ET-A2N1	MSS	THCA
TCGA-ET-A2N3	MSS	THCA
TCGA-ET-A2N4	MSS	THCA
TCGA-ET-A2N5	MSS	THCA
TCGA-ET-A39I	MSS	THCA
TCGA-ET-A39J	MSS	THCA
TCGA-ET-A39K	MSS	THCA
TCGA-ET-A39L	MSS	THCA
TCGA-ET-A39M	MSS	THCA
TCGA-ET-A39N	MSS	THCA
TCGA-ET-A39O	MSS	THCA
TCGA-ET-A39P	MSS	THCA
TCGA-ET-A39R	MSS	THCA
TCGA-ET-A39S	MSS	THCA

TCGA-ET-A39T	MSS	THCA
TCGA-ET-A3BN	MSS	THCA
TCGA-ET-A3BO	MSS	THCA
TCGA-ET-A3BP	MSS	THCA
TCGA-ET-A3BQ	MSS	THCA
TCGA-ET-A3BS	MSS	THCA
TCGA-ET-A3BT	MSS	THCA
TCGA-ET-A3BU	MSS	THCA
TCGA-ET-A3BV	MSS	THCA
TCGA-ET-A3BW	MSS	THCA
TCGA-ET-A3BX	MSS	THCA
TCGA-ET-A3DO	MSS	THCA
TCGA-ET-A3DQ	MSS	THCA
TCGA-ET-A3DR	MSS	THCA
TCGA-ET-A3DS	MSS	THCA
TCGA-ET-A3DT	MSS	THCA
TCGA-ET-A3DU	MSS	THCA
TCGA-ET-A3DV	MSS	THCA
TCGA-ET-A3DW	MSS	THCA
TCGA-ET-A40P	MSS	THCA
TCGA-ET-A40Q	MSS	THCA
TCGA-ET-A40R	MSS	THCA
TCGA-ET-A40S	MSS	THCA
TCGA-ET-A40T	MSS	THCA
TCGA-ET-A4KN	MSS	THCA
TCGA-ET-A4KQ	MSS	THCA
TCGA-EU-5904	MSS	KIRC
TCGA-EU-5905	MSS	KIRC
TCGA-EU-5906	MSS	KIRC
TCGA-EU-5907	MSS	KIRC
TCGA-EV-5901	MSS	KIRP
TCGA-EV-5902	MSS	KIRP
TCGA-EV-5903	MSS	KIRP
TCGA-EW-A1IW	MSS	BRCA
TCGA-EW-A1IX	MSS	BRCA
TCGA-EW-A1IY	MSS	BRCA
TCGA-EW-A1IZ	MSI-H	BRCA
TCGA-EW-A1J1	MSS	BRCA
TCGA-EW-A1J2	MSS	BRCA
TCGA-EW-A1J3	MSS	BRCA
TCGA-EW-A1J5	MSS	BRCA
TCGA-EW-A1J6	MSS	BRCA
TCGA-EW-A1OV	MSI-H	BRCA
TCGA-EW-A1OX	MSI-H	BRCA
TCGA-EW-A1OY	MSS	BRCA
TCGA-EW-A1OZ	MSI-H	BRCA
TCGA-EW-A1P0	MSS	BRCA
TCGA-EW-A1P1	MSI-H	BRCA
TCGA-EW-A1P3	MSS	BRCA
TCGA-EW-A1P4	Intermediate	BRCA
TCGA-EW-A1P5	MSS	BRCA
TCGA-EW-A1P6	MSS	BRCA

TCGA-EW-A1P7	Intermediate	BRCA
TCGA-EW-A1P8	MSS	BRCA
TCGA-EW-A1PA	Intermediate	BRCA
TCGA-EW-A1PB	MSI-H	BRCA
TCGA-EW-A1PD	MSI-H	BRCA
TCGA-EW-A1PE	Intermediate	BRCA
TCGA-EW-A1PG	MSS	BRCA
TCGA-EW-A2FS	Intermediate	BRCA
TCGA-EW-A2FV	MSI-H	BRCA
TCGA-EW-A2FW	MSS	BRCA
TCGA-EW-A6SA	MSS	BRCA
TCGA-EW-A6SB	MSS	BRCA
TCGA-EW-A6SC	MSS	BRCA
TCGA-EW-A6SD	MSS	BRCA
TCGA-EX-A1H5	MSS	CESC
TCGA-EX-A69L	MSS	CESC
TCGA-EX-A69M	MSS	CESC
TCGA-EX-A8YF	MSS	CESC
TCGA-EY-A1GC	MSS	UCEC
TCGA-EY-A1GF	MSI-H	UCEC
TCGA-EY-A1GJ	MSS	UCEC
TCGA-EY-A1GK	MSI-H	UCEC
TCGA-EY-A1GO	MSI-H	UCEC
TCGA-EY-A1GQ	MSI-H	UCEC
TCGA-EY-A1GS	MSS	UCEC
TCGA-EY-A1GU	MSI-H	UCEC
TCGA-EY-A1H0	MSI-H	UCEC
TCGA-EY-A212	MSS	UCEC
TCGA-EY-A215	MSI-H	UCEC
TCGA-EY-A2OM	MSI-H	UCEC
TCGA-EY-A2OO	MSS	UCEC
TCGA-EY-A2OP	MSI-H	UCEC
TCGA-EY-A2OQ	MSS	UCEC
TCGA-EY-A4KR	MSS	UCEC
TCGA-EY-A547	MSI-H	UCEC
TCGA-EY-A548	MSI-H	UCEC
TCGA-EY-A549	MSI-H	UCEC
TCGA-EY-A5W2	MSI-H	UCEC
TCGA-EY-A72D	MSS	UCEC
TCGA-EZ-7264	MSS	LGG
TCGA-F1-6177	MSI-H	STAD
TCGA-F1-6874	MSI-H	STAD
TCGA-F1-A448	MSI-H	STAD
TCGA-F1-A72C	MSS	STAD
TCGA-F2-6880	MSS	PAAD
TCGA-F2-7273	MSS	PAAD
TCGA-F2-7276	MSS	PAAD
TCGA-F2-A44G	MSS	PAAD
TCGA-F2-A7TX	MSS	PAAD
TCGA-F2-A8YN	MSS	PAAD
TCGA-F4-6459	MSS	COAD
TCGA-F4-6460	MSS	COAD

TCGA-F4-6461	MSS	COAD
TCGA-F4-6463	MSS	COAD
TCGA-F4-6569	MSS	COAD
TCGA-F4-6570	MSI-H	COAD
TCGA-F4-6703	MSS	COAD
TCGA-F4-6704	MSS	COAD
TCGA-F4-6806	MSS	COAD
TCGA-F4-6807	MSS	COAD
TCGA-F4-6808	MSS	COAD
TCGA-F4-6809	MSS	COAD
TCGA-F4-6854	MSS	COAD
TCGA-F4-6855	MSS	COAD
TCGA-F4-6856	MSI-H	COAD
TCGA-F5-6464	MSS	READ
TCGA-F5-6465	MSS	READ
TCGA-F5-6571	MSS	READ
TCGA-F5-6702	MSS	READ
TCGA-F5-6810	MSS	READ
TCGA-F5-6811	MSS	READ
TCGA-F5-6812	MSS	READ
TCGA-F5-6813	MSS	READ
TCGA-F5-6814	MSS	READ
TCGA-F5-6861	MSS	READ
TCGA-F5-6863	MSS	READ
TCGA-F5-6864	MSS	READ
TCGA-F6-A8O3	MSS	LGG
TCGA-F6-A8O4	MSS	LGG
TCGA-F7-7848	MSS	HNSC
TCGA-F7-8298	MSS	HNSC
TCGA-F7-8489	MSS	HNSC
TCGA-F7-A50G	MSS	HNSC
TCGA-F7-A50I	MSS	HNSC
TCGA-F7-A50J	MSS	HNSC
TCGA-F7-A61S	MSS	HNSC
TCGA-F7-A61V	MSS	HNSC
TCGA-F7-A61W	MSS	HNSC
TCGA-F7-A620	MSS	HNSC
TCGA-F7-A622	MSS	HNSC
TCGA-F7-A623	MSS	HNSC
TCGA-F7-A624	MSI-H	HNSC
TCGA-F9-A7Q0	MSS	KIRP
TCGA-F9-A7VF	MSS	KIRP
TCGA-F9-A8NY	MSS	KIRP
TCGA-F9-A97G	MSS	KIRP
TCGA-FA-A4BB	MSS	DLBC
TCGA-FA-A4XK	MSS	DLBC
TCGA-FA-A6HN	MSS	DLBC
TCGA-FA-A6HO	MSS	DLBC
TCGA-FA-A7DS	MSS	DLBC
TCGA-FA-A7Q1	MSS	DLBC
TCGA-FA-A82F	MSS	DLBC
TCGA-FA-A86F	MSS	DLBC

TCGA-FB-A4P6	MSS	PAAD
TCGA-FB-A5VM	MSS	PAAD
TCGA-FB-A78T	MSS	PAAD
TCGA-FB-A7DR	MSS	PAAD
TCGA-FB-AAPP	MSS	PAAD
TCGA-FB-AAPQ	MSS	PAAD
TCGA-FB-AAPS	MSS	PAAD
TCGA-FB-AAPU	MSS	PAAD
TCGA-FB-AAPY	MSS	PAAD
TCGA-FB-AAPZ	MSS	PAAD
TCGA-FB-AAQ0	MSS	PAAD
TCGA-FB-AAQ1	MSS	PAAD
TCGA-FB-AAQ2	MSS	PAAD
TCGA-FB-AAQ3	MSS	PAAD
TCGA-FB-AAQ6	MSS	PAAD
TCGA-FC-7708	MSS	PRAD
TCGA-FC-7961	MSS	PRAD
TCGA-FC-A4JI	MSS	PRAD
TCGA-FC-A5OB	MSS	PRAD
TCGA-FC-A66V	MSS	PRAD
TCGA-FC-A6HD	MSS	PRAD
TCGA-FC-A8O0	MSS	PRAD
TCGA-FD-A3B3	MSS	BLCA
TCGA-FD-A3B4	MSS	BLCA
TCGA-FD-A3B6	MSS	BLCA
TCGA-FD-A3B8	MSS	BLCA
TCGA-FD-A3SJ	MSS	BLCA
TCGA-FD-A3SL	MSS	BLCA
TCGA-FD-A3SM	MSS	BLCA
TCGA-FD-A3SN	MSS	BLCA
TCGA-FD-A3SO	MSS	BLCA
TCGA-FD-A3SP	MSS	BLCA
TCGA-FD-A3SQ	MSS	BLCA
TCGA-FD-A3SR	MSS	BLCA
TCGA-FD-A3SS	MSS	BLCA
TCGA-FD-A43N	MSS	BLCA
TCGA-FD-A43P	MSS	BLCA
TCGA-FD-A43S	MSS	BLCA
TCGA-FD-A43U	MSS	BLCA
TCGA-FD-A43X	MSS	BLCA
TCGA-FD-A5BY	MSS	BLCA
TCGA-FD-A5BZ	MSS	BLCA
TCGA-FD-A5C0	MSS	BLCA
TCGA-FD-A5C1	MSS	BLCA
TCGA-FD-A62N	MSS	BLCA
TCGA-FD-A62O	MSS	BLCA
TCGA-FD-A62P	MSS	BLCA
TCGA-FD-A62S	MSS	BLCA
TCGA-FD-A6TA	MSS	BLCA
TCGA-FD-A6TB	MSS	BLCA
TCGA-FD-A6TC	MSS	BLCA
TCGA-FD-A6TD	MSS	BLCA

TCGA-FD-A6TE	MSS	BLCA
TCGA-FD-A6TF	MSS	BLCA
TCGA-FD-A6TG	MSS	BLCA
TCGA-FD-A6TH	MSS	BLCA
TCGA-FD-A6TI	MSS	BLCA
TCGA-FD-A6TK	MSS	BLCA
TCGA-FE-A22Z	MSS	THCA
TCGA-FE-A230	MSS	THCA
TCGA-FE-A231	MSS	THCA
TCGA-FE-A232	MSS	THCA
TCGA-FE-A233	MSS	THCA
TCGA-FE-A234	MSS	THCA
TCGA-FE-A235	MSS	THCA
TCGA-FE-A236	MSS	THCA
TCGA-FE-A237	MSS	THCA
TCGA-FE-A23A	MSS	THCA
TCGA-FE-A3PA	MSS	THCA
TCGA-FE-A3PB	MSS	THCA
TCGA-FE-A3PC	MSS	THCA
TCGA-FE-A3PD	MSS	THCA
TCGA-FF-8041	MSS	DLBC
TCGA-FF-8042	MSS	DLBC
TCGA-FF-8043	MSS	DLBC
TCGA-FF-8046	MSS	DLBC
TCGA-FF-8047	MSS	DLBC
TCGA-FF-8061	MSS	DLBC
TCGA-FF-8062	MSI-H	DLBC
TCGA-FF-A7CQ	MSS	DLBC
TCGA-FF-A7CR	MSS	DLBC
TCGA-FF-A7CW	MSS	DLBC
TCGA-FF-A7CX	MSS	DLBC
TCGA-FG-5962	MSS	LGG
TCGA-FG-5963	MSS	LGG
TCGA-FG-5963	MSS	LGG
TCGA-FG-5964	MSS	LGG
TCGA-FG-5965	MSS	LGG
TCGA-FG-5965	MSS	LGG
TCGA-FG-5965	MSS	LGG
TCGA-FG-6688	MSS	LGG
TCGA-FG-6689	MSS	LGG
TCGA-FG-6690	MSS	LGG
TCGA-FG-6691	MSS	LGG
TCGA-FG-6692	MSS	LGG
TCGA-FG-7636	MSS	LGG
TCGA-FG-7637	MSS	LGG
TCGA-FG-7638	MSS	LGG
TCGA-FG-7641	MSS	LGG
TCGA-FG-7643	MSS	LGG
TCGA-FG-8186	MSS	LGG
TCGA-FG-8187	MSS	LGG
TCGA-FG-8188	MSS	LGG
TCGA-FG-8189	MSS	LGG

TCGA-FG-A4MU	MSS	LGG
TCGA-FG-A60J	MSS	LGG
TCGA-FG-A60K	MSS	LGG
TCGA-FG-A60L	MSS	LGG
TCGA-FG-A6IZ	MSS	LGG
TCGA-FG-A6J1	MSS	LGG
TCGA-FG-A6J3	MSS	LGG
TCGA-FG-A70Y	MSS	LGG
TCGA-FG-A70Z	MSS	LGG
TCGA-FG-A710	MSS	LGG
TCGA-FG-A711	MSS	LGG
TCGA-FG-A713	MSS	LGG
TCGA-FG-A87N	MSS	LGG
TCGA-FG-A87Q	MSS	LGG
TCGA-FI-A2CY	MSS	UCEC
TCGA-FI-A2D0	MSI-H	UCEC
TCGA-FI-A2D2	Intermediate	UCEC
TCGA-FI-A2D4	MSI-H	UCEC
TCGA-FI-A2D6	MSI-H	UCEC
TCGA-FI-A2EU	MSS	UCEC
TCGA-FI-A2EW	MSS	UCEC
TCGA-FI-A2EX	MSS	UCEC
TCGA-FI-A2EY	MSS	UCEC
TCGA-FI-A2F4	MSI-H	UCEC
TCGA-FI-A2F8	MSS	UCEC
TCGA-FI-A3PX	MSS	UCEC
TCGA-FJ-A3Z7	MSS	BLCA
TCGA-FJ-A3Z9	MSS	BLCA
TCGA-FJ-A3ZE	MSS	BLCA
TCGA-FJ-A3ZF	MSS	BLCA
TCGA-FJ-A871	MSS	BLCA
TCGA-FK-A3S3	MSS	THCA
TCGA-FK-A3SB	MSS	THCA
TCGA-FK-A3SD	MSS	THCA
TCGA-FK-A3SE	MSS	THCA
TCGA-FK-A3SG	MSS	THCA
TCGA-FK-A3SH	MSS	THCA
TCGA-FK-A4UB	MSS	THCA
TCGA-FM-8000	MSI-H	DLBC
TCGA-FN-7833	MSS	LGG
TCGA-FP-7829	MSS	STAD
TCGA-FP-8099	MSS	STAD
TCGA-FP-8209	MSS	STAD
TCGA-FP-8211	MSS	STAD
TCGA-FP-8631	MSS	STAD
TCGA-FP-A4BE	MSI-H	STAD
TCGA-FP-A4BF	MSS	STAD
TCGA-FP-A8CX	MSS	STAD
TCGA-FP-A9TM	MSS	STAD
TCGA-FR-A2OS	MSS	SKCM
TCGA-FR-A3R1	MSS	SKCM
TCGA-FR-A3YN	MSS	SKCM

TCGA-FR-A3YO	MSS	SKCM
TCGA-FR-A44A	MSS	SKCM
TCGA-FR-A69P	MSS	SKCM
TCGA-FR-A726	MSS	SKCM
TCGA-FR-A728	MSS	SKCM
TCGA-FR-A729	MSS	SKCM
TCGA-FR-A7U8	MSS	SKCM
TCGA-FR-A7U9	MSS	SKCM
TCGA-FR-A7UA	MSS	SKCM
TCGA-FR-A8YC	MSS	SKCM
TCGA-FR-A8YD	MSS	SKCM
TCGA-FR-A8YE	MSS	SKCM
TCGA-FS-A1YW	MSS	SKCM
TCGA-FS-A1YX	MSS	SKCM
TCGA-FS-A1YY	MSS	SKCM
TCGA-FS-A1Z0	MSS	SKCM
TCGA-FS-A1Z3	MSS	SKCM
TCGA-FS-A1Z4	MSS	SKCM
TCGA-FS-A1Z7	MSS	SKCM
TCGA-FS-A1ZA	MSS	SKCM
TCGA-FS-A1ZB	MSS	SKCM
TCGA-FS-A1ZC	MSS	SKCM
TCGA-FS-A1ZD	MSS	SKCM
TCGA-FS-A1ZE	MSS	SKCM
TCGA-FS-A1ZF	MSS	SKCM
TCGA-FS-A1ZG	MSS	SKCM
TCGA-FS-A1ZH	MSS	SKCM
TCGA-FS-A1ZJ	MSS	SKCM
TCGA-FS-A1ZK	MSS	SKCM
TCGA-FS-A1ZM	MSS	SKCM
TCGA-FS-A1ZN	MSS	SKCM
TCGA-FS-A1ZP	MSS	SKCM
TCGA-FS-A1ZQ	MSS	SKCM
TCGA-FS-A1ZR	MSS	SKCM
TCGA-FS-A1ZS	MSS	SKCM
TCGA-FS-A1ZT	MSS	SKCM
TCGA-FS-A1ZU	MSS	SKCM
TCGA-FS-A1ZW	MSS	SKCM
TCGA-FS-A1ZY	MSS	SKCM
TCGA-FS-A1ZZ	MSS	SKCM
TCGA-FS-A4F0	MSS	SKCM
TCGA-FS-A4F2	MSS	SKCM
TCGA-FS-A4F4	MSS	SKCM
TCGA-FS-A4F8	MSS	SKCM
TCGA-FS-A4F9	MSS	SKCM
TCGA-FS-A4FC	MSS	SKCM
TCGA-FS-A4FD	MSS	SKCM
TCGA-FT-A3EE	MSS	BLCA
TCGA-FT-A61P	MSS	BLCA
TCGA-FU-A23K	MSS	CESC
TCGA-FU-A23L	MSS	CESC
TCGA-FU-A3TQ	MSS	CESC

TCGA-FU-A3TX	MSS	CESC
TCGA-FU-A3WB	MSS	CESC
TCGA-FU-A3YQ	MSS	CESC
TCGA-FU-A57G	MSS	CESC
TCGA-FU-A770	MSS	CESC
TCGA-FV-A23B	MSS	LIHC
TCGA-FV-A2QQ	MSS	LIHC
TCGA-FV-A2QR	MSS	LIHC
TCGA-FV-A3I0	MSS	LIHC
TCGA-FV-A3I1	MSS	LIHC
TCGA-FV-A3R2	MSS	LIHC
TCGA-FV-A3R3	MSS	LIHC
TCGA-FW-A3I3	MSS	SKCM
TCGA-FW-A3R5	MSS	SKCM
TCGA-FW-A3TU	MSS	SKCM
TCGA-FW-A3TV	MSS	SKCM
TCGA-FW-A5DX	MSS	SKCM
TCGA-FW-A5DY	MSS	SKCM
TCGA-FX-A76Y	MSS	SARC
TCGA-FX-A8OO	MSS	SARC
TCGA-FY-A2QD	MSS	THCA
TCGA-FY-A3BL	MSS	THCA
TCGA-FY-A3I5	MSS	THCA
TCGA-FY-A3ON	MSS	THCA
TCGA-FY-A3R6	MSS	THCA
TCGA-FY-A3R7	MSS	THCA
TCGA-FY-A3R8	MSS	THCA
TCGA-FY-A3R9	MSS	THCA
TCGA-FY-A3RA	MSS	THCA
TCGA-FY-A3TY	MSS	THCA
TCGA-FY-A3W9	MSS	THCA
TCGA-FY-A3WA	MSS	THCA
TCGA-FY-A3YR	MSS	THCA
TCGA-FY-A40K	MSS	THCA
TCGA-FY-A40L	MSS	THCA
TCGA-FY-A40M	MSS	THCA
TCGA-FY-A40N	MSS	THCA
TCGA-FY-A4B0	MSS	THCA
TCGA-FY-A4B3	MSS	THCA
TCGA-FY-A4B4	MSS	THCA
TCGA-FY-A76V	MSS	THCA
TCGA-FZ-5919	MSS	PAAD
TCGA-FZ-5920	MSS	PAAD
TCGA-FZ-5921	MSS	PAAD
TCGA-FZ-5922	MSS	PAAD
TCGA-FZ-5923	MSS	PAAD
TCGA-FZ-5924	MSS	PAAD
TCGA-FZ-5926	MSS	PAAD
TCGA-G2-A2EC	MSS	BLCA
TCGA-G2-A2EF	MSS	BLCA
TCGA-G2-A2EJ	MSS	BLCA
TCGA-G2-A2EK	MSS	BLCA

TCGA-G2-A2EL	MSS	BLCA
TCGA-G2-A2EO	MSS	BLCA
TCGA-G2-A2ES	MSS	BLCA
TCGA-G2-A3VY	MSS	BLCA
TCGA-G2-AA3B	MSS	BLCA
TCGA-G2-AA3C	MSS	BLCA
TCGA-G2-AA3D	MSS	BLCA
TCGA-G2-AA3F	MSS	BLCA
TCGA-G3-A25S	MSS	LIHC
TCGA-G3-A25T	MSS	LIHC
TCGA-G3-A25U	MSS	LIHC
TCGA-G3-A25V	MSS	LIHC
TCGA-G3-A25W	MSS	LIHC
TCGA-G3-A25Y	MSS	LIHC
TCGA-G3-A25Z	MSS	LIHC
TCGA-G3-A3CG	MSS	LIHC
TCGA-G3-A3CH	MSS	LIHC
TCGA-G3-A3CJ	MSI-H	LIHC
TCGA-G3-A3CK	MSS	LIHC
TCGA-G3-A6UC	MSS	LIHC
TCGA-G3-A7M5	MSS	LIHC
TCGA-G3-A7M6	MSS	LIHC
TCGA-G3-A7M7	MSS	LIHC
TCGA-G3-A7M8	MSS	LIHC
TCGA-G3-A7M9	MSS	LIHC
TCGA-G3-AAUZ	MSS	LIHC
TCGA-G3-AAV0	MSS	LIHC
TCGA-G3-AAV1	MSS	LIHC
TCGA-G3-AAV2	MSS	LIHC
TCGA-G3-AAV3	MSS	LIHC
TCGA-G3-AAV4	MSS	LIHC
TCGA-G3-AAV5	MSS	LIHC
TCGA-G3-AAV6	MSS	LIHC
TCGA-G3-AAV7	MSS	LIHC
TCGA-G4-6293	MSS	COAD
TCGA-G4-6294	MSS	COAD
TCGA-G4-6295	MSS	COAD
TCGA-G4-6297	MSS	COAD
TCGA-G4-6298	MSS	COAD
TCGA-G4-6299	MSS	COAD
TCGA-G4-6302	MSS	COAD
TCGA-G4-6303	MSS	COAD
TCGA-G4-6304	Intermediate	COAD
TCGA-G4-6306	MSS	COAD
TCGA-G4-6307	MSS	COAD
TCGA-G4-6309	MSI-H	COAD
TCGA-G4-6310	MSS	COAD
TCGA-G4-6311	MSS	COAD
TCGA-G4-6314	MSS	COAD
TCGA-G4-6315	MSS	COAD
TCGA-G4-6317	MSS	COAD
TCGA-G4-6317	MSS	COAD

TCGA-G4-6320	MSI-H	COAD
TCGA-G4-6321	MSS	COAD
TCGA-G4-6322	MSS	COAD
TCGA-G4-6323	MSS	COAD
TCGA-G4-6586	MSI-H	COAD
TCGA-G4-6588	MSI-H	COAD
TCGA-G4-6625	MSS	COAD
TCGA-G4-6626	MSS	COAD
TCGA-G4-6627	MSS	COAD
TCGA-G4-6628	MSI-H	COAD
TCGA-G5-6233	MSS	READ
TCGA-G5-6235	MSS	READ
TCGA-G5-6572	MSS	READ
TCGA-G5-6572	MSS	READ
TCGA-G5-6641	MSS	READ
TCGA-G6-A5PC	MSS	KIRC
TCGA-G6-A8L6	MSS	KIRC
TCGA-G6-A8L7	MSS	KIRC
TCGA-G6-A8L8	MSS	KIRC
TCGA-G7-6789	MSS	KIRP
TCGA-G7-6790	MSS	KIRP
TCGA-G7-6792	MSS	KIRP
TCGA-G7-6793	MSS	KIRP
TCGA-G7-6795	MSS	KIRP
TCGA-G7-6796	MSS	KIRP
TCGA-G7-6797	MSS	KIRP
TCGA-G7-7501	MSS	KIRP
TCGA-G7-7502	MSS	KIRP
TCGA-G7-A4TM	MSS	KIRP
TCGA-G7-A8LB	MSS	KIRP
TCGA-G7-A8LC	MSS	KIRP
TCGA-G7-A8LD	MSS	KIRP
TCGA-G7-A8LE	MSS	KIRP
TCGA-G8-6324	MSI-H	DLBC
TCGA-G8-6325	MSI-H	DLBC
TCGA-G8-6326	MSI-H	DLBC
TCGA-G8-6906	MSI-H	DLBC
TCGA-G8-6907	MSI-H	DLBC
TCGA-G8-6909	MSI-H	DLBC
TCGA-G8-6914	MSI-H	DLBC
TCGA-G9-6329	MSS	PRAD
TCGA-G9-6332	MSS	PRAD
TCGA-G9-6333	MSS	PRAD
TCGA-G9-6336	MSS	PRAD
TCGA-G9-6338	MSS	PRAD
TCGA-G9-6339	MSS	PRAD
TCGA-G9-6342	MSS	PRAD
TCGA-G9-6343	MSS	PRAD
TCGA-G9-6347	MSS	PRAD
TCGA-G9-6348	MSS	PRAD
TCGA-G9-6351	MSS	PRAD
TCGA-G9-6353	MSS	PRAD

TCGA-G9-6354	MSS	PRAD
TCGA-G9-6356	MSS	PRAD
TCGA-G9-6361	MSS	PRAD
TCGA-G9-6362	MSS	PRAD
TCGA-G9-6363	MSS	PRAD
TCGA-G9-6364	MSS	PRAD
TCGA-G9-6365	MSS	PRAD
TCGA-G9-6367	MSS	PRAD
TCGA-G9-6369	MSS	PRAD
TCGA-G9-6370	MSS	PRAD
TCGA-G9-6371	MSS	PRAD
TCGA-G9-6373	MSS	PRAD
TCGA-G9-6377	MSS	PRAD
TCGA-G9-6378	MSS	PRAD
TCGA-G9-6379	MSS	PRAD
TCGA-G9-6384	MSS	PRAD
TCGA-G9-6385	MSS	PRAD
TCGA-G9-6494	MSS	PRAD
TCGA-G9-6496	MSS	PRAD
TCGA-G9-6498	MSS	PRAD
TCGA-G9-6499	MSS	PRAD
TCGA-G9-7509	MSS	PRAD
TCGA-G9-7522	MSS	PRAD
TCGA-G9-A9S0	MSS	PRAD
TCGA-G9-A9S4	MSS	PRAD
TCGA-G9-A9S7	MSS	PRAD
TCGA-GC-A3BM	MSS	BLCA
TCGA-GC-A3I6	MSS	BLCA
TCGA-GC-A3OO	MSS	BLCA
TCGA-GC-A3RC	MSS	BLCA
TCGA-GC-A3RD	MSS	BLCA
TCGA-GC-A3WC	MSS	BLCA
TCGA-GC-A3YS	MSS	BLCA
TCGA-GC-A6I1	MSS	BLCA
TCGA-GC-A6I3	MSS	BLCA
TCGA-GD-A2C5	MSS	BLCA
TCGA-GD-A3OP	MSS	BLCA
TCGA-GD-A3OQ	MSS	BLCA
TCGA-GD-A3OS	MSS	BLCA
TCGA-GD-A6C6	MSS	BLCA
TCGA-GD-A76B	MSS	BLCA
TCGA-GE-A2C6	MSS	THCA
TCGA-GF-A2C7	MSS	SKCM
TCGA-GF-A3OT	MSS	SKCM
TCGA-GF-A4EO	MSS	SKCM
TCGA-GF-A6C8	MSS	SKCM
TCGA-GF-A6C9	MSS	SKCM
TCGA-GF-A769	MSS	SKCM
TCGA-GH-A9DA	MSS	CESC
TCGA-GI-A2C8	Intermediate	BRCA
TCGA-GJ-A3OU	MSS	LIHC
TCGA-GJ-A6C0	MSS	LIHC

TCGA-GJ-A9DB	MSS	LIHC
TCGA-GK-A6C7	MSS	KIRC
TCGA-GL-6846	MSS	KIRP
TCGA-GL-7773	MSS	KIRP
TCGA-GL-7966	MSS	KIRP
TCGA-GL-8500	MSS	KIRP
TCGA-GL-A9DC	MSS	KIRP
TCGA-GL-A9DD	MSS	KIRP
TCGA-GL-A9DE	MSS	KIRP
TCGA-GM-A2D9	MSS	BRCA
TCGA-GM-A2DB	MSS	BRCA
TCGA-GM-A2DC	MSS	BRCA
TCGA-GM-A2DD	MSS	BRCA
TCGA-GM-A2DF	MSS	BRCA
TCGA-GM-A2DH	MSS	BRCA
TCGA-GM-A2DI	MSS	BRCA
TCGA-GM-A2DK	MSS	BRCA
TCGA-GM-A2DL	MSS	BRCA
TCGA-GM-A2DM	MSS	BRCA
TCGA-GM-A2DN	Intermediate	BRCA
TCGA-GM-A2DO	MSS	BRCA
TCGA-GM-A3NY	MSS	BRCA
TCGA-GM-A3XN	MSS	BRCA
TCGA-GM-A4E0	MSS	BRCA
TCGA-GM-A5PX	MSS	BRCA
TCGA-GN-A262	MSS	SKCM
TCGA-GN-A263	MSS	SKCM
TCGA-GN-A264	MSS	SKCM
TCGA-GN-A265	MSS	SKCM
TCGA-GN-A266	MSS	SKCM
TCGA-GN-A267	MSS	SKCM
TCGA-GN-A268	MSS	SKCM
TCGA-GN-A269	MSS	SKCM
TCGA-GN-A26A	MSS	SKCM
TCGA-GN-A26C	MSS	SKCM
TCGA-GN-A4U3	MSS	SKCM
TCGA-GN-A4U4	MSS	SKCM
TCGA-GN-A4U5	MSS	SKCM
TCGA-GN-A4U7	MSS	SKCM
TCGA-GN-A4U8	MSS	SKCM
TCGA-GN-A4U9	MSS	SKCM
TCGA-GN-A8LK	MSS	SKCM
TCGA-GN-A8LL	MSS	SKCM
TCGA-GN-A8LN	MSS	SKCM
TCGA-GN-A9SD	MSS	SKCM
TCGA-GR-7351	MSI-H	DLBC
TCGA-GR-7353	MSI-H	DLBC
TCGA-GR-A4D4	MSS	DLBC
TCGA-GR-A4D5	MSS	DLBC
TCGA-GR-A4D6	MSS	DLBC
TCGA-GR-A4D9	MSS	DLBC
TCGA-GS-A9TQ	MSS	DLBC

TCGA-GS-A9TT	MSS	DLBC
TCGA-GS-A9TU	MSS	DLBC
TCGA-GS-A9TV	MSS	DLBC
TCGA-GS-A9TW	MSS	DLBC
TCGA-GS-A9TX	MSS	DLBC
TCGA-GS-A9TY	MSS	DLBC
TCGA-GS-A9TZ	MSS	DLBC
TCGA-GS-A9U3	MSS	DLBC
TCGA-GS-A9U4	MSS	DLBC
TCGA-GU-A42Q	MSS	BLCA
TCGA-GU-A42R	MSS	BLCA
TCGA-GU-A762	MSS	BLCA
TCGA-GU-A763	MSS	BLCA
TCGA-GU-A764	MSS	BLCA
TCGA-GU-A766	MSS	BLCA
TCGA-GU-A767	MSS	BLCA
TCGA-GU-AATO	MSS	BLCA
TCGA-GU-AATP	MSS	BLCA
TCGA-GU-AATQ	MSS	BLCA
TCGA-GV-A3JV	MSS	BLCA
TCGA-GV-A3JX	MSS	BLCA
TCGA-GV-A3QF	MSS	BLCA
TCGA-GV-A3QG	MSS	BLCA
TCGA-GV-A3QH	MSS	BLCA
TCGA-GV-A3QK	MSS	BLCA
TCGA-GV-A40E	MSS	BLCA
TCGA-GV-A40G	MSS	BLCA
TCGA-GV-A6ZA	MSS	BLCA
TCGA-H2-A26U	MSS	THCA
TCGA-H2-A2K9	MSS	THCA
TCGA-H2-A3RH	MSS	THCA
TCGA-H2-A3RI	MSS	THCA
TCGA-H2-A421	MSS	THCA
TCGA-H2-A422	MSS	THCA
TCGA-H4-A2HO	MSS	BLCA
TCGA-H4-A2HQ	MSS	BLCA
TCGA-H6-8124	MSS	PAAD
TCGA-H6-A45N	MSS	PAAD
TCGA-H7-7774	MSS	HNSC
TCGA-H7-8501	MSS	HNSC
TCGA-H7-8502	MSS	HNSC
TCGA-H7-A6C4	MSS	HNSC
TCGA-H7-A6C5	MSS	HNSC
TCGA-H7-A76A	MSS	HNSC
TCGA-H8-A6C1	MSS	PAAD
TCGA-H9-A6BX	MSS	PRAD
TCGA-H9-A6BY	MSS	PRAD
TCGA-HC-7075	MSS	PRAD
TCGA-HC-7077	MSS	PRAD
TCGA-HC-7079	MSS	PRAD
TCGA-HC-7080	MSS	PRAD
TCGA-HC-7081	MSS	PRAD

TCGA-HC-7209	MSS	PRAD
TCGA-HC-7210	MSS	PRAD
TCGA-HC-7213	MSS	PRAD
TCGA-HC-7231	MSS	PRAD
TCGA-HC-7232	MSS	PRAD
TCGA-HC-7233	MSS	PRAD
TCGA-HC-7736	MSS	PRAD
TCGA-HC-7740	MSS	PRAD
TCGA-HC-7740	MSS	PRAD
TCGA-HC-7742	MSS	PRAD
TCGA-HC-7747	MSS	PRAD
TCGA-HC-7748	MSS	PRAD
TCGA-HC-7817	MSS	PRAD
TCGA-HC-7818	MSS	PRAD
TCGA-HC-7819	MSS	PRAD
TCGA-HC-7820	MSS	PRAD
TCGA-HC-7821	MSS	PRAD
TCGA-HC-8213	MSS	PRAD
TCGA-HC-8216	MSS	PRAD
TCGA-HC-8264	MSS	PRAD
TCGA-HC-8265	MSS	PRAD
TCGA-HC-A48F	MSS	PRAD
TCGA-HC-A4ZV	MSS	PRAD
TCGA-HC-A631	MSS	PRAD
TCGA-HC-A632	MSS	PRAD
TCGA-HC-A6AL	MSS	PRAD
TCGA-HC-A6AN	MSS	PRAD
TCGA-HC-A6AO	MSS	PRAD
TCGA-HC-A6AP	MSS	PRAD
TCGA-HC-A6AQ	MSS	PRAD
TCGA-HC-A6AS	MSS	PRAD
TCGA-HC-A6HX	MSS	PRAD
TCGA-HC-A6HY	MSS	PRAD
TCGA-HC-A76W	MSS	PRAD
TCGA-HC-A76X	MSS	PRAD
TCGA-HC-A8CY	MSS	PRAD
TCGA-HC-A8D0	MSS	PRAD
TCGA-HC-A8D1	MSS	PRAD
TCGA-HC-A9TE	MSS	PRAD
TCGA-HC-A9TH	MSS	PRAD
TCGA-HD-7229	MSS	HNSC
TCGA-HD-7753	MSS	HNSC
TCGA-HD-7754	MSS	HNSC
TCGA-HD-7831	MSS	HNSC
TCGA-HD-7832	MSS	HNSC
TCGA-HD-8224	MSS	HNSC
TCGA-HD-8314	MSS	HNSC
TCGA-HD-8634	MSS	HNSC
TCGA-HD-8635	MSS	HNSC
TCGA-HD-A4C1	MSS	HNSC
TCGA-HD-A633	MSS	HNSC
TCGA-HD-A634	MSS	HNSC

TCGA-HD-A6HZ	MSS	HNSC
TCGA-HD-A6I0	MSS	HNSC
TCGA-HE-7128	MSS	KIRP
TCGA-HE-7129	MSS	KIRP
TCGA-HE-7130	MSS	KIRP
TCGA-HE-A5NK	MSS	KIRP
TCGA-HF-7131	MSS	STAD
TCGA-HF-7132	MSI-H	STAD
TCGA-HF-7133	MSS	STAD
TCGA-HF-A5NB	MSI-H	STAD
TCGA-HG-A2PA	MSS	CESC
TCGA-HG-A9SC	MSS	CESC
TCGA-HI-7168	MSS	PRAD
TCGA-HI-7169	MSS	PRAD
TCGA-HI-7171	MSS	PRAD
TCGA-HM-A4S6	MSS	CESC
TCGA-HM-A6W2	MSS	CESC
TCGA-HM-A6W2	MSS	CESC
TCGA-HN-A2NL	MSS	BRCA
TCGA-HN-A2OB	MSS	BRCA
TCGA-HQ-A2OE	MSS	BLCA
TCGA-HQ-A5ND	MSS	BLCA
TCGA-HQ-A5NE	MSS	BLCA
TCGA-HR-A2OG	MSS	SKCM
TCGA-HR-A2OH	MSS	SKCM
TCGA-HR-A5NC	MSS	SKCM
TCGA-HS-A5N8	MSS	SARC
TCGA-HS-A5N9	MSS	SARC
TCGA-HT-7467	MSS	LGG
TCGA-HT-7468	MSS	LGG
TCGA-HT-7470	MSS	LGG
TCGA-HT-7472	MSS	LGG
TCGA-HT-7473	MSS	LGG
TCGA-HT-7474	MSS	LGG
TCGA-HT-7475	MSS	LGG
TCGA-HT-7476	MSS	LGG
TCGA-HT-7477	MSS	LGG
TCGA-HT-7478	MSS	LGG
TCGA-HT-7479	MSS	LGG
TCGA-HT-7480	MSS	LGG
TCGA-HT-7481	MSS	LGG
TCGA-HT-7483	MSS	LGG
TCGA-HT-7485	MSS	LGG
TCGA-HT-7601	MSS	LGG
TCGA-HT-7602	MSS	LGG
TCGA-HT-7604	MSS	LGG
TCGA-HT-7605	MSS	LGG
TCGA-HT-7607	MSS	LGG
TCGA-HT-7608	MSS	LGG
TCGA-HT-7609	MSS	LGG
TCGA-HT-7611	MSS	LGG
TCGA-HT-7616	MSS	LGG

TCGA-HT-7676	MSS	LGG
TCGA-HT-7677	MSS	LGG
TCGA-HT-7680	MSS	LGG
TCGA-HT-7681	MSS	LGG
TCGA-HT-7686	MSS	LGG
TCGA-HT-7691	MSS	LGG
TCGA-HT-7693	MSS	LGG
TCGA-HT-7694	MSS	LGG
TCGA-HT-7695	MSS	LGG
TCGA-HT-7855	MSS	LGG
TCGA-HT-7856	MSS	LGG
TCGA-HT-7857	MSS	LGG
TCGA-HT-7858	MSS	LGG
TCGA-HT-7860	MSS	LGG
TCGA-HT-7873	MSS	LGG
TCGA-HT-7874	MSS	LGG
TCGA-HT-7875	MSS	LGG
TCGA-HT-7877	MSS	LGG
TCGA-HT-7879	MSS	LGG
TCGA-HT-7880	MSS	LGG
TCGA-HT-7881	MSS	LGG
TCGA-HT-7882	MSS	LGG
TCGA-HT-7884	MSS	LGG
TCGA-HT-7902	MSS	LGG
TCGA-HT-8010	MSS	LGG
TCGA-HT-8011	MSS	LGG
TCGA-HT-8012	MSS	LGG
TCGA-HT-8013	MSS	LGG
TCGA-HT-8015	MSS	LGG
TCGA-HT-8018	MSS	LGG
TCGA-HT-8019	MSS	LGG
TCGA-HT-8104	MSS	LGG
TCGA-HT-8105	MSS	LGG
TCGA-HT-8106	MSS	LGG
TCGA-HT-8107	MSS	LGG
TCGA-HT-8108	MSS	LGG
TCGA-HT-8109	MSS	LGG
TCGA-HT-8110	MSS	LGG
TCGA-HT-8111	MSS	LGG
TCGA-HT-8113	MSS	LGG
TCGA-HT-8114	MSS	LGG
TCGA-HT-8558	MSS	LGG
TCGA-HT-8563	MSS	LGG
TCGA-HT-8564	MSI-H	LGG
TCGA-HT-A5R5	MSS	LGG
TCGA-HT-A5R7	MSS	LGG
TCGA-HT-A5R9	MSS	LGG
TCGA-HT-A5RA	MSS	LGG
TCGA-HT-A5RB	MSS	LGG
TCGA-HT-A5RC	MSS	LGG
TCGA-HT-A614	MSS	LGG
TCGA-HT-A615	MSS	LGG

TCGA-HT-A616	MSS	LGG
TCGA-HT-A617	MSS	LGG
TCGA-HT-A618	MSS	LGG
TCGA-HT-A619	MSS	LGG
TCGA-HT-A61A	MSS	LGG
TCGA-HT-A61B	MSS	LGG
TCGA-HT-A61C	MSS	LGG
TCGA-HT-A74H	MSS	LGG
TCGA-HT-A74J	MSS	LGG
TCGA-HT-A74K	MSS	LGG
TCGA-HT-A74L	MSS	LGG
TCGA-HT-A74O	MSS	LGG
TCGA-HU-8238	MSS	STAD
TCGA-HU-8243	MSS	STAD
TCGA-HU-8244	MSS	STAD
TCGA-HU-8245	MSS	STAD
TCGA-HU-8249	MSS	STAD
TCGA-HU-8602	MSI-H	STAD
TCGA-HU-8604	MSS	STAD
TCGA-HU-8608	MSS	STAD
TCGA-HU-8610	MSS	STAD
TCGA-HU-A4G2	MSS	STAD
TCGA-HU-A4G3	MSS	STAD
TCGA-HU-A4G6	MSS	STAD
TCGA-HU-A4G8	MSI-H	STAD
TCGA-HU-A4G9	MSI-H	STAD
TCGA-HU-A4GC	MSS	STAD
TCGA-HU-A4GD	MSS	STAD
TCGA-HU-A4GF	MSS	STAD
TCGA-HU-A4GH	MSS	STAD
TCGA-HU-A4GJ	MSS	STAD
TCGA-HU-A4GN	MSI-H	STAD
TCGA-HU-A4GP	MSS	STAD
TCGA-HU-A4GQ	MSI-H	STAD
TCGA-HU-A4GT	MSI-H	STAD
TCGA-HU-A4GU	MSI-H	STAD
TCGA-HU-A4GX	MSI-H	STAD
TCGA-HU-A4GY	MSS	STAD
TCGA-HU-A4H2	MSS	STAD
TCGA-HU-A4H3	MSI-H	STAD
TCGA-HU-A4H4	MSI-H	STAD
TCGA-HU-A4H5	MSS	STAD
TCGA-HU-A4H6	MSS	STAD
TCGA-HU-A4H8	MSI-H	STAD
TCGA-HU-A4HB	MSS	STAD
TCGA-HU-A4HD	MSS	STAD
TCGA-HV-A7OL	MSS	PAAD
TCGA-HV-A7OP	MSS	PAAD
TCGA-HV-AA8V	MSS	PAAD
TCGA-HV-AA8X	MSS	PAAD
TCGA-HW-7486	MSS	LGG
TCGA-HW-7487	MSS	LGG

TCGA-HW-7489	MSS	LGG
TCGA-HW-7490	MSS	LGG
TCGA-HW-7491	MSS	LGG
TCGA-HW-7493	MSS	LGG
TCGA-HW-7495	MSS	LGG
TCGA-HW-8319	MSS	LGG
TCGA-HW-8320	MSS	LGG
TCGA-HW-8321	MSS	LGG
TCGA-HW-8322	MSS	LGG
TCGA-HW-A5KJ	MSS	LGG
TCGA-HW-A5KK	MSS	LGG
TCGA-HW-A5KL	MSS	LGG
TCGA-HW-A5KM	MSS	LGG
TCGA-HZ-7289	MSS	PAAD
TCGA-HZ-7918	MSS	PAAD
TCGA-HZ-7919	MSS	PAAD
TCGA-HZ-7920	MSS	PAAD
TCGA-HZ-7922	MSS	PAAD
TCGA-HZ-7923	MSS	PAAD
TCGA-HZ-7924	MSS	PAAD
TCGA-HZ-7925	MSS	PAAD
TCGA-HZ-7926	MSS	PAAD
TCGA-HZ-8001	MSS	PAAD
TCGA-HZ-8002	MSS	PAAD
TCGA-HZ-8003	MSS	PAAD
TCGA-HZ-8005	MSS	PAAD
TCGA-HZ-8315	MSS	PAAD
TCGA-HZ-8317	MSS	PAAD
TCGA-HZ-8519	MSS	PAAD
TCGA-HZ-8636	MSS	PAAD
TCGA-HZ-8637	MSS	PAAD
TCGA-HZ-8638	MSS	PAAD
TCGA-HZ-A49H	MSS	PAAD
TCGA-HZ-A49I	MSS	PAAD
TCGA-HZ-A4BH	MSS	PAAD
TCGA-HZ-A4BK	MSS	PAAD
TCGA-HZ-A77O	MSS	PAAD
TCGA-HZ-A77P	MSS	PAAD
TCGA-HZ-A77Q	MSS	PAAD
TCGA-HZ-A8P0	MSS	PAAD
TCGA-HZ-A8P1	MSS	PAAD
TCGA-HZ-A9TJ	MSS	PAAD
TCGA-HZ-A9TJ	MSS	PAAD
TCGA-IA-A83S	MSS	KIRP
TCGA-IA-A83T	MSS	KIRP
TCGA-IA-A83V	MSS	KIRP
TCGA-IA-A83W	MSS	KIRP
TCGA-IB-7644	MSS	PAAD
TCGA-IB-7645	MSS	PAAD
TCGA-IB-7646	MSS	PAAD
TCGA-IB-7647	MSS	PAAD
TCGA-IB-7649	MSS	PAAD

TCGA-IB-7651	MSS	PAAD
TCGA-IB-7652	MSS	PAAD
TCGA-IB-7654	MSS	PAAD
TCGA-IB-7885	MSS	PAAD
TCGA-IB-7886	MSS	PAAD
TCGA-IB-7887	MSS	PAAD
TCGA-IB-7889	MSS	PAAD
TCGA-IB-7890	MSS	PAAD
TCGA-IB-7891	MSS	PAAD
TCGA-IB-7893	MSS	PAAD
TCGA-IB-7897	MSS	PAAD
TCGA-IB-8126	MSS	PAAD
TCGA-IB-8127	MSS	PAAD
TCGA-IB-A5SO	MSS	PAAD
TCGA-IB-A5SP	MSS	PAAD
TCGA-IB-A5SQ	MSS	PAAD
TCGA-IB-A5SS	MSS	PAAD
TCGA-IB-A5ST	MSS	PAAD
TCGA-IB-A6UF	MSS	PAAD
TCGA-IB-A6UG	MSS	PAAD
TCGA-IB-A7LX	MSS	PAAD
TCGA-IB-A7M4	MSS	PAAD
TCGA-IB-AAUM	MSS	PAAD
TCGA-IB-AAUN	MSS	PAAD
TCGA-IB-AAUO	MSS	PAAD
TCGA-IB-AAUP	MSS	PAAD
TCGA-IB-AAUQ	MSS	PAAD
TCGA-IB-AAUR	MSS	PAAD
TCGA-IB-AAUS	MSS	PAAD
TCGA-IB-AAUT	MSS	PAAD
TCGA-IB-AAUU	MSS	PAAD
TCGA-IB-AAUV	MSS	PAAD
TCGA-IB-AAUW	MSS	PAAD
TCGA-IC-A6RE	MSS	ESCA
TCGA-IC-A6RF	MSS	ESCA
TCGA-IE-A4EH	MSS	SARC
TCGA-IE-A6BZ	MSS	SARC
TCGA-IF-A4AK	MSS	SARC
TCGA-IG-A3YA	MSS	ESCA
TCGA-IG-A4P3	MSS	ESCA
TCGA-IG-A4QT	MSS	ESCA
TCGA-IG-A51D	MSS	ESCA
TCGA-IG-A5S3	MSS	ESCA
TCGA-IG-A625	MSS	ESCA
TCGA-IG-A6QS	MSS	ESCA
TCGA-IG-A7DP	MSS	ESCA
TCGA-IG-A8O2	MSS	ESCA
TCGA-IG-A97H	MSS	ESCA
TCGA-IG-A97I	MSS	ESCA
TCGA-IH-A3EA	MSS	SKCM
TCGA-IK-7675	MSS	LGG
TCGA-IM-A3EB	MSS	THCA

TCGA-IM-A3ED	MSS	THCA
TCGA-IM-A3U2	MSS	THCA
TCGA-IM-A41Y	MSS	THCA
TCGA-IM-A41Z	MSS	THCA
TCGA-IM-A420	Intermediate	THCA
TCGA-IM-A4EB	MSS	THCA
TCGA-IN-7808	MSS	STAD
TCGA-IN-8462	MSS	STAD
TCGA-IN-8663	MSS	STAD
TCGA-IN-A6RI	MSS	STAD
TCGA-IN-A6RJ	MSS	STAD
TCGA-IN-A6RL	MSS	STAD
TCGA-IN-A6RN	MSS	STAD
TCGA-IN-A6RO	MSS	STAD
TCGA-IN-A6RP	MSS	STAD
TCGA-IN-A6RR	MSS	STAD
TCGA-IN-A6RS	MSS	STAD
TCGA-IN-A7NR	MSS	STAD
TCGA-IN-A7NT	MSS	STAD
TCGA-IN-A7NU	MSS	STAD
TCGA-IN-AB1V	MSS	STAD
TCGA-IN-AB1X	MSS	STAD
TCGA-IQ-7630	MSS	HNSC
TCGA-IQ-7631	MSS	HNSC
TCGA-IQ-7632	MSS	HNSC
TCGA-IQ-A61E	MSS	HNSC
TCGA-IQ-A61G	MSS	HNSC
TCGA-IQ-A61H	MSS	HNSC
TCGA-IQ-A61I	MSS	HNSC
TCGA-IQ-A61J	MSS	HNSC
TCGA-IQ-A61K	MSS	HNSC
TCGA-IQ-A61L	MSS	HNSC
TCGA-IQ-A61O	MSS	HNSC
TCGA-IQ-A6SG	MSS	HNSC
TCGA-IQ-A6SH	MSS	HNSC
TCGA-IR-A3LF	MSS	CESC
TCGA-IR-A3LK	MSS	CESC
TCGA-IW-A3M6	MSS	SARC
TCGA-IZ-8195	MSS	KIRP
TCGA-IZ-8195	MSI-H	KIRP
TCGA-IZ-8196	MSS	KIRP
TCGA-IZ-A6M8	MSS	KIRP
TCGA-IZ-A6M9	MSS	KIRP
TCGA-J1-A4AH	MSS	LUSC
TCGA-J2-8192	MSS	LUAD
TCGA-J2-A4AD	MSS	LUAD
TCGA-J2-A4AE	MSS	LUAD
TCGA-J2-A4AG	MSS	LUAD
TCGA-J4-8200	MSS	PRAD
TCGA-J4-A67K	MSS	PRAD
TCGA-J4-A67L	MSS	PRAD
TCGA-J4-A67M	MSS	PRAD

TCGA-J4-A67N	MSS	PRAD
TCGA-J4-A67O	MSS	PRAD
TCGA-J4-A67Q	MSS	PRAD
TCGA-J4-A67R	MSS	PRAD
TCGA-J4-A67S	MSS	PRAD
TCGA-J4-A67T	MSS	PRAD
TCGA-J4-A6G1	MSS	PRAD
TCGA-J4-A6G3	MSS	PRAD
TCGA-J4-A6M7	MSS	PRAD
TCGA-J4-A83I	MSS	PRAD
TCGA-J4-A83J	MSS	PRAD
TCGA-J4-A83K	MSS	PRAD
TCGA-J4-A83L	MSS	PRAD
TCGA-J4-A83M	MSS	PRAD
TCGA-J4-A83N	MSS	PRAD
TCGA-J4-AATV	MSS	PRAD
TCGA-J4-AATZ	MSS	PRAD
TCGA-J4-AAU2	MSS	PRAD
TCGA-J7-6720	MSS	KIRP
TCGA-J7-8537	MSS	KIRP
TCGA-J7-A8I2	MSS	KIRP
TCGA-J8-A3O2	MSS	THCA
TCGA-J8-A3O2	MSS	THCA
TCGA-J8-A3YD	MSS	THCA
TCGA-J8-A3YE	MSS	THCA
TCGA-J8-A3YF	MSS	THCA
TCGA-J8-A3YH	MSS	THCA
TCGA-J8-A3YH	MSS	THCA
TCGA-J8-A42S	MSS	THCA
TCGA-J8-A4HW	MSS	THCA
TCGA-J8-A4HW	MSS	THCA
TCGA-J8-A4HY	MSS	THCA
TCGA-J9-A52D	MSS	PRAD
TCGA-J9-A8CK	MSS	PRAD
TCGA-J9-A8CL	MSS	PRAD
TCGA-J9-A8CM	MSS	PRAD
TCGA-J9-A8CN	MSS	PRAD
TCGA-J9-A8CP	MSS	PRAD
TCGA-JL-A3YW	MSS	BRCA
TCGA-JL-A3YX	MSS	BRCA
TCGA-JU-AAVI	MSS	UCEC
TCGA-JV-A75J	MSS	SARC
TCGA-JW-A5VK	MSS	CESC
TCGA-JW-A852	MSS	CESC
TCGA-JW-AAVH	MSS	CESC
TCGA-JY-A6FA	MSS	ESCA
TCGA-JY-A6FB	MSS	ESCA
TCGA-JY-A6FD	MSS	ESCA
TCGA-JY-A6FE	MSS	ESCA
TCGA-JY-A6FG	MSS	ESCA
TCGA-JY-A6FH	MSS	ESCA
TCGA-JY-A938	MSS	ESCA

TCGA-JY-A939	MSS	ESCA
TCGA-JY-A93C	MSS	ESCA
TCGA-JY-A93D	MSS	ESCA
TCGA-JY-A93E	MSS	ESCA
TCGA-JY-A93F	MSS	ESCA
TCGA-K1-A6RT	MSS	SARC
TCGA-K1-A6RU	MSS	SARC
TCGA-K1-A6RV	MSS	SARC
TCGA-K4-A3WS	MSS	BLCA
TCGA-K4-A3WU	MSS	BLCA
TCGA-K4-A3WV	MSS	BLCA
TCGA-K4-A4AB	MSS	BLCA
TCGA-K4-A54R	MSS	BLCA
TCGA-K4-A5RH	MSS	BLCA
TCGA-K4-A5RI	MSS	BLCA
TCGA-K4-A5RJ	MSS	BLCA
TCGA-K4-A6FZ	MSS	BLCA
TCGA-K4-A6MB	MSS	BLCA
TCGA-K4-A83P	MSS	BLCA
TCGA-K4-AAQO	MSS	BLCA
TCGA-K7-A6G5	MSS	LIHC
TCGA-K7-AAU7	MSS	LIHC
TCGA-KB-A6F5	MSS	STAD
TCGA-KB-A6F7	MSS	STAD
TCGA-KB-A93G	MSS	STAD
TCGA-KB-A93H	MSS	STAD
TCGA-KB-A93J	MSS	STAD
TCGA-KC-A4BL	MSS	PRAD
TCGA-KC-A4BN	MSS	PRAD
TCGA-KC-A4BO	MSS	PRAD
TCGA-KC-A4BR	MSS	PRAD
TCGA-KC-A7F3	MSS	PRAD
TCGA-KC-A7F5	MSS	PRAD
TCGA-KC-A7F6	MSS	PRAD
TCGA-KC-A7FA	MSS	PRAD
TCGA-KC-A7FD	MSS	PRAD
TCGA-KC-A7FE	MSS	PRAD
TCGA-KH-A6WC	MSS	ESCA
TCGA-KJ-A3U4	MSS	UCEC
TCGA-KK-A59V	MSI-H	PRAD
TCGA-KK-A59X	MSS	PRAD
TCGA-KK-A59Z	MSS	PRAD
TCGA-KK-A5A1	MSS	PRAD
TCGA-KK-A6DY	MSS	PRAD
TCGA-KK-A6E0	MSS	PRAD
TCGA-KK-A6E1	MSS	PRAD
TCGA-KK-A6E2	MSS	PRAD
TCGA-KK-A6E3	MSS	PRAD
TCGA-KK-A6E4	MSS	PRAD
TCGA-KK-A6E5	MSS	PRAD
TCGA-KK-A6E6	MSS	PRAD
TCGA-KK-A6E7	MSS	PRAD

TCGA-KK-A6E8	MSS	PRAD
TCGA-KK-A7AP	MSS	PRAD
TCGA-KK-A7AQ	MSS	PRAD
TCGA-KK-A7AU	MSS	PRAD
TCGA-KK-A7AV	MSS	PRAD
TCGA-KK-A7AW	MSS	PRAD
TCGA-KK-A7AY	MSS	PRAD
TCGA-KK-A7AZ	MSS	PRAD
TCGA-KK-A7B0	MSS	PRAD
TCGA-KK-A7B1	MSS	PRAD
TCGA-KK-A7B2	MSS	PRAD
TCGA-KK-A7B3	MSS	PRAD
TCGA-KK-A7B4	MSS	PRAD
TCGA-KK-A8I4	MSS	PRAD
TCGA-KK-A8I5	MSS	PRAD
TCGA-KK-A8I6	MSS	PRAD
TCGA-KK-A8I7	MSS	PRAD
TCGA-KK-A8I8	MSS	PRAD
TCGA-KK-A8I9	MSS	PRAD
TCGA-KK-A8IA	MSS	PRAD
TCGA-KK-A8IB	MSS	PRAD
TCGA-KK-A8IC	MSS	PRAD
TCGA-KK-A8ID	MSS	PRAD
TCGA-KK-A8IF	MSS	PRAD
TCGA-KK-A8IG	MSS	PRAD
TCGA-KK-A8IH	MSS	PRAD
TCGA-KK-A8II	MSS	PRAD
TCGA-KK-A8IJ	MSS	PRAD
TCGA-KK-A8IK	MSS	PRAD
TCGA-KK-A8IL	MSS	PRAD
TCGA-KK-A8IM	MSS	PRAD
TCGA-KL-8323	MSS	KICH
TCGA-KL-8324	MSS	KICH
TCGA-KL-8325	MSS	KICH
TCGA-KL-8326	MSS	KICH
TCGA-KL-8327	MSS	KICH
TCGA-KL-8328	MSS	KICH
TCGA-KL-8329	MSS	KICH
TCGA-KL-8330	MSS	KICH
TCGA-KL-8331	MSS	KICH
TCGA-KL-8332	MSS	KICH
TCGA-KL-8333	MSS	KICH
TCGA-KL-8334	MSS	KICH
TCGA-KL-8335	MSS	KICH
TCGA-KL-8336	MSS	KICH
TCGA-KL-8337	MSS	KICH
TCGA-KL-8338	MSS	KICH
TCGA-KL-8339	MSS	KICH
TCGA-KL-8340	MSS	KICH
TCGA-KL-8341	MSS	KICH
TCGA-KL-8342	MSS	KICH
TCGA-KL-8343	MSS	KICH

TCGA-KL-8344	MSS	KICH
TCGA-KL-8345	MSS	KICH
TCGA-KL-8346	MSS	KICH
TCGA-KM-8438	MSS	KICH
TCGA-KM-8439	MSS	KICH
TCGA-KM-8440	MSS	KICH
TCGA-KM-8441	MSS	KICH
TCGA-KM-8442	MSS	KICH
TCGA-KM-8443	MSS	KICH
TCGA-KM-8476	MSS	KICH
TCGA-KM-8477	MSS	KICH
TCGA-KN-8418	MSS	KICH
TCGA-KN-8419	MSS	KICH
TCGA-KN-8421	MSS	KICH
TCGA-KN-8422	MSS	KICH
TCGA-KN-8423	MSS	KICH
TCGA-KN-8424	MSS	KICH
TCGA-KN-8425	MSS	KICH
TCGA-KN-8426	MSS	KICH
TCGA-KN-8427	MSS	KICH
TCGA-KN-8428	MSS	KICH
TCGA-KN-8429	MSS	KICH
TCGA-KN-8430	MSS	KICH
TCGA-KN-8431	MSS	KICH
TCGA-KN-8432	MSS	KICH
TCGA-KN-8433	MSS	KICH
TCGA-KN-8434	MSS	KICH
TCGA-KN-8435	MSS	KICH
TCGA-KN-8436	MSS	KICH
TCGA-KN-8437	MSS	KICH
TCGA-KO-8403	MSS	KICH
TCGA-KO-8404	MSS	KICH
TCGA-KO-8405	MSS	KICH
TCGA-KO-8406	MSS	KICH
TCGA-KO-8407	MSS	KICH
TCGA-KO-8408	MSS	KICH
TCGA-KO-8409	MSS	KICH
TCGA-KO-8410	MSS	KICH
TCGA-KO-8411	MSS	KICH
TCGA-KO-8413	MSS	KICH
TCGA-KO-8414	MSS	KICH
TCGA-KO-8415	MSS	KICH
TCGA-KO-8416	MSS	KICH
TCGA-KP-A3W3	MSS	UCEC
TCGA-KP-A3W4	MSS	UCEC
TCGA-KQ-A41N	MSS	BLCA
TCGA-KQ-A41O	MSS	BLCA
TCGA-KQ-A41P	MSS	BLCA
TCGA-KQ-A41Q	MSS	BLCA
TCGA-KQ-A41R	MSS	BLCA
TCGA-KQ-A41S	MSS	BLCA
TCGA-KR-A7K0	MSS	LIHC

TCGA-KR-A7K2	MSS	LIHC
TCGA-KR-A7K7	MSS	LIHC
TCGA-KR-A7K8	MSS	LIHC
TCGA-KS-A41F	MSS	THCA
TCGA-KS-A41I	MSS	THCA
TCGA-KS-A41J	MSS	THCA
TCGA-KS-A41L	MSS	THCA
TCGA-KS-A4I1	MSS	THCA
TCGA-KS-A4I3	MSS	THCA
TCGA-KS-A4I5	MSS	THCA
TCGA-KS-A4I7	MSS	THCA
TCGA-KS-A4I9	MSS	THCA
TCGA-KS-A4IB	MSS	THCA
TCGA-KS-A4IC	MSS	THCA
TCGA-KS-A4ID	MSS	THCA
TCGA-KT-A74X	MSS	LGG
TCGA-KT-A7W1	MSS	LGG
TCGA-KU-A66S	MSS	HNSC
TCGA-KU-A66T	MSS	HNSC
TCGA-KU-A6H7	MSS	HNSC
TCGA-KU-A6H7	MSS	HNSC
TCGA-KU-A6H8	MSS	HNSC
TCGA-KV-A6GD	MSS	KIRP
TCGA-KV-A6GE	MSS	KIRP
TCGA-KV-A74V	MSS	KIRP
TCGA-L1-A7W4	MSS	PAAD
TCGA-L3-A4E7	MSS	LUSC
TCGA-L3-A524	MSS	LUSC
TCGA-L4-A4E5	MSS	LUAD
TCGA-L4-A4E6	MSS	LUAD
TCGA-L5-A43J	MSI-H	ESCA
TCGA-L5-A4OE	MSS	ESCA
TCGA-L5-A4OF	MSS	ESCA
TCGA-L5-A4OG	MSS	ESCA
TCGA-L5-A4OH	MSS	ESCA
TCGA-L5-A4OI	MSI-H	ESCA
TCGA-L5-A4OM	MSS	ESCA
TCGA-L5-A4ON	MSS	ESCA
TCGA-L5-A4OO	MSS	ESCA
TCGA-L5-A4OP	MSS	ESCA
TCGA-L5-A4OS	MSS	ESCA
TCGA-L5-A4OU	MSS	ESCA
TCGA-L5-A4OX	MSS	ESCA
TCGA-L5-A88S	MSS	ESCA
TCGA-L5-A88T	MSS	ESCA
TCGA-L5-A88V	MSS	ESCA
TCGA-L5-A88W	MSS	ESCA
TCGA-L5-A88Y	MSS	ESCA
TCGA-L5-A88Z	MSS	ESCA
TCGA-L5-A891	MSS	ESCA
TCGA-L5-A893	MSS	ESCA
TCGA-L5-A8NE	MSS	ESCA

TCGA-L5-A8NF	MSS	ESCA
TCGA-L5-A8NG	MSS	ESCA
TCGA-L5-A8NH	MSS	ESCA
TCGA-L5-A8NI	MSS	ESCA
TCGA-L5-A8NJ	MSS	ESCA
TCGA-L5-A8NK	MSS	ESCA
TCGA-L5-A8NL	MSS	ESCA
TCGA-L5-A8NM	MSI-H	ESCA
TCGA-L5-A8NN	MSS	ESCA
TCGA-L5-A8NQ	MSS	ESCA
TCGA-L5-A8NR	MSS	ESCA
TCGA-L5-A8NS	MSS	ESCA
TCGA-L5-A8NT	MSS	ESCA
TCGA-L5-A8NU	MSS	ESCA
TCGA-L5-A8NV	MSS	ESCA
TCGA-L5-A8NW	MSS	ESCA
TCGA-L6-A4EQ	MSS	THCA
TCGA-L6-A4ET	MSS	THCA
TCGA-L6-A4EU	MSS	THCA
TCGA-L7-A6VZ	MSS	ESCA
TCGA-L9-A443	MSS	LUAD
TCGA-L9-A444	MSS	LUAD
TCGA-L9-A50W	MSS	LUAD
TCGA-L9-A5IP	MSS	LUAD
TCGA-L9-A743	MSS	LUAD
TCGA-L9-A7SV	MSS	LUAD
TCGA-L9-A8F4	MSS	LUAD
TCGA-LA-A446	MSS	LUSC
TCGA-LA-A7SW	MSS	LUSC
TCGA-LB-A7SX	MSS	PAAD
TCGA-LB-A8F3	MSS	PAAD
TCGA-LB-A9Q5	MSS	PAAD
TCGA-LC-A66R	MSS	BLCA
TCGA-LD-A66U	MSS	BRCA
TCGA-LD-A74U	MSS	BRCA
TCGA-LD-A7W5	MSS	BRCA
TCGA-LD-A7W6	MSS	BRCA
TCGA-LD-A9QF	MSS	BRCA
TCGA-LG-A6GG	MSS	LIHC
TCGA-LG-A9QC	MSS	LIHC
TCGA-LG-A9QD	MSS	LIHC
TCGA-LH-A9QB	MSS	SKCM
TCGA-LI-A67I	MSS	SARC
TCGA-LK-A4NW	MSS	MESO
TCGA-LK-A4NY	MSS	MESO
TCGA-LK-A4NZ	MSS	MESO
TCGA-LK-A4O0	MSS	MESO
TCGA-LK-A4O2	MSS	MESO
TCGA-LK-A4O4	MSS	MESO
TCGA-LK-A4O5	MSS	MESO
TCGA-LK-A4O6	MSS	MESO
TCGA-LK-A4O7	MSS	MESO

TCGA-LL-A5YL	MSS	BRCA
TCGA-LL-A5YM	MSS	BRCA
TCGA-LL-A5YN	MSS	BRCA
TCGA-LL-A6FP	MSS	BRCA
TCGA-LL-A6FQ	MSS	BRCA
TCGA-LL-A6FR	MSS	BRCA
TCGA-LL-A73Y	MSS	BRCA
TCGA-LL-A73Z	MSS	BRCA
TCGA-LL-A740	MSS	BRCA
TCGA-LL-A7SZ	MSS	BRCA
TCGA-LL-A7T0	MSS	BRCA
TCGA-LL-A8F5	MSS	BRCA
TCGA-LL-A9Q3	MSS	BRCA
TCGA-LN-A49P	MSS	ESCA
TCGA-LN-A49U	MSS	ESCA
TCGA-LN-A49X	MSS	ESCA
TCGA-LN-A4A2	MSS	ESCA
TCGA-LN-A4A3	MSS	ESCA
TCGA-LN-A4A4	MSS	ESCA
TCGA-LN-A4A8	MSS	ESCA
TCGA-LN-A4A9	MSS	ESCA
TCGA-LN-A4MQ	MSS	ESCA
TCGA-LN-A5U5	MSS	ESCA
TCGA-LN-A5U6	MSS	ESCA
TCGA-LN-A5U7	MSS	ESCA
TCGA-LN-A7HV	MSS	ESCA
TCGA-LN-A7HW	MSS	ESCA
TCGA-LN-A7HX	MSS	ESCA
TCGA-LN-A7HY	MSS	ESCA
TCGA-LN-A7HZ	MSS	ESCA
TCGA-LN-A8HZ	MSS	ESCA
TCGA-LN-A8I0	MSS	ESCA
TCGA-LN-A8I1	MSS	ESCA
TCGA-LN-A9FO	MSS	ESCA
TCGA-LN-A9FP	MSS	ESCA
TCGA-LN-A9FQ	MSS	ESCA
TCGA-LP-A7HU	MSS	CESC
TCGA-LQ-A4E4	MSS	BRCA
TCGA-LT-A5Z6	MSS	BLCA
TCGA-LT-A8JT	MSS	BLCA
TCGA-M7-A71Y	MSS	PRAD
TCGA-M7-A71Z	MSS	PRAD
TCGA-M7-A720	MSS	PRAD
TCGA-M7-A721	MSS	PRAD
TCGA-M7-A722	MSS	PRAD
TCGA-M7-A723	MSS	PRAD
TCGA-M7-A724	MSS	PRAD
TCGA-M7-A725	MSS	PRAD
TCGA-MA-AA3W	MSS	CESC
TCGA-MA-AA3X	MSS	CESC
TCGA-MA-AA3Y	MSS	CESC
TCGA-MA-AA3Z	MSS	CESC

TCGA-MA-AA41	MSS	CESC
TCGA-MA-AA42	Intermediate	CESC
TCGA-MA-AA43	MSS	CESC
TCGA-MB-A5Y8	MSS	SARC
TCGA-MB-A8JK	MSS	SARC
TCGA-MB-A8JL	MSS	SARC
TCGA-MF-A522	MSS	LUSC
TCGA-MG-AAMC	MSS	PRAD
TCGA-MH-A854	MSS	KIRP
TCGA-MH-A855	MSS	KIRP
TCGA-MH-A856	MSS	KIRP
TCGA-MH-A857	MSS	KIRP
TCGA-MI-A75C	MSS	LIHC
TCGA-MI-A75E	MSS	LIHC
TCGA-MI-A75G	MSS	LIHC
TCGA-MI-A75H	MSS	LIHC
TCGA-MI-A75I	MSS	LIHC
TCGA-MJ-A68H	MSS	SARC
TCGA-MJ-A68J	MSS	SARC
TCGA-MJ-A850	MSS	SARC
TCGA-MK-A4N7	MSS	THCA
TCGA-MK-A4N9	MSS	THCA
TCGA-MK-A84Z	MSS	THCA
TCGA-MM-A84U	MSS	KIRC
TCGA-MN-A4N1	MSS	LUAD
TCGA-MN-A4N4	MSS	LUAD
TCGA-MN-A4N5	MSS	LUAD
TCGA-MO-A47P	MSS	SARC
TCGA-MP-A4SV	MSS	LUAD
TCGA-MP-A4SW	MSS	LUAD
TCGA-MP-A4SY	MSS	LUAD
TCGA-MP-A4T2	MSS	LUAD
TCGA-MP-A4T4	MSS	LUAD
TCGA-MP-A4T6	MSS	LUAD
TCGA-MP-A4T7	MSS	LUAD
TCGA-MP-A4T8	MSS	LUAD
TCGA-MP-A4T9	MSS	LUAD
TCGA-MP-A4TA	MSS	LUAD
TCGA-MP-A4TC	MSS	LUAD
TCGA-MP-A4TD	MSS	LUAD
TCGA-MP-A4TE	MSS	LUAD
TCGA-MP-A4TF	MSS	LUAD
TCGA-MP-A4TH	MSS	LUAD
TCGA-MP-A4TI	MSS	LUAD
TCGA-MP-A4TJ	MSS	LUAD
TCGA-MP-A4TK	MSS	LUAD
TCGA-MP-A5C7	MSS	LUAD
TCGA-MQ-A4KX	MSS	MESO
TCGA-MQ-A4LC	MSS	MESO
TCGA-MQ-A4LI	MSS	MESO
TCGA-MQ-A4LJ	MSS	MESO
TCGA-MQ-A4LM	MSS	MESO

TCGA-MQ-A4LP	MSS	MESO
TCGA-MQ-A4LV	MSS	MESO
TCGA-MQ-A6BL	MSS	MESO
TCGA-MQ-A6BQ	MSS	MESO
TCGA-MQ-A6BR	MSS	MESO
TCGA-MQ-A6BS	MSS	MESO
TCGA-MR-A520	MSS	LIHC
TCGA-MR-A8JO	MSS	LIHC
TCGA-MS-A51U	MSS	BRCA
TCGA-MT-A51W	MSS	HNSC
TCGA-MT-A51X	MSS	HNSC
TCGA-MT-A67A	MSS	HNSC
TCGA-MT-A67D	MSS	HNSC
TCGA-MT-A67F	MSS	HNSC
TCGA-MT-A67G	MSS	HNSC
TCGA-MT-A7BN	MSS	HNSC
TCGA-MU-A51Y	MSS	CESC
TCGA-MU-A5YI	MSS	CESC
TCGA-MU-A8JM	MSS	CESC
TCGA-MX-A5UG	MSS	STAD
TCGA-MX-A5UJ	MSI-H	STAD
TCGA-MX-A663	MSS	STAD
TCGA-MX-A666	MSS	STAD
TCGA-MY-A5BD	MSS	CESC
TCGA-MY-A5BE	MSS	CESC
TCGA-MY-A5BF	MSS	CESC
TCGA-MY-A913	MSS	CESC
TCGA-MZ-A5BI	MSS	HNSC
TCGA-MZ-A6I9	MSS	HNSC
TCGA-MZ-A7D7	MSS	HNSC
TCGA-N1-A6IA	MSS	SARC
TCGA-N5-A4R8	MSS	UCS
TCGA-N5-A4RA	MSS	UCS
TCGA-N5-A4RD	MSS	UCS
TCGA-N5-A4RF	MSS	UCS
TCGA-N5-A4RJ	MSS	UCS
TCGA-N5-A4RM	MSS	UCS
TCGA-N5-A4RN	MSS	UCS
TCGA-N5-A4RO	MSS	UCS
TCGA-N5-A4RS	MSS	UCS
TCGA-N5-A4RT	MSS	UCS
TCGA-N5-A4RU	MSS	UCS
TCGA-N5-A4RV	MSS	UCS
TCGA-N5-A59E	MSS	UCS
TCGA-N5-A59F	MSS	UCS
TCGA-N6-A4V9	MSS	UCS
TCGA-N6-A4VC	MSS	UCS
TCGA-N6-A4VD	MSS	UCS
TCGA-N6-A4VE	MSS	UCS
TCGA-N6-A4VF	MSS	UCS
TCGA-N6-A4VG	MSS	UCS
TCGA-N7-A4Y0	MSI-H	UCS

TCGA-N7-A4Y5	MSS	UCS
TCGA-N7-A4Y8	MSS	UCS
TCGA-N7-A59B	MSS	UCS
TCGA-N8-A4PI	MSS	UCS
TCGA-N8-A4PL	MSS	UCS
TCGA-N8-A4PM	MSS	UCS
TCGA-N8-A4PN	MSS	UCS
TCGA-N8-A4PO	MSS	UCS
TCGA-N8-A4PP	MSS	UCS
TCGA-N8-A4PQ	MSS	UCS
TCGA-N8-A56S	MSS	UCS
TCGA-N9-A4PZ	MSS	UCS
TCGA-N9-A4Q1	MSS	UCS
TCGA-N9-A4Q3	MSS	UCS
TCGA-N9-A4Q4	MSS	UCS
TCGA-N9-A4Q7	MSS	UCS
TCGA-N9-A4Q8	MSS	UCS
TCGA-NA-A4QV	MSS	UCS
TCGA-NA-A4QW	MSS	UCS
TCGA-NA-A4QX	MSS	UCS
TCGA-NA-A4QY	MSS	UCS
TCGA-NA-A4R0	MSS	UCS
TCGA-NA-A4R1	Intermediate	UCS
TCGA-NA-A5I1	MSS	UCS
TCGA-NC-A5HD	MSS	LUSC
TCGA-NC-A5HE	MSS	LUSC
TCGA-NC-A5HF	MSS	LUSC
TCGA-NC-A5HG	MSS	LUSC
TCGA-NC-A5HH	MSS	LUSC
TCGA-NC-A5HI	MSS	LUSC
TCGA-NC-A5HJ	MSS	LUSC
TCGA-NC-A5HK	MSS	LUSC
TCGA-NC-A5HL	MSS	LUSC
TCGA-NC-A5HM	MSS	LUSC
TCGA-NC-A5HN	MSS	LUSC
TCGA-NC-A5HO	MSS	LUSC
TCGA-NC-A5HP	MSS	LUSC
TCGA-NC-A5HQ	MSS	LUSC
TCGA-NC-A5HR	MSS	LUSC
TCGA-NC-A5HT	MSS	LUSC
TCGA-ND-A4W6	MSS	UCS
TCGA-ND-A4WA	MSS	UCS
TCGA-ND-A4WC	MSS	UCS
TCGA-ND-A4WF	MSS	UCS
TCGA-NF-A4WU	MSS	UCS
TCGA-NF-A4WX	MSS	UCS
TCGA-NF-A4X2	MSS	UCS
TCGA-NF-A5CP	MSS	UCS
TCGA-NG-A4VU	MSS	UCS
TCGA-NG-A4VW	MSS	UCS
TCGA-NH-A50U	MSS	COAD
TCGA-NH-A5IV	MSI-H	COAD

TCGA-NH-A6GA	MSS	COAD
TCGA-NH-A6GB	MSS	COAD
TCGA-NH-A6GC	MSS	COAD
TCGA-NH-A8F7	MSS	COAD
TCGA-NH-A8F7	MSS	COAD
TCGA-NH-A8F8	MSS	COAD
TCGA-NI-A8LF	MSS	LIHC
TCGA-NJ-A4YF	MSS	LUAD
TCGA-NJ-A4YG	MSS	LUAD
TCGA-NJ-A4YI	MSS	LUAD
TCGA-NJ-A4YP	MSS	LUAD
TCGA-NJ-A4YQ	MSS	LUAD
TCGA-NJ-A55A	MSS	LUAD
TCGA-NJ-A55O	MSS	LUAD
TCGA-NJ-A55R	MSS	LUAD
TCGA-NJ-A7XG	MSS	LUAD
TCGA-NK-A5CR	MSS	LUSC
TCGA-NK-A5CT	MSS	LUSC
TCGA-NK-A5CX	MSS	LUSC
TCGA-NK-A5D1	MSS	LUSC
TCGA-NK-A7XE	MSS	LUSC
TCGA-NQ-A57I	MSS	MESO
TCGA-NQ-A638	MSS	MESO
TCGA-O1-A52J	MSS	LUAD
TCGA-O2-A52N	MSS	LUSC
TCGA-O2-A52Q	MSS	LUSC
TCGA-O2-A52S	MSS	LUSC
TCGA-O2-A52V	MSS	LUSC
TCGA-O2-A5IB	MSS	LUSC
TCGA-O8-A75V	MSS	LIHC
TCGA-O9-A75Z	MSS	KIRP
TCGA-OD-A75X	MSS	SKCM
TCGA-OE-A75W	MSS	PAAD
TCGA-OL-A5RZ	MSS	BRCA
TCGA-OL-A66H	MSS	BRCA
TCGA-OL-A66I	MSS	BRCA
TCGA-OL-A66J	MSS	BRCA
TCGA-OL-A66K	MSS	BRCA
TCGA-OL-A66L	MSS	BRCA
TCGA-OL-A66N	MSS	BRCA
TCGA-OL-A66O	MSS	BRCA
TCGA-OL-A66P	MSS	BRCA
TCGA-OL-A6VO	MSS	BRCA
TCGA-OL-A6VQ	MSS	BRCA
TCGA-OL-A6VR	MSS	BRCA
TCGA-OL-A97C	MSS	BRCA
TCGA-OX-A56R	MSS	GBM
TCGA-OY-A56P	MSS	OV
TCGA-OY-A56Q	MSS	OV
TCGA-P3-A5Q5	MSS	HNSC
TCGA-P3-A5Q6	MSS	HNSC
TCGA-P3-A5QA	MSS	HNSC

TCGA-P3-A5QE	MSS	HNSC
TCGA-P3-A5QF	MSS	HNSC
TCGA-P3-A6SW	MSS	HNSC
TCGA-P3-A6SX	MSS	HNSC
TCGA-P3-A6T0	MSS	HNSC
TCGA-P3-A6T2	MSS	HNSC
TCGA-P3-A6T3	MSS	HNSC
TCGA-P3-A6T4	MSS	HNSC
TCGA-P3-A6T5	MSS	HNSC
TCGA-P3-A6T6	MSS	HNSC
TCGA-P3-A6T7	MSS	HNSC
TCGA-P3-A6T8	MSS	HNSC
TCGA-P4-AAVK	MSS	KIRP
TCGA-P4-AAVL	MSS	KIRP
TCGA-P4-AAVM	MSS	KIRP
TCGA-P4-AAVO	MSS	KIRP
TCGA-P5-A5ET	MSS	LGG
TCGA-P5-A5EU	MSS	LGG
TCGA-P5-A5EV	MSS	LGG
TCGA-P5-A5EW	MSS	LGG
TCGA-P5-A5EX	MSS	LGG
TCGA-P5-A5EY	MSS	LGG
TCGA-P5-A5EZ	MSS	LGG
TCGA-P5-A5F0	MSS	LGG
TCGA-P5-A5F1	MSS	LGG
TCGA-P5-A5F2	MSS	LGG
TCGA-P5-A5F4	MSS	LGG
TCGA-P5-A5F6	MSS	LGG
TCGA-P5-A72U	MSS	LGG
TCGA-P5-A72W	MSS	LGG
TCGA-P5-A72X	MSS	LGG
TCGA-P5-A72Z	MSS	LGG
TCGA-P5-A730	MSS	LGG
TCGA-P5-A731	MSS	LGG
TCGA-P5-A733	MSS	LGG
TCGA-P5-A735	MSS	LGG
TCGA-P5-A736	MSS	LGG
TCGA-P5-A737	MSS	LGG
TCGA-P5-A77W	MSS	LGG
TCGA-P5-A77X	MSS	LGG
TCGA-P5-A780	MSS	LGG
TCGA-P5-A781	MSS	LGG
TCGA-P7-A5NX	MSS	PCPG
TCGA-P7-A5NY	MSS	PCPG
TCGA-P7-A5NY	MSS	PCPG
TCGA-P8-A5KC	MSS	PCPG
TCGA-P8-A5KD	MSS	PCPG
TCGA-P8-A6RX	MSS	PCPG
TCGA-P8-A6RY	MSS	PCPG
TCGA-PC-A5DK	MSS	SARC
TCGA-PC-A5DL	MSS	SARC
TCGA-PC-A5DM	MSS	SARC

TCGA-PC-A5DN	MSS	SARC
TCGA-PC-A5DP	MSS	SARC
TCGA-PE-A5DD	MSS	BRCA
TCGA-PG-A5BC	MSS	UCEC
TCGA-PG-A6IB	MSI-H	UCEC
TCGA-PG-A7D5	MSS	UCEC
TCGA-PG-A914	MSS	UCEC
TCGA-PG-A915	MSS	UCEC
TCGA-PG-A916	MSS	UCEC
TCGA-PG-A917	MSI-H	UCEC
TCGA-PJ-A8JU	MSS	KIRP
TCGA-PL-A8LV	MSS	BRCA
TCGA-PL-A8LX	MSS	BRCA
TCGA-PL-A8LY	MSS	BRCA
TCGA-PL-A8LZ	MSS	BRCA
TCGA-PN-A8MA	MSS	CESC
TCGA-PQ-A6FI	MSS	BLCA
TCGA-PQ-A6FN	MSS	BLCA
TCGA-PR-A5PF	MSS	PCPG
TCGA-PR-A5PG	MSS	PCPG
TCGA-PR-A5PH	MSS	PCPG
TCGA-PZ-A5RE	MSS	PAAD
TCGA-Q1-A6DT	MSS	CESC
TCGA-Q1-A6DV	MSS	CESC
TCGA-Q1-A6DW	MSS	CESC
TCGA-Q1-A73O	MSS	CESC
TCGA-Q1-A73P	MSS	CESC
TCGA-Q1-A73Q	MSS	CESC
TCGA-Q1-A73R	MSS	CESC
TCGA-Q1-A73S	MSS	CESC
TCGA-Q3-A5QY	MSS	PAAD
TCGA-Q3-AA2A	MSS	PAAD
TCGA-Q9-A6FU	MSS	ESCA
TCGA-Q9-A6FW	MSS	ESCA
TCGA-QA-A7B7	MSS	LIHC
TCGA-QB-A6FS	MSS	SKCM
TCGA-QB-AA9O	MSS	SKCM
TCGA-QC-A6FX	MSS	SARC
TCGA-QC-A7B5	MSS	SARC
TCGA-QC-AA9N	MSS	SARC
TCGA-QD-A8IV	MSS	THCA
TCGA-QF-A5YS	MSS	UCEC
TCGA-QF-A5YT	MSS	UCEC
TCGA-QG-A5Z2	MSI-H	COAD
TCGA-QH-A65R	MSS	LGG
TCGA-QH-A65S	MSS	LGG
TCGA-QH-A65V	MSS	LGG
TCGA-QH-A65X	MSS	LGG
TCGA-QH-A65Z	MSS	LGG
TCGA-QH-A6CS	MSS	LGG
TCGA-QH-A6CU	MSS	LGG
TCGA-QH-A6CV	MSS	LGG

TCGA-QH-A6CW	MSS	LGG
TCGA-QH-A6CX	MSS	LGG
TCGA-QH-A6CY	MSS	LGG
TCGA-QH-A6CZ	MSS	LGG
TCGA-QH-A6X3	MSS	LGG
TCGA-QH-A6X4	MSS	LGG
TCGA-QH-A6X5	MSS	LGG
TCGA-QH-A6X8	MSS	LGG
TCGA-QH-A6X9	MSS	LGG
TCGA-QH-A6XA	MSS	LGG
TCGA-QH-A6XC	MSS	LGG
TCGA-QH-A86X	MSS	LGG
TCGA-QH-A870	MSS	LGG
TCGA-QK-A64Z	MSS	HNSC
TCGA-QK-A652	MSS	HNSC
TCGA-QK-A6IF	MSS	HNSC
TCGA-QK-A6IG	MSS	HNSC
TCGA-QK-A6IH	MSS	HNSC
TCGA-QK-A6II	MSS	HNSC
TCGA-QK-A6IJ	MSS	HNSC
TCGA-QK-A6V9	MSS	HNSC
TCGA-QK-A6VB	MSI-H	HNSC
TCGA-QK-A6VC	MSS	HNSC
TCGA-QK-A8Z7	MSS	HNSC
TCGA-QK-A8Z8	MSS	HNSC
TCGA-QK-A8Z9	MSS	HNSC
TCGA-QK-A8ZA	MSS	HNSC
TCGA-QK-A8ZB	MSS	HNSC
TCGA-QK-AA3J	MSS	HNSC
TCGA-QK-AA3K	MSS	HNSC
TCGA-QL-A97D	MSS	COAD
TCGA-QM-A5NM	MSS	UCS
TCGA-QN-A5NN	MSS	UCS
TCGA-QQ-A5V2	MSS	SARC
TCGA-QQ-A5V9	MSS	SARC
TCGA-QQ-A5VA	MSS	SARC
TCGA-QQ-A5VB	MSS	SARC
TCGA-QQ-A5VC	MSS	SARC
TCGA-QQ-A5VD	MSS	SARC
TCGA-QQ-A8VB	MSS	SARC
TCGA-QQ-A8VD	MSS	SARC
TCGA-QQ-A8VF	MSI-H	SARC
TCGA-QQ-A8VG	MSS	SARC
TCGA-QQ-A8VH	MSS	SARC
TCGA-QR-A6GO	MSS	PCPG
TCGA-QR-A6GR	MSS	PCPG
TCGA-QR-A6GS	MSS	PCPG
TCGA-QR-A6GT	MSS	PCPG
TCGA-QR-A6GU	MSS	PCPG
TCGA-QR-A6GW	MSS	PCPG
TCGA-QR-A6GX	MSS	PCPG
TCGA-QR-A6GY	MSS	PCPG

TCGA-QR-A6GZ	MSS	PCPG
TCGA-QR-A6GZ	MSS	PCPG
TCGA-QR-A6H0	MSS	PCPG
TCGA-QR-A6H1	MSS	PCPG
TCGA-QR-A6H2	MSS	PCPG
TCGA-QR-A6H3	MSS	PCPG
TCGA-QR-A6H4	MSS	PCPG
TCGA-QR-A6H5	MSS	PCPG
TCGA-QR-A6H6	MSS	PCPG
TCGA-QR-A6ZZ	MSS	PCPG
TCGA-QR-A700	MSS	PCPG
TCGA-QR-A702	MSS	PCPG
TCGA-QR-A703	MSS	PCPG
TCGA-QR-A705	MSS	PCPG
TCGA-QR-A706	MSS	PCPG
TCGA-QR-A707	MSS	PCPG
TCGA-QR-A708	MSS	PCPG
TCGA-QR-A70A	MSS	PCPG
TCGA-QR-A70C	MSS	PCPG
TCGA-QR-A70D	MSS	PCPG
TCGA-QR-A70E	MSS	PCPG
TCGA-QR-A70G	MSS	PCPG
TCGA-QR-A70H	MSS	PCPG
TCGA-QR-A70I	MSS	PCPG
TCGA-QR-A70J	MSS	PCPG
TCGA-QR-A70K	MSS	PCPG
TCGA-QR-A70M	MSS	PCPG
TCGA-QR-A70N	MSS	PCPG
TCGA-QR-A70O	MSS	PCPG
TCGA-QR-A70P	MSS	PCPG
TCGA-QR-A70Q	MSS	PCPG
TCGA-QR-A70R	MSS	PCPG
TCGA-QR-A70T	MSS	PCPG
TCGA-QR-A70U	MSS	PCPG
TCGA-QR-A70V	MSS	PCPG
TCGA-QR-A70W	MSS	PCPG
TCGA-QR-A70X	MSS	PCPG
TCGA-QR-A7IN	MSS	PCPG
TCGA-QR-A7IP	MSS	PCPG
TCGA-QS-A5YR	MSI-H	UCEC
TCGA-QS-A744	MSS	UCEC
TCGA-QS-A8F1	MSS	UCEC
TCGA-QT-A5XJ	MSS	PCPG
TCGA-QT-A5XK	MSS	PCPG
TCGA-QT-A5XL	MSS	PCPG
TCGA-QT-A5XM	MSS	PCPG
TCGA-QT-A5XN	MSS	PCPG
TCGA-QT-A5XO	MSS	PCPG
TCGA-QT-A5XP	MSS	PCPG
TCGA-QT-A69Q	MSS	PCPG
TCGA-QT-A7U0	MSS	PCPG
TCGA-QU-A6IL	MSS	PRAD

TCGA-QU-A6IM	MSS	PRAD
TCGA-QU-A6IN	MSS	PRAD
TCGA-QU-A6IO	MSS	PRAD
TCGA-QU-A6IP	MSS	PRAD
TCGA-R2-A69V	MSS	CESC
TCGA-R3-A69X	MSS	BLCA
TCGA-R5-A7O7	MSS	STAD
TCGA-R5-A7ZE	MSS	STAD
TCGA-R5-A7ZF	MSS	STAD
TCGA-R5-A7ZI	MSI-H	STAD
TCGA-R5-A7ZR	MSS	STAD
TCGA-R5-A804	MSS	STAD
TCGA-R5-A805	MSS	STAD
TCGA-R6-A6DN	MSS	ESCA
TCGA-R6-A6DQ	MSS	ESCA
TCGA-R6-A6KZ	MSS	ESCA
TCGA-R6-A6L4	MSS	ESCA
TCGA-R6-A6L6	MSS	ESCA
TCGA-R6-A6XG	MSS	ESCA
TCGA-R6-A6Y0	MSS	ESCA
TCGA-R6-A6Y2	MSS	ESCA
TCGA-R6-A8W5	MSS	ESCA
TCGA-R6-A8W8	MSS	ESCA
TCGA-R6-A8WC	MSS	ESCA
TCGA-R6-A8WG	MSS	ESCA
TCGA-R8-A6MK	MSS	LGG
TCGA-R8-A6ML	MSS	LGG
TCGA-R8-A6MO	MSS	LGG
TCGA-R8-A6YH	MSS	LGG
TCGA-R8-A73M	MSS	LGG
TCGA-RA-A741	MSS	CESC
TCGA-RB-A7B8	MSS	PAAD
TCGA-RB-AA9M	MSS	PAAD
TCGA-RC-A6M3	MSS	LIHC
TCGA-RC-A6M4	MSS	LIHC
TCGA-RC-A6M5	MSS	LIHC
TCGA-RC-A6M6	MSS	LIHC
TCGA-RC-A7S9	MSS	LIHC
TCGA-RC-A7SB	MSS	LIHC
TCGA-RC-A7SF	MSS	LIHC
TCGA-RC-A7SH	MSS	LIHC
TCGA-RC-A7SK	MSS	LIHC
TCGA-RD-A7BS	MSS	STAD
TCGA-RD-A7BT	MSS	STAD
TCGA-RD-A7BW	MSS	STAD
TCGA-RD-A7C1	MSS	STAD
TCGA-RD-A8MV	MSS	STAD
TCGA-RD-A8MW	MSS	STAD
TCGA-RD-A8N0	MSS	STAD
TCGA-RD-A8N1	MSS	STAD
TCGA-RD-A8N2	MSS	STAD
TCGA-RD-A8N4	MSS	STAD

TCGA-RD-A8N5	MSS	STAD
TCGA-RD-A8N6	MSS	STAD
TCGA-RD-A8N9	MSS	STAD
TCGA-RD-A8NB	MSI-H	STAD
TCGA-RE-A7BO	MSS	ESCA
TCGA-RG-A7D4	MSS	LIHC
TCGA-RL-AAAS	MSS	PAAD
TCGA-RM-A68T	MSS	PCPG
TCGA-RM-A68W	MSS	PCPG
TCGA-RN-A68Q	MSS	SARC
TCGA-RN-AAAQ	MSS	SARC
TCGA-RP-A690	MSS	SKCM
TCGA-RP-A693	MSS	SKCM
TCGA-RP-A694	MSS	SKCM
TCGA-RP-A695	MSS	SKCM
TCGA-RP-A6K9	MSS	SKCM
TCGA-RQ-A68N	MSS	DLBC
TCGA-RQ-A6JB	MSS	DLBC
TCGA-RQ-AAAT	MSS	DLBC
TCGA-RR-A6KA	MSS	GBM
TCGA-RR-A6KB	MSS	GBM
TCGA-RR-A6KC	MSS	GBM
TCGA-RS-A6TO	MSS	HNSC
TCGA-RS-A6TP	MSS	HNSC
TCGA-RT-A6Y9	MSS	PCPG
TCGA-RT-A6YA	MSS	PCPG
TCGA-RT-A6YC	MSS	PCPG
TCGA-RU-A8FL	MSS	COAD
TCGA-RW-A67V	MSS	PCPG
TCGA-RW-A67W	MSS	PCPG
TCGA-RW-A67X	MSS	PCPG
TCGA-RW-A67Y	MSS	PCPG
TCGA-RW-A680	MSS	PCPG
TCGA-RW-A681	MSS	PCPG
TCGA-RW-A684	MSS	PCPG
TCGA-RW-A685	MSS	PCPG
TCGA-RW-A686	MSS	PCPG
TCGA-RW-A686	MSS	PCPG
TCGA-RW-A688	MSS	PCPG
TCGA-RW-A689	MSS	PCPG
TCGA-RW-A68A	MSS	PCPG
TCGA-RW-A68B	MSS	PCPG
TCGA-RW-A68C	MSS	PCPG
TCGA-RW-A68D	MSS	PCPG
TCGA-RW-A68F	MSS	PCPG
TCGA-RW-A68G	MSS	PCPG
TCGA-RW-A7CZ	MSS	PCPG
TCGA-RW-A7D0	MSS	PCPG
TCGA-RW-A8AZ	MSS	PCPG
TCGA-RX-A8JQ	MSS	PCPG
TCGA-RY-A83X	MSS	LGG
TCGA-RY-A83Y	MSS	LGG

TCGA-RY-A83Z	MSS	LGG
TCGA-RY-A840	MSS	LGG
TCGA-RY-A843	MSS	LGG
TCGA-RY-A845	MSS	LGG
TCGA-RY-A847	MSS	LGG
TCGA-RZ-AB0B	MSS	UVM
TCGA-S2-AA1A	MSS	LUAD
TCGA-S3-A6ZF	MSS	BRCA
TCGA-S3-A6ZG	MSS	BRCA
TCGA-S3-A6ZH	MSS	BRCA
TCGA-S3-AA0Z	MSS	BRCA
TCGA-S3-AA10	MSS	BRCA
TCGA-S3-AA11	MSS	BRCA
TCGA-S3-AA12	MSS	BRCA
TCGA-S3-AA14	MSS	BRCA
TCGA-S3-AA15	MSS	BRCA
TCGA-S3-AA17	MSS	BRCA
TCGA-S4-A8RM	MSS	PAAD
TCGA-S4-A8RO	MSS	PAAD
TCGA-S4-A8RP	MSS	PAAD
TCGA-S5-A6DX	MSS	BLCA
TCGA-S5-AA26	MSS	BLCA
TCGA-S6-A8JW	MSS	TGCT
TCGA-S6-A8JX	MSS	TGCT
TCGA-S6-A8JY	MSS	TGCT
TCGA-S7-A7WL	MSS	PCPG
TCGA-S7-A7WM	MSS	PCPG
TCGA-S7-A7WN	MSS	PCPG
TCGA-S7-A7WO	MSS	PCPG
TCGA-S7-A7WP	MSS	PCPG
TCGA-S7-A7WQ	MSS	PCPG
TCGA-S7-A7WR	MSS	PCPG
TCGA-S7-A7WT	MSS	PCPG
TCGA-S7-A7WU	MSS	PCPG
TCGA-S7-A7WV	MSS	PCPG
TCGA-S7-A7WW	MSS	PCPG
TCGA-S7-A7WX	MSS	PCPG
TCGA-S7-A7X0	MSS	PCPG
TCGA-S7-A7X1	MSS	PCPG
TCGA-S7-A7X2	MSS	PCPG
TCGA-S8-A6BV	MSS	ESCA
TCGA-S8-A6BW	MSS	ESCA
TCGA-S9-A6TS	MSS	LGG
TCGA-S9-A6TU	MSS	LGG
TCGA-S9-A6TV	MSS	LGG
TCGA-S9-A6TW	MSS	LGG
TCGA-S9-A6TX	MSS	LGG
TCGA-S9-A6TY	MSS	LGG
TCGA-S9-A6TZ	MSS	LGG
TCGA-S9-A6U0	MSS	LGG
TCGA-S9-A6U1	MSS	LGG
TCGA-S9-A6U2	MSS	LGG

TCGA-S9-A6U5	MSS	LGG
TCGA-S9-A6U6	MSS	LGG
TCGA-S9-A6U8	MSS	LGG
TCGA-S9-A6U9	MSS	LGG
TCGA-S9-A6UA	MSS	LGG
TCGA-S9-A6UB	MSS	LGG
TCGA-S9-A6WE	MSS	LGG
TCGA-S9-A6WG	MSS	LGG
TCGA-S9-A6WH	MSS	LGG
TCGA-S9-A6WI	MSS	LGG
TCGA-S9-A6WL	MSS	LGG
TCGA-S9-A6WM	MSS	LGG
TCGA-S9-A6WN	MSS	LGG
TCGA-S9-A6WO	MSS	LGG
TCGA-S9-A6WP	MSS	LGG
TCGA-S9-A6WQ	MSS	LGG
TCGA-S9-A7IQ	MSS	LGG
TCGA-S9-A7IS	MSS	LGG
TCGA-S9-A7IX	MSS	LGG
TCGA-S9-A7IY	MSS	LGG
TCGA-S9-A7IZ	MSS	LGG
TCGA-S9-A7J0	MSS	LGG
TCGA-S9-A7J1	MSS	LGG
TCGA-S9-A7J2	MSS	LGG
TCGA-S9-A7J3	MSS	LGG
TCGA-S9-A7QW	MSS	LGG
TCGA-S9-A7QX	MSS	LGG
TCGA-S9-A7QY	MSS	LGG
TCGA-S9-A7QZ	MSS	LGG
TCGA-S9-A7R1	MSS	LGG
TCGA-S9-A7R2	MSS	LGG
TCGA-S9-A7R3	MSS	LGG
TCGA-S9-A7R4	MSS	LGG
TCGA-S9-A7R7	MSS	LGG
TCGA-S9-A7R8	MSS	LGG
TCGA-S9-A89V	MSS	LGG
TCGA-S9-A89Z	MSS	LGG
TCGA-SA-A6C2	MSS	PCPG
TCGA-SB-A6J6	MSS	TGCT
TCGA-SB-A76C	MSS	TGCT
TCGA-SC-A6LM	MSS	MESO
TCGA-SC-A6LN	MSS	MESO
TCGA-SC-A6LP	MSS	MESO
TCGA-SC-A6LQ	MSS	MESO
TCGA-SC-A6LR	MSS	MESO
TCGA-SC-AA5Z	MSS	MESO
TCGA-SG-A6Z4	MSS	SARC
TCGA-SG-A6Z7	MSS	SARC
TCGA-SG-A849	MSS	SARC
TCGA-SH-A7BC	MSS	MESO
TCGA-SH-A7BD	MSS	MESO
TCGA-SH-A7BH	MSS	MESO

TCGA-SI-A71O	MSS	SARC
TCGA-SI-A71O	MSS	SARC
TCGA-SI-A71P	MSS	SARC
TCGA-SI-A71Q	MSS	SARC
TCGA-SI-AA8B	MSS	SARC
TCGA-SI-AA8C	MSS	SARC
TCGA-SJ-A6ZI	MSI-H	UCEC
TCGA-SJ-A6ZJ	MSS	UCEC
TCGA-SL-A6J9	MSS	UCEC
TCGA-SL-A6JA	MSI-H	UCEC
TCGA-SN-A6IS	MSS	TGCT
TCGA-SN-A84W	MSS	TGCT
TCGA-SN-A84X	MSS	TGCT
TCGA-SN-A84Y	MSS	TGCT
TCGA-SO-A8JP	MSS	TGCT
TCGA-SP-A6QC	MSS	PCPG
TCGA-SP-A6QD	MSS	PCPG
TCGA-SP-A6QF	MSS	PCPG
TCGA-SP-A6QG	MSS	PCPG
TCGA-SP-A6QH	MSS	PCPG
TCGA-SP-A6QI	MSS	PCPG
TCGA-SP-A6QJ	MSS	PCPG
TCGA-SP-A6QK	MSS	PCPG
TCGA-SQ-A6I4	MSS	PCPG
TCGA-SQ-A6I6	MSS	PCPG
TCGA-SR-A6MP	MSS	PCPG
TCGA-SR-A6MQ	MSS	PCPG
TCGA-SR-A6MR	MSS	PCPG
TCGA-SR-A6MS	MSS	PCPG
TCGA-SR-A6MT	MSS	PCPG
TCGA-SR-A6MU	MSS	PCPG
TCGA-SR-A6MV	MSS	PCPG
TCGA-SR-A6MX	MSS	PCPG
TCGA-SR-A6MX	MSS	PCPG
TCGA-SR-A6MX	MSS	PCPG
TCGA-SR-A6MY	MSS	PCPG
TCGA-SR-A6MZ	MSS	PCPG
TCGA-SR-A6N0	MSS	PCPG
TCGA-SS-A7HO	MSS	COAD
TCGA-SU-A7E7	MSS	PRAD
TCGA-SW-A7EA	MSI-H	STAD
TCGA-SW-A7EB	MSS	STAD
TCGA-SX-A71R	MSS	KIRP
TCGA-SX-A71S	MSS	KIRP
TCGA-SX-A71U	MSS	KIRP
TCGA-SX-A71V	MSS	KIRP
TCGA-SX-A71W	MSS	KIRP
TCGA-SX-A7SL	MSS	KIRP
TCGA-SX-A7SM	MSS	KIRP
TCGA-SX-A7SN	MSS	KIRP
TCGA-SX-A7SO	MSS	KIRP
TCGA-SX-A7SP	MSS	KIRP

TCGA-SX-A7SQ	MSS	KIRP
TCGA-SX-A7SR	MSS	KIRP
TCGA-SX-A7SS	MSS	KIRP
TCGA-SX-A7SU	MSS	KIRP
TCGA-SY-A9G0	MSS	BLCA
TCGA-SY-A9G5	MSS	BLCA
TCGA-T1-A6J8	MSS	LIHC
TCGA-T2-A6WX	MSS	HNSC
TCGA-T2-A6WZ	MSS	HNSC
TCGA-T2-A6X0	MSS	HNSC
TCGA-T2-A6X2	MSS	HNSC
TCGA-T3-A92M	MSS	HNSC
TCGA-T3-A92N	MSS	HNSC
TCGA-T7-A92I	MSS	KIRC
TCGA-T9-A92H	MSS	COAD
TCGA-TK-A8OK	MSS	PRAD
TCGA-TM-A7C3	MSS	LGG
TCGA-TM-A7C4	MSS	LGG
TCGA-TM-A7C5	MSS	LGG
TCGA-TM-A7CA	MSS	LGG
TCGA-TM-A7CF	MSS	LGG
TCGA-TM-A7CF	MSS	LGG
TCGA-TM-A84B	MSS	LGG
TCGA-TM-A84C	MSS	LGG
TCGA-TM-A84F	MSS	LGG
TCGA-TM-A84G	MSS	LGG
TCGA-TM-A84H	MSS	LGG
TCGA-TM-A84I	MSS	LGG
TCGA-TM-A84J	MSS	LGG
TCGA-TM-A84L	MSS	LGG
TCGA-TM-A84M	MSS	LGG
TCGA-TM-A84O	MSS	LGG
TCGA-TM-A84Q	MSS	LGG
TCGA-TM-A84R	MSS	LGG
TCGA-TM-A84S	MSS	LGG
TCGA-TM-A84T	MSS	LGG
TCGA-TN-A7HI	MSS	HNSC
TCGA-TN-A7HJ	MSS	HNSC
TCGA-TN-A7HL	MSS	HNSC
TCGA-TP-A8TT	MSS	PRAD
TCGA-TP-A8TV	MSS	PRAD
TCGA-TQ-A7RF	MSS	LGG
TCGA-TQ-A7RG	MSS	LGG
TCGA-TQ-A7RH	MSS	LGG
TCGA-TQ-A7RI	MSS	LGG
TCGA-TQ-A7RJ	MSS	LGG
TCGA-TQ-A7RK	MSS	LGG
TCGA-TQ-A7RK	MSS	LGG
TCGA-TQ-A7RM	MSS	LGG
TCGA-TQ-A7RN	MSS	LGG
TCGA-TQ-A7RO	MSS	LGG
TCGA-TQ-A7RP	MSS	LGG

TCGA-TQ-A7RQ	MSS	LGG
TCGA-TQ-A7RR	MSS	LGG
TCGA-TQ-A7RS	MSS	LGG
TCGA-TQ-A7RU	MSS	LGG
TCGA-TQ-A7RV	MSS	LGG
TCGA-TQ-A7RV	MSS	LGG
TCGA-TQ-A7RW	MSS	LGG
TCGA-TQ-A8XE	MSS	LGG
TCGA-TQ-A8XE	MSS	LGG
TCGA-TS-A7OY	MSS	MESO
TCGA-TS-A7P0	MSS	MESO
TCGA-TS-A7P3	MSS	MESO
TCGA-TS-A7P6	MSS	MESO
TCGA-TS-A7P8	MSS	MESO
TCGA-TS-A7PB	MSS	MESO
TCGA-TS-A8AI	MSS	MESO
TCGA-TS-A8AS	MSS	MESO
TCGA-TS-A8AV	MSS	MESO
TCGA-TS-A8AY	MSS	MESO
TCGA-TT-A6YJ	MSS	PCPG
TCGA-TT-A6YK	MSS	PCPG
TCGA-TT-A6YN	MSS	PCPG
TCGA-TT-A6YO	MSS	PCPG
TCGA-TT-A6YP	MSS	PCPG
TCGA-UB-A7MA	MSS	LIHC
TCGA-UB-A7MB	MSS	LIHC
TCGA-UB-A7MC	MSS	LIHC
TCGA-UB-A7MD	MSS	LIHC
TCGA-UB-A7ME	MSS	LIHC
TCGA-UB-A7MF	MSS	LIHC
TCGA-UB-AA0U	MSS	LIHC
TCGA-UB-AA0V	MSS	LIHC
TCGA-UC-A7PD	MSS	CESC
TCGA-UC-A7PF	MSS	CESC
TCGA-UC-A7PG	MSS	CESC
TCGA-UC-A7PG	MSS	CESC
TCGA-UC-A7PI	MSS	CESC
TCGA-UD-AAC5	MSS	MESO
TCGA-UD-AAC7	MSS	MESO
TCGA-UE-A6QT	MSS	SARC
TCGA-UE-A6QU	MSS	SARC
TCGA-UF-A718	MSS	HNSC
TCGA-UF-A719	MSS	HNSC
TCGA-UF-A71A	MSS	HNSC
TCGA-UF-A71A	MSS	HNSC
TCGA-UF-A71B	MSS	HNSC
TCGA-UF-A71D	MSS	HNSC
TCGA-UF-A71E	MSS	HNSC
TCGA-UF-A7J9	MSS	HNSC
TCGA-UF-A7JA	MSS	HNSC
TCGA-UF-A7JC	MSS	HNSC
TCGA-UF-A7JD	MSS	HNSC

TCGA-UF-A7JF	MSS	HNSC
TCGA-UF-A7JH	MSS	HNSC
TCGA-UF-A7JJ	MSS	HNSC
TCGA-UF-A7JK	MSS	HNSC
TCGA-UF-A7JO	MSS	HNSC
TCGA-UF-A7JS	MSS	HNSC
TCGA-UF-A7JT	MSS	HNSC
TCGA-UF-A7JV	MSS	HNSC
TCGA-UL-AAZ6	MSS	BRCA
TCGA-UN-AAZ9	MSS	KIRP
TCGA-UP-A6WW	MSS	HNSC
TCGA-US-A774	MSS	PAAD
TCGA-US-A776	MSS	PAAD
TCGA-US-A779	MSS	PAAD
TCGA-US-A77E	MSS	PAAD
TCGA-US-A77G	MSS	PAAD
TCGA-US-A77J	MSS	PAAD
TCGA-UT-A88C	MSS	MESO
TCGA-UT-A88D	MSS	MESO
TCGA-UT-A88E	MSS	MESO
TCGA-UT-A88G	MSS	MESO
TCGA-UT-A97Y	MSS	MESO
TCGA-UU-A93S	MSS	BRCA
TCGA-UY-A78K	MSS	BLCA
TCGA-UY-A78L	MSS	BLCA
TCGA-UY-A78M	MSS	BLCA
TCGA-UY-A78N	MSS	BLCA
TCGA-UY-A78O	MSS	BLCA
TCGA-UY-A78P	MSS	BLCA
TCGA-UY-A8OB	MSS	BLCA
TCGA-UY-A8OC	MSS	BLCA
TCGA-UY-A8OD	MSS	BLCA
TCGA-UY-A9PA	MSS	BLCA
TCGA-UY-A9PB	MSS	BLCA
TCGA-UY-A9PD	MSS	BLCA
TCGA-UY-A9PE	MSS	BLCA
TCGA-UY-A9PF	MSS	BLCA
TCGA-UY-A9PH	MSS	BLCA
TCGA-UZ-A9PJ	MSS	KIRP
TCGA-UZ-A9PK	MSS	KIRP
TCGA-UZ-A9PL	MSS	KIRP
TCGA-UZ-A9PM	MSS	KIRP
TCGA-UZ-A9PN	MSS	KIRP
TCGA-UZ-A9PO	MSS	KIRP
TCGA-UZ-A9PP	MSS	KIRP
TCGA-UZ-A9PQ	MSS	KIRP
TCGA-UZ-A9PR	MSS	KIRP
TCGA-UZ-A9PS	MSS	KIRP
TCGA-UZ-A9PS	MSS	KIRP
TCGA-UZ-A9PU	MSS	KIRP
TCGA-UZ-A9PV	MSS	KIRP
TCGA-UZ-A9PX	MSS	KIRP

TCGA-UZ-A9PZ	MSS	KIRP
TCGA-UZ-A9Q0	MSS	KIRP
TCGA-UZ-A9Q1	MSS	KIRP
TCGA-V1-A8MF	MSS	PRAD
TCGA-V1-A8MG	MSS	PRAD
TCGA-V1-A8MJ	MSS	PRAD
TCGA-V1-A8MK	MSS	PRAD
TCGA-V1-A8ML	MSS	PRAD
TCGA-V1-A8MM	MSS	PRAD
TCGA-V1-A8MU	MSS	PRAD
TCGA-V1-A8WL	MSS	PRAD
TCGA-V1-A8WN	MSS	PRAD
TCGA-V1-A8WS	MSS	PRAD
TCGA-V1-A8WV	MSS	PRAD
TCGA-V1-A8WW	MSS	PRAD
TCGA-V1-A8X3	MSS	PRAD
TCGA-V1-A9O5	MSS	PRAD
TCGA-V1-A9O5	MSS	PRAD
TCGA-V1-A9O7	MSS	PRAD
TCGA-V1-A9O9	MSS	PRAD
TCGA-V1-A9OA	MSS	PRAD
TCGA-V1-A9OF	MSS	PRAD
TCGA-V1-A9OH	MSS	PRAD
TCGA-V1-A9OL	MSS	PRAD
TCGA-V1-A9OQ	MSS	PRAD
TCGA-V1-A9OT	MSS	PRAD
TCGA-V1-A9OX	MSS	PRAD
TCGA-V1-A9OY	MSS	PRAD
TCGA-V1-A9Z7	MSS	PRAD
TCGA-V1-A9Z8	MSS	PRAD
TCGA-V1-A9Z9	MSS	PRAD
TCGA-V1-A9ZG	MSS	PRAD
TCGA-V1-A9ZI	MSS	PRAD
TCGA-V1-A9ZK	MSS	PRAD
TCGA-V1-A9ZR	MSS	PRAD
TCGA-V3-A9ZX	MSS	UVM
TCGA-V3-A9ZY	MSS	UVM
TCGA-V4-A9E5	MSS	UVM
TCGA-V4-A9E7	MSS	UVM
TCGA-V4-A9E8	MSS	UVM
TCGA-V4-A9E9	MSS	UVM
TCGA-V4-A9EA	MSS	UVM
TCGA-V4-A9EC	MSS	UVM
TCGA-V4-A9ED	MSS	UVM
TCGA-V4-A9EE	MSS	UVM
TCGA-V4-A9EF	MSS	UVM
TCGA-V4-A9EH	MSS	UVM
TCGA-V4-A9EI	MSS	UVM
TCGA-V4-A9EJ	MSS	UVM
TCGA-V4-A9EK	MSS	UVM
TCGA-V4-A9EL	MSS	UVM
TCGA-V4-A9EM	MSS	UVM

TCGA-V4-A9EO	MSS	UVM
TCGA-V4-A9EQ	MSS	UVM
TCGA-V4-A9ES	MSS	UVM
TCGA-V4-A9ET	MSS	UVM
TCGA-V4-A9EU	MSS	UVM
TCGA-V4-A9EV	MSS	UVM
TCGA-V4-A9EW	MSS	UVM
TCGA-V4-A9EX	MSS	UVM
TCGA-V4-A9EY	MSS	UVM
TCGA-V4-A9EZ	MSS	UVM
TCGA-V4-A9F0	MSS	UVM
TCGA-V4-A9F1	MSS	UVM
TCGA-V4-A9F2	MSS	UVM
TCGA-V4-A9F3	MSS	UVM
TCGA-V4-A9F4	MSS	UVM
TCGA-V4-A9F5	MSS	UVM
TCGA-V4-A9F7	MSS	UVM
TCGA-V4-A9F8	MSS	UVM
TCGA-V5-A7RB	MSS	ESCA
TCGA-V5-A7RC	MSS	ESCA
TCGA-V5-A7RC	MSS	ESCA
TCGA-V5-A7RE	MSS	ESCA
TCGA-V5-AASV	MSS	ESCA
TCGA-V5-AASW	MSS	ESCA
TCGA-V5-AASX	MSS	ESCA
TCGA-V7-A7HQ	MSS	BRCA
TCGA-V9-A7HT	MSS	KIRP
TCGA-VB-A8QN	MSS	DLBC
TCGA-VD-A8K7	MSS	UVM
TCGA-VD-A8K8	MSS	UVM
TCGA-VD-A8K9	MSS	UVM
TCGA-VD-A8KA	MSS	UVM
TCGA-VD-A8KB	MSS	UVM
TCGA-VD-A8KD	MSS	UVM
TCGA-VD-A8KE	MSS	UVM
TCGA-VD-A8KF	MSS	UVM
TCGA-VD-A8KG	MSS	UVM
TCGA-VD-A8KH	MSS	UVM
TCGA-VD-A8KI	MSS	UVM
TCGA-VD-A8KJ	MSS	UVM
TCGA-VD-A8KK	MSS	UVM
TCGA-VD-A8KL	MSS	UVM
TCGA-VD-A8KM	MSS	UVM
TCGA-VD-A8KN	MSS	UVM
TCGA-VD-A8KO	MSS	UVM
TCGA-VD-AA8M	MSS	UVM
TCGA-VD-AA8N	MSS	UVM
TCGA-VD-AA8O	MSS	UVM
TCGA-VD-AA8P	MSS	UVM
TCGA-VD-AA8Q	MSS	UVM
TCGA-VD-AA8R	MSS	UVM
TCGA-VD-AA8S	MSS	UVM

TCGA-VD-AA8T	MSS	UVM
TCGA-VF-A8A8	MSS	TGCT
TCGA-VF-A8A9	MSS	TGCT
TCGA-VF-A8AA	MSS	TGCT
TCGA-VF-A8AB	MSS	TGCT
TCGA-VF-A8AC	MSS	TGCT
TCGA-VF-A8AD	MSS	TGCT
TCGA-VF-A8AE	MSS	TGCT
TCGA-VG-A8LO	MSS	OV
TCGA-VM-A8C8	MSS	LGG
TCGA-VM-A8C9	MSS	LGG
TCGA-VM-A8CA	MSS	LGG
TCGA-VM-A8CB	MSS	LGG
TCGA-VM-A8CD	MSS	LGG
TCGA-VM-A8CE	MSS	LGG
TCGA-VM-A8CF	MSS	LGG
TCGA-VM-A8CH	MSS	LGG
TCGA-VN-A88I	MSS	PRAD
TCGA-VN-A88K	MSS	PRAD
TCGA-VN-A88L	MSS	PRAD
TCGA-VN-A88M	MSS	PRAD
TCGA-VN-A88N	MSS	PRAD
TCGA-VN-A88O	MSS	PRAD
TCGA-VN-A88P	MSS	PRAD
TCGA-VN-A88Q	MSS	PRAD
TCGA-VN-A88R	MSS	PRAD
TCGA-VN-A943	MSS	PRAD
TCGA-VP-A872	MSS	PRAD
TCGA-VP-A875	MSS	PRAD
TCGA-VP-A876	MSS	PRAD
TCGA-VP-A878	MSS	PRAD
TCGA-VP-A879	MSS	PRAD
TCGA-VP-A87B	MSS	PRAD
TCGA-VP-A87C	MSS	PRAD
TCGA-VP-A87D	MSS	PRAD
TCGA-VP-A87E	MSS	PRAD
TCGA-VP-A87H	MSS	PRAD
TCGA-VP-A87J	MSS	PRAD
TCGA-VP-A87K	MSS	PRAD
TCGA-VP-AA1N	MSS	PRAD
TCGA-VQ-A8DL	MSS	STAD
TCGA-VQ-A8DT	MSS	STAD
TCGA-VQ-A8DU	MSS	STAD
TCGA-VQ-A8DV	MSS	STAD
TCGA-VQ-A8DZ	MSS	STAD
TCGA-VQ-A8E0	MSS	STAD
TCGA-VQ-A8E2	MSS	STAD
TCGA-VQ-A8E3	MSI-H	STAD
TCGA-VQ-A8E7	MSS	STAD
TCGA-VQ-A8P2	MSI-H	STAD
TCGA-VQ-A8P3	MSS	STAD
TCGA-VQ-A8P5	MSS	STAD

TCGA-VQ-A8P8	MSS	STAD
TCGA-VQ-A8PB	MSI-H	STAD
TCGA-VQ-A8PC	MSS	STAD
TCGA-VQ-A8PD	MSS	STAD
TCGA-VQ-A8PE	MSS	STAD
TCGA-VQ-A8PF	MSS	STAD
TCGA-VQ-A8PH	MSS	STAD
TCGA-VQ-A8PJ	MSS	STAD
TCGA-VQ-A8PK	MSS	STAD
TCGA-VQ-A8PM	MSS	STAD
TCGA-VQ-A8PO	MSI-H	STAD
TCGA-VQ-A8PP	MSI-H	STAD
TCGA-VQ-A8PQ	MSS	STAD
TCGA-VQ-A8PS	MSS	STAD
TCGA-VQ-A8PT	MSI-H	STAD
TCGA-VQ-A8PU	MSS	STAD
TCGA-VQ-A8PX	MSI-H	STAD
TCGA-VQ-A8PY	MSS	STAD
TCGA-VQ-A8PZ	MSS	STAD
TCGA-VQ-A91A	MSS	STAD
TCGA-VQ-A91D	MSI-H	STAD
TCGA-VQ-A91E	MSI-H	STAD
TCGA-VQ-A91K	MSI-H	STAD
TCGA-VQ-A91N	MSS	STAD
TCGA-VQ-A91Q	MSS	STAD
TCGA-VQ-A91S	MSS	STAD
TCGA-VQ-A91U	MSS	STAD
TCGA-VQ-A91V	MSS	STAD
TCGA-VQ-A91W	MSS	STAD
TCGA-VQ-A91X	MSS	STAD
TCGA-VQ-A91Y	MSS	STAD
TCGA-VQ-A91Z	MSS	STAD
TCGA-VQ-A922	MSS	STAD
TCGA-VQ-A923	MSS	STAD
TCGA-VQ-A924	MSI-H	STAD
TCGA-VQ-A925	MSS	STAD
TCGA-VQ-A927	MSS	STAD
TCGA-VQ-A928	MSS	STAD
TCGA-VQ-A92D	MSS	STAD
TCGA-VQ-A94O	MSS	STAD
TCGA-VQ-A94P	MSS	STAD
TCGA-VQ-A94R	MSS	STAD
TCGA-VQ-A94T	MSS	STAD
TCGA-VQ-A94U	MSS	STAD
TCGA-VQ-AA64	MSS	STAD
TCGA-VQ-AA68	MSS	STAD
TCGA-VQ-AA69	MSS	STAD
TCGA-VQ-AA6A	MSS	STAD
TCGA-VQ-AA6B	MSS	STAD
TCGA-VQ-AA6D	MSI-H	STAD
TCGA-VQ-AA6F	MSS	STAD
TCGA-VQ-AA6G	MSS	STAD

TCGA-VQ-AA6I	MSS	STAD
TCGA-VQ-AA6J	MSS	STAD
TCGA-VQ-AA6K	MSS	STAD
TCGA-VR-A8EO	MSS	ESCA
TCGA-VR-A8EP	MSS	ESCA
TCGA-VR-A8EQ	MSS	ESCA
TCGA-VR-A8ER	MSS	ESCA
TCGA-VR-A8ET	MSS	ESCA
TCGA-VR-A8EU	MSS	ESCA
TCGA-VR-A8EW	MSS	ESCA
TCGA-VR-A8EX	MSS	ESCA
TCGA-VR-A8EY	MSS	ESCA
TCGA-VR-A8EZ	MSS	ESCA
TCGA-VR-A8Q7	MSS	ESCA
TCGA-VR-AA4D	MSS	ESCA
TCGA-VR-AA4G	MSS	ESCA
TCGA-VR-AA7B	MSS	ESCA
TCGA-VR-AA7D	MSS	ESCA
TCGA-VR-AA7I	MSS	ESCA
TCGA-VS-A8EB	MSS	CESC
TCGA-VS-A8EC	MSS	CESC
TCGA-VS-A8EG	MSS	CESC
TCGA-VS-A8EH	MSS	CESC
TCGA-VS-A8EI	MSS	CESC
TCGA-VS-A8EJ	MSS	CESC
TCGA-VS-A8EK	MSS	CESC
TCGA-VS-A8EL	MSS	CESC
TCGA-VS-A8Q8	MSS	CESC
TCGA-VS-A8Q9	MSS	CESC
TCGA-VS-A8QA	MSS	CESC
TCGA-VS-A8QC	MSS	CESC
TCGA-VS-A8QF	MSS	CESC
TCGA-VS-A8QH	MSS	CESC
TCGA-VS-A8QM	MSS	CESC
TCGA-VS-A94W	MSS	CESC
TCGA-VS-A94X	MSS	CESC
TCGA-VS-A94Y	MSS	CESC
TCGA-VS-A94Z	MSI-H	CESC
TCGA-VS-A950	MSS	CESC
TCGA-VS-A952	MSS	CESC
TCGA-VS-A953	MSS	CESC
TCGA-VS-A954	MSS	CESC
TCGA-VS-A957	MSS	CESC
TCGA-VS-A958	MSS	CESC
TCGA-VS-A959	MSS	CESC
TCGA-VS-A9U5	MSS	CESC
TCGA-VS-A9U6	MSI-H	CESC
TCGA-VS-A9U7	MSS	CESC
TCGA-VS-A9UA	MSS	CESC
TCGA-VS-A9UB	MSS	CESC
TCGA-VS-A9UC	MSS	CESC
TCGA-VS-A9UD	MSS	CESC

TCGA-VS-A9UH	MSS	CESC
TCGA-VS-A9UI	MSS	CESC
TCGA-VS-A9UJ	MSI-H	CESC
TCGA-VS-A9UL	MSS	CESC
TCGA-VS-A9UM	MSS	CESC
TCGA-VS-A9UO	MSS	CESC
TCGA-VS-A9UP	MSS	CESC
TCGA-VS-A9UQ	MSS	CESC
TCGA-VS-A9UR	MSS	CESC
TCGA-VS-A9UT	MSS	CESC
TCGA-VS-A9UU	MSS	CESC
TCGA-VS-A9UV	MSS	CESC
TCGA-VS-A9UY	MSS	CESC
TCGA-VS-A9UZ	MSS	CESC
TCGA-VS-A9V0	MSS	CESC
TCGA-VS-A9V1	MSS	CESC
TCGA-VS-A9V2	MSS	CESC
TCGA-VS-A9V3	MSS	CESC
TCGA-VS-A9V4	MSS	CESC
TCGA-VS-A9V5	MSS	CESC
TCGA-VS-AA62	MSS	CESC
TCGA-VT-A80G	MSS	SARC
TCGA-VT-A80J	MSS	SARC
TCGA-VT-A80J	MSS	SARC
TCGA-VT-AB3D	MSS	SARC
TCGA-VV-A829	MSS	LGG
TCGA-VV-A86M	MSS	LGG
TCGA-VW-A7QS	MSS	LGG
TCGA-VW-A8FI	MSS	LGG
TCGA-W2-A7H5	MSS	PCPG
TCGA-W2-A7H7	MSS	PCPG
TCGA-W2-A7HA	MSS	PCPG
TCGA-W2-A7HB	MSS	PCPG
TCGA-W2-A7HC	MSS	PCPG
TCGA-W2-A7HD	MSS	PCPG
TCGA-W2-A7HE	MSS	PCPG
TCGA-W2-A7HF	MSS	PCPG
TCGA-W2-A7HH	MSS	PCPG
TCGA-W2-A7UY	MSS	PCPG
TCGA-W3-A824	Intermediate	SKCM
TCGA-W3-A825	MSS	SKCM
TCGA-W3-A828	MSS	SKCM
TCGA-W3-AA1O	MSS	SKCM
TCGA-W3-AA1Q	MSS	SKCM
TCGA-W3-AA1R	MSS	SKCM
TCGA-W3-AA1V	MSS	SKCM
TCGA-W3-AA1W	MSS	SKCM
TCGA-W3-AA21	MSS	SKCM
TCGA-W4-A7U2	MSS	TGCT
TCGA-W4-A7U3	MSS	TGCT
TCGA-W4-A7U4	MSS	TGCT
TCGA-W5-AA2G	MSS	CHOL

TCGA-W5-AA2H	MSS	CHOL
TCGA-W5-AA2I	MSS	CHOL
TCGA-W5-AA2J	MSS	CHOL
TCGA-W5-AA2M	MSS	CHOL
TCGA-W5-AA2O	MSS	CHOL
TCGA-W5-AA2Q	MSS	CHOL
TCGA-W5-AA2R	MSS	CHOL
TCGA-W5-AA2T	MSS	CHOL
TCGA-W5-AA2U	MSS	CHOL
TCGA-W5-AA2W	MSS	CHOL
TCGA-W5-AA2X	MSS	CHOL
TCGA-W5-AA2Z	MSS	CHOL
TCGA-W5-AA30	MSS	CHOL
TCGA-W5-AA31	MSS	CHOL
TCGA-W5-AA33	MSS	CHOL
TCGA-W5-AA34	MSS	CHOL
TCGA-W5-AA36	MSS	CHOL
TCGA-W5-AA38	MSS	CHOL
TCGA-W5-AA39	MSS	CHOL
TCGA-W6-AA0S	MSS	CHOL
TCGA-W6-AA0T	MSS	CHOL
TCGA-W7-A93N	MSS	CHOL
TCGA-W7-A93O	MSS	CHOL
TCGA-W7-A93P	MSS	CHOL
TCGA-W8-A86G	MSS	BRCA
TCGA-W9-A837	MSS	LGG
TCGA-WA-A7GZ	MSS	HNSC
TCGA-WA-A7H4	MSS	HNSC
TCGA-WB-A80K	MSS	PCPG
TCGA-WB-A80L	MSS	PCPG
TCGA-WB-A80M	MSS	PCPG
TCGA-WB-A80N	MSS	PCPG
TCGA-WB-A80O	MSS	PCPG
TCGA-WB-A80P	MSS	PCPG
TCGA-WB-A80Q	MSS	PCPG
TCGA-WB-A80V	MSS	PCPG
TCGA-WB-A80Y	MSS	PCPG
TCGA-WB-A814	MSS	PCPG
TCGA-WB-A815	MSS	PCPG
TCGA-WB-A816	MSS	PCPG
TCGA-WB-A817	MSS	PCPG
TCGA-WB-A818	MSS	PCPG
TCGA-WB-A819	MSS	PCPG
TCGA-WB-A81A	MSS	PCPG
TCGA-WB-A81D	MSS	PCPG
TCGA-WB-A81E	MSS	PCPG
TCGA-WB-A81F	MSS	PCPG
TCGA-WB-A81G	MSS	PCPG
TCGA-WB-A81H	MSS	PCPG
TCGA-WB-A81I	MSS	PCPG
TCGA-WB-A81J	MSS	PCPG
TCGA-WB-A81K	MSS	PCPG

TCGA-WB-A81M	MSS	PCPG
TCGA-WB-A81N	MSS	PCPG
TCGA-WB-A81P	MSS	PCPG
TCGA-WB-A81Q	MSS	PCPG
TCGA-WB-A81R	MSS	PCPG
TCGA-WB-A81S	MSS	PCPG
TCGA-WB-A81T	MSS	PCPG
TCGA-WB-A81V	MSS	PCPG
TCGA-WB-A81W	MSS	PCPG
TCGA-WB-A820	MSS	PCPG
TCGA-WB-A821	MSS	PCPG
TCGA-WB-A822	MSS	PCPG
TCGA-WC-A87T	MSS	UVM
TCGA-WC-A87U	MSS	UVM
TCGA-WC-A87W	MSS	UVM
TCGA-WC-A87Y	MSS	UVM
TCGA-WC-A880	MSS	UVM
TCGA-WC-A881	MSS	UVM
TCGA-WC-A882	MSS	UVM
TCGA-WC-A883	MSS	UVM
TCGA-WC-A884	MSS	UVM
TCGA-WC-A885	MSS	UVM
TCGA-WC-A888	MSS	UVM
TCGA-WC-A88A	MSS	UVM
TCGA-WC-AA9A	MSS	UVM
TCGA-WC-AA9E	MSS	UVM
TCGA-WD-A7RX	MSS	CHOL
TCGA-WE-A8K1	MSS	SKCM
TCGA-WE-A8K4	MSS	SKCM
TCGA-WE-A8K5	MSS	SKCM
TCGA-WE-A8K6	MSS	SKCM
TCGA-WE-A8ZM	MSS	SKCM
TCGA-WE-A8ZN	MSS	SKCM
TCGA-WE-A8ZO	MSS	SKCM
TCGA-WE-A8ZQ	MSS	SKCM
TCGA-WE-A8ZR	MSS	SKCM
TCGA-WE-A8ZT	MSS	SKCM
TCGA-WE-A8ZX	MSS	SKCM
TCGA-WE-A8ZY	MSS	SKCM
TCGA-WE-AA9Y	MSS	SKCM
TCGA-WE-AAA0	MSS	SKCM
TCGA-WE-AAA3	MSS	SKCM
TCGA-WE-AAA4	MSS	SKCM
TCGA-WH-A86K	MSS	LGG
TCGA-WJ-A86L	MSS	LIHC
TCGA-WK-A8XQ	MSS	SARC
TCGA-WK-A8XS	MSS	SARC
TCGA-WK-A8XT	MSS	SARC
TCGA-WK-A8XY	MSS	SARC
TCGA-WK-A8XZ	MSS	SARC
TCGA-WK-A8Y0	MSS	SARC
TCGA-WL-A834	MSS	CESC

TCGA-WN-A9G9	MSS	KIRP
TCGA-WN-AB4C	MSS	KIRP
TCGA-WP-A9GB	MSS	SARC
TCGA-WQ-A9G7	MSI-H	LIHC
TCGA-WQ-AB4B	MSS	LIHC
TCGA-WR-A838	MSS	OV
TCGA-WS-AB45	MSI-H	COAD
TCGA-WT-AB41	MSS	BRCA
TCGA-WT-AB44	MSS	BRCA
TCGA-WW-A8ZI	MSS	PRAD
TCGA-WX-AA44	MSS	LIHC
TCGA-WX-AA46	MSS	LIHC
TCGA-WX-AA47	MSS	LIHC
TCGA-WY-A858	MSS	LGG
TCGA-WY-A859	MSS	LGG
TCGA-WY-A85A	MSS	LGG
TCGA-WY-A85B	MSS	LGG
TCGA-WY-A85C	MSS	LGG
TCGA-WY-A85D	MSS	LGG
TCGA-WY-A85E	MSS	LGG
TCGA-WZ-A7V3	MSS	TGCT
TCGA-WZ-A7V4	MSS	TGCT
TCGA-WZ-A7V5	MSS	TGCT
TCGA-WZ-A8D5	MSS	TGCT
TCGA-X2-A95T	MSS	SARC
TCGA-X3-A8G4	MSS	TGCT
TCGA-X4-A8KQ	MSS	PRAD
TCGA-X4-A8KS	MSS	PRAD
TCGA-X6-A7W8	MSS	SARC
TCGA-X6-A7WA	MSS	SARC
TCGA-X6-A7WB	MSS	SARC
TCGA-X6-A7WC	MSS	SARC
TCGA-X6-A7WD	MSS	SARC
TCGA-X6-A8C2	MSS	SARC
TCGA-X6-A8C3	MSS	SARC
TCGA-X6-A8C4	MSS	SARC
TCGA-X6-A8C5	MSS	SARC
TCGA-X6-A8C6	MSS	SARC
TCGA-X6-A8C7	MSS	SARC
TCGA-X7-A8D6	MSS	THYM
TCGA-X7-A8D8	MSS	THYM
TCGA-X7-A8D9	MSS	THYM
TCGA-X7-A8DB	MSS	THYM
TCGA-X7-A8DC	MSS	THYM
TCGA-X7-A8DD	MSS	THYM
TCGA-X7-A8DE	MSS	THYM
TCGA-X7-A8DF	MSS	THYM
TCGA-X7-A8DG	MSS	THYM
TCGA-X7-A8DI	MSS	THYM
TCGA-X7-A8DJ	MSS	THYM
TCGA-X7-A8M0	MSS	THYM
TCGA-X7-A8M1	MSS	THYM

TCGA-X7-A8M3	MSS	THYM
TCGA-X7-A8M4	MSS	THYM
TCGA-X7-A8M5	MSS	THYM
TCGA-X7-A8M6	MSS	THYM
TCGA-X7-A8M7	MSS	THYM
TCGA-X7-A8M8	MSS	THYM
TCGA-X8-AAAR	MSS	ESCA
TCGA-X9-A971	MSS	SARC
TCGA-X9-A973	MSS	SARC
TCGA-XA-A8JR	MSS	PRAD
TCGA-XC-AA0X	MSS	LUSC
TCGA-XD-AAUG	MSS	PAAD
TCGA-XD-AAUH	MSS	PAAD
TCGA-XD-AAUI	MSS	PAAD
TCGA-XD-AAUL	MSS	PAAD
TCGA-XE-A8H1	MSS	TGCT
TCGA-XE-A8H4	MSS	TGCT
TCGA-XE-A8H5	MSS	TGCT
TCGA-XE-A9SE	MSS	TGCT
TCGA-XE-AANI	MSS	TGCT
TCGA-XE-AANJ	MSS	TGCT
TCGA-XE-AANR	MSS	TGCT
TCGA-XE-AANV	MSS	TGCT
TCGA-XE-AAO3	MSS	TGCT
TCGA-XE-AAO4	MSS	TGCT
TCGA-XE-AAO6	MSS	TGCT
TCGA-XE-AAOB	MSS	TGCT
TCGA-XE-AAOC	MSS	TGCT
TCGA-XE-AAOD	MSS	TGCT
TCGA-XE-AAOF	MSS	TGCT
TCGA-XE-AAOJ	MSS	TGCT
TCGA-XE-AAOL	MSS	TGCT
TCGA-XF-A8HB	MSS	BLCA
TCGA-XF-A8HC	MSS	BLCA
TCGA-XF-A8HD	MSS	BLCA
TCGA-XF-A8HE	MSS	BLCA
TCGA-XF-A8HF	MSS	BLCA
TCGA-XF-A8HG	MSS	BLCA
TCGA-XF-A8HH	MSS	BLCA
TCGA-XF-A8HI	MSS	BLCA
TCGA-XF-A9SG	MSS	BLCA
TCGA-XF-A9SH	MSS	BLCA
TCGA-XF-A9SI	MSS	BLCA
TCGA-XF-A9SJ	MSS	BLCA
TCGA-XF-A9SK	MSS	BLCA
TCGA-XF-A9SL	MSS	BLCA
TCGA-XF-A9SM	MSS	BLCA
TCGA-XF-A9SP	MSS	BLCA
TCGA-XF-A9ST	MSS	BLCA
TCGA-XF-A9SU	MSS	BLCA
TCGA-XF-A9SV	MSS	BLCA
TCGA-XF-A9SW	MSS	BLCA

TCGA-XF-A9SX	MSS	BLCA
TCGA-XF-A9SY	MSS	BLCA
TCGA-XF-A9SZ	MSS	BLCA
TCGA-XF-A9T0	MSS	BLCA
TCGA-XF-A9T2	Intermediate	BLCA
TCGA-XF-A9T3	MSS	BLCA
TCGA-XF-A9T4	MSS	BLCA
TCGA-XF-A9T5	MSS	BLCA
TCGA-XF-A9T6	MSS	BLCA
TCGA-XF-A9T8	MSS	BLCA
TCGA-XF-AAME	MSS	BLCA
TCGA-XF-AAMF	MSS	BLCA
TCGA-XF-AAMG	MSS	BLCA
TCGA-XF-AAMH	MSS	BLCA
TCGA-XF-AAMJ	MSS	BLCA
TCGA-XF-AAML	MSS	BLCA
TCGA-XF-AAMQ	MSS	BLCA
TCGA-XF-AAMR	MSS	BLCA
TCGA-XF-AAMT	MSS	BLCA
TCGA-XF-AAMW	MSS	BLCA
TCGA-XF-AAMX	MSS	BLCA
TCGA-XF-AAMY	MSS	BLCA
TCGA-XF-AAMZ	MSS	BLCA
TCGA-XF-AAN0	MSS	BLCA
TCGA-XF-AAN1	MSS	BLCA
TCGA-XF-AAN2	MSS	BLCA
TCGA-XF-AAN3	MSS	BLCA
TCGA-XF-AAN4	MSS	BLCA
TCGA-XF-AAN5	MSS	BLCA
TCGA-XF-AAN7	MSS	BLCA
TCGA-XF-AAN8	MSS	BLCA
TCGA-XG-A823	MSS	PCPG
TCGA-XH-A853	MSS	THYM
TCGA-XJ-A83F	MSS	PRAD
TCGA-XJ-A83G	MSS	PRAD
TCGA-XJ-A83H	MSS	PRAD
TCGA-XJ-A9DI	MSS	PRAD
TCGA-XJ-A9DK	MSS	PRAD
TCGA-XJ-A9DQ	MSS	PRAD
TCGA-XJ-A9DX	MSS	PRAD
TCGA-XK-AAIR	MSS	PRAD
TCGA-XK-AAIV	MSS	PRAD
TCGA-XK-AAIW	MSI-H	PRAD
TCGA-XK-AAJ3	MSS	PRAD
TCGA-XK-AAJA	MSS	PRAD
TCGA-XK-AAJP	MSS	PRAD
TCGA-XK-AAJR	MSS	PRAD
TCGA-XK-AAJT	MSS	PRAD
TCGA-XK-AAJU	MSS	PRAD
TCGA-XK-AAK1	MSS	PRAD
TCGA-XM-A8R8	MSS	THYM
TCGA-XM-A8R9	MSS	THYM

TCGA-XM-A8RB	MSS	THYM
TCGA-XM-A8RC	MSS	THYM
TCGA-XM-A8RD	MSS	THYM
TCGA-XM-A8RE	MSS	THYM
TCGA-XM-A8RF	MSS	THYM
TCGA-XM-A8RG	MSS	THYM
TCGA-XM-A8RH	MSS	THYM
TCGA-XM-A8RI	MSS	THYM
TCGA-XM-A8RL	MSS	THYM
TCGA-XM-AAZ1	MSS	THYM
TCGA-XM-AAZ2	MSS	THYM
TCGA-XN-A8T3	MSS	PAAD
TCGA-XN-A8T5	MSS	PAAD
TCGA-XP-A8T6	MSS	ESCA
TCGA-XP-A8T7	MSS	ESCA
TCGA-XP-A8T8	MSS	ESCA
TCGA-XQ-A8TA	MSS	PRAD
TCGA-XQ-A8TB	MSS	PRAD
TCGA-XR-A8TC	MSS	LIHC
TCGA-XR-A8TD	MSS	LIHC
TCGA-XR-A8TE	MSS	LIHC
TCGA-XR-A8TF	MSS	LIHC
TCGA-XR-A8TG	MSS	LIHC
TCGA-XS-A8TJ	MSS	CESC
TCGA-XT-AASU	MSS	MESO
TCGA-XU-A92O	MSS	THYM
TCGA-XU-A92Q	MSS	THYM
TCGA-XU-A92R	MSS	THYM
TCGA-XU-A92T	MSS	THYM
TCGA-XU-A92U	MSS	THYM
TCGA-XU-A92V	MSS	THYM
TCGA-XU-A92W	MSS	THYM
TCGA-XU-A92X	MSS	THYM
TCGA-XU-A92Y	MSS	THYM
TCGA-XU-A92Z	MSS	THYM
TCGA-XU-A931	MSS	THYM
TCGA-XU-A932	MSS	THYM
TCGA-XU-A933	MSS	THYM
TCGA-XU-A936	MSS	THYM
TCGA-XU-AAXW	MSS	THYM
TCGA-XU-AAXX	MSS	THYM
TCGA-XU-AAXY	MSS	THYM
TCGA-XU-AAXZ	MSS	THYM
TCGA-XU-AAY0	MSS	THYM
TCGA-XV-A9VZ	MSS	SKCM
TCGA-XV-A9W2	MSS	SKCM
TCGA-XV-A9W5	MSS	SKCM
TCGA-XV-AAZV	MSS	SKCM
TCGA-XV-AAZW	MSS	SKCM
TCGA-XV-AAZY	MSS	SKCM
TCGA-XV-AB01	MSS	SKCM
TCGA-XX-A899	MSS	BRCA

TCGA-XX-A89A	MSS	BRCA
TCGA-XY-A89B	MSS	TGCT
TCGA-XY-A8S2	MSS	TGCT
TCGA-XY-A8S3	MSS	TGCT
TCGA-XY-A9T9	MSS	TGCT
TCGA-Y6-A8TL	MSS	PRAD
TCGA-Y6-A9XI	MSS	PRAD
TCGA-Y8-A894	MSS	KIRP
TCGA-Y8-A895	MSS	KIRP
TCGA-Y8-A896	MSS	KIRP
TCGA-Y8-A897	MSS	KIRP
TCGA-Y8-A898	MSS	KIRP
TCGA-Y8-A8RY	MSS	KIRP
TCGA-Y8-A8RZ	MSS	KIRP
TCGA-Y8-A8S0	MSS	KIRP
TCGA-Y8-A8S1	MSS	KIRP
TCGA-YA-A8S7	MSS	LIHC
TCGA-YB-A89D	MSS	PAAD
TCGA-YC-A89H	MSS	BLCA
TCGA-YC-A8S6	MSS	BLCA
TCGA-YC-A9TC	MSS	BLCA
TCGA-YD-A89C	MSS	SKCM
TCGA-YD-A9TA	MSS	SKCM
TCGA-YD-A9TB	MSS	SKCM
TCGA-YF-AA3L	MSS	BLCA
TCGA-YF-AA3M	MSS	BLCA
TCGA-YG-AA3N	MSS	SKCM
TCGA-YG-AA3O	MSS	SKCM
TCGA-YG-AA3P	MSS	SKCM
TCGA-YH-A8SY	MSS	PAAD
TCGA-YJ-A8SW	MSS	PRAD
TCGA-YL-A8HJ	MSS	PRAD
TCGA-YL-A8HK	MSS	PRAD
TCGA-YL-A8HL	MSS	PRAD
TCGA-YL-A8HM	MSS	PRAD
TCGA-YL-A8HO	MSS	PRAD
TCGA-YL-A8S8	MSS	PRAD
TCGA-YL-A8S9	MSS	PRAD
TCGA-YL-A8SA	MSS	PRAD
TCGA-YL-A8SB	MSS	PRAD
TCGA-YL-A8SC	MSS	PRAD
TCGA-YL-A8SF	MSS	PRAD
TCGA-YL-A8SH	MSS	PRAD
TCGA-YL-A8SI	MSS	PRAD
TCGA-YL-A8SJ	MSS	PRAD
TCGA-YL-A8SK	MSS	PRAD
TCGA-YL-A8SL	MSS	PRAD
TCGA-YL-A8SO	MSS	PRAD
TCGA-YL-A8SP	MSS	PRAD
TCGA-YL-A8SQ	MSS	PRAD
TCGA-YL-A8SR	MSS	PRAD
TCGA-YL-A9WH	MSS	PRAD

TCGA-YL-A9WI	MSS	PRAD
TCGA-YL-A9WJ	MSS	PRAD
TCGA-YL-A9WK	MSS	PRAD
TCGA-YL-A9WL	MSS	PRAD
TCGA-YL-A9WX	MSS	PRAD
TCGA-YL-A9WY	MSS	PRAD
TCGA-YR-A95A	MSS	CHOL
TCGA-YS-A95B	MSS	MESO
TCGA-YS-A95C	MSS	MESO
TCGA-YT-A95D	MSS	THYM
TCGA-YT-A95E	MSS	THYM
TCGA-YT-A95F	MSS	THYM
TCGA-YT-A95G	MSS	THYM
TCGA-YT-A95H	MSS	THYM
TCGA-YU-A90P	MSS	TGCT
TCGA-YU-A90Q	MSS	TGCT
TCGA-YU-A90S	MSS	TGCT
TCGA-YU-A90W	MSS	TGCT
TCGA-YU-A90Y	MSS	TGCT
TCGA-YU-A912	MSS	TGCT
TCGA-YU-A94D	MSS	TGCT
TCGA-YU-A94I	MSS	TGCT
TCGA-YU-AA4L	MSS	TGCT
TCGA-YU-AA61	MSS	TGCT
TCGA-YY-A8LH	MSS	PAAD
TCGA-YZ-A980	MSS	UVM
TCGA-YZ-A982	MSS	UVM
TCGA-YZ-A983	MSS	UVM
TCGA-YZ-A984	MSS	UVM
TCGA-YZ-A985	MSS	UVM
TCGA-Z2-A8RT	MSS	SKCM
TCGA-Z2-AA3S	MSS	SKCM
TCGA-Z2-AA3V	MSS	SKCM
TCGA-Z4-A8JB	MSS	SARC
TCGA-Z4-A9VC	MSS	SARC
TCGA-Z4-AAPF	MSS	SARC
TCGA-Z4-AAPG	MSS	SARC
TCGA-Z5-AAPL	MSS	PAAD
TCGA-Z6-A8JD	MSS	ESCA
TCGA-Z6-A8JE	MSS	ESCA
TCGA-Z6-A9VB	MSS	ESCA
TCGA-Z6-AAPN	MSS	ESCA
TCGA-Z7-A8R5	MSS	BRCA
TCGA-Z7-A8R6	MSS	BRCA
TCGA-ZA-A8F6	MSS	STAD
TCGA-ZB-A961	MSS	THYM
TCGA-ZB-A962	MSS	THYM
TCGA-ZB-A963	MSS	THYM
TCGA-ZB-A964	MSS	THYM
TCGA-ZB-A965	MSS	THYM
TCGA-ZB-A966	MSI-H	THYM
TCGA-ZB-A969	MSS	THYM

TCGA-ZB-A96A	MSS	THYM
TCGA-ZB-A96B	MSS	THYM
TCGA-ZB-A96C	MSS	THYM
TCGA-ZB-A96D	MSS	THYM
TCGA-ZB-A96E	MSS	THYM
TCGA-ZB-A96F	MSS	THYM
TCGA-ZB-A96G	MSS	THYM
TCGA-ZB-A96H	MSS	THYM
TCGA-ZB-A96I	MSS	THYM
TCGA-ZB-A96K	MSS	THYM
TCGA-ZB-A96L	MSS	THYM
TCGA-ZB-A96M	MSS	THYM
TCGA-ZB-A96O	MSS	THYM
TCGA-ZB-A96P	MSS	THYM
TCGA-ZB-A96Q	MSS	THYM
TCGA-ZB-A96R	MSS	THYM
TCGA-ZB-A96V	MSS	THYM
TCGA-ZC-AAA7	MSS	THYM
TCGA-ZC-AAAA	MSS	THYM
TCGA-ZC-AAAF	MSS	THYM
TCGA-ZC-AAAH	MSS	THYM
TCGA-ZD-A8I3	MSS	CHOL
TCGA-ZF-A9R0	MSS	BLCA
TCGA-ZF-A9R1	MSS	BLCA
TCGA-ZF-A9R2	MSS	BLCA
TCGA-ZF-A9R3	MSS	BLCA
TCGA-ZF-A9R4	MSS	BLCA
TCGA-ZF-A9R5	MSS	BLCA
TCGA-ZF-A9R7	MSS	BLCA
TCGA-ZF-A9R9	MSS	BLCA
TCGA-ZF-A9RC	MSS	BLCA
TCGA-ZF-A9RD	MSS	BLCA
TCGA-ZF-A9RE	MSS	BLCA
TCGA-ZF-A9RF	MSS	BLCA
TCGA-ZF-A9RG	MSS	BLCA
TCGA-ZF-A9RL	MSS	BLCA
TCGA-ZF-A9RM	MSS	BLCA
TCGA-ZF-A9RN	MSS	BLCA
TCGA-ZF-AA4N	MSS	BLCA
TCGA-ZF-AA4R	MSS	BLCA
TCGA-ZF-AA4T	MSS	BLCA
TCGA-ZF-AA4U	MSS	BLCA
TCGA-ZF-AA4V	MSS	BLCA
TCGA-ZF-AA4W	Intermediate	BLCA
TCGA-ZF-AA4X	MSS	BLCA
TCGA-ZF-AA51	MSS	BLCA
TCGA-ZF-AA52	MSS	BLCA
TCGA-ZF-AA53	MSS	BLCA
TCGA-ZF-AA54	MSS	BLCA
TCGA-ZF-AA56	MSS	BLCA
TCGA-ZF-AA58	MSS	BLCA
TCGA-ZF-AA5H	MSS	BLCA

TCGA-ZF-AA5N	MSS	BLCA
TCGA-ZF-AA5P	MSS	BLCA
TCGA-ZG-A8QW	MSS	PRAD
TCGA-ZG-A8QX	MSS	PRAD
TCGA-ZG-A8QY	MSS	PRAD
TCGA-ZG-A8QZ	MSS	PRAD
TCGA-ZG-A9KY	MSS	PRAD
TCGA-ZG-A9L0	MSS	PRAD
TCGA-ZG-A9L1	MSS	PRAD
TCGA-ZG-A9L2	MSS	PRAD
TCGA-ZG-A9L4	MSS	PRAD
TCGA-ZG-A9L5	MSS	PRAD
TCGA-ZG-A9L6	MSS	PRAD
TCGA-ZG-A9L9	MSS	PRAD
TCGA-ZG-A9LB	MSS	PRAD
TCGA-ZG-A9LM	MSS	PRAD
TCGA-ZG-A9LN	MSS	PRAD
TCGA-ZG-A9LS	MSS	PRAD
TCGA-ZG-A9LU	MSS	PRAD
TCGA-ZG-A9LY	MSS	PRAD
TCGA-ZG-A9LZ	MSS	PRAD
TCGA-ZG-A9M4	MSS	PRAD
TCGA-ZG-A9MC	MSS	PRAD
TCGA-ZG-A9N3	MSS	PRAD
TCGA-ZG-A9ND	MSS	PRAD
TCGA-ZG-A9NI	MSS	PRAD
TCGA-ZH-A8Y1	MSS	CHOL
TCGA-ZH-A8Y2	MSS	CHOL
TCGA-ZH-A8Y3	MSS	CHOL
TCGA-ZH-A8Y4	MSS	CHOL
TCGA-ZH-A8Y5	MSS	CHOL
TCGA-ZH-A8Y6	MSS	CHOL
TCGA-ZH-A8Y7	MSI-H	CHOL
TCGA-ZH-A8Y8	MSS	CHOL
TCGA-ZJ-A8QO	MSS	CESC
TCGA-ZJ-A8QQ	MSS	CESC
TCGA-ZJ-A8QR	MSS	CESC
TCGA-ZJ-AAX4	MSS	CESC
TCGA-ZJ-AAX8	MSS	CESC
TCGA-ZJ-AAXA	MSS	CESC
TCGA-ZJ-AAXB	MSS	CESC
TCGA-ZJ-AAXD	MSS	CESC
TCGA-ZJ-AAXF	MSS	CESC
TCGA-ZJ-AAXI	MSS	CESC
TCGA-ZJ-AAXJ	MSS	CESC
TCGA-ZJ-AAXN	MSS	CESC
TCGA-ZJ-AAXT	MSS	CESC
TCGA-ZJ-AAXU	MSS	CESC
TCGA-ZJ-AB0H	MSS	CESC
TCGA-ZJ-AB0I	MSS	CESC
TCGA-ZK-AAYZ	MSS	CHOL
TCGA-ZL-A9V6	MSS	THYM

TCGA-ZM-AA05	MSS	TGCT
TCGA-ZM-AA06	MSS	TGCT
TCGA-ZM-AA0B	MSS	TGCT
TCGA-ZM-AA0D	MSS	TGCT
TCGA-ZM-AA0E	MSS	TGCT
TCGA-ZM-AA0F	MSS	TGCT
TCGA-ZM-AA0H	MSS	TGCT
TCGA-ZM-AA0N	MSS	TGCT
TCGA-ZN-A9VQ	Intermediate	MESO
TCGA-ZN-A9VS	MSS	MESO
TCGA-ZN-A9VU	MSS	MESO
TCGA-ZP-A9CV	MSS	LIHC
TCGA-ZP-A9CY	MSS	LIHC
TCGA-ZP-A9CZ	MSS	LIHC
TCGA-ZP-A9D0	MSS	LIHC
TCGA-ZP-A9D1	MSS	LIHC
TCGA-ZP-A9D2	MSS	LIHC
TCGA-ZP-A9D4	MSS	LIHC
TCGA-ZQ-A9CR	MSS	STAD
TCGA-ZR-A9CJ	MSS	ESCA
TCGA-ZS-A9CD	MSS	LIHC
TCGA-ZS-A9CE	MSS	LIHC
TCGA-ZS-A9CF	MSS	LIHC
TCGA-ZS-A9CF	MSS	LIHC
TCGA-ZS-A9CG	MSS	LIHC
TCGA-ZT-A8OM	MSS	THYM
TCGA-ZU-A8S4	MSS	CHOL
TCGA-ZX-AA5X	MSS	CESC

Supplemental Table 2. Inferred MSI diagnosis for tumors from whole genome sequencing

TCGA ID	MSI diagnosis	Cancer type
TCGA-02-2483	MSS	GBM
TCGA-02-2485	MSS	GBM
TCGA-04-1331	MSS	OV
TCGA-04-1347	MSS	OV
TCGA-04-1349	MSS	OV
TCGA-04-1367	MSS	OV
TCGA-04-1371	MSS	OV
TCGA-04-1514	MSS	OV
TCGA-04-1542	MSS	OV
TCGA-05-4389	MSS	LUAD
TCGA-05-4395	MSS	LUAD
TCGA-05-4396	MSS	LUAD
TCGA-05-4397	MSS	LUAD
TCGA-05-5429	MSS	LUAD
TCGA-06-0124	MSS	GBM
TCGA-06-0125	MSS	GBM
TCGA-06-0125	MSS	GBM
TCGA-06-0128	MSS	GBM
TCGA-06-0145	MSS	GBM
TCGA-06-0152	MSS	GBM
TCGA-06-0152	MSS	GBM
TCGA-06-0155	MSS	GBM
TCGA-06-0157	MSS	GBM
TCGA-06-0171	MSS	GBM
TCGA-06-0171	MSS	GBM
TCGA-06-0185	MSS	GBM
TCGA-06-0188	MSS	GBM
TCGA-06-0190	MSS	GBM
TCGA-06-0190	MSS	GBM
TCGA-06-0210	MSS	GBM
TCGA-06-0210	MSS	GBM
TCGA-06-0211	MSS	GBM
TCGA-06-0211	MSS	GBM
TCGA-06-0214	MSS	GBM
TCGA-06-0221	MSS	GBM
TCGA-06-0221	MSS	GBM
TCGA-06-0648	MSS	GBM
TCGA-06-0686	MSS	GBM
TCGA-06-0744	MSS	GBM
TCGA-06-0745	MSS	GBM
TCGA-06-0877	MSS	GBM
TCGA-06-0881	MSS	GBM
TCGA-06-1086	MSS	GBM
TCGA-06-2557	MSS	GBM
TCGA-06-2570	MSS	GBM
TCGA-06-5411	MSS	GBM
TCGA-06-5415	MSS	GBM
TCGA-09-1666	MSS	OV
TCGA-09-2045	MSS	OV
TCGA-09-2050	MSS	OV

TCGA-10-0934	MSS	OV
TCGA-10-0937	MSS	OV
TCGA-10-0938	MSS	OV
TCGA-13-0723	MSS	OV
TCGA-13-0725	MSS	OV
TCGA-13-0727	MSS	OV
TCGA-13-0751	MSS	OV
TCGA-13-0890	MSS	OV
TCGA-13-0906	MSS	OV
TCGA-13-0912	MSS	OV
TCGA-13-1411	MSS	OV
TCGA-13-1477	MSS	OV
TCGA-13-1487	MSS	OV
TCGA-13-1491	MSS	OV
TCGA-14-0786	MSS	GBM
TCGA-14-1034	MSS	GBM
TCGA-14-1034	MSS	GBM
TCGA-14-1401	MSS	GBM
TCGA-14-1402	MSS	GBM
TCGA-14-1402	MSS	GBM
TCGA-14-1454	MSS	GBM
TCGA-14-1459	MSS	GBM
TCGA-14-1823	MSS	GBM
TCGA-14-2554	MSS	GBM
TCGA-15-1444	MSS	GBM
TCGA-16-1063	MSS	GBM
TCGA-16-1460	MSS	GBM
TCGA-18-3408	MSS	LUSC
TCGA-18-4721	MSS	LUSC
TCGA-19-1389	MSS	GBM
TCGA-19-1389	MSS	GBM
TCGA-19-2620	MSS	GBM
TCGA-19-2624	MSS	GBM
TCGA-19-2629	MSS	GBM
TCGA-19-5960	MSS	GBM
TCGA-21-1076	MSS	LUSC
TCGA-21-1078	MSS	LUSC
TCGA-21-1082	MSS	LUSC
TCGA-21-1083	MSS	LUSC
TCGA-22-1016	MSS	LUSC
TCGA-22-5477	MSS	LUSC
TCGA-22-5485	MSS	LUSC
TCGA-22-5492	MSS	LUSC
TCGA-23-1110	MSS	OV
TCGA-23-1118	MSS	OV
TCGA-23-1124	MSS	OV
TCGA-24-0980	MSS	OV
TCGA-24-0982	MSS	OV
TCGA-24-1103	MSS	OV
TCGA-24-1419	MSS	OV
TCGA-24-1466	MSS	OV
TCGA-24-1544	MSS	OV

TCGA-24-1548	MSS	OV
TCGA-24-1552	MSS	OV
TCGA-24-1557	MSS	OV
TCGA-24-1558	MSS	OV
TCGA-24-1562	MSS	OV
TCGA-24-1614	MSS	OV
TCGA-24-2024	MSS	OV
TCGA-24-2290	MSS	OV
TCGA-25-1319	MSS	OV
TCGA-25-1632	MSS	OV
TCGA-25-1634	MSS	OV
TCGA-25-2391	MSS	OV
TCGA-25-2400	MSS	OV
TCGA-26-1438	MSS	GBM
TCGA-26-5132	MSS	GBM
TCGA-26-5135	MSS	GBM
TCGA-27-1831	MSS	GBM
TCGA-27-2523	MSS	GBM
TCGA-27-2528	MSS	GBM
TCGA-29-1710	MSS	OV
TCGA-32-1970	MSS	GBM
TCGA-33-4586	MSS	LUSC
TCGA-34-2596	MSS	LUSC
TCGA-34-2600	MSS	LUSC
TCGA-34-5240	MSS	LUSC
TCGA-36-1570	MSS	OV
TCGA-36-1571	MSS	OV
TCGA-36-1574	MSS	OV
TCGA-37-4135	MSS	LUSC
TCGA-38-4628	MSS	LUAD
TCGA-38-4630	MSS	LUAD
TCGA-43-3920	MSS	LUSC
TCGA-44-2656	MSS	LUAD
TCGA-44-2656	MSS	LUAD
TCGA-44-2666	MSS	LUAD
TCGA-44-2668	MSS	LUAD
TCGA-44-2668	MSS	LUAD
TCGA-44-3917	MSS	LUAD
TCGA-44-3917	MSS	LUAD
TCGA-44-3918	MSS	LUAD
TCGA-44-4112	MSS	LUAD
TCGA-44-4112	MSS	LUAD
TCGA-44-5645	MSS	LUAD
TCGA-44-5645	MSS	LUAD
TCGA-44-6146	MSS	LUAD
TCGA-44-6147	MSS	LUAD
TCGA-44-6147	MSS	LUAD
TCGA-44-6148	MSS	LUAD
TCGA-44-6775	MSS	LUAD
TCGA-49-4486	MSS	LUAD
TCGA-49-6742	MSS	LUAD
TCGA-50-5066	MSS	LUAD

TCGA-50-5930	MSS	LUAD
TCGA-50-5932	MSS	LUAD
TCGA-50-6591	MSS	LUAD
TCGA-50-6597	MSS	LUAD
TCGA-52-7812	MSS	LUSC
TCGA-55-1594	MSS	LUAD
TCGA-55-1596	MSS	LUAD
TCGA-55-6972	MSS	LUAD
TCGA-55-6982	MSS	LUAD
TCGA-55-6984	MSS	LUAD
TCGA-55-6986	MSS	LUAD
TCGA-55-7281	MSS	LUAD
TCGA-56-1622	MSS	LUSC
TCGA-56-7582	MSS	LUSC
TCGA-60-2695	MSS	LUSC
TCGA-60-2698	MSS	LUSC
TCGA-60-2711	MSS	LUSC
TCGA-60-2713	MSS	LUSC
TCGA-60-2719	MSS	LUSC
TCGA-60-2726	MSS	LUSC
TCGA-61-2000	MSS	OV
TCGA-61-2095	MSS	OV
TCGA-64-1678	MSS	LUAD
TCGA-64-1680	MSS	LUAD
TCGA-66-2744	MSS	LUSC
TCGA-66-2756	MSS	LUSC
TCGA-66-2757	MSS	LUSC
TCGA-66-2759	MSS	LUSC
TCGA-66-2766	MSS	LUSC
TCGA-66-2789	MSS	LUSC
TCGA-66-2793	MSS	LUSC
TCGA-66-2795	MSS	LUSC
TCGA-67-3771	MSS	LUAD
TCGA-67-6215	MSS	LUAD
TCGA-73-4659	MSS	LUAD
TCGA-73-4666	MSS	LUAD
TCGA-75-5147	MSS	LUAD
TCGA-75-6203	MSS	LUAD
TCGA-75-7030	MSS	LUAD
TCGA-77-6843	MSS	LUSC
TCGA-77-7139	MSS	LUSC
TCGA-78-7143	MSS	LUAD
TCGA-78-7146	MSS	LUAD
TCGA-78-7156	MSS	LUAD
TCGA-78-7158	MSS	LUAD
TCGA-78-7535	MSS	LUAD
TCGA-85-8052	MSS	LUSC
TCGA-85-8277	MSS	LUSC
TCGA-90-7767	MSS	LUSC
TCGA-91-6840	MSS	LUAD
TCGA-91-6847	MSS	LUAD
TCGA-92-8064	MSS	LUSC

TCGA-94-7943	MSS	LUSC
TCGA-97-8171	MSS	LUAD
TCGA-98-8022	MSS	LUSC
TCGA-A1-A0SM	MSS	BRCA
TCGA-A2-A04P	MSS	BRCA
TCGA-A2-A04Q	MSS	BRCA
TCGA-A2-A04T	MSS	BRCA
TCGA-A2-A04X	MSS	BRCA
TCGA-A2-A0CM	MSS	BRCA
TCGA-A2-A0D0	MSS	BRCA
TCGA-A2-A0D1	MSS	BRCA
TCGA-A2-A0D2	MSS	BRCA
TCGA-A2-A0D4	MSS	BRCA
TCGA-A2-A0EY	MSS	BRCA
TCGA-A2-A0YG	MSS	BRCA
TCGA-A2-A259	MSS	BRCA
TCGA-A2-A25B	MSS	BRCA
TCGA-A2-A3XX	MSS	BRCA
TCGA-A2-A3Y0	MSS	BRCA
TCGA-A3-3308	MSS	KIRC
TCGA-A3-3324	MSS	KIRC
TCGA-A3-3363	MSS	KIRC
TCGA-A3-3370	MSS	KIRC
TCGA-A3-3372	MSS	KIRC
TCGA-A3-3387	MSS	KIRC
TCGA-A4-A48D	MSS	KIRP
TCGA-A4-A4ZT	MSS	KIRP
TCGA-A5-A0GA	MSI-H	UCEC
TCGA-A6-2680	MSS	COAD
TCGA-A6-2681	MSS	COAD
TCGA-A6-2683	MSS	COAD
TCGA-A6-3807	MSS	COAD
TCGA-A6-6141	MSS	COAD
TCGA-A6-6781	MSI-H	COAD
TCGA-A6-A565	MSS	COAD
TCGA-A6-A566	MSS	COAD
TCGA-A6-A567	MSS	COAD
TCGA-A6-A56B	MSS	COAD
TCGA-A7-A0CE	MSS	BRCA
TCGA-A7-A26G	MSS	BRCA
TCGA-A7-A26J	MSS	BRCA
TCGA-A7-A26J	MSS	BRCA
TCGA-A8-A075	MSS	BRCA
TCGA-A8-A07B	MSS	BRCA
TCGA-A8-A07I	MSS	BRCA
TCGA-A8-A08B	MSS	BRCA
TCGA-A8-A08L	MSS	BRCA
TCGA-A8-A08S	MSS	BRCA
TCGA-A8-A092	MSS	BRCA
TCGA-A8-A094	MSS	BRCA
TCGA-A8-A09I	MSS	BRCA
TCGA-A8-A09X	MSS	BRCA

TCGA-AA-3514	MSS	COAD
TCGA-AA-3516	MSI-H	COAD
TCGA-AA-3518	MSI-H	COAD
TCGA-AA-3529	MSS	COAD
TCGA-AA-3534	MSS	COAD
TCGA-AA-3555	MSS	COAD
TCGA-AA-3664	MSS	COAD
TCGA-AA-3666	MSS	COAD
TCGA-AA-3685	MSS	COAD
TCGA-AA-3956	MSS	COAD
TCGA-AA-3977	MSS	COAD
TCGA-AA-3994	MSS	COAD
TCGA-AA-A00N	MSS	COAD
TCGA-AA-A00R	MSI-H	COAD
TCGA-AA-A01R	MSI-H	COAD
TCGA-AA-A01S	MSS	COAD
TCGA-AA-A01T	MSS	COAD
TCGA-AA-A01V	MSS	COAD
TCGA-AA-A01X	MSS	COAD
TCGA-AA-A02O	MSS	COAD
TCGA-AA-A02Y	MSS	COAD
TCGA-AA-A03F	MSS	COAD
TCGA-AB-2905	MSS	LAML
TCGA-AB-2906	MSS	LAML
TCGA-AB-2907	MSS	LAML
TCGA-AB-2963	MSS	LAML
TCGA-AB-2964	MSS	LAML
TCGA-AB-2965	MSS	LAML
TCGA-AB-2966	MSS	LAML
TCGA-AB-2967	MSS	LAML
TCGA-AB-2968	MSS	LAML
TCGA-AB-2970	MSS	LAML
TCGA-AB-2971	MSS	LAML
TCGA-AB-2972	MSS	LAML
TCGA-AB-2973	MSS	LAML
TCGA-AB-2974	MSS	LAML
TCGA-AB-2975	MSS	LAML
TCGA-AB-2976	MSS	LAML
TCGA-AB-2977	MSS	LAML
TCGA-AB-2978	MSS	LAML
TCGA-AB-2979	MSS	LAML
TCGA-AB-2980	MSS	LAML
TCGA-AB-2981	MSS	LAML
TCGA-AB-2982	MSS	LAML
TCGA-AB-2983	MSS	LAML
TCGA-AB-2985	MSS	LAML
TCGA-AB-2986	MSS	LAML
TCGA-AB-2987	MSS	LAML
TCGA-AB-2988	MSS	LAML
TCGA-AB-2990	MSS	LAML
TCGA-AB-2991	MSS	LAML
TCGA-AB-2992	MSS	LAML

TCGA-AB-2993	MSS	LAML
TCGA-AB-2994	MSS	LAML
TCGA-AB-2995	MSS	LAML
TCGA-AB-2996	MSS	LAML
TCGA-AB-2997	MSS	LAML
TCGA-AB-2998	MSS	LAML
TCGA-AB-2999	MSS	LAML
TCGA-AB-3000	MSS	LAML
TCGA-AB-3001	MSS	LAML
TCGA-AB-3002	MSS	LAML
TCGA-AB-3005	MSS	LAML
TCGA-AB-3007	MSS	LAML
TCGA-AB-3008	MSS	LAML
TCGA-AB-3009	MSS	LAML
TCGA-AB-3011	MSS	LAML
TCGA-AB-3012	MSS	LAML
TCGA-AC-A2BK	MSS	BRCA
TCGA-AD-6964	MSI-H	COAD
TCGA-AD-A5EJ	MSI-H	COAD
TCGA-AD-A5EK	MSS	COAD
TCGA-AF-2689	MSS	READ
TCGA-AF-2691	MSS	READ
TCGA-AF-3913	MSS	READ
TCGA-AG-3574	MSS	READ
TCGA-AG-3582	MSS	READ
TCGA-AG-3593	MSS	READ
TCGA-AG-3727	MSS	READ
TCGA-AG-3885	MSS	READ
TCGA-AG-3890	MSS	READ
TCGA-AG-3896	MSS	READ
TCGA-AG-3901	MSS	READ
TCGA-AG-4007	MSS	READ
TCGA-AG-4008	MSS	READ
TCGA-AG-4015	MSS	READ
TCGA-AG-A002	MSS	READ
TCGA-AG-A032	MSS	READ
TCGA-AJ-A23M	MSS	UCEC
TCGA-AK-3428	MSS	KIRC
TCGA-AK-3454	MSS	KIRC
TCGA-AK-3455	MSS	KIRC
TCGA-AL-3467	MSS	KIRP
TCGA-AL-3468	MSS	KIRP
TCGA-AL-3472	MSS	KIRP
TCGA-AN-A04D	MSS	BRCA
TCGA-AN-A0AT	MSS	BRCA
TCGA-AN-A0G0	MSS	BRCA
TCGA-AN-A0XR	MSS	BRCA
TCGA-AO-A03L	MSS	BRCA
TCGA-AO-A03N	MSS	BRCA
TCGA-AO-A0J2	MSS	BRCA
TCGA-AO-A0J4	MSS	BRCA
TCGA-AO-A0J6	MSS	BRCA

TCGA-AO-A0JM	MSS	BRCA
TCGA-AO-A124	MSS	BRCA
TCGA-AO-A12H	MSS	BRCA
TCGA-AP-A051	MSI-H	UCEC
TCGA-AP-A052	MSS	UCEC
TCGA-AP-A05A	MSS	UCEC
TCGA-AP-A05D	MSS	UCEC
TCGA-AP-A0LE	MSI-H	UCEC
TCGA-AP-A0LF	MSS	UCEC
TCGA-AQ-A04J	MSS	BRCA
TCGA-AR-A0TX	MSS	BRCA
TCGA-AR-A1AY	MSS	BRCA
TCGA-AR-A24Z	MSS	BRCA
TCGA-AR-A256	MSS	BRCA
TCGA-AR-A2LK	MSS	BRCA
TCGA-AX-A05S	MSI-H	UCEC
TCGA-AX-A06B	MSS	UCEC
TCGA-AX-A1C8	MSS	UCEC
TCGA-AX-A1CI	MSS	UCEC
TCGA-AX-A2H5	MSS	UCEC
TCGA-AY-A54L	MSS	COAD
TCGA-AZ-4315	MSS	COAD
TCGA-AZ-6601	MSI-H	COAD
TCGA-B0-5094	MSS	KIRC
TCGA-B0-5695	MSS	KIRC
TCGA-B1-A47N	MSS	KIRP
TCGA-B1-A47O	MSS	KIRP
TCGA-B2-3924	MSS	KIRC
TCGA-B2-4099	MSS	KIRC
TCGA-B2-4101	MSS	KIRC
TCGA-B2-4102	MSS	KIRC
TCGA-B2-5633	MSS	KIRC
TCGA-B2-5635	MSS	KIRC
TCGA-B3-3925	MSS	KIRP
TCGA-B3-3926	MSS	KIRP
TCGA-B3-4103	MSS	KIRP
TCGA-B3-4104	MSS	KIRP
TCGA-B5-A0K3	MSS	UCEC
TCGA-B5-A0K8	MSS	UCEC
TCGA-B5-A11H	MSI-H	UCEC
TCGA-B5-A11I	MSS	UCEC
TCGA-B5-A1MY	MSS	UCEC
TCGA-B6-A0I1	MSS	BRCA
TCGA-B6-A0I2	MSS	BRCA
TCGA-B6-A0I6	MSS	BRCA
TCGA-B6-A0IJ	MSS	BRCA
TCGA-B6-A0IQ	MSS	BRCA
TCGA-B6-A0RE	MSS	BRCA
TCGA-B6-A0RT	MSS	BRCA
TCGA-B6-A0RU	MSS	BRCA
TCGA-B6-A0WX	MSS	BRCA
TCGA-B6-A0X5	MSS	BRCA

TCGA-B9-4115	MSS	KIRP
TCGA-B9-4116	MSS	KIRP
TCGA-B9-4617	MSS	KIRP
TCGA-B9-A44B	MSS	KIRP
TCGA-BA-4076	MSS	HNSC
TCGA-BA-4077	MSS	HNSC
TCGA-BA-5149	MSS	HNSC
TCGA-BA-5153	MSS	HNSC
TCGA-BA-5556	MSS	HNSC
TCGA-BA-6869	MSS	HNSC
TCGA-BA-6872	MSS	HNSC
TCGA-BA-6873	MSS	HNSC
TCGA-BA-A4IH	MSS	HNSC
TCGA-BB-4225	MSS	HNSC
TCGA-BC-A216	MSS	LIHC
TCGA-BC-A217	MSS	LIHC
TCGA-BG-A18C	MSS	UCEC
TCGA-BH-A0AV	MSS	BRCA
TCGA-BH-A0B3	MSS	BRCA
TCGA-BH-A0B9	MSS	BRCA
TCGA-BH-A0BW	MSS	BRCA
TCGA-BH-A0DG	MSS	BRCA
TCGA-BH-A0DT	MSS	BRCA
TCGA-BH-A0E0	MSS	BRCA
TCGA-BH-A0EA	MSS	BRCA
TCGA-BH-A0H0	MSS	BRCA
TCGA-BH-A0H6	MSS	BRCA
TCGA-BH-A0WA	MSS	BRCA
TCGA-BH-A18R	MSS	BRCA
TCGA-BH-A18U	MSS	BRCA
TCGA-BH-A1FC	MSS	BRCA
TCGA-BJ-A0Z2	MSS	THCA
TCGA-BJ-A0ZB	MSS	THCA
TCGA-BJ-A191	MSS	THCA
TCGA-BJ-A28V	MSS	THCA
TCGA-BJ-A45K	MSS	THCA
TCGA-BK-A0CC	MSS	UCEC
TCGA-BK-A139	MSS	UCEC
TCGA-BL-A0C8	MSS	BLCA
TCGA-BL-A13J	MSS	BLCA
TCGA-BL-A13J	MSS	BLCA
TCGA-BP-4326	MSS	KIRC
TCGA-BP-4327	MSS	KIRC
TCGA-BP-4781	MSS	KIRC
TCGA-BP-4807	MSS	KIRC
TCGA-BP-4968	MSS	KIRC
TCGA-BP-5010	MSS	KIRC
TCGA-BP-5168	MSS	KIRC
TCGA-BR-4255	MSS	STAD
TCGA-BR-4280	MSI-H	STAD
TCGA-BR-6452	MSI-H	STAD
TCGA-BR-6456	MSS	STAD

TCGA-BR-6564	MSS	STAD
TCGA-BR-7722	MSS	STAD
TCGA-BR-8373	MSS	STAD
TCGA-BR-8381	MSS	STAD
TCGA-BR-8486	MSS	STAD
TCGA-BR-8682	MSS	STAD
TCGA-BR-8690	MSS	STAD
TCGA-BR-A4J4	MSS	STAD
TCGA-BS-A0U9	MSS	UCEC
TCGA-BT-A20Q	MSS	BLCA
TCGA-BT-A20T	MSS	BLCA
TCGA-BT-A20V	MSS	BLCA
TCGA-BT-A2LA	MSS	BLCA
TCGA-BT-A3PH	MSS	BLCA
TCGA-BT-A3PJ	MSS	BLCA
TCGA-BW-A5NP	MSS	LIHC
TCGA-C4-A0F7	MSS	BLCA
TCGA-C5-A0TN	MSS	CESC
TCGA-C5-A1BF	MSS	CESC
TCGA-C5-A1BJ	MSS	CESC
TCGA-C5-A1BN	MSS	CESC
TCGA-C5-A1M8	MSS	CESC
TCGA-C5-A1M9	MSS	CESC
TCGA-C5-A1MI	MSS	CESC
TCGA-C5-A1ML	MSS	CESC
TCGA-C5-A1MQ	MSS	CESC
TCGA-C5-A2LT	MSS	CESC
TCGA-C5-A2LV	MSS	CESC
TCGA-C5-A2LY	MSS	CESC
TCGA-C8-A12L	MSS	BRCA
TCGA-C8-A12Q	MSS	BRCA
TCGA-C8-A130	MSS	BRCA
TCGA-CA-6717	MSS	COAD
TCGA-CA-6718	MSS	COAD
TCGA-CC-5260	MSS	LIHC
TCGA-CC-5261	MSS	LIHC
TCGA-CD-5799	MSS	STAD
TCGA-CD-5802	MSS	STAD
TCGA-CD-8529	MSS	STAD
TCGA-CF-A27C	MSS	BLCA
TCGA-CF-A3MF	MSS	BLCA
TCGA-CG-4442	MSI-H	STAD
TCGA-CG-4443	MSS	STAD
TCGA-CG-4474	MSS	STAD
TCGA-CG-5723	MSI-H	STAD
TCGA-CG-5724	MSS	STAD
TCGA-CG-5730	MSS	STAD
TCGA-CJ-4639	MSS	KIRC
TCGA-CJ-4870	MSS	KIRC
TCGA-CJ-4878	MSS	KIRC
TCGA-CJ-4885	MSS	KIRC
TCGA-CJ-4899	MSS	KIRC

TCGA-CJ-4918	MSS	KIRC
TCGA-CJ-5681	MSS	KIRC
TCGA-CJ-5682	MSS	KIRC
TCGA-CJ-6033	MSS	KIRC
TCGA-CN-4737	MSS	HNSC
TCGA-CN-4741	MSS	HNSC
TCGA-CN-5365	MSS	HNSC
TCGA-CN-5374	MSS	HNSC
TCGA-CN-6011	MSS	HNSC
TCGA-CN-6989	MSS	HNSC
TCGA-CN-6994	MSS	HNSC
TCGA-CQ-6225	MSS	HNSC
TCGA-CQ-6228	MSS	HNSC
TCGA-CR-5249	MSS	HNSC
TCGA-CR-5250	MSS	HNSC
TCGA-CR-6467	MSS	HNSC
TCGA-CR-6470	MSS	HNSC
TCGA-CR-6472	MSS	HNSC
TCGA-CR-6480	MSS	HNSC
TCGA-CR-6482	MSS	HNSC
TCGA-CR-6487	MSS	HNSC
TCGA-CR-6491	MSS	HNSC
TCGA-CR-7382	MSS	HNSC
TCGA-CR-7385	MSS	HNSC
TCGA-CR-7391	MSS	HNSC
TCGA-CR-7404	MSS	HNSC
TCGA-CS-5395	MSS	LGG
TCGA-CS-6186	MSS	LGG
TCGA-CS-6665	MSS	LGG
TCGA-CS-6668	MSS	LGG
TCGA-CS-6669	MSS	LGG
TCGA-CV-5431	MSS	HNSC
TCGA-CV-5432	MSS	HNSC
TCGA-CV-5442	MSS	HNSC
TCGA-CV-5443	MSS	HNSC
TCGA-CV-5973	MSS	HNSC
TCGA-CV-6433	MSS	HNSC
TCGA-CV-6956	MSS	HNSC
TCGA-CV-6961	MSS	HNSC
TCGA-CV-7090	MSS	HNSC
TCGA-CV-7100	MSS	HNSC
TCGA-CV-7180	MSS	HNSC
TCGA-CV-7255	MSS	HNSC
TCGA-CV-7416	MSS	HNSC
TCGA-CV-7432	MSS	HNSC
TCGA-CW-5585	MSS	KIRC
TCGA-CW-6087	MSS	KIRC
TCGA-CW-6093	MSS	KIRC
TCGA-CX-7086	MSS	HNSC
TCGA-CZ-4856	MSS	KIRC
TCGA-CZ-5453	MSS	KIRC
TCGA-CZ-5454	MSS	KIRC

TCGA-CZ-5987	MSS	KIRC
TCGA-D1-A16G	MSS	UCEC
TCGA-D1-A1NU	MSS	UCEC
TCGA-D3-A1Q1	MSS	SKCM
TCGA-D3-A1Q5	MSS	SKCM
TCGA-D3-A3MO	MSS	SKCM
TCGA-D5-6540	MSI-H	COAD
TCGA-D7-5579	MSS	STAD
TCGA-D7-6519	MSS	STAD
TCGA-D7-6527	MSS	STAD
TCGA-D7-6528	MSS	STAD
TCGA-D7-6815	MSS	STAD
TCGA-D7-6822	MSS	STAD
TCGA-D7-8570	MSS	STAD
TCGA-D7-A4YX	MSS	STAD
TCGA-D8-A27F	MSS	BRCA
TCGA-D8-A27H	MSS	BRCA
TCGA-D9-A148	MSS	SKCM
TCGA-DA-A1HV	MSS	SKCM
TCGA-DA-A1HW	MSS	SKCM
TCGA-DA-A1HY	MSS	SKCM
TCGA-DA-A1I0	MSS	SKCM
TCGA-DA-A1I2	MSS	SKCM
TCGA-DA-A1I8	MSS	SKCM
TCGA-DA-A1IC	MSS	SKCM
TCGA-DA-A3F3	MSS	SKCM
TCGA-DA-A3F5	MSS	SKCM
TCGA-DA-A3F8	MSS	SKCM
TCGA-DB-5278	MSS	LGG
TCGA-DD-A1EB	MSS	LIHC
TCGA-DD-A1EJ	MSS	LIHC
TCGA-DD-A3A6	MSS	LIHC
TCGA-DD-A3A8	MSS	LIHC
TCGA-DD-A3A9	MSS	LIHC
TCGA-DD-A4NA	MSS	LIHC
TCGA-DD-A4NB	MSS	LIHC
TCGA-DD-A4NE	MSS	LIHC
TCGA-DD-A4NG	MSS	LIHC
TCGA-DE-A0Y3	MSS	THCA
TCGA-DE-A2OL	MSS	THCA
TCGA-DE-A3KN	MSS	THCA
TCGA-DG-A2KJ	MSS	CESC
TCGA-DH-A669	MSS	LGG
TCGA-DI-A1NN	MSS	UCEC
TCGA-DJ-A13L	MSS	THCA
TCGA-DJ-A13R	MSS	THCA
TCGA-DJ-A13W	MSS	THCA
TCGA-DJ-A1QL	MSS	THCA
TCGA-DJ-A2Q1	MSS	THCA
TCGA-DJ-A2Q2	MSS	THCA
TCGA-DJ-A3US	MSS	THCA
TCGA-DK-A1A5	MSS	BLCA

TCGA-DK-A1A6	MSS	BLCA
TCGA-DK-A1A7	MSS	BLCA
TCGA-DK-A1AA	MSS	BLCA
TCGA-DK-A1AE	MSS	BLCA
TCGA-DK-A1AG	MSS	BLCA
TCGA-DK-A3IL	MSS	BLCA
TCGA-DQ-5625	MSS	HNSC
TCGA-DQ-5629	MSS	HNSC
TCGA-DS-A0VL	MSS	CESC
TCGA-DU-5870	MSS	LGG
TCGA-DU-5870	MSS	LGG
TCGA-DU-5872	MSS	LGG
TCGA-DU-5872	MSS	LGG
TCGA-DU-5874	MSS	LGG
TCGA-DU-6397	MSS	LGG
TCGA-DU-6401	MSS	LGG
TCGA-DU-6404	MSS	LGG
TCGA-DU-6404	MSS	LGG
TCGA-DU-6407	MSS	LGG
TCGA-DU-6407	MSS	LGG
TCGA-DU-7009	MSS	LGG
TCGA-DU-7013	MSS	LGG
TCGA-DU-7301	MSS	LGG
TCGA-DV-5566	MSS	KIRC
TCGA-DX-A1KU	MSS	SARC
TCGA-DX-A1KW	MSS	SARC
TCGA-DX-A1L0	MSS	SARC
TCGA-DX-A1L2	MSS	SARC
TCGA-DX-A1L3	MSS	SARC
TCGA-DX-A23R	MSS	SARC
TCGA-DX-A240	MSS	SARC
TCGA-DX-A2IZ	MSS	SARC
TCGA-DX-A2J0	MSS	SARC
TCGA-DX-A2J4	MSS	SARC
TCGA-DX-A3LS	MSS	SARC
TCGA-DX-A3LT	MSS	SARC
TCGA-DX-A3LU	MSS	SARC
TCGA-DX-A3LW	MSS	SARC
TCGA-DX-A3LY	MSS	SARC
TCGA-DX-A3M1	MSS	SARC
TCGA-DX-A3U5	MSS	SARC
TCGA-DX-A3U6	MSS	SARC
TCGA-DX-A3U7	MSS	SARC
TCGA-DX-A3U8	MSS	SARC
TCGA-DX-A48U	MSS	SARC
TCGA-DX-A6Z2	MSS	SARC
TCGA-E1-5318	MSS	LGG
TCGA-E1-5319	MSS	LGG
TCGA-E2-A109	MSS	BRCA
TCGA-E2-A14P	MSS	BRCA
TCGA-E2-A14X	MSS	BRCA
TCGA-E2-A152	MSS	BRCA

TCGA-E2-A15E	MSS	BRCA
TCGA-E2-A15H	MSS	BRCA
TCGA-E2-A15K	MSS	BRCA
TCGA-E2-A15K	MSS	BRCA
TCGA-E2-A1LG	MSS	BRCA
TCGA-E2-A1LK	MSS	BRCA
TCGA-E2-A1LL	MSS	BRCA
TCGA-E6-A1LZ	MSS	UCEC
TCGA-E8-A418	MSS	THCA
TCGA-E9-A1NH	MSS	BRCA
TCGA-EB-A24D	MSS	SKCM
TCGA-ED-A459	MSS	LIHC
TCGA-ED-A4XI	MSS	LIHC
TCGA-EE-A185	MSS	SKCM
TCGA-EE-A29B	MSS	SKCM
TCGA-EE-A2A0	MSS	SKCM
TCGA-EE-A2GN	MSS	SKCM
TCGA-EE-A2GT	MSS	SKCM
TCGA-EE-A2M5	MSS	SKCM
TCGA-EE-A2MI	MSS	SKCM
TCGA-EE-A3J5	MSS	SKCM
TCGA-EE-A3JI	MSS	SKCM
TCGA-EI-6917	MSS	READ
TCGA-EK-A2PK	MSS	CESC
TCGA-EK-A2R9	MSS	CESC
TCGA-EK-A2RE	MSS	CESC
TCGA-EK-A2RL	MSS	CESC
TCGA-EK-A2RM	MSS	CESC
TCGA-EL-A3CV	MSS	THCA
TCGA-EL-A3CX	MSS	THCA
TCGA-EL-A3MY	MSS	THCA
TCGA-EL-A3T0	MSS	THCA
TCGA-EL-A3TB	MSS	THCA
TCGA-EL-A4K6	MSS	THCA
TCGA-EM-A22O	MSS	THCA
TCGA-EM-A2CN	MSS	THCA
TCGA-EM-A2CP	MSS	THCA
TCGA-EM-A2CU	MSS	THCA
TCGA-EM-A2OV	MSS	THCA
TCGA-EM-A2OW	MSS	THCA
TCGA-EM-A3AL	MSS	THCA
TCGA-EM-A3AQ	MSS	THCA
TCGA-EM-A3FL	MSS	THCA
TCGA-EM-A3FR	MSS	THCA
TCGA-EO-A1Y8	MSS	UCEC
TCGA-EP-A26S	MSS	LIHC
TCGA-EP-A2KB	MSS	LIHC
TCGA-EP-A3RK	MSS	LIHC
TCGA-EQ-5647	MSS	STAD
TCGA-ER-A19D	MSS	SKCM
TCGA-ER-A19E	MSS	SKCM
TCGA-ER-A19J	MSS	SKCM

TCGA-ER-A19L	MSS	SKCM
TCGA-ER-A19T	MSS	SKCM
TCGA-ER-A19T	MSS	SKCM
TCGA-ER-A2NF	MSS	SKCM
TCGA-ER-A2NF	MSS	SKCM
TCGA-ER-A3ES	MSS	SKCM
TCGA-ES-A2HS	MSS	LIHC
TCGA-ES-A2HT	MSS	LIHC
TCGA-ET-A2N1	MSS	THCA
TCGA-ET-A3DV	MSS	THCA
TCGA-EW-A1P8	MSS	BRCA
TCGA-EW-A1PB	MSS	BRCA
TCGA-EW-A1PC	MSS	BRCA
TCGA-EW-A1PH	MSS	BRCA
TCGA-EW-A3U0	MSS	BRCA
TCGA-EX-A1H5	MSS	CESC
TCGA-EY-A1GS	MSS	UCEC
TCGA-EY-A1GW	MSS	UCEC
TCGA-EZ-7264	MSS	LGG
TCGA-F1-6177	MSI-H	STAD
TCGA-F1-6875	MSS	STAD
TCGA-F5-6814	MSS	READ
TCGA-FD-A3N5	MSS	BLCA
TCGA-FD-A3N6	MSS	BLCA
TCGA-FE-A22Z	MSS	THCA
TCGA-FG-5964	MSS	LGG
TCGA-FG-5965	MSS	LGG
TCGA-FG-7643	MSS	LGG
TCGA-FG-8182	MSS	LGG
TCGA-FG-A4MT	MSS	LGG
TCGA-FG-A4MT	MSS	LGG
TCGA-FK-A3S3	MSS	THCA
TCGA-FK-A3SD	MSS	THCA
TCGA-FK-A3SE	MSS	THCA
TCGA-FP-7998	MSS	STAD
TCGA-FS-A1ZD	MSS	SKCM
TCGA-FS-A1ZK	MSS	SKCM
TCGA-FS-A1ZP	MSS	SKCM
TCGA-FS-A1ZU	MSS	SKCM
TCGA-FT-A3EE	MSS	BLCA
TCGA-FV-A2QQ	MSS	LIHC
TCGA-FV-A3R2	MSS	LIHC
TCGA-FV-A3R3	MSS	LIHC
TCGA-FV-A495	MSS	LIHC
TCGA-FV-A496	MSS	LIHC
TCGA-FV-A4ZQ	MSS	LIHC
TCGA-FX-A2QS	MSS	SARC
TCGA-FX-A3NJ	MSS	SARC
TCGA-FX-A3RE	MSS	SARC
TCGA-FX-A48G	MSS	SARC
TCGA-FY-A2QD	MSS	THCA
TCGA-G3-A25S	MSS	LIHC

TCGA-G3-A25T	MSS	LIHC
TCGA-G3-A25Y	MSS	LIHC
TCGA-G3-A5SL	MSS	LIHC
TCGA-GD-A2C5	MSS	BLCA
TCGA-GI-A2C9	MSS	BRCA
TCGA-GL-A4EM	MSS	KIRP
TCGA-GM-A2DF	MSS	BRCA
TCGA-GM-A3XL	MSS	BRCA
TCGA-GN-A262	MSS	SKCM
TCGA-GN-A264	MSS	SKCM
TCGA-GN-A266	MSS	SKCM
TCGA-GN-A26A	MSS	SKCM
TCGA-GN-A26C	MSS	SKCM
TCGA-H4-A2HQ	MSS	BLCA
TCGA-HB-A43Z	MSS	SARC
TCGA-HB-A5W3	MSS	SARC
TCGA-HD-7753	MSS	HNSC
TCGA-HE-A5NI	MSS	KIRP
TCGA-HE-A5NK	MSS	KIRP
TCGA-HE-A5NL	MSS	KIRP
TCGA-HF-7136	MSS	STAD
TCGA-HT-7695	MSS	LGG
TCGA-HT-8104	MSS	LGG
TCGA-HT-A5R7	MSS	LGG
TCGA-HT-A61B	MSS	LGG
TCGA-HU-8245	MSS	STAD
TCGA-HU-8608	MSS	STAD
TCGA-HU-A4G6	MSS	STAD
TCGA-HU-A4H0	MSS	STAD
TCGA-HW-7486	MSS	LGG
TCGA-IA-A40Y	MSS	KIRP
TCGA-IE-A4EI	MSS	SARC
TCGA-IE-A4EK	MSS	SARC
TCGA-IF-A4AJ	MSS	SARC
TCGA-IG-A3YB	MSS	ESCA
TCGA-IG-A97I	MSS	ESCA
TCGA-IK-7675	MSS	LGG
TCGA-IN-7806	MSS	STAD
TCGA-IS-A3K7	MSS	SARC
TCGA-IS-A3KA	MSS	SARC
TCGA-IW-A3M4	MSS	SARC
TCGA-IW-A3M5	MSS	SARC
TCGA-JY-A93C	MSS	ESCA
TCGA-K1-A3PN	MSS	SARC
TCGA-K1-A3PN	MSS	SARC
TCGA-KL-8325	MSS	KICH
TCGA-KL-8328	MSS	KICH
TCGA-KL-8330	MSS	KICH
TCGA-KL-8331	MSS	KICH
TCGA-KL-8332	MSS	KICH
TCGA-KL-8333	MSS	KICH
TCGA-KL-8334	MSS	KICH

TCGA-KL-8337	MSS	KICH
TCGA-KL-8341	MSS	KICH
TCGA-KL-8342	MSS	KICH
TCGA-KL-8343	MSS	KICH
TCGA-KL-8344	MSS	KICH
TCGA-KL-8346	MSS	KICH
TCGA-KM-8438	MSS	KICH
TCGA-KM-8439	MSS	KICH
TCGA-KM-8443	MSS	KICH
TCGA-KM-8476	MSS	KICH
TCGA-KM-8477	MSS	KICH
TCGA-KN-8418	MSS	KICH
TCGA-KN-8419	MSS	KICH
TCGA-KN-8421	MSS	KICH
TCGA-KN-8422	MSS	KICH
TCGA-KN-8424	MSS	KICH
TCGA-KN-8425	MSS	KICH
TCGA-KN-8426	MSS	KICH
TCGA-KN-8428	MSS	KICH
TCGA-KN-8429	MSS	KICH
TCGA-KN-8430	MSS	KICH
TCGA-KN-8431	MSS	KICH
TCGA-KN-8432	MSS	KICH
TCGA-KN-8434	MSS	KICH
TCGA-KN-8435	MSS	KICH
TCGA-KN-8437	MSS	KICH
TCGA-KO-8405	MSS	KICH
TCGA-KO-8406	MSS	KICH
TCGA-KO-8407	MSS	KICH
TCGA-KO-8409	MSS	KICH
TCGA-KO-8410	MSS	KICH
TCGA-KO-8416	MSS	KICH
TCGA-KO-8417	MSS	KICH
TCGA-L5-A4OF	MSS	ESCA
TCGA-L5-A4OJ	MSS	ESCA
TCGA-L5-A4OR	MSS	ESCA
TCGA-L5-A891	MSS	ESCA
TCGA-L5-A8NE	MSS	ESCA
TCGA-L5-A8NN	MSS	ESCA
TCGA-L6-A4ET	MSS	THCA
TCGA-L7-A6VZ	MSS	ESCA
TCGA-LN-A49L	MSS	ESCA
TCGA-LN-A49M	MSS	ESCA
TCGA-LN-A49Y	MSS	ESCA
TCGA-LN-A4A1	MSS	ESCA
TCGA-LN-A4A4	MSS	ESCA
TCGA-LN-A5U5	MSS	ESCA
TCGA-LN-A8I1	MSS	ESCA
TCGA-MH-A55W	MSS	KIRP
TCGA-MH-A560	MSS	KIRP
TCGA-MH-A561	MSS	KIRP
TCGA-MO-A47R	MSS	SARC

TCGA-N1-A6IA	MSS	SARC
TCGA-NH-A50T	MSS	COAD
TCGA-NH-A50V	MSS	COAD
TCGA-PD-A5DF	MSS	LIHC
TCGA-QG-A5YW	MSS	COAD
TCGA-QG-A5YX	MSS	COAD
TCGA-QG-A5Z1	MSS	COAD
TCGA-QG-A5Z2	MSI-H	COAD
TCGA-TM-A7CF	MSS	LGG
TCGA-TM-A7CF	MSS	LGG
TCGA-TQ-A7RK	MSS	LGG
TCGA-TQ-A7RK	MSS	LGG
TCGA-TQ-A7RV	MSS	LGG
TCGA-TQ-A7RV	MSS	LGG
TCGA-TQ-A8XE	MSS	LGG
TCGA-V5-A7RC	MSS	ESCA
TCGA-V5-A7RC	MSS	ESCA
TCGA-WP-A9GB	MSS	SARC
TCGA-X2-A95T	MSS	SARC

Supplemental Table 3. Summary of inferred MSI diagnoses from whole genome sequencing

	Fraction of Cases (Count)	
Cancer Type (TCGA Code)	**MSS**	**MSI-H**
BLCA	1 (24)	0 (0)
BRCA	1 (98)	0 (0)
CESC	1 (20)	0 (0)
COAD	0.79 (37)	0.21 (10)
ESCA	1 (19)	0 (0)
GBM	1 (61)	0 (0)
HNSC	1 (50)	0 (0)
KICH	1 (40)	0 (0)
KIRC	1 (41)	0 (0)
KIRP	1 (23)	0 (0)
LAML	1 (46)	0 (0)
LGG	1 (43)	0 (0)
LIHC	1 (32)	0 (0)
LUAD	1 (55)	0 (0)
LUSC	1 (41)	0 (0)
OV	1 (52)	0 (0)
READ	1 (18)	0 (0)
SARC	1 (41)	0 (0)
SKCM	1 (42)	0 (0)
STAD	0.87 (34)	0.13 (5)
THCA	1 (40)	0 (0)
UCEC	0.83 (24)	0.17 (5)

Supplemental Table 4. Microsatellites most informative for MSI per cancer type (p value)

Chromosome	Start Position	End Position	Gene(s) or distance to closest genes (dist)	UCEC	STAD	READ	PRAD	OV	LUSC	LUAD	LGG	KIRC	GBM	ESCA	DLBC	COAD	CESC	BRCA
15	65744267	65744286	DPP8	1.51E-10	1.78E-22	0.020209	1	0.057143	0.070613	1	1	0.02027	1	1	1	5.27E-13	1	0.167646
20	34099165	34099180	CEP250	1.13E-08	4.6E-21	1	1	1	1	1	1	0.027027	1	1	0.4	4.1E-08	1	0.184968
16	12145683	12145699	SNX29	2.17E-17	1.11E-20	1	0.03013	1	1	1	1	0.034881	1	1	1	1.83E-11	0.000187	0.00086
7	107575782	107575819	LAMB1	7.63E-06	0.002792	1	1	0.405542	1	0.321647	1	1	1	1	0.071429	3.11E-05	1	0.086303
16	56718015	56718036	MT1X	1.04E-08	3.34E-15	1	1	1	1	1	1	1	0.020833	1	1	2.86E-09	0.041096	0.36351
16	75674252	75674271	KARS	7.94E-23	2.87E-36	1.03E-05	0.023621	0.146337	0.000201	0.049991	1	0.025889	0.035294	0.027027	1	1.57E-35	7.05E-05	0.007429
18	649879	649895	TYMSOS	2.63E-36	1.03E-33	0.001053	0.000127	0.105188	0.002963	0.000358	1	0.024194	0.000566	0.030303	1	1.18E-38	0.000618	1.51E-07
2	128770731	128770743	SAP130	2.48E-13	5.53E-22	1	1	1	1	1	1	1	1	1	1	1.12E-12	1	0.017313
1	172577864	172577879	SUCO	1.28E-29	1.38E-22	0.00202	1	1	1	0.059353	1	1	1.67E-05	1	1	2.46E-22	0.020408	3.21E-06
1	52403174	52403187	RAB3B	3.5E-07	8.45E-16	0.166667	1	1	0.007143	1	1	1	1	0.025	1	0.000248	1	0.000705
1	92763091	92763128	GLMN	7.19E-11	3.89E-26	0.000111	1	1	0.082651	0.078702	1	1	1	0.105263	1	1.37E-25	1	1
10	74690437	74690455	OIT3	1.15E-15	5.03E-13	0.003659	1	1	1	1	1	1	1	1	1	5.57E-14	1	0.169852
11	118885668	118885701	CCDC84	3.57E-10	1.68E-16	9.19E-07	1	1	1	1	1	0.006803	1	0.016393	1	1.36E-17	1	0.048247
2	179407763	179407779	MIR548N,TTN-AS1	1.47E-29	2.98E-33	0.000247	0.009346	0.086957	0.066834	1	1	1	0.077586	1	1	7.61E-14	1	0.003514
8	134125650	134125662	TG	3.49E-17	1.1E-23	0.047619	0.008734	0.077519	0.025773	0.000474	1	0.021898	0.000229	0.000529	1	1.52E-06	0.000244	0.000126
1	144905992	144906020	NBPF20,NBPF9,PDE4DIP	3.57E-11	8E-08	0.006897	1	1	1	1	1	1	1	1	1	2.17E-07	1	0.014315
1	154562617	154562636	ADAR	2.76E-18	1.1E-13	0.003759	1	1	1	0.017778	1	1	1	1	1	5.77E-09	0.044195	0.004385
1	220284112	220284124	RNU5F-1	6.42E-20	1.24E-25	0.001012	0.008547	1	1	1	1	1	0.134034	0.014706	1	5.78E-11	0.000686	7.72E-05
1	46597496	46597508	PIK3R3	1.83E-09	3.6E-17	0.065027	1	0.110342	1	1	1	1	1	1	1	8.7E-11	1	0.07598
1	94497662	94497673	ABCA4	3.14E-06	6.91E-14	1	1	1	1	0.017241	1	1	1	1	1	6.13E-05	0.070779	0.012658
11	65273547	65273582	MALAT1	3.49E-11	3.59E-16	1	1	1	0.092248	1	1	1	0.009015	1	1	1	1	1
17	36477914	36477929	MRPL45	9.96E-14	2.21E-21	0.164048	1	1	1	1	1	1	0.003319	1	1	5.03E-09	0.001681	1
17	66038979	66038999	KPNA2	2.17E-09	1.19E-29	1	1	1	1	1	1	0.075472	1	1	1	1.11E-16	0.004141	0.007284
17	78343198	78343215	LOC100294362	0.721023	4.27E-12	1	1	1	1	1	1	1	0.286266	1	1	1.2E-05	1	0.020193
19	14827076	14827089	ZNF333	9.91E-18	6.49E-14	1	0.035317	1	0.02765	1	1	1	1	0.015625	1	9.17E-14	0.034091	0.055556
2	152424933	152424962	NEB	1.15E-14	6.96E-17	1	0.010417	1	1	0.013043	1	0.015625	0.086915	0.028986	0.263158	1.75E-26	0.094622	0.176705
2	33500751	33500763	LTBP1	8.49E-06	3.68E-09	0.079699	1	1	1	0.020161	1	1	0.054795	1	1	0.004416	0.012987	0.002837
2	70456452	70456465	TIA1	9.68E-26	2.25E-28	0.017544	1	0.066116	1	0.013889	1	0.011628	0.114551	1	1	8.79E-27	1	1.32E-07
22	29879265	29879302	NEFH	0.109645	3.75E-08	1	0.004975	1	1	0.015564	1	1	1	1	1	0.015883	1	1
3	172052897	172052914	FNDC3B	2.9E-28	4.26E-36	0.000846	0.004566	0.060811	1	1	1	0.007143	1	1	1	9.06E-17	1	0.011286
6	36452603	36452620	KCTD20	1.66E-22	6.6E-29	8.39E-06	1	0.229482	0.126414	0.000845	1	1	1	0.001681	1	2.83E-32	0.000974	1.18E-06
9	30689085	30689104	LINC01242(dist=280633),ACO1(dist=1695497)	1.47E-18	3.86E-14	0.000161	1	0.041667	1	1	1	0.041771	1	0.166667	1	3.97E-33	1	0.003533
1	215914883	215914896	USH2A	5.51E-08	1.85E-16	0.023256	1	1	0.005225	0.03661	1	0.014286	0.005746	1	1	5.2E-07	1	1.96E-05
1	225707271	225707295	ENAH	8.51E-25	7.88E-21	0.003507	1	1	0.029412	1	1	1	1	1	1	3E-18	0.020202	0.00139
10	99198507	99198528	EXOSC1	5.94E-07	9.01E-17	0.002105	1	1	1	1	1	0.019481	1	1	1	3.82E-12	0.057681	0.095574
11	9878320	9878353	LOC101928008	0.004335	2.01E-06	1	1	1	1	1	1	1	1	1	1	0.255814	1	0.113112
12	51053873	51053889	DIP2B	1.34E-12	6.98E-19	0.005848	1	1	0.08893	0.035209	1	1	1	1	1	1.06E-05	1	0.018852
19	55501348	55501365	NLRP2	1.04E-08	8.28E-18	1	1	0.429063	0.006565	1	1	0.028369	1	1	1	7.74E-16	1	0.013821
2	9558905	9558924	ITGB1BP1	5.37E-23	2.42E-24	0.065789	0.008772	1	1	1	1	0.058428	1	1	1	2.07E-23	1	0.116097
20	30818497	30818514	POFUT1	2.72E-14	7.99E-24	1	0.000129	1	1	1	1	0.053684	1	1	1	0.015789	0.001403	1
20	31954819	31954834	CDK5RAP1	3.77E-24	6.16E-24	0.076923	0.015968	1	1	1	1	1	5.89E-06	0.02	1	2.94E-26	1	0.000817
21	34907636	34907654	GART	2.36E-21	5.55E-29	0.003279	0.012097	1	0.03913	1	1	0.019231	1	0.021739	1	9.36E-19	1	0.018063
3	37360696	37360708	GOLGA4	1.03E-16	2.47E-19	0.004525	1	1	1	1	1	1	1	0.02439	1	1.01E-20	0.012346	0.114654
6	30619285	30619302	C6orf136	3.76E-07	1.86E-26	1	1	1	1	0.051054	1	1	0.078947	1	1	0.008422	1	0.045045
7	100843369	100843385	MOGAT3	1.19E-12	6.35E-25	1	1	1	1	1	1	0.021739	0.037207	1	1	1.93E-09	1	6.79E-05
8	13072066	13072084	DLC1	3.42E-07	1.33E-10	1	1	0.249265	1	1	1	1	1	1	1	2.43E-08	1	1
1	181714466	181714481	CACNA1E	3.7E-08	1.19E-18	1	1	0.071942	0.009406	1	1	1	0.167048	1	1	0.003077	0.024691	0.000363
1	237060945	237060970	MTR	1.8E-15	4.17E-21	0.002221	1	1	1	0.000471	1	1	1	0.014925	1	7.45E-19	1	0.000427
1	3697538	3697562	LRRC47	0.003424	1.41E-09	1	1	1	1	1	1	1	0.114656	0.027027	0.142857	0.004926	0.021505	1
1	67292737	67292748	WDR78	0.005608	6.19E-10	1	1	1	1	0.022222	1	1	1	1	1	3.32E-09	1	0.086915
10	116196143	116196156	ABLIM1	8.4E-19	8.05E-14	0.047619	1	1	0.042056	1	1	1	1	0.000784	1	9.25E-10	1	0.003773
12	4645161	4645173	C12orf4	6.63E-23	2.1E-28	0.122024	0.008696	0.065868	0.033981	0.015873	1	0.025862	1	1	1	3E-15	1	6.1E-06
14	39594134	39594146	GEMIN2	1.79E-15	4.36E-24	0.008737	0.012739	1	0.052174	0.005814	0.005051	1	0.12069	0.017857	1	1.36E-19	1	0.000152
14	57101560	57101576	TMEM260	2.55E-20	1.93E-24	0.006721	0.008511	1	1	0.032191	1	0.103824	0.133746	1	1	9.96E-11	1	0.000956
15	52561891	52561907	MYO5C	1.79E-24	1.36E-18	0.093702	1	0.093906	1	0.001449	1	1	0.101519	0.000512	1	3.67E-21	9.43E-06	0.258514
15	65739356	65739384	DPP8	2.53E-13	1.81E-16	0.087719	0.01956	1	1	1	1	1	1	1	1	7.8E-12	1	0.117071
15	94841981	94842010	MCTP2	0.002721	3.66E-11	1	1	1	1	1	1	1	1	0.021277	1	0.285714	1	1
16	15159022	15159039	PDXDC1,RRN3	2.71E-14	5.76E-25	0.000398	1	0.114551	1	1	1	1	1	0.024691	1	1.07E-28	0.057132	0.011073
17	1582787	1582825	PRPF8	5.34E-17	4.6E-11	0.008865	0.008368	1	0.064499	1	1	0.017857	1	1	1	0.003629	0.000618	0.005055
19	37155495	37155509	ZNF461	5.71E-18	3.79E-14	0.007389	1	1	0.000985	1	0.027027	0.023256	1	1	1	2.19E-05	1	4.89E-05
19	51919434	51919447	LOC100129083,SIGLEC10	8.48E-17	4.44E-16	0.001639	1	1	0.041284	0.012	1	0.044439	0.043796	0.000673	1	4.95E-11	0.034884	8.77E-07
2	178364328	178364342	AGPS	1.63E-29	1.35E-21	0.24883	1	0.070588	0.012577	0.043663	1	0.021429	1	0.000726	1	9.42E-07	0.001242	0.004624
2	227968771	227968782	COL4A4	5.4E-09	1.62E-13	0.1	1	1	1	1	1	1	1	1	1	0.002122	0.034884	0.001956
2	228680153	228680168	CCL20	2.64E-26	8.57E-34	0.015873	1	1	1	0.087666	1	0.039798	0.0003	1	1	5.57E-09	0.052632	0.000564
20	60587772	60587788	TAF4	5.91E-07	1.72E-31	0.076923	0.029701	1	0.090396	1	1	0.112269	1	1	1	1.06E-07	1	0.00556
3	137892531	137892543	DBR1	1.01E-06	9.04E-16	1	0.008658	1	0.031963	1	1	1	1	1	1	0.043245	1	0.006392
3	146177594	146177608	PLSCR2	5.53E-17	1.72E-26	0.000117	1	0.276043	1	1	1	1	0.17666	0.029412	0.003008	8.95E-20	0.003891	0.058463
3	58296209	58296232	RPP14	5.31E-14	4.54E-19	1	1	1	0.016497	0.037657	1	1	0.011921	0.086957	1	1.45E-14	0.000137	0.002426
3	97605460	97605472	CRYBG3	1.15E-15	5.65E-25	0.000264	0.004902	1	0.048913	0.045621	1	1	0.045752	1	1	1.87E-16	1	1
6	80910611	80910635	BCKDHB	1.05E-28	9.58E-24	0.000183	0.00939	0.322051	1	0.03448	1	0.041663	0.158623	0.003322	0.076923	1.54E-11	1.42E-05	8.08E-05
7	131130509	131130538	MKLN1	1.59E-09	1.19E-12	0.055556	0.005025	0.121622	1	1	1	1	1	0.013699	1	1.37E-06	0.024096	2.65E-05
7	135098181	135098192	CNOT4	0.000874	9.25E-10	1	1	1	1	1	1	1	1	0.040816	1	0.000471	1	0.000176
8	133984814	133984834	TG	1.54E-12	2.39E-32	0.0002	0.00885	0.136582	1	1	1	1	1	1	0.298246	2.67E-18	1	1
8	51314734	51314761	SNTG1	6.43E-11	1.12E-14	0.019231	1	0.205534	1	1	1	0.017857	1	1	1	2.67E-12	1	0.069069
8	67759411	67759438	C8orf44-SGK3,SGK3	3.48E-20	4.74E-28	0.000144	1	0.125743	0.077319	1	1	0.01626	0.110638	0.00101	1	4.44E-13	0.063987	0.000375
9	88650586	88650609	GOLM1	0.010307	6.56E-11	1	1	1	1	0.029142	1	1	1	1	1	1	1	0.00439
1	16248728	16248740	SPEN	1.07E-07	9.82E-16	0.034483	1	0.210986	1	1	1	0.015625	3.08E-05	1	1	1.76E-06	0.000584	0.001851
10	26825151	26825168	APBB1IP	1.29E-13	6.26E-35	0.007843	0.008811	0.019719	0.008323	3.79E-05	1	0.072262	0.215168	1	1	4.2E-18	1	0.00031
11	85979636	85979669	EED	0.000267	0.359874	0.140428	1	0.44873	1	1	1	1	1	1	0.176471	0.000153	1	0.030052
12	50867998	50868014	LARP4	1.27E-13	5.53E-23	0.0724	1	1	0.005102	0.057542	1	1	1	1	1	2.33E-16	1	1
13	51522081	51522094	RNASEH2B	7.77E-16	6.71E-23	0.000611	1	0.084809	1	1	1	1	0.0002	1	1	8.99E-07	1	0.028168
13	77644856	77644877	MYCBP2	8.42E-26	7.84E-26	0.016365	1	0.155545	0.136165	1	0.004739	1	1	0.090909	1	6.4E-22	1	0.312977
15	64717845	64717857	TRIP4	7.53E-14	8.15E-15	1	1	1	0.049224	0.000523	1	1	0.001763	1	1	2.23E-13	1	8.11E-06
17	19850675	19850696	AKAP10	5.46E-08	2.01E-12	0.027668	1	1	1	0.043473	1	1	1	1	1	6.8E-17	1	0.003726
19	11447769	11447783	RAB3D	1.18E-11	3.38E-21	0.055556	1	1	0.051282	0.025974	1	1	0.006303	0.066667	1	4.82E-09	1	1
2	153004816	153004839	STAM2	1.29E-12	5.26E-14	0.0625	1	1	0.072892	1	1	1	0.004126	1	1	3E-11	1	0.003169
2	228356364	228356398	AGFG1	4.38E-09	5.87E-16	0.006494	1	0.214402	0.102775	1	1	0.032967	1	1	1	6.49E-12	0.012406	0.380716
2	236877066	236877084	AGAP1	3.73E-17	8.62E-20	0.006368	0.039683	1	0.19517	0.097194	1	1	1	0.014493	1	3.85E-26	0.001099	0.14813
2	37487341	37487353	PRKD3	1.32E-10	1.4E-10	0.001586	0.009709	1	1	1	1	1	0.004922	0.000565	1	3.35E-11	0.000672	0.239826
2	61308569	61308585	KIAA1841	2.36E-25	3.01E-32	0.041667	1	1	1	0.000489	1	0.021978	2.14E-07	0.028571	1	8.51E-33	0.000325	0.010176
2	95816017	95816037	ZNF514	8.15E-07	1.02E-21	0.004898	1	1	1	0.053951	1	0.015267	1	0.083333	1	1.28E-08	1	0.139082
20	33338325	33338339	NCOA6	6.37E-16	5.91E-32	0.009662	1	1	0.029703	1	1	0.034884	0.06338	0.016949	1	2.57E-11	0.055164	0.063729
20	34430474	34430486	PHF20	7.13E-17	2.9E-26	0.044444	0.010582	0.075269	0.027473	0.012987	1	0.03125	0.069231	0.013333	1	7.39E-13	1	0.004392
22	25153810	25153836	PIWIL3	2.04E-09	8.74E-10	0.020993	0.025209	0.499888	0.062223	1	1	1	1	1	1	3.38E-08	0.029412	0.107629
3	121515940	121515953	IQCB1	1.09E-23	7.18E-32	0.015873	1	1	1	0.016	1	1	0.00019	0.016949	1	1.62E-07	1	0.000312
3	158526942	158526966	MFSD1	2.14E-19	3.31E-17	0.001279	1	1	1	0.000117	1	1	1	1	1	7.78E-22	0.032609	0.002288
3	169992958	169992994	PRKCI	1.34E-22	9.32E-24	2.29E-05	0.031556	0.108351	1	1	1	0.058596	1	1	1	9.87E-30	1	0.000112
3	39453367	39453378	RPSA	6.24E-10	2.21E-09	0.230769	1	1	1	1	1	1	0.046512	1	1	0.027569	1	0.011861
4	107133861	107133873	TBCK	4.19E-13	5.78E-23	0.06014	1	0.172663	1	1	1	1	0.002238	1	1	4.21E-08	0.075472	0.109836
4	156725681	156725695	GUCY1B3	8.36E-15	2.01E-11	0.009805	1	0.133177	0.166278	0.016598	0.016667	1	1	1	1	1.96E-10	0.00925	0.01178
7	75185990	75186002	HIP1	2.48E-24	4.46E-24	1	0.010471	1	1	0.000319	1	0.026229	1	0.020833	1	1.34E-14	1	0.110383
7	91714092	91714106	AKAP9	1.9E-20	9.4E-24	0.088195	0.01937	0.057692	1	0.012448	1	1	1.33E-06	1	1	9.61E-17	0.038961	0.118446
8	120856021	120856034	DSCC1	6.05E-19	5.16E-36	0.000305	1	1	1	0.060592	1	0.008403	0.002136	1	1	6.3E-10	1	0.065789
8	79629738	79629753	ZC2HC1A	7.36E-16	2.63E-22	0.139373	1	0.336532	1	1	1	0.028673	1	1	1	1.61E-11	1	9.7E-05
9	130116724	130116736	GARNL3	4.67E-15	1.52E-13	0.055556	1	1	1	1	0.004065	1	1	1	1	8.5E-05	1	1
X	10491233	10491259	MID1	1.98E-10	3.55E-09	0.002558	0.036197	1	1	0.119076	1	1	1	1	1	7.87E-18	1	0.003857
1	100684334	100684355	DBT	8.68E-11	8.99E-22	0.002262	1	1	1	1	1	1	0.103448	0.013699	1	6.6E-20	0.034884	0.004798
1	151403334	151403346	POGZ	2.02E-18	4.94E-16	0.149798	1	1	1	0.034113	1	1	1	1	1	2.53E-05	0.018868	0.063492
1	155671899	155671929	DAP3	7.72E-17	6.67E-26	0.047619	1	1	0.093203	1	1	1	0.00138	1	1	5.24E-08	0.012195	0.043114
1	155747369	155747381	GON4L	5.21E-10	2.36E-11	1	0.009132	1	0.02439	1	1	1	1	1	1	1.65E-10	1	0.059387
1	161091805	161091832	DEDD	1.52E-07	1.5E-05	0.356296	1	1	1	1	1	1	1	1	1	0.000884	1	0.027778
1	166962119	166962131	MAEL	3.06E-07	1.9E-23	0.105263	1	0.110512	1	1	0.003891	1	0.027408	1	1	3.05E-05	1	0.101424
1	201081283	201081293	CACNA1S	2.89E-05	4.73E-05	0.096774	0.043011	1	0.10643	1	1	0.039406	0.022291	1	0.294118	0.019236	1	0.630474
1	23636874	23636886	HNRNPR	2.43E-15	9.78E-21	0.018182	1	1	0.022222	0.020202	1	1	5.46E-05	1	1	1.15E-05	0.042857	0.000121
1	241663902	241663941	FH	6.85E-05	0.064951	0.057143	1	1	1	1	1	1	1	1	1	0.000126	1	0.021351
1	3549854	3549874	WRAP73	6.28E-07	2.37E-29	0.073171	0.009217	1	1	1	1	1	0.103448	1	1	7.4E-08	0.003911	1
1	82452554	82452578	LPHN2	1.52E-05	7.14E-21	0.005845	1	0.159676	1	0.017241	1	1	0.187678	1	1	2.58E-10	0.037037	0.025641
10	94774082	94774094	EXOC6	3.81E-11	8.45E-08	1	1	1	0.023622	1	1	1	1	1	1	8.27E-14	1	0.0625
11	108188266	108188280	ATM	7.69E-14	8.17E-21	0.0375	0.008889	0.179175	0.035897	0.015936	1	1	1	1	1	7.15E-13	0.027027	0.065156
11	118369265	118369290	KMT2A	1.1E-14	1.31E-36	0.014286	1	1	1	0.001824	1	0.015267	0.084173	1	0.058824	7.16E-08	1	9.87E-05
11	93490699	93490715	C11orf54	0.001045	1.97E-23	0.133333	0.012422	0.065421	1	1	1	1	1	1	1	0.000752	1	0.040816
12	118588746	118588795	TAOK3	1.32E-10	2.4E-06	0.002976	1	1	1	1	1	1	0.144148	1	1	4.44E-11	1	0.06326
12	122017894	122017916	KDM2B	1.94E-10	9.66E-40	0.002801	1	1	1	1	1	0.012903	1	0.022222	1	1.17E-08	0.026549	0.097589
14	35497274	35497286	SRP54	1.13E-24	4.77E-22	0.00508	1	0.089697	0.00805	0.000575	1	0.017241	1	0.027778	1	2.88E-15	1	0.00101
14	91633483	91633498	C14orf159	4.05E-11	7.63E-14	1	1	1	1	0.015873	1	1	0.004586	1	1	0.212121	1	0.003074
14	95574594	95574608	DICER1	2.63E-11	2.31E-19	0.1	1	0.134947	0.092159	0.051419	1	1	0.032258	0.142857	1	1.55E-09	1	0.022037
15	44057578	44057590	PDIA3	1.96E-12	2.9E-19	1	1	1	1	1	1	1	0.064286	1	1	1.63E-07	1	1
15	90229786	90229798	PEX11A	7.56E-18	1.43E-18	0.06383	1	1	1	0.015504	1	1	0.034014	0.089852	1	4.46E-11	1	4.22E-05
16	15758744	15758761	NDE1	6.69E-08	4.91E-20	0.08	1	1	1	0.037875	1	1	1	0.333333	1	5.69E-17	1	0.010245
16	31202698	31202716	FUS	3.41E-13	1.7E-10	0.000263	0.007843	1	1	1	1	0.011976	1	1	1	5.32E-15	0.000413	0.046008
16	71808499	71808519	AP1G1	1.67E-14	1.25E-17	0.076923	1	1	0.018405	0.0181	1	1	0.003774	1	1	8.85E-22	1	0.022602
17	35988718	35988739	DDX52	4.65E-10	8.48E-16	1	1	1	1	0.013699	1	0.026667	1	1	1	1.14E-05	1	0.00078
19	34872355	34872367	GPI	5.5E-11	7.85E-19	1	1	1	0.034483	1	1	1	0.000135	1	1	5.16E-08	1	0.067568
19	36145409	36145425	COX6B1	5.67E-30	6.24E-28	0.068966	1	0.061069	0.060137	0.022305	1	0.031619	0.053846	1	1	7.52E-22	0.012987	2.94E-06
2	102979238	102979250	IL18R1	2.63E-12	6.23E-19	0.083333	0.010152	1	0.025157	0.00012	1	1	0.003552	0.047619	1	9.05E-15	1	0.260387
2	103343275	103343295	MFSD9	6.47E-07	2.41E-13	0.000234	1	1	0.035573	1	1	1	1	1	1	3.54E-28	1	0.019769
2	200800572	200800585	TYW5	2.98E-19	1.47E-24	0.00188	1	1	0.15439	0.056195	1	0.01	0.060606	1	1	1.61E-13	1	8.09E-06
2	66796098	66796109	MEIS1	2.06E-27	4.01E-25	0.000403	4.69E-05	1	8.75E-06	0.028301	1	0.164048	0.003506	0.000784	1	7.34E-20	0.000101	0.000353
2	74754818	74754830	AUP1	4.41E-10	3.87E-27	1	1	1	1	0.036948	1	1	1	1	1	2.67E-18	1	6.09E-05

20	52675132	52675153	BCAS1	5.8E-08	5.4E-15	0.049383	1	1	1	1	1	1	1	1	1	1.56E-12	1	0.198933
3	160134195	160134221	SMC4	4.18E-06	7.1E-27	0.0625	0.011173	0.0625	0.033333	0.019737	1	0.035714	0.013158	1	1	2.05E-19	1	1
3	180680880	180680908	FXR1	6.35E-10	6.06E-08	0.181422	1	1	1	1	1	1	1	1	1	6.26E-06	1	1
3	194159705	194159736	ATP13A3	2.14E-14	3.93E-16	0.019608	1	0.069444	0.026549	1	1	0.015267	0.02994	1	1	3.34E-12	0.040541	0.000442
3	19498221	19498253	KCNH8	6.97E-17	2.5E-12	0.000925	0.009217	1	1	1	1	0.011494	0.004523	1	1	6.74E-13	1	0.013681
3	33725814	33725828	CLASP2	8.63E-20	3.5E-26	0.097561	0.009479	1	0.03	0.000987	1	0.034041	1	0.016129	0.238095	9.36E-13	0.021505	0.000278
4	128621144	128621158	INTU	3.6E-18	2.7E-25	1	1	1	0.032609	1	1	1	3.4E-06	0.015625	1	7.59E-19	1	0.009935
4	16362275	16362287	TAPT1-AS1(dist=102465),LDB2(dist=140878)	1.36E-12	8.03E-19	0.151636	1	0.166298	0.035358	0.074042	1	1	0.00234	1	0.368421	4.27E-11	1	0.11845
4	25315637	25315653	ZCCHC4	7.89E-25	7.52E-28	0.000594	0.040646	1	0.022141	1	1	0.001832	0.001395	1	0.066667	2.47E-19	1	0.13533
4	78815272	78815284	MRPL1	2.22E-11	3.45E-17	0.041667	1	1	1	0.043592	1	1	0.060241	0.017544	1	2E-14	1	0.164331
5	31435975	31435987	DROSHA	7.13E-14	2.52E-15	0.072054	0.009132	0.081301	0.010309	1	1	1	1	0.018519	1	1.15E-07	1	0.065574
6	10926514	10926528	SYCP2L	2.36E-17	6.47E-16	0.08	1	1	0.025723	0.084067	1	1	3.3E-05	0.035088	1	3.51E-08	0.007103	0.036238
6	15651642	15651656	DTNBP1	1.64E-32	3.1E-30	0.001329	1	1	0.064891	1	0.00813	1	1	0.015152	1	1.41E-23	0.071408	1.11E-07
7	100319680	100319696	EPO	5.87E-48	1.51E-23	0.057545	1	1	0.000419	0.013158	1	0.012346	1	0.056729	1	7.69E-18	4.51E-06	0.017851
7	86522420	86522432	KIAA1324L	8.04E-09	9.68E-23	0.00439	1	0.098704	0.02439	0.022831	1	0.022989	3.93E-08	0.166667	0.296296	2.63E-14	0.034483	0.021585
7	95818864	95818897	SLC25A13	3.2E-12	4.26E-11	0.007541	1	1	0.004592	1	1	0.013889	1	1	1	8.07E-08	1	0.211483
8	63948170	63948202	GGH	6.69E-12	1.38E-18	0.268571	0.03661	1	1	1	1	1	1	0.052632	0.2	3.24E-21	1	0.00031
9	102730697	102730712	STX17	1.59E-30	4.73E-30	0.000515	1	1	0.040541	0.040979	1	1	6.84E-05	0.018519	1	1.35E-19	1	0.000551
9	131743701	131743715	NUP188	4.55E-17	7.2E-29	0.039999	0.009091	1	0.043689	1	1	1	9.38E-05	1	1	3.36E-16	0.034483	5.67E-07
9	33062183	33062195	SMU1	4.57E-08	8.69E-17	1	1	0.042855	0.02	0.150651	1	1	0.440717	0.020408	0.066667	4.51E-06	0.06014	0.011678
9	80343587	80343612	GNAQ	4.29E-14	4.97E-27	0.014401	0.009132	1	1	0.001091	1	1	0.188619	0.002558	0.2	1.52E-19	0.091783	0.019664
9	90343456	90343467	CTSL	9.21E-10	2.03E-09	1	1	1	1	1	1	1	1	1	1	0.000123	1	0.007126
1	109839063	109839079	MYBPHL	3.34E-08	8.38E-08	1	1	1	1	1	1	1	1	1	1	0.000642	1	0.105438
1	12398426	12398437	VPS13D	0.000903	1.16E-09	1	1	1	1	1	1	1	0.003342	0.016393	1	7.97E-07	1	0.002338
1	150799125	150799138	ARNT	2.98E-09	2.38E-26	0.002885	0.010811	1	1	0.000478	1	1	1	1	1	1.56E-19	1	0.001173
1	160268834	160268846	COPA	1.99E-14	3.78E-22	0.007212	1	1	1	1	1	0.016529	0.058824	1	1	1.12E-10	1	0.063131
1	222904869	222904881	BROX	6.01E-27	5.06E-33	4.59E-06	0.008621	1	1	6.75E-06	1	0.037733	1	1	1	4.84E-29	1	0.157939
1	57349140	57349151	C8A	5.13E-10	2.64E-14	0.00363	1	1	0.040201	1	0.004016	1	1	1	0.263158	1.86E-09	1	0.032806
1	67154730	67154748	SGIP1	1.73E-11	3.2E-23	0.146154	0.001326	0.309696	1	1	0.048673	0.170399	0.001823	1	1	2.93E-10	0.020161	0.031043
1	84956161	84956173	RPF1	1.68E-21	7.07E-31	0.003279	0.000141	1	1	0.080281	1	0.022556	0.00136	0.033898	0.464286	9.52E-19	1	0.00168
10	112044559	112044572	MXI1	1.41E-20	8.85E-13	0.008865	0.008929	0.125196	1	0.012552	1	1	0.096039	0.055556	1	2.02E-05	1	0.078431
10	75576885	75576896	CAMK2G	7.32E-06	7.75E-10	0.019285	0.005556	1	0.038462	1	0.010989	1	0.115013	1	1	4.23E-05	1	0.118171
11	118626215	118626227	DDX6	2.05E-10	3.81E-21	0.022727	1	1	1	0.025478	1	0.032787	1	0.000546	1	2.07E-10	1	0.049383
11	46703002	46703014	ARHGAP1	4.7E-12	1.65E-14	1	1	1	1	0.000141	1	1	1	1	1	7.03E-15	1	0.00377
11	73429947	73429972	RAB6A	1.32E-10	1.02E-20	0.059701	1	1	0.039773	1	1	1	1	0.028986	1	7.32E-11	1	0.00026
12	90005161	90005173	ATP2B1	2.31E-20	5.49E-26	0.04	1	1	0.000767	0.000493	1	0.034333	0.000739	0.033898	1	5.13E-16	1	0.007961
14	76349004	76349024	TTLL5	3.23E-12	2.62E-07	1	1	1	1	1	1	1	1	1	1	0.003186	0.028169	1
15	30010328	30010349	TJP1	3.41E-24	7.29E-32	6.17E-05	1	1	0.07374	1	1	0.021898	1	0.024691	1	1.78E-20	1	0.183042
15	36910962	36910982	C15orf41	1.84E-17	1.96E-17	0.001681	1	1	0.202155	1	1	1	1	1	1	1.98E-07	1	7.14E-05
15	65847112	65847125	PTPLAD1	4.35E-16	1.79E-13	1	1	1	1	1	1	1	0.027211	0.041667	1	4.88E-13	1	0.000168
2	102785158	102785171	IL1R1	1.1E-13	2.48E-07	0.006974	0.075242	1	1	1	0.009479	0.052623	0.038095	1	0.296296	4.12E-22	1	0.000512
2	102959416	102959427	IL1RL1	7.43E-09	3.03E-22	1	1	0.080645	1	1	1	1	1	1	1	2E-12	0.030769	0.000138
2	166018764	166018775	SCN3A	0.094209	0.000247	1	1	1	1	1	1	1	1	1	0.235294	0.000605	1	1
2	179595571	179595589	TTN	0.000139	3.78E-17	0.000111	1	1	0.029126	0.097194	0.013889	1	0.041203	1	1	0.000827	1	1
2	183960133	183960155	DUSP19	2.11E-10	3.93E-23	0.08951	0.018735	0.132264	0.066332	0.001796	0.00463	0.020548	0.042424	1	1	2.73E-11	1	5.56E-06
2	188225486	188225497	CALCRL	2.58E-07	3.28E-12	1	1	0.081967	0.027027	1	1	1	1	1	1	1.4E-08	1	0.113615
21	34117067	34117080	PAXBP1	4.11E-22	3.96E-38	0.036364	1	1	0.039896	0.000604	1	0.027273	1	0.016949	1	6.56E-21	2.71E-05	0.088267
21	34635068	34635095	IFNAR2	8.15E-10	1.04E-10	1	1	1	0.129452	0.11059	1	0.037313	1	1	1	0.001531	0.001695	1
21	47821449	47821460	PCNT	0.001334	9.86E-11	1	0.013605	1	0.019417	0.031746	1	1	0.014225	1	1	7.15E-08	1	0.017391
22	39482241	39482254	APOBEC3G	4.41E-11	3.94E-15	0.03693	1	1	1	1	1	1	1	1	1	3.78E-08	1	0.004318
3	179481971	179482004	USP13	2.2E-07	0.160421	0.01063	1	1	1	1	1	1	1	1	0.087719	0.000418	0.08	0.000286
3	33877500	33877534	PDCD6IP	2.39E-11	2.46E-09	1	1	1	1	1	1	1	1	1	1	6.45E-07	1	0.001597
3	9730522	9730543	MTMR14	8.51E-10	7.13E-11	1	1	1	1	1	0.004695	1	1	1	1	5.47E-06	1	1
4	187627659	187627676	FAT1	3.26E-16	1.06E-23	0.001095	0.069093	0.146456	0.000274	0.079507	1	0.056526	0.157325	1	1	3.95E-08	0.001947	0.475902
5	52358761	52358775	ITGA2	2.19E-29	4.31E-24	0.030303	1	0.064086	1	0.000268	1	1	0.174754	1	1	1.22E-26	1	0.001818
6	30573637	30573656	PPP1R10	1.11E-15	1.06E-22	0.007103	1	1	0.141671	0.11438	1	0.088517	1	1	0.192308	7.53E-23	1	0.000221
6	31832356	31832372	SLC44A4	1.94E-13	1.8E-26	1	0.000268	0.088496	0.028169	0.031934	1	0.019608	1	1	1	5.53E-15	1	0.077267
6	6318921	6318936	F13A1	1.93E-07	1.85E-17	1	0.028708	1	1	0.048478	1	1	1	0.130435	1	4.43E-06	1	0.575859
7	5087800	5087822	RBAK,RBAK-RBAKDN	1.74E-13	1.18E-12	0.001587	1	1	0.034653	0.013043	1	1	0.041916	0.000584	1	1.47E-05	0.001403	0.000873
8	68140383	68140394	ARFGEF1	2.38E-15	1.82E-29	0.001587	0.006494	1	1	0.023256	0.011236	1	3.4E-05	0.016949	1	1.76E-20	0.073148	0.000125
8	75944409	75944422	CRISPLD1	1.62E-13	1.81E-14	0.105195	1	0.108302	0.178083	0.004778	0.031674	0.030417	1	0.0625	0.202797	4.05E-14	0.015624	0.008233
9	114295951	114295963	ZNF483	9.65E-08	1.08E-16	1	1	0.080775	1	1	1	0.013158	1	1	1	2.51E-09	1	1
9	8525217	8525230	PTPRD	0.000547	9.27E-13	1	0.02809	0.134615	0.083291	0.000151	1	1	0.00498	1	1	0.464286	1	0.083333
X	132888207	132888236	GPC3	8.1E-11	9.29E-15	0.007974	1	1	1	0.015564	1	0.032387	1	1	1	4.85E-12	1	0.011712
1	112305406	112305423	DDX20	7.75E-27	9.36E-21	0.002912	0.015066	1	0.111463	1	1	0.036142	1	0.012658	1	2.66E-25	1	0.001866
1	12368705	12368721	VPS13D	4.32E-15	8.11E-25	0.008564	0.008696	1	0.029703	1	1	1	0.065693	1	1	1.58E-16	1	0.0058
1	151384052	151384067	POGZ	3.73E-16	3.05E-32	1	0.000258	0.065574	0.059246	1	1	1	0.055901	1	1	1.5E-23	0.022472	0.005769
1	216373476	216373489	USH2A	8.85E-18	1.99E-15	0.017618	0.014706	1	1	0.015707	1	1	1	1	1	6.92E-15	1	0.056522
1	221875661	221875686	DUSP10	4.57E-16	3.96E-24	1	0.008969	1	0.060137	1	1	1	0.053691	0.000887	1	2.35E-09	1	0.064
1	44588267	44588285	KLF17	0.011311	4.61E-12	1	1	1	1	1	1	1	1	1	1	0.001179	1	0.143769
10	104620163	104620174	C10orf32-ASMT	0.000547	1.42E-09	1	1	1	1	1	1	1	1	1	1	1.48E-07	1	1
10	127789605	127789616	ADAM12	8.78E-07	0.000283	1	1	1	1	1	1	1	0.00053	1	1	0.00072	0.037975	0.077236
10	15828685	15828696	FAM188A	3.23E-05	1.82E-15	1	1	1	1	1	1	1	1	1	1	4.31E-07	1	0.143867
10	17646048	17646060	PTPLA	1.13E-17	7.39E-18	0.032258	0.01875	0.067568	0.058127	0.05954	1	0.015038	0.002584	0.036364	1	1.96E-16	0.020833	0.189642
10	38260558	38260601	ZNF25	6.45E-06	1	0.030303	1	1	1	1	1	1	1	1	0.507246	0.007489	1	0.000917
11	108121410	108121426	ATM	3.83E-18	5.07E-28	0.031621	1	1	0.000194	0.098606	1	0.033753	0.000743	0.08	1	3.57E-05	0.04878	0.037948
12	112579878	112579890	TRAFD1	4.49E-08	1.03E-18	1	1	1	1	0.022222	1	1	1	1	1	8.25E-12	1	0.048048
13	23808732	23808745	SGCG	5.78E-18	2.01E-23	0.00097	1	1	1	0.034555	1	1	0.001931	0.030769	1	3.47E-14	0.025974	0.247027
13	76430622	76430633	LMO7	8.47E-08	5.18E-11	1	1	1	0.02551	1	1	1	1	1	1	0.000158	1	1
14	45716018	45716030	MIS18BP1	2.36E-10	4.28E-15	0.042553	1	1	0.029412	1	1	1	0.002203	0.015385	1	2.42E-17	0.055164	0.000256
14	94046445	94046483	UNC79	0.004323	1.91E-05	1	1	1	0.027027	1	1	1	1	1	1	0.030119	1	0.057851
17	62855003	62855017	LRRC37A3	3.55E-20	2.59E-22	0.00266	1	1	0.034483	0.008	1	1	0.097493	0.015152	0.3	3.16E-19	0.002051	0.000169
19	36572251	36572263	WDR62	6.59E-18	4.06E-22	0.00363	1	1	1	0.000751	1	1	0.05042	1	1	1.93E-13	0.019608	0.000387
19	6013202	6013215	LOC100128568	0.00027	1.31E-08	1	1	1	0.015873	1	1	1	1	0.333333	1	0.145299	1	0.058812
2	10928694	10928709	PDIA6	3.95E-15	7.83E-30	0.018423	1	0.158007	0.01226	0.005164	1	1	1	1	0.142857	9.22E-15	0.08	0.010738
2	136511898	136511910	UBXN4	4.22E-08	4.86E-18	0.084181	1	0.012721	0.056807	1	1	1	0.283616	1	1	7.52E-06	1	0.302411
2	158275111	158275135	CYTIP	1.14E-20	4.79E-23	0.000191	1	1	1	1	1	1	1	0.014925	1	3.52E-24	0.061211	0.000153
2	192225477	192225514	MYO1B	8.45E-05	0.002933	1	1	0.045961	1	1	1	1	1	1	0.002259	3.28E-08	1	0.216111
3	122259738	122259756	PARP9	0.186885	1.59E-07	0.00363	1	1	1	0.053801	1	0.000949	1	1	0.227273	1.01E-08	1	0.282056
3	185641778	185641789	TRA2B	0.000631	7.14E-07	1	1	1	1	1	1	0.01	1	1	1	4.6E-07	1	3.2E-05
3	45500178	45500191	LARS2	2.04E-12	1.66E-09	1	1	1	0.059837	1	1	0.038458	1	0.058824	0.272727	1.45E-10	0.027027	0.02313
3	52676065	52676079	PBRM1	2.72E-16	8.92E-23	0.076169	0.014815	0.161829	1	1	1	1	0.002162	1	1	1.88E-10	0.002353	0.000141
4	119666217	119666241	SEC24D	1.95E-18	3.71E-30	0.065789	1	1	0.038647	1	1	1	1	0.026316	1	1.99E-20	1	0.000664
4	128814425	128814449	PLK4	2.19E-13	4.68E-35	0.000565	0.011834	0.068627	0.121249	1	1	0.027027	0.133921	0.042553	1	1.82E-30	0.016667	0.008488
4	160274602	160274613	RAPGEF2	0.00087	0.000288	1	1	1	1	1	1	1	1	1	1	5.13E-07	1	0.047872
5	147793666	147793680	FBXO38	6.31E-20	1.21E-26	0.14976	1	1	0.056169	0.014706	1	1	0.061947	1	1	6E-13	0.002646	0.003423
5	59901692	59901704	DEPDC1B	1.92E-17	4.11E-21	0.068966	1	1	0.090307	0.036444	1	0.009434	0.122956	0.002463	1	6.78E-08	1	0.010322
5	65081745	65081758	NLN	1.07E-11	1.11E-20	0.018197	1	1	1	1	1	1	1	0.026316	1	5.87E-08	0.055556	0.004114
6	143382254	143382285	AIG1	0.001986	0.099696	1	1	1	1	1	1	1	1	1	1	0.000869	0.024096	1
6	46636556	46636581	SLC25A27	1.08E-15	1.69E-19	5.78E-06	0.004545	1	0.004634	1	1	1	1	1	1	3.27E-22	1	0.006785
7	102727051	102727067	ARMC10	7.76E-38	9.56E-44	0.027037	1	1	0.001182	0.026667	1	0.032651	0.057554	0.000351	1	8.04E-23	0.028302	0.007555
7	107875143	107875165	NRCAM	1.64E-23	4.48E-21	0.000584	0.017429	1	0.040816	1	1	1	1	1	1	8.43E-14	1	4.53E-05
7	137076100	137076123	DGKI	1.62E-14	3.58E-22	2.4E-05	0.009346	1	1	0.012712	0.003906	1	1	1	1	3.9E-08	1	0.078176
8	127595047	127595058	FAM84B(dist=24336),PCAT1(dist=430341)	1.51E-17	1.91E-25	1	0.019184	1	1	1	1	1	0.057471	1	1	3.92E-11	1	0.001147
8	130874614	130874639	FAM49B	8.45E-24	8.92E-30	0.000966	1	1	0.034286	1	0.008299	0.009709	0.056738	0.016667	1	2.82E-20	0.068947	7.29E-05
8	23114189	23114218	CHMP7	0.001738	6.69E-09	0.058824	1	1	1	1	1	0.033193	1	1	1	0.029872	1	0.190932
8	74897025	74897036	TMEM70(dist=2007),LY96(dist=6528)	4.49E-06	4.59E-15	1	1	1	0.032258	1	1	1	1	1	1	3.5E-05	1	0.020234
X	100666907	100666921	HNRNPH2,RPL36A-HNRNPH2	8.12E-16	1.13E-16	0.01658	1	0.188435	0.037915	0.004878	1	1	0.07438	1	0.24	4.33E-07	1	0.032212
X	154009592	154009603	MPP1	9.85E-06	9.91E-09	1	1	1	1	0.018072	1	1	1	1	1	0.001313	1	1
X	69504063	69504115	RAB41	3.66E-08	1.85E-07	0.107071	1	1	1	1	1	1	0.052632	1	1	1.38E-08	1	0.116334
1	165712555	165712571	TMCO1	1.7E-26	5.83E-25	0.057143	1	1	1	0.000463	1	0.006579	1	1	1	1.71E-31	1	1
1	207753824	207753846	CR1	2.27E-22	4.64E-26	0.01941	1	0.005128	1	0.000308	1	1	1	0.058824	1	2E-12	1	0.00019
1	209974528	209974550	IRF6	8.76E-09	2.02E-11	0.095238	1	0.116514	1	1	1	1	1	0.00025	1	4.69E-11	1	0.001487
1	22082967	22082999	USP48	4.4E-05	7.07E-18	0.175084	1	1	0.054783	1	1	1	1	1	1	3.95E-08	0.028846	0.033617
10	120867694	120867705	FAM45B	5.28E-07	7.18E-09	1	1	1	1	1	1	0.014706	0.062016	1	1	4.27E-08	0.050633	0.144451
10	12708721	12708732	CAMK1D	2.04E-06	1.95E-10	0.079184	1	0.145629	0.036145	1	1	1	1	1	1	0.004685	1	0.237611
11	83180169	83180185	DLG2	1.29E-22	2.1E-22	0.00565	1	0.416563	1	0.196404	1	0.069244	0.050413	1	1	1.58E-14	0.000325	0.002209
12	54920288	54920301	NCKAP1L	1.02E-14	5.39E-13	1	1	0.212121	0.05695	0.036779	0.004184	1	1	1	1	3.5E-10	0.000529	0.00128
12	8692327	8692338	CLEC4E	1.17E-09	6.62E-20	0.214286	0.00032	0.095183	1	0.000273	1	0.017094	1	0.071429	0.111111	0.003796	1	1
13	115015966	115015983	CDC16	7.76E-11	1.7E-12	1	1	1	1	1	1	1	1	1	1	0.021132	1	1
13	37011617	37011628	CCNA1	4.05E-05	1.93E-22	0.241667	0.020887	1	1	0.014634	1	1	1	0.142857	1	2.16E-09	1	1
13	79216356	79216381	RNF219	8.49E-32	1.14E-34	2.53E-06	1	0.10929	0.038647	0.015385	1	1	1	0.000426	1	6.25E-34	1	5.67E-06
14	74426284	74426298	COQ6	7.5E-18	4.87E-21	0.05	1	1	0.011976	0.014423	1	0.03065	1	0.014706	1	1.54E-15	1	0.061321
15	66794298	66794311	RPL4	7.41E-18	2.71E-24	1	0.009259	1	0.000677	0.011364	1	1	1	1	1	3.32E-10	1	0.000103
15	83808031	83808046	HDGFRP3	9.38E-19	3.61E-26	0.139373	0.000211	1	0.001229	0.061208	1	1	2.62E-07	1	1	1.34E-11	0.030303	1.17E-05
17	30687599	30687612	ZNF207	3.18E-16	5.22E-18	1.58E-05	1	1	1	1	1	0.066646	0.049645	0.071429	1	3.05E-12	1	0.013051
17	57278908	57278920	PRR11	1.19E-25	6.56E-32	0.008547	1	0.037037	0.002445	0.022321	1	0.016807	0.053691	0.002221	1	9.17E-09	0.025974	2.09E-06
17	58153603	58153615	HEATR6	4.33E-14	6.85E-12	1	0.024793	1	1	1	1	1	0.073036	1	1	0.004797	1	0.124693
17	67178764	67178794	ABCA10	6.6E-08	1.23E-15	1	1	1	3.1E-05	0.044838	1	1	1	1	1	2.71E-08	0.012658	0.201249
18	6870798	6870817	ARHGAP28	0.003024	1.81E-11	1	1	0.142669	0.024242	1	1	1	1	1	1	0.000633	1	1
18	9954233	9954247	VAPA	1.67E-13	4.97E-17	1	1	1	1	0.050171	1	1	1	0.027397	0.294118	6.65E-12	0.020619	0.000194
19	10090461	10090482	COL5A3	8.73E-24	2.51E-24	0.252906	0.00939	0.13617	0.101957	0.049172	0.0125	0.022727	1	0.031746	1	7.18E-20	0.022472	1
19	9771286	9771300	ZNF562	6.76E-23	4.59E-31	0.003077	0.029998	0.036641	0.297233	0.001035	1	0.033753	0.13617	0.086957	1	1.03E-12	0.077647	0.023378
2	109371849	109371865	RANBP2	6.22E-21	7.14E-14	0.003507	1	1	1	1	1	1	1	0.03125	1	4.88E-30	0.001604	2.62E-08
2	109421324	109421335	CCDC138	0.000402	1.39E-12	1	1	1	0.058596	0.038926	1	1	1	1	0.333333	8.42E-09	0.041667	0.196902
2	197654578	197654593	GTF3C3	3.28E-28	7.58E-26	6.59E-05	0.010204	0.077419	0.025316	1	1	1	1	0.000565	1	8.36E-16	0.036145	0.000981
2	209113048	209113059	IDH1	0.022928	2.08E-09	0.002551	1	1	1	1	1	0.016529	1	0.037037	1	5.23E-05	1	1
2	27597190	27597204	SNX17	2.69E-22	1.86E-24	0.007742	1	0.064935	1	0.000299	1	0.036527	0.041379	0.031746	1	2.73E-17	0.001532	3.75E-05
2	61319728	61319740	KIAA1841	5.88E-06	1.03E-17	0.057692	0.010471	1	1	0.022222	1	1	0.053191	1	1	4.68E-17	1	0.07326
2	73635899	73635911	ALMS1	4.26E-07	3.99E-06	0.005984	1	1	0.030303	1	1	0.029851	0.006036	1	1	1.55E-06	1	0.137993
3	129123327	129123355	EFCAB12	0.000225	2.42E-10	0.007317	1	1	1	0.031744	1	1	1	1	1	1.09E-11	1	0.161206

3	179501968	179502006	USP13	1.05E-12	3.89E-10	0.040816	1	1	1	1	1	1	1	1	0.3	2E-12	1	0.039934
3	69111084	69111116	UBA3	3.09E-18	1.78E-20	0.015625	1	1	1	1	1	1	7.09E-05	1	1	4.41E-09	1	0.004073
3	93768420	93768439	ARL13B	1.13E-08	4.15E-11	0.003507	1	1	1	1	1	1	1	0.019608	1	1.59E-18	0.000316	0.000323
4	170077834	170077845	SH3RF1	3.59E-07	1.11E-10	0.058824	1	1	1	1	1	1	0.013495	0.018868	1	5.24E-09	1	0.023971
5	1260515	1260532	TERT	0.051823	0.000515	1	1	1	1	1	1	1	1	1	1	0.186813	1	1
5	130939025	130939037	RAPGEF6	3.3E-05	2.32E-11	0.003484	1	1	0.025974	1	1	1	0.003056	1	1	2.23E-19	1	0.037697
6	122733490	122733508	HSF2	1.08E-16	2.77E-20	1.23E-06	0.027649	1	0.060745	1	1	1	1	1	1	1.46E-14	0.033898	1
6	99817699	99817713	COQ3	4.02E-21	8.76E-25	7.98E-05	0.015625	0.06383	1	0.013953	1	0.045108	1	1	1	2.49E-14	1	0.005639
7	123329060	123329093	WASL	4.07E-08	0.000278	0.034709	1	1	0.177066	0.329837	1	0.075472	0.561657	1	1	0.026525	1	0.058845
7	64275470	64275486	ZNF138	2.86E-26	3.91E-24	0.028894	1	1	1	1	1	0.006849	1	0.052281	1	1.7E-12	1	0.001978
8	103287850	103287864	UBR5	3.56E-45	1.03E-37	0.03125	1	0.208179	0.000671	0.016807	1	0.050413	9.57E-05	0.027027	1	1.61E-33	0.001488	0.000156
8	24348425	24348437	LOC101929294,LOC101929315	6.5E-07	4.19E-17	1.18E-05	1	0.070922	1	0.000397	1	0.017391	0.003339	0.034483	0.2	1.09E-14	1	0.001072
8	37704283	37704295	BRF2	3.15E-05	3.67E-27	0.163043	1	1	0.000827	1	1	0.060593	0.057971	1	1	1.46E-05	1	0.070779
9	116039089	116039115	PRPF4	3.51E-07	2.87E-21	0.071429	1	1	1	1	1	0.013333	1	1	1	0.018403	1	0.00141
9	125827752	125827764	RABGAP1	6.7E-19	7.51E-22	0.029412	1	1	1	0.039212	0.004348	1	0.073821	1	1	2.12E-07	0.028846	1.63E-06
9	127287158	127287183	NR6A1	3.68E-18	1.13E-25	0.007974	1	0.079137	0.033019	0.00034	1	1	0.067114	1	1	1.65E-17	1	0.357585
9	133364619	133364644	ASS1	4.49E-08	2.29E-09	1	1	1	1	1	1	1	1	1	1	8.32E-06	1	0.045161
X	123204978	123204993	STAG2	8.15E-17	2.13E-22	0.036364	1	0.026738	1	1	1	1	0.012541	0.017857	1	9.14E-17	1	0.005042
1	116202126	116202161	VANGL1	0.000156	1.26E-05	1	1	1	1	1	1	1	0.082609	0.111111	1	0.006494	1	0.018893
1	153949135	153949147	JTB	4.06E-21	6.17E-30	0.003086	0.010256	1	0.081042	1	1	0.008	0.06338	1	1	8.61E-14	1	0.059701
1	156203572	156203588	PMF1,PMF1-BGLAP	3.65E-16	6.82E-17	0.009524	1	1	1	1	1	1	1	1	1	3.72E-11	0.001344	0.000116
1	210536178	210536190	HHAT	3.49E-12	3.15E-12	0.023469	1	1	1	1	1	1	1	0.013333	1	2.94E-06	1	0.056872
1	236721452	236721466	HEATR1	1.07E-09	5.12E-17	1	0.013986	1	1	1	1	1	1	1	1	3.87E-11	1	0.069444
1	63998326	63998338	EFCAB7	1.32E-15	2.61E-20	1	1	0.122017	0.066332	1	1	1	1	1	1	7.05E-19	0.023529	0.009495
10	102716310	102716330	FAM178A	4.26E-09	1.34E-05	1	1	1	1	0.012876	1	0.016529	1	1	1	1.71E-08	1	0.156496
10	26998490	26998502	PDSS1	1.1E-10	7.04E-11	0.079365	0.004348	0.076923	1	1	1	1	0.068966	1	1	3.84E-09	1	0.048518
10	88834244	88834265	GLUD1	1.14E-12	1.5E-20	0.006721	0.005181	0.06015	1	1	1	0.023529	1	1	1	5.95E-23	0.034483	1
10	98709108	98709119	LCOR	0.000259	1.39E-13	1	1	1	1	1	1	1	1	1	1	3.81E-05	0.086918	1
11	118247264	118247277	UBE4A	1.06E-18	2.93E-21	0.00266	0.032431	0.308893	0.004409	0.096084	1	1	0.00024	1	1	7.05E-08	0.003301	0.078472
11	119145463	119145476	CBL	2.96E-17	8.78E-21	0.039474	0.010989	1	0.022727	0.000518	1	0.015873	1	1	1	6.15E-14	0.094077	0.000153
11	65270090	65270116	MALAT1	0.000146	5.98E-10	0.035714	1	1	1	1	1	0.016949	1	1	1	0.215686	1	1
12	111926224	111926237	ATXN2	2.57E-17	4.29E-17	0.001586	0.01227	1	0.028902	1	1	1	0.051282	1	1	7.37E-15	0.042254	0.072848
12	118463653	118463672	RFC5	2.17E-19	8.9E-16	0.068966	1	1	1	1	1	0.019608	0.054645	1	1	2.15E-19	1	0.000129
12	122481641	122481656	BCL7A	0.000142	4.94E-17	1	0.024	1	1	1	1	0.045193	1	1	1	0.095238	1	0.188732
12	22063251	22063266	ABCC9	3.3E-13	6.43E-22	0.3	0.040096	0.020909	0.022453	0.175365	1	1	0.043478	1	1	0.000424	1	0.008585
12	50867692	50867704	LARP4	4.49E-05	2.76E-13	1	1	1	1	0.000363	1	1	0.054348	0.00085	1	9.87E-07	0.001399	0.06
12	6858889	6858905	MLF2	2.96E-11	2.08E-21	1	0.018349	0.119076	0.005844	1	1	0.02439	0.045045	1	1	9.88E-05	0.06383	8.58E-06
14	103915242	103915254	MARK3	5.32E-12	2.58E-20	0.000324	0.005181	1	0.041885	1	1	1	5.46E-05	1	1	5.93E-20	1	1
16	4700318	4700337	MGRN1	3.9E-10	6.7E-18	1	1	1	1	0.049715	0.03	0.012195	1	1	1	2.9E-19	0.026316	0.053104
16	67805993	67806026	RANBP10	2.06E-09	9.84E-08	0.005464	1	1	1	0.094873	1	1	1	1	1	2.44E-10	1	0.002461
17	18785823	18785842	PRPSAP2	1.26E-10	7.48E-23	0.01063	0.005076	1	1	0.04477	1	1	9.27E-10	0.055556	1	1.48E-10	1	1
17	39723415	39723439	KRT9	1.29E-11	5.34E-14	1	1	0.561531	0.011478	1	1	0.000701	0.116564	1	1	0.005526	1	0.018022
17	46190093	46190110	SNX11	1.19E-10	1.54E-07	0.00058	1	1	1	0.040298	1	1	1	1	1	8.63E-16	1	0.001295
17	66041871	66041886	KPNA2	4.25E-18	1.47E-28	0.130435	0.034286	0.149967	1	0.118384	1	0.079334	0.034986	1	1	6.39E-06	0.006171	0.355177
18	30913142	30913153	CCDC178	3.67E-05	9.89E-13	0.001107	0.007407	0.075	0.021505	1	1	1	0.096774	1	1	1.06E-12	0.027778	1
18	66367726	66367742	TMX3	3.51E-21	1.22E-22	0.000247	0.02005	0.182234	1	0.038551	1	1	1	0.000966	1	1.58E-26	0.000882	0.049921
19	40587849	40587876	ZNF780A	4.79E-07	7.21E-11	0.001057	1	1	1	1	1	0.032787	1	1	0.176471	3.98E-10	1	0.016838
19	9645753	9645773	ZNF426	6.74E-05	5.24E-08	0.108108	1	0.059524	1	0.042323	1	1	0.026667	1	1	1.83E-05	1	0.132077
2	112854563	112854576	TMEM87B	1.08E-18	4.37E-28	0.047619	0.015464	1	1	1	1	1	0.000251	1	0.363636	7.88E-29	1	0.225776
2	120620092	120620108	PTPN4	7.11E-24	1.6E-29	0.109015	0.015228	0.067568	1	1	1	0.036364	0.101846	0.001111	1	1.27E-24	1	1.41E-07
2	157370018	157370033	GPD2	6.94E-28	3.55E-25	0.011094	0.004505	0.047904	0.095388	0.016194	1	1	0.102775	1	0.272727	2.09E-24	0.027778	0.000682
2	201534173	201534187	AOX1	6E-17	2.24E-27	0.004267	0.000279	1	0.044554	0.046237	0.004587	1	1	1	1	6.94E-12	0.001161	0.003183
2	228159652	228159677	LOC654841	1.58E-16	4.33E-32	0.001474	0.100689	0.229761	6.15E-06	0.030973	1	0.035714	8.41E-05	1	1	0.006019	0.022395	0.000338
2	238277142	238277163	COL6A3	2.81E-06	1.5E-06	1	1	0.066667	1	1	1	1	1	0.018868	1	1.83E-08	0.000699	0.10499
2	242263615	242263626	SEPT2	1.5E-05	4.26E-10	0.057692	1	0.107543	1	0.025773	1	1	1	1	1	4.48E-13	0.048479	0.067797
2	27708007	27708031	IFT172	2.29E-10	3.26E-18	0.052632	1	1	1	1	0.012397	1	5.77E-07	0.018519	1	2.79E-14	0.033333	0.073171
2	29125053	29125064	WDR43	9.37E-12	4.5E-19	0.076169	1	1	0.089082	1	1	1	1	0.072054	1	1.77E-13	1	1
2	37113791	37113809	STRN	0.001288	0.000415	0.002463	1	1	1	1	1	1	1	1	1	3.43E-07	1	0.004525
2	70463334	70463348	TIA1	2.61E-18	4.14E-16	0.023031	1	0.053333	1	1	0.004032	0.05245	1	0.016393	1	1.07E-08	0.046512	0.019429
20	50713983	50714011	ZFP64	3.93E-08	1.19E-19	0.065574	1	1	1	1	1	0.008	1	1	1	3.27E-07	1	1
22	29682873	29682894	EWSR1	2.84E-29	7.44E-23	0.076169	1	1	0.033981	1	0.004525	1	1	0.027397	1	5.73E-18	0.034884	0.000398
22	46679850	46679864	TTC38	4.18E-28	2.44E-40	0.018519	1	1	0.001885	1	1	1	0.039735	0.014286	1	4.72E-22	0.002443	2.77E-09
3	113655096	113655108	GRAMD1C	1.98E-14	6.9E-25	0.139373	0.004464	1	1	1	1	1	1	0.03125	1	4.12E-11	0.014085	0.149318
3	130733046	130733058	ASTE1	1.02E-20	2.54E-24	2E-05	0.019277	0.063291	0.001301	1	1	0.026316	0.010145	1	1	3.02E-16	1	0.002018
3	132173004	132173026	DNAJC13	4.74E-15	1.37E-24	0.002487	1	0.068966	0.039773	0.000271	1	1	0.067164	1	1	1.13E-27	0.001174	0.162734
3	141622616	141622641	ATP1B3	0.007304	0.000307	1	0.006329	1	1	1	1	1	1	1	1	0.000888	0.029412	0.058824
3	146167163	146167186	PLSCR2	5.51E-11	1.25E-14	0.024066	0.009804	1	0.058467	0.024896	1	0.008772	1	0.042553	1	2.35E-06	1	0.000113
3	45776875	45776914	SACM1L	7.05E-13	1.41E-16	0.004408	1	1	1	0.046325	1	0.009091	0.008717	1	1	1.03E-11	0.06665	0.326464
3	50339381	50339395	HYAL1	2.12E-09	3.19E-06	1	1	1	1	1	1	1	0.017857	0.103841	1	1.52E-06	1	1
4	140262240	140262251	NAA15	0.000189	1.2E-09	1	1	1	1	0.013986	1	1	1	0.021739	0.15	7.63E-07	1	1
4	146076632	146076644	OTUD4	2.62E-14	1.3E-14	0.000108	1	0.363691	1	0.00878	1	1	0.000514	1	1	5.38E-15	1	0.006121
4	160253030	160253041	RAPGEF2	1.52E-06	4.95E-07	0.136213	1	1	0.026316	1	1	1	1	1	1	4.74E-11	1	0.005445
4	26417055	26417080	RBPJ	2.7E-12	4.15E-23	0.06298	4.39E-05	1	0.126736	0.031432	1	1	1	0.032258	1	4.15E-19	1	0.030353
5	112720977	112720988	MCC	1.43E-08	3.78E-11	0.287449	1	1	1	1	1	1	1	0.029412	1	1.76E-05	1	0.124064
6	147635318	147635347	STXBP5	3.86E-13	6.32E-05	0.073375	1	0.651242	0.035645	1	1	1	0.05041	1	0.53268	1.29E-07	1	0.039785
7	115891736	115891750	TES	2.37E-18	5.45E-16	0.06	1	1	0.111776	0.053801	1	1	4.48E-05	1	1	4.12E-08	0.065918	0.000951
7	26883761	26883776	SKAP2	6.76E-24	3.17E-32	0.000109	1	0.201192	1	0.003678	1	1	0.223367	1	0.083333	2.81E-14	0.000733	0.013429
7	29407518	29407543	CHN2	9.68E-06	9.23E-09	0.064516	1	0.086207	1	1	1	1	1	1	1	3.91E-07	0.030769	1
7	73279233	73279260	WBSCR28	0.035716	1.18E-07	1	1	0.355284	1	0.000965	0.012121	1	0.130279	1	1	0.021451	1	0.000433
8	38880851	38880862	ADAM9	1.23E-06	8.86E-09	0.064516	1	1	1	1	1	1	0.082569	0.015385	1	3.91E-07	0.059249	0.01474
8	68334940	68334952	CPA6	9.92E-11	2.81E-11	0.120192	1	1	1	1	1	1	0.026667	1	1	2.3E-09	1	0.024346
8	70516957	70516974	SULF1	0.000396	3.16E-09	1	1	1	0.127113	1	1	1	0.034483	1	1	2.58E-05	1	0.050505
8	74585483	74585494	STAU2	1.81E-05	4.28E-11	1	0.01227	1	1	1	1	1	1	0.033898	1	9.78E-08	1	0.160013
9	125511990	125512001	OR1L6	3.57E-07	1.36E-12	1	1	1	0.072048	0.022222	1	1	1	1	0.375	4.61E-09	1	0.004058
9	2083313	2083338	SMARCA2	1.13E-17	3.03E-25	0.040816	0.005376	1	0.004835	0.014085	1	1	1	1	1	2.23E-14	1	0.030488
1	101194965	101194977	VCAM1	1.36E-12	6.43E-12	1	0.061054	1	0.007225	0.104484	1	1	0.02304	0.094077	0.333333	0.011748	0.057971	0.095965
1	107866731	107866743	NTNG1	4.19E-08	1.15E-11	0.117647	1	0.152632	1	0.02216	1	0.082867	0.031915	1	1	0.0021	1	1
1	108160260	108160273	VAV3	7.02E-17	6.87E-15	0.537602	1	1	1	1	1	1	0.312831	1	1	2.03E-14	0.057545	0.001756
1	155701055	155701071	DAP3	4.07E-25	1.84E-21	0.001142	1	1	2.42E-05	1	1	0.017241	1	0.014085	1	8.04E-25	0.038462	0.001058
1	160461188	160461199	SLAMF6	4.58E-05	2.09E-10	1	1	1	1	1	1	1	1	1	1	0.000608	1	0.125262
1	200559220	200559231	KIF14	0.007219	4.15E-05	0.007937	1	0.03125	1	1	1	1	1	1	1	0.006371	1	1
1	245222673	245222684	EFCAB2	0.016124	2.35E-07	0.066667	1	1	1	1	1	1	1	1	1	0.013586	1	1
10	116605738	116605750	FAM160B1	3.53E-21	3.08E-28	0.014872	1	0.041667	0.022388	1	1	0.02381	0.018956	1	1	9.43E-15	1	0.003168
10	91483908	91483928	KIF20B	3.86E-07	2.57E-18	0.0114	1	1	1	1	1	0.017544	1	1	1	2.36E-10	0.016949	0.123429
12	107080617	107080640	LOC100287944	9.64E-07	7.6E-05	0.122984	0.009615	0.414176	1	1	1	1	1	1	0.018182	0.028592	0.033333	0.053711
12	125587478	125587491	AACS	1.42E-14	3.9E-35	1.3E-06	1	0.075208	0.000498	1	1	1	1	1	1	3.9E-23	0.031915	0.012255
12	416046	416060	KDM5A	1.26E-17	1.11E-21	0.001161	0.026596	1	0.141011	0.159471	1	0.069848	0.017304	0.037736	1	5.35E-12	0.055936	0.063187
12	56213978	56213991	ORMDL2	1.53E-14	7.36E-18	0.115294	1	0.142857	0.06868	0.000385	1	1	5.5E-06	1	1	8.93E-08	0.017857	0.001022
12	56744020	56744045	STAT2	3.03E-12	1.61E-13	0.079365	1	0.015962	1	1	1	1	1	0.019608	1	0.000158	0.001536	0.000599
12	66716618	66716630	HELB	1.14E-19	2.77E-17	0.004706	0.017897	0.079755	0.026042	1	1	1	0.040936	0.016667	1	1.81E-09	0.046512	0.003841
13	115007533	115007545	CDC16	3.29E-12	7.16E-17	1	1	0.248706	0.034283	0.037293	1	0.01626	1	1	1	6.24E-14	1	1
14	95571635	95571647	DICER1	6.64E-10	5.14E-24	0.034694	1	1	1	0.047331	1	1	1	1	1	7.13E-10	1	0.041509
15	40505736	40505754	BUB1B	0.002406	5.1E-06	0.083333	1	1	1	1	1	1	1	1	1	0.027429	1	0.116667
16	22579717	22579776	LOC653786	7.76E-10	0.113006	0.005026	1	1	1	1	1	0.03463	1	1	0.006106	2.67E-05	0.071408	1
16	70176311	70176336	PDPR	5.45E-29	9.9E-17	0.145253	1	0.1322	1	1	1	0.035926	1	0.000699	1	4.05E-10	0.000631	0.025931
17	17041157	17041168	MPRIP	3.72E-05	2.43E-08	0.045455	1	1	1	1	1	0.029412	1	0.037736	1	0.002544	1	0.018182
17	2238741	2238760	TSR1	9.32E-13	4.57E-19	0.044444	0.024615	0.120192	1	1	1	1	1	1	1	1.41E-14	0.041667	0.23453
17	40457520	40457546	STAT5A	7.56E-11	6.99E-10	0.024425	1	1	1	1	1	1	1	1	1	0.001594	1	0.143551
19	34832292	34832305	KIAA0355	7.05E-10	7.91E-11	1	1	1	0.02381	1	1	1	1	1	1	7.61E-06	1	0.13389
2	141625630	141625642	LRP1B	1.41E-07	4.24E-13	0.008207	1	1	0.200965	0.0199	1	1	1	1	1	6.13E-11	0.000427	0.001993
2	165365365	165365376	GRB14	7.6E-06	2.33E-15	1	0.00641	1	0.017241	1	1	0.019608	0.145833	1	1	1.84E-05	1	0.000114
2	175246386	175246411	CIR1	1.32E-09	2.57E-26	0.147313	1	1	1	0.014851	1	1	1	1	1	1.68E-17	1	0.000968
2	202137288	202137313	CASP8	9.31E-07	1.49E-08	1	1	1	1	1	1	1	1	1	1	0.011218	1	1
2	55559651	55559667	CCDC88A	8.63E-24	1.93E-17	0.014401	0.0181	1	0.209463	0.061208	1	0.05084	1	0.036364	1	1.48E-18	0.022472	2.41E-06
2	55907799	55907810	PNPT1	5.88E-08	1.52E-06	0.002449	1	1	1	1	1	1	1	1	1	0.000246	1	0.072398
20	37187110	37187134	RALGAPB	7.44E-08	6.68E-09	1	1	0.162921	1	1	1	0.008772	1	1	1	7.43E-12	1	0.146601
20	402971	402984	RBCK1	0.008791	1.55E-11	1	1	1	1	1	1	1	0.060823	1	1	1	1	1
21	30925853	30925869	GRIK1	5.45E-18	3.34E-17	0.011927	1	1	0.025451	0.100341	0.029167	1	1	1	1	1.9E-05	0.020408	0.26918
3	164905648	164905660	SLITRK3	4.01E-20	2.32E-23	0.061274	4.98E-05	0.067485	0.081777	1	1	1	1	1	0.363636	9.33E-17	1	0.073429
3	167000006	167000017	ZBBX	1.7E-06	5.23E-14	0.044444	1	1	1	1	1	1	0.060811	1	1	1.06E-09	1	0.162359
3	179103328	179103352	MFN1	1.92E-08	1.02E-07	0.139373	1	1	1	1	1	1	1	1	0.007353	4.69E-05	1	0.188029
4	79847634	79847654	PAQR3	1.67E-08	8.91E-15	1	1	1	0.025381	1	1	1	1	1	1	2.65E-17	1	0.067449
5	109049507	109049530	MAN2A1	3.66E-19	2.89E-22	0.002714	1	0.30402	0.094673	0.059508	1	1	1	0.037037	0.24	2.73E-11	1	0.001038
5	118487582	118487593	DMXL1	0.001997	1.45E-08	0.000726	1	1	1	0.046915	1	1	1	1	1	1.7E-09	1	0.073375
5	134086670	134086684	CAMLG	5.35E-20	6.11E-22	0.001442	0.012658	1	1	1	1	1	1	0.018182	1	4.27E-24	0.026667	5.07E-05
5	146773709	146773725	DPYSL3	4.09E-13	6.52E-14	0.057143	1	0.073529	0.012903	1	1	1	0.051724	0.092262	1	5.94E-10	0.041447	1
5	151180439	151180475	G3BP1	4.35E-10	3.9E-05	0.000161	1	0.084619	1	1	1	0.017544	1	1	1	9.53E-22	0.021978	0.001645
5	154305379	154305390	GEMIN5	2.38E-06	6.57E-12	1	1	1	0.066648	1	1	1	1	1	1	7.16E-06	0.045455	1
5	33546113	33546143	ADAMTS12	9.68E-08	1.56E-08	0.000117	1	0.016948	1	1	1	1	0.17666	0.000452	1	2.08E-13	1	0.010189
5	33561022	33561043	ADAMTS12	1.24E-13	1.49E-32	0.027473	1	0.063383	0.100595	0.023041	1	0.113122	0.064516	0.00404	1	0.023736	0.077895	0.00029
5	43536904	43536916	PAIP1	5.23E-06	1.07E-09	0.042553	1	1	0.067017	0.038737	1	1	0.070463	1	1	2.87E-07	1	0.25937
5	83432985	83433037	EDIL3	2.12E-08	0.020547	0.088235	0.035791	0.52186	0.202315	1	1	1	1	1	0.005882	0.048789	1	0.007164
6	107420417	107420451	BEND3	9.58E-08	5.49E-22	0.023469	1	0.253937	1	1	1	0.045455	1	0.036364	0.005848	5.23E-09	0.000398	0.007458
6	76728583	76728598	IMPG1	1.53E-21	3.42E-22	0.00425	1	0.122686	1	1	1	1	0.001045	0.077647	1	2.02E-15	0.043478	0.006558
6	90452808	90452835	MDN1	2.49E-11	7.09E-20	0.002353	0.010204	1	1	1	1	0.015385	0.0625	0.041667	0.285714	3.03E-11	1	0.202163
7	40234742	40234756	SUGCT	1.28E-24	2.32E-17	0.201128	0.021164	0.332585	0.236662	1	1	1	0.209748	0.079184	0.108392	3.37E-20	0.036364	2.03E-05
7	7572355	7572381	COL28A1	3.76E-25	3.29E-35	0.002899	0.008929	1	0.02139	1	1	0.047613	1	1	1	9.95E-22	0.000439	9.3E-06
7	87485539	87485551	SLC25A40	6.08E-16	1.87E-17	0.011723	1	1	0.036364	0.042776	1	1	1	1	1	1.67E-15	0.042553	0.221313
7	92900502	92900527	CCDC132	4.55E-24	1.3E-31	3.68E-05	0.015504	0.035294	1	0.088184	1	1	0.051282	1	1	1.13E-37	0.000584	0.008798
8	95186510	95186526	CDH17	4.12E-34	2.28E-32	0.015015	0.000112	0.220665	0.072868	1	1	0.039212	1	0.06298	1	5.66E-16	1	4.66E-05
9	131456159	131456172	SET	2.85E-26	2.32E-35	0.033898	1	1	0.045065	7.61E-06	1	1	0.002962	0.000414	0.25	6.67E-21	0.022222	0.015051

9	132838831	132838842	GPR107	4.86E-07	2.34E-12	1	1	1	1	1	1	1	0.028986	1	1	1.79E-05	1	0.085293
X	101409243	101409271	BEX5	6.01E-23	1.73E-11	0.000161	1	0.067227	1	0.015326	1	1	1	0.028571	1	5.26E-17	0.081186	0.022574
X	111090289	111090311	TRPC5	3.99E-09	2.69E-12	1	1	0.142665	1	0.016736	1	1	1	0.055556	1	2.23E-05	0.012346	0.036645
X	117530912	117530925	WDR44	2.84E-25	1.86E-17	1	1	0.05	1	0.044242	1	1	1	0.021277	1	1.12E-11	0.037037	0.000116
X	15607586	15607598	ACE2	2.63E-15	2.35E-15	0.076169	1	1	0.027523	0.052109	1	1	1.56E-06	0.037037	1	2.12E-14	1	0.003455
1	153955601	153955614	RAB13	9.95E-14	5.12E-18	0.074627	1	1	1	0.000807	1	1	0.000323	1	1	5.35E-10	1	1
1	183176970	183176986	LAMC2	1.98E-15	1.88E-16	0.04878	0.039502	1	0.235644	1	1	1	1	0.090909	1	9.12E-15	1	0.056804
1	230798864	230798876	COG2	2.45E-21	2.32E-12	0.001442	1	1	0.040201	0.016461	1	0.045449	0.058065	1	1	3.75E-17	0.00084	0.00172
1	235316088	235316100	RBM34	9.59E-08	4E-07	1	1	1	0.054598	1	1	1	1	0.033333	1	2.74E-09	1	0.059633
1	236737874	236737886	HEATR1	1.51E-13	2.56E-15	0.153627	1	0.0625	0.000433	0.014563	1	0.021978	0.071429	1	1	1.65E-08	1	0.007703
10	102739143	102739159	MRPL43,SEMA4G	0.002728	3.18E-17	1	0.073708	0.068164	0.034483	1	1	1	1	1	1	5.9E-17	1	0.001197
10	114297930	114297954	VTI1A	3.02E-06	4.6E-08	1	1	1	1	1	1	1	1	0.028571	1	5.74E-09	0.033333	0.089953
10	32575773	32575785	EPC1	8.52E-15	2.71E-28	1	1	0.081633	0.035503	1	1	0.027273	0.045113	0.028571	1	2.07E-21	0.020202	0.000104
10	69716602	69716614	HERC4	6.84E-16	8.6E-24	0.158163	1	1	1	1	0.012448	1	0.149736	0.033898	0.384615	4.81E-15	0.021978	0.000482
10	7747034	7747047	ITIH2	2.4E-13	2.76E-12	0.006452	1	1	1	1	1	1	0.07	1	1	6.04E-08	1	0.000234
11	75316787	75316823	MAP6	2.19E-09	1.14E-09	1	1	1	1	1	1	0.016807	0.061856	0.02381	1	9.02E-09	1	1
12	104461711	104461723	HCFC2	3.75E-23	1.67E-29	1	0.032651	1	0.030303	0.042662	1	0.133181	5.96E-08	0.019231	1	3.32E-16	0.039216	9.39E-06
12	107398862	107398876	CRY1	9.28E-22	3.69E-26	1	1	0.005368	0.018868	0.058125	1	0.03947	0.000108	1	1	7.39E-08	1	4.04E-08
12	40716037	40716052	LRRK2	2.69E-20	5.69E-17	0.009307	1	0.070064	1	1	1	1	0.152585	1	1	5.63E-15	0.118688	0.00261
13	113527868	113527879	ATP11A	2.46E-10	2.44E-16	0.005571	1	0.051095	1	0.021739	1	1	1	1	1	8.22E-16	0.000529	8.33E-05
13	28609813	28609824	FLT3	0.000154	7.83E-11	1	1	1	1	1	1	1	1	1	1	1.64E-08	1	0.025028
14	35899480	35899493	NFKBIA(dist=25520),INSM2(dist=103755)	2.41E-23	1.96E-20	0.073915	1	1	0.003412	0.044242	1	1	1	0.021739	1	4.39E-25	0.021739	0.000341
14	73079138	73079150	RGS6(dist=45900),DPF3(dist=6854)	9.28E-07	1.37E-23	1	0.000116	0.044248	0.038213	0.000152	0.00578	1	0.006348	1	1	0.010989	1	0.020619
14	91467510	91467532	RPS6KA5	3.2E-05	3.73E-09	1	1	1	1	1	1	1	1	1	1	7.77E-08	0.036585	0.086207
15	75909933	75909947	SNUPN	2.77E-12	1.56E-13	1	1	1	1	1	1	0.015267	0.015748	0.333333	1	5.48E-14	1	0.003257
16	30975312	30975326	SETD1A	1.37E-09	1.11E-11	1	1	1	1	1	1	1	0.026786	1	1	0.000111	1	0.006741
17	17931884	17931902	ATPAF2	6.66E-07	4.13E-11	0.042254	1	1	1	1	1	1	1	0.020833	0.290323	8.08E-17	1	0.542944
17	33445416	33445427	RAD51L3-RFFL	1.29E-05	4.09E-14	1	0.026549	1	1	1	1	1	1	0.03125	1	0.001739	1	1
18	24039893	24039904	KCTD1	3.62E-08	8.02E-25	1	1	1	1	1	1	1	0.05036	1	1	0.000983	1	1
18	77737714	77737726	TXNL4A	4E-12	3.09E-19	0.000966	1	1	0.00023	1	1	0.032609	0.081395	1	1	2.28E-13	1	1
2	100079130	100079164	REV1	7.03E-05	3.59E-06	1	1	1	0.055556	1	1	1	1	1	1	0.001534	1	0.066667
2	141272360	141272372	LRP1B	5.21E-14	3.65E-13	0.007103	0.013423	0.133986	0.118312	1	1	0.044113	1	0.113636	1	2.64E-10	1	0.068706
2	143913281	143913292	ARHGAP15	0.026418	8.82E-10	0.115294	1	1	1	1	1	0.015038	1	1	1	6.05E-07	1	1
2	167138320	167138331	SCN9A	4.45E-10	3.6E-22	0.00895	0.01227	1	1	0.010935	0.016949	1	0.115385	0.001639	0.231304	2.71E-14	0.025316	0.012795
2	174094381	174094392	MLK7-AS1	1.06E-08	6.07E-14	1	1	0.140784	1	1	1	1	1	1	1	3.4E-08	1	0.07837
20	37191391	37191408	RALGAPB	2.2E-21	4.33E-23	0.000111	1	0.219261	0.032967	0.047707	1	0.014184	1	0.000426	1	3.22E-24	0.020619	0.105841
20	60861505	60861519	OSBPL2	5.09E-05	9.03E-23	1	0.013575	1	1	1	0.008889	0.021053	1	0.027778	1	5.45E-06	0.051282	0.018939
21	34878454	34878468	GART	2.32E-08	1.02E-08	1	1	1	0.02381	0.020202	1	1	0.089127	1	1	3E-06	1	1
21	36080444	36080459	CLIC6	1	1	1	1	0.096154	1	1	1	1	1	1	1	0.158416	1	1
21	46602483	46602497	ADARB1	9.23E-16	2.16E-23	1	1	1	0.001162	1	1	1	0.106023	1	1	5.56E-11	0.002501	0.100735
3	113166840	113166859	SPICE1	1.41E-06	1.3E-08	0.000699	1	1	1	1	1	1	1	1	1	2.39E-10	1	1
3	132166148	132166162	DNAJC13	1.39E-23	3.52E-23	0.001639	0.019184	1	1	1	1	1	0.056928	0.000966	1	2.49E-16	0.001279	0.000383
3	179333753	179333764	NDUFB5	8.31E-07	1.47E-10	0.130303	1	1	1	0.024631	1	1	1	0.032787	1	3.04E-07	1	0.149436
3	186522293	186522308	RFC4	5.42E-21	1.1E-20	0.065574	1	1	1	1	1	0.014925	0.012331	0.014925	1	2.71E-21	0.021739	0.000609
3	19959707	19959719	EFHB	3.75E-08	7.11E-29	0.046512	0.02	0.0625	0.049074	0.059874	1	0.083333	8.74E-05	1	1	3.04E-14	0.002096	4.34E-06
3	28304768	28304779	CMC1	3.27E-07	3.1E-06	0.069767	1	1	1	1	1	1	1	0.033898	1	5.79E-08	1	0.009829
4	145659167	145659178	HHIP	5.06E-09	3.27E-08	0.125	1	1	1	1	1	1	0.085714	0.015152	1	0.15	1	0.141582
4	155180652	155180681	DCHS2	0.000199	0.000526	0.004538	1	0.399064	1	1	1	0.015385	0.231496	1	1	0.000514	1	0.008284
4	54265883	54265894	FIP1L1	2.3E-10	3.65E-17	0.00202	1	1	1	1	1	1	0.213481	0.0125	1	2.35E-10	0.043956	0.126371
5	137763868	137763912	KDM3B	8.39E-07	1.19E-08	0.088235	0.005405	1	0.037234	1	1	1	1	1	1	7.34E-05	0.027397	0.118831
5	14388797	14388816	TRIO	4.59E-18	1.3E-20	0.004354	1	0.077844	0.04	1	1	1	1	1	1	5.8E-24	1	0.020425
5	413428	413452	AHRR	2E-09	0.001034	1	1	0.207196	0.00061	1	1	1	0.074601	1	0.0625	0.22531	0.007974	0.006453
5	7896957	7896969	MTRR	1.39E-11	4.75E-17	0.001279	1	1	1	0.026515	1	1	0.057692	0.028986	1	2.02E-18	1	0.118059
6	52768392	52768408	GSTA3	3.19E-21	2.77E-13	0.003165	1	0.113725	1	1	1	1	0.015873	1	0.25	6.2E-12	0.001357	2.15E-06
7	123332378	123332391	WASL	6.96E-16	5.76E-19	0.001207	0.010152	1	0.061054	0.022321	1	0.030887	1	0.055556	1	3.13E-14	1	1
7	151874147	151874157	KMT2C	2.29E-09	4.09E-18	1	1	1	0.056738	1	1	1	1	0.04878	1	0.003687	1	0.003764
7	84671609	84671620	SEMA3D	5.99E-07	4.96E-12	1	1	1	1	0.005814	1	1	0.065574	1	1	0.000394	1	1
7	92020452	92020465	ANKIB1	2.57E-10	2.12E-28	0.000219	1	0.150456	0.028986	1	1	1	1	1	1	3.34E-17	1	3.21E-06
8	80831393	80831407	MRPS28	1.42E-32	7.74E-32	0.000816	0.010638	1	1	0.000276	1	0.014388	0.092613	0.05	0.105263	3.58E-23	1	1.26E-06
9	13193320	13193332	MPDZ	4.36E-16	2.96E-15	0.089852	1	0.060811	1	1	1	0.013889	1	0.017857	1	7.02E-06	0.037037	0.007733
X	18183097	18183113	BEND2	1.33E-12	4.43E-19	0.045455	0.004673	0.197186	0.066645	0.013216	1	1	0.155956	1	1	0.001302	0.2	0.000922
X	48136515	48136526	SSX1(dist=9636),SSX9(dist=24459)	2.44E-14	8.9E-24	1	1	0.088355	1	1	1	1	1	1	1	0.000104	0.064501	0.007774
X	48214185	48214200	SSX3	1.25E-42	1.4E-26	0.000302	1	0.171332	1	0.000247	1	0.046869	0.004667	0.001442	1	2.22E-27	0.001852	2.51E-06
1	116234024	116234041	VANGL1	0.002156	7.32E-07	1	1	1	1	1	1	1	1	1	1	0.182692	1	1
1	116655183	116655197	MAB21L3	1.1E-14	3.9E-26	0.058824	1	0.095238	0.025236	0.000479	1	1	1	0.029851	1	6.5E-08	0.053684	0.000789
1	153994527	153994552	NUP210L	1.01E-06	1.65E-06	1	1	0.068182	1	1	1	1	0.131579	0.018182	1	0.020886	1	0.045113
1	169586220	169586233	SELP	1.94E-11	2.15E-24	0.005288	1	1	1	0.023148	1	1	1	1	1	6.34E-16	1	0.002739
1	28086989	28087014	FAM76A	0.011603	0.00277	1	1	1	1	1	1	1	1	1	1	0.18	1	1
1	3788978	3788992	DFFB	7.37E-09	7.83E-08	0.150769	1	1	1	1	1	1	1	1	1	4.29E-07	1	0.299278
1	71535064	71535075	ZRANB2	2.78E-07	5.67E-09	1	1	1	1	1	0.004831	1	1	1	1	4.14E-05	1	0.080851
1	79383748	79383762	ELTD1	1.47E-17	1.59E-23	0.00049	0.029555	0.002878	0.038251	0.026785	1	1	1	1	0.263158	5.04E-24	1	0.050392
1	86246998	86247012	COL24A1	6.06E-12	2.56E-18	1	1	1	1	0.035853	1	1	0.004735	1	1	0.004141	1	0.004186
10	105139888	105139903	TAF5	5.59E-19	7.04E-20	0.012987	1	0.043165	1	0.030149	1	1	1	1	1	3.32E-07	1	0.00324
10	81667391	81667414	LOC100288974	7.94E-08	9.37E-11	0.01087	1	1	1	0.039698	0.004505	0.043712	1	0.1	0.142857	0.000107	0.001498	1
11	108004919	108004941	ACAT1	3.89E-09	5.34E-20	0.00489	1	1	1	0.046915	1	1	1	0.05	0.3	8.2E-15	1	0.038748
11	118454476	118454495	ARCN1	4E-09	1.2E-13	1	1	1	0.035533	1	1	0.03292	0.075092	1	1	1.31E-10	0.00101	0.141403
12	104515109	104515121	NFYB	1.67E-20	7.41E-28	0.15847	0.006667	0.033333	0.002757	1	1	1	0.067416	1	1	4.26E-09	1	0.013187
12	133375066	133375092	GOLGA3	4.02E-09	2.84E-31	1	1	1	1	0.041837	1	1	1	1	1	2.58E-09	1	1
12	45771901	45771918	ANO6	1.13E-18	1.44E-15	0.00058	1	1	1	1	1	0.012987	0.04142	0.000452	1	1.13E-24	0.042553	0.000611
12	66531936	66531947	TMBIM4	8.52E-05	3.22E-12	1	0.013333	1	0.001941	1	1	1	0.083333	1	1	0.001096	1	0.008567
13	37596114	37596125	SUPT20H	8.19E-07	1.31E-12	0.023256	7.57E-05	1	1	1	1	1	1	1	1	4.11E-09	1	0.000781
13	73409508	73409522	PIBF1	8.9E-30	1.23E-27	3.06E-05	0.045065	0.177254	2.4E-05	0.008867	1	0.121081	0.012602	0.047619	1	1.34E-23	0.111016	0.083782
15	25232026	25232045	PWAR5	0.567068	0.006148	1	1	1	0.114638	1	1	1	1	1	1	0.111111	1	1
15	44852433	44852444	EIF3J	4.2E-10	1.53E-10	0.065574	1	1	0.0375	0.039698	1	1	1	1	1	1.83E-09	0.045977	0.004522
15	80460576	80460591	FAH	2.27E-22	5.93E-31	0.000705	1	1	0.049528	1	0.004545	0.020833	0.113543	0.003507	1	2.18E-19	0.033898	7.74E-06
16	69965396	69965409	WWP2	1.98E-06	1.58E-19	0.099942	1	1	0.034483	1	1	1	1	1	1	1.76E-07	0.003812	0.004983
17	31324330	31324379	SPACA3	9.88E-05	0.008604	0.090909	0.031412	1	1	1	1	1	1	1	0.031579	0.000532	1	0.009636
17	34151245	34151260	TAF15	1.19E-22	2.89E-21	0.04918	1	0.266241	0.00136	1	1	0.050413	1	0.035714	1	2.85E-19	1	0.001936
17	35696841	35696853	ACACA	2.32E-14	1.84E-16	0.086957	1	1	1	1	1	1	1	0.000481	1	7.81E-12	1	1
17	58525202	58525229	APPBP2	1.72E-18	1.56E-20	1	1	1	1	1	1	1	1	1	1	6.82E-09	0.014286	0.05974
18	9279678	9279703	ANKRD12	1.41E-07	4.35E-19	0.002634	1	1	1	1	0.008734	0.013514	1	0.055164	1	9.92E-12	0.023529	0.004593
2	114475433	114475444	SLC35F5	0.001689	7.52E-08	0.027027	1	1	1	1	1	1	1	1	1	0.000244	0.027397	1
2	192011485	192011497	STAT4	2.85E-24	2.26E-19	0.006368	0.004608	1	0.091321	1	1	1	1	1	1	3.45E-20	0.011364	0.000387
2	28521140	28521152	BRE	2.29E-07	4.98E-16	0.003846	1	1	1	1	1	0.017391	0.057971	1	1	0.000197	1	0.004245
2	64323751	64323763	PELI1	3.96E-27	7.96E-19	0.066102	1	0.059603	0.026882	1	1	1	1	1	1	5.65E-25	1	8.76E-05
2	8998775	8998788	MBOAT2	1.18E-13	4.18E-21	6.14E-06	6.57E-05	1	1	0.080176	1	1	1	0.05	1	1.92E-13	1	0.144327
3	129168854	129168881	IFT122	3.31E-35	3.35E-18	0.000122	1	1	1	1	1	1	1	0.00037	1	1.35E-14	0.061211	5.07E-05
3	160083950	160083968	IFT80	1.78E-05	9.35E-15	0.119318	1	1	1	1	1	1	1	0.022222	1	1.15E-05	1	0.098446
3	37845264	37845282	ITGA9-AS1	0.139822	0.011679	1	1	1	1	1	1	1	1	1	1	0.244186	1	0.066667
3	41756845	41756856	ULK4	1.11E-09	3.02E-11	0.025641	1	0.2	1	1	1	1	1	0.027397	1	2.19E-09	0.030769	0.169482
3	43756577	43756612	ABHD5	1.05E-07	0.030955	0.19937	1	1	1	1	1	0.052796	1	1	0.014286	0.001722	1	0.012479
4	54327211	54327223	LNX1	3.41E-10	2.84E-14	0.001753	1	0.037405	1	1	1	1	0.098101	1	0.384615	9.66E-10	1	0.218637
4	78806528	78806540	MRPL1	2.69E-06	1.32E-06	1	1	1	0.06	1	1	0.022222	1	1	1	8.46E-07	1	0.001469
5	126847109	126847120	MEGF10(dist=50199),PRRC1(dist=6181)	0.006942	4.83E-09	1	1	1	1	1	1	1	1	1	0.166667	0.000681	1	0.043011
5	32057910	32057923	PDZD2	8.99E-19	1.58E-14	0.017857	1	1	0.016949	0.069742	1	1	1	1	1	2.85E-20	0.001053	0.000156
7	128631979	128631990	TNPO3	2.1E-05	9.93E-13	1	1	0.116689	1	1	1	1	1	1	1	0.001207	1	1
7	151267237	151267248	PRKAG2	3.59E-05	2.5E-11	0.057143	1	1	0.03125	1	1	1	1	1	1	0.003317	1	0.153601
7	2641048	2641083	IQCE	2.78E-09	1.2E-10	0.004141	1	1	0.027149	1	1	1	1	1	1	1.07E-11	1	0.026653
7	75155143	75155157	PMS2P3	7.4E-26	2.81E-17	0.115294	1	1	1	1	1	1	1	0.015625	1	1.04E-17	0.049074	0.065753
7	8110836	8110848	GLCCI1	5.36E-20	2.23E-16	0.001282	1	1	0.069424	0.01105	1	1	1	1	1	9.91E-10	1	1
8	22053163	22053178	BMP1	5.75E-08	1.48E-18	0.2	1	1	1	1	1	1	0.051282	0.013889	1	1.02E-07	1	1
8	42761288	42761308	HOOK3	2.24E-18	4.85E-24	0.00266	3.97E-05	1	1	1	1	1	1	1	1	1.3E-13	1	0.178294
X	46510851	46510901	SLC9A7	4.7E-08	6.53E-16	0.047619	1	1	1	1	1	0.02	1	1	1	2.45E-05	1	1
1	151380720	151380737	POGZ	9.78E-20	1.9E-17	0.048387	4.69E-05	1	0.021053	1	1	0.03065	1	1	1	1.83E-14	1	0.00358
1	207240818	207240829	PFKFB2	2.69E-05	5.77E-10	0.08599	1	1	1	1	1	1	1	0.037736	1	6.98E-07	1	0.056338
1	207737670	207737691	CR1	0.000235	0.679087	1	1	1	1	1	1	1	1	1	0.093407	0.001163	1	0.058167
1	235826382	235826396	LYST	1.59E-09	1.41E-17	0.08	1	1	1	1	1	0.000644	0.000731	1	0.2	0.000146	1	0.179491
1	28218773	28218784	RPA2	0.000115	2.84E-13	0.009009	1	0.04918	1	1	1	1	1	1	1	1.04E-06	1	0.000164
1	28785729	28785740	PHACTR4	1.74E-07	9.61E-15	0.330435	1	0.041667	0.060227	1	1	1	1	1	1	4.24E-11	0.027397	0.010789
1	41456808	41456823	CTPS1	3.93E-33	1.31E-28	0.1	0.006803	0.112676	1	0.048641	1	1	1	0.000546	1	9.8E-16	1	3.11E-05
1	62740780	62740792	KANK4	1.74E-10	1.71E-20	0.005348	1	0.048611	1	0.024272	1	1	0.029197	1	1	1.01E-08	1	0.110376
1	89449508	89449520	RBMXL1	4.99E-21	2.88E-28	1	0.011561	1	0.003497	0.029762	1	0.012821	0.076087	1	1	5.68E-23	0.022222	0.008479
1	99762456	99762467	LPPR4	2.24E-06	5.87E-11	1	1	1	0.101618	1	1	0.020833	1	1	1	4.87E-07	1	4.59E-06
10	112360315	112360333	SMC3	7.66E-28	1.89E-24	8.23E-07	0.00905	1	1	0.024631	1	1	1	0.07997	1	1.18E-37	1.13E-06	0.014225
10	127483396	127483423	UROS	1.97E-08	9.27E-08	0.016158	1	1	1	1	1	1	1	1	1	2.69E-07	0.026316	0.182432
11	126174242	126174254	DCPS	0.004635	0.000362	1	0.039022	1	0.016949	1	1	1	1	1	1	2.43E-05	1	0.07337
11	134118382	134118401	THYN1	1.07E-10	5.1E-22	0.119898	0.010101	1	0.056195	0.001386	1	1	1	1	1	7.74E-08	1	0.003725
11	65268479	65268492	MALAT1	1.7E-10	8.25E-26	0.176471	0.000614	1	0.019481	0.00077	1	0.014286	0.002466	1	1	0.005848	0.03125	0.030887
13	48664556	48664569	MED4	4.7E-18	4.08E-35	0.000117	0.011299	1	1	1	1	1	0.095754	1	1	2.37E-25	0.015385	9.54E-05
13	76370755	76370769	LMO7	7.78E-16	3.22E-08	0.035088	1	0.164921	0.37805	1	1	0.10913	1	0.117647	1	4.73E-16	1	0.031761
14	21960425	21960451	TOX4	0.000119	8.67E-09	0.068182	0.007937	1	1	0.000442	1	1	1	1	1	6.85E-06	1	1
15	22709277	22709288	GOLGA8DP	1.62E-06	7.53E-11	0.166667	1	1	1	1	1	1	1	0.017544	1	0.230769	0.03125	1
15	42714195	42714207	ZNF106	2.17E-09	6.17E-13	0.176136	1	0.059701	1	1	1	1	0.049837	1	1	1.7E-10	1	1
15	48826427	48826440	FBN1	2.66E-14	4.43E-25	0.199507	0.010417	0.115284	0.146337	0.07084	1	0.043791	1	0.044444	1	6E-06	0.053333	0.017892
17	15909736	15909747	TTC19	0.000179	9.13E-12	1	1	0.081967	1	1	1	1	1	1	1	0.000248	1	0.09816
2	223158424	223158439	PAX3	0.024074	2.19E-07	1	1	0.09434	1	1	1	1	1	0.021739	1	0.001742	1	0.059633
2	228109615	228109654	LOC654841	2.17E-06	8.73E-08	0.04	1	0.236135	0.062242	1	1	1	1	0.066667	1	7.65E-05	1	0.440242
20	16359356	16359369	KIF16B	3.48E-07	6.89E-21	0.019231	1	1	0.000778	0.188029	1	0.015873	0.315011	0.033333	1	5.82E-11	1	0.111024
22	30781774	30781790	RNF215	5.99E-10	8.18E-19	1	1	1	0.02168	1	1	1	0.020408	1	1	0.000321	1	1
3	48491343	48491366	ATRIP	1.93E-18	6.34E-28	0.098305	1	1	0.001806	0.018293	1	0.094622	1	0.000496	1	6.98E-23	1	0.007721
4	113107829	113107845	C4orf32	2.91E-19	3.64E-32	0.048387	1	0.012294	1	1	1	1	0.002249	1	1	9.93E-20	0.027027	0.001336

4	153268227	153268252	FBXW7	6.19E-20	1.24E-15	0.189337	1	1	1	1	1	1	1	1	1	9.91E-18	1	1.61E-07
4	169612452	169612484	PALLD	4.69E-10	1.68E-09	0.011868	0.010256	0.050279	1	1	1	1	0.001854	0.000605	1	2.46E-18	0.024096	1
4	48136087	48136098	TXK	6.32E-05	2.82E-11	1	0.014184	1	1	1	1	1	1	1	1	2.25E-05	0.051282	0.079365
5	10405809	10405822	MARCH6	3.34E-18	4.75E-18	0.057971	1	1	1	0.00037	1	1	1.78E-05	0.058824	1	2.61E-20	1	0.064
5	14485161	14485175	TRIO	4.2E-38	1.79E-31	5.69E-05	1	1	2.88E-05	0.001578	1	0.02909	0.010255	0.000649	1	4.44E-28	1	7.16E-05
5	147795682	147795713	FBXO38	9.55E-12	1.16E-14	0.004141	1	0.143603	1	1	1	0.019108	1	1	1	4.16E-09	1	0.132259
5	33881669	33881683	ADAMTS12	0.000171	1.76E-19	0.142857	1	1	1	0.04807	1	1	1	1	1	2.97E-05	1	1
5	34945797	34945810	DNAJC21	1.88E-09	7.55E-18	0.074746	0.010152	1	0.027778	0.023148	1	1	1	1	1	5.06E-18	1	7.39E-05
5	37326073	37326084	NUP155	7.44E-08	5.3E-08	1	0.005747	1	0.013333	1	1	1	0.126167	1	1	1	1	1
6	144758647	144758660	UTRN	2.79E-11	3.19E-11	1	1	1	1	1	1	1	0.00053	1	1	1.31E-05	1	0.000499
6	24589046	24589057	KIAA0319	8.81E-13	3.97E-15	0.001948	0.011696	1	1	5.57E-05	1	1	1	0.004267	1	6.41E-15	1	0.049057
6	90432565	90432587	MDN1	3.3E-07	3.3E-16	0.014286	1	1	1	1	1	1	1	0.027027	1	3.44E-08	1	0.054892
7	135256008	135256041	NUP205	4.85E-11	1.03E-14	0.090865	1	1	1	1	1	1	1	1	1	1.27E-16	1	0.075843
7	48048728	48048739	SUN3	6.73E-06	2.28E-08	1	1	1	1	1	1	1	0.043956	1	1	6.95E-07	0.015625	0.036018
7	87005287	87005312	CROT	1.07E-12	1.2E-12	0.08599	1	1	0.030303	1	1	1	0.017167	1	0.181818	6.02E-10	1	0.000918
7	94042504	94042515	COL1A2	5.27E-07	2.83E-20	0.043478	1	0.454545	0.012195	1	1	1	0.2	1	1	7.78E-09	0.044776	0.002162
8	141293914	141293943	TRAPPC9	6.97E-19	5.91E-28	0.080782	0.000242	0.11171	0.000939	1	0.00431	1	1.39E-07	1	1	3.88E-06	1	0.062189
8	59337246	59337258	UBXN2B	2.19E-11	1.82E-14	0.002551	1	0.089127	0.025078	1	1	0.016129	1	1	1	1.53E-08	0.025	0.003014
8	98817552	98817571	LAPTM4B	5.8E-09	4.46E-14	0.217376	1	1	0.036269	1	1	1	1	1	1	5.94E-08	1	0.000123
9	163927	163943	CBWD1	1.69E-19	3.61E-28	0.001894	0.00028	1	1	1	1	1	1	0.003846	1	2.29E-30	0.00013	0.000867
9	75420448	75420463	TMC1	2.37E-21	3.03E-18	2.48E-06	0.010929	1	1	1	0.008734	0.014599	0.155545	0.00202	0.1875	1.05E-17	1	0.003654
X	107827760	107827773	COL4A5	3.47E-16	3.84E-14	0.003393	1	1	1	1	1	1	0.047244	1	1	2.63E-14	1	8.95E-07
X	129343603	129343614	ZNF280C	3.83E-07	4.97E-07	1	1	1	1	1	1	1	0.069767	1	1	0.000153	1	0.075342
X	135292012	135292028	FHL1	3.62E-06	2.07E-13	1	1	1	0.003378	1	1	1	1	1	1	0.000748	0.04	1
10	74874082	74874112	NUDT13	3.88E-42	2.93E-23	0.001261	1	0.192972	1	1	1	0.007874	1	0.000512	1	4.76E-19	0.022989	1.45E-05
2	99936265	99936280	TXNDC9	1.96E-41	4.6E-25	3.08E-05	1	1	0.01	0.016949	1	0.035872	1	0.032787	1	1.19E-36	0.024096	5.95E-06
3	10018739	10018754	EMC3	7.09E-40	4.68E-42	0.000435	0.054412	0.070796	0.001877	1	1	0.001439	0.048077	1	1	8.2E-14	0.001262	5.89E-05
20	37146131	37146146	RALGAPB	3.04E-39	1.03E-39	0.047619	1	1	1	3.66E-06	1	1	6.35E-10	0.000529	1	1.68E-23	0.002333	4.43E-09
2	201778717	201778733	ORC2	8.73E-38	1.44E-11	0.000273	1	1	0.023256	0.016393	1	0.025862	1	0.000546	1	3.82E-32	0.000309	0.000109
4	115586972	115586988	UGT8	9.83E-38	9.77E-10	0.057971	1	0.04878	1	1	1	1	1	0.000481	1	6.55E-36	0.065918	0.00152
18	180211	180228	USP14	3.6E-37	2.68E-17	0.009231	0.036496	0.186967	0.014048	0.090594	1	1	1	0.001948	1	6.06E-15	0.010638	0.000236
6	111329221	111329239	RPF2	4.33E-37	8.31E-33	0.002082	0.000115	1	0.133511	1	1	1	0.220566	0.000466	0.250256	6.29E-38	0.001113	0.001235
X	48631645	48631660	GLOD5	5.93E-37	1.25E-18	0.106324	1	1	0.159261	0.012346	1	1	0.036036	0.083333	1	4.18E-09	0.000582	0.004174
10	18280054	18280071	SLC39A12	6.64E-37	1.52E-18	0.039409	0.060745	0.262776	0.097969	0.10137	1	0.002121	1	0.064516	1	9.96E-11	4.9E-06	1
X	20204548	20204563	RPS6KA3	1.26E-36	1.04E-19	0.04918	1	1	0.053571	0.030612	1	0.006803	1	0.006536	1	1.85E-25	0.011364	5.74E-05
5	36123065	36123135	LMBRD2	1.78E-36	2.55E-15	1.03E-06	0.012346	1	0.015152	1	1	0.007752	0.033898	0.025316	1	5.76E-29	0.047619	0.001155
1	78432506	78432521	FUBP1	2.29E-36	1.91E-29	0.098305	0.018391	0.06135	1	0.048379	0.00939	0.085981	3.71E-07	1	1	2.98E-21	0.030769	0.039272
9	104306988	104307005	RNF20	1.43E-35	2.54E-22	0.135043	1	0.038835	1	1	1	1	1	0.057545	0.166667	2.15E-07	0.030303	0.005546
X	106092450	106092473	TBC1D8B	2.06E-35	1.3E-07	3.51E-06	1	1	1	1	1	1	1	0.012195	1	2.91E-36	0.000539	1
19	34951356	34951371	UBA2	2.56E-35	9.43E-06	0.002551	1	1	1	0.117647	1	1	1	0.0125	1	1.03E-16	0.000135	0.000256
5	172578549	172578567	BNIP1	3.33E-35	9.43E-28	4.25E-06	1	0.164032	1	1	1	0.054228	0.105792	0.042553	1	5.33E-35	0.004263	0.453131
12	124242458	124242472	ATP6V0A2	5.61E-35	1.97E-18	1	1	1	1	1	1	0.045796	0.001858	0.000649	0.28	4.63E-18	0.001532	1.74E-07
2	120714401	120714418	PTPN4	9.29E-35	1.11E-38	1.31E-05	1	1	0.031963	0.001313	1	1	1	0.000466	1	2.97E-26	0.025316	0.002305
4	146031236	146031253	ABCE1	1.39E-34	1.29E-17	3.16E-06	0.012739	0.241249	0.037383	1	0.022989	0.014599	0.068066	0.000426	1	3.47E-37	0.000239	0.000263
2	44445604	44445617	PPM1B	2.68E-34	3.75E-23	0.298246	0.021108	1	1	1	1	0.028846	0.09853	0.023256	1	2.82E-17	0.000816	0.004441
9	125655308	125655324	RC3H2	3.8E-34	5.49E-23	0.000512	1	1	0.039732	0.031913	1	1	1.23E-05	1	1	5.31E-29	1	0.029024
5	41909830	41909846	C5orf51	4.11E-34	7.27E-21	0.06298	1	0.016637	0.035971	1	1	1	0.134828	0.000627	1	9.79E-26	1.01E-05	0.026643
14	53513439	53513452	DDHD1	4.19E-34	9.93E-24	0.090865	1	1	1	0.023077	1	1	0.096039	0.000649	1	7.33E-26	0.001207	0.000479
1	39751172	39751188	MACF1	4.38E-34	7.05E-12	0.092262	1	1	1	0.101618	1	1	1	1	1	3.1E-17	0.012903	7.04E-05
X	23693084	23693098	PRDX4	5.17E-34	4.02E-22	1	1	1	1	1	1	1	1	0.021739	1	4.9E-23	0.001567	0.002114
7	98639904	98639917	SMURF1	8.37E-34	8.62E-14	0.107143	1	1	1	0.000309	1	0.02027	1	0.000887	1	1.17E-10	0.000414	0.001186
16	74372596	74372618	LOC283922	8.57E-34	1.17E-17	1	1	0.068027	0.030151	0.000113	1	0.013793	1	0.000699	1	1.49E-15	0.04	1.96E-06
7	74608740	74608754	GTF2IP1,LOC100093631	1.43E-33	1.14E-42	0.029306	0.005376	1	0.030864	0.014151	1	0.02909	0.075161	0.000452	1	6.05E-27	4.35E-05	0.000257
1	39929162	39929178	MACF1	1.55E-33	1.84E-11	0.044818	1	1	1	1	1	0.027874	1	0.013333	1	4.35E-15	0.051606	0.006028
X	129267464	129267478	AIFM1	1.69E-33	4.3E-34	0.004281	1	0.059603	0.02907	7.68E-05	1	1	0.000282	0.04	1	1.54E-20	0.037037	0.006298
X	52654536	52654550	SSX8	1.87E-33	6.58E-23	0.01087	0.01105	1	1	0.014778	1	0.030887	1	0.047619	1	2.03E-20	0.00188	1.56E-09
10	95549836	95549852	LGI1	1.17E-32	9.17E-13	0.136364	1	1	1	1	1	0.05775	0.160967	0.002105	1	0.000278	0.001142	0.001479
10	90362299	90362324	LIPJ	1.33E-32	2.46E-14	0.23	1	0.022555	0.127154	1	1	1	0.010587	0.014493	1	0.000118	0.003381	0.560263
6	34735652	34735670	SNRPC	1.37E-32	1.67E-10	0.101215	1	1	0.049383	1	1	1	1	1	1	2.55E-11	0.001669	5.25E-05
11	49056627	49056644	TRIM49B	1.71E-32	1.69E-14	0.004724	1	1	1	1	1	1	1	0.105263	0.25223	2.05E-18	0.000446	0.506466
8	100160282	100160300	VPS13B	5.77E-32	2.33E-24	5.83E-06	0.02941	1	1	1	1	1	1	0.001948	1	7.54E-28	1	0.01514
11	88068256	88068270	CTSC	5.89E-32	4.59E-19	0.037298	1	0.103488	0.004275	1	1	0.026935	1	0.002353	0.004329	9.73E-26	0.005599	1.44E-05
3	5249962	5249976	EDEM1	6.37E-32	2.76E-40	5.72E-05	1	1	1	0.028317	0.00369	1	1	1	1	5.09E-24	0.012658	0.000926
5	55034756	55034770	DDX4	8.71E-32	2.67E-32	0.001185	1	1	0.001645	1	1	1	1	1	1	9.98E-14	1	1.28E-06
2	55883509	55883523	PNPT1	9.02E-32	8.61E-25	2.78E-05	0.030768	1	0.001057	1	1	1	0.027211	0.03125	1	3.32E-31	0.000316	6.37E-05
4	44691795	44691810	GUF1	1.5E-31	1.63E-12	0.000762	1	0.226284	0.140665	1	1	1	0.058009	0.261084	1	1.93E-25	0.148148	0.000266
6	146256315	146256344	SHPRH	2.34E-31	4.39E-12	0.006394	1	1	0.072141	0.014851	1	0.006289	1	0.014286	1	2.6E-18	1	1.13E-05
20	33225781	33225808	PIGU	2.76E-31	3.65E-24	0.01	1	0.047619	0.035556	1	1	0.044771	1	0.032258	1	6.22E-06	0.000686	0.013754
X	79991590	79991604	BRWD3	2.8E-31	3.43E-08	1	1	1	0.096341	1	1	1	1	0.001948	1	2.9E-16	0.001111	5.69E-06
6	89638988	89639004	RNGTT	3.15E-31	5.37E-23	6.43E-05	1	0.071429	0.087457	0.019277	1	0.015625	1	0.015873	1	1.35E-37	8.72E-05	3.64E-05
9	19299209	19299224	DENND4C	3.83E-31	4.07E-16	0.006209	0.010989	1	1	1	1	1	0.074049	0.015385	1	1.73E-27	0.000301	3.95E-08
9	114341239	114341255	PTGR1	6.35E-31	7.35E-22	0.005042	0.009615	1	0.04375	1	1	1	1	0.017241	1	2.26E-26	0.020833	0.05
15	101550861	101550877	LRRK1	7.09E-31	1.12E-27	0.011364	1	1	0.081482	0.006105	1	1	0.058674	0.002797	1	9.03E-12	1	0.007947
3	52696310	52696322	PBRM1	9.24E-31	1.68E-17	2.64E-05	0.004348	1	0.046942	0.037733	0.003984	1	1	0.014493	1	1.84E-24	0.000766	5.21E-06
X	129546260	129546274	RBMX2	9.63E-31	3.04E-30	0.269841	1	0.084746	1	1	1	1	0.024194	0.058824	1	5.16E-09	0.000438	0.084619
12	104714847	104714867	TXNRD1	9.66E-31	8.99E-32	0.000536	1	1	0.002632	1	1	0.045796	1	0.001948	0.468966	5.17E-29	1	0.03035
16	19063220	19063235	TMC7	1.37E-30	7.44E-27	0.130279	0.017429	0.105534	0.010659	0.024194	0.012658	0.077888	0.038462	0.033898	0.238095	6.76E-26	0.000999	7.15E-05
7	114303617	114303633	FOXP2	1.66E-30	1.36E-14	0.014857	0.004101	1	0.034188	1	1	0.157115	1	0.027778	1	6.55E-25	0.01982	0.000864
17	30293149	30293164	SUZ12	2.84E-30	2.93E-12	0.003759	0.016667	0.03125	1	1	1	0.028469	0.011628	0.000754	1	3.32E-30	0.000926	0.172779
3	196088809	196088826	UBXN7	4.17E-30	3.45E-15	0.009015	1	0.05303	0.080775	0.053502	1	1	1	1	1	1.59E-33	1	0.058234
1	173795803	173795821	DARS2	4.18E-30	7.78E-27	1	0.004566	0.005042	0.104564	0.000489	0.017699	1	1	0.016129	1	7.06E-14	0.000821	0.06204
5	94842718	94842730	TTC37	4.71E-30	4.1E-29	0.001298	4.65E-05	0.005589	0.021739	0.025751	1	1	0.000319	0.2	1	1.09E-34	1	1.19E-05
X	110494528	110494543	CAPN6	5.21E-30	2.51E-13	0.001083	1	0.019645	1	0.00885	1	1	1	0.020408	1	4.68E-14	1	0.000343
12	48360947	48360961	TMEM106C	5.63E-30	9.88E-33	0.092437	0.000193	1	0.091641	0.006001	1	1	4.45E-09	0.001815	1	4E-25	0.037037	0.000246
1	113159364	113159384	ST7L	5.72E-30	1.45E-24	0.046875	1	1	0.01227	0.000469	1	0.013423	0.048625	0.018182	1	2.6E-32	0.002558	0.015181
3	20189528	20189540	KAT2B	6.34E-30	5.16E-15	0.14976	1	0.107063	1	1	1	1	1	0.001536	1	2.77E-24	0.027027	0.0071
2	48032740	48032754	MSH6	6.85E-30	1.48E-25	0.027668	0.061054	1	0.045198	0.06785	1	0.058596	0.002944	0.032258	0.065359	4.8E-27	1	0.033071
X	19606999	19607014	SH3KBP1	6.95E-30	2.67E-13	0.01087	1	1	1	0.008333	1	0.027586	0.02381	0.090909	1	3.25E-06	1	0.000941
1	33087567	33087584	ZBTB8OS	7.24E-30	2.22E-22	0.000362	1	1	0.069544	1	1	1	1	0.000333	1	5.39E-28	2.8E-05	0.000456
4	76528928	76528945	CDKL2	1.12E-29	1.07E-22	1.27E-05	1	1	1	0.091682	1	0.025078	1	1	1	3.13E-22	1	0.000204
2	64112697	64112719	UGP2	1.24E-29	3.11E-37	0.004329	1	0.071429	0.081806	0.037971	1	0.022556	9.32E-06	0.000565	1	2.82E-16	0.000974	0.014958
12	95488339	95488354	FGD6	1.71E-29	1.85E-37	0.019608	1	0.013548	0.000714	0.000221	1	1	1	0.000903	1	3.78E-16	0.001548	2.63E-07
6	152728079	152728093	SYNE1	1.74E-29	2.24E-14	0.003896	1	1	1	0.018473	1	0.02381	1	0.004354	0.084615	3.63E-16	0.034483	0.472977
6	152740681	152740695	SYNE1	2.69E-29	9.24E-17	0.068361	1	0.086378	0.168026	0.155032	1	1	0.199311	0.005845	0.098039	2.85E-25	0.060976	0.00522
10	74906122	74906136	ECD	2.87E-29	2.13E-16	0.009524	1	1	0.078919	1	1	0.035553	1	1	1	5.06E-15	0.052281	0.004411
5	132408905	132408918	HSPA4	3.39E-29	5.14E-23	0.098662	1	1	0.001194	0.064083	0.004329	1	0.00042	1	0.066667	4.37E-07	1	0.083035
7	135099044	135099059	CNOT4	4.05E-29	2.36E-28	0.006048	0.01	1	0.074048	0.043099	1	1	1.22E-06	1	1	1.37E-11	0.027397	0.000553
20	58497481	58497497	SYCP2	4.2E-29	1.95E-13	1.93E-05	1	1	1	0.06383	1	1	0.047059	0.000381	1	1.66E-27	0.020202	0.002292
13	21370398	21370412	XPO4	4.95E-29	3.1E-16	0.113122	1	1	1	0.016393	1	1	0.086494	1	1	4.83E-17	0.000137	0.000997
2	207027356	207027368	EEF1B2	5.71E-29	4.01E-34	1	0.010204	1	0.003082	1	1	1	0.007225	1	1	3.17E-16	0.013333	0.004238
1	114092111	114092124	MAGI3	6.37E-29	9.13E-16	1	1	1	1	1	0.034188	1	1	0.020408	1	5.41E-18	0.07997	0.105513
1	176105710	176105723	RFWD2	8.24E-29	6.7E-18	0.082447	1	0.002408	1	0.053563	1	0.006849	1	0.032258	1	8.05E-21	1	0.002119
6	97000341	97000356	UFL1	8.4E-29	3.23E-17	0.006048	1	1	0.000976	1	1	0.020548	1	0.074074	1	1.05E-13	0.010695	0.010056
X	44949951	44949963	KDM6A	8.7E-29	1.12E-17	0.032787	1	0.011471	1	0.055545	1	1	1	1	1	7.1E-19	0.010526	0.00053
X	148582573	148582585	IDS	8.84E-29	8.05E-20	1	1	1	1	1	1	1	0.131075	0.000784	0.190476	3.49E-11	1	3.04E-05
5	172421760	172421776	ATP6V0E1	9.23E-29	1.08E-12	0.00036	1	1	1	1	1	0.003583	1	0.037736	0.052632	8.57E-34	0.027778	4.81E-07
2	203417391	203417403	BMPR2	9.23E-29	3.4E-20	0.117551	0.024615	1	0.026596	1	1	0.020833	1	1	1	2.32E-13	1	7.47E-05
14	76638065	76638087	GPATCH2L	9.32E-29	3.99E-18	0.012097	1	1	1	0.02551	1	1	1	0.001053	1	1.13E-10	3.08E-05	2.62E-05
X	19380975	19380993	MAP3K15	9.58E-29	1.52E-24	9.19E-07	1	1	1	0.072515	1	0.025889	1	0.115385	1	4.16E-21	0.039022	0.018899
6	17669262	17669277	NUP153	2.27E-28	5.14E-20	0.00369	0.015075	1	1	0.057679	1	0.00271	0.037313	0.027778	1	1.16E-22	0.13027	0.000147
6	116912033	116912049	RWDD1	2.48E-28	1.05E-17	0.009307	1	0.205859	1	1	1	0.090172	1	0.048387	1	3.78E-19	0.074976	0.000106
2	54146387	54146400	PSME4	2.55E-28	2.15E-23	0.123337	0.005291	1	1	1	1	0.006623	0.033333	1	1	1.33E-24	0.000287	4.29E-05
1	150297334	150297351	PRPF3	2.78E-28	1.11E-22	1	1	0.075441	0.109733	0.119486	1	0.070401	0.002061	0.017544	1	3.37E-27	1	0.003545
1	32381592	32381607	PTP4A2	2.79E-28	5.12E-19	0.000191	1	1	1	1	1	1	1	1	1	5.75E-36	0.052281	0.026712
4	141448595	141448610	ELMOD2	3.24E-28	1.26E-21	0.006908	0.008439	0.12064	0.042553	0.022026	0.012712	0.045449	1	0.001142	1	2.45E-21	0.000658	0.131773
6	70040500	70040513	BAI3	3.47E-28	7.16E-13	0.043478	1	1	0.136175	1	0.012195	1	1	0.007212	1	2.1E-16	0.023529	0.002167
14	91372685	91372700	RPS6KA5	4.01E-28	3.64E-26	0.221369	1	1	0.055046	1	1	0.065772	1	1	1	2.3E-22	1	0.004739
7	138434066	138434081	ATP6V0A4	4.89E-28	1.98E-25	0.007103	1	0.188221	0.063332	0.062051	1	0.079176	0.046192	0.125	0.356296	3.23E-24	1	0.138534
19	6908675	6908689	EMR1	5.27E-28	1.8E-19	0.245161	1	1	0.067394	0.065482	1	0.0895	1	0.084472	1	1.24E-10	0.023529	0.170332
12	96704958	96704972	CDK17	5.76E-28	5.72E-20	0.025641	1	1	0.206116	1	1	1	0.107819	0.060606	1	5.15E-10	1	1
15	64496611	64496630	CSNK1G1	5.81E-28	1.23E-19	7.71E-05	1	1	0.124849	1	1	1	1	1	1	3.64E-17	1	0.39032
17	27829588	27829602	TAOK1	5.94E-28	1.73E-21	0.098305	1	1	0.032258	1	1	1	1	1	1	3.99E-13	0.003418	0.000493
2	179548695	179548712	TTN	6.16E-28	8.61E-19	0.000894	1	1	1	0.103632	1	1	1	0.000414	1	6.51E-28	0.121081	0.001839
11	59626477	59626491	TCN1	6.8E-28	2.96E-29	0.001107	1	0.291802	0.137324	0.069089	1	0.000435	0.229188	0.4	0.25	3.59E-15	1	1.12E-08
19	38282490	38282505	ZNF573(dist=12260),LOC644554(dist=25546)	7.07E-28	3.92E-20	0.000639	1	1	0.173878	1	1	1	1	0.035088	0.033333	1.79E-14	1	0.555667
7	36465606	36465622	ANLN	7.07E-28	8.94E-21	0.000183	0.027272	1	1	0.005072	1	0.019481	0.049383	0.012048	1	8.86E-32	0.00056	0.000461
22	41551231	41551249	EP300	7.4E-28	3.62E-24	0.076923	1	1	1	1	1	0.012987	1	0.2	1	3.74E-22	1	0.02566
12	81239721	81239737	LIN7A	8.1E-28	5.32E-12	0.000894	0.010309	0.11754	0.027273	0.02459	1	1	1	0.043478	0.263158	1.54E-15	0.003891	8.61E-06
12	129360344	129360381	GLT1D1	8.64E-28	1.58E-22	2.36E-05	1	1	1	0.034218	1	0.013605	1	0.04	1	3.51E-10	0.022727	1
2	15536509	15536532	NBAS	1.31E-27	4.5E-14	0.002096	0.025	1	0.057143	1	1	1	1	0.000649	1	2.2E-34	0.003173	6E-08
5	147785802	147785816	FBXO38	1.34E-27	2.97E-31	0.000673	0.023738	1	0.011559	0.074215	0.02	0.038275	1	0.05	1	4.62E-16	0.000949	0.012319
6	42611936	42611951	UBR2	1.51E-27	6.59E-29	0.000481	0.009852	0.049296	0.025641	0.026785	1	0.007634	2.6E-06	0.059249	0.230769	4.78E-14	0.003734	0.010123
11	8486375	8486389	STK33	1.55E-27	4.19E-32	0.00327	1	1	1	1	1	0.030417	0.017442	1	1	3.02E-26	1	1.08E-05
4	146046123	146046135	ABCE1	1.62E-27	3.78E-25	0.003659	1	0.174397	1	1	1	1	1	0.000391	1	1.23E-20	1	1.31E-05
9	34017005	34017043	UBAP2	1.76E-27	1.68E-11	0.003049	1	1	1	1	1	1	1	0.001317	0.023715	1.77E-25	0.064501	0.007871
17	54981571	54981588	TRIM25	1.77E-27	2.63E-26	0.007974	0.036361	0.010512	0.007076	1	1	1	1	0.037037	1	2.24E-25	0.037736	1.14E-10
8	54742095	54742107	ATP6V1H	1.78E-27	5.5E-22	0.077647	1	1	0.028571	1	0.004425	1	0.004508	1	0.285714	7.58E-14	0.000546	0.001613
14	64460536	64460551	SYNE2	1.84E-27	1.23E-14	0.00013	0.027027	1	0.018631	0.224795	1	0.068473	0.008536	1	1	2.92E-18	1	0.000432
15	37391752	37391765	MEIS2	1.91E-27	6.84E-24	0.127536	1	1	1	1	1	1	1	1	1	1.21E-18	0.026316	1
12	57006059	57006072	BAZ2A	2.02E-27	3.33E-08	1	1	1	1	1	1	0.009091	1	0.032258	1	1.29E-21	1	0.009813
1	115226990	115227003	AMPD1	2.2E-27	2.76E-13	0.085678	0.009174	1	1	1	1	0.019231	1	0.068182	1	1.68E-17	0.000391	0.000946

1	158260878	158260892	CD1C	2.63E-27	3.73E-08	0.136591	1	0.089841	0.117543	1	1	0.02909	0.05817	0.028571	1	1.1E-12	1	0.021466
8	39775377	39775390	IDO1	2.71E-27	5.68E-17	0.113384	1	1	1	1	1	1	1	1	1	8.02E-10	1	0.009087
19	34945331	34945344	UBA2	2.76E-27	3.15E-27	0.029851	1	1	0.071194	0.027778	1	0.009346	0.055556	1	1	2.33E-15	0.000287	0.000831
2	87122096	87122121	ANAPC1P1	3.21E-27	1.08E-12	0.007742	1	1	0.053563	1	1	1	1	0.033898	1	2.39E-20	1.37E-05	0.223944
3	108224685	108224701	MYH15	3.61E-27	2.7E-25	0.011868	1	0.204267	0.000777	1	1	0.074045	0.051724	1	1	1.92E-27	0.012821	7.07E-08
6	88221097	88221109	SLC35A1	3.74E-27	2.66E-20	1	1	0.208116	1	1	1	1	1	1	1	1.69E-14	0.044195	0.000762
4	39233719	39233734	MIR1273H	3.79E-27	2.05E-24	0.001442	1	1	1	0.000372	1	0.045796	1.34E-05	0.079184	1	1.74E-20	0.000903	0.000202
2	219341717	219341730	USP37	3.95E-27	5.11E-20	0.000278	1	1	0.013514	1	1	1	1	1	1	5.98E-23	0.012048	0.0563
20	34435246	34435270	PHF20	4.01E-27	4.69E-19	0.08216	1	1	1	0.014493	1	0.026786	1	0.031746	1	2.02E-22	1	5.52E-07
15	22848150	22848166	TUBGCP5	4.46E-27	1.41E-19	0.006645	1	1	1	1	1	1	1	1	1	3.42E-14	0.029412	1.25E-06
12	42835328	42835365	PPHLN1	5.73E-27	1.81E-05	0.086957	1	1	1	1	1	0.007092	1	0.015625	1	1.8E-13	1	2.56E-05
4	39511530	39511543	MIR1273H	5.81E-27	4.21E-24	0.00895	0.062001	0.48066	0.082152	0.006	1	0.008772	0.000702	1	1	5.14E-12	0.12	0.000144
7	107336262	107336274	SLC26A4	5.85E-27	8.07E-13	1	1	1	1	0.007813	1	1	1	1	1	5.59E-16	0.107071	9.33E-07
5	14678762	14678776	OTULIN	6.01E-27	1.21E-14	0.08	0.012821	1	1	1	1	1	1	0.000402	1	4.57E-18	1	0.044944
8	30933816	30933829	WRN	6.78E-27	1.12E-17	0.010274	1	1	1	0.037497	1	0.019802	0.05618	1	1	1.8E-28	1	0.000131
19	21350520	21350533	ZNF431	7.67E-27	2.9E-26	0.033333	1	0.163647	0.065772	1	1	0.084864	0.057143	0.015385	1	7.3E-13	0.034884	5.1E-05
8	23712066	23712089	STC1	7.9E-27	2.05E-28	0.000168	0.000606	1	0.186019	0.150101	1	1	1	0.000439	1	5.72E-24	1	7.84E-05
X	135115669	135115681	SLC9A6	9.03E-27	3.54E-28	0.058824	1	0.000306	1	1	1	0.029961	1	1	1	2.36E-18	0.002896	0.001693
7	138453892	138453909	ATP6V0A4	9.3E-27	9.62E-18	1	1	0.338135	0.024446	0.072864	1	0.001721	0.087391	0.04878	1	1.35E-10	0.069549	0.054898
6	108076870	108076886	SCML4	1E-26	1.88E-17	0.006719	1	1	1	0.062053	1	1	0.021429	0.065027	1	1.01E-12	1	0.163512
11	125763610	125763624	PUS3	1.01E-26	2.68E-20	1	1	1	0.105969	0.013636	1	0.047244	0.101519	0.005348	1	3.46E-21	0.094077	0.000716
12	64491002	64491019	SRGAP1	1.11E-26	1.27E-28	0.000611	1	0.042735	0.001046	0.016598	1	0.031619	0.039474	0.001081	1	2.94E-20	2.66E-07	0.136087
3	16636093	16636108	DAZL	1.13E-26	2.74E-08	1	1	0.096608	1	1	1	0.081818	0.059524	0.016949	0.298246	1.73E-18	0.0833	0.001678
6	71571688	71571707	SMAP1	1.45E-26	4.97E-09	0.000496	1	0.139558	0.053147	1	1	1	1	1	0.214286	3.21E-23	1	0.001886
22	30051705	30051722	NF2	1.72E-26	4.02E-08	4.52E-05	1	1	1	1	1	1	1	0.06014	1	4.27E-40	0.002971	0.000637
16	67384060	67384075	LRRC36	1.77E-26	6.45E-18	0.003884	1	0.202709	1	0.105171	1	1	1	0.001107	1	1.53E-09	1	0.007862
13	115011550	115011564	CDC16	1.79E-26	5.45E-06	0.000936	1	1	1	1	1	1	0.012987	0.031746	1	1.33E-21	1	0.012262
2	236817336	236817351	AGAP1	1.84E-26	1.54E-17	1	0.067227	1	0.208568	1	1	0.005598	1	0.002885	1	1.88E-13	1	0.010786
14	75199555	75199568	FCF1	1.88E-26	2.01E-16	0.055556	1	0.129353	0.001225	0.021277	1	0.007576	1	1	1	6.13E-13	0.027778	0.02077
2	64331815	64331833	PELI1	2.08E-26	1.94E-30	0.002225	1	0.201985	0.100883	0.105168	1	0.096087	0.156108	0.024096	1	2.42E-18	1	0.001203
1	117605130	117605145	TTF2	2.09E-26	3.04E-06	0.001087	0.016129	1	1	1	1	1	1	0.142857	0.315789	2.02E-28	1	0.00031
12	72067966	72067980	THAP2	2.3E-26	8.05E-20	0.009231	1	1	1	1	1	0.007519	4.52E-05	1	0.066667	1.16E-09	0.004152	5.21E-05
9	133498229	133498245	FUBP3	2.56E-26	6.69E-20	0.000853	1	1	0.048774	1	1	0.000716	1	0.003418	1	1.97E-42	0.002181	0.000101
20	35695535	35695562	RBL1	3.44E-26	3.54E-22	7.31E-05	1	1	0.018692	1	1	1	1	0.033898	1	4.26E-34	0.000255	0.001065
14	104465128	104465144	TDRD9	4.05E-26	2.24E-23	2.8E-05	1	1	1	1	1	1	0.037879	1	1	6.97E-20	0.011364	8.13E-05
9	15472611	15472623	PSIP1	4.18E-26	6.14E-30	0.004193	1	0.065342	1	1	1	0.036864	0.051948	1	1	1.76E-19	4.35E-05	0.044329
16	19619602	19619617	C16orf62	4.58E-26	6.93E-26	0.002414	1	0.042404	0.073877	1	1	0.035928	1	0.043478	1	1.7E-12	0.076897	0.000397
3	71008341	71008362	FOXP1	4.64E-26	5.43E-27	0.001488	0.041375	1	1	0.093778	1	1	1	0.062004	1	1.84E-30	0.096914	5.08E-05
2	239241445	239241460	TRAF3IP1	4.7E-26	5.94E-23	0.000345	0.015152	1	0.026738	0.056325	0.009615	0.007937	1	0.034483	1	2.65E-27	0.000101	0.003537
6	116914112	116914128	RWDD1	4.92E-26	3.5E-29	1	1	0.011724	0.068783	1	1	1	0.080775	0.027397	1	4.14E-09	0.000686	5.6E-05
2	183832100	183832113	NCKAP1	5.56E-26	2.91E-22	0.030769	1	0.065772	0.004105	1	1	0.017391	1	0.095238	1	3.12E-16	1	0.145267
1	220369745	220369758	RAB3GAP2	5.65E-26	1.06E-18	0.044444	0.072141	0.005665	0.000406	0.075345	1	0.004202	1	1	1	1.43E-15	0.088195	0.079282
2	203079025	203079039	SUMO1	7.14E-26	1.92E-09	0.003418	1	1	1	1	1	1	0.04	1	1	2.47E-26	0.010279	6.98E-06
12	22215194	22215212	CMAS	7.87E-26	6.17E-11	0.005348	0.12069	1	1	0.090909	1	1	1	0.041667	0.010989	3.12E-15	0.013514	0.004219
1	94964139	94964155	ABCD3	8.28E-26	1.25E-31	8.25E-05	0.019704	0.261595	0.135291	0.076889	1	1	1	1	1	3.84E-34	0.004736	0.001048
6	117243181	117243196	RFX6	8.38E-26	3.71E-21	0.068418	1	1	0.134256	1	1	0.044771	1	1	1	4.61E-10	0.000926	0.001148
4	103505784	103505799	NFKB1	9.17E-26	5.39E-15	0.004765	1	1	0.122552	1	1	1	1	0.052632	0.337662	3.69E-14	0.071429	0.019987
17	40881033	40881048	EZH1	9.24E-26	5.47E-18	0.027768	1	1	0.033193	1	1	0.029412	1	0.033333	1	4.35E-11	1	0.003732
2	61145498	61145512	REL	9.33E-26	6.87E-22	0.074746	1	1	1	1	1	1	0.117986	0.027778	1	8.69E-21	1	2.68E-05
3	180679235	180679250	FXR1	9.84E-26	2.28E-16	0.001174	0.025236	0.064815	0.00023	1	1	0.00813	1	1	1	4.28E-19	0.011628	0.000294
X	44386435	44386460	FUNDC1	1.04E-25	1.15E-11	0.002714	1	0.058824	1	1	1	1	1	1	1	2.12E-26	1	3.97E-07
2	141294271	141294299	LRP1B	1.04E-25	1.04E-09	6.52E-06	1	1	1	0.031432	1	1	1	0.046154	1	1.86E-13	0.091382	1
4	71888332	71888348	DCK	1.06E-25	1.35E-13	0.007389	1	1	1	1	1	1	0.008621	0.020408	1	8.61E-06	1	0.010222
20	7921106	7921120	HAO1	1.09E-25	4.21E-27	0.001481	1	1	1	1	1	0.06473	1	1	1	2.64E-25	0.089342	2.9E-05
1	86435957	86435971	COL24A1	1.11E-25	1.27E-30	0.000982	1	1	1	0.078322	1	1	3.62E-07	0.00266	1	2.31E-21	0.027778	0.000242
3	10128965	10128985	FANCD2,FANCD2OS	1.11E-25	5.32E-12	0.003702	1	0.070922	1	0.013514	1	0.012579	1	1	1	2.68E-18	1	0.001522
17	74736999	74737016	MFSD11	1.19E-25	4.26E-23	0.002283	0.055989	0.168157	0.052853	0.007756	1	0.113526	1	0.030769	0.222222	3.71E-21	1	0.070631
15	65273147	65273161	SPG21	1.38E-25	6.01E-14	0.013256	0.041447	0.001333	1	1	1	0.023077	1	0.000784	1	2.46E-12	0.055164	0.000124
16	24574691	24574710	RBBP6	1.39E-25	3.74E-18	0.018939	1	0.162504	1	1	1	1	1	0.017544	0.095238	5.79E-22	0.048479	1
6	20758808	20758822	CDKAL1	1.43E-25	3.13E-21	0.001639	0.006289	0.281689	0.061839	0.003922	1	0.090044	0.041184	0.003759	1	7.44E-28	0.023256	0.010587
17	8417006	8417020	MYH10	1.54E-25	1.08E-28	0.021132	0.000345	1	0.090333	0.012022	1	1	0.000275	0.115385	0.230769	3.95E-19	0.000496	0.003078
3	172046695	172046709	FNDC3B	1.59E-25	2.09E-13	0.001815	0.060606	1	1	1	1	0.037037	0.002338	0.054054	1	9.88E-19	0.007545	0.003494
6	64289938	64289954	PTP4A1	1.69E-25	1.81E-42	0.007389	1	0.114638	0.000544	1	1	1	1	1	1	1.74E-10	0.041881	0.001461
9	86354663	86354679	GKAP1	1.97E-25	1.96E-14	0.000234	1	1	1	0.000295	1	0.013889	0.000509	0.050949	1	1.3E-21	0.028302	0.000355
12	107237602	107237626	RIC8B	2.05E-25	2.26E-27	0.001815	1	1	0.001984	3.53E-06	1	1	0.000457	0.028571	1	4.4E-22	0.000219	0.013816
6	129955151	129955165	ARHGAP18	2.06E-25	5.21E-15	0.146154	1	1	0.018984	1	0.050505	0.126349	0.176034	0.096721	0.071429	2.76E-10	1	0.08698
13	28133956	28133972	LNX2	2.12E-25	2.02E-39	1.09E-05	0.000296	0.188235	0.00213	0.001012	1	1	1	0.00037	1	5.27E-38	0.000135	1.82E-08
1	179089233	179089251	ABL2	2.18E-25	1.05E-20	0.041667	1	1	0.026738	1	1	0.016	1	0.037736	1	5.15E-19	0.041096	0.001579
1	229662901	229662916	ABCB10	2.21E-25	3.17E-18	0.012565	1	1	0.073862	0.086747	1	0.058051	1	1	1	2.85E-16	0.001998	0.002214
12	8813345	8813362	MFAP5	2.42E-25	0.003497	0.081081	1	0.107053	1	1	1	1	1	0.000686	1	1.66E-12	0.004146	1
12	31435608	31435620	FAM60A	2.57E-25	6.74E-26	0.117551	0.010363	1	0.000483	1	1	1	0.03012	0.015385	1	2.1E-12	1	0.031744
3	176751870	176751887	TBL1XR1	2.59E-25	1.28E-12	1	1	1	0.086167	1	1	0.006897	1	0.034483	1	7.05E-10	1	9.8E-05
5	96342077	96342093	LNPEP	2.62E-25	1.34E-07	0.006988	1	0.419248	1	1	1	0.04717	0.01075	0.08	0.022059	2.6E-23	0.04918	1
3	160955882	160955898	NMD3	2.62E-25	5.97E-24	0.361647	1	0.073503	0.321486	0.277218	1	0.038372	1	1	1	6.11E-12	1	0.01771
3	71739332	71739345	EIF4E3	2.79E-25	1.54E-21	1	0.01766	0.04908	0.078498	1	1	1	1	0.033333	1	9.69E-26	0.027397	0.01202
22	30772228	30772244	KIAA1656	3.03E-25	1.61E-32	1	1	1	0.030611	0.044048	1	0.052623	0.130266	0.000882	1	1.45E-12	1	1.42E-05
1	99164246	99164260	SNX7	3.23E-25	8.96E-19	0.074074	0.00625	1	0.047899	0.001763	1	1	1	1	1	2.02E-19	0.002899	0.172312
10	27333121	27333134	ANKRD26	3.25E-25	1.34E-13	0.202742	1	0.419248	1	1	0.050847	1	0.08951	0.037037	0.073529	1.86E-23	0.000265	0.004512
15	40005793	40005806	FSIP1	3.25E-25	6.74E-22	0.007103	0.014925	0.076389	1	0.003332	1	0.000342	1	0.006585	0.333333	4.91E-19	1	0.00165
1	46739974	46739989	RAD54L	3.55E-25	7.96E-05	0.003173	1	1	0.102564	1	1	1	1	0.016949	1	6.89E-23	0.034091	0.003276
18	43445730	43445748	EPG5	3.78E-25	1.13E-21	0.046154	0.047518	1	0.071886	1	1	0.116261	0.001241	0.03125	1	1.2E-20	0.060593	0.000521
3	113222099	113222114	SPICE1	3.88E-25	7.52E-14	0.001488	1	1	1	1	1	1	0.064501	0.039216	1	2.68E-27	0.036364	0.003693
13	98634737	98634749	IPO5	3.94E-25	1.64E-15	0.002221	1	1	0.016043	1	1	0.018182	1	0.014925	1	6.73E-15	0.020619	0.000231
18	33058318	33058335	INO80C	4.13E-25	2.01E-05	0.113122	1	1	1	1	1	1	1	1	1	7.15E-30	0.182366	0.000777
6	64419024	64419039	PHF3	4.22E-25	1.17E-31	0.377778	0.027272	0.11697	1	0.03396	1	0.037912	0.000438	0.043478	1	0.000106	1	5.69E-07
4	164440461	164440474	TMA16	4.72E-25	2.43E-09	0.00339	0.025641	0.060345	1	1	1	1	1	0.045455	1	3.97E-21	0.033898	0.003845
10	32327037	32327053	KIF5B	4.74E-25	1.43E-23	0.058824	1	1	0.015504	1	1	0.007092	1	0.026316	1	4.48E-20	1	0.001186
6	100403812	100403827	MCHR2	4.85E-25	1.5E-16	0.036116	1	0.141404	7.86E-05	1	1	0.02388	1	0.035897	1	1.58E-11	0.076169	3.74E-05
10	70056619	70056632	PBLD	5.24E-25	1.44E-35	0.113384	1	1	0.026316	0.040719	1	0.04958	0.00077	0.0625	1	1.62E-23	1	0.000116
11	108141955	108141971	ATM	5.5E-25	1.28E-19	0.000418	1	1	0.087103	1	1	1	1	0.014925	0.190476	2.56E-20	0.001577	8.57E-05
2	135887514	135887528	RAB3GAP1	5.65E-25	3.86E-10	0.030769	1	1	1	1	1	1	0.015385	0.032787	0.272727	1.44E-23	1	0.07719
X	24760276	24760289	POLA1	6.02E-25	5.73E-13	0.245351	1	1	1	1	1	1	0.0122	0.042553	0.428571	3.9E-15	0.011268	0.042883
5	6623405	6623418	NSUN2	6.05E-25	2.57E-18	0.003846	0.009524	1	0.000279	1	1	0.013605	0.002229	0.059249	1	6.78E-17	0.025641	0.003164
18	43487885	43487905	EPG5	6.29E-25	2.32E-21	0.022569	1	0.233247	1	1	1	1	1	0.02439	0.111111	5.39E-17	1	0.004041
5	180481216	180481233	BTNL9	6.99E-25	1.93E-26	2.52E-05	1	1	1	0.023256	1	1	1	1	1	1.43E-24	0.072375	0.000201
18	6873646	6873663	ARHGAP28	7.56E-25	1.29E-19	0.118415	1	1	0.076344	0.01938	1	1	1	0.047619	0.411765	4.79E-16	0.033333	7.08E-05
4	39501722	39501754	MIR1273H	7.62E-25	1.79E-08	1.38E-05	1	0.242772	0.131698	1	1	1	1	0.029851	0.238095	2.16E-30	1	0.048196
2	160092703	160092716	WDSUB1	7.89E-25	1.12E-09	0.000496	1	1	1	1	1	0.014286	0.008547	0.015625	1	9.97E-16	1	5.68E-07
8	96069973	96069988	NDUFAF6	7.94E-25	1.81E-20	0.107071	1	1	1	1	1	0.015873	0.017857	0.002551	1	4.87E-27	1	0.05211
2	74089266	74089281	STAMBP	8.18E-25	3.02E-13	1	1	1	1	0.075949	1	1	1	0.029412	1	5.7E-33	1	0.04856
15	42503953	42503965	TMEM87A	8.18E-25	2.94E-35	0.124863	0.000216	0.151623	1	0.040298	0.005556	0.014493	0.027211	1	1	8.39E-18	1	0.002336
7	152144203	152144216	FABP5P3(dist=4103),LINC01003(dist=16993)	8.4E-25	3.89E-29	0.006541	1	0.01607	0.079963	0.082644	1	0.018182	1	0.000887	1	8.75E-22	0.067398	0.011688
18	25727760	25727775	CDH2	9.77E-25	4.71E-22	0.245161	1	0.067485	1	1	1	0.027874	1	1	1	3.61E-13	0.006048	0.001507
11	47701629	47701642	AGBL2	1.06E-24	2.6E-27	9.58E-06	1	1	1	1	1	1	1	1	1	9.73E-15	0.012048	1.22E-05
X	138864932	138864946	ATP11C	1.2E-24	1.1E-20	0.04918	1	0.283624	1	1	1	0.013605	0.046512	1	1	1.99E-23	0.093693	0.041901
6	53138203	53138233	ELOVL5	1.24E-24	2.81E-15	0.061265	1	1	0.176003	1	1	1	0.106293	0.000426	1	1.21E-06	1	0.010065
1	47123898	47123914	ATPAF1	1.29E-24	2.19E-14	7.78E-05	1	1	1	0.009979	1	1	0.095684	0.045455	1	2.42E-32	1	0.010063
6	13316780	13316795	TBC1D7	1.34E-24	7.77E-31	0.002801	0.00012	1	0.035897	1	1	0.039063	0.123165	0.030303	1	9.38E-06	1	0.022259
4	83376098	83376111	ENOPH1	1.37E-24	2.59E-18	0.008737	1	0.061404	1	1	1	1	0.021583	1	1	1.7E-14	1	0.008991
8	67969596	67969610	COPS5	1.39E-24	1.72E-25	0.000627	1	0.152144	1	1	1	1	5.43E-05	0.02	1	6.92E-15	1	0.003407
7	6064470	6064488	EIF2AK1	1.44E-24	1.24E-07	0.002347	1	1	0.055936	1	1	0.014286	1	1	1	1.01E-22	1	0.000215
2	209195472	209195485	PIKFYVE	1.56E-24	2.3E-23	0.000512	0.018306	1	0.081384	1	1	0.038706	0.076401	0.05	1	1.63E-15	1	0.001077
1	167871297	167871312	ADCY10	1.57E-24	5.53E-27	0.029641	1	0.253529	1	0.00039	1	1	0.03125	0.055556	1	8.01E-18	1	0.027527
6	149846372	149846387	PPIL4	1.6E-24	7.74E-20	0.000316	1	0.176032	0.036364	1	1	0.014184	0.037037	0.000699	1	9.49E-24	1	0.167384
3	33626219	33626236	CLASP2	1.6E-24	3.24E-14	2.19E-05	1	0.142032	0.081876	1	1	0.044439	1	0.00202	1	1.17E-27	1	1
20	47649496	47649525	ARFGEF2	1.7E-24	7.73E-12	8.74E-05	1	1	1	1	1	0.007143	1	1	1	2.85E-27	1	7.53E-06
2	47635523	47635537	MSH2	1.71E-24	2.04E-26	0.002414	1	1	0.027273	0.000614	1	0.06473	4.73E-08	0.000699	1	1.16E-24	0.0125	0.000521
1	247729206	247729223	GCSAML	1.8E-24	6.53E-10	0.100566	1	0.076892	1	1	1	1	1	0.027778	1	3.33E-22	0.037037	0.257673
5	78416973	78416990	BHMT	2.04E-24	9.53E-31	0.206213	0.000494	1	0.105438	1	1	0.007092	1	1	1	7.11E-21	0.068966	0.024214
10	24784014	24784030	KIAA1217	2.15E-24	9.28E-12	0.142683	1	1	0.041237	1	1	0.056928	1	1	1	5.02E-13	1	0.005715
2	120567392	120567406	PTPN4	2.27E-24	3.39E-23	0.006697	1	0.106234	0.079768	1	1	0.016	0.044776	0.069549	0.227273	1.12E-10	0.012658	0.003231
7	63454255	63454269	MIR4283-2(dist=372708),LINC01005(dist=30527)	2.27E-24	6.3E-15	0.133333	1	1	0.086167	1	1	0.0009	1	0.160798	1	4.62E-05	1	0.000224
10	16824085	16824108	RSU1	2.29E-24	1.23E-22	0.0021	0.008889	1	0.035354	0.046777	0.004115	0.021277	1	1	1	2.21E-19	1	0.007382
1	9633387	9633400	SLC25A33	2.38E-24	7.28E-17	0.107306	0.034483	0.138684	0.043239	1	1	1	0.129385	0.000673	1	4.42E-19	0.044118	0.086595
1	100542702	100542718	HIAT1	2.38E-24	1.02E-17	0.221369	1	0.181338	0.026144	0.044072	1	0.02027	0.078125	0.000426	1	1.43E-15	0.029412	0.021249
8	33356825	33356839	MAK16	2.52E-24	8.7E-14	1.79E-06	1	0.159021	1	1	1	1	0.021277	0.016129	0.318182	3.19E-22	0.000274	3.09E-06
12	132539500	132539513	EP400	2.52E-24	1.53E-33	1	1	0.043478	0.056807	0.039896	1	0.018868	1	0.028986	1	1.07E-19	0.038462	0.000384
20	33033065	33033083	ITCH	2.89E-24	3.52E-19	0.000348	1	1	0.047163	1	1	1	1	0.00037	1	1.69E-15	0.003587	0.046294
14	39591613	39591627	GEMIN2	3.01E-24	1.82E-11	1	0.109091	0.216575	1	0.08216	1	0.011597	1	1	1	4.36E-27	0.013187	1
7	97939975	97939988	BAIAP2L1	3.04E-24	6.88E-19	2.05E-06	1	1	0.017241	1	1	1	0.024691	0.017544	0.2	5.79E-15	0.032967	0.005059
1	212241691	212241730	DTL	3.12E-24	5.32E-08	0.207729	1	1	1	1	1	1	1	0.001279	1	3.95E-07	0.061842	0.165963
10	21461410	21461435	NEBL	3.22E-24	5.47E-17	0.00363	1	1	1	1	1	0.047994	1	0.020408	1	1.31E-23	0.014493	0.006339
9	19334957	19334970	DENND4C	3.36E-24	5.15E-29	0.005889	0.009009	0.044025	0.000293	1	1	1	7.95E-06	0.003279	0.3	7.18E-17	1	1.75E-05
X	19037666	19037686	GPR64	3.56E-24	1.42E-05	1	0.15625	1	1	1	1	1	0.158884	0.000627	0.214286	5.54E-28	0.076241	0.004957
6	126249747	126249771	NCOA7	3.57E-24	3.36E-24	1	1	0.115602	1	1	1	0.041663	0.101519	0.012658	1	6.2E-09	1	1
3	37550027	37550040	ITGA9	3.67E-24	9.4E-13	0.001947	1	1	0.108008	1	1	0.029961	1	1	1	1.62E-20	1	0.043257
1	95615737	95615761	TMEM56,TMEM56-RWDD3	3.84E-24	6.08E-16	1	1	1	1	1	1	0.012987	1	0.00303	0.190476	3.67E-17	0.092262	0.004272
10	94266330	94266346	IDE	3.85E-24	3.46E-18	0.088235	1	0.099008	1	1	1	0.007092	0.034333	1	1	2.01E-10	1	0.001132
3	58351660	58351690	PXK	4.06E-24	1.74E-09	0.003702	1	1	1	1	1	0.02388	1	0.028571	1	8.33E-30	0.000686	0.024722
15	63571279	63571293	APH1B	4.07E-24	1.98E-18	0.011927	1	1	1	0.040816	1	0.043011	1	0.004193	1	7.5E-12	1	6.63E-06
11	110128925	110128941	RDX	4.38E-24	1.58E-17	0.001822	1	1	1	1	1	0.059912	1	0.052632	1	7.15E-31	0.03125	2.59E-07

13	50586051	50586064	DLEU2	4.51E-24	1.07E-26	0.061224	1	0.011144	0.030303	1	1	0.027118	0.052326	0.036364	1	1.74E-21	0.029641	0.164639
1	153617510	153617526	CHTOP	4.77E-24	1.61E-16	0.163043	0.033149	0.162921	0.000965	0.046777	1	1	1	0.000391	1	2.48E-07	1.58E-05	0.021233
6	70459209	70459222	LMBRD1	4.86E-24	1.93E-16	0.000101	0.010638	1	0.05613	1	1	0.019802	1	1	1	2.63E-16	0.054795	0.002578
6	100988266	100988280	ASCC3	4.94E-24	8.15E-21	1	1	1	0.001122	0.018405	1	0.02749	1	1	0.238095	7.51E-30	0.030303	1
7	33217071	33217084	BBS9	5.49E-24	4.7E-31	0.044963	1	0.050847	1	1	0.00431	1	0.102121	1	1	1.67E-14	0.017241	0.023177
5	36629801	36629815	SLC1A3	5.55E-24	2.31E-18	0.000405	0.012422	1	0.044776	1	0.014493	1	1	0.025641	1	7.68E-15	8.23E-06	0.000245
9	131715001	131715017	NUP188	5.93E-24	8.62E-22	0.000208	0.015873	0.09703	1	1	1	1	1	0.002177	1	4.43E-23	1	0.276412
5	122940980	122941019	CSNK1G3	6.38E-24	1.29E-13	0.063987	1	1	0.082804	1	1	1	0.000345	0.000439	1	8.68E-13	1	0.000845
15	58974349	58974361	ADAM10	6.53E-24	6.91E-22	0.076923	1	1	1	1	1	1	1	0.015873	1	7.25E-13	0.022727	8.36E-06
17	30500816	30500828	RHOT1	7.04E-24	6.4E-34	0.004281	1	1	0.069695	0.007605	1	0.012346	1	0.021739	1	7.03E-17	0.024691	1
22	44083327	44083345	EFCAB6	7.13E-24	4.71E-07	0.043608	1	1	1	1	1	0.059701	1	0.006394	1	2.9E-23	0.064501	0.112456
X	52674318	52674335	SSX7	7.22E-24	1.56E-06	0.013213	1	1	1	1	1	1	1	1	1	2.91E-21	1	2.58E-05
2	33586464	33586479	LTBP1	7.28E-24	0.000146	0.185714	1	1	1	1	1	0.054545	1	1	1	2.09E-09	0.019591	8.14E-05
X	83403148	83403160	RPS6KA6	8.44E-24	1.97E-08	0.071429	1	1	0.013889	0.019048	1	1	1	0.034483	0.26087	8.34E-11	0.000974	0.000541
19	47700438	47700453	SAE1	8.49E-24	1.75E-26	0.189947	1	0.177066	1	1	1	0.019048	0.002919	0.016667	1	5.22E-18	0.011765	2.39E-06
16	3808052	3808066	CREBBP	9.43E-24	1.7E-25	9.19E-07	0.010152	1	1	1	1	0.047994	1	1	0.28	1.29E-25	0.117647	0.004188
2	32117217	32117230	MEMO1	1.11E-23	3.7E-31	0.00439	0.004587	1	0.05491	1	1	0.02909	0.114638	1	1	1.85E-29	0.033333	0.085546
9	73164596	73164610	TRPM3	1.11E-23	6.17E-19	0.171717	0.008658	0.220665	1	0.000698	1	1	1	1	1	9.79E-10	1	0.005835
9	97555228	97555242	C9orf3	1.13E-23	1.64E-35	0.044776	0.005376	1	0.095678	0.000303	1	1	1	0.000496	0.024631	9.86E-23	1.37E-05	0.001916
X	151996539	151996552	CETN2	1.15E-23	1.51E-16	1	1	1	1	0.141512	1	1	0.139332	1	1	3.21E-06	1	0.001094
14	68582259	68582279	RAD51B	1.16E-23	6.47E-21	0.002714	1	1	0.04186	0.002094	1	0.013514	0.052632	0.013889	1	8.94E-30	0.031915	0.079546
21	30356973	30356986	LTN1	1.21E-23	1.02E-16	0.092593	1	0.056593	0.075161	1	1	1	1	1	1	2.79E-15	0.03125	5.93E-06
21	27136460	27136473	GABPA	1.35E-23	2.78E-21	0.000546	1	1	1	1	0.00463	0.013889	1	1	1	1.13E-24	1	0.002233
7	139097271	139097295	C7orf55-LUC7L2,LUC7L2	1.38E-23	8.07E-32	0.001317	1	0.19065	0.000233	1	1	0.000363	0.000116	0.018519	1	5.22E-20	1	0.009165
14	60616914	60616937	DHRS7	1.43E-23	2.39E-15	0.054545	1	1	1	0.040265	1	0.020408	1	1	1	3.79E-25	0.030928	8.79E-06
6	128330423	128330435	PTPRK	1.5E-23	1.46E-30	0.003484	0.005128	0.158935	0.037736	0.019139	1	0.053563	0.040984	0.016129	1	3.76E-18	1	0.002286
14	103192774	103192791	RCOR1	1.54E-23	9.54E-15	0.007937	1	0.009886	0.335337	1	1	0.012579	1	1	1	8.42E-10	0.047619	0.271301
7	95775848	95775863	SLC25A13	1.55E-23	6.18E-25	0.006209	0.026577	0.045455	0.049587	0.037972	1	1	2.8E-06	0.002096	0.230769	6.52E-23	0.001111	0.00013
8	96047806	96047820	NDUFAF6	1.57E-23	1.93E-14	0.013549	1	0.074113	1	0.093458	1	1	0.112584	0.086207	1	2E-21	1	0.001163
9	21861902	21861914	MTAP	1.58E-23	1.36E-24	0.09375	0.014423	0.146098	0.076163	0.014851	1	1	0.061842	0.153846	1	4.4E-19	1	0.042253
22	39079920	39079936	TOMM22	1.58E-23	1.94E-07	0.000175	1	1	1	1	1	1	1	0.030303	1	2.45E-21	0.02439	0.131876
14	23870220	23870234	MYH6	1.69E-23	2.07E-08	0.094077	1	1	1	1	1	1	0.095188	1	1	2.31E-10	0.012821	0.059748
2	48734331	48734349	PPP1R21	1.7E-23	0.000167	0.000443	0.136364	0.074394	1	1	1	1	1	0.022727	1	1.28E-33	0.04	0.216562
8	30569609	30569622	GSR	1.78E-23	1.72E-30	0.013213	1	1	1	0.016878	0.004082	1	0.003923	0.018519	1	1.37E-18	0.024691	2.33E-05
13	115002097	115002111	CDC16	1.82E-23	1.82E-18	1	1	1	0.07823	1	1	1	0.07337	0.011905	1	0.0004	1	0.060628
13	102235764	102235780	ITGBL1	1.94E-23	2.09E-20	0.011723	0.02765	0.101961	1	0.118439	1	0.085849	1	0.074074	0.24	2.28E-26	0.002449	0.381991
8	38138934	38138975	WHSC1L1	1.95E-23	7.88E-13	1	1	1	1	1	1	0.008264	1	1	1	6.07E-18	1	0.01081
5	134015495	134015508	SEC24A	2.01E-23	2.52E-29	0.007937	1	1	0.142616	0.085261	1	1	1	1	1	6.38E-08	1	0.015173
1	173490547	173490571	SLC9C2	2.07E-23	9.55E-20	0.001081	0.008969	0.072222	1	1	1	0.021277	1	0.013514	1	1.46E-24	1	0.055276
8	110535444	110535460	PKHD1L1	2.21E-23	8.01E-24	0.009009	1	0.33471	0.137149	0.163179	1	0.071406	1	0.032258	0.055556	1.59E-10	1	0.218409
4	57897508	57897530	IGFBP7	2.25E-23	2.07E-17	0.125	0.004785	1	1	1	1	1	1.4E-06	1	1	1.22E-05	0.001488	0.06599
22	16404838	16404857	POTEH(dist=116901),OR11H1(dist=43967)	2.26E-23	0.111111	0.004239	1	1	1	1	1	1	1	0.005746	0.016206	2.97E-17	9.69E-06	0.024853
X	19024426	19024440	GPR64	2.28E-23	6.81E-23	1	1	0.066667	1	1	1	1	0.004662	1	1	1.52E-14	5.26E-05	0.001597
X	134033226	134033239	MOSPD1	2.33E-23	5.86E-23	0.001639	1	0.145249	1	0.041318	1	1	1	0.015625	1	2.98E-13	0.028169	0.005706
1	22030115	22030132	USP48	2.53E-23	3.94E-31	0.066667	1	1	1	1	0.004219	1	1	1	1	1E-10	0.001433	0.00021
2	162081128	162081140	TANK	2.6E-23	1.57E-21	0.073171	1	1	0.010929	1	1	1	1	0.000414	1	3.33E-21	0.02381	0.120928
8	38940143	38940157	ADAM9	2.84E-23	9.2E-30	0.017857	0.018072	0.071429	0.037736	1	0.005128	1	0.034783	0.041667	1	1.06E-22	1	2.2E-05
21	33312539	33312554	HUNK	3.05E-23	2E-10	0.000466	1	1	1	1	1	1	0.001122	1	1	1.01E-17	0.021739	0.007046
1	233295992	233296007	PCNXL2	3.26E-23	6.59E-12	0.001753	1	0.053846	1	1	1	0.015152	0.001845	1	1	1.07E-12	1	0.002097
3	178937630	178937642	PIK3CA	3.66E-23	8.49E-10	0.054545	1	1	1	1	1	1	1	0.027778	1	8.65E-14	0.000903	0.000201
6	52400479	52400497	TRAM2	3.67E-23	1.33E-12	0.001221	1	1	1	1	0.038961	1	1	1	1	4.45E-16	1	5.38E-05
1	63044645	63044661	DOCK7	3.67E-23	2.55E-22	0.003129	1	0.076923	1	0.004034	1	1	1	1	1	5.64E-31	1	0.00493
1	53267474	53267488	ZYG11B	3.76E-23	7.37E-11	1	1	1	1	1	1	1	1	0.001753	0.184211	1.85E-20	0.026667	0.002559
12	97051927	97051940	CDK17(dist=257561),NEDD1(dist=249061)	3.96E-23	3.48E-18	0.005832	1	1	0.075648	0.011466	1	0.049174	0.143433	1	0.054945	5.54E-15	1	1
8	96260054	96260070	C8orf37	4.06E-23	8.86E-19	0.002381	1	1	1	1	1	0.041954	1	1	1	1.66E-22	1	0.001144
4	25160732	25160748	SEPSECS	5.03E-23	1.49E-08	0.026245	1	1	0.252552	0.077895	1	0.062242	0.046779	0.02439	1	7.17E-19	0.001317	0.000698
11	18379446	18379459	GTF2H1	5.13E-23	1E-05	1	1	1	1	0.153846	1	1	1	1	1	3E-15	0.021277	0.283561
3	124397249	124397262	KALRN	5.38E-23	4.65E-17	0.199507	0.0625	1	1	1	1	0.042324	0.197749	0.035714	1	1.92E-06	1	0.114673
5	134015250	134015288	SEC24A	5.55E-23	6.63E-25	0.044776	1	1	1	0.004255	1	1	1	0.028571	1	6.3E-16	0.043011	0.059524
3	160233406	160233421	KPNA4	5.78E-23	8.8E-21	0.111801	0.029125	0.093788	0.03448	1	1	1	0.045113	1	1	2.36E-14	1	2.39E-06
7	122757719	122757733	SLC13A1	5.82E-23	1.39E-06	0.004267	1	1	1	0.090865	1	0.014925	0.031915	1	1	4.45E-16	1	1
15	76205523	76205536	FBXO22	6.01E-23	9.97E-21	0.086957	1	0.079967	1	0.038607	1	0.033193	0.083795	1	1	1.82E-09	1	0.000325
2	230653669	230653682	TRIP12	6.05E-23	5.09E-18	0.018418	1	1	0.059837	1	1	0.045449	1	0.053684	1	4.23E-13	2.8E-05	7.98E-05
10	103567665	103567680	MGEA5	6.17E-23	1.22E-30	0.323406	1	0.05625	1	0.017422	1	0.037497	1	1	1	4.22E-23	0.039474	0.006331
6	129905035	129905050	ARHGAP18	6.44E-23	2.27E-13	0.02913	1	0.059322	1	1	1	1	1	1	1	7.26E-12	0.011364	0.112506
X	15332451	15332469	ASB11	6.65E-23	9.44E-17	0.037037	1	0.325891	1	1	1	1	1	0.079184	1	1.52E-08	0.11101	0.053161
10	121675238	121675251	SEC23IP	6.86E-23	3.9E-20	1	1	0.278728	1	1	1	0.059467	1	0.016393	1	3.02E-20	1	0.009251
7	29771546	29771561	DPY19L2P3(dist=43687),WIPF3(dist=74609)	6.91E-23	6.79E-17	0.027778	1	0.371128	1	1	1	0.030303	1	0.046875	1	1.48E-11	0.048479	0.008133
2	48033875	48033909	MSH6	7.31E-23	2.38E-07	0.00219	1	1	1	1	1	0.021583	1	0.025974	1	1.73E-08	1	0.000668
14	36334905	36334921	BRMS1L	7.31E-23	3.81E-11	0.109015	1	1	1	0.028037	1	1	1	1	1	1.36E-21	0.045193	0.001343
19	327260	327277	MIER2	7.6E-23	6.98E-36	0.001261	0.024767	0.270929	0.152585	0.106288	1	1	1.06E-09	0.015385	1	9.2E-17	0.027027	0.013184
18	21120381	21120398	NPC1	7.89E-23	8.07E-08	0.166387	1	1	1	0.184766	1	0.013333	0.033193	1	1	2.63E-12	1	0.003394
2	120831654	120831667	EPB41L5	8.14E-23	6.12E-14	0.08951	1	1	0.116689	0.029412	1	0.010101	1	1	1	3.02E-15	1	0.003294
7	16676082	16676097	ANKMY2	8.79E-23	1.08E-07	0.002484	1	1	1	1	1	1	1	0.000426	1	2.14E-28	1	0.038638
1	231094050	231094067	TTC13	9.21E-23	3.32E-14	7.98E-05	1	0.173993	0.141361	0.032965	1	1	0.068356	1	1	9.43E-22	1	0.000719
18	44424651	44424667	PIAS2	1.02E-22	1.03E-13	0.157895	1	1	1	1	1	1	1	0.000754	1	2.11E-14	0.001025	0.003023
2	211521213	211521243	CPS1	1.03E-22	3.82E-10	0.01658	1	1	0.01053	1	1	0.082804	7.36E-05	0.016667	1	1.12E-21	1	4.07E-05
5	169020337	169020350	SPDL1	1.05E-22	5.24E-12	8.35E-05	0.034884	1	1	1	0.016949	1	0.039022	1	1	8.28E-16	0.043478	1
12	2997058	2997074	RHNO1	1.07E-22	2.77E-12	0.095188	1	0.13982	0.021053	1	1	0.006757	1	0.033333	0.090909	2.01E-16	4.2E-05	0.002713
6	136710669	136710685	MAP7	1.13E-22	1.19E-21	0.045455	1	1	0.15616	0.003674	1	1	7.41E-07	0.181818	1	4.71E-16	0.001894	0.01457
14	58690427	58690451	ACTR10	1.16E-22	1.55E-16	0.006368	1	1	0.07098	0.043854	1	1	0.001781	0.03125	1	7.87E-19	0.000717	3.04E-05
X	114871127	114871141	PLS3	1.25E-22	1.55E-22	0.025641	1	1	0.02963	1	1	1	1	0.032787	1	9.67E-10	0.005102	0.042031
5	115167564	115167575	ATG12	1.28E-22	5.07E-15	0.01944	0.013514	0.176034	1	1	1	1	1	1	1	3.38E-10	0.024691	0.007704
15	82517622	82517671	EFTUD1	1.31E-22	0.000616	0.000474	1	1	1	1	1	0.016667	1	0.000649	1	1.02E-25	0.001025	0.000792
12	111160513	111160526	PPP1CC	1.34E-22	5.51E-15	0.004267	1	0.101056	0.017045	1	1	1	1	1	1	1.39E-12	0.098718	0.026969
3	32571823	32571841	DYNC1LI1	1.4E-22	5.94E-09	0.001539	0.014286	1	1	1	1	1	1	1	1	1.85E-36	1	0.282426
8	89128708	89128722	MMP16	1.47E-22	2.49E-19	0.02473	1	0.045893	1	0.017241	1	1	0.154881	0.038462	1	4.23E-17	1	4.24E-07
5	41862862	41862875	OXCT1	1.62E-22	3.89E-17	0.041667	1	1	1	1	1	1	1	0.017857	1	5.9E-17	1	0.00016
12	130883554	130883568	RIMBP2	1.68E-22	5.83E-16	0.037037	0.043356	1	0.180801	1	1	1	0.037497	0.029851	1	5.19E-14	1	1
7	66747794	66747810	PMS2P4	1.81E-22	2.15E-08	0.1	1	1	1	1	1	1	0.037736	1	1	0.04329	0.030612	0.002585
1	11134470	11134485	EXOSC10	1.99E-22	1.71E-21	1	0.010101	0.044872	0.052014	0.000216	1	1	1	1	1	1.77E-19	1	0.001814
1	113657018	113657033	LRIG2	2.01E-22	1.2E-24	0.145299	1	0.004645	1	0.050465	1	1	0.005255	0.001783	0.1	4.44E-12	0.072054	0.127496
4	40123997	40124010	N4BP2	2.01E-22	8.46E-10	0.057692	1	0.068182	1	1	1	0.006897	1	1	1	2.32E-14	1	0.000156
4	88986745	88986761	PKD2	2.11E-22	2.93E-18	0.002636	1	0.192171	1	1	1	0.012821	1	0.002463	0.3	1.05E-18	1	0.020953
5	118576096	118576110	DMXL1	2.14E-22	7.21E-25	0.231061	1	1	1	1	1	0.045108	1	0.000481	1	1.73E-07	1	0.0009
16	22271671	22271685	EEF2K	2.33E-22	5.52E-23	0.066667	0.01676	0.177966	0.005666	0.116693	1	0.052632	1	0.040816	1	1.01E-08	0.095188	0.001512
X	135095655	135095677	SLC9A6	2.5E-22	4.51E-08	0.002558	1	1	1	1	1	0.016667	0.000565	1	1	4.19E-15	1	0.003397
20	30142484	30142500	HM13	2.56E-22	4.9E-16	0.012987	0.038961	1	1	1	1	0.05817	1	0.035714	1	1.84E-13	0.033333	8.56E-07
9	112184972	112184987	PTPN3	2.6E-22	4.26E-24	0.010279	0.077042	1	1	1	1	0.000673	0.022555	0.146853	1	8.08E-10	1	0.001465
20	50292756	50292777	ATP9A	2.61E-22	2.7E-13	0.003418	1	1	0.061224	1	1	1	0.028986	1	1	3.83E-12	0.030303	0.262681
X	36156447	36156461	CHDC2	2.69E-22	9.35E-16	0.038462	1	0.048354	1	0.017699	0.018519	1	1	0.073375	1	5.82E-17	0.050847	0.020737
14	96916232	96916246	AK7	2.77E-22	1.51E-05	0.00339	1	1	1	1	1	1	1	0.009398	1	2.58E-17	0.108764	0.010616
2	234916771	234916787	TRPM8	2.81E-22	1.21E-23	0.002179	1	0.193856	0.039896	0.046147	1	1	1	0.027397	1	4.34E-28	0.001373	1.95E-05
12	76780051	76780066	OSBPL8	2.88E-22	7.96E-12	0.018956	1	0.271021	0.039474	1	1	1	1	0.085714	1	2.93E-29	0.003049	0.002065
1	200080464	200080490	NR5A2	2.9E-22	3.95E-13	0.01	1	0.065934	1	0.013333	1	0.014815	1	1	1	1.6E-10	0.000965	3.55E-07
17	73515055	73515068	TSEN54	2.96E-22	3.03E-32	0.123912	0.007463	0.044586	0.054878	0.000518	1	1	1	0.016949	1	7.02E-14	1	0.008376
17	40850552	40850587	CNTNAP1	3.04E-22	4.82E-08	0.083333	1	1	1	1	1	1	1	0.002551	1	7.58E-10	0.000361	0.241589
12	63964640	63964653	DPY19L2	3.06E-22	1.57E-18	1	1	0.155768	0.065403	8.9E-06	1	1	1	1	1	2.27E-14	0.000701	0.046595
4	151835502	151835539	LRBA	3.27E-22	6.19E-21	0.045455	1	0.154513	1	0.035008	1	1	1	0.032787	1	4.24E-15	1	0.000441
13	30854363	30854376	KATNAL1	3.28E-22	2.44E-18	1	1	1	1	0.031579	1	0.043239	0.017545	1	1	3.84E-11	1	0.03304
3	138248009	138248026	CEP70	3.7E-22	6.53E-14	0.000111	1	1	1	1	1	0.041954	0.030303	0.033898	1	1.89E-33	0.001242	0.000301
5	86679495	86679514	RASA1	3.81E-22	5.94E-07	0.000144	1	1	0.041667	1	1	1	1	0.028986	1	1.9E-37	1	4.27E-06
20	13140617	13140637	SPTLC3	4.21E-22	3.44E-25	0.000324	0.010309	1	1	0.014599	1	1	0.05	0.014085	0.125	1.47E-11	0.03125	1.06E-05
12	110006724	110006738	MMAB	4.22E-22	1.13E-18	0.058824	1	1	1	1	1	1	0.010204	1	1	2.93E-29	0.032609	0.000197
2	61577667	61577680	USP34	4.39E-22	4.73E-32	0.053684	1	0.05625	1	1	1	0.008547	0.041667	0.001317	1	7.78E-30	0.037037	0.000663
2	101885656	101885675	CNOT11	4.55E-22	5.99E-27	0.000722	1	0.068966	1	0.015686	1	1	1	1	1	2.16E-23	1	0.002292
8	30969355	30969369	WRN	4.61E-22	2.04E-23	0.009614	1	1	0.058241	1	1	1	0.0895	0.03125	1	1.24E-17	1	1
5	178030941	178030955	CLK4	4.86E-22	1.27E-26	9.6E-05	1	1	0.122932	0.037971	1	1	1	0.05	1	1.08E-24	1	0.00538
6	70840124	70840137	COL19A1	4.91E-22	1.86E-19	0.006446	1	1	0.085981	1	1	0.026087	0.05042	0.053571	1	3.87E-28	0.014085	0.000112
2	207013834	207013846	NDUFS1	5.07E-22	3.13E-19	2.52E-05	1	1	0.001145	0.00037	1	0.013514	0.015001	1	1	1.57E-16	0.045193	1.94E-06
21	33982072	33982086	C21orf59	5.17E-22	2.06E-13	0.042857	1	0.051613	1	1	1	1	0.011993	0.033898	1	6.81E-14	0.036145	0.038168
15	51768755	51768768	DMXL2	5.19E-22	4.82E-21	0.070779	1	1	1	0.011173	1	1	0.08	1	1	2.36E-20	1	0.000408
X	44918221	44918236	KDM6A	5.55E-22	2.55E-18	0.003173	1	1	1	0.038213	1	0.029519	1	1	1	4.04E-25	1	0.072222
14	20763824	20763838	TTC5	5.7E-22	2.28E-25	0.07997	1	1	1	1	1	1	0.039735	1	1	5.03E-17	1	0.038043
17	1326754	1326769	CRK	6.31E-22	2.43E-27	0.244703	1	1	1	1	1	1	1	0.012987	1	2.62E-10	0.044688	0.002705
2	170062201	170062216	LRP2	6.43E-22	1.69E-20	0.002849	0.014388	0.103488	0.104843	6.3E-05	1	1	0.059588	0.015873	1	4.21E-09	0.052281	7.41E-06
18	59942586	59942600	KIAA1468	6.45E-22	2.64E-21	0.01658	1	0.090909	0.002011	0.055238	1	0.012987	1	0.025641	1	9.07E-25	0.057692	4.04E-05
15	55972660	55972674	PRTG	6.47E-22	1.39E-29	1.74E-05	1	0.046113	0.00385	0.002598	1	0.01626	1	1	1	6.56E-19	0.116772	0.003519
X	153994469	153994482	DKC1	6.85E-22	1.56E-23	0.042553	0.004695	1	1	0.01444	1	1	0.129268	1	1	2.56E-14	1	0.003861
3	132169705	132169718	DNAJC13	7.4E-22	3.19E-16	0.027841	0.022038	0.06	0.100482	0.000533	1	1	0.063226	0.00037	1	7.17E-31	0.000999	0.257388
12	45269439	45269452	NELL2	8.61E-22	9.41E-13	0.217376	1	0.070568	1	0.036527	1	1	1	1	0.333333	9.4E-21	0.04	1
15	64231569	64231591	DAPK2	8.96E-22	9.25E-19	0.046512	1	1	1	1	1	1	1	0.015873	0.095238	7.23E-11	0.038462	0.004144
15	52185961	52185975	TMOD3	9.41E-22	2.69E-21	0.087416	0.016129	0.579844	0.000348	0.165488	1	0.088517	0.028952	0.035714	0.181818	4.12E-11	0.048193	0.229952
7	35189891	35189905	DPY19L2P1	9.46E-22	1.25E-10	0.003507	1	0.440281	0.020833	1	1	1	0.018258	0.086207	0.125	4.99E-12	0.053333	0.014953
5	50122645	50122660	PARP8	9.6E-22	1.91E-18	0.008737	1	0.010724	0.017544	0.107657	1	0.000127	0.001542	1	0.384615	2.91E-32	0.051948	0.010036
15	54586266	54586278	UNC13C	9.74E-22	1.62E-18	0.101633	1	0.164921	0.013784	0.12281	1	0.016129	0.181818	1	1	2.65E-18	0.002754	0.024482
4	114176848	114176860	ANK2	9.8E-22	2.25E-27	0.007937	0.013393	1	0.004938	0.014787	0.016461	0.019481	0.103376	0.017544	1	1.89E-11	0.058824	0.001363
10	115380483	115380497	NRAP	9.85E-22	2.99E-28	1.36E-05	5.13E-05	1	0.026738	0.013216	1	0.020408	1	0.043478	1	9.27E-16	1	0.059322
11	121367557	121367571	SORL1	9.88E-22	2.2E-18	0.284211	1	1	0.125962	1	1	0.027681	1	0.033333	1	7.85E-12	0.087391	0.000787
X	154133316	154133329	F8	1.01E-21	3.93E-16	0.28369	0.030769	1	1	1	1	1	1	1	1	4.39E-12	1	1.72E-06
4	42592935	42592965	ATP8A1	1.04E-21	4.23E-09	0.424761	1	1	0.13964	1	1	0.024793	4.35E-05	0.136591	1	0.00015	1	0.569023

1	54395673	54395692	HSPB11	1.16E-21	1.64E-15	0.005665	0.040537	0.079365	1	0.123877	1	1	1	1	1	6.93E-24	0.027027	0.25037
14	31191658	31191682	SCFD1	1.16E-21	3.76E-26	0.107071	0.029849	1	0.00197	0.000716	1	0.065201	1	0.000381	1	9.73E-23	1	0.314844
4	178357514	178357527	AGA	1.17E-21	1.29E-20	0.033898	1	1	1	0.011561	1	1	1	0.028571	1	1.07E-18	0.189947	0.035587
19	9361740	9361752	OR7E24	1.24E-21	0.000377	0.000225	1	1	1	0.043478	1	1	1	0.001399	1	6.36E-10	0.020408	1
18	19119813	19119828	ESCO1	1.28E-21	3.02E-16	0.000148	1	1	1	1	1	1	0.045752	0.000414	1	3.29E-30	1	0.011057
9	27062802	27062816	IFT74	1.31E-21	2.03E-24	0.052632	1	1	1	1	1	1	1	1	1	1.14E-14	1	1.11E-05
12	21639528	21639542	RECQL	1.32E-21	5.72E-08	0.00262	1	0.372314	1	1	1	1	0.066927	0.053571	0.090909	4.38E-23	1	0.000357
3	113169372	113169386	SPICE1	1.35E-21	2.96E-22	0.000263	0.005025	1	1	1	1	1	1	0.018182	1	4.4E-25	1	0.378494
X	118679315	118679331	CXorf56	1.37E-21	2.22E-32	5.78E-05	0.016632	1	0.052279	1	1	0.028267	0.002392	1	1	1.79E-09	1	0.376579
8	74204423	74204438	RPL7	1.4E-21	7.77E-30	0.111111	1	0.125721	0.198319	1	1	0.030187	0.118211	1	1	3E-13	0.018423	2.26E-06
1	155679543	155679557	DAP3	1.41E-21	1.23E-19	1	0.010582	0.164309	0.035712	1	1	1	0.054795	0.027027	1	3.89E-06	0.004426	0.059149
8	87111362	87111382	ATP6V0D2	1.44E-21	2.03E-05	1	0.028986	1	1	1	1	1	1	1	1	7.43E-06	1	0.002656
8	86180906	86180924	CA13	1.46E-21	1.1E-07	0.02223	1	1	1	1	1	1	1	1	0.086957	1.73E-22	0.131698	0.17103
X	154578865	154578881	LOC101927830,TMLHE-AS1	1.5E-21	2.16E-07	0.001783	1	1	1	1	1	1	1	0.031746	0.333333	2.65E-09	0.037975	0.078272
9	134049353	134049366	NUP214	1.5E-21	9.73E-25	0.074074	1	0.049587	1	1	1	1	1	0.2	1	5.55E-12	1	1.26E-05
5	137451460	137451472	NME5	1.55E-21	4.81E-22	0.008547	0.01005	1	0.028846	1	1	1	1	0.014706	1	4.7E-09	1	0.000358
X	135481956	135481970	GPR112	1.68E-21	2.71E-19	0.012256	0.016393	0.068966	1	0.000283	1	1	0.069744	0.071429	1	1.16E-14	1	0.030243
2	95766553	95766567	MRPS5	1.69E-21	1.71E-08	1	1	1	1	1	1	1	1	1	1	4.39E-20	1	0.004699
20	46270911	46270923	NCOA3	1.89E-21	1.14E-21	0.16996	1	0.131689	1	0.007576	1	1	0.040698	1	0.2	4.83E-10	0.061842	0.001146
14	96848565	96848580	GSKIP	1.9E-21	7.83E-18	0.016679	1	1	0.009709	0.0004	1	0.014085	0.036864	1	1	7.52E-14	0.045977	0.00192
1	182812410	182812425	DHX9	2.03E-21	5.03E-19	1	1	1	1	1	1	1	1	0.001948	1	5.16E-09	0.036585	0.251576
20	35672436	35672456	RBL1	2.07E-21	3.51E-15	0.002763	1	1	1	1	1	1	1	1	1	1.71E-28	0.055556	0.092555
1	63270823	63270838	ATG4C	2.08E-21	1.32E-09	0.000458	1	1	1	1	1	1	0.051274	0.001695	1	6.75E-14	1	0.081303
5	125820276	125820292	GRAMD3	2.09E-21	6.52E-14	0.215686	1	0.070513	0.048276	1	1	0.047238	0.065342	1	1	1.18E-08	0.058385	0.139569
16	15162143	15162165	PDXDC1,RRN3	2.19E-21	7.31E-11	0.00439	1	1	1	1	1	1	0.035294	0.035088	1	2.45E-26	0.025974	0.000766
16	56508722	56508734	OGFOD1	2.19E-21	1.22E-13	0.008217	1	1	0.026432	1	1	1	0.070685	1	1	5.26E-08	0.022989	0.087019
15	63447932	63447960	RPS27L	2.25E-21	9.44E-22	0.001242	1	1	1	1	1	1	0.059524	1	1	1.05E-17	1	7.04E-05
5	118500981	118501000	DMXL1	2.31E-21	5.32E-11	0.000578	1	1	1	1	1	1	1	0.016949	0.310345	9.03E-28	0.000325	0.003771
7	76883792	76883819	CCDC146	2.34E-21	3.85E-20	0.019608	0.00995	1	1	0.045578	1	1	0.056738	0.016949	1	9.02E-12	0.037037	0.001184
4	41015553	41015566	APBB2	2.56E-21	3.24E-24	1	1	0.259382	0.034188	0.006231	0.009524	0.007634	5.71E-06	0.125	0.315789	2.49E-12	0.04	0.000709
7	120739962	120739978	CPED1	2.6E-21	9.53E-17	0.069767	0.03	0.061211	0.107448	1	1	1	0.003703	0.066667	1	2.41E-20	1	0.00205
19	33406199	33406229	CEP89	2.69E-21	1.6E-12	0.000439	1	1	1	1	1	0.027778	1	1	1	1.77E-16	0.063815	0.000293
4	128812230	128812245	PLK4	2.79E-21	3.64E-33	0.000853	0.027906	0.19517	0.072787	0.018349	1	0.014815	9.6E-07	0.125	1	3.03E-29	0.04	4.09E-06
15	73418741	73418756	NEO1	2.99E-21	2.63E-16	1	1	1	1	0.02193	0.00885	0.017544	1.97E-05	0.030303	1	1.73E-08	1	0.000639
15	101019693	101019705	CERS3	3.11E-21	7.12E-20	0.013495	1	1	1	0.001812	1	0.013072	0.034014	0.016949	1	4.13E-12	0.03125	0.000142
2	173848186	173848214	RAPGEF4	3.24E-21	5.55E-15	0.107071	1	0.095562	1	0.001997	1	1	0.15149	1	0.2	2.09E-08	1	0.133823
3	195010023	195010035	ACAP2	3.27E-21	1.15E-11	1	1	1	1	1	1	1	0.013889	1	1	1.02E-16	8.74E-05	1
1	220269426	220269439	RNU5F-1	3.54E-21	2.69E-12	0.045455	1	1	1	0.012121	1	1	0.036232	0.037037	1	2.89E-10	0.050308	0.05615
11	74000180	74000195	P4HA3	3.56E-21	0.000104	0.02	1	1	1	1	1	1	0.111022	0.031746	1	4E-14	1	0.024231
4	16510058	16510073	LDB2	3.62E-21	1.81E-08	0.002096	0.030303	0.132445	0.039474	1	1	0.03524	1	1	1	3.39E-20	1	0.06338
2	118854094	118854108	INSIG2	3.86E-21	3.16E-16	0.139373	1	1	0.269522	0.000964	1	0.061762	1	1	0.066667	2.28E-14	0.002016	0.235051
1	223156384	223156419	DISP1	4.07E-21	2.33E-21	0.030769	1	1	1	0.043122	0.005988	1	4.63E-06	0.033333	1	4.72E-32	0.024691	0.002749
2	64195997	64196012	VPS54	4.25E-21	1.8E-06	0.002246	1	1	0.081633	1	1	1	0.032967	1	0.1875	1.08E-20	1	0.132715
4	123109034	123109048	KIAA1109	4.65E-21	2.85E-18	0.003484	0.020151	0.061069	1	0.033262	0.009009	1	0.003611	1	1	0.000217	1	2.25E-05
9	79968285	79968309	VPS13A	4.69E-21	5.66E-16	1.1E-05	1	1	1	1	1	1	1	0.030769	1	4.5E-25	0.063143	1
21	37706065	37706077	MORC3	4.72E-21	2.01E-24	0.000111	0.000143	0.069231	0.084701	0.043057	1	0.028069	0.038462	0.015625	1	1.06E-31	1	0.052764
3	138193025	138193038	ESYT3	4.88E-21	1.93E-30	1	0.017241	1	0.034884	0.017937	1	0.029961	0.003478	1	0.142857	3.66E-12	0.000274	0.285163
8	131193153	131193166	ASAP1	5.02E-21	6.59E-28	9.53E-05	1	0.028605	0.013314	1	1	1	0.246467	0.045455	0.333333	1.07E-21	1	0.010186
3	44815871	44815883	KIF15	5.03E-21	3.04E-20	0.0833	0.00578	1	0.000958	1	1	1	1	0.055164	1	4.3E-13	0.00084	0.066327
11	86120270	86120294	CCDC81	5.04E-21	2.82E-20	0.00106	1	1	0.014706	0.01105	1	0.006667	1	1	1	5.05E-16	0.127536	0.000141
3	100438778	100438810	TFG	5.13E-21	6.57E-25	0.038462	0.005208	1	1	0.015707	1	1	1	1	1	6.56E-21	0.000301	0.028791
5	159841492	159841507	SLU7	5.28E-21	3.2E-22	1	1	0.130466	1	1	0.004717	1	1	0.029851	1	5.43E-14	1	0.0629
9	118164375	118164388	DEC1	5.53E-21	5.67E-16	0.033898	0.024895	0.116761	1	1	1	1	0.025157	0.079184	1	6.46E-16	1	4.14E-05
17	17152363	17152377	COPS3	5.58E-21	1.53E-22	0.20863	1	1	1	1	1	0.003522	1	0.133333	0.125	2.15E-11	0.226481	0.036301
15	59094494	59094508	FAM63B	5.7E-21	7.49E-12	0.099942	0.013333	1	1	1	1	1	0.080612	0.001587	0.357143	2.26E-17	0.168116	0.026872
8	53543090	53543106	RB1CC1	6.29E-21	8.67E-06	5.78E-06	1	1	1	1	1	0.014286	1	0.014706	1	9E-31	0.037037	0.001666
17	7811876	7811889	CHD3	6.36E-21	7.63E-21	0.002797	1	0.21946	0.056459	1	1	1	0.000808	0.033898	0.272727	2.51E-15	1	2.45E-06
1	22033369	22033411	USP48	6.38E-21	9.89E-20	7.98E-05	0.01956	1	1	1	1	1	1	0.015873	1	6.38E-19	1	0.003422
5	115628120	115628134	COMMD10	6.51E-21	5.38E-21	0.090994	0.021053	0.415993	0.11352	0.129116	1	0.029412	0.252552	0.069444	1	9.69E-07	0.01342	0.000452
6	18258299	18258311	DEK	6.57E-21	3.31E-22	0.002885	1	1	1	0.010638	1	0.015873	0.044643	0.014085	1	2.98E-18	0.000309	0.000694
12	53861636	53861650	PCBP2	6.64E-21	5.86E-28	1	0.014151	1	0.074442	0.004606	0.009662	1	1	0.006342	1	9.3E-22	0.023256	1.64E-05
1	79358743	79358761	ELTD1	6.69E-21	1.79E-08	0.019385	1	0.200829	1	0.163647	1	0.018519	1	1	1	1.14E-09	0.050949	0.434012
X	24745018	24745047	POLA1	6.78E-21	1.25E-06	0.029851	1	0.10643	1	1	1	1	0.009804	1	1	1.42E-21	0.061842	0.0006
1	115280193	115280207	CSDE1	7.04E-21	8.36E-13	6.17E-05	1	1	1	1	1	1	0.089127	1	1	3.48E-17	1	0.00012
9	88287588	88287615	AGTPBP1	7.25E-21	2.9E-23	0.000231	1	1	0.023952	1	1	0.016949	0.082018	0.027778	1	9.1E-09	0.001807	0.004081
11	71155778	71155805	DHCR7	7.44E-21	7.69E-06	0.077922	0.025	1	1	1	1	1	1	1	1	1.26E-16	1	0.001383
13	48828102	48828118	ITM2B	7.62E-21	6.8E-17	0.000322	0.011696	1	1	1	1	0.012739	0.109655	1	1	1.69E-23	1	0.003395
20	16025192	16025206	MACROD2	7.64E-21	3.06E-20	0.034483	1	1	1	1	1	0.017391	1	1	1	1.72E-10	0.000439	0.112424
19	6026288	6026302	RFX2	7.76E-21	2.88E-29	2.86E-06	0.004464	0.008886	1	1	1	1	0.045198	0.037975	1	1.91E-22	0.002088	0.009306
7	105122891	105122924	PUS7	7.79E-21	1.59E-17	0.000123	1	1	1	1	1	0.007576	0.131075	0.030769	1	9.01E-15	1	0.052376
9	116044905	116044921	PRPF4	7.96E-21	6.63E-23	0.012502	1	1	1	1	1	1	1	1	1	2.28E-25	1	0.094122
11	16117460	16117478	SOX6	7.97E-21	5.26E-11	0.023416	1	0.05	1	1	1	1	1	0.013514	0.142857	2.06E-16	0.056593	0.348976
17	15517060	15517073	CDRT1	8.58E-21	2.64E-06	0.00555	1	1	0.075208	1	1	1	9.13E-05	1	1	1.26E-13	1	0.020459
19	15511205	15511221	AKAP8L	8.83E-21	5.39E-17	0.001753	1	1	0.021447	1	1	1	1	0.142857	1	6.01E-28	1	0.01
4	113506885	113506900	ZGRF1	9.1E-21	1.76E-09	0.000289	1	1	1	1	1	1	1	0.033333	1	2.08E-13	1	2.72E-06
12	89995053	89995065	ATP2B1	9.2E-21	1.55E-18	0.065217	1	1	0.019355	1	0.014493	0.044439	1	1	1	2.23E-11	1	0.000306
5	139907713	139907738	ANKHD1,ANKHD1-EIF4EBP3	9.49E-21	9.92E-09	0.00439	0.024096	1	1	1	1	0.014599	1	1	1	1.52E-18	0.023256	0.008849
14	73959703	73959720	C14orf169	9.62E-21	2.14E-20	0.055945	1	0.069292	0.018683	0.06894	1	0.096618	0.206138	1	1	2.13E-34	1	0.086414
2	61566824	61566839	USP34	9.68E-21	6.31E-10	0.003604	1	1	1	1	1	1	0.025862	1	1	5.83E-23	1	0.003461
10	50686600	50686614	ERCC6	9.78E-21	3.27E-17	1	1	0.06865	0.034091	1	1	0.018692	0.000174	1	1	0.00245	0.029412	0.008087
6	100006295	100006309	CCNC	1.03E-20	3.33E-21	0.047619	1	1	0.040708	1	1	1	0.025641	0.000754	1	4.79E-18	0.046238	0.000154
13	26151184	26151196	ATP8A2	1.04E-20	1.62E-28	0.000466	1	0.07619	1	1	1	1	0.014493	0.015385	1	5.72E-15	1	0.000109
1	168165767	168165781	TIPRL	1.08E-20	6.26E-23	0.010274	1	1	0.149259	0.194476	1	0.033333	1	1	0.125	1.64E-21	1	0.010583
16	69293926	69293945	SNTB2	1.09E-20	2.81E-27	0.000417	0.008547	1	0.007664	1	1	1	1	1	1	2.14E-14	1	0.000142
6	24412431	24412445	MRS2	1.1E-20	1.19E-18	0.005199	1	1	0.004598	1	0.017467	1	0.037975	1	0.098039	1.03E-24	0.006541	0.000609
12	118675984	118675997	TAOK3	1.1E-20	2.74E-20	0.016679	1	1	0.037736	0.017021	1	0.045108	1	1	1	8.11E-16	1	1
4	85556378	85556414	CDS1	1.12E-20	9.04E-13	0.012903	1	1	1	1	1	1	1	1	1	3.84E-12	1	6.09E-06
9	79820192	79820224	VPS13A	1.14E-20	2.74E-19	1	0.009091	0.074766	1	0.017094	1	1	1	0.022222	1	6.45E-21	1	1
3	158407930	158407945	GFM1	1.23E-20	4.7E-27	1	0.020997	0.216575	0.000567	1	1	0.075924	0.160967	0.028571	1	7.79E-17	0.074976	0.001521
1	154227292	154227307	UBAP2L	1.27E-20	2.13E-18	0.050806	1	1	1	0.311014	1	1	0.003901	0.030303	1	2.02E-17	0.005889	1E-05
7	92129161	92129183	PEX1	1.27E-20	7.64E-10	0.014006	0.001058	0.15526	0.001817	0.001439	1	1	0.009995	0.081081	1	4E-05	1	0.01153
15	41770639	41770652	RTF1	1.27E-20	6.2E-36	0.122984	0.000242	1	0.030769	0.003281	1	1	1	1	0.090909	1.54E-10	1	0.000461
2	99614595	99614609	TSGA10	1.35E-20	1.95E-15	0.001053	1	1	1	1	1	1	1	0.000402	1	5.83E-15	0.022989	0.007449
11	102272460	102272474	TMEM123	1.37E-20	1.13E-21	0.001639	1	1	0.005094	1	1	1	0.114176	0.077647	1	2.59E-15	1	0.000211
1	114940202	114940243	TRIM33	1.4E-20	5.59E-19	0.01648	0.018293	1	1	0.022922	1	1	1	1	1	7.2E-19	0.068066	1
11	55656437	55656451	TRIM51	1.51E-20	3.12E-22	0.014286	0.010256	1	0.250063	0.003399	0.014218	0.044195	0.006589	0.060606	0.081319	7.56E-15	1	0.083364
10	25140413	25140425	PRTFDC1	1.52E-20	2.74E-24	0.005263	1	1	0.032558	0.000343	1	1	1	1	1	6.91E-07	0.018868	0.014644
2	131883287	131883301	PLEKHB2	1.55E-20	2.9E-22	1	0.031913	0.049587	1	0.020779	1	0.012739	0.001417	1	0.1	1.22E-23	0.023529	0.011392
1	149900985	149901002	MTMR11	1.55E-20	3.34E-19	6.52E-06	1	0.0625	1	1	0.010949	0.007519	1	0.014493	1	3.11E-17	0.035714	0.002107
7	94040345	94040362	COL1A2	1.66E-20	6.81E-06	0.178197	1	1	1	0.064501	1	1	1	0.02439	1	7.33E-12	1	0.024568
19	21558818	21558831	ZNF738	1.67E-20	1.1E-18	1	1	1	0.048951	1	1	0.030187	1	1	1	2.36E-18	1	0.003054
20	2474136	2474149	ZNF343	1.81E-20	2.92E-15	0.04918	0.000123	1	1	1	1	0.026755	1	1	1	4.47E-18	0.04	1
11	49088577	49088602	TRIM64C(dist=7913),FOLH1(dist=79585)	1.81E-20	3.81E-17	0.000144	1	0.272623	1	0.011504	1	0.030864	0.404345	0.040541	0.115385	7.13E-20	0.021397	0.019728
7	31132235	31132249	ADCYAP1R1	1.84E-20	1.27E-21	1	0.008403	0.134426	1	1	1	1	0.000558	1	0.1875	3.14E-08	1	0.025692
16	20803249	20803265	ACSM3,ERI2	1.86E-20	1.06E-12	0.004523	1	1	0.028267	1	1	1	1	0.043478	1	8.36E-20	0.000466	0.000451
12	104077096	104077126	STAB2	1.86E-20	3.33E-15	0.000234	1	1	0.032432	1	1	1	1	1	1	1.07E-21	0.001899	0.026391
10	70962143	70962162	SUPV3L1	1.96E-20	1.15E-23	0.044444	1	0.129306	1	1	1	1	0.030769	0.0625	1	3.31E-16	1	0.070866
2	61622374	61622387	USP34	1.98E-20	3.93E-13	0.066102	0.006135	1	1	1	1	0.016393	1	0.016949	0.416667	2.16E-14	0.042254	0.04723
1	47325299	47325313	CYP4Z2P	2.22E-20	1.45E-19	0.009015	1	0.020804	0.033493	0.096508	1	1	1	0.006993	1	1.27E-16	0.044944	0.441343
3	108672335	108672350	GUCA1C	2.26E-20	8.26E-09	0.046264	1	1	1	1	1	0.0727	0.085671	1	1	3.8E-08	1	0.012448
6	145095545	145095558	UTRN	2.41E-20	2.89E-11	0.022147	0.078431	1	1	1	1	1	1	1	1	2.51E-23	1	0.024521
6	163899794	163899807	QKI	2.62E-20	5.65E-29	0.004862	0.005682	0.064268	1	0.014706	1	0.044113	1	0.094077	1	5.46E-20	1	0.009737
1	211280724	211280748	KCNH1	2.65E-20	4.5E-23	0.005046	1	0.007211	0.016497	0.000146	1	0.000915	0.0002	1	0.097007	1.14E-15	1	0.177975
15	50782416	50782446	USP8	2.65E-20	2.96E-22	1	1	1	0.034247	0.000505	1	1	1	1	1	1.13E-21	1	0.00016
10	27054255	27054277	ABI1	2.7E-20	1.1E-07	1	1	1	1	1	1	1	1	1	1	1.81E-13	1	0.00288
3	51266880	51266895	DOCK3	2.71E-20	3.26E-05	0.05	1	1	1	1	1	1	1	0.029851	0.285714	4.9E-17	0.030303	0.0044
3	180320897	180320910	TTC14	2.76E-20	1.55E-30	0.000282	4.08E-05	0.160364	0.023669	0.000346	1	0.069748	2.74E-05	0.000754	1	1.93E-26	0.040541	6.99E-05
1	176050430	176050447	RFWD2	2.97E-20	5.03E-18	3.81E-05	1	1	1	1	1	0.025236	1	0.025	1	1.31E-22	0.018692	0.000194
6	70966421	70966435	COL9A1	3.01E-20	4.71E-13	0.006965	1	1	0.015639	0.055546	1	1	1	1	1	3.15E-07	1	0.003092
4	93225752	93225765	GRID2	3.03E-20	5.08E-11	0.098305	1	1	1	1	1	0.00885	1	0.03125	1	2.96E-17	0.073148	0.017576
7	102825987	102826001	DPY19L2P2	3.42E-20	8.58E-26	0.006368	1	0.015242	1	1	1	1	1	0.000391	0.05	2.05E-14	1	0.250573
2	15676703	15676717	NBAS	3.7E-20	1.35E-25	0.076923	0.019048	1	0.001884	0.024096	0.004739	1	1	0.032787	1	5.78E-13	0.065201	0.00634
5	36629504	36629545	SLC1A3	3.73E-20	0.00017	0.016129	1	0.11754	0.081836	1	1	1	1	0.025	1	3.96E-18	1	0.013221
19	34302673	34302689	KCTD15	3.76E-20	1.31E-23	1	0.008403	1	0.061389	0.062699	0.010909	0.048951	0.056486	0.015625	1	5.76E-20	0.058812	0.003681
16	21623935	21623964	METTL9	3.88E-20	2.23E-12	0.000109	1	1	1	0.035952	1	1	1	0.012658	1	2.31E-17	1	0.038881
18	30275526	30275539	KLHL14	4.09E-20	7.48E-11	0.172704	0.027027	1	1	1	1	0.014184	1	1	1	1.3E-12	0.002353	1
6	49815873	49815888	CRISP1	4.17E-20	7.22E-13	0.000494	1	1	1	1	1	1	1	1	1	1.4E-09	1	0.002117
3	108081175	108081187	HHLA2	4.22E-20	1.5E-06	0.068493	0.015625	1	1	1	1	1	1	0.030303	1	8.42E-12	0.012346	0.000234
12	26628357	26628369	ITPR2	4.37E-20	9.96E-13	0.15361	1	1	1	1	1	1	1	1	1	6.6E-16	1	1
11	113697927	113697939	USP28	4.41E-20	6.05E-24	0.001586	1	0.061728	1	1	1	1	1	1	1	9.24E-17	0.035294	1.47E-05
5	170837513	170837527	NPM1	4.48E-20	9.11E-17	0.0114	1	1	1	1	1	0.022727	1	0.030303	1	1.49E-12	1	0.039566
11	74053485	74053497	PGM2L1	4.55E-20	6.42E-29	0.003912	1	1	0.037915	0.011858	1	1	0.114551	1	1	3.96E-19	0.000106	8.18E-06
15	20666397	20666411	HERC2P3	4.71E-20	9.93E-15	0.018113	1	1	1	0.000166	1	0.034014	0.057336	0.212766	0.277778	3.17E-13	0.107937	0.215068
6	20548795	20548808	CDKAL1	4.83E-20	3.03E-18	0.068966	1	1	0.037838	1	1	0.029412	0.001179	0.001442	1	8.33E-21	1	0.012523
17	57937792	57937807	TUBD1	4.84E-20	1.35E-25	9.98E-06	0.023529	1	0.070151	0.071242	0.013953	1	1	0.018182	1	1.61E-24	0.000882	0.000121
10	7755088	7755101	ITIH2	4.91E-20	3.41E-10	0.047619	0.022989	1	0.027273	1	1	1	0.000869	1	1	5.09E-09	1	0.113483
3	160141656	160141671	SMC4	4.91E-20	4.03E-12	0.062004	0.016129	1	1	1	1	0.026402	0.023077	1	1	2.29E-18	1	0.216542
13	77750765	77750791	MYCBP2	4.97E-20	2.63E-18	0.064935	1	1	1	1	1	0.013605	1	1	1	3.41E-17	1	0.050746
2	228771819	228771838	DAW1	5.01E-20	1.02E-07	0.00339	1	1	1	1	1	1	1	1	1	6.61E-10	0.0625	0.001219
12	62972198	62972223	MON2	5.69E-20	2.53E-11	0.009307	1	1	1	1	1	0.007937	1	0.000673	0.222222	8.45E-18	1	0.017105
1	155884155	155884167	KIAA0907	5.85E-20	1.27E-17	0.001174	1	1	1	0.048774	1	0.01227	1	0.018182	1	2.75E-14	0.037975	0.000649

8	97296205	97296220	PTDSS1	5.95E-20	2.16E-15	0.053684	1	1	1	1	1	0.036197	1	1	1	1.14E-22	1	0.001486
5	78936847	78936860	PAPD4	6.59E-20	5.13E-25	0.016129	1	1	1	1	1	1	0.029412	0.001057	1	1.6E-17	1	0.002024
3	130653386	130653399	ATP2C1	6.93E-20	6.08E-11	0.046154	1	1	1	1	1	1	0.013333	1	1	1.06E-17	0.05	2.03E-05
11	73984657	73984669	P4HA3	7.06E-20	2.43E-28	0.035088	1	1	1	4.18E-06	1	1	1	0.025	1	2.39E-13	0.001948	0.001147
3	111873902	111873917	SLC9C1	7.56E-20	8.99E-15	7.18E-05	0.044771	1	0.019248	0.244847	1	1	0.028718	0.102041	0.269841	3.01E-27	0.057971	0.000369
2	198267243	198267257	SF3B1	7.67E-20	3.52E-19	0.095188	1	1	1	0.02809	1	0.019868	1	0.117647	1	3.46E-17	1	1
6	18148155	18148167	TPMT	7.74E-20	2.99E-16	0.028571	1	1	1	1	1	0.007299	1	1	1	1.53E-14	0.034483	0.114046
14	52957731	52957750	TXNDC16	7.79E-20	5.39E-09	0.003604	1	0.157115	1	1	1	1	1	0.222222	1	1.7E-20	1	0.06227
6	44364261	44364277	CDC5L	8.27E-20	1.14E-24	1.22E-05	1	1	0.047619	1	1	0.018293	1	1	1	3.67E-13	0.03125	0.004771
11	17526254	17526267	USH1C	8.32E-20	2.54E-25	0.210526	1	1	1	1	1	0.03065	1	0.016667	1	7.27E-07	0.065918	0.24343
21	38498341	38498356	TTC3	8.66E-20	5.44E-16	0.035714	1	1	0.093697	1	1	1	0.000138	1	0.166667	1.44E-12	0.033333	0.000542
9	128064242	128064260	GAPVD1	8.97E-20	5.14E-17	0.000803	1	0.00294	1	1	1	1	0.11288	1	1	1.24E-16	0.037207	0.48408
9	17464479	17464491	CNTLN	9.05E-20	2.82E-27	1	0.036807	1	0.101045	0.019231	1	1	0.000128	1	1	2.19E-17	0.055936	0.041534
11	108058769	108058785	NPAT	9.12E-20	4.66E-14	0.226335	1	1	0.005098	1	1	1	1	0.09375	1	1.02E-26	1	0.01229
X	48054294	48054306	SSX5	9.26E-20	1.06E-17	1	1	1	1	0.034856	1	0.015625	0.046053	1	1	1.63E-13	1	3.78E-05
X	22244528	22244549	PHEX	9.37E-20	4.83E-16	1	1	0.049484	0.111005	1	1	1	0.146095	0.034483	0.000327	6.62E-09	0.074976	0.000616
18	70532185	70532210	NETO1	9.55E-20	4.88E-06	0.133192	1	1	1	1	1	1	1	1	1	9.48E-11	1	2.9E-07
1	116940481	116940497	ATP1A1-AS1	9.86E-20	2.29E-37	0.125	1	0.171332	1	0.000501	1	1	0.088563	1	1	5.98E-06	0.034483	0.005397
2	28464369	28464382	BRE	1.01E-19	2.31E-05	0.027027	1	1	1	1	1	0.019608	1	1	1	1.34E-11	1	0.000353
8	3611416	3611429	CSMD1	1.06E-19	1.52E-14	0.111801	1	1	1	0.079571	1	1	0.038462	1	1	1.84E-29	0.033333	1.03E-05
8	108315599	108315615	ANGPT1	1.07E-19	5.04E-22	0.234274	1	1	1	1	1	1	1	0.052973	1	3.42E-14	7.46E-05	0.001027
12	50152601	50152618	TMBIM6	1.14E-19	2.59E-11	9.77E-05	1	1	1	1	1	1	1	1	1	1.31E-22	1	0.330159
2	64069277	64069293	UGP2	1.15E-19	1.35E-27	1	1	1	0.034314	1	0.008734	0.034932	0.099228	0.024691	1	9.11E-09	0.032609	1.12E-05
9	33280749	33280775	CHMP5	1.17E-19	1.29E-17	0.00327	0.009852	1	1	1	1	0.018182	0.076308	1	1	5.68E-19	0.059988	0.040857
X	2343183	2343213	DHRSX	1.18E-19	5.54E-17	4.72E-05	1	0.011905	0.023243	1	1	0.024	1	0.001763	1	4.48E-25	4.05E-05	0.000854
8	87680406	87680418	CNGB3	1.19E-19	3.3E-20	1	1	0.253295	0.047801	0.024589	1	0.027681	1	1	0.065934	9.22E-14	0.016935	0.05336
3	21606027	21606040	ZNF385D-AS1	1.19E-19	1.41E-11	0.462451	1	0.585977	1	1	1	0.304878	1	0.117647	0.035714	4.23E-09	1	0.088421
2	86998651	86998676	RMND5A	1.21E-19	3.22E-12	0.101633	0.000148	0.167625	0.00523	0.103138	1	1	0.139325	1	1	2.48E-10	0.083734	0.214339
5	94903575	94903589	ARSK	1.26E-19	2.56E-12	0.211144	0.009524	1	0.004058	1	1	1	1	0.033898	1	2.5E-14	0.00223	0.024704
13	77792099	77792113	MYCBP2	1.32E-19	7.85E-19	0.033898	0.018306	0.017282	1	1	1	1	0.052632	0.027397	1	5.88E-22	1	2.11E-05
3	123332875	123332892	MYLK-AS1	1.33E-19	1.35E-25	0.009307	0.023529	0.24607	0.084462	0.04395	1	1	1	1	0.181818	4.19E-21	0.104265	0.109309
6	38905667	38905680	LOC100131047	1.35E-19	2.94E-19	0.001536	1	1	0.043478	1	1	1	1	0.033333	1	1.87E-21	0.078919	0.000519
7	65426054	65426069	GUSB	1.35E-19	2.18E-34	0.085678	1	1	1	0.09296	0.004831	0.044643	0.061856	0.028571	1	3.63E-17	0.033333	1.84E-05
7	151884279	151884292	KMT2C	1.39E-19	1.57E-13	0.012097	1	1	1	1	1	0.016529	0.000142	1	1	1.33E-09	0.034483	0.000637
3	42660489	42660508	LOC101928323	1.39E-19	7.16E-13	0.031715	1	1	1	1	1	0.059159	1	0.034884	1	6.55E-22	0.054045	0.002916
14	91365646	91365664	RPS6KA5	1.4E-19	5.83E-15	0.000673	1	0.075581	1	1	1	1	0.05746	1	1	1.9E-18	1	9.75E-08
2	114689047	114689061	ACTR3	1.48E-19	1.56E-07	0.136185	0.035714	1	1	1	1	1	1	0.055164	1	9.29E-18	0.074976	0.001445
5	72185591	72185607	TNPO1	1.48E-19	3.63E-24	0.000853	1	1	0.08649	0.04629	0.00463	1	1	0.068361	1	5.68E-16	1	0.011015
8	142161666	142161681	DENND3	1.57E-19	1.13E-29	0.003587	0.020253	1	1	0.059309	1	1	1	1	1	1.45E-25	0.013699	0.013665
12	69214081	69214094	MDM2	1.58E-19	9.86E-13	0.069549	1	0.125262	1	0.039996	1	1	0.001122	1	1	7.95E-12	0.011236	0.003747
11	124624705	124624721	ESAM	1.6E-19	2.03E-28	0.029412	1	1	6.02E-05	0.000571	1	0.021127	1	1	1	3.23E-14	1	0.000572
14	32142544	32142557	NUBPL	1.61E-19	2.97E-12	0.144944	1	1	0.285337	1	1	1	1	0.001815	1	5.76E-26	0.026316	0.001818
13	103257289	103257311	TPP2	1.62E-19	2.25E-22	0.01277	1	1	0.02649	1	1	1	1	0.028986	1	3.66E-30	0.036145	1.68E-05
3	148858987	148859001	HPS3	1.64E-19	1.89E-21	0.043478	1	1	0.305593	1	0.021739	1	0.027586	0.041667	0.26087	9.28E-14	0.144001	0.027877
1	197150249	197150268	ZBTB41	1.68E-19	4.21E-18	0.00188	1	1	0.039106	1	1	0.01626	1	1	1	1.42E-19	1	0.000221
17	45234760	45234774	CDC27	1.69E-19	5.24E-10	0.163647	1	1	0.11892	0.10281	1	1	0.18697	1	1	9.78E-17	0.2	0.001864
21	38564530	38564545	TTC3	1.7E-19	4.16E-08	0.076897	1	1	1	0.012195	1	1	1	1	1	1.31E-17	1	1
12	100496478	100496498	UHRF1BP1L	1.7E-19	9.08E-06	3.97E-06	1	0.093647	1	1	1	0.044586	1	0.086957	1	3.57E-23	1	0.000104
X	153357614	153357628	MECP2	1.75E-19	5.46E-17	0.090909	1	0.10643	0.125995	0.020548	1	1	0.001905	0.086957	1	5.63E-14	0.000644	0.000394
19	46206021	46206037	QPCTL	1.75E-19	2.83E-16	0.421739	1	1	1	1	1	0.038645	0.045977	1	1	1.27E-11	1	0.019851
17	66039938	66039951	KPNA2	1.78E-19	3.37E-30	0.04918	0.015625	0.205044	0.182717	0.067063	1	0.00885	1	1	1	1.23E-19	0.000784	0.03527
X	106028279	106028291	RNF128	1.8E-19	3.93E-23	1	1	0.10939	0.091321	1	1	0.027523	0.002392	1	1	4.78E-16	0.067398	1.55E-05
12	85285920	85285938	SLC6A15	1.8E-19	8.25E-19	4.63E-06	1	0.311836	0.245428	1	1	1	1	0.02381	0.003096	2.36E-18	1	1
5	93294451	93294463	FAM172A	1.86E-19	5.13E-28	0.03125	0.02216	1	0.09296	0.031556	1	1	0.011405	1	1	1.2E-14	1	0.001085
6	24515330	24515350	ALDH5A1	1.93E-19	1.11E-12	0.25178	1	1	1	1	1	1	1	1	1	1.04E-28	0.018692	0.013381
14	21964623	21964635	TOX4	2.06E-19	3.09E-14	1	1	1	1	0.031913	1	0.013423	1	0.000466	1	1.49E-23	1	1E-06
5	58270446	58270485	PDE4D	2.17E-19	3.13E-23	5.69E-05	1	1	1	1	0.009756	1	0.297572	1	1	5.58E-06	1	0.015383
2	232025952	232025967	PSMD1	2.32E-19	2.79E-08	0.147905	1	1	1	1	1	0.02749	0.000539	1	1	4.49E-11	1	0.031946
6	11714639	11714665	ADTRP	2.32E-19	2.6E-09	0.000115	1	1	1	1	1	0.041663	1	1	0.238095	6.33E-27	1	0.001321
17	45105631	45105644	RPRML(dist=49017),ARL17A(dist=3308)	2.36E-19	5.14E-20	1	1	0.166364	0.009615	0.000552	1	0.019608	0.014675	1	1	1.58E-15	0.000649	0.003885
6	119296378	119296399	FAM184A	2.42E-19	3.03E-07	1	0.036585	1	1	1	1	1	1	1	0.135714	9.97E-12	1	0.308823
4	159590922	159590934	C4orf46	2.48E-19	2.87E-22	0.062004	1	1	1	1	1	0.048774	0.026786	1	1	3.24E-20	0.045455	2.38E-05
6	158049351	158049365	ZDHHC14	2.49E-19	1.56E-19	1	1	0.086022	1	0.104075	1	0.042254	0.132565	0.019608	0.2	1.04E-18	0.001317	0.000707
2	234178624	234178640	ATG16L1	2.61E-19	2.57E-30	0.003301	1	0.032488	0.138664	0.079562	1	0.000233	0.106944	0.016129	1	1.4E-14	0.028037	0.044503
9	36058785	36058815	RECK	2.92E-19	9.95E-17	0.008535	1	1	0.043478	0.031412	1	1	1	0.025	1	1.09E-09	0.110262	0.002398
17	16041578	16041592	NCOR1	3.08E-19	1.37E-10	0.066667	1	1	1	1	1	1	1	1	1	1.41E-15	0.042254	4.83E-06
11	117152291	117152314	RNF214	3.14E-19	2.17E-39	0.039216	8.27E-05	0.0625	0.041237	0.000813	1	0.03125	6.02E-09	0.016667	1	4.69E-16	1	1.96E-05
5	122359456	122359480	PPIC	3.23E-19	6.18E-15	0.005102	1	1	1	0.016129	1	1	1	0.033898	1	3E-17	1	0.000103
7	104707158	104707171	KMT2E	3.24E-19	2.54E-19	0.050847	1	1	0.040265	0.04807	0.004651	1	0.0875	1	1	0.000162	1	0.000239
10	98325237	98325262	TM9SF3	3.26E-19	9.7E-16	0.00303	1	1	1	1	1	0.029961	2.33E-05	1	1	2.21E-11	1	3.99E-08
1	237619875	237619890	RYR2	3.28E-19	4.02E-17	0.153846	1	0.457185	0.271368	0.277585	1	1	0.002612	1	1	3.22E-10	1	0.004022
11	43342281	43342311	API5	3.31E-19	1.22E-07	0.050847	1	1	1	1	1	0.027118	1	0.029851	1	0.001666	1	0.010774
18	29238076	29238091	B4GALT6	3.43E-19	4.02E-16	0.115224	1	1	0.012795	0.257369	1	1	0.059988	1	1	4.35E-16	1	9.98E-05
17	39522910	39522922	KRT33B	3.44E-19	4.51E-20	0.000496	1	1	1	1	1	1	1	0.000565	0.315789	3.25E-12	0.016667	0.16352
14	58674823	58674838	ACTR10	3.53E-19	1.1E-18	1	1	1	1	0.093333	1	1	1	0.04	1	3.05E-20	1	0.048857
2	111406968	111406984	BUB1	3.57E-19	8.94E-29	0.000601	0.008032	0.155773	1	1	1	0.013072	1	0.013514	0.2	1.28E-24	1	0.002756
11	63149670	63149682	SLC22A9	3.62E-19	1.18E-26	0.048387	1	1	1	0.000995	1	0.013699	0.003754	0.057971	1	3.88E-18	0.022989	1.94E-05
9	8341280	8341300	PTPRD	3.64E-19	2.06E-21	0.003173	1	1	0.127487	1	1	1	0.181306	0.035714	1	1.68E-18	1	0.170791
11	78154810	78154823	NARS2	3.67E-19	1.31E-19	1	1	0.088496	1	0.019324	1	0.023438	0.001735	1	1	8.03E-08	0.04878	0.281238
1	24978892	24978909	SRRM1	3.68E-19	6.15E-11	0.118415	1	0.093407	0.043478	0.088608	0.086207	1	1	0.017241	1	5.83E-16	0.001151	0.027211
1	54252939	54252952	NDC1	3.82E-19	2.47E-25	0.004902	0.008584	1	0.078225	0.012048	1	1	1	0.125	1	2.63E-12	1	0.004866
2	191523855	191523879	NAB1	3.87E-19	1.02E-07	0.038462	1	1	1	1	1	1	1	0.015152	1	1.73E-08	1	1
11	57505520	57505534	TMX2-CTNND1	3.92E-19	6.51E-14	0.003798	1	1	0.035874	1	1	0.013699	0.044444	0.222222	1	2.02E-09	1	0.009884
8	104922508	104922534	RIMS2	3.94E-19	1.72E-30	0.039051	1	1	0.101957	4.87E-05	1	0.02459	1	0.035714	1	0.000447	1	0.04211
9	36109839	36109853	RECK	3.96E-19	3.45E-21	0.04918	0.008439	1	1	0.049477	1	1	1	1	1	2.15E-12	1	1.25E-06
8	38839302	38839316	HTRA4	4.12E-19	2.48E-25	0.044118	1	1	1	1	0.008969	1	0.118294	1	1	8.41E-22	0.001373	0.003732
12	76763092	76763106	OSBPL8	4.2E-19	2.43E-09	1	1	1	0.134187	0.126963	0.033058	0.025641	1	1	0.052632	1.89E-14	1	0.099367
15	23333801	23333815	HERC2P2	4.22E-19	6.3E-10	0.037037	1	1	1	1	1	1	1	0.000816	1	1.32E-11	0.016667	0.000588
7	74172385	74172400	GTF2I	4.34E-19	8.5E-07	0.019285	1	1	1	0.017241	1	0.009615	0.006593	1	1	7.82E-08	0.002177	0.000856
11	68338491	68338520	PPP6R3	4.36E-19	1.05E-09	0.001753	1	1	0.034091	1	1	0.015152	0.044118	1	1	6.44E-21	0.00028	0.013477
1	89614950	89614962	GBP7	4.38E-19	2.98E-14	1	1	1	1	0.021008	0.004808	1	0.05298	0.115294	0.529412	5.5E-12	1	0.083871
7	74119460	74119488	LOC101926943	4.59E-19	1.14E-27	0.030303	1	0.138951	0.038278	0.02521	1	0.028469	1	1	1	6.22E-09	0.026316	1.51E-05
14	20857306	20857321	TEP1	4.59E-19	1.33E-12	0.009484	1	1	1	1	1	1	1	1	0.230769	3.16E-25	1	0.000335
16	24185815	24185831	PRKCB	4.76E-19	1.29E-13	8.35E-05	1	1	1	1	1	1	1	0.042254	1	1.09E-25	0.00508	0.002709
15	55841195	55841209	PYGO1	4.8E-19	1.24E-21	4.34E-06	0.005348	0.088235	0.023529	1	1	0.025316	0.000814	1	1	2.55E-26	1	1.55E-05
1	92108274	92108288	CDC7(dist=116953),TGFBR3(dist=37612)	4.86E-19	1.42E-07	0.000936	0.0833	1	0.101974	1	1	0.015504	0.047994	1	1	2.22E-18	1	0.309594
8	42323207	42323223	SLC20A2	4.98E-19	8.14E-12	1	1	1	1	1	1	1	1	0.030303	1	0.016449	0.009804	0.015993
17	29508819	29508836	NF1	5.07E-19	7.64E-19	3.01E-06	0.008772	0.18697	0.035	0.02	1	0.011561	1	1	1	7.41E-39	1	0.001263
12	10205420	10205435	CLEC9A	5.14E-19	2.68E-10	0.007541	0.053571	1	0.02381	1	1	1	1	1	1	1.58E-23	0.024096	0.000527
18	29435778	29435795	TRAPPC8	5.16E-19	3.49E-09	0.00257	1	1	0.084472	1	1	1	0.011628	1	1	6.89E-24	0.176471	1
17	29195444	29195460	ATAD5	5.35E-19	1.32E-10	0.000252	1	1	1	1	1	1	1	0.03125	1	9.3E-22	0.022472	0.000961
3	41877473	41877487	ULK4	5.73E-19	2.07E-18	4.63E-06	1	1	1	0.014851	1	1	1	1	1	3.47E-23	0.046779	0.437257
4	55131001	55131019	PDGFRA	5.76E-19	7.18E-17	0.031602	1	1	0.090854	0.155947	1	1	1	0.054414	1	5.49E-13	0.000455	8.79E-07
1	92765880	92765892	RPAP2	6.01E-19	4.49E-17	0.06	1	1	0.034041	1	0.020833	1	1	1	1	4.71E-13	1	0.123142
12	104712858	104712885	TXNRD1	6.23E-19	9.14E-16	0.029412	1	1	1	1	1	1	1	1	1	8E-09	0.035294	0.0019
3	75466006	75466019	MIR4444-1(dist=202307),FAM86DP(dist=4684)	6.23E-19	8.33E-13	0.141414	1	1	0.07997	1	1	1	1	0.037037	0.044118	6.02E-20	1	1
X	40588605	40588618	MED14	6.32E-19	1.04E-09	0.001587	1	0.138256	0.024096	0.039216	1	1	1	0.037037	1	8.98E-14	0.000749	2.28E-05
22	46739288	46739300	TRMU	6.52E-19	2.79E-14	0.006446	1	1	1	1	1	1	1	0.017241	1	3.39E-20	1	2.44E-05
12	56380950	56380964	RAB5B	6.87E-19	4.34E-22	1	0.009346	1	0.103376	1	1	1	0.034091	0.014706	0.333333	5.92E-20	0.010753	0.000681
12	102468721	102468748	NUP37	6.98E-19	1.7E-11	0.004024	1	1	1	1	1	0.022222	1	1	1	8.99E-17	0.023529	0.055118
7	72879898	72879914	BAZ1B	7E-19	1.13E-19	0.001317	1	1	0.061714	0.02439	1	1	1	0.027778	1	1.13E-16	1	0.068571
21	19653342	19653355	TMPRSS15	7.04E-19	1.43E-21	7.98E-05	0.040462	0.165086	0.100775	0.009897	1	0.134977	0.009858	1	0.002051	2.51E-17	0.022989	0.027347
X	79937622	79937634	BRWD3	7.17E-19	2.23E-11	0.125859	1	0.062508	1	1	1	0.049993	1	0.006452	1	9.57E-16	1	0.471544
4	166215662	166215692	KLHL2	7.36E-19	0.034479	8.35E-05	1	1	1	1	1	1	1	1	1	1.73E-11	0.001807	0.082667
4	9710633	9710651	MIR548I2(dist=152696),DRD5(dist=72607)	7.41E-19	1.13E-07	0.008564	1	1	1	1	1	0.019231	1	1	1	9.25E-22	1	0.021381
20	37395979	37396016	ACTR5	7.47E-19	2.08E-08	0.125	1	1	1	1	1	0.014706	1	1	1	6.48E-05	0.028169	0.001781
3	112719791	112719808	GTPBP8	7.64E-19	1.2E-15	0.213523	1	1	0.113526	1	1	1	0.097969	1	0.052632	2.45E-20	1	7.43E-05
17	39776817	39776829	KRT17	7.64E-19	8.64E-25	1	0.004762	0.059701	0.000671	0.03543	1	0.01875	1	0.029412	1	2.78E-14	0.022472	1
17	59857599	59857611	BRIP1	7.7E-19	7.45E-22	1	0.018912	1	1	1	1	1	0.00176	0.016667	1	1.82E-15	0.033333	0.00301
2	85589223	85589237	ELMOD3	8.16E-19	1.3E-08	1	1	1	1	1	1	0.007874	1	0.026667	1	1.24E-19	0.021978	2.65E-07
13	113965002	113965017	LAMP1	8.5E-19	1.19E-32	0.136364	1	1	1	0.000251	1	0.018182	1	0.034483	0.333333	3.68E-10	0.034091	0.106141
3	132363752	132363765	NPHP3-ACAD11	8.55E-19	2.16E-16	0.030303	0.035926	0.248669	0.026846	0.039896	1	1	1	0.016129	1	1.14E-09	1	0.016184
15	41060070	41060085	DNAJC17	8.56E-19	3.58E-26	1	1	1	0.010417	1	1	0.043474	1	0.039216	0.090909	1.05E-07	1	4.81E-05
15	41364265	41364305	INO80	8.78E-19	3.83E-20	0.003053	0.006329	1	0.018868	1	1	1	1	1	1	1.07E-08	1	0.000196
13	111076981	111076999	COL4A2	8.8E-19	8.34E-12	0.011858	1	0.345983	1	1	1	1	1	0.028571	1	0.068793	0.004236	0.158745
19	9528423	9528438	ZNF266	8.82E-19	1.67E-19	0.055069	0.006494	1	0.000883	1	1	0.041447	0.054545	0.038462	1	1.1E-07	1	1
6	157495951	157495966	ARID1B	9.21E-19	2.11E-37	0.000316	1	0.095652	0.049254	0.001501	1	1	1	1	1	4.14E-33	1	0.03567
6	131948816	131948831	MED23	9.34E-19	9.67E-09	0.000539	1	0.275843	0.049992	1	1	1	0.001457	0.083333	0.275862	2.28E-09	0.065918	0.006746
5	137474284	137474295	NME5	9.61E-19	1.43E-15	0.035714	1	1	0.042373	1	1	1	1	1	1	8.62E-16	1	0.001024
2	87049358	87049371	CD8B	9.68E-19	6.37E-17	0.003896	1	0.005961	1	1	1	1	1	1	1	5.07E-12	1	4.76E-05
10	45984725	45984740	MARCH8	1.1E-18	2.32E-07	1	1	0.011555	1	1	1	1	1	1	1	1.88E-10	0.027778	0.136939
X	3539376	3539390	PRKX	1.13E-18	3.57E-11	0.006963	1	0.147477	0.001099	1	1	0.053863	0.021739	1	1	2.66E-12	0.00202	6.64E-05
4	99214537	99214549	RAP1GDS1	1.13E-18	1.87E-08	3.08E-05	1	1	0.018182	0.014286	1	1	1	1	1	9.98E-13	1	0.10761
19	22836873	22836886	ZNF492	1.17E-18	2.39E-20	1	1	0.347976	0.167199	0.047865	1	0.046506	0.083297	0.004808	0.007353	1.78E-14	0.000294	7.57E-06
6	102124470	102124483	GRIK2	1.18E-18	6.02E-13	0.020993	1	0.055556	0.054536	1	0.024	1	0.001213	0.001488	0.5	5.46E-18	0.025641	0.042736
21	30339205	30339217	LTN1	1.18E-18	3.87E-21	1	1	1	1	1	1	1	0.001212	1	1	1.96E-18	0.013514	0.078756
8	133854714	133854728	PHF20L1	1.21E-18	2.65E-20	0.007353	1	1	1	1	1	1	1	0.020408	1	2.16E-05	1	2.33E-05
X	19086800	19086823	GPR64	1.22E-18	1.15E-21	0.046875	1	1	0.081384	0.013274	1	0.007463	0.109006	0.065217	1	1.86E-16	0.025316	0.000681
X	41530655	41530668	CASK	1.23E-18	1.71E-12	0.144944	1	0.236749	1	0.091547	1	1	1	0.017544	0.307692	1.51E-11	1	0.560965
12	118821800	118821813	SUDS3	1.23E-18	4.55E-14	0.00565	0.038462	1	1	1	1	1	0.144001	0.079184	0.171569	1.26E-19	0.038961	0.018568
13	39608335	39608360	PROSER1	1.24E-18	5.88E-28	0.000627	0.019851	1	1	1	1	1	1	1	0.272727	1.89E-29	1	0.229747

12	110834030	110834049	ANAPC7	1.25E-18	2.99E-14	2.25E-06	1	0.039683	1	1	1	0.012195	1	0.166667	1	1.85E-34	0.025641	0.219596
12	43826277	43826290	ADAMTS20	1.27E-18	2.12E-22	0.171047	0.039116	1	0.004427	1	1	0.028069	0.122328	1	1	8.9E-09	1	0.303035
10	101124157	101124170	CNNM1	1.35E-18	6.92E-12	0.146853	1	1	1	1	1	1	1	0.101633	1	1.66E-13	0.022727	0.026643
X	18800531	18800548	PPEF1	1.43E-18	0.000344	0.065068	1	1	1	1	1	1	1	1	0.473846	3.28E-30	0.063987	0.025679
4	17841869	17841881	NCAPG	1.46E-18	6.82E-29	0.000504	0.020887	1	0.083795	0.066058	0.004587	0.019608	1	1	1	1.6E-21	0.012987	0.00773
2	173435578	173435593	PDK1	1.47E-18	1.43E-06	0.006721	1	1	1	1	1	1	1	1	1	1.28E-26	1	0.025613
7	94740524	94740538	PPP1R9A	1.48E-18	7.07E-18	0.001739	1	1	1	0.031746	1	1	1	0.084181	0.090909	4.34E-15	0.027778	0.012377
2	98866980	98866995	VWA3B	1.67E-18	5.07E-16	0.008737	1	0.124872	0.080775	1	1	0.0125	0.00161	0.027027	1	8.41E-12	0.037037	0.156832
2	135703650	135703664	CCNT2	1.69E-18	2.87E-21	0.050847	1	1	0.038462	0.020833	1	1	1	0.037037	1	2.32E-20	1	0.006686
11	134072616	134072632	NCAPD3	1.75E-18	4E-12	0.054054	1	1	0.084864	1	1	1	1	0.023256	1	1.76E-12	1	0.000859
8	107704921	107704955	OXR1	1.76E-18	6.88E-20	0.000673	0.009615	0.105188	1	1	1	1	1.17E-05	0.000452	1	1.07E-14	1	0.028469
1	12330939	12330953	VPS13D	1.87E-18	5.72E-12	0.004862	1	1	0.042324	0.000483	1	1	0.059988	1	1	2.57E-15	1	0.020588
7	66489771	66489787	TYW1	1.92E-18	2.48E-06	0.085714	1	0.126167	1	1	1	0.017699	1	1	1	7.76E-09	0.157591	1
12	69980447	69980462	CCT2	1.94E-18	1.82E-17	0.052281	1	1	0.0199	0.038458	1	1	1	1	1	2.13E-13	1	0.001203
7	112555294	112555307	C7orf60	1.95E-18	1.83E-12	1	1	0.06	1	0.011407	1	1	1	1	1	8.06E-13	1	0.146601
4	52928352	52928371	SPATA18	1.98E-18	2.7E-26	0.011858	0.002125	0.408639	0.019488	0.05475	1	0.015349	2.62E-06	0.069767	1	2.49E-05	1	0.055034
1	35885037	35885058	ZMYM4	2.04E-18	1.85E-23	1	1	1	0.033333	1	1	1	1	1	1	9.6E-14	1.09E-05	0.062972
12	69042454	69042468	RAP1B	2.06E-18	1.93E-07	0.123912	1	1	1	1	1	0.030534	0.034483	0.001242	1	1E-18	1	0.002294
5	70837260	70837275	BDP1	2.11E-18	2.5E-29	0.004707	1	1	1	0.000168	1	1	1	0.060606	1	1.64E-22	0.027397	0.177442
14	45330466	45330477	FSCB(dist=353967),C14orf28(dist=36030)	2.12E-18	2.67E-07	0.055556	0.015625	0.069307	1	0.017857	1	1	1	0.08216	0.181818	1.53E-11	0.067398	1
4	38937316	38937329	FAM114A1	2.13E-18	6.35E-14	0.035088	1	1	0.075682	0.009479	1	1	0.052796	1	1	4.39E-17	0.036145	0.001052
X	16761748	16761764	SYAP1	2.14E-18	2.22E-20	0.249012	1	1	1	1	1	1	1	1	1	0.000799	1	0.001944
14	35242702	35242726	BAZ1A	2.19E-18	0.000477	0.000335	1	0.160967	1	1	1	1	1	1	1	4.49E-28	1	2.67E-05
20	36431202	36431215	CTNNBL1	2.19E-18	9.81E-34	0.15556	1	0.042254	0.000853	0.000514	1	1	5.05E-05	1	1	6.57E-16	1	0.043165
12	96379650	96379675	HAL	2.2E-18	6.16E-11	0.032258	0.017544	1	1	1	1	1	1	1	1	8.63E-09	0.034483	0.009889
3	121720514	121720530	ILDR1	2.23E-18	3.8E-33	0.199417	0.044843	0.059379	0.018722	1	1	1	1	1	0.142857	2.31E-18	1	0.238604
3	172003831	172003845	FNDC3B	2.3E-18	8.68E-12	1	1	0.192962	0.188125	1	1	1	1	0.085714	1	3.68E-20	0.188235	0.319969
8	104075165	104075177	ATP6V1C1	2.52E-18	2.99E-23	0.000481	1	1	0.039801	1	1	1	0.119291	1	1	4.58E-15	0.042777	0.134558
18	18588229	18588257	ROCK1	2.52E-18	1.19E-09	0.001402	1	1	1	1	1	0.007937	1	1	0.214286	1.33E-08	1	0.179218
17	58013510	58013529	RPS6KB1	2.56E-18	8.53E-16	0.044776	0.01	1	1	1	1	1	0.068945	1	1	1.82E-15	1	6.57E-05
14	88407716	88407730	GALC	2.72E-18	2.99E-28	0.030769	1	0.285337	0.058515	1	1	0.110512	0.002031	0.166667	0.166667	9.78E-06	1	0.038217
2	222290623	222290635	EPHA4	2.74E-18	1.17E-14	0.119898	0.005747	1	0.011236	0.038001	1	1	1	0.019231	1	5.1E-10	1	0.003024
10	8111345	8111359	GATA3	2.76E-18	1.06E-13	0.289231	1	1	0.049383	0.000255	1	1	1	0.045455	1	0.000625	0.000191	0.027235
1	65138787	65138801	CACHD1	2.77E-18	4.85E-25	0.015336	0.027874	0.379795	1	0.000684	1	0.000571	9.66E-05	0.175084	1	6.59E-21	0.00925	0.553866
19	37721404	37721419	ZNF383	2.79E-18	2.14E-09	1	1	1	1	0.030928	1	0.006897	1	1	1	9.63E-22	0.003484	0.003076
1	47581121	47581151	CYP4Z1	3E-18	2.5E-06	0.002162	0.0125	1	1	1	1	0.013699	1	1	1	1.3E-13	0.024691	0.10447
1	33402334	33402352	RNF19B	3.07E-18	4.77E-20	7.63E-05	0.059511	0.194207	1	0.051492	1	0.102192	1	1	1	7.77E-38	1	0.149812
2	211179765	211179777	MYL1	3.1E-18	1.17E-26	0.109524	0.020134	1	0.079334	0.000453	1	0.013699	1.59E-06	0.045455	1	3.98E-09	0.011139	0.001415
2	230656987	230657001	TRIP12	3.12E-18	1.2E-24	0.001142	0.027906	1	0.016484	1	1	0.019608	1	1	0.272727	2.74E-24	0.117647	0.00121
5	161322652	161322664	GABRA1	3.15E-18	2.68E-18	0.044118	1	1	1	1	1	1	1	1	1	7.84E-12	1	0.015396
2	62063093	62063111	FAM161A	3.24E-18	1.54E-30	0.001329	0.070485	0.591131	0.310812	0.122474	1	1	1.59E-06	0.069444	1	6.91E-36	1	0.000351
11	33374613	33374626	HIPK3	3.26E-18	9.48E-21	0.00752	1	0.077267	1	0.074215	0.022222	0.026786	1	1	1	5.35E-24	0.042553	0.028061
17	55016354	55016369	COIL	3.27E-18	4.83E-18	0.049684	1	0.073529	1	0.047612	1	1	1	0.05	1	2.81E-18	1	0.013592
10	12226870	12226882	NUDT5	3.38E-18	1.83E-11	0.000171	1	1	1	0.050732	1	1	1	1	0.214286	4.36E-19	0.024096	0.000415
17	58289521	58289533	USP32	3.39E-18	6.04E-09	9.38E-05	1	1	1	1	1	1	0.008065	1	0.333333	1.18E-20	1	0.014859
1	63128836	63128850	DOCK7	3.41E-18	1.63E-28	8.35E-05	1	0.054264	1	1	1	1	1	1	1	4.96E-14	1	0.00686
2	48688258	48688273	PPP1R21	3.5E-18	3.18E-20	0.01944	0.004695	1	1	1	1	0.007874	1	0.05	1	2.79E-16	1	0.058454
6	49415351	49415368	MUT	3.52E-18	2.84E-22	6.94E-06	0.04958	0.00251	0.04958	1	0.025641	0.014184	1	1	1	8.71E-33	1	0.005345
5	145647187	145647210	RBM27	3.7E-18	6.14E-25	3.42E-05	1	1	1	9.25E-06	1	1	1	1	1	2.38E-18	0.039474	0.00356
3	112289576	112289599	SLC35A5	3.71E-18	5.73E-07	0.041096	1	1	1	1	1	1	0.021277	1	0.421053	1.13E-18	0.043478	0.006614
X	135080623	135080653	SLC9A6	3.77E-18	8.53E-17	0.222856	1	0.142032	0.000393	0.176891	1	1	0.011536	0.018868	0.529231	4.05E-19	0.029412	0.405077
5	77745712	77745752	SCAMP1	3.81E-18	7.28E-22	1	1	1	1	0.000256	1	1	1.5E-06	0.015625	0.1	3.67E-10	1	5E-06
12	123703074	123703086	MPHOSPH9	3.87E-18	3.21E-27	4.27E-05	0.018823	1	0.089056	0.051164	1	0.03	1	0.018519	1	3.86E-27	0.027027	0.007098
8	28707622	28707636	INTS9	3.88E-18	2.94E-27	0.000111	1	0.011645	0.000623	1	1	0.02888	1	0.025641	1	1.75E-22	1	0.000995
1	109856836	109856854	SORT1	4.22E-18	4.38E-12	0.030769	1	1	0.055118	0.004275	1	0.05084	1	1	1	9.67E-10	0.050847	0.000407
6	37328387	37328414	RNF8	4.23E-18	2.79E-05	0.113122	1	1	1	1	1	1	1	1	1	1.57E-06	1	0.0003
7	24789116	24789134	DFNA5	4.27E-18	2.9E-18	0.009231	1	1	0.004665	1	1	1	1	0.034483	1	1.97E-09	1	0.160762
X	3238003	3238028	MXRA5	4.27E-18	7.59E-09	0.032787	1	0.060606	1	0.039604	1	1	1	1	1	7.9E-13	0.04918	9E-05
9	86920104	86920135	SLC28A3	4.32E-18	4.29E-09	0.007974	1	0.01474	1	1	1	0.040265	1	0.047899	1	2.14E-15	0.019231	0.38977
2	110925982	110925995	NPHP1	4.34E-18	1.83E-17	0.11103	1	0.068027	1	0.015936	1	1	1	0.030303	1	3.81E-18	0.070568	0.001842
12	99117397	99117414	APAF1	4.38E-18	3.69E-34	0.002259	0.071886	1	0.000273	0.003618	1	1	0.00682	0.054545	1	9.31E-11	0.042553	0.023855
19	54603097	54603118	OSCAR	4.42E-18	1.94E-08	0.02593	1	1	1	1	1	1	1	1	1	2.9E-28	1	0.061321
20	18505555	18505576	SEC23B	4.5E-18	2.42E-17	0.073529	1	0.010724	1	1	1	1	0.046729	1	1	2.72E-16	1	0.005054
2	189859434	189859447	COL3A1	4.58E-18	6.73E-18	0.001639	1	1	0.08716	0.008772	1	0.001596	1	0.058824	1	1.96E-11	7E-05	0.106526
7	121699789	121699802	PTPRZ1	4.65E-18	2.29E-15	0.054054	0.011494	1	1	2.47E-05	1	1	8.69E-07	0.017857	1	0.000193	1	0.02798
1	158584103	158584116	SPTA1	4.65E-18	2.14E-07	1	1	0.019823	0.151883	1	1	1	1	0.050847	0.15	5.62E-24	0.002687	0.082428
5	145508515	145508535	LARS	4.67E-18	1.26E-13	0.035714	1	0.061224	1	1	0.004926	0.030769	0.053333	0.033333	1	3.21E-11	0.00037	1
1	197053561	197053577	ASPM	4.74E-18	2.3E-17	0.0002	1	0.238785	1	1	1	0.05613	1	0.053571	1	9.32E-30	1	0.004853
10	30605169	30605182	MTPAP	4.87E-18	4.14E-16	0.000974	1	0.146988	1	1	1	1	1	1	1	2.41E-30	0.0833	0.010772
7	84751249	84751273	SEMA3D	5.03E-18	9.12E-05	0.020449	1	1	1	1	1	1	1	1	1	1.04E-09	0.018182	0.022347
15	49064607	49064620	CEP152	5.27E-18	2.08E-08	0.12	0.032607	1	1	1	1	1	1	0.03125	0.25	0.000158	0.040816	0.000373
17	54554821	54554839	ANKFN1	5.41E-18	4.77E-12	0.084472	1	1	1	0.068473	1	1	0.113526	0.079184	1	1.43E-18	0.014925	0.005716
10	90034667	90034679	RNLS	5.53E-18	2.07E-16	0.012903	1	1	0.034014	1	1	0.009091	0.044688	1	1	6.82E-06	1	0.003154
13	25911034	25911067	NUPL1	5.58E-18	7.57E-14	0.001094	0.012658	1	1	0.0375	1	0.012821	1	0.00188	1	5.86E-13	0.054545	0.026869
4	48381682	48381704	SLAIN2	5.62E-18	4.77E-12	1	1	1	0.005097	1	1	1	0.000147	1	1	1.38E-10	0.032258	0.013665
17	66141017	66141032	LINC00674(dist=8947),LOC440461(dist=53769)	5.67E-18	3.76E-12	0.091916	1	0.240285	0.02963	1	1	1	1	0.000726	1	1.45E-08	0.064501	0.144146
2	11332238	11332250	ROCK2	5.73E-18	3.45E-24	0.001174	1	0.126626	0.035354	1	1	1	1	1	1	8.41E-18	0.015873	0.005085
3	132179072	132179085	DNAJC13	5.87E-18	2.14E-13	0.004152	1	1	0.004078	0.057957	1	1	1	0.017857	1	3.91E-12	1	0.033186
20	49354351	49354368	PARD6B	5.94E-18	4.91E-12	1	1	1	1	0.073171	1	1	0.067797	0.016667	1	2.89E-17	0.000402	0.180209
9	52625	52641	FAM138C(dist=16761),PGM5P3-AS1(dist=20049)	6.03E-18	5.71E-20	5.15E-06	0.008403	1	0.104031	0.002502	1	1	1	0.033333	0.333333	1.08E-12	1	0.01696
15	50596341	50596355	GABPB1	6.19E-18	1.01E-26	0.009307	0.035317	1	0.039216	1	1	0.014184	1	0.222222	1	2.77E-29	1	1.49E-05
1	245021291	245021305	HNRNPU	6.2E-18	4.04E-21	0.171047	1	0.101618	0.083506	1	0.035354	0.000932	0.002996	0.030303	1	2.84E-21	0.046779	0.000248
18	13671976	13671989	FAM210A	6.3E-18	1.36E-18	1	1	0.099228	0.051274	1	1	1	1	0.030303	1	1.53E-11	0.057692	0.0173
X	129265852	129265866	AIFM1	6.3E-18	2.34E-19	1	0.02	0.040268	1	0.014085	1	0.009709	0.061947	0.2	1	3.31E-06	1	0.003563
8	124822507	124822519	FAM91A1	6.42E-18	6.04E-32	0.017241	1	1	1	1	0.006061	1	0.05	1	1	1.39E-19	1	0.139635
1	110592048	110592068	STRIP1	6.44E-18	7.09E-16	0.00404	1	1	1	0.088309	1	0.044316	1	1	1	1.36E-14	0.035714	0.017997
2	139318332	139318366	SPOPL	6.49E-18	2.01E-07	0.222856	0.02168	1	0.106855	1	1	1	0.002191	0.061058	1	1.35E-20	0.052973	0.475078
2	152359276	152359297	NEB	6.51E-18	1.93E-11	0.002449	1	1	1	1	1	0.01626	1	0.073375	0.028571	1.7E-21	0.022727	0.004254
14	58825825	58825847	ARID4A	6.71E-18	1.19E-08	0.000161	1	1	1	0.028169	1	1	1	0.071429	1	8.9E-32	1	2.4E-05
11	134064516	134064540	NCAPD3	6.75E-18	2.53E-18	1	0.011494	1	0.001709	0.025078	1	1	1	1	1	2.72E-14	1	0.011313
4	89352469	89352487	HERC6	6.79E-18	1.46E-24	0.000556	0.00495	1	0.068356	0.000352	1	1	0.011364	0.016949	1	5.3E-25	1	0.002278
4	79754716	79754728	BMP2K	6.86E-18	1.12E-20	0.099942	1	0.350921	1	0.002145	1	0.038645	1	0.014925	1	7.58E-14	0.058241	0.040973
14	45587186	45587199	FKBP3	6.92E-18	1.91E-23	0.044444	1	1	0.174889	0.000251	1	1	0.120834	1	1	7.39E-14	0.013699	6.05E-05
12	105540322	105540335	KIAA1033	6.93E-18	1.72E-14	0.001565	1	1	1	1	1	1	0.057681	1	1	3.48E-14	1	0.000334
5	128990138	128990150	ADAMTS19	6.93E-18	3.58E-17	0.145299	1	0.221318	1	0.05363	0.004082	0.028673	0.103973	1	1	1.77E-07	0.001403	0.003884
6	4943999	4944022	CDYL	7.2E-18	1.68E-13	0.071429	1	1	1	1	1	1	1	1	0.071429	2.27E-07	1	0.005057
12	109510086	109510099	USP30	7.21E-18	1.52E-22	4.03E-05	1	1	0.018293	0.00089	1	1	1	0.000605	1	2.15E-29	0.000234	0.071038
9	135161760	135161780	SETX	7.28E-18	7.06E-18	0.08	1	0.06902	0.060796	1	1	1	1	1	0.071429	1E-10	1	0.407059
11	27414071	27414102	LGR4	7.33E-18	0.008696	0.00512	1	1	1	1	1	1	1	0.026667	1	6.93E-19	0.001807	0.160641
7	130139660	130139674	MEST	7.33E-18	3.78E-13	1	1	1	1	1	1	0.029739	0.00032	0.002262	1	5.42E-08	1	0.012528
5	161494990	161495003	GABRG2	7.56E-18	2.68E-23	1	1	0.066176	1	1	1	0.013158	1	0.125	1	4.82E-11	1	0.143555
11	124007701	124007714	VWA5A	7.69E-18	2.04E-28	1	0.012658	1	0.028986	0.000493	1	1	0.002088	0.032258	1	8.84E-08	0.151383	0.120337
4	159618683	159618709	ETFDH	7.71E-18	2.47E-20	0.124884	1	0.052632	0.032864	1	1	1	0.002919	0.016667	1	1.04E-16	1	0.004442
15	73580950	73580962	NEO1	8.03E-18	5.11E-13	0.000982	1	0.080357	1	1	1	0.009804	0.053846	1	1	1.03E-14	0.047059	0.001101
21	37760118	37760134	CHAF1B	8.14E-18	1.68E-23	1	1	1	1	1	1	1	1	1	1	1.34E-16	0.022727	0.000855
20	50781298	50781310	ZFP64	8.36E-18	2.2E-17	0.043478	1	0.072871	0.104077	0.035474	0.022727	1	0.051095	1	0.193676	7.36E-08	1	0.052193
4	83970297	83970312	COPS4	8.36E-18	3.55E-30	0.04918	0.009804	1	1	0.012048	1	1	0.000186	0.025641	0.105263	1.32E-16	1	0.003971
14	101506158	101506169	MIR376A1,MIR376A2,MIR376B,MIR654;MIR376C	8.57E-18	1.09E-13	1	1	1	1	1	1	1	0.02439	0.00135	0.285714	4.05E-15	0.073171	0.010004
11	86198529	86198542	ME3	8.68E-18	1.8E-10	0.129944	1	1	1	1	1	1	1	0.001242	1	5.13E-12	0.030303	1
14	55629650	55629664	DLGAP5	9.26E-18	2.69E-09	1	1	1	1	1	1	1	1	1	1	4.18E-22	0.039474	0.000116
16	4873743	4873761	GLYR1	9.54E-18	5.52E-25	0.091795	0.000449	0.012691	1	0.000514	1	0.12049	1	0.049684	1	7.53E-06	0.007611	0.243023
6	42559866	42559879	UBR2	9.72E-18	4.47E-20	0.001815	0.004831	0.225457	1	0.031556	1	0.052623	0.007929	0.030769	1	1.65E-09	1	0.256839
2	183841691	183841704	NCKAP1	9.76E-18	4.36E-13	0.041667	0.000333	1	1	1	1	1	1	0.02	1	1.34E-17	0.028169	0.004493
6	111702448	111702460	REV3L	9.85E-18	4.18E-22	0.015789	1	0.00401	0.001403	0.001574	1	0.058596	0.001045	0.12	1	3.6E-06	0.043478	0.360232
7	94157572	94157605	CASD1	9.95E-18	3.1E-13	0.00752	1	1	1	0.032607	1	0.06665	1	1	1	2.89E-13	0.076897	0.004603
9	98703711	98703723	ERCC6L2	1.01E-17	2.64E-19	1	0.004545	1	1	1	1	0.026577	1	0.000605	0.294118	4.02E-16	0.013699	0.005119
14	50760968	50760980	L2HGDH	1.05E-17	2.34E-18	0.001221	0.009615	0.103093	1	0.013274	0.004587	1	0.183712	0.037736	1	4.28E-12	0.027027	0.237172
15	48764655	48764676	FBN1	1.06E-17	4.61E-12	0.013563	1	0.123714	0.087815	1	1	0.045108	1	1	1	4.66E-06	0.056593	0.254178
6	131997990	131998015	ENPP3	1.08E-17	5.54E-09	0.001357	1	1	0.03065	1	1	1	1	1	1	1.71E-10	0.078919	6.23E-07
14	74443828	74443841	ENTPD5	1.14E-17	1.11E-21	1	0.018475	1	0.016129	1	1	1	1	0.021277	1	1.8E-10	1	0.003347
8	89499214	89499230	MMP16(dist=159497),LOC101929709(dist=1230397)	1.15E-17	4.01E-23	0.049367	1	0.065574	4.93E-05	1	1	0.020979	0.058333	0.02	1	2.53E-25	0.096721	0.085586
9	20448058	20448086	MLLT3	1.16E-17	9.25E-22	0.102041	1	1	1	1	1	1	1	1	1	1.46E-08	1	0.002493
10	70252822	70252837	SLC25A16	1.18E-17	1.42E-20	0.001481	0.020101	0.069075	0.013423	1	1	1	1	1	0.166667	1.2E-19	0.229774	0.034092
7	117867960	117867983	ANKRD7	1.19E-17	8.66E-05	0.014225	1	0.261173	1	1	1	1	1	0.005288	1	1.92E-16	0.068164	0.015405
1	158326447	158326459	CD1E	1.25E-17	7.6E-10	0.133181	0.027027	1	1	1	1	0.056928	1	0.003759	0.065934	4.3E-07	1	0.274592
5	96093391	96093408	CAST	1.25E-17	2.48E-07	0.000219	1	1	1	1	1	1	1	1	0.296296	1.39E-27	0.052973	4.69E-05
6	133093231	133093247	SLC18B1	1.25E-17	1.6E-12	1	0.009709	1	1	0.001936	1	1	0.078095	1	1	8.54E-09	0.004146	0.183046
2	203817257	203817270	CARF	1.29E-17	4.94E-17	0.176136	1	0.146815	0.105726	0.053801	1	1	0.000167	1	1	5.83E-07	0.000466	0.079468
14	59787325	59787338	DAAM1	1.3E-17	4.95E-16	0.000496	0.009852	0.196535	1	1	1	0.006849	1	1	1	3.69E-32	1	2.44E-05
15	81187286	81187297	CEMIP	1.38E-17	1.71E-21	0.172078	1	0.047619	0.052901	1	1	1	0.000711	0.015385	1	1.35E-21	0.102199	0.146092
6	166578165	166578177	T	1.39E-17	6.15E-23	0.020749	0.00885	0.095562	0.11897	1	1	0.022556	0.06273	1	1	5.03E-10	1	0.399855
5	14390989	14391001	TRIO	1.4E-17	1.61E-22	0.038462	1	1	0.037433	1	1	0.026402	1	1	1	1.28E-14	1	1
18	14214318	14214331	ANKRD20A5P	1.45E-17	7.58E-13	0.095238	1	1	0.026144	0.011364	1	1	1	0.043478	1	0.006048	0.068361	0.247888
3	69112658	69112688	UBA3	1.49E-17	2.6E-15	0.009015	1	1	1	1	1	0.05084	1	1	1	1.17E-25	1	3.4E-05
1	170927570	170927588	MROH9	1.5E-17	2.06E-13	0.000398	1	1	0.004173	0.061208	1	1	1	1	0.529231	1.6E-18	1	0.139873
5	110438000	110438014	WDR36	1.52E-17	9.22E-12	1	1	0.234193	0.111111	1	1	1	1	1	1	1.35E-11	0.103158	1
12	105538270	105538287	KIAA1033	1.53E-17	5.29E-14	0.074627	1	1	1	1	1	1	1	1	1	3.07E-22	0.091382	0.00336
20	480602	480627	CSNK2A1	1.56E-17	6.23E-11	0.000161	1	0.026556	1	1	1	0.011834	1	0.035088	1	1.67E-15	1	0.001473
6	110048489	110048501	FIG4	1.57E-17	1.08E-14	0.00202	1	0.059454	0.033263	1	1	0.11281	0.002433	1	1	2.55E-07	1	0.086883
5	180482303	180482317	BTNL9	1.59E-17	3.41E-19	0.009524	0.011429	1	1	1	0.005988	0.015504	0.003516	1	1	4.02E-10	0.002646	1.5E-05
12	56504143	56504159	PA2G4	1.59E-17	3.48E-24	7.63E-05	1	1	0.066464	1	1	0.075441	1	0.025	1	1.42E-20	0.014706	0.204122

22	40755427	40755439	ADSL	1.61E-17	8.83E-09	0.000117	1	1	1	1	1	1	1	0.03125	0.263158	1.47E-16	1	0.003753
16	31196218	31196237	FUS	1.63E-17	7.46E-23	1	0.008658	0.045455	0.04	0.019157	1	1	0.002408	1	1	3.3E-07	0.000301	1
1	215931901	215931935	USH2A	1.63E-17	7.98E-16	0.157614	1	1	0.089056	1	1	1	1.25E-07	1	1	1.65E-09	1	1
19	22585521	22585535	ZNF98	1.64E-17	5.63E-17	0.02162	1	0.007611	0.143899	1	1	1	1	0.006266	1	6.05E-15	0.09035	0.000342
4	20706067	20706080	PACRGL	1.68E-17	3.96E-12	0.063492	1	1	1	1	1	1	1	1	1	3.71E-14	0.058385	0.002146
8	109462215	109462229	EMC2	1.72E-17	1.08E-23	2.69E-05	1	1	1	1	1	1	1	0.074746	1	9.91E-20	1	0.169605
11	16117684	16117698	SOX6	1.76E-17	2.06E-24	0.133192	1	1	1	1	1	0.02749	1	0.032787	1	6.22E-10	9.77E-06	4.97E-05
10	101992923	101992938	CWF19L1	1.81E-17	1.71E-31	0.002262	1	1	1	1	1	1	0.088517	0.000754	1	1.54E-18	0.000802	0.000117
11	107518175	107518187	ELMOD1	1.82E-17	4.86E-16	0.006697	1	1	0.027624	1	1	1	0.005689	0.000512	1	1.1E-14	0.001142	0.000267
12	112515954	112515966	NAA25	1.93E-17	2.57E-14	0.037975	1	1	0.012987	1	1	1	1	0.019231	1	1.43E-14	0.057545	1
18	59942746	59942760	KIAA1468	1.97E-17	3.07E-08	0.219809	1	0.257945	1	1	1	0.013986	1	1	0.385965	3.37E-17	1	0.001006
14	36218039	36218056	RALGAPA1P	1.97E-17	2.8E-12	1.23E-05	1	1	1	1	1	1	1	1	1	8.16E-26	0.015873	9.45E-06
17	53014442	53014457	TOM1L1	2.02E-17	7.4E-22	0.003623	0.02459	0.010755	0.083636	0.110596	1	0.131212	4.39E-05	0.064516	1	0.0003	1	0.003948
15	43927623	43927636	CATSPER2	2.02E-17	1.69E-29	1	1	1	1	0.057678	1	0.025723	0.047945	0.028571	1	5.76E-11	1	0.009283
2	21226218	21226230	APOB	2.06E-17	6.85E-24	0.013495	0.011299	0.006266	0.000176	0.00302	1	0.016393	0.033893	0.1	1	7.27E-12	1	0.00157
17	5044640	5044653	USP6	2.11E-17	4.06E-11	0.037736	0.008197	1	0.003393	1	1	0.043161	0.000206	1	1	3.23E-15	1	0.026645
3	107910327	107910342	IFT57	2.14E-17	1.83E-21	0.267274	1	0.005865	0.167582	1	1	1	1	0.000726	1	1.59E-11	0.013889	0.000649
12	25678995	25679008	LMNTD1	2.14E-17	4.39E-18	0.013733	1	1	0.189624	1	0.008969	0.028673	0.010362	0.000529	0.227273	3.49E-17	1	0.001229
4	128817905	128817919	PLK4	2.15E-17	2.78E-14	0.107071	1	1	1	1	1	0.037556	1	0.033898	1	1.03E-28	0.037037	4.56E-06
X	100793432	100793449	ARMCX4(dist=42634),ARMCX1(dist=12065)	2.2E-17	4.34E-14	0.020158	1	0.592092	0.044607	0.002878	1	0.032651	0.006747	1	1	8.31E-21	0.026667	0.337436
3	50112589	50112605	RBM6	2.25E-17	5.45E-15	1	0.022472	1	1	1	1	0.014388	0.043474	1	1	7.66E-11	1	0.002803
X	67741418	67741434	YIPF6	2.29E-17	2.84E-08	0.076923	1	1	1	1	1	1	1	0.105263	1	5.53E-12	1	0.000321
5	108168451	108168468	FER	2.33E-17	2.12E-11	0.006807	1	0.264543	1	1	0.010811	1	0.141361	0.060606	1	8.6E-12	0.055556	1
22	17063605	17063619	OR11H1(dist=613801),CCT8L2(dist=8029)	2.39E-17	4.2E-16	0.015618	0.035294	1	1	1	1	1	1	1	1	6.79E-18	0.055556	1
9	69127139	69127155	PGM5P2	2.45E-17	6.54E-12	0.002177	1	0.046074	1	1	1	1	1	1	1	7.95E-17	0.009993	1
19	4947062	4947076	UHRF1	2.7E-17	1.95E-18	0.046512	1	1	0.043057	0.029573	1	1	0.058824	1	0.215686	2.71E-09	1	0.007322
8	37611414	37611428	ERLIN2	2.72E-17	1.76E-28	0.103383	1	0.113783	0.003518	0.066506	1	1	0.087457	0.071429	1	8.51E-12	1	0.001297
7	26247984	26247997	CBX3	2.73E-17	4.95E-17	0.127869	1	0.0375	1	0.095562	1	0.008547	0.052083	0.00085	1	4.44E-18	0.08105	1
8	17422434	17422446	SLC7A2	2.76E-17	1.97E-16	0.041667	0.000686	0.062548	0.0625	1	1	1	1	0.018182	1	1.59E-09	1	0.000651
16	10567751	10567778	ATF7IP2	2.76E-17	2.32E-06	6.14E-06	1	1	1	1	1	1	1	1	1	5.38E-28	0.021053	0.11999
12	28412398	28412416	CCDC91	2.83E-17	7.22E-13	0.000486	1	0.053846	0.057471	1	1	0.007937	1	1	1	9.31E-23	1	0.003177
4	74285182	74285210	ALB	2.83E-17	5.48E-11	0.023256	1	1	0.057554	1	1	1	1	1	1	5.68E-12	1	0.031339
11	3381798	3381814	ZNF195	2.84E-17	1.09E-20	0.090909	0.011173	1	1	1	1	0.024767	1	0.027027	1	3.42E-12	1	0.034695
17	20639183	20639199	LOC100287072	2.91E-17	0.004902	0.142669	1	1	1	1	1	1	1	0.001142	0.241379	8.76E-16	0.023256	0.006138
6	163235158	163235170	PACRG	2.93E-17	8.56E-19	0.069767	0.005263	0.284396	1	0.001037	1	0.015267	0.006891	1	1	7.65E-14	0.09035	0.004304
15	34168207	34168221	AVEN	2.94E-17	1.19E-10	1	1	1	1	1	1	1	1	1	1	2.09E-17	1	0.004056
13	53239754	53239767	SUGT1	3.04E-17	1.08E-14	0.086207	1	1	0.015038	0.03012	1	1	1	0.022727	1	3.46E-14	0.033333	0.170581
12	88926290	88926302	KITLG	3.06E-17	1.7E-15	0.006446	1	0.019961	0.088191	0.086157	1	0.025641	1	0.015873	1	1.46E-14	1	0.001514
13	80095130	80095156	NDFIP2	3.1E-17	6.8E-15	0.047619	1	0.071406	1	1	1	1	1	1	1	1.78E-07	0.034483	0.004527
12	68690765	68690777	MDM1	3.31E-17	2.1E-12	0.032787	1	1	1	1	1	0.018349	0.007546	1	1	1.39E-14	1	0.001071
20	18511458	18511473	SEC23B	3.31E-17	7.56E-16	0.001998	1	1	1	0.049254	1	1	1	1	1	3.22E-19	1	0.000963
4	147628705	147628716	TTC29	3.34E-17	2.08E-08	0.308943	1	1	1	0.024315	1	1	1	0.070175	1	1.17E-09	0.048479	6.02E-05
11	18591715	18591730	UEVLD	3.44E-17	6.78E-14	1	1	1	1	1	1	1	1	0.136364	0.1	1.06E-14	0.073171	0.062881
10	7684120	7684132	ITIH5	3.46E-17	1.49E-13	0.078125	1	1	1	0.032785	1	1	1	1	1	1.08E-10	0.023529	0.003244
12	97306603	97306631	NEDD1	3.47E-17	1.32E-13	0.000263	1	1	1	1	1	0.008475	1	0.001207	1	2.62E-23	1	0.000101
14	56078699	56078713	KTN1	3.5E-17	5.36E-10	0.126618	1	1	1	0.045796	1	0.026549	1	0.001107	1	5.3E-07	1	0.008132
11	120348128	120348148	ARHGEF12	3.52E-17	9.87E-10	0.022147	1	1	1	1	1	1	1	1	1	4.5E-17	0.052281	0.106149
1	181752769	181752784	CACNA1E	3.57E-17	6.71E-08	1	1	1	1	1	1	0.035714	0.002134	0.032258	0.143281	0.000524	0.024691	0.224922
2	56611386	56611398	CCDC85A	3.69E-17	5.66E-17	0.25946	0.021917	0.012664	1	1	1	1	0.001169	0.03125	1	8.02E-08	1	0.15495
2	10187764	10187775	KLF11	3.79E-17	1.97E-16	1	1	1	0.058522	1	1	1	0.037313	1	1	6.15E-06	0.029412	0.004886
18	67614674	67614695	CD226	4.09E-17	6.39E-17	0.000578	1	1	0.000663	1	1	1	0.182449	0.069767	0.416667	1.47E-17	1	0.002888
11	49883972	49883985	LOC440040(dist=52003),OR4C13(dist=89958)	4.12E-17	1.2E-11	0.001344	0.042662	1	0.234693	0.062485	1	0.097969	1	1	0.539243	5.03E-14	0.038462	0.002814
1	236714292	236714311	HEATR1	4.19E-17	5.32E-09	0.005102	1	1	1	1	1	1	1	1	1	7.46E-11	1	0.032924
1	225607366	225607387	LBR	4.2E-17	1.48E-21	0.002347	0.006329	1	1	0.024691	1	1	1	1	1	3.54E-14	1	0.000413
12	98989187	98989199	SLC25A3	4.22E-17	1.6E-29	1	0.017977	1	1	0.018868	1	1	1	0.03125	1	1.64E-15	0.034091	1.7E-05
X	84523274	84523298	ZNF711	4.31E-17	0.000164	0.107306	1	1	1	1	1	1	1	1	1	2.11E-29	1	0.233736
15	98513086	98513103	ARRDC4	4.78E-17	1.76E-09	0.003659	1	0.023165	1	1	1	0.068473	1	0.057545	1	2.8E-14	1	0.005281
6	155126680	155126709	SCAF8	4.82E-17	0.000524	0.010274	1	1	1	1	1	1	0.024096	1	1	1.69E-06	0.038961	1
9	103027226	103027243	INVS	4.93E-17	2.27E-09	0.000113	1	0.078313	1	1	1	1	1	1	1	8.91E-23	1	0.029562
19	12128923	12128937	ZNF433	4.97E-17	4.34E-13	0.003702	1	1	1	0.04532	1	1	1	0.033898	1	1.91E-17	0.032609	0.000636
3	191888452	191888477	FGF12	5.03E-17	3.64E-28	0.028986	1	1	0.159471	0.058125	1	0.106234	1	1	0.25	1.85E-09	0.033333	0.000217
2	187531848	187531874	ITGAV	5.11E-17	6.35E-13	0.035088	1	1	0.06602	0.02	1	1	1	0.027778	1	1.11E-17	1	1
20	23473522	23473535	CST8	5.24E-17	1.32E-18	0.166387	0.023529	1	0.000509	1	1	1	0.046053	1	1	5.75E-08	0.013158	0.000622
5	38958956	38958971	RICTOR	5.31E-17	2.26E-11	0.000123	1	1	1	1	1	1	1	0.015873	1	1.71E-16	1	0.012582
11	59368218	59368235	OSBP	5.35E-17	1.11E-27	0.000122	0.013889	0.007847	0.001212	0.001754	1	0.015038	1	0.050949	1	3.72E-26	0.030928	0.243354
2	217280250	217280286	SMARCAL1	5.4E-17	9.92E-17	0.012255	1	1	1	1	1	0.013889	1	1	1	1.08E-05	1	1
3	125179711	125179723	SNX4	5.41E-17	1.1E-21	0.032787	1	1	1	0.022222	1	1	0.073708	0.013514	1	4.4E-18	0.033708	0.003439
14	96800846	96800858	ATG2B	5.78E-17	5.02E-16	0.156002	1	0.18697	1	0.000106	1	1	1	0.02381	1	3.63E-18	0.000342	0.003366
12	40258687	40258699	SLC2A13	5.91E-17	4.82E-18	0.143955	1	1	0.037433	1	1	0.050413	1	0.032787	1	3.9E-19	1	3.69E-07
3	101575877	101575895	NFKBIZ	5.95E-17	1.67E-24	0.161905	1	1	0.000952	0.014778	1	1	1	1	1	3.92E-10	1	0.025825
15	56946703	56946733	ZNF280D	5.96E-17	1.09E-20	0.06014	1	1	1	1	1	1	0.00112	1	1	1.11E-23	0.036145	0.146279
4	148578917	148578929	PRMT9	6.11E-17	2.03E-14	1	1	1	0.132626	1	1	1	1	1	1	1.97E-18	1	0.125242
19	54264352	54264364	MIR516A2	6.12E-17	1.2E-17	0.00439	0.012739	1	1	0.036779	1	1	1	1	1	1.21E-10	0.000244	0.000496
22	41545024	41545039	EP300	6.42E-17	1.87E-34	0.005845	0.051012	1	0.00385	0.066231	1	1	0.044444	0.111111	1	2.66E-26	1	0.070381
6	158322872	158322901	SNX9	6.5E-17	7.6E-23	0.001815	1	1	1	1	1	0.021583	0.004173	1	1	1.57E-12	0.082867	0.002411
6	32147291	32147312	RNF5P1	6.51E-17	1.67E-36	0.001111	6.96E-05	1	0.001133	0.020779	0.011429	1	1	0.026316	1	8.98E-36	1	0.137283
X	134025421	134025436	MOSPD1	6.75E-17	7.59E-29	0.003507	0.043663	0.075	1	0.011811	1	1	0.013514	1	1	2.09E-24	1	0.12673
1	237965133	237965146	RYR2	6.86E-17	3.68E-13	0.018462	0.022388	0.10901	1	0.075441	1	0.050413	0.1797	0.000816	1	5.14E-06	0.003301	0.012513
2	15753307	15753321	DDX1	6.93E-17	5.5E-10	0.000161	1	0.138961	1	1	1	1	0.079184	0.079184	0.3125	3.59E-17	1	0.007831
X	119676896	119676908	CUL4B	7.21E-17	6E-11	1	1	1	0.099318	0.05084	1	0.007463	1	1	1	1.21E-11	1	0.001986
20	47615074	47615089	ARFGEF2	7.27E-17	2.91E-06	0.020158	1	0.302725	1	1	1	0.04065	0.018732	1	0.008333	3.62E-09	1	0.009395
2	162877041	162877054	DPP4	7.41E-17	1.09E-05	0.189947	1	1	1	1	1	0.014085	1	1	1	8.46E-15	0.027778	0.194878
X	18323348	18323361	SCML2	7.57E-17	2.21E-18	0.088195	1	0.050855	0.051538	1	1	1	8.26E-05	1	1	1.67E-17	1	0.003686
4	113568126	113568140	LARP7	7.6E-17	1.13E-26	0.009614	1	0.288133	1	1	1	1	3.49E-07	1	1	4.86E-22	0.000717	0.010109
5	150282674	150282694	ZNF300	7.6E-17	6.38E-27	0.213523	0.011905	0.112674	0.222413	1	1	0.009615	1	1	0.192308	4.2E-17	0.133157	0.030281
X	119675354	119675368	CUL4B	7.74E-17	4.45E-10	0.000192	1	0.044586	1	0.016064	1	1	0.004559	1	1	1.03E-08	1	0.098481
5	55252984	55253000	IL6ST	7.81E-17	5.83E-11	0.006993	1	1	1	1	1	0.02069	0.139977	1	1	1.27E-09	0.023529	0.049075
4	141484371	141484383	UCP1	8.06E-17	4.48E-19	0.001695	0.017738	0.042933	1	1	1	1	1	0.047619	1	8.41E-11	1	0.02531
X	14625399	14625415	GLRA2	8.07E-17	4.56E-20	0.020833	1	1	0.08139	1	1	1	1	0.034483	1	5.77E-17	1	0.387087
15	43307839	43307852	UBR1	8.08E-17	1.38E-25	0.000107	0.02005	0.075949	1	0.059985	1	0.02439	0.005363	0.022222	1	5.28E-17	0.039216	2.41E-06
10	114910667	114910685	TCF7L2	8.16E-17	7.44E-12	0.034483	1	1	1	1	1	1	1	1	0.135714	8.18E-15	1	0.173242
X	96171416	96171435	DIAPH2	8.47E-17	0.002741	0.004024	1	0.07871	1	1	1	1	1	0.001317	1	6.18E-31	0.039798	0.16194
1	110551590	110551602	AHCYL1	8.9E-17	4.76E-14	1	0.016129	1	1	1	1	1	1	0.030303	1	3.29E-14	1	8.51E-05
6	17675386	17675402	NUP153	8.91E-17	8.27E-16	0.005984	1	0.090044	1	0.035712	1	1	0.029851	1	0.291667	2.82E-23	1	7.78E-05
3	186295417	186295431	DNAJB11	9.14E-17	1.85E-13	0.011092	1	1	1.31E-05	1	1	1	1	1	0.017544	5.18E-15	0.001242	0.270638
7	116409675	116409691	MET	9.19E-17	1.31E-21	0.207729	1	1	0.286738	1	1	1	1	0.2	1	1.71E-17	0.032258	0.131559
3	10094206	10094220	FANCD2	9.28E-17	1.27E-13	0.01277	1	1	1	1	1	1	0.018634	1	1	1.74E-15	0.020833	0.05652
4	184567431	184567444	RWDD4	9.46E-17	2.36E-16	0.002393	0.006803	0.061947	1	1	1	1	1	1	1	4.25E-19	0.028986	1
X	48053437	48053450	SSX5	9.5E-17	0.125232	0.138274	1	0.102485	1	1	1	1	0.106607	0.02	1	6.06E-13	0.000414	0.020473
10	89720622	89720649	PTEN	9.51E-17	2.39E-05	0.000345	1	0.221958	0.028571	1	1	0.007463	1	0.031746	0.263158	1.98E-21	1	0.070997
6	13597295	13597307	SIRT5	9.61E-17	6.48E-20	1	1	1	1	1	1	1	1	1	1	3.84E-07	0.000999	0.197016
2	110922055	110922080	NPHP1	9.65E-17	7.3E-32	8.71E-05	1	1	0.000305	1	1	1	1	1	1	6.15E-14	1	0.000813
11	16339918	16339934	SOX6	1E-16	6.66E-14	0.254002	1	0.209252	0.094427	0.00089	1	0.02909	7.27E-05	1	1	1.91E-20	0.140967	4.23E-05
12	13364426	13364437	EMP1	1E-16	8.13E-17	0.003342	1	1	1	1	1	0.048381	1	1	1	6.8E-15	1	0.000598
1	112240038	112240059	RAP1A	1.01E-16	5.5E-19	0.007307	1	1	1	1	1	1	1	1	1	2.95E-17	1	0.35316
5	74011541	74011556	HEXB	1.03E-16	1.13E-27	0.004558	0.014706	0.242051	1	1	1	0.014815	0.000104	0.037037	1	1.24E-13	0.001053	0.00769
2	136527318	136527332	UBXN4	1.04E-16	3.56E-26	0.042146	1	1	0.001543	0.021834	1	1	0.049587	1	1	7.29E-06	0.004236	0.00494
17	67178976	67178992	ABCA10	1.05E-16	9.27E-20	0.00262	0.03125	0.356903	1.55E-05	0.009421	1	0.060388	0.331736	1	0.277778	6.62E-15	1	0.011884
4	25366051	25366071	ZCCHC4	1.08E-16	1.31E-14	0.000461	1	1	1	1	1	1	0.053571	0.019608	1	7.92E-16	1	0.009612
5	137507104	137507121	BRD8	1.12E-16	2.49E-14	0.142229	1	0.44837	0.004173	0.012586	1	0.110149	0.002617	1	1	2.32E-07	0.00098	2.85E-08
10	34573008	34573020	PARD3	1.19E-16	4.14E-20	0.001242	1	1	0.029557	0.000456	1	0.019868	0.000359	0.016949	0.505495	1.09E-14	0.041237	0.163284
12	110454085	110454114	ANKRD13A	1.2E-16	3.23E-05	0.044118	1	1	1	1	1	1	1	1	1	1.82E-21	1	0.144451
2	112625555	112625566	ANAPC1	1.2E-16	1.42E-16	0.015873	1	1	0.033333	1	1	1	0.034483	1	1	1.71E-17	0.02439	0.000273
15	72875521	72875535	ARIH1	1.21E-16	1.23E-26	0.007937	1	0.083333	0.036364	1	1	1	1	1	1	4.53E-15	1	0.0324
2	69553369	69553389	GFPT1	1.23E-16	3.08E-12	1	1	0.228955	1	1	1	1	1	1	1	7.12E-11	0.000325	0.006743
12	15776223	15776244	EPS8	1.24E-16	1.62E-19	0.037736	1	1	0.040936	1	1	0.022222	0.053191	1	1	7.52E-15	0.011494	0.002379
15	81427705	81427719	C15orf26	1.26E-16	4.44E-16	0.00199	1	1	1	0.000383	1	1	0.075682	0.014085	1	3.49E-18	1	0.16239
14	58949210	58949223	KIAA0586	1.26E-16	1.01E-05	0.057692	0.0625	1	1	1	1	1	0.071408	1	1	4.47E-09	0.044944	0.009579
20	4839890	4839911	SLC23A2	1.3E-16	1.3E-21	0.006061	0.005263	0.046358	1	1	1	0.013986	0.051852	0.039216	1	3.33E-12	0.08105	8.93E-06
14	53180739	53180777	PSMC6	1.31E-16	6.73E-17	0.009231	1	1	1	1	1	1	0.026316	1	1	2.7E-05	0.013333	0.005833
11	119144791	119144809	CBL	1.33E-16	3.6E-12	0.047456	1	1	1	1	1	0.014493	1	1	1	2.68E-15	0.021739	0.185191
7	95125050	95125067	ASB4	1.33E-16	3.87E-15	0.004706	1	0.118294	1	1	1	0.05084	1	0.0625	0.204678	7.4E-19	1	1
1	10408837	10408852	KIF1B	1.34E-16	0.004314	0.153573	1	1	1	1	1	1	1	0.06	0.227273	1.05E-17	1	0.010973
20	2552802	2552817	TMC2	1.35E-16	1.41E-15	0.006266	1	0.159676	0.026042	0.115577	1	0.018182	1	0.013514	0.128205	4.29E-14	1	0.012748
14	60587879	60587900	PCNXL4	1.39E-16	7.58E-12	6.43E-05	0.013453	0.038944	1	1	1	1	1	0.052973	1	3.52E-23	1	0.293346
9	20346363	20346406	MLLT3	1.46E-16	1.87E-12	0.00339	0.070568	1	0.07802	1	1	0.013072	1	0.055936	1	2.34E-14	0.022222	0.0001
1	150804401	150804418	ARNT	1.47E-16	7.93E-06	0.064039	0.026667	1	1	1	1	1	1	0.030303	1	1.13E-09	0.123571	0.009488
1	185269100	185269122	IVNS1ABP	1.48E-16	2.51E-17	0.047619	1	0.059322	1	1	1	1	1	1	1	3.36E-21	0.021053	0.00664
5	70841097	70841109	BDP1	1.49E-16	1.07E-09	0.172704	1	1	1	1	1	1	0.030928	1	1	1.2E-06	1	0.015987
17	19744865	19744877	ULK2	1.5E-16	2.9E-13	0.000222	1	1	1	0.061208	1	0.051716	1	1	0.133333	1.47E-07	0.096774	6.79E-05
22	38766061	38766082	LOC400927	1.51E-16	5.24E-11	0.00188	1	0.183184	1	1	0.008584	1	1	0.054414	1	2.23E-21	1	1
14	51348281	51348299	ABHD12B	1.52E-16	1.25E-34	0.060084	0.048035	0.32791	0.194999	0.00701	1	0.135174	3.46E-08	0.105263	1	3.92E-15	1	0.021514
20	10273694	10273715	SNAP25	1.54E-16	1.1E-19	0.000142	0.009132	0.090861	1	1	1	1	1	1	1	2.37E-08	0.01087	0.00357
11	10794578	10794590	CTR9	1.55E-16	1.21E-11	1	0.01995	1	1	1	1	1	1	1	1	1.46E-13	0.034884	0.041401
15	50920509	50920523	TRPM7	1.56E-16	1.75E-12	0.06298	1	1	3.65E-05	1	1	0.009259	0.000383	1	1	2.83E-16	1	0.112191
21	33979904	33979922	C21orf59	1.6E-16	4.22E-20	0.00023	1	1	1	1	1	1	1	1	1	3.01E-18	1	0.000339
11	14539315	14539332	PSMA1	1.61E-16	4.34E-14	0.001036	1	0.035361	1	0.067416	1	0.072924	0.1	1	0.017544	7.16E-25	0.143955	0.377841
6	7595241	7595255	SNRNP48	1.77E-16	5.46E-13	0.010274	1	1	0.033557	1	1	1	1	0.000673	0.3	1.64E-12	0.002714	0.07451
6	88126360	88126373	C6orf165	1.81E-16	4.22E-13	0.099942	1	0.070866	1	0.043791	1	0.008333	1	0.058824	1	2.07E-10	0.024691	0.016391
2	108520601	108520629	RGPD4(dist=11601),SLC5A7(dist=82366)	1.85E-16	0.181818	0.00496	1	1	1	1	1	1	1	0.039216	1	3.18E-26	0.031746	1
X	24597303	24597330	PCYT1B	1.85E-16	0.015595	1	1	0.172252	1	1	1	1	1	1	1	3.02E-09	1	0.418391

14	92549604	92549623	ATXN3	1.87E-16	4.35E-19	0.057692	0.010695	1	1	0.008584	1	1	1	1	1	4.63E-10	1	0.000191
12	72004884	72004926	ZFC3H1	1.89E-16	1.13E-22	0.064516	1	1	1	0.044854	1	1	1	1	1	5.61E-16	0.031579	0.38447
4	39347146	39347159	MIR1273H	1.93E-16	0.00018	1	1	1	1	1	1	1	0.019048	0.022222	1	7.86E-15	0.002262	0.00136
1	114372332	114372354	AP4B1-AS1	2.02E-16	2.03E-16	1	1	1	0.171001	0.043122	1	0.090044	0.028952	1	0.05	6.79E-13	1	0.00687
12	88482779	88482791	CEP290	2.08E-16	5.78E-14	0.076923	0.014706	1	1	0.01626	1	1	1	0.000512	1	4.05E-15	1	1
12	53470811	53470838	SPRYD3	2.12E-16	7.63E-15	1	1	1	1	0.01105	0.009901	1	1	1	1	1.3E-06	0.024096	2.13E-06
1	112958898	112958910	CTTNBP2NL	2.12E-16	3.83E-20	0.103841	0.009091	1	1	0.022624	1	1	1	1	1	1.94E-07	0.014286	0.107335
3	15613279	15613304	HACL1	2.14E-16	6.22E-23	0.103383	0.009569	1	1	0.003762	1	1	1	0.181818	1	3.83E-15	1	0.008527
6	96982111	96982125	UFL1	2.16E-16	1.04E-09	1	1	0.06665	1	0.000784	1	1	0.02439	1	1	1.06E-11	0.068361	0.020208
16	57249981	57250000	RSPRY1	2.16E-16	7.02E-27	0.308104	1	0.023344	1	0.094272	1	0.024315	1	0.008547	0.083333	5.38E-27	1	0.003465
X	105912591	105912604	CXorf57	2.2E-16	3.11E-06	1	1	0.061644	1	1	1	1	1	1	1	2.43E-11	1	0.01157
1	14057425	14057439	PRDM2	2.2E-16	2.44E-33	0.004354	1	0.083333	0.003795	0.049072	0.013274	1	1	1	1	2.99E-25	1	0.00037
1	210411266	210411281	SERTAD4	2.27E-16	2.2E-19	1	0.011494	1	0.076474	1	1	1	1	1	1	3.58E-24	0.034483	0.000545
12	118673483	118673495	TAOK3	2.28E-16	6.71E-06	0.048643	1	1	1	1	1	1	1	1	0.056373	4.98E-12	0.055556	0.047998
X	113965679	113965691	HTR2C	2.29E-16	3.72E-18	0.050847	0.004695	1	1	0.051054	1	1	1	0.105263	1	1.14E-15	1	0.043478
11	55035809	55035822	TRIM48	2.3E-16	5.74E-14	0.084181	0.031579	1	1	0.02476	1	1	0.000229	0.150769	0.444444	2.33E-09	0.019285	0.168574
10	35314130	35314161	CUL2	2.33E-16	9.48E-12	1.23E-06	0.032258	0.252783	0.075924	0.042254	1	0.006897	1	0.000974	1	4.56E-27	0.029126	0.091993
10	5788110	5788126	FAM208B	2.35E-16	7.42E-27	0.009231	1	0.056953	0.015295	1	0.048458	0.073036	0.034466	1	1	1.08E-08	0.051606	0.020736
2	166758447	166758460	TTC21B	2.36E-16	9.07E-11	1	1	1	1	0.038213	1	1	1	0.000333	1	5.29E-12	0.000274	0.176682
3	121202433	121202476	POLQ	2.41E-16	4.18E-18	0.000536	1	1	1	0.061762	1	1	1	1	1	1.38E-25	1	0.00248
4	141481203	141481225	UCP1	2.42E-16	1.58E-07	3.88E-05	0.012658	1	1	1	1	1	1	1	1	4.65E-11	0.027027	0.003374
X	70594925	70594942	BCYRN1	2.49E-16	1.76E-10	1	1	1	1	0.141954	1	1	1	0.002646	0.022222	1.68E-09	0.057681	0.001634
3	112253193	112253208	ATG3	2.5E-16	3.36E-10	0.000583	1	0.142123	1	1	1	1	0.213433	0.034483	1	2.03E-13	0.172625	0.001353
X	24833074	24833092	POLA1	2.51E-16	7.87E-14	0.088235	1	1	1	0.134034	1	1	0.044113	1	1	2.77E-10	0.028169	0.198948
3	113377481	113377493	KIAA2018	2.53E-16	1.68E-32	0.000264	0.021898	0.053097	0.001136	0.03	1	0.036864	0.002506	0.001586	1	3.25E-23	0.02381	0.000553
2	197643854	197643870	GTF3C3	2.54E-16	2.23E-12	1	1	1	1	1	1	1	1	1	1	1.92E-09	1	0.046832
6	33408890	33408917	SYNGAP1	2.57E-16	8E-07	0.000342	1	0.026772	0.159676	1	1	1	1	1	1	2.11E-06	1	0.033744
14	59790749	59790763	DAAM1	2.58E-16	7.76E-09	0.187097	1	1	0.013158	1	1	0.013699	1	1	1	0.001584	0.000802	0.011225
18	319944	319956	COLEC12	2.61E-16	7.84E-15	0.019926	0.019417	0.048276	0.126349	1	1	1	1	1	1	1.14E-12	1	0.122871
9	5811331	5811349	ERMP1	2.66E-16	1.71E-11	0.000452	0.008969	1	0.038251	0.004566	1	1	1	1	1	3.32E-06	1	1.33E-06
10	94694025	94694037	EXOC6	2.7E-16	5.85E-17	0.005199	1	1	1	1	0.010811	1	0.183389	0.034483	1	6.71E-16	0.104572	0.002279
2	179363909	179363925	MIR548N	2.76E-16	3.48E-17	0.006048	1	1	1	1	1	1	1	0.016667	1	4.03E-20	1	0.004369
15	91303325	91303352	BLM	2.84E-16	2.26E-06	0.003507	1	1	1	1	1	1	1	0.000381	1	5.47E-13	0.028302	0.115421
13	39435552	39435564	FREM2	2.85E-16	5.17E-26	0.019231	0.009804	1	1	0.064888	1	1	0.00195	0.037736	1	4.15E-13	0.011628	0.001546
6	167447489	167447501	FGFR1OP	2.86E-16	4.34E-13	0.037736	0.061211	1	1	0.026755	1	1	1	1	1	2.67E-13	1	0.136163
4	47746602	47746616	CORIN	2.87E-16	5.73E-25	0.04	0.010471	0.251549	0.035085	0.04807	1	0.009091	0.101124	0.033898	1	4.03E-10	1	0.005651
3	57850505	57850518	SLMAP	2.94E-16	1.08E-28	0.065027	0.008511	1	0.001393	1	1	1	0.027397	1	1	1.05E-17	0.011236	0.002533
16	72050826	72050853	DHODH	2.96E-16	9.58E-06	0.071429	0.045455	1	1	1	1	1	1	0.015873	1	2.26E-12	0.044118	0.014085
8	9619159	9619173	TNKS	3.05E-16	6.51E-13	0.095238	1	1	0.024169	1	1	1	1	1	1	9.03E-05	1	0.02523
10	14572298	14572309	FAM107B	3.06E-16	9.87E-13	0.061224	1	0.229756	1	0.026086	1	1	0.059406	1	1	5.84E-09	0.035714	0.056106
19	14857187	14857203	EMR2	3.18E-16	7.55E-19	0.003072	1	1	1	1	1	1	0.089841	1	1	6.34E-23	0.04918	0.019159
6	167453519	167453532	FGFR1OP	3.19E-16	5.94E-09	0.279202	1	0.591354	0.313057	1	0.043478	0.076336	1	0.021277	0.111111	3.27E-07	1	0.083094
1	32384716	32384728	PTP4A2	3.28E-16	5.56E-11	1	1	1	1	1	1	1	1	0.04878	1	6.82E-07	0.018868	0.168964
2	27824348	27824360	ZNF512	3.3E-16	1.19E-16	0.04918	0.008368	1	1	0.022642	1	1	1	1	1	1.17E-14	1	0.002215
8	38961268	38961280	ADAM9	3.35E-16	3.87E-10	0.055556	1	1	0.035294	1	1	0.015625	0.025806	1	1	1.97E-07	0.019608	0.00387
3	137981439	137981456	ARMC8,NME9	3.37E-16	1.25E-06	0.001565	1	0.192088	1	1	1	1	1	1	1	8.63E-13	0.055936	0.000193
18	43258919	43258936	SLC14A2	3.38E-16	6.3E-09	1	0.037975	0.270886	1	1	1	1	1	1	1	1.69E-05	1	0.249778
1	197705275	197705289	DENND1B	3.42E-16	1.53E-12	0.00439	1	1	1	1	1	0.03125	0.086447	1	0.132609	1.07E-18	0.04	0.080621
10	74899343	74899356	ECD	3.53E-16	2.75E-28	1	1	1	1	0.047471	1	0.088235	1.83E-08	0.014706	1	2.22E-12	1	0.006254
2	172305163	172305189	DCAF17	3.65E-16	4.79E-18	0.054545	1	0.312072	1	1	1	1	0.05303	1	1	3.66E-13	0.101052	0.006283
4	1701673	1701686	SLBP	3.66E-16	2.68E-18	0.055556	1	1	1	1	1	0.022727	1	1	1	1.64E-21	1	2.25E-05
2	32095023	32095056	MEMO1	3.71E-16	3.72E-09	7.87E-06	1	1	1	1	1	0.014493	0.019802	1	1	4.58E-25	1	0.006874
15	43430749	43430765	TMEM62	3.78E-16	1.73E-23	0.001442	1	1	0.082317	1	1	0.093517	0.014514	1	0.304348	1.36E-23	1	0.307079
20	60963346	60963359	RPS21	3.82E-16	3.11E-16	1	0.180727	1	1	0.002322	1	0.105188	1	0.08951	0.315789	9.63E-06	1	0.20474
11	14063262	14063275	SPON1	3.91E-16	4.58E-10	1	1	0.002584	1	1	1	1	1	1	1	1.31E-09	0.0625	0.02378
11	700526	700541	TMEM80	3.94E-16	5.29E-17	0.184135	0.070175	1	0.186351	0.022275	1	0.00382	1.79E-05	1	1	8.99E-11	1	2.2E-07
13	25839869	25839885	MTMR6	3.95E-16	1.5E-14	0.090909	1	1	0.018405	1	1	0.06473	1	1	0.4	1.62E-07	1	1
8	101725020	101725049	PABPC1	3.96E-16	2E-13	0.009015	1	0.181945	1	1	1	1	1	0.027027	0.054348	4.66E-14	1	0.00024
12	31820564	31820578	METTL20	3.97E-16	8.09E-24	0.009307	0.000195	1	0.010929	0.001492	1	0.061628	0.001845	1	1	3.05E-13	1	0.000169
4	178262605	178262628	NEIL3	3.99E-16	1.45E-15	0.076923	0.026086	1	1	0.036882	1	1	1	1	0.083333	5.29E-06	0.060593	0.005733
13	113818805	113818818	PROZ	4.2E-16	3.21E-17	1	0.013605	1	1	0.001662	1	1	1	0.021277	1	7E-16	0.003279	0.012327
2	39046321	39046333	DHX57	4.33E-16	7.59E-22	0.03125	1	0.067114	1	1	1	1	1	0.133333	1	9.02E-15	0.003953	0.006763
1	6291918	6291933	ICMT	4.38E-16	9.64E-10	1	0.075924	1	1	1	1	1	0.117527	1	1	1.48E-05	0.024096	0.001829
6	37897811	37897845	ZFAND3	4.41E-16	3.89E-06	0.007974	1	1	0.02381	1	1	1	0.01626	0.028986	1	8.21E-08	1	0.058968
2	101581294	101581308	NPAS2	4.48E-16	5.58E-16	0.068418	1	1	0.013764	0.000652	1	0.021277	0.090862	1	1	6.61E-09	1	0.000704
18	61064220	61064237	VPS4B	4.48E-16	4.28E-16	1	1	1	1	1	1	0.039022	1	1	1	5.09E-06	0.001753	0.003322
1	22079457	22079473	USP48	4.57E-16	4.7E-12	0.007863	1	1	1	1	1	1	1	1	1	5.31E-18	1	0.001166
14	97022161	97022182	PAPOLA	4.62E-16	4.11E-20	0.001753	1	1	1	1	1	1	0.216898	1	1	8.49E-10	1	0.00371
13	49684436	49684450	FNDC3A	4.68E-16	3.21E-16	1	1	0.084112	0.068966	1	1	1	0.073708	0.027778	1	2.8E-10	1	0.000344
7	38810880	38810895	VPS41	4.82E-16	2.02E-11	0.314091	1	1	0.08	1	1	0.045796	1	0.125	1	2.33E-10	0.076923	0.001314
15	76168406	76168425	UBE2Q2	4.86E-16	1.08E-16	0.187097	1	1	0.027026	1	1	0.07497	1	1	1	2.07E-08	1	0.010159
12	122017848	122017866	KDM2B	4.88E-16	8.66E-25	1	1	1	1	1	1	0.015038	1	0.001357	1	2.56E-07	0.047899	0.264386
21	34901037	34901079	GART	4.89E-16	0.000312	0.065789	1	1	1	1	1	0.017857	1	1	1	2.26E-17	1	1
12	52139669	52139683	SCN8A	4.92E-16	9.68E-10	0.017742	1	1	1	0.051716	1	1	0.044444	0.020833	1	9.4E-05	1	0.210466
9	133498017	133498047	FUBP3	4.99E-16	3.94E-07	0.000219	1	0.104095	1	1	1	1	1	0.069748	0.153846	2.59E-28	1	4.92E-07
2	44569739	44569755	PREPL	5.1E-16	9.69E-13	0.006361	1	1	0.068966	0.063492	1	1	1	1	1	3.4E-09	1	0.018929
1	174188216	174188243	RABGAP1L	5.23E-16	1.01E-21	0.058824	1	1	0.068747	0.018182	1	0.032387	0.053333	1	1	1.19E-19	1	0.013259
5	54710072	54710091	SKIV2L2	5.25E-16	3.51E-07	0.002246	1	0.089589	1	1	1	1	1	1	1	8.43E-21	1	0.005927
16	15501658	15501670	MPV17L	5.26E-16	3.91E-17	0.00752	0.017964	0.006692	1	1	1	0.045802	1	0.02439	1	1.27E-11	1	0.088135
7	102912317	102912336	DPY19L2P2	5.4E-16	1.01E-12	0.05	1	1	1	1	1	1	1	0.001442	1	8.94E-15	1	0.01228
21	38092247	38092259	SIM2	5.84E-16	2.55E-14	1	0.040462	1	0.526229	1	1	0.123429	0.024958	0.051724	1	0.00164	0.001852	0.123175
10	18875051	18875063	NSUN6	5.85E-16	5.79E-09	1	0.025	1	1	1	1	1	1	0.033333	1	0.000658	1	1
8	121455551	121455586	MRPL13	5.89E-16	2.27E-10	0.009015	1	0.092664	0.120547	1	1	1	1	1	1	2.14E-16	1	6.48E-05
1	10468005	10468021	PGD	5.99E-16	1.97E-17	0.23913	1	1	1	1	1	1	0.003672	0.017544	1	4.66E-07	1	0.010311
1	231502230	231502245	EGLN1	6.11E-16	2.29E-09	0.002976	1	1	0.069544	1	1	1	0.110638	1	1	1.37E-08	0.036585	1.28E-06
1	150676674	150676692	HORMAD1	6.16E-16	4.95E-05	9.16E-05	1	1	1	1	1	1	1	0.001815	1	1.37E-33	1	0.000536
2	191537793	191537809	NAB1	6.29E-16	1.23E-17	0.001976	0.03012	0.304092	1	1	1	0.035461	1	1	1	2.02E-08	1	0.208331
22	24040564	24040577	GUSBP11	6.51E-16	4.07E-18	0.298246	1	1	0.034483	1	1	1	1	0.026316	1	0.006838	0.037037	0.000989
5	54424226	54424238	CDC20B	6.69E-16	1.89E-17	0.007742	1	0.325399	0.112191	0.017937	1	0.041954	1	1	1	1.65E-19	0.032967	0.046715
19	41188890	41188901	NUMBL	6.72E-16	1.46E-16	0.039216	0.011976	1	1	1	0.017143	1	0.039216	1	1	1.08E-11	0.030303	0.002055
6	20548763	20548778	CDKAL1	6.86E-16	4.9E-15	0.15556	0.0833	0.100354	1	1	1	0.014925	1	0.036364	1	1.31E-26	1	0.020619
15	50901929	50901943	TRPM7	6.94E-16	6.09E-09	0.035897	1	0.216047	1	1	1	0.082474	1	1	1	4.14E-12	0.015345	0.025643
4	166388811	166388838	CPE	7.09E-16	1.56E-20	0.055556	1	1	0.036364	1	1	1	0.002758	0.066102	1	3.55E-19	1.05E-05	0.07438
11	28113094	28113107	KIF18A	7.16E-16	6.84E-20	0.086957	0.009901	1	0.018405	0.020725	0.005495	0.000123	0.061224	1	1	1.9E-14	0.045455	0.002555
2	157352734	157352747	GPD2	7.21E-16	1.06E-07	0.000277	1	1	1	0.02069	1	1	1	0.027778	1	1.78E-09	1	0.070588
9	95618605	95618618	ZNF484	7.28E-16	6.85E-21	0.02223	0.019417	0.238848	0.392739	0.073864	1	1	0.341154	1	0.071429	1.75E-10	1	0.196978
18	57684454	57684466	PMAIP1(dist=112916),MC4R(dist=354098)	7.37E-16	2.28E-09	0.166317	1	1	1	1	1	0.040812	0.000883	0.029412	1	1.02E-17	1	9.22E-06
8	117864952	117864973	RAD21	7.52E-16	1.94E-15	0.054054	1	1	0.007634	1	1	1	1	0.017241	1	1.09E-11	1	0.012976
9	77550305	77550323	TRPM6(dist=47295),C9orf40(dist=11176)	7.58E-16	3.79E-16	0.000722	0.00059	0.19073	1	1	1	1	0.037936	1	1	3.36E-09	1	0.017191
16	69492952	69492989	CYB5B	7.69E-16	3.82E-12	0.008202	1	1	1	0.062648	1	0.001333	1	0.050847	0.238095	1.22E-18	1	0.11624
6	90366329	90366347	LOC101929057	7.75E-16	4.19E-28	0.226335	0.097238	0.595295	0.005895	1	0.031873	1	0.142631	0.02029	1	4.11E-16	1	0.000646
16	3433714	3433726	ZSCAN32	7.8E-16	1.84E-23	0.042857	1	1	0.077748	1	1	1	0.001307	1	1	1.4E-16	1	0.005704
17	29157881	29157892	CRLF3(dist=6103),ATAD5(dist=1131)	7.92E-16	3.23E-08	0.035088	1	1	1	1	1	1	0.018182	1	1	2.28E-14	0.050308	0.004571
16	31435918	31435935	ITGAD	8.05E-16	9.48E-13	0.055556	1	1	1	1	1	1	1	1	1	1.91E-14	1	0.00026
6	123545159	123545186	TRDN	8.11E-16	0.000193	0.047456	1	1	1	1	1	0.036232	1	0.016949	1	5.77E-10	1	0.000585
8	65537104	65537116	CYP7B1	8.24E-16	1.79E-15	0.001536	1	1	0.028736	1	1	1	1	1	1	1.86E-11	1	0.120928
6	116264386	116264400	FRK	8.39E-16	1.22E-07	0.012256	1	1	1	1	1	1	1	1	0.277778	1.86E-17	1	0.127287
12	64679694	64679708	C12orf56	8.47E-16	2.49E-10	0.000746	1	1	1	1	1	1	1	0.059249	1	1.53E-09	0.025974	1.79E-08
2	211527815	211527840	CPS1	8.67E-16	2.73E-14	2.8E-05	1	0.065201	1	1	1	0.018349	1	1	1	1.15E-12	0.000481	0.137905
8	74495112	74495130	STAU2	8.68E-16	2.82E-23	0.047619	0.005128	1	1	1	1	1	1	1	1	4.55E-17	1	0.000117
8	101933023	101933037	YWHAZ	8.71E-16	1.19E-21	0.212698	0.000123	1	0.000519	0.000317	1	0.009259	1	0.002463	1	4.82E-24	0.001681	0.003367
2	196912236	196912247	DNAH7	8.73E-16	3.4E-18	0.001282	1	0.167224	1	1	1	1	0.063492	0.032787	1	5.38E-15	1	0.006667
15	44216559	44216573	FRMD5	8.85E-16	8.62E-12	0.001681	1	0.029913	1	1	1	1	1	0.064516	1	6.37E-09	1	0.198784
2	64335290	64335301	PELI1	8.87E-16	3.44E-18	0.021739	1	0.170787	1	0.018433	1	0.031915	0.050505	0.015625	1	1.03E-13	1	0.01457
7	150918586	150918602	ABCF2	9.01E-16	1.22E-32	0.103383	1	1	0.070151	0.000281	1	0.009709	1	0.026316	1	1.3E-14	0.029851	0.000467
3	78695353	78695364	ROBO1	9.18E-16	2.88E-20	0.014225	1	0.187678	0.032432	0.072436	1	1	1	1	1	7.31E-17	1.54E-05	0.004257
3	50091941	50091957	RBM6	9.26E-16	5.36E-12	0.24217	1	1	1	1	1	0.014493	1	1	1	0.000317	1	0.030912
1	241954005	241954024	WDR64	9.47E-16	7.41E-16	0.001011	0.0631	0.522254	0.055287	0.000762	1	1	0.26177	1	1	7.04E-08	1	0.000143
9	78748972	78748993	PCSK5	9.51E-16	1.31E-15	1	1	1	1	1	1	1	0.158774	1	1	4.51E-15	1	0.049612
X	109416688	109416703	TMEM164	9.56E-16	2.1E-08	1	1	1	0.009417	1	1	0.057132	1	1	1	1.8E-12	1	0.062144
5	96116095	96116125	ERAP1	9.64E-16	4.19E-09	1	1	0.352891	1	0.084906	0.015152	1	1	0.004193	1	0.001659	0.002414	5.71E-06
16	90141288	90141302	PRDM7	9.81E-16	1.9E-17	0.000101	1	0.270929	0.003705	1	1	1	1	0.011614	0.3125	3.78E-31	1	0.000466
11	14316128	14316148	RRAS2	9.94E-16	5.26E-11	0.096341	1	0.07874	1	1	0.010204	1	0.000608	1	1	4.13E-20	1	0.020252
1	21307733	21307759	EIF4G3	1.01E-15	0.001218	1	1	1	1	1	1	1	1	1	1	4.51E-05	1	1
13	99890849	99890862	MIR548AN	1.01E-15	1.4E-33	0.004941	0.005076	0.048193	6.16E-05	0.000349	1	0.02381	0.106417	0.142857	1	1.64E-14	1	0.003038
7	2406737	2406755	EIF3B	1.04E-15	2.9E-11	0.000324	1	0.280306	1	0.065789	1	0.164032	5.86E-05	0.000466	1	6.15E-12	1	4.5E-07
2	197531518	197531530	CCDC150	1.04E-15	2.59E-07	1	0.009709	1	1	1	1	1	0.142157	0.000466	1	1.84E-08	0.022989	0.045455
20	57611828	57611841	SLMO2-ATP5E	1.05E-15	6.13E-08	0.035088	1	1	1	0.038462	1	1	1	1	1	1.36E-18	0.012658	0.003459
1	169560727	169560740	SELP	1.06E-15	1.55E-13	0.163323	1	1	0.16768	1	1	0.013986	1	1	1	5.06E-18	1	0.211903
12	56500502	56500515	PA2G4	1.08E-15	7.87E-27	0.130303	1	0.136166	0.124071	0.121803	0.021053	1	0.113101	0.033333	1	1.18E-15	0.037037	0.28581
2	128263363	128263377	IWS1	1.1E-15	1.9E-26	0.107143	1	0.116883	1	0.000293	1	1	0.101618	1	1	2.53E-06	1	0.022336
3	160249220	160249234	KPNA4	1.17E-15	3.35E-12	1	1	1	1	1	1	1	6.94E-05	1	1	7.99E-10	0.025974	0.16678
1	236744720	236744735	HEATR1	1.19E-15	5.84E-14	0.277328	1	1	1	0.060959	0.033613	1	0.092965	0.045455	1	7E-05	1	0.248581
12	31289662	31289674	DDX11(dist=31937),FAM60A(dist=143846)	1.2E-15	1.98E-18	0.25	0.012422	0.052632	0.013605	1	1	0.055036	0.002338	1	1	0.4	0.002162	0.000272
15	72864384	72864397	ARIH1	1.22E-15	2.97E-20	1	1	0.279828	1	1	1	1	0.033113	1	1	3.19E-09	0.035294	5E-07
14	81953889	81953901	SEL1L	1.33E-15	2.43E-23	0.042553	0.010526	0.078947	1	0.035162	1	1	1	1	1	8.39E-10	1	0.086914
4	74010555	74010571	ANKRD17	1.36E-15	1.5E-13	0.006048	0.01087	1	1	1	1	1	1	0.023256	1	1.14E-16	0.000381	4.76E-05
14	58471378	58471390	C14orf37	1.41E-15	1.68E-20	0.024769	0.00013	1	0.03352	0.020833	0.004132	0.025	0.09901	1	1	4.82E-12	0.067398	1
2	27659821	27659845	NRBP1	1.44E-15	1.54E-24	0.077922	1	0.152701	1	1	1	1	0.035294	1	1	3.14E-14	1	0.150382
6	17669303	17669328	NUP153	1.46E-15	1.53E-07	0.067568	0.012048	1	1	1	1	1	1	0.015385	1	1.92E-08	1	0.009858
2	201719258	201719275	CLK1	1.47E-15	2.63E-10	0.003659	1	0.453087	0.04192	1	1	1	0.009705	0.11103	1	1.28E-13	1	1

8	62550924	62550938	ASPH	1.49E-15	6.5E-29	0.001364	0.02046	1	1	1	0.008658	0.015385	1	1	1	2.76E-22	0.110262	0.038123
3	147120444	147120470	ZIC4	1.53E-15	1.08E-16	0.00565	1	1	1	0.058238	1	1	0.087912	1	1	1.49E-10	1	0.009352
17	38451739	38451755	CDC6	1.55E-15	5.78E-14	0.04918	1	1	0.029412	1	1	1	1	0.041667	1	2.4E-16	1	0.014777
7	137782593	137782609	AKR1D1	1.56E-15	1.06E-16	0.007143	1	0.068376	0.11812	1	1	0.017544	1	0.03125	0.333333	4.81E-06	0.05	0.056432
8	42798394	42798409	HOOK3	1.56E-15	6.21E-17	1	1	1	1	1	1	0.031871	0.009524	1	1	6.98E-10	1	9.85E-07
15	45028919	45028931	TRIM69	1.56E-15	1.1E-08	1	1	0.574975	1	0.129353	1	0.202329	0.001326	1	1	6.81E-06	1	0.034297
5	60170512	60170537	ERCC8	1.61E-15	8.17E-11	0.002347	1	1	0.034483	1	1	1	1	0.016393	1	2.19E-15	1	4.97E-05
8	30954244	30954280	WRN	1.61E-15	1.7E-09	0.025997	1	1	1	1	1	0.045108	1	1	1	0.001617	1	0.060317
20	44429633	44429646	DNTTIP1	1.66E-15	2.21E-09	0.08951	1	1	1	0.020725	1	1	1	1	0.25	2.09E-09	0.021978	0.228297
X	54042926	54042942	PHF8	1.67E-15	1.16E-11	1	1	0.04918	1	1	1	1	1	0.333333	1	2.58E-07	1	0.000116
10	101510104	101510123	CUTC	1.68E-15	2.4E-14	1	0.009174	0.071895	1	1	1	1	1	0.000402	1	9.06E-07	0.029412	0.230104
21	40871690	40871717	SH3BGR	1.68E-15	4.34E-10	0.001442	1	1	1	1	1	1	1	0.015625	1	5.8E-10	0.037037	0.066519
5	138704323	138704348	PAIP2,SLC23A1	1.71E-15	1.76E-07	0.044118	1	1	1	1	1	1	1	0.033898	1	2.63E-10	1	0.003722
12	21644428	21644447	RECQL	1.74E-15	1.54E-11	0.006368	1	1	1	1	1	1	1	0.0625	1	6.91E-26	1	0.158201
11	22296094	22296106	ANO5	1.75E-15	1.21E-25	0.370448	1	0.466731	0.076889	1	1	1	1	1	0.142857	5.76E-07	1	0.000591
2	172582088	172582125	DYNC1I2	1.8E-15	9.12E-05	1	1	1	1	1	1	1	1	0.062004	0.142857	3.17E-28	0.035714	0.161057
5	101574897	101574911	SLCO4C1	1.83E-15	1.71E-15	0.006765	1	0.116388	1	0.081593	1	0.104082	1	1	0.222222	1.12E-17	1	0.048305
3	138341284	138341300	FAIM	1.85E-15	1.65E-06	0.009936	0.093023	1	0.11812	1	1	1	1	1	1	4.01E-10	0.172016	0.054299
22	44074070	44074102	EFCAB6	1.92E-15	3.04E-08	0.003246	1	1	1	1	1	1	1	1	0.391304	2.82E-18	1	0.001195
2	217329413	217329447	SMARCAL1	1.93E-15	5.57E-17	0.006061	0.009804	0.123429	1	1	1	1	1	1	1	5.08E-06	1	0.005342
20	13695824	13695839	ESF1	2.04E-15	7.82E-07	0.001053	1	1	1	0.017241	1	1	1	1	1	4.94E-12	1	0.269769
12	88566358	88566370	TMTC3	2.06E-15	3.5E-21	1	1	1	0.01875	1	1	0.044688	0.003634	0.020408	1	4.64E-09	1	0.348272
3	179298584	179298597	ACTL6A	2.06E-15	1.47E-10	0.118305	1	1	0.001237	1	1	0.015152	1	0.002484	0.307692	6.98E-16	1	0.063463
2	55863360	55863372	PNPT1	2.1E-15	2.93E-09	0.355556	0.071429	1	1	0.0122	1	1	0.240001	0.034483	0.125	1.21E-11	1	4.8E-05
4	122590883	122590899	ANXA5	2.17E-15	1.47E-18	0.003507	1	1	1	0.082311	0.039526	1	0.003852	0.030303	1	2.92E-15	1	0.095174
3	37176656	37176670	LRRFIP2	2.25E-15	2.3E-23	6.43E-05	1	0.052288	0.045045	1	1	0.014815	0.161206	1	1	8.4E-11	0.055556	0.004361
16	72832618	72832635	ZFHX3	2.26E-15	8.48E-21	0.003953	1	1	0.127113	1	1	1	1	1	1	3.14E-14	0.034483	0.065201
19	11411997	11412010	TSPAN16	2.29E-15	1.54E-23	0.004525	0.009259	1	0.000403	1	1	0.018692	1	1	1	3.63E-17	1	9.36E-05
17	66904031	66904045	ABCA8	2.3E-15	5.71E-12	0.000725	1	0.184111	1	1	1	1	0.070401	0.1	1	2.12E-13	0.029412	0.005419
14	39619587	39619599	TRAPPC6B	2.31E-15	4.43E-10	0.066667	1	1	1	0.047332	1	1	1	1	1	0.000144	0.012987	0.006801
11	108014684	108014704	ACAT1	2.32E-15	3.72E-10	0.00339	0.065	0.222636	0.160926	0.169518	0.015075	1	0.256522	0.074074	1	2.13E-08	0.020928	0.002392
12	56197331	56197344	SARNP	2.32E-15	2.59E-08	1	1	1	1	0.02168	1	1	1	0.033898	1	0.003815	0.02439	0.267533
10	25273311	25273328	ENKUR	2.34E-15	9.87E-07	0.218487	1	0.03937	1	1	1	1	1	1	1	6.3E-09	1	0.001756
4	123374811	123374832	IL2	2.38E-15	6.69E-10	0.02223	1	1	1	0.021186	1	0.024	0.007482	1	1	1.27E-07	1	0.000345
10	90676384	90676397	STAMBPL1	2.42E-15	4.58E-12	0.027778	1	1	0.05042	1	1	1	0.025641	1	0.375	1.76E-15	1	0.002865
17	80430359	80430375	NARF	2.44E-15	1.29E-12	0.142857	0.059159	0.251675	1	1	1	1	1	0.044444	1	8.97E-05	1	0.207652
6	155109168	155109189	SCAF8	2.5E-15	1.81E-19	0.004152	1	1	0.054635	1	0.005556	1	1	0.018182	1	1.7E-12	1	0.059764
22	42415224	42415240	WBP2NL	2.52E-15	1.51E-20	8.1E-05	1	0.007785	1	1	1	1	1	1	1	1.49E-15	1	7.35E-05
3	38257551	38257583	OXSR1	2.55E-15	3.78E-10	0.000636	1	1	1	1	1	1	1	1	1	6.71E-24	1	1.84E-07
9	130243534	130243551	LRSAM1	2.59E-15	3.68E-16	0.061265	1	1	1	1	1	1	1	1	1	6.13E-10	2.4E-05	0.34631
5	50055456	50055473	PARP8	2.6E-15	5.2E-10	0.00549	1	0.174337	1	0.153002	1	0.070588	1	0.094077	0.222222	8.17E-24	1	0.031361
14	21936762	21936776	RAB2B	2.65E-15	2.38E-21	0.04	1	0.011657	0.099451	1	1	1	1	0.059701	1	5.6E-20	1	0.36563
7	73666736	73666750	RFC2	2.65E-15	1.95E-24	1	0.026431	0.068027	0.001716	0.047611	1	0.032387	0.003497	1	1	3.83E-11	1	1.9E-07
3	42599049	42599064	SEC22C	2.7E-15	4.95E-18	0.001442	1	1	1	0.004934	1	1	0.062242	0.018868	1	1.37E-14	0.071429	1
7	134626034	134626049	CALD1	2.75E-15	2.61E-19	0.199457	1	1	0.116388	0.002061	0.008621	0.038213	1	1	0.136364	2.41E-18	1	0.002535
8	101629995	101630010	SNX31	2.75E-15	1.4E-18	0.12037	1	1	1	1	1	1	0.04142	1	1	6.37E-15	1	0.000791
3	160138723	160138736	SMC4	2.78E-15	2.85E-15	0.002976	1	1	0.045455	1	1	0.015385	0.03	0.016949	1	6.7E-13	1	0.003459
12	97311376	97311393	NEDD1	2.81E-15	3.48E-22	1	1	0.409703	0.057787	1	1	0.039474	1	1	0.120588	2.9E-19	1	0.003014
4	104066176	104066191	CENPE	2.81E-15	5.86E-22	0.003279	1	0.176099	1	1	1	1	0.050308	0.000402	1	2.49E-19	0.026316	0.04417
12	51323672	51323684	METTL7A	2.82E-15	4.71E-35	0.030303	0.01087	1	0.035533	0.012987	1	0.03947	0.050955	0.018868	1	4.16E-15	0.047619	0.145738
X	134708007	134708023	DDX26B	2.83E-15	7.58E-11	1	1	1	1	1	1	1	0.039683	1	1	2.89E-15	1	0.005195
5	94206957	94206971	MCTP1	2.84E-15	6.99E-05	0.138274	1	0.123144	0.012987	0.063987	1	1	1	0.052632	1	4.2E-13	0.022727	0.026844
7	81695842	81695859	CACNA2D1	2.89E-15	1.32E-14	8.46E-05	1	1	1	1	1	1	1	0.015385	1	4.96E-24	0.025316	0.246267
15	44944221	44944233	SPG11	2.89E-15	1.57E-15	0.010695	1	1	1	1	1	1	1	1	1	2.93E-09	0.035714	0.005517
13	24410498	24410511	MIPEP	2.92E-15	1.54E-18	0.074074	1	0.067901	0.034653	1	1	0.036142	1	1	1	9.11E-06	1	0.000148
3	43385025	43385042	SNRK	2.93E-15	6.83E-07	1	1	1	1	1	1	1	1	1	1	3.23E-08	0.034483	1
5	37027560	37027590	NIPBL	2.96E-15	3.33E-14	0.000308	1	1	1	1	1	1	1	0.063987	1	3.03E-25	1	1
2	208611699	208611715	CCNYL1	3.04E-15	6.06E-12	0.109524	1	1	1	1	1	1	1	0.02439	0.1875	1.35E-08	0.067212	0.001258
13	33637913	33637928	KL	3.06E-15	4.51E-12	0.002484	1	0.192278	0.018593	0.004101	1	0.053563	0.392164	0.010989	1	2.25E-11	1	0.033167
12	57882764	57882777	MARS	3.1E-15	1.46E-27	1	1	1	1	0.049682	1	1	1.17E-05	1	1	5.12E-15	1	0.051402
7	72159820	72159832	TYW1B	3.21E-15	2.22E-12	0.118415	1	1	1	1	1	0.021978	1	1	1	4.14E-16	0.001604	0.002132
6	100957763	100957779	ASCC3	3.27E-15	3.18E-17	1	1	1	1	1	1	1	7.75E-05	1	1	7.11E-09	1	0.098164
16	21809188	21809208	RRN3P1	3.28E-15	1.68E-09	0.000649	1	1	1	1	1	1	1	0.017241	1	5.82E-20	0.042254	4.03E-05
6	82930437	82930451	IBTK	3.29E-15	6.97E-18	0.012502	0.024631	0.21655	1	0.052164	1	1	1	0.038462	1	9.41E-13	0.029851	0.185315
2	186692859	186692872	FSIP2	3.33E-15	3.79E-13	1	1	1	0.099923	1	1	1	0.001818	1	1	1.57E-12	1	0.013754
17	57762402	57762414	CLTC	3.33E-15	4.87E-27	0.05	0.013072	0.090909	0.001414	0.000224	1	1	0.056258	0.032787	1	9.04E-05	1	0.17864
11	48970767	48970782	OR4A47(dist=459493),TRIM49B(dist=82370)	3.5E-15	1.54E-10	0.000382	1	1	1	1	1	1	0.1797	0.120192	1	1.58E-17	1	0.00983
9	130127691	130127703	GARNL3	3.54E-15	2.89E-18	0.000982	1	0.411251	0.178083	1	1	1	0.127223	1	1	2.16E-23	1	1
1	236590675	236590687	EDARADD	3.71E-15	2.43E-15	1	1	1	0.016807	1	1	0.001084	1	1	1	1.28E-12	0.038961	0.004561
1	109525421	109525434	WDR47	3.81E-15	5.34E-17	0.00188	1	1	0.027778	1	1	1	0.0625	1	1	1.88E-20	0.046875	0.000216
6	136932603	136932616	MAP3K5	3.86E-15	5.23E-11	1	1	1	1	0.034783	1	1	0.018182	1	1	4.36E-08	1	0.003309
17	19749952	19749969	ULK2	3.88E-15	1.99E-20	1	1	1	1	1	1	0.020134	0.144766	1	1	2.86E-25	1	0.000101
17	10543281	10543296	MYH3	3.9E-15	6.3E-09	0.403782	1	0.414396	1	0.057377	1	1	0.005961	1	0.006061	1.18E-05	0.012097	0.00018
17	60374173	60374189	TBC1D3P2(dist=21157),EFCAB3(dist=73390)	3.96E-15	1.66E-11	0.239448	1	1	1	1	1	0.060364	0.001001	0.04918	0.428571	2.14E-14	0.011005	0.539381
6	7410735	7410747	RIOK1	4E-15	1.58E-10	0.113122	1	1	1	1	1	1	0.00813	1	1	6.14E-19	0.025641	0.000266
2	55874657	55874673	PNPT1	4.06E-15	0.000683	0.08951	1	0.07997	1	1	1	1	1	1	1	2.45E-15	1	0.00021
14	65472874	65472892	MAX	4.07E-15	9.37E-26	0.000442	1	0.057532	0.120838	0.290959	1	0.045161	0.041577	0.030303	1	1.12E-16	1	0.014453
5	10394911	10394930	MARCH6	4.07E-15	2.31E-05	0.000253	1	1	1	1	1	1	1	1	1	3.03E-23	1	0.079082
6	43538501	43538513	XPO5	4.1E-15	9.48E-14	0.084472	1	1	1	1	1	1	0.017699	1	1	1.76E-13	1	1
X	150573322	150573335	VMA21	4.22E-15	1.03E-17	0.004707	1	0.128375	1	1	1	1	0.001233	1	1	3.61E-08	0.00223	0.194874
20	46266543	46266558	NCOA3	4.28E-15	1.21E-29	0.032787	0.005714	0.071429	0.006673	1	1	1	0.106307	1	1	3.74E-26	0.035294	0.000206
22	36157175	36157187	RBFOX2	4.32E-15	1.73E-09	0.044776	1	0.137953	1	1	1	1	1	1	1	2.84E-16	1	0.001561
10	61956386	61956407	ANK3	4.41E-15	1.51E-09	0.04878	1	0.109879	0.003267	1	1	0.019355	1	0.064516	1	3.47E-11	0.021277	0.00618
3	47103861	47103876	SETD2	4.51E-15	8.68E-14	0.072054	0.019002	0.116813	1	1	1	1	0.175373	0.051282	0.028571	1.51E-06	0.084746	0.070749
6	167416662	167416676	FGFR1OP	4.52E-15	2.26E-09	0.066667	1	0.108614	1	1	1	0.009259	0.0005	1	1	9.26E-09	1	0.001096
11	107904512	107904524	CUL5	4.67E-15	3.23E-18	1	0.004608	1	0.000995	1	1	1	1	0.027027	1	8.64E-16	1	0.084567
2	64139831	64139844	VPS54	4.76E-15	1.28E-20	0.000342	1	0.042553	0.00163	1	1	0.017699	1	1	0.227273	1.44E-24	0.020833	8.15E-05
11	5687320	5687338	TRIM5	4.76E-15	8.98E-13	0.003805	1	1	1	1	1	1	1	0.030303	0.25	2.36E-21	1	0.000171
X	107464327	107464339	COL4A6	4.86E-15	4.72E-13	0.052632	1	0.075188	1	0.000216	1	1	1	0.060606	1	7.69E-05	0.033708	0.063444
6	84649715	84649747	CYB5R4	4.91E-15	2.27E-19	1	1	0.009705	1	0.051805	1	1	1	0.027027	1	2.77E-22	0.022222	0.000199
19	1057776	1057790	ABCA7	4.98E-15	1.46E-17	1	1	1	1	1	1	1	1	1	1	0.037926	1	0.007988
6	133138067	133138082	RPS12	5.01E-15	9.61E-22	1	0.039216	1	1	0.004087	1	0.10929	0.026707	0.008535	1	1.68E-09	1	0.088565
19	1825786	1825805	REXO1	5.18E-15	6.48E-08	0.213675	1	1	0.022662	1	1	0.012658	1	0.04	1	5.94E-21	0.091382	0.00612
4	22444251	22444267	GPR125	5.2E-15	0.000344	0.082447	1	1	1	1	1	1	0.103365	1	1	6.07E-13	1	1.93E-05
5	95224700	95224719	ELL2	5.37E-15	1.32E-06	0.001563	1	1	1	1	1	0.012739	1	0.037736	1	8.88E-26	0.047619	0.002041
8	90933269	90933296	OSGIN2	5.38E-15	1.52E-22	0.05	0.024315	0.04	1	0.023585	1	1	7.52E-07	1	1	2.63E-08	0.038961	0.00325
4	15839700	15839712	CD38	5.57E-15	7.72E-16	0.098305	1	0.076923	1	1	1	0.08105	1	0.004141	1	4.62E-08	1	0.095371
7	77797468	77797490	MAGI2	5.9E-15	2.03E-05	0.052632	1	1	1	1	1	1	0.051813	1	1	0.000217	0.028302	0.000733
1	25679278	25679290	TMEM50A	6.04E-15	0.001508	7.31E-05	1	1	1	1	1	1	1	1	1	4.52E-16	1	7.19E-06
2	191155233	191155245	HIBCH	6.08E-15	4.04E-07	1	1	0.064103	1	1	1	0.015504	1	0.001681	1	1E-08	1	0.000731
14	96770942	96770967	ATG2B	6.16E-15	7.94E-16	0.000343	1	0.313162	0.018625	1	1	1	1	1	0.019763	6.44E-26	0.007218	0.165981
19	16591361	16591374	CALR3	6.3E-15	4.82E-09	0.168116	1	1	1	1	1	1	1	1	1	1.94E-08	0.04878	0.000179
2	109066220	109066248	GCC2	6.44E-15	7.81E-07	0.136185	1	0.442295	0.029412	1	1	0.026229	1	1	1	3.47E-08	1	0.292141
3	138400782	138400796	PIK3CB	6.55E-15	1.51E-15	0.06383	1	1	0.027027	0.082804	1	1	1	0.018182	0.49	2.05E-12	0.001567	0.016887
10	128780161	128780172	DOCK1	6.55E-15	5.71E-09	0.054545	1	1	1	0.084701	1	1	0.066372	1	1	1.71E-05	0.055164	0.134599
1	211545442	211545459	TRAF5	6.78E-15	7.28E-12	0.43	1	1	0.000219	0.01359	1	1	0.012246	0.001998	1	2.94E-09	0.039022	0.229251
3	122471407	122471434	HSPBAP1	6.87E-15	1.8E-07	0.04	1	1	1	1	1	1	0.040988	0.003805	0.272727	4.32E-22	1	0.012242
3	47604262	47604281	CSPG5	7.07E-15	1.09E-10	0.078431	0.006135	1	0.000762	0.033708	1	0.021505	1	1	1	1.07E-06	1	1
14	55636060	55636079	DLGAP5	7.08E-15	6.27E-06	0.000289	1	1	0.186971	1	1	0.001445	1	1	1	2.6E-20	1	0.443164
15	73567127	73567163	NEO1	7.16E-15	0.002568	0.003702	1	1	1	1	1	1	1	1	1	1.63E-12	1	0.00037
11	59836986	59836998	MS4A3	7.35E-15	2.48E-14	1	0.005405	0.051852	0.054935	1	1	1	0.102871	1	1	1.65E-14	0.022222	0.005085
1	114186351	114186362	MAGI3	7.39E-15	2.56E-23	0.052632	0.010582	1	0.019231	1	1	1	0.09375	0.013333	1	7.69E-16	1	0.196731
17	10317164	10317176	MYHAS	7.68E-15	9.17E-23	0.000584	0.008929	0.025401	0.035	1	0.0125	1	1	1	1	1.68E-19	1	0.002879
14	64496810	64496822	MIR548AZ	7.87E-15	6.82E-16	0.010885	0.007353	1	1	1	1	1	1	1	1	5.21E-13	1	1
2	48046012	48046035	FBXO11	8.32E-15	1.6E-33	0.000144	1	1	1	0.015038	1	0.029961	1	0.033333	1	5.14E-20	1	0.000139
9	19078116	19078132	HAUS6	8.58E-15	6.14E-11	0.272483	1	1	1	1	1	0.018405	1	0.034483	0.36	1.38E-22	1	0.007648
6	110113763	110113776	FIG4	8.67E-15	9.16E-09	1	1	1	1	0.018823	1	1	0.003596	0.093702	0.467836	8.17E-07	0.151636	0.062606
20	9360821	9360845	PLCB4	8.72E-15	6E-11	0.061224	1	0.038462	1	0.03012	1	1	1	0.031746	0.235294	3.51E-20	1	1
2	152293320	152293334	RIF1	8.79E-15	5.78E-11	1	1	1	1	1	1	1	0.020833	1	1	1.44E-18	0.001807	1
11	122928926	122928953	HSPA8	9.02E-15	3.54E-17	0.000816	1	1	1	1	1	1	1	1	0.275862	6.24E-25	1	0.223646
1	175116046	175116071	TNN	9.03E-15	4.99E-29	0.26629	1	1	0.050518	1	1	0.038213	0.150567	0.049074	1	2.5E-21	1	0.110369
3	3216976	3216988	CRBN	9.04E-15	1.99E-23	0.044776	1	1	1	0.015717	1	1	0.003006	1	1	1.69E-13	1	0.000103
11	3424760	3424773	TSSC2	9.21E-15	5.99E-12	1	0.01814	1	1	1	1	0.006061	1	0.029412	1	5.34E-18	0.034483	0.11929
7	16704933	16704945	BZW2	9.37E-15	2.56E-14	0.068182	1	0.048077	1	1	1	1	1	1	1	8.82E-09	1	4.97E-05
7	152055766	152055780	KMT2C	9.42E-15	2.21E-20	1	1	1	0.081836	1	0.008969	0.018182	0.061404	0.030303	1	4.98E-18	1	0.003345
14	45696752	45696769	MIS18BP1	9.43E-15	1.51E-12	0.010695	1	0.040677	1	0.06292	1	0.025641	1	1	1	7.94E-09	0.125	0.046979
8	30464719	30464734	GTF2E2	9.47E-15	1.18E-14	0.001586	1	1	1	1	1	1	1	1	1	1.05E-20	1	0.072308
10	118891992	118892021	VAX1	9.53E-15	2.03E-30	0.033898	1	1	1	0.022222	1	0.014599	1	1	1	1.59E-17	1	0.187449
8	82713832	82713849	SNX16	9.7E-15	5.74E-13	0.002463	1	1	1	0.078621	1	0.039063	1	1	1	1.66E-06	1	0.088567
21	34655334	34655346	IL10RB	9.93E-15	2.17E-19	0.050847	1	1	0.003807	1	1	1	1	0.015625	1	5.44E-12	0.036145	0.000196
1	75042626	75042650	ERICH3	1E-14	6E-10	0.058824	1	0.083587	0.097899	1	1	1	1	1	1	2.06E-13	1	0.001021
13	111340025	111340053	CARS2	1.01E-14	8.23E-27	0.284211	0.000155	1	0.003891	0.014801	0.022059	1	1	1	1	0.011594	0.046154	1
2	64210968	64210991	VPS54	1.01E-14	1.24E-23	0.036364	0.006579	0.067416	0.027027	0.034483	1	1	0.108764	1	1	1.8E-07	0.033708	0.062914
15	89533168	89533181	MFGE8(dist=76505),ABHD2(dist=98200)	1.02E-14	7.49E-18	0.044118	1	1	1	0.058351	0.004425	1	0.000257	1	1	9.96E-06	0.007832	0.295153
1	235938388	235938400	LYST	1.07E-14	8.9E-12	0.019285	1	0.053691	1	1	1	1	2.57E-06	1	1	3.09E-09	1	0.103469
11	86868352	86868374	TMEM135	1.07E-14	3.92E-21	0.006963	0.043122	0.356736	0.181771	1	1	0.016	0.0598	0.028571	1	3.87E-18	1	0.087278
11	4139450	4139465	RRM1	1.13E-14	8.53E-11	1	1	1	1	1	1	0.043165	0.392636	0.137931	1	1.35E-15	1	0.230751
12	27877126	27877148	MRPS35	1.13E-14	2.91E-13	1	1	0.042254	1	1	1	1	1	1	1	8.57E-05	0.051606	0.00061
X	101138438	101138450	ZMAT1	1.14E-14	9.74E-11	0.03125	0.014493	1	1	0.022535	1	1	1	1	1	1.41E-13	1	0.106157
9	3937244	3937266	GLIS3	1.14E-14	4.28E-07	0.04	1	0.084507	0.019231	1	1	1	0.022727	1	1	4.25E-09	0.027027	0.000131
14	64443258	64443278	MIR548AZ	1.14E-14	1.08E-31	0.01277	0.042969	1	0.229348	0.004728	1	0.127113	0.131689	0.005288	0.091304	2.64E-14	0.022472	0.076411

2	61300548	61300568	KIAA1841	1.15E-14	2.28E-12	0.035714	1	1	1	1	1	1	1	0.032258	1	2.89E-09	0.036145	0.072046
X	11308610	11308629	ARHGAP6	1.18E-14	6.2E-09	0.054545	1	1	1	1	1	1	1	1	1	6.42E-20	1	0.015306
3	127820493	127820505	RUVBL1	1.19E-14	3.32E-17	0.061538	1	1	0.054054	1	0.009804	0.014925	0.001134	0.017544	1	1.11E-11	1	1
1	112303077	112303090	DDX20	1.2E-14	6.14E-24	0.007317	0.020151	1	1	0.002062	0.008299	0.047619	0.008808	1	1	2.53E-14	1	0.018716
4	151850226	151850239	LRBA	1.2E-14	2.55E-31	0.056729	0.009709	1	1	0.083288	1	1	1	1	1	1.56E-18	1	2.05E-05
1	167889145	167889160	MPC2	1.21E-14	1.07E-10	0.107071	0.021563	1	1	0.075976	1	1	0.000173	0.020408	0.206897	8.33E-15	1	1
4	22449028	22449052	GPR125	1.26E-14	4.58E-11	0.065027	1	1	1	0.023904	1	1	1	0.027778	1	2.74E-15	0.023256	0.047165
2	88825315	88825330	TEX37	1.26E-14	6.34E-08	1	0.055556	1	1	1	1	1	1	1	0.157895	5.69E-17	0.06	0.027048
15	59806473	59806486	FAM81A	1.31E-14	1.72E-13	0.081081	1	1	0.041447	1	1	1	0.021505	0.040816	1	2.71E-21	0.015873	5.58E-05
12	16713487	16713501	LMO3	1.36E-14	3.46E-11	0.002236	1	0.167504	0.435526	1	0.016129	0.001781	0.214955	0.008097	1	1.54E-10	1	0.053878
16	47399670	47399687	ITFG1	1.37E-14	9.4E-24	7.98E-05	1	0.035256	0.303909	1	1	1	1	1	0.214286	6.48E-32	1	0.012119
12	56354988	56355010	PMEL	1.43E-14	1.08E-11	0.007692	1	1	1	1	1	1	1	1	1	8.33E-13	0.05	0.230987
5	70809269	70809285	BDP1	1.43E-14	7.51E-27	0.00266	0.001407	1	0.001084	0.138095	1	0.040984	1	0.004354	1	1.7E-16	0.001681	0.029793
19	55044241	55044256	KIR3DX1	1.43E-14	1.55E-19	0.001142	1	0.071244	1	0.077456	1	0.015385	0.020332	0.047619	1	7.41E-14	0.030769	9.72E-05
9	15458080	15458092	SNAPC3	1.44E-14	5.01E-08	0.008471	1	0.461537	0.001984	1	1	1	0.001797	0.071429	0.001471	1.23E-05	0.021277	0.317533
4	185694877	185694891	ACSL1	1.45E-14	1.13E-07	0.01063	1	1	1	1	1	1	0.117953	1	1	8.86E-16	1	0.012891
4	141448696	141448718	ELMOD2	1.47E-14	9.04E-10	0.000191	1	0.111801	1	1	1	1	1	1	1	1.41E-20	1	1
6	7413094	7413107	RIOK1	1.52E-14	2.27E-09	0.084472	1	0.004857	0.09798	1	1	1	1	0.000426	1	4.66E-22	1	0.004135
X	12994867	12994886	TMSB4X	1.53E-14	1.03E-33	0.039216	1	0.153559	1	0.03322	1	1	1	1	1	2.68E-18	1	0.004015
2	66670211	66670223	MEIS1	1.53E-14	2.72E-14	0.000512	1	1	0.000222	1	1	1	1	1	1	4.8E-19	1	0.007322
14	71517327	71517341	PCNX	1.53E-14	1.21E-20	1	0.029998	0.069444	0.05	0.059985	1	1	1	1	1	6.29E-15	1	0.00031
19	54545084	54545096	VSTM1	1.65E-14	7.03E-11	1	1	1	0.111776	0.034555	1	1	1	1	1	3.72E-10	1	0.033386
17	40880759	40880775	EZH1	1.65E-14	1.8E-18	7E-05	1	1	1	0.056726	1	1	1	1	1	2.74E-15	1	0.124693
16	5129689	5129703	ALG1	1.68E-14	8.51E-17	0.009662	0.006098	1	0.012121	0.000474	1	0.019048	1	0.076169	1	6.07E-23	0.046875	1.49E-05
5	112876889	112876907	YTHDC2	1.69E-14	4.92E-07	0.163043	1	0.206361	1	1	1	1	1	1	1	0.000226	1	0.509886
6	70589407	70589419	COL19A1	1.69E-14	2.4E-06	0.129944	1	1	0.027273	1	1	1	1	1	1	1.41E-06	0.022989	0.002583
12	38423269	38423280	NONE(dist=NONE),ALG10B(dist=287277)	1.7E-14	1.42E-10	1	1	1	0.104564	1	1	0.032387	1	1	1	0.114551	1	0.00724
17	35979746	35979761	DDX52	1.71E-14	1.39E-09	0.002912	0.006711	1	1	1	1	0.006711	0.001732	1	1	2.09E-25	1	1
7	87526550	87526563	DBF4	1.73E-14	6.31E-17	1	1	0.164578	0.182405	0.155236	1	1	0.359623	0.085714	0.083333	1.99E-05	1	0.50557
13	25355954	25355978	RNF17	1.73E-14	6.27E-12	0.010084	1	0.09798	0.020833	1	1	1	0.070463	0.001422	1	8.35E-10	0.099942	0.028648
15	35149313	35149327	AQR	1.73E-14	5.41E-18	0.103158	0.006289	1	0.068008	0.032256	1	1	0.000663	1	1	1.11E-17	0.035294	0.001175
12	102512024	102512037	NUP37	1.76E-14	8.3E-11	0.005319	1	1	1	1	1	1	3.95E-06	1	1	9.5E-05	1	1
16	10783088	10783102	TEKT5	1.77E-14	1.09E-22	0.105195	1	1	1	1	1	1	1	0.047619	1	1.34E-13	0.00565	0.003826
14	21189177	21189196	RNASE4(dist=20416),EDDM3A(dist=24903)	1.78E-14	4.39E-15	1	1	1	1	1	1	1	1	1	1	1.36E-14	1	1
2	238896494	238896511	UBE2F-SCLY	1.83E-14	0.004903	0.108764	1	1	1	1	1	0.042857	1	0.04878	1	3.41E-09	1	1
20	3245219	3245232	C20orf194	1.84E-14	2.55E-07	4.41E-05	1	1	1	0.023256	1	1	1	0.017241	1	2.38E-12	0.026667	3E-05
21	40181937	40181956	ETS2	1.88E-14	5.24E-09	0.067797	1	1	1	0.014599	1	0.013423	1	0.029851	1	4.8E-19	0.035294	0.109574
5	150846858	150846882	SLC36A1	1.94E-14	1.08E-06	0.000152	1	1	1	1	1	0.013699	1	0.030303	1	2.77E-22	0.08105	0.035414
2	118860645	118860670	INSIG2	2E-14	6.53E-19	0.010315	1	1	0.031746	1	1	1	0.047613	0.039216	1	0.000305	0.031915	0.000326
3	150282051	150282075	EIF2A	2.05E-14	6.41E-07	0.044118	1	1	1	1	1	1	1	0.000627	1	3.21E-22	0.002714	0.12487
X	129483202	129483222	SLC25A14	2.16E-14	1.64E-11	0.035714	1	1	1	1	1	1	1	0.018868	1	2.75E-09	0.001947	0.124385
1	161332091	161332106	SDHC	2.16E-14	1.29E-12	1	1	1	0.117527	1	1	1	1	1	1	2.58E-16	1	0.041054
1	70742532	70742545	ANKRD13C	2.17E-14	5.23E-08	0.055556	1	1	0.035714	1	0.009009	1	1	1	1	1.73E-06	1	0.229342
12	72019989	72020018	ZFC3H1	2.2E-14	5.72E-11	0.016365	1	1	0.403142	1	1	0.060345	0.004242	0.108108	0.395257	2.97E-10	1	0.005625
4	113178966	113178979	AP1AR	2.23E-14	3.29E-10	1	1	0.063492	1	1	1	1	1	0.001057	1	2.68E-18	0.055556	1
18	48584855	48584872	SMAD4	2.24E-14	1.45E-15	0.113122	1	0.161823	1	1	1	0.035292	1	1	1	4.8E-15	1	0.011779
3	160131236	160131250	SMC4	2.24E-14	1.77E-19	0.119879	1	1	0.001457	1	1	1	0.00885	0.014085	1	1.97E-12	1	0.359516
8	10065325	10065339	MSRA	2.25E-14	3.91E-12	0.107143	1	1	1	1	1	1	0.03937	1	0.153846	2.23E-12	1	0.098774
X	62974288	62974301	ARHGEF9	2.25E-14	3.97E-05	0.004451	1	1	0.081967	1	1	1	1	1	1	1.74E-13	1	0.003464
20	48562797	48562813	RNF114	2.28E-14	2.96E-13	0.12807	1	0.250684	1	0.02909	1	0.006211	1	0.030303	1	1.13E-23	0.034483	0.00035
1	28233572	28233599	RPA2	2.28E-14	1.22E-18	1	1	1	1	1	1	0.015385	1	1	1	2.97E-14	1	0.002147
X	133407417	133407443	CCDC160(dist=27609),PHF6(dist=99899)	2.28E-14	0.00049	1	0.025641	1	1	1	1	1	0.02381	1	1	0.001398	1	0.100472
11	112099294	112099311	PTS	2.3E-14	1.08E-12	0.076923	1	1	1	1	1	1	0.047613	1	1	1.79E-06	1	0.120643
1	186330695	186330709	MIR548F1	2.33E-14	7.74E-08	0.000673	0.010638	1	1	1	1	1	1	1	1	1.12E-19	0.002281	0.019821
11	76727866	76727878	ACER3	2.34E-14	2.56E-12	0.184135	1	1	1	1	1	1	1	1	1	9.82E-15	1	0.032835
14	39602843	39602863	GEMIN2	2.36E-14	2.34E-20	1	1	0.053763	1	0.039366	1	1	0.012225	1	1	5.49E-07	0.000301	5.69E-07
4	5851234	5851250	CRMP1	2.38E-14	1.38E-10	0.004267	1	1	1	0.177518	1	1	1	0.157895	1	1.47E-09	1	0.021888
8	42295130	42295156	SLC20A2	2.39E-14	2.95E-08	0.004193	0.019231	1	0.030303	1	1	1	1	0.015152	1	6.49E-14	0.02439	7.26E-06
3	185155430	185155442	MAP3K13	2.42E-14	3.07E-26	0.234274	0.043689	0.115053	9.81E-05	0.077446	1	0.049505	0.000483	0.005348	1	8.81E-13	0.001753	8.02E-05
6	166831580	166831594	RPS6KA2	2.43E-14	2.13E-19	0.15	0.005525	1	1	1	0.005076	0.088195	1	0.027027	1	0.000733	0.034483	1
1	118502087	118502108	WDR3	2.48E-14	4.02E-07	0.000605	1	1	1	1	1	1	1	0.032787	1	1.18E-12	1	0.052795
3	190338028	190338060	IL1RAP	2.5E-14	1.82E-08	0.006965	1	0.345983	0.030303	1	1	1	0.029126	0.022727	1	5.6E-13	1	0.000721
7	5239305	5239336	WIPI2	2.55E-14	4.23E-19	0.003418	0.005	1	1	1	1	0.041447	1	0.014493	1	3.87E-22	1	1.53E-05
1	75614380	75614410	LHX8	2.58E-14	1.43E-08	0.100085	1	0.143778	1	0.178104	1	1	0.216531	1	0.000565	5.61E-16	0.065574	0.025757
5	108516618	108516640	FER	2.58E-14	9.31E-13	1	1	0.075553	0.056526	1	1	1	1	1	0.1875	3.15E-11	0.036145	0.000772
X	109507669	109507681	AMMECR1	2.6E-14	4.8E-21	0.163323	1	1	1	1	1	1	8.98E-05	1	1	4.49E-17	1	0.00336
2	202593915	202593943	ALS2	2.6E-14	2E-12	0.064103	1	1	1	1	1	1	1	1	1	7.65E-12	1	0.004395
11	116629734	116629748	BUD13	2.66E-14	2.13E-14	0.044963	1	1	1	0.117194	1	0.243229	0.185688	0.012195	0.023715	1.81E-18	0.008097	0.024367
7	151921037	151921049	KMT2C	2.66E-14	7.67E-10	0.000949	0.015152	0.081876	1	1	1	0.039996	1	0.029412	1	4.82E-17	1	0.255721
4	71693494	71693508	GRSF1	2.7E-14	1.01E-22	0.001695	0.006494	1	0.057471	7.25E-05	1	1	1	1	1	2.09E-14	1	0.002776
7	103206001	103206013	RELN	2.73E-14	1.49E-09	0.237903	1	0.084344	0.002926	1	1	0.000322	0.324331	1	1	1.24E-07	0.15625	0.160489
13	25416104	25416116	RNF17	2.76E-14	1.17E-09	1	0.011173	1	1	1	1	1	1	1	1	1.64E-15	1	0.003486
1	179271948	179271961	SOAT1	2.78E-14	2.33E-10	0.033898	1	1	0.043161	0.053754	1	1	0.00048	1	1	1.49E-07	1	2.01E-06
11	35327841	35327853	SLC1A2	2.79E-14	1.56E-07	0.014286	1	1	1	0.067774	1	1	1	1	1	0.000825	1	0.002967
5	63803508	63803522	RGS7BP	2.79E-14	4.1E-22	0.161841	1	1	0.003303	1	1	0.020408	0.001738	0.041667	1	1.21E-13	0.042857	0.172833
15	43720155	43720172	RNU6-28P	2.94E-14	1.36E-12	0.05	1	0.044406	1	1	1	1	0.113401	1	1	1.05E-08	1	0.037417
8	72958691	72958714	LOC100132891	2.96E-14	9.98E-10	1	1	0.281611	1	1	1	0.02381	1	1	1	4.06E-05	1	0.001541
3	139077527	139077541	COPB2	2.97E-14	6.72E-10	0.002262	1	1	1	0.046385	1	0.02459	1	1	1	7.71E-10	0.064516	0.142068
1	114495348	114495383	HIPK1	3.06E-14	9.91E-14	0.000437	1	1	1	0.021097	1	1	1	0.027397	1	1.3E-16	1	0.003976
10	71647196	71647209	COL13A1	3.09E-14	7.46E-16	0.00303	1	1	1	0.058051	0.049587	1	0.028504	1	0.294118	6.53E-10	9.43E-05	0.007681
8	124382376	124382403	ATAD2	3.11E-14	1.69E-20	0.053152	0.014815	0.066038	1	0.009091	1	1	1	0.001681	1	7.46E-14	0.000414	0.005874
5	108203451	108203465	FER	3.17E-14	8.55E-12	0.030949	1	1	1	0.097493	1	1	1	1	0.25974	1.5E-09	0.000656	0.224334
6	84650214	84650226	CYB5R4	3.2E-14	3.22E-10	0.007545	1	1	1	0.045448	1	1	0.035714	1	1	5.19E-16	0.028169	0.026204
2	231940295	231940307	PSMD1	3.25E-14	1.26E-18	1	1	1	1	4.65E-05	1	1	1	1	1	1.37E-18	1	0.109353
12	987533	987549	WNK1	3.34E-14	8.65E-07	1	1	0.440717	1	1	1	1	1	1	1	4.86E-11	1	0.030912
4	44685236	44685248	GUF1	3.35E-14	5.14E-14	0.096341	1	1	1	1	1	1	0.091382	0.028986	0.25	3.81E-17	0.094622	0.282714
11	10820663	10820688	EIF4G2	3.37E-14	1.23E-16	0.198122	1	1	0.000106	0.084974	1	0.080499	0.116154	0.02	1	1.9E-10	1	0.038499
2	214794938	214794951	SPAG16	3.37E-14	2.31E-10	0.022267	1	1	1	1	1	0.012987	1	1	1	2.62E-06	1	0.036212
1	103356072	103356097	COL11A1	3.44E-14	1.49E-07	0.02162	1	1	1	1	1	1	1	1	0.15	2.43E-10	0.052973	0.128659
5	134305852	134305866	CATSPER3	3.48E-14	1.11E-19	0.005682	1	0.126849	1	1	1	0.014388	1	1	1	3.45E-13	1	0.000261
3	44399683	44399706	TCAIM	3.6E-14	5.03E-11	1	1	1	0.043474	0.015707	1	1	1.58E-05	1	1	1.31E-06	0.084472	0.181592
4	57871748	57871762	POLR2B	3.63E-14	3.87E-07	0.19937	1	0.188648	1	1	1	1	0.030612	1	0.083333	4.35E-05	0.08105	0.458581
1	214825289	214825312	CENPF	3.7E-14	0.00091	0.003279	1	0.046053	1	1	1	1	1	0.03125	1	3.16E-22	1	0.001599
14	50146547	50146565	POLE2	3.7E-14	4.46E-09	0.084746	1	1	1	1	1	1	1	1	1	5.89E-16	1	0.010912
13	50098426	50098438	PHF11	3.71E-14	1.72E-14	0.070175	0.017241	0.038462	1	1	1	0.007407	1	0.017241	1	4.44E-16	1	0.086378
15	37242440	37242455	MEIS2	3.76E-14	2.45E-12	0.00592	1	0.270915	1	1	1	1	0.12281	1	0.11453	1.52E-15	0.074051	0.445598
17	40856565	40856586	EZH1	3.78E-14	3.96E-14	0.105195	0.012346	1	1	1	1	1	1	0.033333	1	1.41E-18	0.022727	0.023871
2	131888361	131888376	PLEKHB2	3.81E-14	1.11E-12	0.014833	1	0.004016	1	1	1	0.038958	1	1	1	6.29E-12	0.042777	0.001394
6	136429995	136430013	PDE7B	4E-14	2.78E-16	0.002543	0.011173	1	1	1	1	1	1	0.015385	1	1.56E-11	0.000215	0.004026
14	61446607	61446626	TRMT5	4.05E-14	7.68E-20	0.142857	0.008658	0.172932	0.032084	1	1	0.038645	1	0.181818	1	1.33E-07	1	0.401223
3	160395089	160395102	ARL14	4.05E-14	2.2E-13	0.103383	0.016216	1	0.02649	1	1	0.03	1	0.001695	1	4.5E-16	1	0.015272
11	56216401	56216413	OR5R1(dist=30693),OR5M9(dist=13532)	4.16E-14	9.63E-25	0.008471	0.108826	0.443357	0.273586	0.092046	1	0.02888	0.236902	1	0.124562	5.44E-10	0.017903	0.299214
X	15373247	15373259	PIR-FIGF	4.2E-14	9.91E-18	0.04	1	1	0.03947	0.047113	1	1	0.00206	0.029851	1	0.000125	1	6.01E-05
6	90503754	90503779	MDN1	4.23E-14	2.07E-08	0.003246	1	0.04918	1	1	1	1	1	1	1	1.08E-21	1	0.000325
12	73012649	73012663	TRHDE	4.24E-14	1.66E-25	0.00035	1	0.116918	1	9.18E-05	1	1	0.000582	1	0.35	1.45E-14	1	0.252783
4	104068855	104068869	CENPE	4.33E-14	5.04E-11	0.014006	1	1	1	1	1	1	1	1	1	0.000366	1	0.009942
22	32482127	32482141	SLC5A1	4.33E-14	1.71E-21	0.161905	5.03E-05	1	0.063984	1	1	1	1	1	1	4.93E-07	1	0.019069
4	38942697	38942726	FAM114A1	4.39E-14	5.64E-05	0.073529	1	1	1	1	1	0.007246	1	1	1	2.15E-11	0.032258	0.240824
5	150856066	150856091	SLC36A1	4.41E-14	4.1E-15	0.020917	0.006173	1	1	1	1	1	1	0.015873	1	3.37E-14	0.021739	0.000176
2	9593027	9593038	CPSF3	4.68E-14	2.22E-11	0.05	1	1	1	1	1	0.008333	0.045455	1	1	8.55E-11	0.04878	0.003113
5	78373251	78373265	BHMT2	4.73E-14	2.68E-14	0.005153	0.008658	1	1	0.078322	1	0.072924	0.086378	1	1	3.66E-10	1	0.155585
11	18596954	18596979	UEVLD	4.88E-14	3.65E-22	0.002414	1	0.148429	1	0.022422	1	0.048774	1	0.021739	1	3.04E-20	0.014286	0.017139
6	47567210	47567222	CD2AP	4.91E-14	4.38E-12	0.035088	1	0.089241	1	1	1	1	1	1	1	1.46E-18	0.015625	0.000525
4	47886322	47886342	LOC101927179	4.98E-14	1.3E-08	0.002177	0.004525	1	0.039801	1	1	1	0.060241	1	1	3.06E-14	0.000301	0.002797
3	93754286	93754317	ARL13B	5E-14	2.65E-20	0.000556	1	0.072289	1	1	1	1	1	0.043478	1	2.38E-22	1	0.083333
1	154112163	154112180	NUP210L	5.13E-14	2.64E-09	0.01063	1	1	1	1	1	1	1	1	1	2.54E-11	1	0.000565
12	122762763	122762779	CLIP1	5.19E-14	6.15E-36	0.035088	0.026549	0.067985	0.044994	0.105791	1	1	1	0.047619	1	1.04E-06	0.02381	0.086321
2	170917983	170917996	UBR3	5.2E-14	1.04E-21	0.255865	1	0.144924	0.00125	1	1	0.031915	0.01324	0.047619	0.375	1.47E-13	0.124884	0.17263
15	72244247	72244286	MYO9A	5.29E-14	1.74E-17	0.146154	1	0.158506	0.00124	1	1	1	1	0.019608	1	0.00029	1	0.004513
8	65528842	65528854	CYP7B1	5.41E-14	1.1E-07	0.024066	1	0.004517	1	1	1	1	1	0.001317	1	3.71E-15	0.04878	1
13	25899091	25899108	NUPL1	5.49E-14	1.02E-24	0.330435	1	1	0.05187	0.188802	1	1	1	0.048387	1	1.18E-09	1	0.065999
4	56877725	56877748	CEP135	5.5E-14	2.11E-06	0.009025	0.032258	1	0.046779	1	1	1	1	0.027027	1	1.23E-11	0.037736	0.013159
5	86629039	86629073	RASA1	5.51E-14	5.84E-13	7.31E-05	1	1	0.064918	0.019802	1	1	0.031008	1	1	2.91E-10	0.037037	0.120935
17	5367019	5367037	DHX33	5.51E-14	2.76E-11	0.145299	0.053089	0.387432	1	1	1	0.032387	1	0.125	1	6.76E-13	0.142857	1
1	10177680	10177693	UBE4B	5.63E-14	4.57E-21	0.005026	1	1	0.057132	1	1	0.014085	1	1	1	6.75E-21	1	0.000985
17	18708830	18708843	TVP23B	5.71E-14	1.97E-20	0.263158	1	0.003661	1	1	0.019802	1	1	0.009662	0.015038	2.72E-09	0.000101	0.012467
3	33339136	33339148	FBXL2	5.73E-14	1.3E-11	0.138716	1	0.0625	0.024096	1	1	1	1	0.035714	1	3.88E-16	0.013333	0.051414
4	15059945	15059957	LOC101929095	5.76E-14	1.67E-16	0.04878	1	1	0.024096	1	1	1	0.009615	1	1	3.3E-11	1	0.003014
8	71037103	71037115	NCOA2	5.76E-14	1.35E-20	0.001317	0.004673	0.062937	0.035354	1	1	1	0.091206	0.050308	1	4.66E-11	1	7.21E-05
9	135526541	135526560	DDX31	5.82E-14	1.47E-09	0.007742	1	1	1	0.019093	1	0.014815	1	1	1	1.22E-07	0.06665	0.238691
8	35401930	35401941	UNC5D	6.06E-14	6.85E-12	0.001107	1	1	1	1	1	1	1	0.033898	1	2.7E-14	0.004847	1
1	52242432	52242447	OSBPL9	6.17E-14	5.8E-06	9.16E-05	1	1	1	1	1	1	1	1	0.052632	2.21E-12	1	5.76E-05
6	17602786	17602812	FAM8A1	6.23E-14	5.68E-15	0.002976	1	1	0.030075	1	1	0.057143	0.002414	1	1	5.78E-12	0.02439	5.78E-09
15	70963344	70963368	UACA	6.33E-14	4.64E-10	0.002449	1	1	1	1	1	1	1	1	1	3.6E-12	1	0.000385
17	74729588	74729600	METTL23	6.35E-14	1.04E-28	1	1	0.193947	0.053089	0.151223	1	0.016129	2.66E-08	1	0.411765	5.1E-16	0.030303	0.079251
22	30374872	30374885	MTMR3	6.42E-14	2.7E-21	1	0.019184	1	1	1	1	1	0.115602	0.039216	1	1.27E-10	1	0.020845
4	108935768	108935822	HADH	6.72E-14	1.85E-27	1	1	0.085981	1	0.065197	1	1	1.49E-05	1	1	1.63E-12	1	0.175559
20	13561632	13561660	TASP1	6.88E-14	2.34E-13	0.011364	1	0.211308	1	1	1	0.037733	1	1	1	0.00011	1	0.036835
5	176729736	176729749	RAB24	6.89E-14	3.11E-11	1	1	0.187678	0.005882	0.001097	1	0.052632	0.001161	1	0.333333	0.000443	1	0.062272
18	29101215	29101231	DSG2	7.02E-14	4.99E-12	0.006342	1	1	1	1	1	0.015038	1	1	0.05	7.89E-14	1	0.113336
6	117725383	117725399	ROS1	7.03E-14	2.33E-21	0.000481	1	1	0.128865	1	1	0.081267	1	0.013889	0.21875	1.2E-17	1	0.231159

9	135133867	135133881	NTNG2(dist=15647),SETX(dist=2946)	7.31E-14	3.04E-10	0.025441	1	1	1	1	0.019608	0.09853	1	0.020408	0.090909	7.55E-11	0.136185	0.292701
12	3018675	3018690	TULP3	7.45E-14	1.13E-11	0.017501	1	0.122778	0.35987	0.031659	1	1	4.44E-06	0.05	0.014706	2.45E-08	1	0.022485
1	78432647	78432669	FUBP1	7.48E-14	1.55E-06	1	1	1	1	1	1	0.038462	1	1	1	1.57E-10	0.026316	0.000908
1	38483296	38483310	UTP11L	7.52E-14	2.11E-08	1	1	1	1	1	1	1	1	1	0.004762	1.05E-08	0.108764	0.001946
3	130660392	130660405	ATP2C1	7.55E-14	7.67E-13	1	1	0.018365	1	1	1	1	1	0.035714	1	1.21E-12	0.001025	9.26E-05
11	57094842	57094869	SSRP1	7.78E-14	1.2E-24	0.078431	1	0.058065	0.047238	0.035211	1	0.047899	8.51E-05	1	1	1.42E-08	0.011905	0.154594
7	103270629	103270641	RELN	7.88E-14	1.19E-13	0.001815	1	1	1	1	1	0.040265	1	1	1	5.46E-08	1	0.019669
2	27463091	27463105	CAD	7.94E-14	1.67E-26	0.01	0.009434	1	0.002714	0.057681	1	1	1	0.002096	1	2.03E-12	7.31E-05	0.01232
2	37487307	37487330	PRKD3	8.1E-14	1.65E-14	0.008202	1	1	1	1	1	0.008929	1	0.027397	1	1.67E-08	0.001899	1.52E-05
8	95549206	95549231	KIAA1429	8.13E-14	5.7E-13	1	1	0.056738	0.053691	0.02765	1	1	1	1	1	2.19E-10	1	0.018596
5	135496820	135496834	SMAD5	8.44E-14	1.31E-16	0.181422	1	0.03374	1	0.209183	1	0.041954	1	0.085714	1	3.49E-08	0.0625	0.058845
7	106888946	106888972	COG5	8.73E-14	4.55E-21	0.003953	1	0.0151	0.041667	5.13E-06	1	0.016807	2.33E-06	1	1	7.67E-09	0.001025	0.000551
2	11716433	11716447	GREB1	8.75E-14	5.96E-16	1	0.015152	1	1	1	1	0.034333	0.052632	0.019231	1	9.37E-10	0.026316	6.89E-05
2	80101515	80101528	CTNNA2	8.77E-14	5.11E-22	1	1	0.041428	0.168462	0.023256	1	1	1	0.176471	1	1.08E-08	0.121951	0.075472
12	21639385	21639398	RECQL	9.33E-14	2.19E-15	0.112824	1	1	0.289463	0.032609	1	0.032787	1	0.044444	0.039526	6.69E-16	0.128422	0.000447
17	15973417	15973449	NCOR1	9.36E-14	8.37E-30	0.031346	1	0.26571	1	1	1	1	1	1	1	1.17E-08	0.02381	0.148907
21	43549808	43549820	UMODL1	9.57E-14	7.01E-17	1	0.041489	1	0.000964	1	1	1	1	1	1	2.14E-09	1	0.137111
11	118883880	118883892	CCDC84	9.63E-14	5.13E-26	0.055556	1	1	0.026738	1	1	1	0.066372	0.025974	1	1.03E-20	1	0.00049
9	91083260	91083278	SPIN1	9.67E-14	9.71E-05	3.03E-05	1	0.592274	0.235936	1	1	0.066667	1	1	0.079699	4.93E-22	1	0.057339
4	68443006	68443018	STAP1	9.68E-14	1.09E-08	0.002797	1	1	1	1	1	1	1	1	1	1.58E-15	0.022727	0.002597
5	158630629	158630653	RNF145	9.88E-14	1.85E-11	0.058824	1	0.128514	0.001055	0.015936	1	1	1	1	1	0.000231	1	0.109502
1	198711160	198711197	PTPRC	1E-13	3.11E-09	0.009614	1	1	0.051724	1	1	1	1	1	1	1.47E-17	0.042105	1
3	178962491	178962504	KCNMB3	1.02E-13	4.49E-15	0.003488	0.053147	1	1	1	1	0.055739	0.092613	1	0.461538	2.3E-18	1	0.051089
12	42768646	42768660	PPHLN1	1.02E-13	2.95E-16	0.213505	0.009804	1	1	1	1	1	1	1	1	2.61E-14	0.03125	0.001737
12	94575201	94575219	PLXNC1	1.03E-13	9.16E-19	1	1	1	0.076163	0.000143	1	0.023256	1	0.015385	1	2.75E-14	1	1
1	243736210	243736226	AKT3	1.03E-13	8.76E-12	0.125	1	1	0.033489	0.009509	1	0.026577	0.07497	1	1	3.83E-07	1	0.030185
2	99721804	99721820	TSGA10	1.03E-13	2.88E-15	1	0.023529	1	1	5.44E-05	1	1	0.000337	1	1	3E-22	0.065201	0.010939
3	67058329	67058357	KBTBD8	1.03E-13	1.64E-10	0.16996	0.009217	0.039216	1	1	1	0.015504	0.005714	0.015873	1	0.063768	0.001081	0.010462
17	39033672	39033684	KRT20	1.04E-13	1.98E-15	0.006266	1	0.153016	1	1	1	0.019608	0.014702	1	1	9.5E-22	1	0.013566
9	37887570	37887587	SLC25A51	1.05E-13	1.16E-06	0.000746	1	0.184689	0.12069	1	1	1	1	0.019231	1	8.53E-22	0.024691	0.316902
6	17779922	17779935	KIF13A	1.08E-13	6.89E-17	0.042254	1	1	0.023952	1	1	1	0.038275	1	1	1.69E-20	0.044944	0.003813
1	161201297	161201309	NR1I3	1.1E-13	6.55E-16	1	1	1	1	1	1	0.008772	1	1	1	2.29E-07	1	0.022216
3	142231062	142231081	ATR	1.1E-13	2.22E-08	0.074627	1	0.078652	0.08308	1	1	1	1	1	1	1.87E-16	1	0.001485
11	4150238	4150253	RRM1	1.12E-13	6.81E-18	1	0.034483	0.116179	1	0.012739	1	1	1	1	1	8.04E-10	0.1875	0.050573
X	131233588	131233600	FRMD7	1.12E-13	5.5E-11	1	1	0.133733	1	1	1	1	1	1	1	4.17E-23	0.043956	0.007158
20	60711773	60711796	PSMA7	1.13E-13	5.46E-18	0.058824	0.005882	1	1	1	1	1	1	1	1	2.52E-17	0.013699	0.078917
10	61612466	61612479	CCDC6	1.13E-13	2.19E-05	0.018197	0.019231	0.486865	1	1	1	1	1	1	0.116883	7.01E-05	1	0.128255
7	29699910	29699921	LOC646762	1.13E-13	6.47E-05	1	1	1	1	0.036585	1	1	1	1	1	3.91E-08	0.014493	1
X	20194479	20194490	RPS6KA3	1.14E-13	1.84E-11	0.09375	1	0.149588	1	1	1	1	1	0.055936	1	3.46E-18	0.032258	0.0116
2	98907089	98907103	VWA3B	1.14E-13	6.84E-07	0.035088	1	1	1	1	1	1	0.001832	1	1	9.98E-21	0.001207	0.003493
10	64022582	64022593	RTKN2	1.14E-13	1.26E-15	5.14E-06	1	0.004263	1	1	1	1	0.033333	0.014925	1	5.43E-17	0.000861	0.004149
13	100913132	100913161	PCCA	1.17E-13	2.56E-14	0.095238	1	0.067114	1	0.016064	1	1	0.002098	0.027778	1	0.036946	1	2.69E-05
2	101627343	101627360	RPL31,TBC1D8	1.19E-13	2.52E-15	0.018023	1	1	0.128857	1	1	1	1	1	1	9.79E-16	1	4.72E-07
15	45725103	45725138	C15orf48	1.2E-13	9.03E-27	0.096774	0.010101	1	1	1	1	0.012821	1	0.000699	1	9.32E-11	0.000926	1.02E-05
3	56807854	56807869	ARHGEF3	1.2E-13	2.36E-09	0.003229	1	0.061224	0.205859	1	1	1	0.093689	0.028571	1	1.09E-10	1	0.026204
6	62611334	62611348	KHDRBS2	1.2E-13	1.68E-23	0.015015	1	0.124167	1	1	1	1	0.008416	0.040816	1	1.07E-07	0.045455	0.003221
15	83805209	83805222	TM6SF1	1.22E-13	5.29E-15	0.000168	1	0.09853	1	1	1	0.015748	0.046358	0.035714	0.454545	4.76E-17	0.020833	0.004361
4	169190129	169190143	DDX60	1.23E-13	3.35E-09	0.372467	0.035088	0.105599	0.221326	1	1	1	1	1	0.352381	4.75E-14	1	0.000514
3	108276264	108276276	KIAA1524	1.24E-13	2.39E-09	0.055556	1	1	1	1	1	1	0.037313	1	1	1.32E-09	0.076923	0.004442
17	37119364	37119376	FBXO47	1.28E-13	3.44E-09	0.05	1	1	1	1	1	1	0.011905	1	1	2.78E-10	1	2.92E-05
6	102130410	102130422	GRIK2	1.29E-13	8.04E-15	2.35E-06	0.013889	1	1	0.110998	1	0.000164	0.048276	0.031746	1	8.03E-08	1	2.86E-07
1	185120927	185120940	TRMT1L	1.3E-13	1.58E-14	0.001357	1	1	0.023256	0.112046	1	1	1	1	1	1.58E-24	0.012821	1
11	47726034	47726053	AGBL2	1.31E-13	8.08E-14	0.026245	1	1	1	1	1	1	1	0.055936	1	1.67E-17	0.011628	0.002943
1	237024360	237024437	MTR	1.32E-13	0.000264	0.114286	0.024096	1	1	1	1	1	1	1	1	3.34E-07	1	0.137558
2	119739127	119739142	MARCO	1.34E-13	8.3E-17	0.002393	1	0.016279	0.047865	0.00035	1	1	0.029197	0.025	0.090909	1.04E-08	0.08037	0.00413
8	17100456	17100471	CNOT7	1.34E-13	6.77E-15	0.194225	1	0.19175	1	1	1	0.043161	0.004419	0.00605	1	4.7E-15	0.142634	0.044315
16	68155860	68155874	NFATC3	1.35E-13	1.32E-14	0.009524	0.076474	0.158891	0.000134	0.150567	1	1	0.05601	0.000816	1	1.88E-09	6.71E-05	0.668592
12	69090573	69090587	NUP107	1.37E-13	1.88E-15	0.111111	1	0.343147	0.004407	1	1	0.134142	0.001377	0.1875	1	1.51E-06	0.183508	0.195518
17	74286032	74286047	QRICH2	1.37E-13	1.46E-24	1	0.010526	1	1	0.002005	1	1	0.028423	0.333333	1	1.34E-11	1	6.11E-08
3	148901395	148901407	CP	1.4E-13	3.02E-13	0.039216	1	1	1	1	1	1	0.054045	0.028571	1	2.35E-07	1	0.081448
20	43623620	43623658	STK4	1.41E-13	1.04E-13	0.004662	1	1	1	1	0.005464	1	1	1	1	7.87E-10	1	0.000167
5	137013350	137013365	KLHL3	1.43E-13	7.36E-21	0.156667	1	0.083916	0.025424	1	1	1	1	1	1	1.21E-05	1	0.003834
X	46884357	46884368	JADE3	1.44E-13	8.89E-09	0.066667	1	0.164662	1	1	1	1	1	1	1	7.59E-09	0.026316	0.005609
9	123591493	123591522	PSMD5	1.44E-13	6.04E-20	0.054054	1	1	0.022472	1	1	1	1	0.022727	1	1.83E-07	1	0.04
11	102080325	102080341	YAP1	1.46E-13	9.75E-25	1	1	0.261538	0.013289	1	1	0.025723	1	1	1	2.09E-12	0.002299	0.105167
13	50306823	50306836	KPNA3	1.47E-13	3.81E-11	0.018293	1	0.501342	1	0.204556	0.043478	1	0.233316	1	0.333333	3.95E-12	1	0.67761
16	18593648	18593662	ABCC6P1	1.49E-13	0.000395	0.042254	1	1	1	1	1	1	0.066102	1	1	3.08E-09	1	0.002617
2	99788147	99788158	MITD1	1.49E-13	8.12E-24	0.013213	1	0.174641	1	0.022099	1	1	1	0.035088	1	1.38E-10	0.022727	1
7	94181585	94181596	CASD1	1.51E-13	9.15E-07	1	1	1	1	1	1	0.011905	1	1	1	2.57E-13	0.028571	1
19	10741681	10741697	SLC44A2	1.52E-13	5.62E-18	0.000568	1	0.261525	1	1	1	1	0.04404	0.078125	1	6.63E-13	0.006057	0.021038
15	25319287	25319304	SNORD116-10	1.55E-13	4.75E-27	0.227941	1	1	0.00404	1	1	0.032967	0.093689	1	1	0.017544	1	1
1	186647323	186647335	PTGS2	1.56E-13	3.85E-07	0.166317	1	1	1	1	1	1	1	1	1	1.65E-10	1	0.138908
2	162849944	162849956	DPP4	1.56E-13	1.21E-09	0.101215	1	0.238504	1	1	1	1	0.057143	1	0.154799	3E-13	1	3.61E-05
11	47755552	47755570	FNBP4	1.58E-13	1.47E-10	0.011614	1	0.127113	1	0.099318	1	1	1	1	1	7.35E-15	1	0.032524
17	30320860	30320882	SUZ12	1.61E-13	6.27E-14	0.005288	1	0.056355	1	0.001082	1	1	0.009141	0.014706	1	1.23E-06	0.044944	0.000789
1	33799658	33799669	PHC2	1.62E-13	1.25E-17	1	1	1	0.040917	1	1	1	1	1	1	4.87E-14	1	0.000523
5	140963623	140963634	DIAPH1	1.62E-13	0.000353	0.114286	1	0.192278	1	1	1	1	1	1	1	1.49E-09	1	0.133017
1	176913215	176913231	ASTN1	1.62E-13	3.69E-09	0.061497	1	0.071151	0.213433	1	1	1	1	1	0.111111	3.33E-06	0.176471	0.002894
17	28773060	28773074	CPD	1.67E-13	6.6E-12	0.000936	1	1	0.003411	1	1	1	1	0.066667	0.388889	1.24E-14	1	0.037374
12	107002558	107002573	RFX4	1.68E-13	3.72E-16	0.1	1	0.549337	1	0.088452	1	0.058596	0.016543	1	0.052632	1.33E-08	1	0.02933
5	139907750	139907762	ANKHD1,ANKHD1-EIF4EBP3	1.68E-13	7.17E-26	0.053333	1	0.063275	0.053467	1	1	1	0.025	1	1	2.01E-16	1	0.000341
17	11697015	11697027	DNAH9	1.76E-13	7.84E-18	0.001031	1	1	1	0.043854	1	0.008333	1	1	1	6.66E-11	1	1
2	32427092	32427104	SLC30A6	1.8E-13	7.14E-13	0.029851	0.00565	1	0.037234	1	0.00939	1	1	1	1	3.86E-13	0.004762	0.000513
11	58892376	58892387	FAM111B	1.82E-13	3.33E-15	0.000515	1	0.009324	0.029557	1	1	1	1	0.025	1	1.59E-06	1	0.032062
3	196134274	196134313	UBXN7	1.9E-13	8.4E-05	0.004869	1	1	1	1	1	1	1	1	1	7.19E-06	1	0.352422
2	70458050	70458062	TIA1	1.94E-13	1.97E-06	1	1	1	1	1	1	1	1	1	1	3.4E-13	0.048193	0.147687
19	33464253	33464266	C19orf40	1.94E-13	3.07E-21	0.042254	1	1	1	1	1	1	0.156882	1	1	5.6E-16	1	0.006529
14	55612006	55612020	LGALS3	1.96E-13	7.69E-11	0.018423	1	1	1	1	1	1	1	1	1	2.58E-08	0.000606	1
6	31692675	31692687	C6orf25	1.98E-13	1.38E-21	0.004152	0.017582	1	1	1	1	0.029126	1	1	1	2.1E-14	0.02439	0.008025
6	32166160	32166174	NOTCH4	2.04E-13	5.16E-25	0.035088	1	1	1	1	1	0.042857	1	0.00339	1	2.47E-12	1	1
10	120809259	120809271	EIF3A	2.06E-13	7.27E-21	1	1	1	0.082533	1	1	1	0.15667	0.020408	1	7.23E-14	1	0.003975
3	183857809	183857826	EIF2B5	2.07E-13	9.85E-06	1	1	1	1	1	1	1	1	1	1	1.63E-06	0.00056	0.222916
6	168355107	168355119	MLLT4	2.13E-13	5.59E-08	0.171047	1	1	1	1	1	0.030417	1	1	1	1.61E-08	0.038961	0.001828
19	33579248	33579262	GPATCH1	2.15E-13	1.54E-13	0.054545	1	1	1	0.029555	1	1	0.001043	1	1	5.03E-07	1	1
20	31294314	31294329	COMMD7	2.15E-13	1.85E-07	0.005199	1	1	1	0.013245	1	1	1	1	1	2.48E-10	1	0.01862
14	104219578	104219590	PPP1R13B	2.18E-13	7.65E-09	0.020115	1	0.179028	0.1833	0.076401	1	1	1	0.161905	1	1.05E-08	0.008197	0.268073
12	72094530	72094564	TMEM19	2.2E-13	0.003183	1	1	1	1	1	1	1	1	1	1	2.54E-07	1	0.178533
10	27037487	27037499	ABI1	2.21E-13	8.22E-10	0.002151	6.21E-05	0.111111	0.000388	1	1	1	0.038835	0.019608	1	6.46E-08	0.029851	0.000966
3	24270412	24270424	THRB	2.21E-13	4.5E-21	0.003322	0.005525	0.188525	0.021277	1	1	1	0.010517	0.101633	1	6.81E-12	0.042254	0.424288
16	57494395	57494422	COQ9	2.21E-13	3.42E-06	0.041096	1	1	1	1	1	0.015152	1	1	1	4.02E-09	1	1
3	47129781	47129808	SETD2	2.23E-13	3.08E-18	0.008163	1	1	0.030768	1	1	1	0.000537	1	1	2.22E-08	1	1
6	15593319	15593334	DTNBP1	2.33E-13	3.27E-05	0.010232	1	1	1	1	1	1	1	0.012048	1	2.26E-15	0.068164	0.042678
8	59518439	59518456	NSMAF	2.34E-13	5.73E-05	1	1	1	1	1	1	1	1	1	1	2.19E-23	0.003381	1
5	122714134	122714153	CEP120	2.41E-13	0.000787	0.000699	1	1	0.076923	1	1	0.027027	1	1	0.052632	1.45E-14	0.084619	0.275829
19	53905129	53905144	ZNF765	2.42E-13	5.65E-15	0.395604	1	0.233048	0.001732	0.093906	0.059603	0.076897	0.199357	0.076923	1	0.003953	0.027027	0.105421
16	7743418	7743437	RBFOX1	2.42E-13	1.48E-15	0.083333	1	0.049724	0.054217	1	1	0.011561	1	1	1	2.08E-13	1	0.205033
2	86393770	86393811	IMMT	2.44E-13	8.14E-07	0.085106	1	1	0.02381	1	1	1	1	1	1	1.29E-08	0.045455	0.012775
4	79173515	79173527	FRAS1	2.44E-13	7.54E-18	0.252874	1	1	1	1	1	1	1	1	1	3.85E-05	1	0.304008
4	84519775	84519790	AGPAT9	2.48E-13	3.91E-20	0.001478	1	0.297553	0.21418	0.006844	1	0.045802	1	0.171123	0.047386	2.54E-26	0.132086	0.082006
7	138951165	138951177	UBN2	2.51E-13	3.58E-16	0.004862	0.00885	1	0.01105	0.028168	1	1	0.044444	1	1	1.12E-18	0.031746	1
6	152765726	152765738	SYNE1	2.54E-13	1.15E-05	0.010274	1	1	1	1	1	1	0.015152	0.036364	1	2.13E-09	1	0.294317
1	235621851	235621865	B3GALNT2	2.59E-13	4.49E-10	0.18136	1	0.146577	1	0.003237	0.00495	1	0.036232	0.029851	1	1.54E-09	1	0.060606
8	72946622	72946636	LOC100132891	2.61E-13	9.73E-14	0.071429	1	1	1	1	1	1	1	1	0.469697	1.61E-15	1	0.003999
7	21646233	21646254	DNAH11	2.66E-13	0.007937	0.229211	1	1	1	1	1	1	1	1	1	1.33E-13	1	0.000126
2	111721142	111721186	ACOXL	2.69E-13	0.023153	0.079758	1	1	1	1	1	1	1	1	0.166667	2.62E-07	1	0.000332
22	21147581	21147594	PI4KA	2.7E-13	3.32E-14	1	1	1	1	0.066372	1	1	1	1	1	1.94E-11	1	0.019851
X	1464126	1464139	IL3RA	2.72E-13	1.17E-15	0.022569	0.025907	1	1	0.018139	1	0.043011	0.000265	0.007389	0.087719	1.11E-10	0.044963	8.42E-05
12	110924566	110924578	FAM216A	2.74E-13	2.21E-13	1	1	1	1	0.022727	0.005587	1	0.001923	1	1	2.19E-09	0.083333	0.052288
17	44833088	44833123	NSF	2.75E-13	0.009724	0.006988	1	0.056075	1	1	1	0.020979	1	0.029851	1	1.25E-15	1	8.45E-06
11	18231788	18231799	LOC494141	2.76E-13	4.92E-19	0.069767	1	1	1	0.02	1	1	1	1	1	1.19E-14	0.000287	0.027111
3	12571420	12571434	TSEN2	2.8E-13	2.92E-14	0.000999	1	0.070401	1	1	1	1	0.048774	0.04918	1	1.5E-18	0.050949	0.022613
3	179083024	179083036	MFN1	2.8E-13	1.58E-15	0.00013	0.022535	0.057692	1	1	1	1	0.004451	1	1	4.52E-14	0.051282	0.10825
1	24082269	24082286	TCEB3	2.82E-13	7.98E-13	1	0.027778	1	1	1	1	0.024169	1	1	1	3.72E-16	1	1
1	236902532	236902560	ACTN2	2.83E-13	1.73E-18	0.205736	1	0.199357	0.070359	1	1	0.022727	0.00624	0.103383	1	4.05E-10	0.046154	0.134452
14	31424778	31424804	STRN3	2.86E-13	8.08E-12	0.136185	1	1	1	1	1	1	0.078095	1	0.25	2.16E-10	0.01087	0.004712
15	52239617	52239629	LEO1	3.03E-13	8.28E-11	0.014085	1	1	1	0.011952	1	0.015038	1	1	1	1.81E-21	1	0.00046
10	63977011	63977030	RTKN2	3.03E-13	1.63E-18	0.015873	1	0.116391	6.18E-05	0.0826	1	1	0.060544	1	1	0.000105	1	0.008144
5	10397473	10397485	MARCH6	3.08E-13	2.49E-19	0.017501	0.029519	1	1	1	1	1	0.004049	1	1	3.95E-18	0.028986	0.060823
9	7128277	7128289	KDM4C	3.16E-13	2.6E-10	0.000546	1	1	1	1	1	1	1	1	1	9.68E-11	1	0.042553
7	36671720	36671738	AOAH	3.2E-13	2.9E-06	0.043478	1	1	0.056604	1	1	0.029739	1	1	1	7.46E-10	1	0.19931
6	24714681	24714694	C6orf62	3.24E-13	1.79E-10	1	1	1	0.311396	1	1	0.043161	1	1	0.214286	1.33E-05	1	0.248122
5	112927888	112927900	YTHDC2	3.38E-13	3.24E-08	0.158163	1	0.06623	0.17232	1	1	1	1	1	1	6.1E-10	1	0.535494
16	9186735	9186764	C16orf72	3.41E-13	0.000733	1	1	1	1	1	1	1	0.017544	0.015385	1	1.49E-16	1	0.115283
X	154009644	154009656	MPP1	3.45E-13	9.49E-10	0.06383	1	0.286299	0.074976	0.00813	1	1	1	0.032258	1	8.18E-14	1	0.045514
6	142691950	142691968	GPR126	3.46E-13	4.79E-10	6.17E-05	1	0.069231	1	1	1	1	1	1	1	4.39E-12	1	0.047113
2	212495336	212495354	ERBB4	3.47E-13	4.21E-15	0.00936	1	0.111801	0.034682	1	1	1	1	1	0.25	1.65E-05	1	3.22E-06
20	48494613	48494625	SLC9A8	3.52E-13	7.21E-12	0.02439	1	1	1	0.025773	1	0.012048	0.019563	0.031746	1	9.53E-14	0.026667	0.135291
17	43587579	43587591	LRRC37A4P	3.56E-13	5.33E-20	0.000887	1	1	1	1	1	1	1	1	0.2	6.38E-09	0.027397	0.23823
11	19197349	19197361	ZDHHC13	3.59E-13	3.24E-10	1	0.027026	1	1	1	1	0.058467	1	0.017857	1	0.004375	1	0.312902
1	25571794	25571805	RSRP1	3.63E-13	2.27E-13	1	1	1	1	1	1	1	1	0.02	1	8.34E-10	0.046154	9.11E-05
1	154178185	154178198	C1orf189	3.69E-13	3.1E-12	1	1	1	1	0.011494	1	1	1	1	1	4.57E-07	1	0.000345

2	24345196	24345211	FAM228B,PFN4	3.77E-13	3E-09	0.213675	1	1	1	0.035712	1	0.029519	1	1	1	0.000447	1	9.07E-05
16	56535193	56535208	BBS2	3.95E-13	2.21E-16	0.000709	1	0.095184	1	1	1	1	3.14E-05	0.033333	1	3.17E-05	1	1
14	104040415	104040450	APOPT1	3.96E-13	1.87E-05	0.003246	1	1	1	1	1	0.011628	1	1	1	4.4E-21	1	0.009016
7	16505054	16505066	SOSTDC1	4.06E-13	4.25E-05	1	1	1	1	1	1	1	0.414176	0.06383	0.133333	1.77E-05	1	0.141189
2	86683539	86683575	KDM3A	4.08E-13	0.044118	0.0002	1	1	1	1	1	1	1	1	1	3.73E-24	0.063143	0.050671
6	137193301	137193332	PEX7	4.08E-13	4.4E-11	0.057143	1	0.079065	1	1	0.005495	1	0.000138	1	1	6.08E-06	1	0.001776
8	121293133	121293158	COL14A1	4.09E-13	3.99E-08	0.028986	1	0.313659	1	1	1	1	1	1	0.026316	3.47E-11	0.074976	1
9	85926893	85926921	FRMD3	4.09E-13	8.78E-09	0.057495	1	1	1	1	1	1	1	0.062004	1	1.67E-09	0.074976	0.28356
15	43170667	43170727	TTBK2	4.12E-13	0.047113	8.35E-05	1	0.546331	0.104261	1	1	1	1	1	1	2.54E-08	1	0.007691
1	155583131	155583149	MSTO2P	4.18E-13	1.92E-08	0.022569	1	1	1	1	1	1	1	0.001442	1	1.91E-12	0.047059	0.053908
21	10916534	10916548	TPTE	4.21E-13	0.001516	0.193947	1	1	1	1	1	0.029586	1	0.078919	0.315789	8.02E-09	0.01638	0.147831
14	103449863	103449880	CDC42BPB	4.22E-13	2.05E-22	1	1	0.20154	0.067067	1	1	0.013514	0.078621	1	1	0.000335	1	0.005938
11	112832276	112832287	LOC101928847	4.45E-13	1.7E-10	1	1	1	1	0.03125	1	0.019048	1	0.088195	0.176471	2.84E-15	0.073148	4.5E-05
3	148902929	148902942	CP	4.53E-13	5.49E-16	0.193103	1	1	1	1	1	0.064268	0.12064	1	1	8.91E-08	0.027397	0.009323
5	137513369	137513382	BRD8	4.53E-13	1.63E-14	0.086957	1	1	0.242609	1	0.026178	0.07244	0.22998	1	1	4.43E-09	1	0.000418
3	60522571	60522583	FHIT	4.59E-13	1.5E-08	0.058824	1	1	1	0.019417	1	1	1	0.080782	1	0.00035	1	0.002854
4	184174896	184174908	WWC2	4.66E-13	5.03E-08	0.03125	1	1	1	1	1	1	1	0.020408	1	9.59E-11	0.054795	0.383685
12	106500153	106500175	NUAK1	4.69E-13	1.14E-06	0.171717	1	0.180637	1	0.085062	1	0.034041	0.036036	1	1	4.68E-10	1	0.448336
X	32472757	32472777	DMD	4.71E-13	2.58E-10	0.582458	1	0.229682	0.07749	1	1	1	0.002759	0.111111	1	3.73E-11	1	0.032329
1	98011812	98011842	DPYD	4.76E-13	4.21E-17	0.002096	1	1	0.009376	0.039116	1	1	1	0.03125	1	2.74E-13	0.047619	0.000662
10	105990647	105990660	CFAP43	4.87E-13	8.17E-15	1	1	1	0.008621	1	1	1	0.099318	1	1	6.24E-05	1	0.016557
12	28459652	28459664	CCDC91	4.99E-13	7.85E-14	0.08599	1	1	1	0.000143	1	1	0.086494	1	1	2.33E-05	1	6.23E-05
4	123128660	123128687	KIAA1109	5.04E-13	2.02E-09	0.015495	1	1	1	1	1	1	1	1	1	7.79E-10	1	0.065338
11	125488247	125488261	STT3A	5.07E-13	6.99E-28	1	1	0.031746	0.041916	1	1	1	1	0.010989	1	2.03E-09	1	0.049808
1	145456732	145456747	NBPF10,NBPF20,POLR3GL	5.13E-13	9.85E-28	0.003049	0.02564	1	1	1	0.003953	0.057336	1	1	1	2.41E-17	1	0.046066
16	58585178	58585191	CNOT1	5.21E-13	2.03E-15	1	0.011905	1	0.020134	0.042212	1	1	1.03E-07	1	1	1.35E-06	0.030303	0.024125
X	100375865	100375883	CENPI	5.22E-13	1.93E-06	0.046512	1	1	1	1	1	1	1	1	1	0.001627	0.039798	0.02442
8	100287517	100287536	VPS13B	5.24E-13	3.25E-20	0.024656	0.003922	0.000388	0.086371	1	1	1	1	1	1	1.42E-15	1	0.03725
15	83677270	83677285	C15orf40	5.28E-13	1.84E-14	1	1	0.192278	1	0.038294	1	1	0.143603	1	1	0.000133	0.017544	0.000961
21	35094849	35094878	ITSN1	5.31E-13	2.9E-08	0.006266	1	1	1	1	1	0.006579	0.022222	1	1	2.99E-21	0.027778	0.022019
13	43872451	43872468	ENOX1	5.34E-13	5.31E-09	0.00046	1	1	1	1	1	0.076433	1	1	1	2.62E-20	1	0.003109
19	50911947	50911960	POLD1	5.41E-13	4.11E-31	0.1	1	1	0.00014	1	1	0.05	1	0.026316	0.25	5.71E-13	1	1
6	109319962	109319991	SESN1	5.44E-13	2.87E-22	0.005845	0.026086	1	0.053923	0.015094	1	1	1	1	1	5.59E-14	1	1
5	89791609	89791620	POLR3G	5.56E-13	3.58E-09	0.0114	1	1	1	1	1	1	1	1	1	6.85E-13	0.05	0.058621
3	160144007	160144039	SMC4	5.56E-13	3.82E-23	0.000264	1	1	0.066667	0.042857	1	1	1	0.000649	1	1.95E-20	1.48E-05	0.058394
7	104309164	104309177	LHFPL3	5.57E-13	1.6E-08	0.027223	1	0.001077	1	1	1	1	1	1	0.333333	8.3E-06	0.018868	0.105916
1	35826959	35826972	ZMYM4	5.68E-13	7.4E-06	1	1	1	1	1	1	1	1	0.015873	1	1.44E-08	0.0375	0.048593
6	158294098	158294121	SNX9	5.77E-13	1.16E-06	0.088235	1	1	1	1	1	1	1	1	1	8.89E-06	0.031915	0.023709
13	43491778	43491796	EPSTI1	5.86E-13	9.98E-20	0.000615	1	0.043316	1	0.057957	1	1	1	1	1	7.62E-22	1	0.0188
16	46652286	46652305	SHCBP1	6.03E-13	4.62E-07	0.000191	1	1	1	1	1	1	1	1	1	2.28E-09	1	0.122305
15	64687559	64687585	TRIP4	6.17E-13	9.97E-08	1	1	1	0.041375	1	1	1	1	1	1	1.34E-07	1	0.002278
1	204494748	204494783	MDM4	6.18E-13	1.26E-07	0.002105	0.00995	1	1	1	1	1	1	0.037736	1	2.22E-13	0.040541	1
12	30822226	30822240	IPO8	6.25E-13	7.33E-10	0.017544	1	1	1	1	1	0.016529	1	1	1	0.000166	1	0.000587
13	45556282	45556303	NUFIP1	6.39E-13	2.24E-07	0.08	1	1	1	1	1	0.01	1	1	1	4.18E-11	0.046512	1
14	50050396	50050408	RPS29	6.64E-13	1.83E-18	1	1	1	1	1	1	1	0.020833	0.095188	1	1.03E-12	0.035714	0.000165
12	110720351	110720363	ATP2A2	6.8E-13	3.09E-20	1	1	1	0.079702	0.004598	1	1	1.34E-08	1	1	2.01E-15	1	0.072414
X	11793084	11793105	MSL3	6.88E-13	1.67E-13	0.000816	1	1	0.023622	1	1	1	1	0.015873	1	1.43E-08	0.092437	0.142408
1	212142054	212142069	INTS7	7.01E-13	6.23E-12	0.107071	1	1	1	1	1	1	1	1	0.168831	3.42E-14	1	0.01165
2	203384776	203384799	BMPR2	7.11E-13	1.89E-10	0.014286	1	1	0.009346	1	1	1	0.061762	0.083333	0.181818	1.27E-13	1	0.531626
12	14599896	14599919	ATF7IP	7.18E-13	4.27E-17	0.007212	1	0.107075	0.007308	1	1	1	0.044238	0.030769	1	4.23E-15	0.035714	0.005845
6	49423956	49423968	MUT	7.19E-13	5.14E-17	0.00266	1	1	0.068942	1	1	1	0.026549	1	1	2.43E-09	1	0.021569
1	1920434	1920449	CFAP74	7.3E-13	1.71E-13	1	0.018182	1	1	1	1	1	1	0.001317	1	2.56E-07	0.115272	0.059511
12	102131090	102131108	SYCP3	7.34E-13	3.95E-24	0.013213	0.04329	1	1	0.115362	1	0.065772	0.075441	0.3	1	1.11E-17	1	0.201942
14	76420881	76420893	TTLL5	7.43E-13	1.1E-12	0.050568	1	1	0.049992	0.025531	1	1	1	1	1	0.001593	0.102199	1
7	116556086	116556111	CAPZA2	7.49E-13	4.02E-11	0.001185	1	1	1	1	1	1	1	1	1	4.16E-16	0.002896	1
11	9192336	9192365	DENND5A	7.56E-13	6.15E-11	0.021719	1	1	0.104404	1	1	1	1	1	1	7.4E-06	1	0.000756
12	95498747	95498778	FGD6	7.72E-13	2.2E-12	0.172078	1	1	1	1	1	0.019355	1	1	1	7.14E-16	1	0.00542
7	6485740	6485753	DAGLB	7.79E-13	1.18E-18	1	0.009709	1	1	1	1	1	0.120104	1	1	7.18E-06	1	0.030487
13	77818089	77818117	MYCBP2	7.93E-13	0.008358	0.072464	1	1	1	1	1	1	1	1	1	1.23E-18	1	2.73E-05
6	30557379	30557397	ABCF1	8.14E-13	3.14E-09	0.284091	0.044776	1	1	1	1	0.064241	1	1	1	3.29E-10	0.166667	0.005093
10	98336613	98336626	TM9SF3	8.17E-13	1.67E-24	0.193103	1	1	0.132264	1	1	1	0.055546	1	1	1.49E-10	0.059249	0.017286
16	21559162	21559174	SLC7A5P2(dist=27397),LOC101927814(dist=41845)	8.21E-13	2.63E-07	1	1	1	1	1	1	1	1	0.014925	1	9.03E-13	0.000861	0.060345
16	19451273	19451297	TMC5	8.74E-13	1.38E-18	0.081081	1	1	1	0.031681	1	1	1	1	1	6.07E-06	1	0.082503
15	59009930	59009941	ADAM10	8.88E-13	1.62E-11	0.046154	0.007874	1	1	1	1	1	1	1	1	3.08E-15	0.047619	1
15	55789793	55789806	DYX1C1-CCPG1	8.96E-13	3.94E-20	0.025	1	1	1	0.050271	0.015625	1	0.098834	1	1	4.76E-06	0.142857	0.021872
2	86348737	86348749	PTCD3	9.37E-13	3.74E-09	1	1	0.069565	0.011561	1	1	1	0.073684	0.028571	1	2.09E-08	1	1
21	30435646	30435668	CCT8	9.45E-13	5.32E-27	0.117551	0.010417	1	0.022059	1	1	1	0.059406	1	1	1.01E-14	1	1.32E-06
12	89853387	89853405	POC1B	9.49E-13	1.35E-13	4.11E-06	1	1	0.065201	1	1	1	1	0.000439	1	5.25E-30	0.00297	0.006665
13	58299427	58299446	PCDH17	9.52E-13	4.59E-21	0.010753	1	0.494003	0.132172	1	1	1	0.242625	0.055556	1	2.05E-10	0.008396	0.552237
6	51503597	51503616	PKHD1	9.64E-13	3.71E-13	0.00752	1	0.065157	0.098288	1	1	1	1	1	1	1.24E-17	0.017391	0.082468
X	122616951	122616978	GRIA3	9.96E-13	1.72E-06	0.052632	1	0.189587	1	1	1	1	1	1	1	5.1E-05	1	0.04698
2	159035618	159035630	CCDC148-AS1	1.01E-12	7.21E-09	1	1	1	1	1	1	0.019417	1	1	1	0.000113	0.025974	0.025191
2	201950159	201950178	NDUFB3	1.01E-12	2.83E-05	0.003509	1	1	1	0.032718	0.008264	1	1	0.017241	0.333333	1.48E-11	1	0.01252
X	12516777	12516790	FRMPD4	1.04E-12	5.53E-16	1	0.021333	1	1	1	0.004444	1	1	1	1	2.17E-08	1	0.212416
1	185834851	185834865	HMCN1	1.08E-12	4.89E-06	0.115385	1	0.240134	1	1	1	1	0.011865	0.000481	1	8.68E-05	0.103371	0.055556
1	247264726	247264738	ZNF669	1.09E-12	3.92E-10	1	1	1	1	0.055889	1	1	0.022222	1	1	0.011293	1	1
1	231396485	231396509	GNPAT	1.11E-12	3.14E-24	0.008547	1	1	1	0.022408	1	0.014286	1	0.025641	1	4.76E-07	0.028986	0.055118
12	59307848	59307866	LRIG3	1.15E-12	2.04E-15	1	0.008547	1	1	0.058579	1	1	1	1	0.05	2.42E-05	1	0.007042
3	132226317	132226330	DNAJC13	1.21E-12	1.93E-09	0.087879	1	1	0.023256	0.041022	1	1	1	0.043478	1	2.34E-08	1	0.111883
1	161829973	161829987	ATF6	1.21E-12	1.02E-06	0.006061	6.64E-05	1	1	1	1	0.016949	0.103365	1	0.285714	1.41E-12	0.00085	0.030311
15	69714622	69714658	KIF23	1.22E-12	2.14E-18	0.129944	1	1	1	1	1	1	1	0.000512	1	1.26E-11	1	0.174415
9	99233431	99233444	HABP4	1.22E-12	0.022122	1	1	0.439542	0.254969	1	1	1	1	1	1	3.73E-07	0.071408	0.05541
7	5567254	5567271	ACTB	1.24E-12	7.41E-11	1	1	0.113821	0.00565	1	1	1	1	0.026667	1	5.46E-14	1	0.325121
18	14188122	14188143	ANKRD20A5P	1.25E-12	6.93E-11	1	1	0.406213	1	0.038551	1	1	0.12377	0.074074	1	7.29E-07	1	0.240414
12	56492195	56492212	ERBB3	1.26E-12	3.26E-08	0.003333	1	0.067961	1	1	1	1	1	0.018868	1	8.39E-08	1	0.017483
17	5013190	5013203	ZNF232	1.26E-12	2.14E-08	1	1	1	1	1	1	1	1	0.25	1	1.16E-08	1	0.00568
15	59399501	59399518	CCNB2	1.27E-12	7.85E-11	0.068966	1	0.306585	1	1	1	1	1	0.016667	1	2.09E-13	1	0.033976
6	76618182	76618195	MYO6	1.27E-12	2.36E-16	0.065027	0.010526	1	0.048773	1	1	1	0.002244	1	1	1.6E-13	0.000261	0.041558
16	9010826	9010844	USP7	1.28E-12	4.6E-07	3.16E-06	1	1	1	1	1	1	0.090853	1	1	7.6E-23	1	0.007335
12	108140266	108140281	LOC101929162	1.3E-12	1.6E-09	1	0.020408	0.140784	1	1	1	0.014286	0.034884	1	0.0625	1.28E-05	0.00196	5.1E-05
7	144245535	144245555	TPK1	1.31E-12	2.5E-09	0.009251	1	1	0.227201	1	1	1	1	1	1	5.44E-07	0.073148	0.004867
2	111397237	111397251	BUB1	1.31E-12	2.52E-09	1	0.120192	0.152262	1	0.011114	1	0.061335	0.057336	1	1	3.87E-07	0.041667	0.017024
12	107360876	107360887	TMEM263	1.32E-12	1.12E-18	0.037736	1	1	0.000628	1	1	1	1	0.027778	1	3.16E-12	1	1
8	104054513	104054532	ATP6V1C1	1.33E-12	1.8E-12	0.032258	0.004484	0.055556	1	1	1	1	1	1	1	6.61E-13	1	0.11267
12	51752085	51752103	GALNT6	1.33E-12	2.57E-23	0.000165	1	1	1	1	1	0.037034	1	0.001357	1	7.91E-12	0.058241	0.008454
21	33068865	33068877	SCAF4	1.33E-12	5.51E-13	0.054545	0.005263	0.079334	0.039773	1	1	0.021429	0.056911	0.028169	1	3.36E-06	0.002687	0.00036
20	8665502	8665518	PLCB1	1.33E-12	2.36E-17	0.14976	1	1	1	1	1	1	1	0.090909	1	7.52E-23	1	0.001024
2	179478746	179478757	MIR548N,TTN-AS1	1.33E-12	3.06E-14	1	1	0.148148	0.000626	1	1	1	0.006171	0.06298	1	6.01E-18	0.037037	0.000121
X	138698652	138698665	MCF2	1.33E-12	1.33E-15	0.152157	1	0.118534	1	1	1	1	1	0.09375	0.4	4.72E-08	1	0.000944
3	65456181	65456211	MAGI1	1.35E-12	4.24E-08	1	0.009756	1	1	1	1	0.020408	1	0.035714	1	2.08E-08	1	0.004016
1	28374836	28374848	EYA3	1.39E-12	0.000236	0.11103	1	1	1	1	1	1	1	0.063987	0.259259	2.12E-14	0.004236	1
3	65439050	65439067	MAGI1	1.41E-12	2.68E-18	0.004762	1	1	1	1	1	1	1	0.020408	1	1.04E-09	0.065027	0.00804
1	168200730	168200743	SFT2D2	1.45E-12	8.33E-14	0.004354	1	0.091837	1	1	0.013514	1	0.013088	1	0.315789	1.04E-09	0.092262	0.001969
3	67559216	67559229	SUCLG2	1.48E-12	1.82E-15	0.009307	1	1	1	1	1	1	1	0.000466	1	2.13E-10	1	0.023024
5	112111302	112111323	APC	1.54E-12	9.13E-15	0.070423	1	1	1	1	1	1	1	1	1	6.45E-07	1	0.153369
17	1558921	1558934	PRPF8	1.54E-12	3.54E-10	0.027451	0.011905	1	1	1	1	1	1	0.0625	1	2.79E-13	1	0.004591
3	191097928	191097944	CCDC50	1.54E-12	3.8E-09	0.018956	1	0.289411	0.28369	1	1	0.001355	1	1	0.352381	7.25E-15	0.000296	0.262523
3	15471528	15471540	EAF1	1.55E-12	0.001088	1	1	0.297553	1	1	1	0.209252	0.288133	1	1	0.021741	1	0.077463
11	32610726	32610740	EIF3M	1.59E-12	7.84E-20	0.00404	0.000106	1	1	1	1	0.02	0.035088	0.066667	1	1.94E-09	1	3.01E-05
6	8417604	8417616	SLC35B3	1.68E-12	2.9E-12	1	1	1	1	1	1	0.016529	1	1	1	1.59E-14	1	0.000155
7	40127710	40127722	CDK13	1.69E-12	3.51E-11	0.111801	1	0.165158	0.033732	1	1	1	0.220566	1	0.315789	1.25E-08	1	1
3	33893929	33893949	PDCD6IP	1.7E-12	0.000714	1.65E-05	1	1	1	1	1	1	1	0.046779	0.275862	5.06E-23	1	0.000423
11	58381663	58381676	ZFP91-CNTF	1.72E-12	3.21E-10	1	1	1	0.04023	1	1	1	1	0.000784	1	7.03E-08	1	0.022947
14	39788501	39788513	CTAGE5	1.72E-12	5.87E-07	0.033898	1	1	1	1	1	1	0.035088	0.015625	1	6.12E-09	1	1
9	98009613	98009626	FANCC	1.75E-12	1.36E-16	4.21E-05	0.011173	1	0.048041	0.013889	1	1	4.88E-05	0.02381	1	7.65E-08	0.022222	0.000232
5	162945387	162945400	MAT2B	1.77E-12	1.52E-12	1	1	1	0.007188	0.081384	1	0.023622	0.102121	0.065574	0.047619	2.79E-08	0.076897	0.230494
8	95547005	95547018	KIAA1429	1.78E-12	2.7E-16	0.005984	1	1	1	0.047865	1	1	0.011114	1	0.222222	3.03E-12	1	0.00971
2	45806939	45806979	SRBD1	1.8E-12	9.7E-17	0.000474	1	1	0.021645	1	1	0.012048	1	1	1	3.61E-11	1	1
3	44846477	44846493	KIF15	1.85E-12	2.3E-12	0.002414	1	0.061538	1	1	1	1	1	0.027027	1	2.3E-27	1	0.002214
8	67753176	67753206	C8orf44-SGK3,SGK3	1.86E-12	0.012031	0.076923	1	1	1	1	1	0.030187	1	1	1	8.83E-15	1	0.001058
14	73535095	73535114	RBM25	1.88E-12	1.94E-09	1	1	0.128477	1	1	1	1	1	1	1	4.36E-11	1	0.377974
16	20749284	20749296	THUMPD1	1.89E-12	4.67E-18	0.000181	0.011236	1	0.059028	0.021739	1	1	0.001077	1	1	1.26E-13	1	1
2	132241502	132241519	RNU6-81P	1.91E-12	9.46E-14	0.161905	1	1	0.148264	1	1	1	1	0.032258	0.230769	2.68E-13	0.098834	1
16	15133783	15133795	NTAN1,PDXDC1	1.95E-12	2.61E-19	0.473504	0.001559	0.345605	0.129695	0.010033	0.023697	1	1.31E-06	0.028571	1	0.000703	1	0.316986
7	81641570	81641584	LOC101927356	1.97E-12	4.03E-13	0.012256	1	0.24441	0.142616	0.003075	0.021552	1	1	1	0.514706	5.17E-15	1	0.020608
10	49632498	49632510	MAPK8	1.98E-12	1.07E-07	1	0.012121	0.082192	0.02381	1	1	1	0.031915	1	1	2.97E-05	1	0.28094
3	136618710	136618721	NCK1	1.98E-12	7.48E-15	0.059935	0.040502	0.066667	0.049528	1	1	1	0.073708	0.130435	1	3.42E-12	1	0.158524
6	138192324	138192336	TNFAIP3	2.01E-12	3.48E-18	0.002912	1	1	1	1	1	0.014599	1	1	1	1.14E-10	1	0.000185
1	196709736	196709747	CFH	2.07E-12	6.49E-17	0.001186	1	0.193103	1	1	1	0.028169	1	1	1	8.14E-12	1	0.000964
2	175246545	175246557	CIR1	2.08E-12	1.14E-33	0.002775	0.005952	0.076923	0.000193	0.000557	1	1	0.000196	1	1	1.3E-17	0.018868	0.019421
8	141754888	141754905	PTK2	2.21E-12	1.91E-11	0.000161	1	1	1	1	1	1	1	1	1	2.72E-14	1	0.005249
15	33218472	33218487	FMN1	2.26E-12	0.00202	0.000154	1	1	1	1	0.2	1	1	0.028169	0.190476	1.7E-17	0.011765	0.020397
X	107918007	107918043	COL4A5	2.26E-12	0.000274	0.01393	1	0.084615	1	1	1	1	1	1	1	3.52E-22	1	0.002244
6	149842148	149842176	PPIL4	2.29E-12	2.66E-16	0.011402	1	1	1	1	1	0.015748	1	1	1	1.16E-12	1	8.62E-06
2	219614190	219614206	TTLL4	2.3E-12	2.32E-08	0.008547	1	1	0.069307	1	1	1	1	1	1	1.02E-06	0.000802	0.034091
6	51930886	51930901	PKHD1	2.38E-12	1.09E-10	0.071429	1	0.314227	1	0.111111	1	0.015748	0.114176	1	0.014286	2.22E-09	0.210521	0.214895
15	65874368	65874380	VWA9	2.4E-12	0.000166	1	1	1	1	1	1	0.028037	1	0.022222	0.154799	3.89E-11	1	4.38E-08
1	197898395	197898415	LHX9	2.47E-12	2.87E-15	0.010315	1	1	0.033816	0.016129	1	0.025889	1	1	1	6.85E-06	0.001536	1
16	71690657	71690671	PHLPP2	2.49E-12	1.63E-05	1	1	1	1	1	1	1	1	1	1	1.5E-06	1	0.125321
X	24084241	24084254	EIF2S3	2.55E-12	7.88E-13	0.065217	1	0.226891	0.005821	0.000236	1	0.151427	0.000657	0.02439	0.266667	5.87E-21	1	6.73E-05
13	26967446	26967495	CDK8	2.57E-12	7.17E-16	1	1	1	1	0.013393	1	1	0.02994	1	1	3.08E-05	1	0.126016

10	94366347	94366370	KIF11	2.61E-12	4.98E-18	0.008471	0.003623	1	0.008523	1	1	1	1	1	1	7.13E-16	1	5.96E-05
15	51017381	51017393	SPPL2A	2.61E-12	1.64E-24	0.016129	1	1	0.028249	1	1	1	1	0.004354	1	1.43E-19	1	6.31E-06
1	36479764	36479778	AGO3	2.61E-12	1.29E-11	0.057692	1	1	1	1	1	0.008065	1	1	1	1.58E-10	1	0.013036
1	94643143	94643154	ARHGAP29	2.67E-12	3.91E-17	0.058824	1	1	1	1	1	1	0.012274	0.022727	1	2.82E-08	1	0.020246
6	165809963	165809979	PDE10A	2.67E-12	3.17E-33	0.000324	1	0.086601	0.027174	1	1	0.026786	1	1	1	3.4E-08	1	0.001191
10	17110577	17110588	CUBN	2.69E-12	4.66E-34	0.058824	1	1	0.039896	0.001442	0.003906	1	1	0.029412	1	1.12E-15	1	0.004239
8	101253085	101253108	SPAG1	2.72E-12	1.11E-09	0.001242	1	0.094287	0.036364	1	1	0.021739	1	1	1	8.54E-12	1	0.009848
12	123103115	123103129	KNTC1	2.81E-12	1.01E-09	0.03008	1	1	1	1	1	0.015267	0.009346	1	1	2.09E-09	1	3.33E-05
15	34380216	34380230	EMC7	2.86E-12	0.000179	1	1	1	1	1	1	0.031619	0.031579	1	1	3.21E-22	1	0.045003
1	173921292	173921316	RC3H1	2.86E-12	0.000616	0.011816	1	1	0.017857	1	1	1	1	1	1	0.000289	1	0.057441
2	87110591	87110608	ANAPC1P1	2.86E-12	2.19E-06	0.130435	1	1	1	1	1	1	1	1	1	2.51E-12	1	0.198554
4	100137292	100137316	ADH6	2.86E-12	2.16E-06	0.085106	0.036697	0.271854	1	0.057792	1	0.062483	1	1	1	4.01E-15	1	0.037908
2	39240584	39240596	SOS1	2.89E-12	7.77E-29	1	1	0.038168	0.040462	0.000316	1	1	0.002579	0.000726	1	1.12E-19	0.024691	0.003147
6	131948469	131948501	MED23	2.94E-12	2.27E-08	0.006036	1	0.059829	1	1	1	1	1	0.028986	1	1.6E-10	0.001316	0.000431
6	42625963	42625974	UBR2	2.96E-12	1.03E-18	0.055556	1	1	1	1	1	1	0.017422	1	1	9.5E-09	0.034483	0.065693
8	131859768	131859803	ADCY8	2.97E-12	2.5E-05	0.002976	1	1	1	1	1	1	1	0.011364	1	7.36E-12	1	0.00011
2	121047044	121047056	RALB	2.98E-12	3.26E-21	1	1	1	1	0.022026	1	1	1	1	1	1.1E-07	1	0.003662
16	74920075	74920089	WDR59	3.04E-12	4.36E-08	0.025997	1	1	1	1	1	1	0.000113	1	1	2.04E-07	1	5.49E-08
17	28811834	28811848	GOSR1	3.04E-12	2.55E-14	0.003702	1	0.125995	0.014085	1	1	1	1	0.017857	1	6.24E-27	0.005889	0.109055
15	44057632	44057645	PDIA3	3.07E-12	1.38E-18	0.05	0.024242	0.061538	0.018018	0.080176	1	1	3.71E-08	0.037037	1	5.32E-12	0.105195	0.001104
5	126866119	126866130	PRRC1	3.08E-12	4.57E-19	0.012987	1	1	0.023529	1	1	1	1	1	1	1.3E-13	1	0.000467
12	122758719	122758730	CLIP1	3.08E-12	2.27E-18	0.004706	1	1	0.059867	0.019417	1	1	0.092593	1	1	2.22E-09	1	0.004625
7	72966422	72966438	BCL7B	3.09E-12	1.55E-14	1	1	1	1	1	1	0.006329	1	1	1	2.89E-07	1	1
5	158126222	158126236	EBF1	3.09E-12	3.08E-13	0.001329	1	1	1	0.014493	1	1	0.022727	0.023256	1	3.44E-20	1	0.014106
7	54819993	54820005	SEC61G	3.09E-12	2.26E-12	1	1	1	1	1	1	1	1	0.000414	1	9.42E-32	0.001919	0.000171
14	75497428	75497440	MLH3	3.1E-12	1.06E-14	1	1	1	0.027778	1	1	1	0.04717	1	1	4.51E-08	0.025641	0.000244
4	3040279	3040293	GRK4	3.21E-12	1.12E-18	0.131034	1	1	1	0.071771	0.030303	1	0.07573	1	1	1.01E-07	1	1
1	95368553	95368604	CNN3	3.24E-12	4.2E-05	0.074627	1	1	1	0.021053	1	1	1	1	1	1.85E-14	1	1
17	62532622	62532635	CEP95	3.25E-12	5.95E-11	1	1	1	1	0.013514	1	1	0.02439	0.018182	1	2.11E-16	0.044118	0.044554
10	96108988	96109000	NOC3L	3.25E-12	4.21E-15	0.004558	1	1	0.0355	1	1	0.011236	0.000173	1	1	1.62E-17	1	0.068966
1	22084284	22084307	USP48	3.26E-12	5.32E-12	0.102564	1	1	1	0.025316	1	1	1	1	1	9.83E-15	1	0.014129
1	86355414	86355428	COL24A1	3.27E-12	0.000129	0.068182	0.047619	1	1	1	1	1	1	0.0833	1	1.45E-06	1	0.10679
2	120366057	120366070	CFAP221	3.27E-12	6.27E-26	0.012987	1	0.12	0.02439	1	1	1	1	0.00303	1	1.43E-12	0.037736	1
13	31195409	31195432	USPL1	3.29E-12	3.94E-16	6.43E-05	1	1	1	1	1	1	1	0.032258	1	2.58E-10	0.042553	0.018792
2	212578379	212578394	ERBB4	3.31E-12	2.17E-15	7.22E-05	1	1	1	1	1	1	0.158405	0.02029	0.401709	3.7E-20	1	0.026722
15	57484572	57484587	TCF12	3.33E-12	1.45E-16	0.026455	1	1	0.136165	1	1	0.019231	1	0.1	1	2.1E-08	1	0.015298
15	75311040	75311051	SCAMP5	3.4E-12	2.59E-07	1	1	1	0.070779	1	1	1	0.037037	1	1	7.61E-05	1	0.010516
1	46726867	46726890	RAD54L	3.54E-12	1.62E-16	0.094077	1	0.072072	0.086284	0.01005	0.01676	1	1	1	1	3.86E-06	1	0.009853
4	186188373	186188388	SNX25	3.57E-12	4.12E-11	0.020197	1	1	1	1	1	1	0.037034	1	1	2.08E-06	1	3.39E-05
2	91887905	91887919	LOC654342(dist=39930),GGT8P(dist=75449)	3.6E-12	4.84E-18	0.000405	1	1	1	1	1	1	1	0.057143	1	3.2E-27	0.002449	0.00061
2	202494630	202494642	TMEM237	3.62E-12	3.31E-09	1	1	1	1	0.020408	1	0.014815	9.8E-05	1	0.017544	4.77E-11	1	1
13	78137932	78137946	SCEL	3.71E-12	6.19E-15	1	1	1	1	0.005541	1	1	0.278062	0.022222	0.071429	2.86E-08	1	0.087896
9	35382559	35382578	UNC13B	3.75E-12	7.82E-16	1	1	1	1	1	1	1	1	1	1	6.36E-09	1	0.060811
19	55420537	55420549	NCR1	3.8E-12	2.05E-12	0.02889	1	1	1	0.018072	1	1	1	1	1	9.82E-11	1	0.011921
15	102287989	102288000	TARSL2(dist=23344),OR4F6(dist=57923)	3.83E-12	1.8E-23	0.25	1	1	0.00413	0.086159	1	1	0.00936	1	1	0.012821	1	4.14E-05
9	86584222	86584234	HNRNPK	3.87E-12	2.83E-16	1	1	1	1	0.017353	1	0.041447	0.004605	1	1	2.31E-07	1	1
12	19410474	19410488	PLEKHA5	3.91E-12	8.12E-16	0.002177	0.018306	0.360056	1	1	1	1	1	0.039216	1	3.04E-08	0.050308	0.000244
22	41550984	41550996	EP300	3.95E-12	6.63E-22	0.004525	1	0.166667	1	0.063474	1	0.038462	0.002621	1	1	5.61E-16	0.098101	2.74E-10
5	153174310	153174322	GRIA1	3.95E-12	1.32E-12	1	0.012987	0.06087	1	1	1	1	1	0.015625	1	1.22E-15	1	9.17E-05
5	68524006	68524019	MRPS36	4.04E-12	2.24E-08	0.307035	1	0.144731	1	1.05E-05	1	0.00125	0.002131	1	1	8.51E-12	1	0.040906
7	133886342	133886370	LRGUK	1.26E-08	4.22E-06	0.002347	1	1	1	1	1	1	1	0.028986	1	7.59E-15	1	0.054795
10	93579111	93579133	TNKS2	4.15E-10	0.000143	0.006908	1	1	1	1	1	1	0.019231	0.052281	1	6.47E-09	0.040816	0.175645
5	86659147	86659159	RASA1	2.46E-11	6.43E-12	1	1	0.149321	1	1	1	1	0.139373	0.016667	1	1.45E-08	1	0.123991
1	89289954	89289966	PKN2	1.16E-10	1.73E-08	1	1	1	1	1	1	1	0.001038	0.001242	1	3.17E-09	1	0.022703
6	108214754	108214783	SEC63	4.2E-06	5.87E-16	0.021739	0.027777	1	0.028571	1	1	1	0.136004	0.014493	1	2.5E-12	1	0.096988
5	159831736	159831748	SLU7	1.03E-08	3.16E-05	0.046875	1	1	1	1	1	1	0.014925	1	1	1.36E-13	1	1
1	212217944	212217961	DTL	9.39E-12	3.63E-12	0.003393	0.013333	1	1	1	1	1	1	1	1	2.37E-31	1	0.227849
14	57072251	57072275	TMEM260	4.85E-06	8.7E-10	0.018868	1	1	1	1	1	0.017857	0.08	1	1	4.38E-05	1	0.159021
6	86387036	86387048	SNORD50A	0.000655	1.02E-08	1	1	1	1	1	1	1	0.001683	1	1	1	0.028169	1
7	131113756	131113779	MKLN1	3.39E-09	2.21E-13	0.034483	0.004673	1	1	1	0.00463	1	1	0.000481	1	1.94E-15	0.000733	0.000131
1	64022708	64022725	EFCAB7	5.13E-12	1.24E-16	0.163043	1	0.414938	1	1	1	1	1	0.013158	1	1.73E-07	0.000549	4.43E-05
15	42632799	42632823	GANC	3.79E-08	7.9E-06	0.066629	1	1	1	1	1	1	1	0.028571	1	0.087723	1	1
2	196762491	196762509	DNAH7	1.77E-10	1.01E-13	2.27E-05	1	1	1	1	1	0.014184	0.011494	0.002162	1	2.13E-16	1	1
7	89982116	89982127	GTPBP10	1E-05	1.86E-07	1	1	0.117647	1	1	1	1	1	1	1	1.31E-06	0.044776	0.00024
8	101936106	101936118	YWHAZ	3.44E-09	9.18E-11	0.010101	1	1	0.022472	1	1	0.025424	1	1	1	1.05E-13	1	0.006384
8	125534481	125534503	TATDN1	9.88E-09	2.5E-11	0.060606	1	1	0.02649	1	1	0.035088	1	1	1	6.53E-06	0.023256	1
1	202736222	202736233	KDM5B	1.87E-09	6.49E-26	0.001502	4.69E-05	1	0.000827	0.019802	1	1	0.099936	0.029851	1	1.38E-16	0.022222	0.065934
10	75497107	75497133	GLUD1P3(dist=1740),SEC24C(dist=6998)	3.82E-06	1.46E-05	1	1	1	1	1	1	1	1	1	1	5.32E-06	0.03	0.091617
11	64715330	64715349	C11orf85	2.14E-11	8.32E-09	0.038462	1	1	1	1	1	1	1	1	1	6.32E-20	0.001465	0.028302
13	37582122	37582135	EXOSC8	5.72E-12	3.75E-11	0.104505	1	1	1	1	1	1	1	1	1	1.33E-16	1	1
13	60348387	60348399	DIAPH3	2.13E-06	1.09E-17	0.043478	1	1	1	1	1	1	1	1	1	9.25E-12	0.035088	0.032258
4	6055625	6055654	JAKMIP1	6.8E-05	1.64E-06	0.199417	1	1	1	1	1	0.018182	1	1	1	7.4E-05	1	0.075803
5	141520013	141520031	NDFIP1	5.82E-12	0.024012	0.001025	1	1	1	1	1	1	1	0.027778	1	1.09E-14	1	7.39E-13
5	58021809	58021820	RAB3C	6.44E-06	8.82E-09	1	1	0.214286	0.009009	0.03524	1	1	1	1	1	2.01E-11	1	0.000895
12	46758392	46758417	SLC38A2	2.23E-05	1.94E-08	1	1	1	1	1	1	1	1	1	1	7.96E-06	1	0.000194
17	33998753	33998764	AP2B1	0.00078	5.26E-16	0.0625	1	1	0.008726	0.040502	1	1	1	1	1	5.49E-05	0.020619	0.177323
18	13099601	13099612	CEP192	1.74E-06	3.31E-08	1	1	0.147905	1	1	1	1	1	1	1	9.05E-07	0.027027	0.008539
18	56412882	56412894	MALT1	5.8E-10	2.69E-10	1	0.022284	1	1	0.03468	1	0.022222	0.1	1	1	2.84E-06	1	0.136164
4	46994972	46994992	GABRA4	0.000968	7.48E-05	1	1	1	1	1	1	0.000125	1	1	0.028571	6.25E-09	1	0.03428
7	33192288	33192300	BBS9	7.36E-08	5.47E-07	0.090909	1	0.008767	1	1	0.005556	1	0.050505	1	1	0.002934	1	0.000106
9	35059646	35059656	VCP	0.010755	6.85E-11	1	1	1	1	1	1	1	1	1	1	2.6E-08	1	0.063143
X	117762109	117762120	DOCK11	3.73E-05	2.47E-08	1	1	1	1	1	1	1	1	1	1	6.62E-05	1	1
1	242264075	242264108	PLD5	4.71E-09	7.15E-12	0.002353	1	1	1	1	1	0.008264	1	1	1	1.42E-07	1	1
13	52025318	52025350	INTS6	0.004806	2.91E-06	0.003279	1	0.090909	1	1	1	1	1	1	1	0.003736	1	0.076923
17	1383742	1383781	MYO1C	2.25E-09	1.13E-23	0.052632	1	1	1	0.041148	1	1	1	0.06298	1	2.86E-07	0.000244	1
19	52819067	52819079	ZNF480	1.81E-08	6.85E-19	0.056604	1	0.106667	1	1	1	0.030303	0.199453	1	1	2.59E-11	1	0.1271
4	119950975	119950989	SYNPO2	9.46E-10	1.22E-15	1	1	1	0.109452	0.409523	1	0.007568	0.003654	0.08951	1	0.000575	0.150312	0.11281
4	164049985	164049997	NAF1	9.63E-06	6.01E-06	1	1	1	1	1	1	1	1	1	1	0.001561	1	1
7	130044323	130044334	CEP41	0.005639	2.4E-05	1	1	1	1	1	1	1	1	1	0.16	1.33E-05	1	0.051852
7	81964578	81964589	CACNA2D1	0.011691	4.76E-11	0.051282	1	0.530787	1	1	1	1	1	1	1	0.005388	1	0.053197
1	23650293	23650315	HNRNPR	5.65E-05	1.61E-05	0.001107	1	0.055556	1	1	1	1	1	1	1	3.65E-06	0.023256	0.017874
12	64474023	64474047	SRGAP1	1.79E-06	6.06E-05	1	1	1	1	1	1	1	1	1	1	0.00336	1	0.267168
12	88473008	88473040	CEP290	3.23E-09	2.07E-07	0.061224	1	1	1	1	1	0.024691	1	1	1	2.89E-09	0.040541	0.003489
14	50121442	50121460	POLE2	1.21E-07	2.17E-13	1	1	1	0.018182	1	1	1	1	1	1	1.82E-11	0.085678	0.004714
15	76577913	76577931	ETFA	3.38E-10	2.7E-06	0.003322	1	1	1	1	1	1	1	1	1	1.95E-09	1	0.042853
2	101521166	101521201	NPAS2	0.000212	3.83E-05	0.077895	1	0.248603	0.144766	0.17498	1	1	1	0.057545	0.269231	8.82E-10	1	0.074222
2	39964206	39964217	THUMPD2	1.52E-10	1.28E-09	0.058824	1	1	1	1	1	0.018349	1	1	1	1.85E-09	1	1
20	35127613	35127626	DLGAP4	3.16E-11	2.95E-10	0.098718	1	0.07767	1	1	1	1	1	0.041667	1	1.27E-08	1	0.02765
4	25777985	25777996	SEL1L3	5.41E-09	3.89E-17	0.095238	1	1	1	1	1	1	1	0.014286	1	9.97E-08	0.028571	1
6	25452453	25452466	LRRC16A	1.07E-11	2.12E-28	1	0.010204	0.11584	0.03271	0.00064	1	0.020408	1	0.000673	1	0.009231	1	0.015748
9	86395372	86395398	GKAP1	1.55E-08	6.68E-05	0.088235	1	1	1	1	1	1	1	0.000426	0.2	1.13E-25	0.000594	1
9	95179829	95179856	OMD	1.49E-05	6.43E-13	0.030769	1	1	1	1	1	1	1	1	1	1.36E-10	1	1
1	159032486	159032497	AIM2	1.71E-10	3.75E-19	0.029412	1	0.058442	0.074566	1	1	1	1	1	1	7.95E-25	0.043011	0.019264
1	62234928	62234939	INADL	0.00211	6.43E-06	0.041667	1	1	1	1	1	1	1	1	1	0.007202	1	0.004008
12	20870033	20870045	SLCO1C1	6.88E-10	4.46E-17	0.005571	1	0.315894	1	1	1	1	0.169207	1	0.193939	4.3E-07	1	0.00155
15	48634311	48634341	DUT	9.69E-11	0.000925	0.125859	1	1	1	1	1	1	1	1	1	1.75E-09	0.001586	1
3	108175734	108175745	MYH15	3.86E-09	4.13E-22	1	0.022284	1	8.83E-05	1	1	1	1	0.016949	1	4.1E-06	0.012195	1
4	113574414	113574425	LARP7	4.68E-09	2.5E-12	1	1	1	1	1	1	1	0.032967	1	1	2.68E-12	1	1
5	170818290	170818301	NPM1	1.7E-07	1.63E-11	0.05	1	1	1	1	1	1	1	1	1	1.52E-07	1	0.000145
7	99128679	99128692	ZKSCAN5	1.99E-10	4.83E-18	0.027778	1	1	1	1	1	1	0.057554	1	1	1.75E-06	0.08105	1
1	229657220	229657241	ABCB10	3.27E-08	6.94E-06	0.003509	1	1	1	1	1	1	1	1	1	4.74E-05	1	0.015061
10	121678931	121678952	SEC23IP	1.12E-07	1.16E-13	0.038462	0.00641	1	0.055739	1	1	1	0.110262	0.041667	1	0.001096	1	0.181407
11	62496623	62496656	TTC9C	0.058008	0.193182	1	1	1	1	1	1	1	1	1	1	0.001345	1	0.081876
11	95561196	95561214	CEP57	1.04E-09	4.75E-06	0.0625	1	1	1	1	1	0.021978	1	1	1	2.38E-09	0.047619	0.007318
16	74542837	74542859	GLG1	4.5E-10	6.17E-20	0.107071	1	0.120006	1	1	1	1	1	0.025316	1	1.17E-08	1	0.001679
17	40986454	40986487	PSME3	1.36E-10	2.07E-11	0.018939	1	0.199336	1	1	1	1	1	1	0.022059	2.86E-19	6.17E-05	0.001154
18	44656709	44656720	HDHD2	1.15E-07	9.53E-06	0.074074	1	1	0.112191	1	1	1	1	1	1	8.36E-08	1	0.065359
2	204156968	204156980	CYP20A1	1.21E-11	1.89E-26	0.021277	1	0.137168	0.064326	1	1	1	0.049296	0.014085	1	2.25E-14	0.044944	0.080119
2	44934524	44934535	CAMKMT	0.00033	1.99E-10	1	1	1	0.084067	1	1	0.016393	1	0.012821	1	2.03E-10	1	0.04661
3	141923491	141923502	GK5	5.31E-05	1.05E-07	1	1	0.058824	1	1	1	1	1	0.035088	1	2.76E-08	1	1
4	79781169	79781185	BMP2K	5.82E-08	1.57E-18	1	1	1	1	1	1	1	1	0.040541	1	0.015789	0.032258	0.008547
5	74722305	74722316	COL4A3BP	3.65E-06	9.93E-13	0.022727	1	1	1	0.006289	1	1	0.1	1	1	1.81E-12	0.055936	0.111022
1	229438530	229438555	RAB4A	1.71E-07	0.01007	0.086957	1	0.055118	1	1	1	1	1	1	1	2.29E-05	1	0.04186
1	94018103	94018114	FNBP1L	7.6E-06	0.000581	0.022222	1	0.0625	1	1	1	1	1	1	1	4.93E-07	1	1
12	122700993	122701012	DIABLO	0.000968	1.04E-10	0.056604	0.012658	1	1	1	1	1	1	1	1	0.004618	1	1
12	26807065	26807090	ITPR2	2.27E-05	4.71E-07	0.075	1	1	1	1	1	0.014706	1	1	1	5.36E-07	1	0.054054
12	99060155	99060173	APAF1	0.00021	0.000379	0.0625	1	1	0.03876	1	1	1	1	0.000784	1	8.24E-06	1	1
4	76583911	76583922	G3BP2	1.13E-05	1.16E-06	1	1	1	1	1	1	1	1	1	1	0.000184	1	1
5	131927539	131927561	RAD50	5.02E-05	3.22E-08	1	1	1	1	0.011111	1	1	1	1	1	1.81E-08	0.015873	1
5	147499874	147499885	SPINK5	5.83E-06	0.000139	0.083333	1	1	1	1	1	1	1	1	1	4.7E-07	1	0.00619
5	912120	912131	TRIP13	0.000216	7.98E-06	1	1	1	1	0.125627	1	1	1	1	0.324111	0.009778	1	0.089377
6	24852682	24852714	FAM65B	6.25E-09	0.000469	0.025439	1	1	1	1	1	1	1	1	1	0.004045	0.030769	0.041237
6	7402813	7402824	RIOK1	8.84E-10	9.09E-10	0.06	1	1	1	0.017467	0.004673	1	1	1	1	1.24E-06	1	0.112862
6	91263309	91263320	MAP3K7	7.83E-08	7.83E-13	1	1	1	0.041092	1	1	1	0.068627	0.018868	1	3.94E-11	1	0.180473
8	32599491	32599517	NRG1	3.71E-07	2.62E-08	0.004762	1	1	1	1	1	1	1	1	1	6.34E-06	1	0.002712
8	67988672	67988683	CSPP1	6.69E-07	3.08E-12	0.073171	0.014815	1	1	1	1	1	1	1	1	6.46E-06	1	0.121619
X	135328309	135328320	MAP7D3	1.75E-06	3.92E-10	0.074074	0.007092	1	0.010101	1	1	1	1	0.030303	1	1.31E-08	1	0.000418
X	22186528	22186539	PHEX-AS1	0.000182	1.06E-05	0.153846	1	1	0.040984	1	1	1	0.027027	1	1	0.003973	1	1
1	155686739	155686757	DAP3	1.04E-09	2.08E-16	0.043478	1	1	1	0.052806	1	0.028673	1	1	1	1.87E-22	0.000594	1
15	42144967	42144979	SPTBN5	3.68E-07	6.09E-15	0.117551	0.032609	1	0.000594	0.074394	1	1	0.072727	1	0.078947	2.11E-07	1	0.025496
17	10411322	10411354	MYHAS	4.86E-12	2.25E-05	0.045649	1	1	0.066667	0.048381	1	0.031127	1	0.042553	0.005882	5.81E-08	0.047619	0.076878

4	69964234	69964245	UGT2B7	0.000761	1.22E-11	1	1	1	0.129461	0.169909	1	0.103632	0.083996	1	0.285714	9.12E-06	0.074976	0.517354
6	121412191	121412203	TBC1D32	9.34E-07	2.36E-10	1	1	1	1	0.004149	1	0.008197	0.002682	1	1	6.56E-08	1	0.000247
7	23239063	23239074	NUPL2	8.46E-11	1.46E-22	1	0.011494	0.182124	1	1	1	1	1	1	1	6.5E-12	0.014085	0.000286
7	63673449	63673467	ZNF735	3.34E-10	1.55E-07	0.085678	0.010989	0.071429	1	1	1	1	1	1	1	2.32E-15	0.013158	0.230515
8	120831492	120831517	TAF2	0.000155	1.31E-07	0.166667	1	1	1	1	1	1	1	1	1	0.000928	1	0.089947
1	100206566	100206577	FRRS1	1	0.000225	1	1	1	1	1	1	1	1	1	1	0.013449	1	1
12	102576299	102576320	PARPBP	3.96E-11	1.28E-09	0.06014	0.018182	1	1	1	1	1	0.079334	1	0.052632	1.38E-15	1	0.395873
17	35771517	35771528	TADA2A	0.010625	6.52E-06	1	1	1	0.000287	1	1	1	1	1	1	0.00016	1	0.074074
18	59894493	59894513	KIAA1468	3.71E-06	5.6E-06	1	1	1	1	1	1	1	0.04878	1	1	1.28E-08	1	0.078818
3	44606820	44606836	ZKSCAN7	4.54E-08	7.83E-09	1	1	1	1	1	1	1	0.025641	0.017241	1	0.002947	1	1
5	82937251	82937262	HAPLN1	1.37E-07	2.24E-26	0.018868	1	0.078658	1	0.046723	1	1	1	0.041667	1	8.48E-12	0.02439	0.050209
7	35218768	35218786	DPY19L2P1	5.41E-10	2.38E-13	0.000209	1	1	1	1	1	1	1	0.037037	1	1.17E-09	1	0.189614
8	62557195	62557207	ASPH	2.4E-10	1.83E-14	0.001815	1	1	0.080775	0.027397	1	1	1	1	0.3	3.77E-12	1	1.49E-06
9	112225552	112225564	PTPN3	1.15E-10	9.22E-15	0.042254	1	1	1	0.056214	1	1	1.74E-05	1	1	2.8E-07	1	0.038501
9	123922400	123922412	CNTRL	5.92E-11	3.67E-18	0.015624	1	1	0.029412	1	0.004405	1	1	0.016667	1	7.14E-08	1	0.006433
1	35826773	35826784	ZMYM4	2.72E-11	1.86E-11	1	1	1	0.029586	1	1	1	1	0.033333	1	5.71E-11	0.036585	0.06422
10	114154662	114154673	ACSL5	2.15E-11	1.46E-19	0.002775	1	0.158163	1	0.087143	1	1	4.24E-05	0.02	1	7.64E-13	1	0.00054
10	116919785	116919796	ATRNL1	2.27E-06	3.05E-08	0.037037	1	1	1	1.32E-05	1	0.018868	0.171717	1	1	7.79E-09	1	0.012783
10	94215457	94215470	IDE	6.63E-09	9.29E-09	0.011402	1	1	1	1	1	1	1	1	1	1.34E-07	1	0.03119
11	108332126	108332138	C11orf65	2.39E-07	3.51E-15	0.041667	1	1	1	0.015504	1	0.016667	0.131579	1	1	2.14E-08	0.028571	1
14	45497556	45497567	FAM179B	0.001813	5.01E-09	0.0625	1	1	0.000549	1	1	1	1	1	1	1.82E-05	1	0.074324
16	57246810	57246821	RSPRY1	2E-07	1.16E-19	0.033898	1	1	0.031412	1	1	1	1	1	1	8.57E-13	1	0.071207
2	109404474	109404507	CCDC138	1.57E-11	4.33E-06	0.006697	1	1	1	1	1	1	1	1	1	2.84E-11	1	0.290924
2	173861105	173861120	RAPGEF4	9.32E-09	2.15E-05	1	1	1	1	1	1	1	0.011905	1	1	1.05E-17	0.011905	1
4	54256108	54256119	FIP1L1	6.14E-09	2.59E-07	0.068182	1	1	1	1	1	1	1	1	1	0.00011	1	0.000889
7	104747784	104747796	KMT2E	1.9E-10	2.33E-10	0.056604	1	1	0.000774	1	1	1	0.114754	1	1	6.85E-09	1	0.002893
8	24811831	24811853	NEFL	0.000749	0.006338	0.153846	1	1	1	1	1	1	0.049383	1	1	0.003423	1	0.008075
X	24516919	24516938	PDK3	5.62E-09	0.000151	0.035088	1	1	1	1	1	1	0.036697	0.035088	1	3.99E-13	0.000605	1
1	163313695	163313707	NUF2	8.67E-09	5.94E-10	0.000247	1	0.071429	1	1	1	1	1	0.03125	1	2.2E-15	0.047619	0.07563
1	215768872	215768883	KCTD3	1.87E-09	2.12E-05	0.08	1	1	1	1	1	1	1	1	1	1.45E-06	0.041667	0.07767
1	67279866	67279877	WDR78	0.000306	0.007133	1	1	1	1	1	1	1	0.08046	1	1	0.010989	1	0.068966
1	68905367	68905378	RPE65	4.63E-05	0.001276	0.047619	1	1	1	1	1	1	0.058824	1	1	0.009167	1	0.069549
1	91402917	91402929	ZNF644	9.04E-12	7.82E-08	0.096721	1	0.050847	0.138439	0.007785	1	1	1	1	1	2.46E-09	0.025316	0.014473
15	86279430	86279457	AKAP13	1.2E-11	4.29E-09	1	1	1	1	1	1	1	1	0.027778	1	4.83E-08	1	0.000574
18	21644075	21644099	TTC39C	0.015893	0.001802	1	1	1	1	1	1	1	1	1	1	0.000334	0.000117	1
4	15826415	15826426	CD38	0.00226	0.000151	0.006452	1	1	1	1	1	1	1	0.014706	0.032967	0.415479	0.006721	0.335266
4	39871117	39871154	PDS5A	0.005899	5.8E-06	0.181452	1	1	1	0.00653	1	1	1	1	1	0.066456	1	1
5	72875091	72875102	UTP15	6.03E-06	2.76E-08	0.001783	1	1	1	0.013514	1	1	1	1	1	1.95E-07	1	0.000179
7	6771663	6771684	ZNF12(dist=25097),PMS2CL(dist=3252)	3.05E-08	4.2E-06	1	0.010638	1	1	1	1	1	1	1	1	0.197674	1	0.000711
9	140006089	140006100	DPP7	0.001187	7.21E-17	1	0.026905	0.178571	1	1	1	1	1	1	1	4.54E-05	1	1
9	94118279	94118310	AUH	0.000474	8.18E-05	1	0.012987	1	1	1	1	1	0.079571	1	1	6.76E-06	0.095188	0.167422
X	52640310	52640321	XAGE1E(dist=94113),SSX8(dist=11664)	3.21E-09	9.45E-09	1	1	1	1	1	1	1	1	1	1	0.000944	0.000861	1
1	39900058	39900076	MACF1	1.52E-11	2.83E-15	0.000204	1	1	1	1	1	1	1	1	0.05	1.37E-14	1	0.06015
10	43199666	43199677	LINC01518(dist=12459),BMS1(dist=78277)	0.002852	5.07E-08	0.000806	1	1	0.032965	0.001604	1	1	1	1	1	0.003468	1	1
13	32360691	32360702	RXFP2	3.47E-10	1.7E-11	1	1	1	0.132626	1	1	0.046296	0.257086	1	0.1	2.16E-12	1	0.03361
13	53007886	53007897	VPS36	1.81E-05	1.96E-22	1	1	1	0.035714	1	1	1	1	1	1	2.04E-12	0.025641	1
15	62250932	62250943	VPS13C	1.74E-08	5.92E-13	0.119318	1	1	1	1	1	1	0.359606	0.020408	1	6.25E-07	0.035714	0.092543
16	57689230	57689261	GPR56	1	0.666362	1	1	0.513464	1	0.054442	1	1	1	1	1	1	1	1
17	58300951	58300962	USP32	3.2E-05	2.46E-11	0.00303	1	1	1	1	1	1	1	1	1	5.09E-10	1	0.066667
2	215821543	215821563	LOC101928103	9.5E-10	2.43E-06	0.078125	0.007937	1	0.046154	1	1	1	1	1	1	0.000694	1	0.017975
2	234746303	234746314	HJURP	3.37E-06	1.78E-07	1	1	1	1	1	1	1	1	1	1	5.89E-09	1	1
21	17236804	17236816	USP25	1.52E-09	0.001423	1	1	1	1	1	1	1	1	1	1	4.91E-05	0.000903	0.004264
4	128996166	128996178	LARP1B	3.06E-07	3.4E-08	0.109015	1	1	1	1	1	1	1	0.016129	1	5.95E-10	0.025641	0.222953
6	109850190	109850201	AK9	5.48E-05	0.000386	0.003171	1	1	0.165711	1	1	1	1	1	0.142857	0.000476	1	0.456441
1	144918011	144918022	NBPF20,NBPF9,PDE4DIP	1.46E-08	8.42E-11	0.006969	1	1	1	1	1	1	1	0.000565	1	1.04E-07	0.000496	1
15	37188705	37188717	MEIS2	1.11E-08	0.154579	1	1	1	1	1	1	1	1	1	1	6.83E-09	0.04878	0.040133
3	48226193	48226204	CDC25A	2.63E-07	5.83E-10	0.096774	1	1	1	1	1	1	1	1	0.043478	2.55E-12	1	0.052288
9	114694383	114694394	MIR4668	2.48E-10	1.18E-18	0.071429	1	1	1	1	1	1	1	0.017857	1	4.11E-07	1	0.051491
9	73240335	73240357	TRPM3	0.000105	6.02E-06	0.119898	1	1	1	1	1	1	1	0.037736	0.2	0.00089	0.051724	0.01961
1	197059221	197059244	ASPM	0.00012	8.1E-10	0.046512	1	1	0.082718	1	1	0.011494	1	1	1	8.81E-07	0.000287	1
10	96448040	96448060	CYP2C18	3.27E-07	2.51E-07	0.001681	1	1	1	1	1	1	1	0.028169	1	9.58E-07	0.023529	1
12	112308870	112308881	MAPKAPK5	0.004446	6.37E-08	0.041667	1	1	1	1	1	0.010638	0.011921	1	1	1.94E-06	1	0.000231
2	206997835	206997847	NDUFS1	6.51E-12	1.64E-17	0.001815	0.008403	1	1	1	1	1	0.053571	0.02	1	1.31E-19	0.030769	0.000112
3	143235916	143235929	SLC9A9	3.28E-07	5.11E-15	0.25	1	1	0.03125	1	1	0.030303	1	0.001422	1	0.027778	1	0.000733
4	155457781	155457826	PLRG1	6.59E-06	1.08E-05	1	1	1	0.021053	1	1	1	1	1	1	1.5E-07	0.029412	1
5	134032954	134032965	SEC24A	1.28E-07	5.2E-12	1	1	1	0.003764	1	1	1	1	1	1	2.88E-05	1	1
5	37051861	37051873	NIPBL	6.18E-11	1.15E-12	0.021277	1	1	0.03125	1	1	1	1	0.014286	1	1.65E-14	0.025316	0.000848
5	70754289	70754302	BDP1	0.012062	7.72E-17	1	1	1	1	1	1	0.025	0.005937	1	0.058824	0.000334	1	0.160418
6	133108763	133108784	SLC18B1	2.57E-09	5.32E-07	0.000117	1	1	1	1	1	1	1	0.033898	1	6.1E-17	0.025641	0.002533
1	201832479	201832492	IPO9	3.65E-09	4.45E-15	1	1	0.005735	1	1	1	1	1	1	1	2.52E-10	1	1
4	42626659	42626674	ATP8A1	5.97E-10	2.19E-12	0.001234	1	1	0.124863	1	1	0.001139	0.114176	1	1	8.96E-13	0.063987	0.000947
5	70848879	70848890	BDP1	1.79E-11	2.35E-09	1	1	1	1	1	1	0.019802	1	0.041667	1	0.000308	1	0.000648
8	71506679	71506718	TRAM1	1.99E-11	2.23E-05	1	1	0.063291	0.029703	1	1	1	1	1	1	0.000515	1	0.004019
8	95861778	95861797	INTS8	4.85E-09	5.69E-11	1	1	1	1	1	1	1	0.166358	1	0.333333	8.82E-12	0.009727	1
9	34088273	34088284	DCAF12	0.005215	1.56E-07	1	1	1	1	1	1	1	1	1	1	3.51E-06	1	1
X	2326742	2326763	DHRSX	4.49E-11	9.35E-05	1	1	1	1	1	1	0.033058	1	0.111111	0.142857	1.89E-14	0.133157	1.38E-06
X	71416534	71416557	PIN4	3.5E-08	1.26E-09	1	1	0.098704	1	1	1	1	1	1	1	3.37E-12	1	1
10	96112578	96112590	NOC3L	7.07E-11	1.31E-07	1	1	1	1	1	1	1	1	0.045455	1	5.32E-05	1	1
7	77221481	77221508	PTPN12	2.09E-08	1.67E-09	1	1	1	1	1	1	1	0.071406	1	0.032967	0.015803	1	0.000236
9	86258319	86258336	IDNK	0.009918	0.000158	1	1	1	1	1	1	1	1	0.035714	1	1.96E-05	1	0.076142
X	15863648	15863678	AP1S2	0.001463	0.033954	1	1	1	1	1	1	1	0.034483	1	1	6.64E-07	1	0.126586
1	8385485	8385496	SLC45A1	1.81E-08	1.14E-05	0.030303	1	0.249012	1	1	1	1	1	1	1	1.87E-11	0.001807	1
10	13271505	13271527	UCMA	4.53E-12	1.47E-05	0.054545	1	1	1	1	1	1	1	1	1	6.18E-08	1	0.010135
12	21791410	21791426	LDHB	1.84E-10	4.01E-17	0.017544	1	0.477477	0.119293	1	1	0.035294	0.01277	0.001057	1	3.15E-15	0.001639	0.011213
4	143181722	143181748	INPP4B	0.000381	0.2	1	1	0.037037	1	1	1	0.008621	1	1	1	3.14E-05	1	1
4	4436579	4436601	STX18	0.000502	3.96E-06	1	1	1	1	1	1	1	0.060606	1	1	0.192982	1	0.004193
5	134007593	134007616	SEC24A	0.028202	0.000509	1	0.007463	1	1	1	1	1	1	1	1	0.000161	1	0.123596
6	149718577	149718593	TAB2	6.1E-12	2.34E-16	0.166667	1	0.191837	1	0.010363	1	1	1	1	1	0.001677	0.030303	1
1	186089102	186089113	MIR548F1	7.27E-10	1.59E-21	0.042146	1	0.042254	1	1	1	1	1	1	1	1.94E-09	0.014286	1
1	52956482	52956493	ZCCHC11	5.27E-07	1.77E-06	0.185714	1	1	0.039604	1	1	1	1	0.017857	1	5.27E-09	0.042254	0.005445
17	35567303	35567314	ACACA	9.46E-05	1.29E-12	0.002775	1	0.010486	1	1	1	1	0.044248	0.036364	1	0.000168	0.016949	1
17	44409890	44409927	LRRC37A	5.32E-12	4.88E-27	0.004449	0.014815	0.052854	0.091206	1	1	1	1	0.004049	1	7.55E-22	0.052281	0.137184
19	36564438	36564455	WDR62	4.01E-06	2.68E-15	1	1	1	1	0.000478	1	0.113821	1	1	1	5.02E-05	0.037037	0.032258
2	107087402	107087425	RGPD3(dist=2601),ST6GAL2(dist=330631)	1.09E-06	0.022526	0.108108	1	1	1	1	1	1	0.050633	1	1	1.38E-08	1	0.006317
4	110433282	110433303	SEC24B	1.66E-11	7.1E-18	0.002177	1	0.144836	1	1	1	1	0.000591	1	0.263158	4.2E-14	0.004236	1
4	151145556	151145586	DCLK2	1.02E-08	0.000461	1	1	1	1	1	1	1	1	1	1	0.000178	1	0.050125
1	216495186	216495197	USH2A	0.000191	5.01E-09	9.38E-05	1	1	0.027027	1	1	1	1	1	1	0.000714	1	0.064516
11	68566834	68566849	CPT1A	3.76E-07	4.54E-09	0.071429	1	0.098592	0.034483	1	1	1	1	1	1	0.000846	1	0.099415
14	60069851	60069862	RTN1	0.03836	1.21E-05	1	1	0.207207	1	1	1	1	0.103448	1	1	0.001488	1	0.019745
18	44424079	44424127	PIAS2	3.31E-07	6.53E-06	0.01944	1	1	1	1	1	1	1	1	1	3.21E-07	0.086918	0.03787
10	96256984	96256998	TBC1D12	2.91E-11	3.23E-07	0.004706	0.016949	1	0.053191	1	1	1	1	1	1	2E-15	1	0.131897
12	105538478	105538491	KIAA1033	1.2E-08	6.52E-15	1	1	1	0.107689	1	1	0.015625	1	1	1	1.04E-05	0.046875	1
12	9706558	9706571	DDX12P(dist=105790),KLRB1(dist=41299)	7.4E-12	7.9E-15	1	1	0.131001	1	1	1	1	0.003165	1	1	0.043478	1	0.000124
2	38975332	38975347	SRSF7	4.57E-11	2.43E-08	0.00363	1	1	1	1	1	1	1	0.060606	1	1.01E-16	1	0.063636
8	48790202	48790212	PRKDC	5.85E-06	1.93E-10	1	1	1	1	1	1	1	1	0.027027	1	7.49E-06	0.06	1
1	87181592	87181615	SH3GLB1	0.628768	0.006391	0.035714	1	1	1	1	1	1	1	1	1	0.002904	1	0.074601
5	148207659	148207671	ADRB2	2.37E-10	0.049209	0.166335	1	0.080386	1	1	1	1	1	0.081633	0.010989	5.08E-12	0.146853	0.038001
8	121502680	121502691	MTBP	1.83E-08	3.22E-10	1	1	0.089109	1	1	1	1	0.027778	0.015873	1	9.67E-08	0.000496	0.144267
8	57389319	57389337	LOC101929415	0.000437	1	0.05601	1	1	1	1	1	1	0.142639	1	1	0.060392	1	0.38424
1	201821196	201821207	IPO9	2.85E-09	9.02E-09	0.04878	1	1	1	0.021898	1	1	0.098039	0.027778	1	4.67E-12	1	0.102564
15	45253674	45253686	C15orf43	4.88E-07	7.51E-13	0.127869	1	1	1	1	1	1	0.008671	0.036364	1	3.51E-13	0.026667	0.008911
18	21293834	21293881	LAMA3	6.61E-08	6.42E-19	1	1	1	1	0.009709	1	1	0.064286	0.02381	1	1.66E-07	1	1
20	35660978	35660989	RBL1	3.23E-06	3.28E-08	1	1	1	1	0.011561	1	1	1	1	1	8.88E-07	1	1
6	160106070	160106081	SOD2	0.002908	0.165563	1	1	1	1	1	1	1	1	1	1	0.005254	0.088195	0.173636
X	153216185	153216195	HCFC1	0.00679	4.63E-09	0.074074	1	0.125	0.00813	1	1	1	0.002899	1	1	8.79E-07	0.034483	1
11	125467134	125467144	STT3A	2.71E-05	0.002831	0.102041	0.028571	1	1	1	1	1	1	0.05	1	1.15E-05	0.068182	0.1536
16	67229793	67229833	E2F4	0.001012	6.43E-05	0.00303	1	0.112401	1	1	1	1	1	1	1	0.000273	1	0.281364
7	101747593	101747605	CUX1	5.18E-07	2.9E-22	0.16996	0.075208	1	0.000503	0.188097	1	1	1	1	1	0.000388	0.042254	0.245417
7	40087320	40087333	CDK13	1.31E-07	1.53E-12	1	1	0.529554	1	0.119291	0.016854	0.100354	1	0.105263	0.25	1.46E-09	0.037037	0.005358
1	101456192	101456203	DPH5	5.8E-06	5.34E-12	1	1	1	0.045872	1	1	1	1	1	1	2.64E-09	1	0.052239
17	78325464	78325475	RNF213	0.000111	2.43E-05	1	1	1	1	1	1	1	1	1	1	3.62E-05	1	1
2	98872570	98872582	VWA3B	3.28E-11	6.87E-20	0.001488	1	0.222689	1	0.013333	1	0.025	0.000477	0.033898	1	1.93E-15	0.045455	0.04802
3	156411774	156411807	TIPARP	0.002287	1.21E-05	0.000605	1	1	0.055556	1	1	1	0.068966	1	1	1.82E-05	1	1
1	217784431	217784441	GPATCH2	5.98E-08	4.95E-06	1	1	1	0.017409	1	1	1	0.089552	0.002646	0.230769	1.27E-13	1	0.038049
1	45212979	45213002	KIF2C	6.07E-06	0.001537	0.003509	1	1	1	1	1	1	1	1	1	9.53E-07	1	0.127782
13	72063066	72063077	DACH1	0.000553	2.23E-08	0.001502	0.016129	1	0.025974	0.033193	1	0.016393	1	1	1	0.000467	0.040816	0.031496
3	154834379	154834396	MME	0.110424	0.150794	1	1	1	1	1	1	1	0.041447	1	1	0.000101	1	0.395643
14	39605621	39605639	GEMIN2	0.000379	2.9E-06	1	1	1	1	1	1	1	1	1	1	7.02E-05	1	0.001565
21	40650627	40650652	BRWD1	1.39E-11	8.11E-16	0.000403	1	0.051282	1	0.023952	1	1	0.09375	0.022222	1	1.44E-18	0.014925	3.3E-05
3	48636506	48636516	UQCRC1	5.14E-08	4.7E-14	0.111111	1	0.111022	1.43E-10	5.65E-06	1	0.019231	0.034393	0.04878	1	0.214286	1	1
4	47901315	47901327	NFXL1	1.27E-11	1.41E-11	1	1	1	0.084472	1	1	1	1	0.086957	0.333333	4.51E-10	1	0.184696
6	160237662	160237680	PNLDC1	1.35E-07	3.04E-07	1	1	1	0.094807	1	1	1	1	0.014706	1	1.41E-07	0.151941	0.207007
1	193038176	193038186	TROVE2	2.14E-06	9.71E-10	1	1	0.0625	1	1	0.014815	0.034483	1	0.054054	1	0.000701	0.040816	0.007452
1	224588833	224588844	WDR26	0.024173	0.001299	1	1	1	1	1	1	1	1	1	1	2.5E-07	1	0.118644
15	44671816	44671837	CASC4	1.83E-10	7.99E-18	0.002718	1	0.301768	1	1	1	1	1	0.026316	1	2.12E-19	0.054536	0.109931
20	4850568	4850578	SLC23A2	2.62E-07	3.92E-13	1	1	1	0.000221	0.046641	0.013245	0.014085	1	1	1	6.05E-07	0.018519	0.011962
3	172080401	172080412	FNDC3B	1.86E-09	4.72E-20	0.021277	1	1	1	0.000713	1	1	0.090909	1	1	2.11E-06	1	0.043396
X	53113895	53113905	TSPYL2	3.97E-09	4.12E-07	0.006209	1	0.079925	1.33E-06	3.84E-05	1	1	0.008045	0.033333	1	1.27E-06	1	0.034986
2	44550339	44550350	PREPL	9.73E-06	2.21E-06	1	1	0.267857	1	1	1	1	0.058824	1	1	2.6E-09	0.067797	0.095238
5	125929000	125929037	ALDH7A1	1.26E-05	1	1	1	1	1	1	1	1	1	1	1	0.065587	1	0.003939
X	129338973	129339002	ZNF280C	6.14E-11	1.66E-07	0.016158	1	1	1	1	1	1	1	1	1	5.24E-12	1	0.121884

1	151535020	151535045	TUFT1	4.34E-07	0.003691	0.054054	1	1	1	1	1	1	1	1	0.1875	0.001327	1	0.250437
6	152539572	152539586	SYNE1	1.91E-10	4.42E-12	0.005473	1	0.580526	0.250065	0.205631	1	1	0.39218	0.088235	0.142857	0.00862	0.05	0.010081
8	75929746	75929756	CRISPLD1	4.63E-06	5.53E-14	1	1	1	1	1	1	0.076169	0.125	1	1	1.48E-11	1	1
11	89914885	89914911	NAALAD2	4.95E-07	0.000344	1	1	0.159261	1	1	1	1	1	1	0.017544	0.016921	1	1
2	70066571	70066582	GMCL1	3.99E-10	7.37E-08	0.068182	1	1	0.16768	1	1	1	0.105189	0.001357	0.004128	2.92E-05	0.005599	0.123374
1	64017377	64017388	EFCAB7	1.54E-05	1.05E-05	0.031746	1	1	1	1	1	0.056065	1	0.016129	1	2.96E-07	1	1
17	37575853	37575874	MED1	9.67E-07	5.75E-06	0.152157	1	1	1	1	1	1	1	1	1	1.51E-07	0.021739	0.116007
9	33311294	33311306	NFX1	3.95E-06	5.24E-08	1	1	0.062992	1	1	1	0.016529	0.031579	1	1	6.37E-10	1	0.185864
12	97331208	97331233	NEDD1	0.048713	0.214026	0.122984	1	0.54538	0.102659	1	1	1	0.025095	1	0.065359	0.000608	1	0.535999
22	26886953	26886982	SRRD	0.029035	0.135835	1	1	1	0.01282	1	1	1	0.185701	0.251515	0.1875	0.000253	1	0.022266
3	52728303	52728323	GNL3	0.000154	0.061458	1	0.006369	0.172704	1	1	1	0.072917	1	1	1	5.3E-05	1	0.017824
6	155143561	155143572	SCAF8	0.000174	8.89E-15	1	1	1	1	1	1	1	1	1	1	7.23E-07	1	0.079208
14	91467393	91467404	RPS6KA5	1.14E-06	7.15E-14	0.187805	1	1	1	1	1	1	1	0.03125	1	5.41E-13	1	0.012301
1	67516191	67516202	SLC35D1	6.48E-06	9.56E-06	0.025641	1	0.391715	0.007879	1	1	0.025	0.343869	1	0.142857	1.51E-11	0.074051	0.193404
10	103771444	103771469	C10orf76	2.99E-09	9.91E-14	1	1	1	1	1	1	1	1	0.070779	1	1E-12	1	0.051095
4	57686807	57686822	SPINK2	1.07E-11	3E-14	0.030593	1	1	1	1	1	0.039732	1	1	1	9.97E-15	1	0.000504
5	38978758	38978770	RICTOR	2.96E-11	5.57E-10	0.02381	1	1	1	1	1	0.008475	1	0.035088	0.117647	1.58E-09	0.044118	0.002413
11	89502007	89502036	TRIM77(dist=50967),TRIM49(dist=28787)	1.58E-06	5.92E-05	0.139373	0.006579	1	1	1	1	1	1	0.044444	1	3.99E-09	1	1
17	5324558	5324611	RPAIN	4.94E-12	4.83E-14	1	0.007874	1	0.002457	0.019481	1	0.017544	1	0.047619	1	2.18E-11	0.103383	1
14	35550467	35550490	LOC101927178	3.88E-11	7.97E-11	0.000137	1	0.051948	1	1	1	0.02459	0.068947	0.018182	1	4.39E-11	0.031915	1
20	13090733	13090745	SPTLC3	2.06E-08	5.14E-12	0.037662	0.031744	1	0.078209	1	1	1	0.146606	1	1	5.53E-08	0.000982	0.160236
17	44806139	44806158	NSF	5.08E-07	6.54E-08	1	1	1	1	1	1	1	0.016129	1	1	5.03E-08	1	0.122471
3	47860685	47860696	DHX30	2.64E-07	7.61E-14	1	1	1	0.037634	1	1	1	1	1	1	5.77E-08	0.065201	0.00389
21	15313079	15313093	CYP4F29P(dist=92394),ANKRD20A11P(dist=3003)	2.26E-06	4.17E-10	1	0.031577	1	1	1	1	1	0.154736	0.088195	1	0.1	0.060976	1
2	171862578	171862590	TLK1	1.33E-08	2.64E-15	0.005772	1	1	0.104077	0.040157	1	1	1	1	1	1.31E-10	1	1
2	54025009	54025020	ERLEC1,GPR75-ASB3	0.000841	4.17E-05	1	1	0.054795	1	0.025	1	1	0.041096	1	1	1.12E-06	1	0.265776
1	115238016	115238032	AMPD1	2.56E-09	1.55E-20	0.084288	1	0.103963	0.331182	0.040319	1	1	0.049005	0.055556	0.1	1.17E-06	0.111024	0.019098
1	207826095	207826106	CR1L	0.000176	1.42E-10	1	1	1	0.173968	1	1	0.094427	0.050413	1	1	0.002561	1	0.31587
16	24820823	24820840	TNRC6A	0.000967	7.98E-07	0.22551	1	0.602348	1	0.140576	1	1	1	1	1	0.002835	1	0.059358
16	28883087	28883097	SH2B1	0.000499	1.14E-11	1	1	1	1	1	1	0.012346	1	1	1	1.12E-08	1	1
3	44826303	44826335	KIF15	2.03E-08	0.000451	0.044548	1	1	1	1	1	0.127138	1	1	0.125	4.04E-12	1	0.006843
4	89579550	89579561	HERC3	0.003748	0.000396	1	1	1	1	1	1	1	0.025974	1	1	0.000809	0.050847	0.148718
17	6662948	6662977	XAF1	0.000386	0.000219	0.048547	1	1	1	1	0.023121	1	0.16544	1	0.423077	7.28E-05	1	0.047887
19	4297855	4297872	TMIGD2	1.67E-09	9.93E-18	1	1	1	0.119868	1	1	0.15129	0.136175	1	1	0.485714	0.005202	1
1	53255587	53255601	ZYG11B	1.45E-08	5.76E-07	0.010788	1	0.172494	1	1	1	1	0.000131	1	0.227273	3.32E-09	1	0.000114
11	113688357	113688368	USP28	3.94E-05	1.43E-12	1	1	0.064103	0.140221	1	1	0.010204	0.02623	1	0.15	8.05E-10	0.039216	0.194331
19	10270725	10270758	DNMT1	1.16E-05	1.43E-10	1	0.061947	0.499599	0.064872	0.085106	0.061069	0.116667	0.252185	1	1	0.001306	1	0.000354
3	112718471	112718512	GTPBP8	0.00032	1.48E-11	0.064516	1	1	1	1	1	1	1	1	1	0.000585	0.014925	0.116733
8	99054836	99054849	RPL30	3.77E-08	3.84E-12	1	1	1	0.065342	1	1	1	0.006251	1	0.166667	1.95E-07	1	0.01928
19	14104688	14104703	RFX1	3.06E-06	1.29E-45	0.002849	3.61E-05	1	0.035088	0.000845	1	1	0.055944	1	1	1.26E-19	1	1
19	11565819	11565831	ELAVL3	1.03E-06	1.9E-35	1	1	1	1	0.002019	1	0.083333	0.000235	1	1	0.066667	1	1
22	35719378	35719394	TOM1	3.68E-08	6.68E-35	0.133333	0.000112	0.183389	1	1	1	0.041096	2.02E-05	1	1	7.96E-06	1	0.044688
4	8472785	8472805	TRMT44	8.38E-09	3.41E-34	0.00555	0.025889	1	1	0.001097	1	1	1	0.016393	1	1.75E-12	0.028571	0.076923
18	60025458	60025474	TNFRSF11A	1.65E-07	5.12E-34	0.142857	1	0.474651	0.187468	1	1	0.024793	0.046478	1	1	4.77E-07	1	0.237923
7	138270744	138270757	TRIM24	9.61E-09	3.47E-31	0.176471	1	1	0.072892	1	1	1	1	1	1	1	1	1
1	44805012	44805054	ERI3	0.000137	1.03E-30	0.008333	1	1	0.02749	1	1	1	0.035088	1	1	5.7E-06	1	1
1	150932953	150932989	SETDB1	2.72E-10	1.06E-30	0.166667	3.49E-05	1	0.058321	1	1	0.064501	1	0.02381	1	1.21E-06	0.028169	0.052973
6	56504477	56504489	RNU6-71P	3.55E-07	1.14E-30	0.022222	0.021447	0.051724	1	0.000287	1	1	2.83E-06	1	1	1.7E-09	1	0.000165
2	79314062	79314073	REG1B	1.11E-11	2.58E-29	1	0.009852	1	1	0.013333	1	1	0.004158	1	1	1.29E-13	0.109994	0.102988
14	104145625	104145642	KLC1	2.91E-10	2.95E-29	0.117647	0.058811	1	0.002063	1	0.008621	0.030928	1	0.058824	1	0.001422	0.001442	0.017477
11	47187055	47187087	ARFGAP2	4.78E-07	5.04E-29	0.076923	0.009132	0.044872	0.06602	0.012245	1	0.007692	1	1	1	6.71E-05	1	0.02917
16	4559351	4559367	HMOX2	1.64E-08	1.28E-28	0.125	1	1	0.035928	0.020305	1	1	0.000308	1	1	0.01685	1	0.014279
9	135773000	135773019	TSC1	6.05E-09	2.55E-28	0.004303	1	1	1	1	1	1	1	1	1	1.54E-20	1	0.017305
7	94989255	94989273	PON3	2.07E-11	3.64E-28	0.002859	0.000324	0.072924	1	1	1	0.05245	1	0.055556	1	1.04E-08	1	0.08793
3	62153593	62153621	PTPRG	0.000122	6.03E-28	0.008737	0.009804	0.031266	0.028757	1	1	0.067568	1	1	0.366667	3.15E-14	1	0.188619
X	100532479	100532505	TAF7L	1.98E-10	1.41E-27	0.156667	1	1	1	1	1	1	1	1	1	1.15E-08	1	0.180081
16	84907499	84907520	CRISPLD2	2.88E-11	5.85E-27	0.006719	1	1	0.000262	0.119934	1	0.068027	0.010413	1	0.111111	1.85E-14	1	0.029757
5	140076413	140076436	HARS2	4.64E-06	6.82E-27	0.166667	1	0.288938	1	0.064082	1	0.019231	0.047904	1	1	9.41E-05	1	0.044444
9	99408079	99408094	AAED1	6.08E-10	2.3E-26	1	0.02857	0.031299	1	1	1	1	0.002504	0.014493	1	1.04E-05	0.001038	0.105669
13	45973231	45973246	SLC25A30	3.12E-09	2.45E-26	0.158163	1	1	0.074227	1	1	1	1	1	1	2.11E-11	0.047619	1
7	106523362	106523383	PIK3CG	5.3E-07	2.76E-26	1	1	1	1	1	0.007067	1	1	1	1	0.001611	1	0.004032
17	62748076	62748093	LOC146880	5.43E-12	2.99E-26	0.142857	0.074915	0.526645	0.156742	0.204799	1	0.314737	0.002941	0.025641	1	0.024242	0.010885	0.001863
14	102476130	102476143	DYNC1H1	9.17E-10	4.87E-26	0.101633	0.019002	1	1	1	1	1	0.047904	1	1	9.46E-11	1	1
7	75651305	75651336	STYXL1	2.55E-07	8.74E-26	0.0625	1	1	0.035533	0.0502	1	0.014599	1	1	1	0.000171	1	1
3	30691871	30691882	TGFBR2	1.93E-07	9.15E-26	0.0114	1	1	0.023952	0.021622	1	1	0.097107	0.000466	1	2.06E-20	0.0125	0.051136
6	55739711	55739726	BMP5	2.67E-09	1.65E-25	0.020408	0.036115	1	1	0.000101	0.005	1	0.0035	1	1	6.23E-13	0.00037	0.003432
3	5024415	5024435	BHLHE40	3.57E-07	1.72E-25	1	0.135251	1	0.130102	0.120255	1	0.033794	5.18E-06	0.040816	1	1.26E-05	0.000999	0.001951
6	137325901	137325917	IL20RA	2.12E-11	1.83E-25	0.25	0.010582	1	0.001139	0.081042	1	0.054545	0.000116	0.04878	1	9.57E-05	1	0.003945
4	76997157	76997173	ART3	3.02E-09	2.56E-25	0.000345	0.008368	0.142663	1	0.034613	1	1	1	0.026316	1	5.75E-28	1	0.019649
19	14153179	14153202	IL27RA	7.35E-11	2.61E-25	1	1	1	0.062001	0.015267	1	1	0.005806	1	1	0.000547	1	1
12	133237753	133237768	POLE	9.97E-08	3.73E-25	0.199507	0.004484	0.144766	0.028302	0.000306	0.007576	0.052623	0.148387	0.090909	0.130435	7.18E-09	0.032258	0.014061
16	70595514	70595525	SF3B3	6.21E-09	4.61E-25	0.002449	0.013889	0.132174	0.037433	0.021368	1	0.017699	1	0.000754	1	1.13E-16	0.027778	1
4	89711690	89711718	FAM13A	5.16E-09	5.31E-25	1	0.008197	1	1	1	1	1	0.069767	1	1	3.26E-08	1	0.176026
10	33496676	33496688	NRP1	6.22E-10	5.48E-25	0.141414	1	1	1	1	1	1	0.14062	0.000391	1	1.07E-07	0.045193	0.051872
19	43919911	43919926	TEX101	2.64E-11	9.25E-25	0.037662	1	1	0.057819	0.091264	1	0.039406	0.044643	1	1	9.54E-06	0.031579	0.169094
17	1584377	1584390	PRPF8	8.5E-08	1.32E-24	1	0.004566	1	1	0.053836	1	1	0.045752	1	1	1.58E-12	1	4.11E-06
17	33288433	33288445	CCT6B	1.29E-09	1.54E-24	1	1	1	0.026882	1	1	1	1	0.014706	1	1.35E-07	1	0.000145
9	34343033	34343047	NUDT2	8.92E-10	1.59E-24	1	0.011834	1	1	1	1	1	0.087391	0.033333	0.333333	2.33E-08	0.095754	1
12	56872770	56872791	GLS2	0.019444	1.63E-24	0.15	1	1	1	1	1	0.050786	0.014198	1	1	0.00121	1	0.392482
7	98649755	98649771	SMURF1	1.08E-10	1.72E-24	0.085617	1	1	0.027027	1	1	0.016393	1	1	1	3.8E-06	1	2.48E-05
6	117026217	117026229	KPNA5	1.73E-08	2.91E-24	0.087879	0.005076	0.040404	0.027027	1	1	0.052973	1	0.03125	1	1.7E-16	1	2.25E-07
17	29325662	29325674	RNF135	4.7E-07	3.28E-24	0.093702	1	1	1	1	1	1	1	1	1	2.88E-08	0.023256	0.07636
20	46282112	46282135	NCOA3	1.09E-09	3.52E-24	0.042146	0.024735	0.08082	0.174532	0.097327	1	0.036585	1	1	1	4.43E-09	1	0.199633
8	22138812	22138831	PIWIL2	2.81E-08	3.79E-24	0.042553	1	0.065217	0.039063	1	1	1	0.009009	0.016667	1	1.23E-14	3.42E-05	0.000374
5	88018369	88018402	MEF2C	1.95E-06	4.13E-24	0.134301	1	1	0.268613	0.041127	1	1	0.00198	0.030303	1	9.34E-06	1	0.055172
12	91372042	91372059	EPYC	4.92E-07	5.51E-24	0.001186	1	0.197251	0.059268	0.111825	1	0.095184	0.030385	1	1	0.006416	0.130303	0.055087
6	152539326	152539345	SYNE1	1.76E-11	5.56E-24	0.008564	1	1	0.001858	0.018018	1	0.027027	0.000212	0.017544	1	3.3E-05	0.039474	0.021178
12	120741303	120741326	SIRT4	4.17E-11	5.77E-24	0.031621	0.012821	0.053191	0.000478	0.010695	1	1	0.039216	0.018519	0.0625	3.17E-06	0.055164	1
8	68139326	68139338	ARFGEF1	2.83E-11	6.07E-24	0.0625	1	1	0.004726	0.00905	1	1	1	0.125	0.130435	1.31E-12	1	0.011473
9	100997485	100997498	TBC1D2	0.001763	8.96E-24	1	1	1	1	0.014545	1	1	2.57E-05	1	1	0.206349	1	1
5	67576330	67576346	PIK3R1	3.35E-08	1.07E-23	0.161348	0.000227	0.041667	1	0.001439	0.022857	0.044118	1.47E-05	1	1	1.97E-11	1	0.199973
21	42823193	42823206	MX1	8.44E-10	1.21E-23	0.035088	0.012121	1	0.021277	0.124872	1	1	9.91E-06	1	1	9.53E-14	1	0.001292
21	32597972	32597988	TIAM1	1.31E-11	1.53E-23	1	1	0.263144	1	1	1	0.097107	0.05881	0.05	1	2.86E-07	1	0.000221
14	91639611	91639627	C14orf159	1.05E-08	1.64E-23	1	1	1	0.028986	0.002742	1	0.103367	1	0.043478	1	1.19E-13	0.038462	0.048748
19	3205810	3205826	NCLN	9.62E-12	2.91E-23	1	1	1	1	0.029739	1	0.022901	1	1	1	0.000464	0.01759	0.162357
7	127251732	127251744	PAX4	7.4E-09	4.02E-23	1	0.021108	1	0.025641	1	1	1	0.166358	1	1	0.000264	0.038462	0.016721
17	39659874	39659890	KRT13	1.03E-08	4.08E-23	0.076923	1	0.111111	0.026667	0.00056	1	0.028571	1	0.015873	1	8.51E-11	0.002414	0.15927
5	77745862	77745874	SCAMP1	2.53E-07	6.13E-23	0.079184	1	1	1	1	1	1	9.93E-05	0.032787	1	7.89E-11	0.013965	0.041245
15	41770598	41770624	RTF1	1.31E-11	7.57E-23	1	1	1	0.00023	0.021164	0.010101	1	0.039022	1	1	0.137353	1	0.000805
1	74901739	74901760	FPGT-TNNI3K,TNNI3K	0.00028	1.24E-22	0.000629	1	0.03825	1	1	1	1	1	0.047899	0.193676	7.53E-22	1	0.589027
1	114224782	114224799	MAGI3	2.75E-11	1.29E-22	0.03374	1	1	0.042301	1	1	0.139786	0.006673	1	0.007353	2.54E-15	0.09434	0.025133
1	32692168	32692186	EIF3I	1.83E-06	2.36E-22	0.385965	0.026666	1	1	0.023437	1	0.010309	1	0.029412	1	1.35E-06	0.027027	0.00706
19	19308821	19308837	RFXANK	3.04E-06	2.4E-22	1	1	1	0.021277	1	1	0.027778	1	1	1	0.111936	1	1
18	67613932	67613959	CD226	3.53E-07	2.55E-22	0.00056	0.021333	0.213505	1	1	1	1	0.054348	1	1	5.65E-08	1	0.272089
19	36259480	36259494	PROSER3	2.58E-07	2.83E-22	1	1	1	1	1	1	1	1	1	1	0.05	0.038645	1
13	41947712	41947725	NAA16	6.95E-10	3.43E-22	1	1	0.119738	0.048332	1	1	1	0.006342	1	1	1.02E-11	1	0.307086
14	68191109	68191127	RDH12	1.41E-08	3.5E-22	0.03008	1	1	0.188605	1	1	1	1	1	0.307692	5.19E-12	1	0.002547
11	94212930	94212942	MRE11A	7.83E-12	4.07E-22	1	1	1	1	1	1	1	0.00237	1	1	5.29E-08	1	5.74E-05
17	38856736	38856749	KRT24	2.01E-08	4.71E-22	0.1	1	1	0.033147	0.027148	1	0.091783	1	1	1	2.78E-07	1	0.013098
15	63063141	63063158	TLN2	2.06E-06	4.96E-22	0.085617	0.016563	0.286266	1	0.241431	1	1	1	1	1	0.000158	1	0.050472
18	40503735	40503751	RIT2	1.7E-11	5.03E-22	0.000122	1	0.307781	1	0.020243	1	1	1	1	1	2.49E-24	0.071429	1
15	59693969	59693985	MYO1E(dist=28898),FAM81A(dist=36387)	0.000234	5.51E-22	3.08E-05	1	0.564528	0.307829	1	1	0.000381	1	1	0.142857	1.09E-12	1	0.015568
3	170715672	170715694	SLC2A2	6.1E-05	5.73E-22	1	0.005464	1	0.021127	1	1	1	0.000155	1	0.298246	5.4E-09	0.032258	1
X	129203198	129203214	ELF4	3.4E-07	5.98E-22	0.005848	1	1	0.143043	1	1	0.073171	0.000913	1	1	0.005574	0.142857	0.177397
5	67584512	67584525	PIK3R1	1.63E-09	6.09E-22	0.000302	1	1	4.64E-06	1	1	0.008621	1	1	1	5.66E-20	0.000658	0.004763
9	740769	740788	KANK1	7.43E-10	6.66E-22	1	1	0.409884	0.010357	1	1	0.067095	1	0.285714	0.333333	6.08E-05	1	0.003806
12	21327652	21327667	SLCO1B1	1.09E-07	6.74E-22	0.070175	1	1	0.003082	0.028435	1	1	0.313396	0.0625	1	2.87E-16	0.02381	0.068694
1	8505744	8505756	RERE	0.002785	7.98E-22	0.333333	1	0.11	1	0.021368	1	1	1	1	1	0.000214	1	0.002151
13	31722620	31722638	HSPH1	2.7E-08	8.85E-22	0.011614	1	0.067334	0.094873	1	1	1	2.81E-07	1	0.039216	2.26E-20	1	0.032039
13	32907535	32907547	BRCA2	7.38E-09	1.16E-21	0.037037	1	0.034965	1	1	1	0.092728	1	1	1	2.78E-18	1	1
11	117261352	117261374	CEP164	1.47E-08	1.17E-21	0.395604	1	1	0.055933	0.036434	1	0.086447	1	1	1	0.008696	0.025316	0.038095
15	48717850	48717884	FBN1	1.98E-11	1.46E-21	0.0114	0.00995	1	0.006897	1	1	1	1	0.055556	1	4.61E-21	1	0.001009
6	17292448	17292460	RBM24	4.48E-10	1.69E-21	0.076923	0.053147	1	1	0.011494	1	0.014085	1	1	1	0.005848	1	0.027778
1	10357206	10357224	KIF1B	1.05E-09	1.74E-21	0.003885	1	0.124387	0.055933	1	1	1	1	1	1	1.03E-22	0.005462	0.232378
9	15433520	15433532	SNAPC3	1.04E-10	1.97E-21	0.083333	1	0.20897	0.042945	1	1	1	0.003378	1	1	1.18E-07	0.051948	0.181331
14	55231286	55231297	SAMD4A	1.54E-11	2.02E-21	0.000171	1	1	1	1	1	1	0.111111	1	1	7.6E-12	0.028571	0.010457
15	63040516	63040533	TLN2	1.58E-10	2.25E-21	0.004348	1	0.133178	1	1	1	1	1	1	1	7.19E-13	1	0.000545
13	52726707	52726730	NEK3	3.76E-11	2.35E-21	0.044118	1	1	0.000569	1	1	1	1	1	1	3.87E-21	1	0.002722
15	57545438	57545449	TCF12	1.28E-10	2.39E-21	0.032258	0.006061	1	1	1	1	0.028986	0.014141	0.016393	1	7.51E-11	1	1
20	58587783	58587794	CDH26	5.32E-08	2.5E-21	1	1	1	1	1	1	1	0.068966	0.014925	1	3.59E-13	0.000466	0.000888
20	55206241	55206253	TFAP2C	4.22E-12	2.54E-21	0.000784	0.000433	1	0.001719	1	1	1	1	0.03125	1	1E-11	0.002281	1
2	179616770	179616786	TTN	0.007917	2.55E-21	0.201991	0.043243	1	2.2E-05	0.002682	1	0.001488	0.408695	1	1	1.43E-15	1	0.333333
2	25875401	25875418	DTNB	1.71E-09	2.84E-21	0.08	1	0.188125	0.11801	1	1	0.094277	1	0.06	1	8.04E-15	1	0.030574
2	203630102	203630124	FAM117B	9.61E-10	3.48E-21	0.004024	1	1	1	1	1	0.036864	0.041667	1	1	2.23E-16	0.071429	0.004352
20	41306488	41306500	PTPRT	1.66E-07	3.81E-21	0.014286	0.0125	1	0.001854	0.097965	1	1	1	0.428571	1	2.64E-07	1	0.04074
19	45540541	45540557	RELB	6.57E-10	3.96E-21	0.176471	1	1	1	1	1	0.010989	1	1	1	0.001095	1	1
14	23495610	23495622	PSMB5	2.17E-11	4.13E-21	1	1	1	1	1.12E-05	1	1	1	1	1	0.00031	1	0.012386
9	78638564	78638576	PCSK5	2.96E-09	4.33E-21	0.001587	0.009804	1	1	0.041148	1	1	0.109879	0.111111	0.0625	3.71E-07	1	0.000241
3	160134241	160134254	SMC4	1.03E-05	5.23E-21	0.00538	1	1	1	1	1	1	1	1	1	1.08E-14	1	0.003587
1	19683355	19683368	CAPZB	8.18E-11	5.48E-21	0.25	0.010695	1	1	0.049744	0.014354	1	0.003193	1	1	3.8E-05	0.055556	1
5	141511525	141511538	NDFIP1	2.03E-11	5.61E-21	1	1	1	1	1	1	0.016807	1	0.25	1	2.56E-18	1	0.000856

3	10301805	10301816	TATDN2	8.18E-11	5.77E-21	0.103383	1	1	0.022346	1	1	0.08253	1	1	1	1.38E-09	0.000402	0.006087
13	73293238	73293264	MZT1	1.69E-10	6.19E-21	0.008547	1	0.227958	1	1	0.012766	0.044439	1	1	1	0.000361	1	0.000229
8	95777578	95777591	DPY19L4	6.96E-11	6.98E-21	1	0.004348	1	0.026738	1	1	1	1	1	1	8.6E-17	1	0.001033
7	2403894	2403908	EIF3B	1.89E-09	7.91E-21	1	1	1	0.026455	1	1	0.008403	0.05042	1	1	7.49E-09	0.04	1
10	21536939	21536956	NEBL-AS1(dist=73087),CASC10(dist=246465)	4.67E-07	8.74E-21	0.008163	1	1	0.027972	1	1	1	1	1	1	2.39E-20	0.058824	0.041459
17	72926288	72926300	OTOP2	8.95E-06	8.86E-21	0.111111	1	1	1	1	1	0.034091	1	1	1	0.018724	0.095238	0.111016
2	38216766	38216779	RMDN2-AS1	2.65E-09	9.2E-21	0.00058	1	0.108392	1	1	1	1	0.146095	0.029851	0.363636	4.81E-20	0.019417	0.0017
20	32803319	32803330	EIF2S2(dist=103234),ASIP(dist=44841)	3.28E-08	1.15E-20	1	1	1	1	0.025862	1	1	1	0.035714	1	2.27E-09	1	0.057692
2	172314644	172314656	DCAF17	5.49E-07	1.66E-20	1	1	1	1	0.001625	1	1	0.102485	0.023256	0.125	3.79E-06	0.044776	0.005372
11	63311954	63311966	MIR3680-1,MIR3680-2	2.29E-08	1.76E-20	1	1	1	0.022222	0.02193	1	1	1	1	1	0.000565	1	1
2	99766927	99766943	C2orf15,TSGA10	1.37E-07	2.29E-20	0.004193	1	1	1	1	1	1	0.052166	1	1	1.59E-08	1	0.048071
5	127522153	127522180	SLC12A2	3.01E-08	2.31E-20	0.046264	1	1	0.215922	1	1	1	1	1	1	1.43E-13	0.008396	0.180918
12	56220974	56220993	DNAJC14	7.94E-05	2.59E-20	0.452851	0.054852	0.358029	0.257051	0.106391	1	0.114656	0.171979	1	1	0.082847	1	0.134676
6	32155249	32155264	PBX2	1.46E-06	3.19E-20	0.066667	1	1	0.025253	0.0125	1	1	0.04	1	1	1.82E-12	0.05	1
1	67098849	67098875	SGIP1	0.000123	3.25E-20	1	1	1	1	1	1	1	1	1	1	6.11E-08	0.044118	1
16	53496428	53496451	RBL2	1.41E-08	3.42E-20	1	1	0.217855	1	0.026882	1	1	0.002388	1	0.181818	1.42E-15	0.041096	0.019022
12	16052767	16052780	STRAP	1.16E-11	3.8E-20	1	1	0.005367	1	1	1	0.034333	1	1	1	1.56E-08	1	0.018098
12	57032216	57032235	ATP5B	5.29E-11	4.65E-20	3.61E-05	1	1	0.042453	0.007299	1	0.019608	1	1	1	1.83E-08	1	1
16	15758514	15758530	NDE1	0.000491	4.66E-20	1	1	1	0.08486	1	1	1	1	1	1	0.001282	1	1
3	14696955	14696967	CCDC174	6.17E-12	6.56E-20	0.00024	1	1	0.096707	1	1	1	1	1	1	6.06E-11	1	0.201212
5	129070812	129070838	ADAMTS19	8.15E-08	6.76E-20	0.066667	0.005348	1	1	1	1	0.044118	0.061856	0.045455	1	4.14E-08	1	0.075472
14	62016387	62016398	PRKCH	9.33E-11	7.11E-20	0.0625	1	1	0.091778	0.035317	1	1	1	1	1	7.46E-05	1	1
8	120800692	120800703	TAF2	4.31E-12	7.87E-20	0.074746	1	1	0.00021	1	1	0.030769	0.297715	1	1	2.82E-12	0.013333	0.007107
11	49196555	49196567	FOLH1	2.39E-11	8.9E-20	9.19E-05	1	1	0.020134	0.02941	1	0.022727	8E-05	1	1	1.11E-10	0.001586	0.000114
2	103281540	103281552	SLC9A2	2.98E-09	1.08E-19	0.199385	0.006452	0.009484	0.153551	1	1	1	0.004158	0.019231	0.066667	6.19E-06	0.015873	0.005599
14	24571860	24571874	PCK2	2.21E-08	1.1E-19	0.156667	1	0.00751	1	0.049115	1	0.029519	1	0.166667	1	0.000289	1	0.109945
12	109701959	109701975	ACACB	1.21E-07	1.19E-19	0.222222	0.027624	0.003011	0.173473	1	0.042857	1	1	0.136364	1	0.000732	1	1
1	75172756	75172771	CRYZ	1.55E-11	1.23E-19	0.020719	1	0.235032	0.221958	0.014963	0.067797	0.000826	0.202537	1	0.214286	2.52E-10	0.028169	0.005998
10	26802633	26802648	APBB1IP	1.11E-05	1.29E-19	0.000117	0.032086	0.201997	0.140221	0.156623	1	1	1	1	0.012821	7.85E-10	0.171047	0.271764
1	218610662	218610680	TGFB2	8.83E-11	1.33E-19	0.009231	0.023715	0.173494	0.08893	2.56E-05	1	1	0.072924	1	1	1.28E-06	1	0.461193
2	114500276	114500287	SLC35F5	8.88E-11	1.53E-19	0.054054	0.020671	0.139558	1	0.027777	1	1	1	1	1	1.81E-13	1	0.007363
17	35550269	35550290	ACACA	7.74E-10	1.57E-19	1	1	1	1	1	1	1	0.054054	0.062004	0.222222	1.61E-19	0.003049	0.024906
11	94230106	94230131	ANKRD49	0.000408	2.04E-19	0.133333	1	1	0.09035	0.013793	1	1	0.001742	1	1	0.010114	1	0.000385
1	213180434	213180459	ANGEL2	8.47E-12	2.37E-19	0.005348	0.063602	1	9.07E-05	1	0.014337	0.028267	0.000838	1	1	1.22E-06	1	0.01047
4	48529683	48529699	FRYL	3.37E-11	2.41E-19	0.012821	1	0.479895	0.128408	1	1	1	0.006897	1	1	4.1E-08	1	6.3E-05
8	121013744	121013756	DEPTOR	2.08E-11	2.42E-19	0.330435	0.014706	1	1	1	1	1	1	0.038462	1	1.14E-07	1	0.103891
11	47840864	47840879	NUP160	5.28E-08	3.78E-19	0.070779	1	1	0.036895	1	1	1	0.286019	0.071429	1	2.35E-09	1	0.000595
2	100006890	100006910	EIF5B	8.68E-12	4.67E-19	0.074627	1	1	0.050243	1	1	1	1	0.046154	0.333333	1.28E-19	1	0.349697
11	118884009	118884025	CCDC84	5.85E-11	5.19E-19	0.003246	1	1	0.047755	1	1	1	1	0.028986	1	5.09E-26	0.126618	0.066108
15	45968237	45968250	SQRDL	0.00024	5.94E-19	1	1	1	1	1	1	1	6.6E-05	0.310345	1	0.059613	1	0.102192
X	100530312	100530326	TAF7L	3.92E-07	5.99E-19	1	1	0.366988	0.00018	0.00157	1	1	1	0.027778	1	0.00966	1	0.041874
6	148761410	148761421	SASH1	9.99E-09	6.09E-19	0.045455	1	0.031737	0.012658	1	1	1	0.095183	0.027397	1	2.64E-10	0.04	0.000248
4	187560860	187560871	FAT1	4.7E-06	6.14E-19	0.026316	1	1	0.001947	0.03125	1	1	0.065359	1	1	8.31E-13	1	0.158935
2	27892022	27892033	SLC4A1AP	1.95E-09	6.22E-19	0.051282	0.028267	1	1	0.025316	1	1	0.058824	1	1	1.79E-07	1	0.084656
18	52927275	52927286	TCF4	0.000926	6.94E-19	0.153627	1	1	1	1	1	1	1	1	1	7.14E-06	1	1
19	36369450	36369462	APLP1	4.97E-10	7.13E-19	0.033898	1	1	0.029126	1	1	1	1	1	1	3.32E-08	0.030612	1
5	79655915	79655929	CRSP8P(dist=8130),ZFYVE16(dist=47903)	1.22E-09	8.56E-19	0.22619	1	1	0.147513	0.033262	1	0.02381	1	1	1	4.11E-05	0.144944	0.008626
9	26906079	26906091	PLAA	2.59E-08	8.76E-19	1	0.03468	1	0.053563	1	1	1	1	0.025641	1	2.64E-10	1	0.002443
15	30406088	30406103	ULK4P3	9.7E-12	9E-19	0.041353	1	1	1	1	1	1	1	1	1	2.04E-15	1	0.000534
7	26411416	26411434	SNX10	1.2E-05	9.36E-19	1	1	1	0.033613	1	1	1	0.096053	1	1	0.004757	1	0.123905
9	33056971	33056996	SMU1	9.67E-06	9.97E-19	1	0.020565	1	0.106888	1	1	0.008197	1	0.078947	0.315789	2.1E-07	1	0.071921
14	92076810	92076822	CATSPERB	1.57E-07	1.05E-18	1	1	0.236519	1	0.027397	1	1	0.01961	1	1	3.06E-12	1	0.002789
6	152702062	152702073	SYNE1-AS1	5.2E-06	1.3E-18	0.020833	1	0.2	1	1	1	0.035714	1	1	1	5.54E-09	1	0.002941
12	6994518	6994534	DSTNP2	1.2E-09	1.33E-18	0.291424	0.017977	1	0.026738	0.017778	1	1	0.044586	1	1	2.13E-10	1	0.005642
9	135523692	135523704	DDX31	1.51E-10	1.4E-18	0.016667	1	1	0.073659	1	1	1	1	0.015152	1	1.26E-10	1	7.46E-07
19	11453412	11453443	TMEM205	2.36E-06	1.57E-18	1	1	1	0.036585	0.02193	1	1	1	1	1	0.00415	0.027778	1
14	81448951	81448962	TSHR	8.17E-06	1.57E-18	0.140212	0.060227	1	0.000592	0.034283	1	1	0.47702	0.175476	1	2.01E-07	0.101215	0.187805
3	57632004	57632015	DENND6A	1.27E-08	1.95E-18	0.257217	0.017429	1	0.069286	1	1	1	1	1	1	1.32E-14	1	0.214475
19	44662274	44662288	ZNF234	7.49E-06	2.01E-18	0.2	0.03012	0.028565	1	0.091787	1	0.065918	1	0.042553	1	2.8E-09	0.048387	0.002801
17	65720150	65720161	NOL11	1.82E-06	2.32E-18	0.058824	1	1	1	0.014085	1	1	1	1	1	0.034832	1	0.144442
16	69385403	69385421	TMED6	1.12E-05	2.33E-18	0.12234	1	0.037313	1	0.012448	1	1	1	0.032258	1	3.62E-06	1	6.83E-06
16	51176119	51176131	SALL1	3.44E-09	2.45E-18	0.002299	1	1	0.020408	1	1	0.044444	1	1	1	2.24E-06	0.032787	0.096914
7	151046112	151046124	NUB1	2.49E-08	2.53E-18	0.001695	1	1	0.025974	0.022831	1	0.008475	1	1	1	1.92E-08	0.040816	0.006051
6	154489255	154489267	IPCEF1,OPRM1	2.65E-11	2.58E-18	1	1	0.041648	0.060962	1	1	1	0.000435	1	1	1.42E-09	0.034091	0.056452
10	116735234	116735260	TRUB1	7.15E-06	2.98E-18	1	1	1	1	1	0.026316	1	1	1	1	0.000567	0.125	1
10	104120731	104120750	GBF1	0.001549	3.07E-18	0.212121	1	0.064935	1	1	1	1	0.162921	1	1	0.000555	0.02	0.029853
3	10429902	10429913	ATP2B2	1.42E-05	3.29E-18	0.16129	1	1	0.042249	1	1	1	0.076923	1	0.133333	6.85E-11	1	0.000428
17	4646533	4646547	ZMYND15	9.58E-08	3.6E-18	0.194737	0.107236	0.020449	0.36072	0.002219	1	0.009709	0.002158	1	1	1.11E-06	1	0.045456
7	23226646	23226667	NUPL2	1.44E-10	3.85E-18	0.179579	1	1	1	1	1	1	0.043478	1	1	3.85E-11	0.001317	9.65E-07
6	90347394	90347406	LYRM2	1.9E-09	4.17E-18	0.056604	1	0.225015	0.007634	0.054534	1	0.016393	0.000881	1	1	7.45E-12	0.028169	1
4	146475243	146475261	SMAD1	2.84E-10	4.23E-18	0.071429	1	0.276043	1	1	1	1	1	1	0.071429	9.99E-09	1	0.004198
8	95507237	95507250	KIAA1429	5.5E-07	4.58E-18	0.002082	1	0.014787	1	1	0.018349	0.07871	1	1	1	3.06E-10	1	0.157149
15	74536285	74536301	CCDC33	0.000217	4.65E-18	1	1	1	0.005541	1	1	1	0.06448	0.041667	1	0.02064	0.035294	1
16	66884343	66884355	CA7	3.7E-08	4.66E-18	0.25	1	1	1	1	1	1	1	0.016667	1	0.0045	1	1
9	103212778	103212790	MSANTD3,MSANTD3-TMEFF1	8.97E-09	5.02E-18	0.061538	1	0.057325	1	1	1	0.015038	0.03065	1	1	8.62E-17	1	0.062809
9	19328009	19328021	DENND4C	3.38E-10	5.42E-18	0.060606	1	1	1	0.038213	0.004695	1	0.000584	0.026316	0.071429	1.55E-05	1	0.094675
6	71009951	71009963	COL9A1	3.32E-10	5.52E-18	0.046749	1	1	0.12281	1	1	1	0.074244	1	0.073529	6.48E-11	0.013333	0.25882
2	64806544	64806556	AFTPH	1.28E-11	5.84E-18	1	0.033331	1	1	1	1	0.042324	1	0.001681	1	3.26E-24	0.019608	0.134383
17	9497478	9497490	CFAP52	6.13E-12	6.18E-18	1	1	1	0.03352	1	1	0.039732	0.051948	0.029412	1	2.29E-12	0.021978	0.008145
10	116203903	116203928	ABLIM1	1.17E-11	6.47E-18	0.05	1	1	0.004034	0.040882	1	1	0.142197	0.015152	1	4.86E-07	1	0.173906
20	33665775	33665786	TRPC4AP	3.46E-09	6.49E-18	0.048387	1	0.049645	0.037559	0.040482	1	1	1	0.03125	1	2.97E-14	0.010526	0.066869
8	12598316	12598327	LONRF1	6.57E-06	6.57E-18	1	1	0.208333	0.000958	1	1	1	1	1	1	5.05E-06	1	1
6	43021976	43021989	MRPL2	7.87E-08	6.65E-18	0.423077	0.059246	1	0.000115	0.003423	1	0.008598	1	1	1	2.18E-06	0.053571	1
14	74875955	74875968	SYNDIG1L	1.09E-07	6.99E-18	1	1	1	1	0.016161	1	0.017241	1	1	1	1.52E-11	0.068966	1
12	82871010	82871021	METTL25	1.48E-08	7.51E-18	0.027778	1	1	1	1	1	1	1	1	1	0.000103	0.085678	0.0033
3	142241692	142241705	ATR	2.43E-10	7.52E-18	1	0.009709	0.122102	1	1	1	1	1	1	1	1.97E-16	0.003891	1
4	68547232	68547242	UBA6	1.58E-09	7.58E-18	1	1	1	1	1	1	1	1	1	1	3.31E-11	1	0.021968
14	21702046	21702071	HNRNPC	8.88E-10	8.01E-18	0.072727	0.00431	0.062112	0.02439	0.025105	1	1	1	0.014925	1	1.68E-15	0.03125	0.002824
21	47647618	47647632	LSS	0.039351	8.57E-18	1	1	1	0.044944	1	1	1	1	1	0.035714	0.044118	0.06383	0.01574
17	35620810	35620826	ACACA	6.33E-10	8.65E-18	0.052632	0.014388	0.066667	0.022388	0.016129	1	1	1	1	1	9.44E-19	1	0.150524
3	52727189	52727200	GNL3	1.06E-05	9.19E-18	0.097561	1	1	0.083734	1	1	1	0.000182	1	1	1.8E-07	0.028571	0.177397
17	46248074	46248089	SKAP1	1.24E-11	9.62E-18	0.023416	1	1	0.080167	1	0.00885	0.019802	1	1	0.2	8.03E-06	1	0.011708
6	151859146	151859161	CCDC170	0.000141	1.05E-17	0.025997	1	0.305135	0.001125	1	0.035176	1	1	1	0.083333	1.21E-09	0.008808	0.002404
5	137506862	137506874	BRD8	1.32E-05	1.07E-17	0.041667	1	1	1	1	1	1	0.028283	1	1	9.61E-13	0.04	0.000164
7	76984752	76984767	GSAP	1.47E-06	1.07E-17	0.105195	0.097739	0.184111	0.233229	1	1	0.043474	0.205141	1	1	5.05E-09	1	0.002224
5	68667019	68667039	RAD17	1.05E-10	1.21E-17	1	1	1	1	1	1	1	1	1	1	0.014778	1	1
2	95783701	95783713	MRPS5	3.4E-07	1.25E-17	1	0.022791	1	1	0.000662	1	1	1	1	1	1.52E-10	1	1
10	120070457	120070469	FAM204A	1.53E-08	1.33E-17	0.109015	1	1	1	1	1	1	0.108515	0.02439	1	9.73E-12	0.130303	0.001549
9	96259883	96259912	FAM120A	1.55E-11	1.39E-17	0.066102	1	1	1	1	1	1	1	1	1	9.97E-08	1	0.048174
12	3935279	3935290	PARP11	9.58E-08	1.41E-17	0.047619	0.011628	1	0.06087	1	1	1	1	1	1	1.84E-08	1	0.00403
15	52571270	52571284	MYO5C	5.58E-12	1.65E-17	2.78E-05	1	1	1	1	1	1	0.116261	1	1	1.5E-16	0.055556	1
2	152236045	152236060	TNFAIP6	5.19E-08	1.67E-17	0.007389	1	1	0.025974	0.042662	1	0.023077	0.000582	1	1	1.44E-10	0.15	0.007688
4	7817686	7817710	AFAP1	2.79E-11	1.75E-17	0.0625	1	0.128431	0.015226	0.088441	0.023697	1	0.051852	1	1	0.001258	1	0.107524
15	63966513	63966528	HERC1	6.82E-09	1.78E-17	0.118305	1	0.215177	0.201199	0.103644	1	1	1	0.019231	1	1.4E-09	1	0.165515
3	62459813	62459846	CADPS	5.81E-12	1.91E-17	0.002387	1	1	1	0.011494	1	1	1	1	1	1.43E-09	1	0.306133
8	86022336	86022348	LRRCC1	7.97E-12	1.94E-17	0.005026	1	1	0.040816	1	1	0.020833	0.05	0.028571	1	8.24E-17	0.019231	1
17	465993	466012	VPS53	6.28E-06	2.12E-17	0.124884	0.014706	1	1	1	1	0.006993	1	0.018182	1	1.11E-07	0.172559	0.038532
8	28651296	28651312	INTS9	5.06E-06	2.18E-17	0.206349	1	0.422926	1	1	1	0.099925	1	1	1	0.000839	1	1
X	108636043	108636070	GUCY2F	2.28E-10	2.25E-17	0.119898	1	0.122485	1	0.000756	1	1	0.003497	0.125	1	8.27E-11	0.032787	0.016575
19	41626438	41626451	CYP2F1	8.22E-11	2.44E-17	0.041667	1	1	0.211979	0.091321	1	0.068164	0.586452	0.070175	1	0.001674	0.093702	0.352257
1	65099701	65099716	CACHD1	6.73E-08	2.6E-17	0.001031	1	1	0.047127	0.099264	1	1	1	1	1	5.34E-26	1	0.000101
4	1806012	1806024	FGFR3	1.19E-08	2.73E-17	1	1	1	0.009022	0.067941	1	1	0.205456	1	1	0.047619	0.051724	0.365537
19	34824582	34824600	KIAA0355	2.69E-10	2.97E-17	0.003484	1	1	0.246402	0.111	1	1	0.111002	1	1	9.82E-17	1	1
14	95999676	95999689	SNHG10	4.86E-05	3.26E-17	1	1	1	0.007261	0.001085	1	1	2.52E-09	0.032258	1	0.1	1	0.032258
1	155671942	155671962	DAP3	8.94E-08	3.39E-17	0.017825	1	1	1	1	1	0.006993	1	1	1	9.75E-11	0.03125	0.03399
1	85575838	85575853	WDR63	2.16E-08	3.45E-17	0.003507	1	1	1	0.000589	1	0.061209	1	1	1	1.48E-18	0.022222	0.004856
4	148457005	148457019	EDNRA	3.99E-05	3.66E-17	0.018197	1	0.1209	1	1	1	1	0.164578	1	0.027569	1.09E-07	1	0.002877
22	44368728	44368741	SAMM50	5.58E-10	3.77E-17	0.11103	0.05111	0.092728	1	0.004871	1	1	0.139977	1	0.304348	7.88E-12	1	0.485294
11	95562535	95562546	CEP57	5.13E-05	3.79E-17	0.098718	1	0.53049	0.140221	1	1	0.018018	0.317532	1	0.230769	3.52E-05	1	0.536501
10	71965991	71966002	PPA1	2.03E-07	4.13E-17	0.05	1	1	1	1	1	1	1	0.032258	1	0.000356	1	1
16	67409030	67409054	LRRC36	1.61E-06	4.26E-17	0.222222	1	1	0.006944	1	1	0.011765	1	1	1	0.007937	1	1
17	59147195	59147217	BCAS3	0.004267	4.35E-17	0.181818	1	1	1	1	1	1	1	0.035714	1	0.008547	1	1
1	114940632	114940645	TRIM33	1.41E-08	4.97E-17	0.055556	1	1	0.19065	0.183547	1	1	0.411804	1	1	2.5E-10	1	0.044935
18	31523144	31523156	NOL4	9.31E-10	5.76E-17	1	0.005814	1	0.059837	1	1	1	1	1	0.333333	6.89E-10	1	0.000497
12	970078	970128	WNK1	4.03E-09	5.89E-17	1	1	0.302725	0.251824	1	1	0.000615	0.025319	1	1	0.010084	1	0.002221
11	26574771	26574790	ANO3	0.000301	6.34E-17	0.090909	0.052796	1	1	1	1	1	1	0.021277	1	0.175951	1	0.048851
10	112649255	112649287	PDCD4	1.44E-07	6.4E-17	0.072727	0.004854	1	0.047619	1	1	0.011765	0.055172	1	1	2.56E-17	0.028571	0.001523
2	220082365	220082377	ABCB6	1.18E-10	6.66E-17	0.01658	1	1	1	0.021552	1	1	0.105178	0.018868	1	1.03E-09	0.068947	0.077928
3	113639062	113639074	GRAMD1C	1.49E-09	8.61E-17	0.033898	1	1	1	1	1	0.021583	0.044444	1	1	1.29E-09	0.026316	0.235877
1	213009178	213009196	SPATA45	2.66E-09	9.19E-17	0.028733	1	1	0.00796	0.139615	1	0.06292	1	1	1	2.31E-27	1	0.001688
20	6077429	6077449	FERMT1	0.000487	9.23E-17	0.031621	1	1	1	0.005299	1	1	1	1	1	5.05E-05	1	0.103488
1	202407189	202407200	PPP1R12B	9.04E-08	1.03E-16	0.041667	0.011111	1	1	1	1	1	1	0.018868	1	1.73E-10	0.052281	1
1	65129233	65129268	CACHD1	2.12E-06	1.14E-16	1	1	1	0.001496	0.018182	1	1	1	1	1	0.001363	0.012821	0.159914
5	81601142	81601155	ATP6AP1L	8.88E-12	1.15E-16	0.058824	1	1	0.005747	1	1	1	1	1	1	5.91E-05	0.001081	1.46E-06
9	88292499	88292521	AGTPBP1	6.06E-12	1.17E-16	0.006061	1	1	1	1	1	1	0.052288	1	1	1.35E-07	1	0.010813
11	59420570	59420588	PATL1	1.39E-09	1.21E-16	0.071429	0.012346	1	1	1	1	1	1	1	1	1.28E-10	1	0.128408
6	56869464	56869475	BEND6	2.73E-10	1.26E-16	1	1	1	0.019868	1	1	1	1	1	1	0.012821	0.08951	0.073733
12	14599855	14599867	ATF7IP	1.01E-11	1.36E-16	0.003896	1	0.074766	0.018519	0.043161	1	1	1	1	1	2.21E-20	0.098305	0.089589
1	201981005	201981023	ELF3	0.036522	1.36E-16	0.395604	1	1	0.071882	1	1	1	1	1	1	0.003923	1	0.001077
10	105752705	105752727	SLK	3.22E-08	1.4E-16	0.051282	1	1	1	1	1	1	7.92E-06	1	1	1.57E-15	1	0.001464
6	44216544	44216556	HSP90AB1	1.25E-10	1.42E-16	0.012097	0.039106	1	0.060039	0.028618	1	0.09798	1	1	1	3.72E-12	0.012704	0.000139

10	122630877	122630889	MIR5694	8.56E-06	1.5E-16	0.002775	6.35E-05	1	0.040323	1	1	0.011628	7.98E-05	0.074074	1	4.73E-06	1	0.014545
16	1612145	1612157	IFT140	5.96E-08	1.56E-16	0.012987	1	1	0.033058	1	1	1	1	1	1	2.47E-08	1	0.201622
12	989800	989815	WNK1	1.76E-07	1.68E-16	1	0.126303	1	0.014769	0.228381	0.056604	0.034483	4.06E-06	1	0.272727	0.000247	1	1
2	11913727	11913739	LPIN1	6.47E-12	1.7E-16	0.003896	0.011236	1	0.084299	1	1	1	0.092613	0.002299	1	1.16E-06	1	0.10996
1	161721402	161721414	DUSP12	3.04E-09	1.7E-16	0.042553	1	0.05303	1	0.019704	1	1	0.042735	1	1	2.81E-12	0.018868	0.012739
2	9515099	9515114	ASAP2	4.33E-08	1.85E-16	0.109524	1	1	1	0.048379	1	0.055036	1	1	1	1.24E-09	0.018182	1
1	151955791	151955814	S100A10	2.48E-07	1.91E-16	1	1	1	1	0.025641	1	1	1	1	1	0.007781	0.025316	0.021532
18	56279052	56279066	ALPK2	8.54E-06	2.01E-16	0.213675	1	0.096491	1	0.014019	0.015075	1	1	1	1	1.38E-08	1	0.001368
5	65088487	65088503	NLN	8.14E-05	2.08E-16	1	1	0.096774	1	0.047238	1	1	1	0.018182	1	2.34E-08	1	0.000246
1	179086419	179086431	ABL2	3.94E-09	2.16E-16	0.044444	1	1	1	0.046915	1	1	0.153846	1	1	0.000117	1	0.001171
12	53573454	53573467	CSAD	1.2E-08	2.17E-16	1	1	1	1	1	1	0.044439	1	1	1	4.28E-05	1	0.023423
1	184692999	184693020	EDEM3	1.66E-09	2.18E-16	0.083333	1	0.040198	1	1	1	1	0.022556	0.000342	1	1.45E-07	1	1
21	42838093	42838104	TMPRSS2	3.32E-09	2.28E-16	0.283838	0.005714	1	0.056526	0.016949	1	1	1	1	1	2.81E-12	0.025316	1
12	7889886	7889934	CLEC4C	4.85E-05	2.28E-16	0.050568	0.036145	1	1	0.084834	1	1	1	0.041667	1	0.000825	0.055556	0.233048
10	76349020	76349033	ADK	8.71E-11	2.37E-16	0.000511	1	1	0.005603	1	1	0.009009	1.01E-07	0.032258	1	1.09E-08	0.054414	0.01291
12	54676165	54676176	HNRNPA1	5.82E-06	2.42E-16	0.040816	0.012346	1	0.025	1	1	1	0.101695	0.063987	1	1.09E-05	1	0.170488
22	31985385	31985398	SFI1	3.22E-07	2.44E-16	0.145299	1	1	1	0.000149	1	1	0.055556	1	1	0.000993	1	0.091483
12	129566284	129566302	TMEM132D	1.49E-07	2.52E-16	0.022569	1	1	1	1	1	0.045045	0.014141	0.070175	0.065359	4.78E-16	0.124875	0.15526
4	68416393	68416409	CENPC(dist=5137),STAP1(dist=8037)	2.23E-08	2.58E-16	1	0.109879	1	0.120554	0.10097	1	1	0.007064	0.023256	1	0.041667	0.033898	1
17	7700419	7700440	DNAH2	0.414628	2.73E-16	0.058824	0.007634	0.11171	1	1	1	1	1	1	1	0.000106	1	0.00694
5	179032860	179032871	RUFY1	1.48E-06	2.74E-16	1	0.008889	1	0.02139	1	1	0.018349	1	0.03125	1	1.51E-06	1	0.003615
11	14501267	14501282	COPB1	9.35E-11	2.81E-16	0.0625	1	1	1	0.000109	1	1	1	1	1	5.33E-14	0.03125	0.050139
17	8397208	8397219	MYH10	2.01E-08	2.81E-16	0.055556	1	1	1	1	1	1	0.075758	0.067212	1	6.99E-10	0.045455	0.147325
19	4430524	4430535	CHAF1A	1.19E-06	2.84E-16	1	1	0.127138	1	0.015075	1	1	1	0.027778	1	2.05E-05	1	0.027273
12	56994331	56994349	BAZ2A	1.55E-07	2.87E-16	1	0.009091	1	0.079967	0.01992	1	1	0.044444	1	1	2.11E-06	1	0.051597
1	45976928	45976939	PRDX1	3.39E-06	3.01E-16	0.034677	1	1	0.044444	1	0.005464	1	1	1	1	0.000302	1	0.139434
12	26816832	26816843	ITPR2	0.001014	3.09E-16	1	1	1	1	0.010753	1	1	1	1	1	0.000212	1	0.065
1	207930564	207930575	CD46	7.17E-06	3.09E-16	0.011858	0.014388	1	0.030612	1	1	1	1	1	1	0.003289	1	1
8	94817177	94817188	TMEM67	2.43E-11	3.41E-16	0.037736	0.010753	0.114286	1	0.016393	1	1	0.074627	1	1	2.74E-12	1	1
7	103828911	103828922	ORC5	2.04E-06	3.49E-16	1	1	1	0.013889	0.011905	1	1	1	1	1	1.08E-05	1	1
19	8438454	8438467	ANGPTL4	0.000204	3.51E-16	1	1	1	1	1	1	1	0.002504	1	1	1	1	0.014925
11	43419087	43419112	TTC17	4.61E-09	3.62E-16	1	1	1	1	1	1	0.014493	1	1	1	0.000333	1	0.02728
19	39909218	39909231	PLEKHG2	1.45E-08	3.64E-16	0.313725	1	1	1	1	1	1	1	1	1	0.091304	0.086957	4.05E-05
4	55976947	55976961	KDR	1.14E-11	3.86E-16	0.000735	1	0.068221	0.196535	1	1	0.03463	1	1	1	2.39E-24	0.007998	0.031174
6	130761525	130761543	TMEM200A	4.52E-09	3.87E-16	0.06383	1	0.080292	0.073659	0.012146	1	1	1	1	1	9.64E-06	1	1
3	195022926	195022944	ACAP2	9.7E-07	3.93E-16	0.006209	1	0.163807	0.093203	1	0.013043	1	0.152871	1	1	1.43E-21	1	0.18614
6	79656600	79656611	PHIP	1.45E-09	4.04E-16	0.006734	1	1	1	1	1	1	1	1	1	8.71E-10	1	0.01168
21	17238572	17238582	USP25	5.42E-05	4.16E-16	1	0.03463	0.017501	0.000229	1	1	1	1	1	1	1.07E-07	0.037037	0.0875
1	22030891	22030902	USP48	1.14E-08	4.22E-16	1	0.01105	1	0.021277	1	1	0.009615	1	0.017241	1	0.007508	0.039474	0.150308
15	84558772	84558783	ADAMTSL3	3.67E-07	4.7E-16	0.061224	1	1	1	1	1	1	1	0.032787	1	3.92E-05	0.038961	0.024057
X	153714027	153714038	UBL4A	0.000192	4.71E-16	1	0.013333	1	0.024793	0.027397	1	1	0.002283	1	0.214286	0.000379	1	0.413055
2	96994050	96994061	ITPRIPL1	0.0001	4.75E-16	1	1	1	1	0.015	1	1	0.213495	1	1	6.45E-08	1	1
13	41382557	41382568	TPTE2P5	1.11E-05	4.78E-16	0.025	1	1	1	0.019737	1	0.016949	1	1	0.333333	0.0004	0.050847	0.030591
X	11200070	11200086	ARHGAP6	1.49E-10	4.83E-16	0.028894	1	0.208829	0.164334	1	1	1	0.000912	1	1	8.51E-15	1	0.075874
5	179150788	179150800	CANX	4.23E-08	4.83E-16	0.04878	0.01	1	0.013605	0.001636	1	1	0.024808	1	0.263158	1.39E-16	1	0.056064
11	1905146	1905158	LSP1	5.48E-09	4.92E-16	0.153846	0.040268	0.241783	0.078912	1	1	0.004303	0.132565	1	1	0.037555	1	0.030409
1	38052867	38052907	GNL2	1.35E-11	5E-16	0.067212	1	0.017896	1	0.044112	1	0.082018	0.177772	1	1	3.85E-06	0.055164	0.000113
12	121004564	121004583	RNF10	0.000683	5.04E-16	0.016158	0.055545	0.085136	0.00028	0.001493	1	1	0.005862	1	1	8.22E-13	1	0.001825
4	77276593	77276604	CCDC158	4.48E-08	5.08E-16	1	1	0.260629	0.037838	1	1	1	0.04386	0.014925	1	3.4E-13	1	0.009879
15	49926993	49927013	DTWD1	6.81E-05	5.74E-16	0.001783	1	1	1	1	1	1	1	0.037037	1	0.01181	1	0.130264
1	42776699	42776711	FOXJ3	4.88E-12	5.84E-16	0.048387	0.028707	1	0.194884	1	1	0.014286	1	0.029851	1	3.77E-24	0.021978	0.030085
2	120712718	120712731	PTPN4	7.53E-12	5.86E-16	0.068182	1	1	0.044316	0.07996	1	0.014085	0.003401	1	0.153846	4.45E-07	1	0.000609
15	65412325	65412337	PDCD7	9.06E-07	5.95E-16	1	1	0.064935	0.037497	1	0.004329	0.018519	0.004419	1	1	0.007628	1	0.141075
6	49459994	49460005	CENPQ	6.7E-11	5.97E-16	1	0.006098	1	1	1	1	0.037207	1	1	1	5.49E-17	0.001053	0.012338
3	58792080	58792092	C3orf67	2.69E-09	6E-16	0.133192	1	0.149775	1	1	1	0.090857	0.003864	1	1	2.37E-11	0.000733	0.067419
19	41895839	41895854	EXOSC5	0.012401	6.25E-16	1	1	1	1	0.041771	1	1	0.066038	1	1	5.02E-07	0.058824	0.005821
10	98412329	98412342	PIK3AP1	2.51E-07	6.29E-16	0.176471	1	1	1	1	1	1	1	1	1	0.037433	0.068966	0.001709
1	22837586	22837604	ZBTB40	3.55E-08	6.31E-16	0.008772	1	1	1	0.013035	1	1	0.002675	1	0.2	4.3E-05	0.087391	0.171569
1	158298679	158298691	CD1B	1.31E-11	6.71E-16	0.005288	0.010309	1	0.035176	0.013274	1	1	1	0.04918	1	1.41E-11	0.02439	1
10	90983403	90983415	LIPA	3.21E-09	6.87E-16	0.074746	1	0.15361	1	0.019512	1	0.021053	1	1	1	8.52E-14	1	0.184325
11	115049203	115049221	CADM1	1.15E-06	7.28E-16	0.125	1	1	1	0.065769	1	0.017699	1	1	1	0.005299	1	0.133921
12	114837219	114837235	TBX5	1.63E-10	7.4E-16	0.004049	0.027272	0.038228	0.045839	0.063273	1	0.025316	0.064482	1	0.076923	1.47E-08	0.08599	0.458021
1	180757007	180757018	XPR1	3.14E-05	7.44E-16	0.261084	1	1	0.027322	1	0.013953	1	1	1	1	1.24E-16	1	0.267579
7	20826270	20826284	SP8	8.63E-11	7.54E-16	0.086957	1	1	0.005236	1	1	1	1	0.037736	1	1.47E-18	0.000439	0.054493
7	130927780	130927804	MKLN1	7.34E-06	7.55E-16	1	1	1	1	1	1	1	1	1	1	0.236364	1	1
2	176995682	176995693	HOXD8	0.000138	8.31E-16	1	1	1	0.000869	0.000236	1	1	1	0.022222	1	1.09E-09	1	0.027397
2	211457713	211457724	CPS1	1.96E-08	8.66E-16	0.1875	1	0.013889	0.035971	1	1	0.031746	1	1	1	6.15E-05	0.042254	0.009099
7	95442405	95442420	DYNC1I1	2.26E-07	8.79E-16	0.279557	1	0.434865	0.102934	0.002513	1	1	0.073505	1	0.125	2.56E-10	1	0.003403
11	134078847	134078858	NCAPD3	4.74E-10	8.93E-16	1	0.011765	1	1	1	1	1	0.034783	0.03125	1	5.86E-13	1	0.001626
16	56448114	56448126	AMFR	7.99E-06	9.68E-16	0.176136	1	1	0.076649	0.040354	1	1	0.081081	1	1	0.000409	1	0.15155
18	47438344	47438355	MYO5B	1.57E-10	1.01E-15	1	1	1	0.031414	1	1	1	0.002747	1	1	3.26E-06	1	0.074303
17	17796875	17796886	TOM1L2	6.85E-07	1.05E-15	0.068182	1	0.179929	0.021505	1	1	1	1	1	0.194737	0.073203	1	0.004219
6	88853530	88853542	CNR1	1.58E-09	1.09E-15	0.000673	1	1	0.03065	1	0.010204	0.02	2.87E-05	0.034483	1	1.49E-08	1	3.81E-05
5	70818329	70818354	BDP1	9.93E-05	1.11E-15	0.054795	1	1	1	1	1	1	1	1	1	3.46E-21	1	0.037313
8	133816999	133817019	PHF20L1	1.31E-05	1.11E-15	0.088889	1	1	0.038462	1	1	1	0.108515	1	1	1.28E-06	1	0.027157
2	220040216	220040231	CNPPD1	1.45E-08	1.13E-15	1	1	1	0.048773	1	0.004545	1	0.190932	1	1	2.63E-11	0.087879	0.17801
7	77006534	77006576	GSAP	4.61E-09	1.14E-15	0.01087	1	1	1	1	1	1	1	1	1	5.81E-05	1	0.037547
5	158526517	158526550	EBF1	0.009245	1.22E-15	0.341158	0.031577	0.127505	0.008625	0.072787	1	0.022727	1	1	0.227273	5.96E-17	1	0.017669
3	124629205	124629243	MUC13	5.56E-06	1.26E-15	0.056338	1	1	1	1	1	1	1	1	0.210526	1.66E-08	1	0.009638
X	15364158	15364186	PIR-FIGF	4.67E-05	1.26E-15	1	1	0.166667	0.010417	1	1	1	1	1	1	7.76E-07	0.017857	0.000788
1	144916415	144916426	NBPF20,NBPF9,PDE4DIP	0.000194	1.29E-15	0.060606	1	1	1	1	1	1	0.06	0.019608	1	7.98E-05	1	0.000696
14	95923421	95923440	SYNE3	0.013076	1.37E-15	1	1	1	0.195423	1	1	0.001344	0.083297	1	1	0.076555	1	0.078139
3	108182168	108182180	MYH15	1.07E-09	1.44E-15	0.002177	1	1	0.039216	1	1	0.014599	1	1	1	1.9E-10	1	0.196099
17	66871570	66871581	ABCA8	0.000198	1.51E-15	0.095238	1	1	1	1	1	1	1	0.033333	1	2.46E-08	1	0.055
2	128854948	128854963	UGGT1	1.17E-08	1.51E-15	0.000278	1	1	1	1	1	1	1	1	1	8.06E-13	1	0.010383
15	86768264	86768280	AGBL1	1.27E-11	1.64E-15	0.003011	0.00813	1	1	1	1	0.035712	1	1	1	3.97E-10	0.00101	0.060386
20	3564453	3564466	ATRN	1.85E-10	1.66E-15	0.050847	1	1	1	1	1	1	0.022222	1	1	0.000352	0.023529	1
14	90458397	90458409	TDP1	5.24E-12	1.7E-15	1	0.014388	1	1	1	1	1	1	1	0.133333	0.000608	1	0.118306
X	117035914	117035926	KLHL13	2.89E-09	1.72E-15	0.069549	1	0.136364	1	0.022727	1	1	0.267606	1	1	1.4E-11	1	4.89E-07
7	148888054	148888067	ZNF398(dist=7936),ZNF282(dist=4510)	3.42E-09	1.81E-15	1	1	1	1	0.019851	1	1	0.067548	0.333333	1	0.000202	0.176471	0.045161
2	58390218	58390231	FANCL	9.29E-08	1.82E-15	0.04878	1	0.152632	1	1	1	1	1	1	1	5.05E-10	0.032258	0.007371
9	96209987	96209999	FAM120AOS	5.33E-10	1.95E-15	0.222986	1	0.220278	0.01677	0.005265	1	0.144595	0.30402	0.076169	0.210526	7.39E-14	1	0.03101
7	151919159	151919171	KMT2C	5.66E-06	1.96E-15	1	1	1	0.022099	1	1	1	1	1	1	2.35E-07	0.02381	0.151739
15	101929632	101929652	PCSK6	0.349845	2.13E-15	1	1	1	0.042553	2.53E-08	1	0.057692	0.116388	1	1	0.003607	1	1
12	49722646	49722658	TROAP	5.83E-06	2.24E-15	1	1	1	0.026316	1	1	1	1	1	1	7.1E-09	0.034483	0.00521
12	101705465	101705490	UTP20	3.5E-07	2.28E-15	0.105263	1	1	1	0.032785	1	0.021053	1	1	1	0.000167	0.030769	0.018049
20	35632021	35632042	RBL1	3.83E-10	2.28E-15	1	1	1	1	0.017647	1	1	1	0.030769	1	1.27E-08	1	0.000489
2	8822892	8822918	ID2	1.12E-08	2.39E-15	0.08951	1	0.176136	1	1	1	1	1	0.021739	1	6.25E-22	1	0.003215
X	35984669	35984680	CXorf22	1.12E-07	2.43E-15	0.045455	1	0.164408	1	1	1	1	1	1	1	2.15E-10	0.042777	0.00943
3	119348345	119348362	PLA1A	6.9E-08	2.44E-15	1	1	0.077381	1	1	1	1	1	1	0.090909	1.05E-07	1	0.000388
13	41814298	41814313	MTRF1	1.34E-10	2.53E-15	0.330279	1	1	1	1	1	0.056593	0.063678	0.025	1	3.4E-09	0.001442	0.029412
1	28929961	28929973	TAF12	2.07E-08	2.55E-15	1	1	1	1	0.031412	1	1	1	1	1	5.84E-09	0.011628	6.31E-06
2	24952712	24952726	NCOA1	2.85E-09	2.56E-15	1	1	0.134518	1	1	1	1	1	1	0.25	0.000908	1	0.001958
9	132595849	132595861	C9orf78	3.06E-10	2.66E-15	1	1	0.085366	1	0.025531	1	1	0.00326	0.015873	1	9.63E-15	1	0.003279
22	39813625	39813640	TAB1	6.59E-09	3.06E-15	0.116883	1	0.050314	1	1	1	1	0.052632	1	1	1.04E-06	1	0.008104
14	39597463	39597482	GEMIN2	1.92E-07	3.17E-15	0.039216	1	1	1	1	1	1	0.000122	0.033333	1	1.8E-09	0.057143	0.002233
10	96025381	96025392	PLCE1	2.69E-06	3.25E-15	0.047619	1	1	0.042324	0.034188	1	0.027027	0.003419	1	1	1.44E-11	1	0.007253
3	32746271	32746301	CNOT10	7.32E-08	3.33E-15	0.068966	1	1	0.076238	1	1	1	0.036585	0.019231	1	1.51E-10	1	1
10	101643723	101643734	DNMBP	8.11E-07	3.39E-15	1	1	0.114583	1	0.035632	1	0.024793	0.114656	1	1	2.19E-07	0.043478	1
17	66033401	66033412	KPNA2	4.26E-05	3.41E-15	1	1	1	1	1	1	0.015625	1	0.000546	1	2.67E-11	0.001442	0.097009
9	98230924	98230947	LOC100507346	9.28E-07	3.42E-15	1	0.010417	1	0.000785	1	1	0.129944	7.01E-07	1	0.000877	5.71E-13	1	0.013549
17	40040422	40040434	ACLY	2.01E-11	3.48E-15	1	1	1	0.025862	1	1	1	0.104167	1	1	3.67E-11	1	1
1	159166612	159166624	CADM3-AS1	3.15E-11	3.67E-15	0.09375	1	1	1	0.000855	1	1	1	1	0.190476	1.24E-05	1	0.083296
15	52903303	52903313	FAM214A	4.29E-09	3.7E-15	1	0.009009	0.359204	1	1	1	1	1	1	1	1.33E-09	0.06	1
2	179330468	179330480	MIR548N	1.04E-10	4.02E-15	1	0.055036	0.230819	1	1	1	1	1	1	0.083333	7.34E-11	0.118305	0.178322
2	43778857	43778869	THADA	0.001784	4.05E-15	0.147313	1	0.016574	1	1	1	1	0.20443	0.006494	0.052632	2.23E-08	0.101974	0.127598
8	53452359	53452373	FAM150A	1.03E-07	4.17E-15	1	1	1	0.417122	1	1	0.063226	0.322181	0.14	1	6.16E-18	1	1
14	74534274	74534284	ALDH6A1	8.52E-06	4.17E-15	0.002899	0.000658	1	1	1	1	1	1	1	1	1.38E-10	1	0.008808
12	15803742	15803753	EPS8	1.86E-07	4.23E-15	0.025	1	0.058824	0.027027	0.05817	1	1	0.125	0.028169	1	1.34E-08	1	0.073684
10	74653468	74653479	OIT3	9.06E-11	4.31E-15	0.094077	1	0.129944	1	1	1	1	0.073171	0.019608	1	6.97E-23	1	0.000183
10	34985197	34985210	PARD3	1.24E-11	4.45E-15	1	0.0375	1	0.008081	0.064268	1	0.076923	1	1	0.038462	4.98E-12	1	0.361585
6	34934996	34935007	ANKS1A	8.25E-08	4.6E-15	0.093023	1	0.133733	1	1	1	1	1	1	1	1.07E-07	0.02439	1
10	60148569	60148580	TFAM	6.94E-12	4.72E-15	0.109524	1	1	0.034884	1	1	0.03524	1	1	1	1.93E-06	1	0.003366
19	54400979	54401003	PRKCG	1.96E-08	4.78E-15	1	0.015385	1	1	0.009901	1	1	1	1	1	0.001054	1	1
6	96971185	96971208	UFL1	2.98E-11	4.89E-15	1.83E-05	0.005319	1	0.062322	1	1	0.046506	0.057692	1	1	1.13E-19	0.0375	1
17	2323953	2323979	METTL16	3.4E-07	5.11E-15	1	1	1	1	0.009524	1	0.015385	0.00046	1	1	0.000511	1	0.000169
11	104878040	104878051	CASP5	6.66E-12	5.18E-15	0.171123	1	1	0.000408	1	1	1	1	1	1	0.000669	1	1
11	101362164	101362178	TRPC6	0.000945	5.49E-15	0.1	1	0.037096	0.081482	1	1	1	0.053563	1	1	0.066629	1	0.0026
5	68564968	68564998	CDK7	2.41E-08	5.53E-15	0.014872	1	0.149489	1	1	1	1	0.066207	0.058824	0.375	9.66E-19	0.005462	0.012283
2	114691801	114691830	ACTR3	1.29E-09	5.64E-15	0.109015	1	1	0.064673	1	1	1	0.153002	1	1	0.000128	1	0.016185
2	128029050	128029077	ERCC3	8.52E-08	5.64E-15	0.004706	1	1	1	1	1	0.03524	0.049668	1	0.176471	0.0011	1	0.004211
8	17504626	17504637	MTUS1	2.27E-08	6.09E-15	0.022222	1	1	1	1	1	1	1	0.000699	1	2.77E-07	0.000351	0.014053
16	31284618	31284634	ITGAM	1.93E-11	6.17E-15	0.000752	1	0.07	1	1	1	0.008772	1	1	1	1.13E-07	0.020408	0.000165
2	25656889	25656901	DTNB	2.27E-05	6.24E-15	0.010428	1	0.21466	0.016839	1	1	1	1	1	0.12782	3.86E-09	0.095238	0.057
10	12240681	12240702	CDC123	7.91E-07	6.76E-15	0.046875	1	1	0.000583	0.068498	0.017937	1	1	0.030303	0.380952	1.07E-10	0.019417	0.000542
12	122966016	122966028	ZCCHC8	7.17E-05	6.83E-15	0.020158	1	1	1	1	0.012987	0.06473	0.001868	1	0.128205	9.45E-08	1	0.064218
X	100093206	100093217	CSTF2	1.32E-06	6.9E-15	1	1	1	1	1	1	1	1	1	1	3.87E-10	1	0.003129
7	6080853	6080867	EIF2AK1	2.49E-05	7.61E-15	0.0608	1	0.092308	1	1	1	1	1	1	1	4.42E-09	1	0.332439
4	79460647	79460664	FRAS1	7.51E-09	7.72E-15	1	0.066648	1	1	1	1	1	0.003857	1	0.111111	0.000545	1	0.014196
9	74859952	74859964	GDA	4.29E-06	7.72E-15	0.370779	1	1	1	1	1	1	0.040506	0.142857	0.142857	0.355955	1	0.647073
7	75573271	75573282	POR	0.003898	7.92E-15	1	1	1	1	0.02381	1	1	0.102941	1	1	0.333333	1	1

6	168348504	168348521	MLLT4	9.66E-07	8.02E-15	0.022222	1	0.103952	0.061479	1	1	0.001053	0.265082	1	0.181818	6.07E-08	1	0.380836
20	271204	271226	C20orf96	2.41E-11	8.04E-15	0.007317	1	1	1	1	1	1	1	0.013333	1	1.59E-23	1	1
2	128608271	128608284	POLR2D	3.87E-11	8.21E-15	0.082447	1	1	1	1	1	0.127138	0.025336	0.054054	0.045796	2.7E-12	0.105195	0.00114
21	47662899	47662934	MCM3AP-AS1	1.05E-06	8.66E-15	1	1	1	0.068942	1	1	1	0.003844	1	1	1.71E-05	1	0.413275
10	12215870	12215884	NUDT5	2.14E-10	8.87E-15	0.008547	1	1	0.002395	0.009043	1	1	1	1	1	1.27E-08	1	0.009636
11	55339545	55339556	OR4C16	1.14E-11	8.88E-15	0.056604	1	1	1	0.011811	1	1	1	0.043478	1	3.28E-12	0.030303	1
14	92258905	92258916	TC2N	6.42E-11	9.05E-15	0.16946	1	1	1	1	1	1	0.00037	0.016393	1	4.17E-09	1	0.067669
11	11969473	11969484	USP47	1.72E-08	9.36E-15	0.032258	1	1	1	0.040646	1	0.028469	1	1	1	3.28E-11	1	1
19	8839038	8839049	ACTL9(dist=29858),OR2Z1(dist=2267)	0.000117	9.56E-15	1	1	1	1	1	1	1	1	1	1	0.166667	0.030769	1
6	150123316	150123329	PCMT1	1.28E-06	9.97E-15	0.127536	1	0.59214	0.257062	1	1	0.007064	0.373566	1	1	4.2E-06	1	1
7	135304090	135304102	NUP205	2.38E-09	1.04E-14	0.093517	1	1	1	0.014706	1	1	1	1	1	2.26E-09	1	0.079511
16	30665449	30665465	PRR14	5.03E-10	1.07E-14	1	0.018223	1	0.021622	1	1	1	0.001517	0.026316	1	0.222687	0.034483	1
11	36302410	36302422	COMMD9	2.69E-11	1.08E-14	0.103841	1	0.296926	0.183603	1	1	1	1	1	1	9.62E-09	1	0.001188
7	75513199	75513231	RHBDD2	8.14E-10	1.14E-14	1	1	1	0.007143	1	1	1	1	1	1	6.12E-07	0.001174	0.041322
10	81925982	81925994	ANXA11	5.58E-12	1.18E-14	1	1	1	1	1	1	1	1	0.066667	0.176471	1.94E-05	0.071429	0.040006
2	70463168	70463180	TIA1	9.58E-12	1.25E-14	1	1	1	1	1	1	1	1	1	1	1.94E-08	0.028986	1
7	103234985	103234997	RELN	9.5E-08	1.28E-14	0.106607	0.022346	0.210414	0.097755	1	1	1	1	1	1	0.012743	0.04878	0.066398
15	90126218	90126232	TICRR	4.29E-11	1.31E-14	0.003072	1	1	1	1	1	1	1	0.03125	1	5.9E-19	1	1
17	71223424	71223438	FAM104A	1.35E-11	1.4E-14	0.130303	0.050725	0.018919	1	1	1	0.032895	1	0.054054	1	2.41E-14	0.041096	0.02066
14	96788613	96788623	ATG2B	2.9E-05	1.53E-14	0.047619	1	1	1	0.033113	1	1	1	0.066667	1	4.54E-13	1	6.35E-05
2	55491007	55491018	MTIF2	1.55E-10	1.59E-14	1	1	0.142634	1	1	1	0.034333	1	1	1	9.76E-12	1	0.265323
3	142274739	142274750	ATR	6.46E-05	1.6E-14	1	0.033753	1	1	1	1	1	0.245161	1	1	4.23E-06	0.029412	0.077419
14	53217376	53217395	STYX	2.14E-05	1.6E-14	1	1	1	0.052623	1	1	1	0.006263	1	1	0.042424	1	0.062718
13	73547700	73547726	PIBF1	0.000349	1.64E-14	0.06383	0.020151	1	1	1	1	0.012048	1	1	1	1.13E-14	1	0.08
18	31709810	31709828	NOL4	0.00086	1.69E-14	0.068966	1	1	0.075161	1	1	0.047619	1	1	1	1.79E-06	1	0.275926
X	77264514	77264533	ATP7A	3.91E-10	1.7E-14	0.045455	1	0.023724	1	1	1	0.027874	1	0.047619	1	1.11E-16	1	0.241772
3	184573472	184573483	VPS8	5.45E-07	1.84E-14	1	1	1	0.000766	1	1	1	1	0.02381	1	2.31E-07	1	0.032049
3	146234962	146234973	PLSCR1	1.6E-07	1.86E-14	0.00266	1	1	1	1	1	1	1	0.022727	1	1.33E-05	0.000565	0.141403
15	37328977	37328996	MEIS2	2.85E-06	1.9E-14	1	1	0.108108	1	1	1	1	1	1	1	1.52E-07	1	1
9	85987879	85987892	FRMD3	4.6E-05	1.97E-14	0.018939	1	1	0.006035	1	1	1	0.368277	1	1	3.35E-06	1	0.005285
2	183995073	183995135	NUP35	2.21E-11	1.98E-14	0.007974	1	0.172663	0.057681	0.053863	1	0.051439	1	1	1	1.98E-16	1	0.266678
16	84124604	84124621	MBTPS1	1.85E-08	2.01E-14	0.036437	1	0.386118	1	0.018126	1	1	1	0.333333	1	2.1E-12	1	0.009163
12	97303682	97303713	NEDD1	1.63E-08	2.03E-14	0.004523	1	0.289411	0.171979	0.115538	1	0.000846	1	1	1	3.42E-11	1	0.034588
3	65361369	65361402	MAGI1	0.000476	2.12E-14	0.00101	1	0.279557	1	1	1	1	0.019231	1	0.357143	1.73E-13	0.093702	0.000399
1	220355521	220355533	RAB3GAP2	1.68E-09	2.13E-14	0.001083	1	0.086957	0.022059	1	0.00495	1	1.16E-06	1	1	3.84E-11	1	0.160926
3	105238890	105238907	ALCAM	7.68E-06	2.14E-14	1	1	0.281689	1	1	1	1	1	0.022727	0.166667	1.1E-09	0.056338	0.479897
21	37619920	37619943	DOPEY2	2.09E-08	2.18E-14	1	1	1	1	0.10815	1	0.028571	0.228317	1	1	4.42E-11	0.077922	1.11E-06
5	138758546	138758559	DNAJC18	0.000257	2.44E-14	0.086207	1	1	1	1	1	1	1	1	1	3.01E-06	1	0.108826
11	122817187	122817199	C11orf63	5.82E-09	2.47E-14	1	0.00905	1	0.026738	1	0.008658	1	1	0.041667	1	1.4E-13	0.043478	1
3	154007618	154007629	DHX36	1.84E-06	2.49E-14	0.022727	0.006803	0.122807	1	1	1	1	0.038462	1	1	1.99E-11	0.02439	1
9	33912102	33912114	UBE2R2	9.2E-09	2.5E-14	0.070175	1	1	1	1	1	0.040323	0.000138	0.04878	0.111111	2.29E-13	0.031746	0.060264
17	9501525	9501545	CFAP52	1.05E-08	2.5E-14	0.042146	1	1	0.00242	1	1	1	0.045977	1	1	1.71E-06	1	0.286489
3	101370529	101370548	ZBTB11	1.46E-10	2.55E-14	0.009231	0.033331	1	1	0.023669	1	0.032651	1	0.333333	1	1.08E-09	1	0.111391
16	3828847	3828870	CREBBP	1.29E-06	2.57E-14	0.001681	0.016807	1	1	0.014388	1	1	0.078947	0.019231	1	7.44E-07	1	0.000679
X	31200799	31200843	DMD	3.08E-09	2.58E-14	0.017094	0.020151	0.679709	0.143384	0.00986	1	0.05084	0.166299	1	1	9.75E-12	0.077895	0.613066
8	75737770	75737785	PI15	7.24E-07	2.6E-14	0.004329	1	1	1	1	1	1	1	0.027778	0.076923	0.001404	0.130279	0.279549
11	46568608	46568621	AMBRA1	3.33E-09	2.79E-14	0.005199	1	1	1	1	1	0.015038	0.063063	1	1	2.89E-07	1	0.003918
10	17164772	17164789	CUBN	6.37E-07	2.86E-14	0.00752	1	0.135399	0.123991	0.096547	1	0.022922	1	1	1	7.45E-19	1	0.01465
3	192516152	192516163	MB21D2	0.000871	2.98E-14	1	1	1	0.013333	1	1	1	1	0.034483	1	0.000136	1	1
14	90735723	90735735	PSMC1	1.51E-10	3.08E-14	0.183508	1	1	1	1	1	1	1	0.068182	1	1.86E-13	0.000219	0.057244
5	180668426	180668444	GNB2L1	1.41E-09	3.23E-14	0.117647	0.015594	1	1	0.016287	1	0.018868	1	1	1	0.001394	1	0.016419
1	24857651	24857670	RCAN3	1.45E-07	3.3E-14	1	0.004219	1	0.043062	1	1	1	1	1	1	7.31E-05	1	0.002375
18	12817106	12817118	PTPN2	8.12E-09	3.35E-14	1	1	0.212698	1	1	1	0.014085	0.195578	1	0.285714	1.23E-06	0.052973	0.21864
1	153516162	153516173	S100A4	1.17E-06	3.47E-14	1	1	1	1	1	1	1	0.129487	0.027397	1	8.63E-09	0.064501	0.000151
14	39620884	39620896	TRAPPC6B	3.72E-10	3.57E-14	0.041667	1	1	0.018868	0.021739	1	1	0.034483	1	1	5.54E-13	1	0.108487
5	145888687	145888714	TCERG1	1.71E-11	3.8E-14	0.000218	1	1	1	1	1	1	0.00283	0.02381	1	1.25E-10	0.033898	0.00016
7	92883250	92883261	CCDC132	2.82E-10	3.82E-14	1	1	1	1	1	0.008696	1	1	1	1	7.27E-15	1	0.000524
14	88454869	88454880	GALC	0.000355	3.93E-14	1	1	0.058824	0.023438	1	1	1	0.075472	1	1	4.38E-06	1	3.71E-06
19	47656338	47656359	SAE1	3.12E-05	4.06E-14	0.002463	1	1	0.014184	1	0.01	0.054414	1	1	1	9.7E-06	0.024096	0.002317
10	13633928	13633944	PRPF18	1.39E-11	4.07E-14	9.16E-05	0.036444	1	0.001275	0.016667	1	1	1	1	1	1.69E-19	0.023529	3.07E-06
9	127765856	127765868	SCAI	3.95E-09	4.21E-14	1	1	1	1	1	0.003759	1	1	1	1	1.89E-15	0.031915	0.010726
3	122811180	122811198	PDIA5	9.88E-08	4.34E-14	0.004706	1	1	1	1	1	1	1	1	1	2.93E-05	1	0.002789
12	50149602	50149635	TMBIM6	2.88E-09	4.36E-14	0.058824	1	1	1	1	1	1	1	1	1	0.00347	1	0.106329
16	67854644	67854670	TSNAXIP1	0.000192	4.42E-14	0.133333	0.010929	1	1	0.022038	1	1	0.166667	1	1	0.013827	1	0.097561
13	21729952	21729979	SKA3	2.49E-11	4.6E-14	0.084472	1	0.04404	0.182717	1	1	1	0.199322	1	1	9.94E-19	0.065918	0.009341
8	42938190	42938204	FNTA	8.05E-09	4.62E-14	0.075	1	1	1	1	1	0.020408	0.010101	0.072727	1	2.03E-15	0.048479	0.072795
12	109685344	109685355	ACACB	4.77E-09	4.67E-14	0.076169	1	1	0.064086	1	1	1	1	1	1	0.004261	1	0.1642
22	21174921	21174932	PI4KA	0.000124	4.86E-14	1	1	0.402998	0.04	1	1	1	1	0.028571	1	0.000364	1	0.006974
16	2115413	2115438	TSC2	0.207453	4.94E-14	1	1	1	1	1	1	0.018519	1	1	1	0.022269	1	1
16	89576879	89576895	SPG7	2.08E-08	5E-14	1	1	0.026923	1	1	1	0.088517	1	0.1	1	9.42E-10	0.027027	1
8	67710676	67710692	C8orf44-SGK3,SGK3	1.13E-10	5.05E-14	0.027397	1	1	1	1	1	1	0.038095	1	1	1.16E-10	1	2.08E-05
12	55354876	55354889	TESPA1	3.73E-11	5.18E-14	1	1	0.006519	0.049709	1	1	1	0.00627	1	1	7.44E-10	1	0.044119
21	44513110	44513140	U2AF1	4.24E-09	5.23E-14	0.047619	1	0.042017	0.019231	1	1	1	1	1	1	0.000103	0.043956	0.002092
14	73465027	73465043	ZFYVE1	0.001807	5.74E-14	1	0.006098	1	1	1	1	0.091783	0.005905	1	1	3.63E-06	1	1
10	28872473	28872498	WAC	2.04E-05	5.9E-14	0.120192	1	1	0.004545	1	1	1	1	1	1	1.24E-12	1	1
1	158637865	158637882	SPTA1	4.93E-09	5.92E-14	0.101215	1	0.05186	0.339666	0.151792	1	1	1	1	1	4.78E-11	1	0.028166
17	30190540	30190551	UTP6	5.43E-09	6.28E-14	1	0.008065	1	0.022472	1	1	0.014493	0.057143	1	1	9.72E-11	0.057143	0.003525
16	46743334	46743369	MYLK3	7.91E-09	6.33E-14	1	1	1	0.062878	1	1	0.038095	1	1	1	6.31E-09	0.119879	0.00237
20	10627473	10627490	JAG1	1.68E-08	6.36E-14	1	1	1	0.05713	1	1	1	1	1	1	8.31E-11	0.054054	1
20	49551780	49551793	ADNP-AS1	1.22E-08	6.51E-14	0.237011	1	1	0.165361	1	1	1	0.116967	0.038462	0.028571	1.45E-13	1	0.51816
2	10269544	10269555	RRM2	0.000332	6.72E-14	0.029412	1	1	1	0.000135	0.007407	0.022727	1	1	1	4.89E-05	1	1
18	77013286	77013297	ATP9B	3.02E-05	7.41E-14	0.003322	1	1	1	1	1	1	0.021337	1	1	3.17E-09	1	0.031323
6	134494708	134494722	SGK1	2.17E-10	7.61E-14	0.184135	1	1	0.002307	1	1	1	1	1	1	2.27E-10	1	0.202484
19	56220430	56220455	NLRP9	3.4E-05	7.61E-14	0.096154	1	1	1	0.02122	1	1	0.049505	1	1	9.04E-05	1	0.066914
1	115260841	115260861	CSDE1	5.89E-05	7.96E-14	1	1	1	1	1	1	1	1	1	1	1.4E-05	1	0.003962
18	12352952	12352964	AFG3L2	9.24E-11	8.19E-14	1	1	1	1	0.020202	1	0.016129	0.003378	1	1	1.01E-07	0.037736	1
2	32983299	32983311	TTC27	4.98E-12	8.2E-14	0.005026	1	1	0.017699	1	1	1	0.025974	1	0.272727	9.56E-17	1	0.001511
5	34818976	34818988	RAI14	7.13E-08	8.25E-14	0.002885	1	0.407111	1	1	1	0.024	1	1	0.090909	4.65E-11	1	0.226155
2	186689258	186689269	FSIP2	1.16E-07	8.41E-14	0.08599	1	1	0.001709	1	1	0.0125	1	1	1	5.66E-13	0.028169	0.000322
9	135152543	135152556	SETX	4.24E-11	8.58E-14	0.083333	1	1	1	1	1	0.039996	0.193824	1	1	1.67E-10	1	0.4241
5	13814976	13814987	DNAH5	3.92E-09	8.96E-14	0.001422	1	1	1	0.025157	1	1	1	1	1	0.019624	0.038961	0.065972
8	117861112	117861124	RAD21	1.8E-05	9.19E-14	0.044118	1	1	1	0.016598	1	1	1	1	1	6.76E-06	0.000325	0.113745
X	148048207	148048223	AFF2	2.47E-05	9.28E-14	1	1	0.265724	1	1	1	0.021053	0.000363	1	1	0.088911	1	0.01063
3	38006175	38006186	CTDSPL	0.001338	9.41E-14	0.052632	1	1	1	0.015873	1	1	0.036364	1	1	1.25E-08	1	0.153995
10	92678870	92678880	ANKRD1	9.51E-06	9.53E-14	0.161905	1	1	0.082152	1	1	1	1	1	1	3.41E-07	1	0.001404
12	15742313	15742345	PTPRO	1.77E-05	9.57E-14	1	1	0.399195	1	1	1	0.023077	1	1	1	2.39E-05	1	0.004566
7	882808	882841	SUN1	1.93E-09	9.67E-14	1	1	0.412602	0.043592	0.03712	1	1	1	0.030303	0.05	1.42E-05	1	0.008727
4	27004737	27004748	STIM2	1.19E-05	9.7E-14	0.003171	1	0.293245	0.03012	1	1	1	1	1	1	4.04E-07	1	0.091603
18	50589652	50589663	DCC	4.15E-05	9.81E-14	1	0.040198	0.090909	1	0.08951	1	1	0.040959	1	1	5.79E-08	0.068361	0.025603
1	223168194	223168216	DISP1	3.75E-06	9.99E-14	0.085714	1	1	1	1	1	1	0.082353	0.02381	1	0.004335	1	0.081197
7	101837331	101837356	CUX1	3.86E-07	1E-13	1	1	1	1	1	1	1	1	1	1	0.000471	1	1
11	9431442	9431466	IPO7	1.15E-06	1.03E-13	1	0.014493	1	1	1	1	1	1	0.034483	1	2.4E-09	1	0.029338
4	99802300	99802325	EIF4E	1.42E-09	1.03E-13	0.004152	1	0.134168	1	1	1	0.017544	1	1	1	2.61E-16	1	0.001001
9	15729855	15729867	CCDC171	9.02E-06	1.05E-13	0.058824	1	1	1	1	1	1	1	1	1	3.95E-06	1	1
1	185060950	185060965	RNF2	2.82E-09	1.06E-13	0.069767	1	1	1	1	1	1	0.063678	1	1	3.37E-05	1	0.013843
16	70693872	70693884	IL34	7.2E-08	1.07E-13	0.113122	0.080427	1	0.01899	0.151988	1	1	0.003834	1	0.005882	1.46E-09	1	0.100302
10	70968804	70968818	SUPV3L1	3.82E-07	1.12E-13	0.313725	1	0.306518	0.069208	1	1	1	1	1	1	0.000169	0.064516	0.004029
8	103236408	103236428	RRM2B	0.000363	1.23E-13	1	1	1	1	0.026548	1	0.013699	0.021127	1	1	7.01E-05	1	0.061047
1	57476485	57476496	DAB1	8.28E-07	1.3E-13	1	1	1	1	1	1	1	1	1	1	0.001112	1	0.010575
4	8176744	8176762	ABLIM2(dist=16185),SH3TC1(dist=24298)	5.27E-08	1.33E-13	0.007257	1	1	1	0.038961	1	1	1	0.15	1	2.16E-18	1	0.000199
14	53347721	53347732	FERMT2	4.59E-05	1.41E-13	1	1	1	1	1	1	1	1	1	1	3.74E-09	1	0.175935
1	154110733	154110745	NUP210L	2.26E-07	1.42E-13	0.379416	1	0.085328	1	0.165515	1	1	1	0.3	0.133333	1.3E-10	1	0.169688
19	23845789	23845807	ZNF675	6.3E-07	1.44E-13	1	1	1	0.010417	0.022727	1	1	1	1	1	1.96E-05	0.003911	0.202709
X	154456644	154456657	VBP1	1.87E-08	1.47E-13	0.166387	1	0.116903	1	0.006994	1	1	0.071726	1	1	1.52E-08	1	0.014412
4	47163234	47163248	GABRB1	1.13E-10	1.48E-13	1	0.000206	0.211979	1	1	0.015748	1	0.03876	0.05	1	3.37E-08	1	0.197431
2	37464877	37464888	NDUFAF7	4.32E-10	1.54E-13	0.115385	0.009709	1	0.04	1	1	1	1	0.022222	1	1.35E-07	0.041667	1
11	128350396	128350418	ETS1	1.52E-07	1.6E-13	0.00303	1	1	0.000617	0.000364	1	1	1	1	1	9.62E-11	1	0.00324
5	134033756	134033767	SEC24A	2.42E-08	1.68E-13	1	1	1	0.040816	1	1	1	1	0.032258	1	0.000154	1	1
2	196738263	196738274	DNAH7	0.000279	1.82E-13	0.000871	1	1	1	0.018692	1	1	1	1	1	1.31E-05	0.014925	1.88E-05
22	29804996	29805007	AP1B1(dist=20424),RFPL1S(dist=27997)	8.41E-05	1.83E-13	1	1	1	1	1	1	1	1	1	1	0.002535	1	0.022989
12	50388296	50388307	RACGAP1	9.6E-07	1.84E-13	0.00363	1	1	1	1	1	1	1	1	1	3.24E-12	1	0.005524
2	20526998	20527011	PUM2	1.89E-10	1.85E-13	1	1	1	1	0.025641	1	1	0.001852	1	1	1.67E-15	1	0.002009
17	30302736	30302748	SUZ12	2.63E-09	1.95E-13	0.004505	1	1	1	1	1	1	1	0.022222	1	4.74E-08	1	0.003355
22	38254768	38254793	EIF3L	0.001512	1.96E-13	1	1	1	1	0.050786	1	1	1	1	1	0.003803	1	1
6	30618688	30618704	C6orf136	2.73E-10	1.98E-13	0.090865	1	1	1	1	1	0.112674	1	0.076923	1	1.83E-14	0.043478	0.00231
1	51032698	51032709	FAF1	9.4E-10	1.99E-13	0.085714	1	0.083333	1	0.032256	1	1	1	1	1	1.77E-06	1	0.104803
17	4880231	4880257	CAMTA2	0.000123	2.09E-13	1	0.005291	1	1	1	1	1	1	1	1	0.000308	1	1
5	112903585	112903598	YTHDC2	4.61E-12	2.1E-13	0.040816	1	0.043478	0.04717	0.000694	1	0.007874	1	1	1	3.9E-17	1	0.025339
1	201754396	201754428	IPO9-AS1,RNU6-79P	4.04E-08	2.34E-09	0.002221	1	1	0.037559	0.216319	0.022472	1	2.64E-06	1	1	8.3E-10	1	0.498934
16	4790059	4790097	C16orf71	0.039633	2.29E-07	1	1	1	1	1	1	0.01626	1	1	1	1	1	1
7	47979920	47979933	PKD1L1	1.07E-09	3.09E-13	0.030303	1	0.083587	0.023585	1	1	1	1	1	1	5.55E-16	0.010989	1
14	62261603	62261633	SNAPC1	1.59E-06	9.21E-12	1	1	1	1	1	0.008163	1	1	0.0625	1	0.000215	1	0.026167
1	52947339	52947366	ZCCHC11	8.18E-12	4.33E-11	0.002885	1	1	0.043956	1	1	1	1	1	1	2.39E-14	1	0.023844
12	7187777	7187796	C1R	0.00026	1.73E-06	0.059701	1	1	1	0.012552	1	1	1	1	0.2	9.74E-05	1	0.196066
12	12974842	12974853	DDX47	1.55E-06	1.82E-08	0.000252	1	1	1	1	1	1	1	1	1	8.01E-05	1	1
14	94066888	94066900	UNC79	1.17E-11	8.4E-10	0.01063	1	1	0.026596	1	1	1	1	0.052632	1	3.55E-10	0.02	0.004269
14	102550069	102550088	HSP90AA1	4.28E-11	8.65E-09	0.000382	1	1	1	1	1	1	0.05	1	1	2.09E-21	0.000618	0.0034
6	112393287	112393299	TUBE1	2.61E-05	9.1E-10	1	1	1	1	1	1	1	1	0.027778	1	0.018388	1	0.180081
1	45479966	45479995	UROD	2.67E-05	2.18E-09	1	1	1	1	1	1	1	1	1	1	3.78E-07	1	1
22	32548036	32548047	C22orf42	0.005046	7.89E-10	0.04878	1	1	1	1	1	1	0.164835	1	1	1.97E-07	1	0.000672
7	646958	646969	LOC101926963	9.85E-07	8.37E-13	1	1	1	1	1	1	1	1	0.025641	1	1.91E-06	0.012721	1

5	179994815	179994842	CNOT6	6.99E-05	0.012833	1	1	1	1	1	1	1	1	1	1	0.000323	1	0.19296
7	99312311	99312322	CYP3A7,CYP3A7-CYP3AP1	8.65E-05	1.87E-10	1	1	1	1	0.022922	1	1	1	0.037037	1	0.000182	1	0.279356
4	1919852	1919863	WHSC1	6.59E-07	1.11E-12	1	1	1	1	1	1	1	1	1	1	5.54E-10	1	0.021053
3	100378512	100378523	GPR128	0.00013	9.4E-11	0.05	1	0.125	0.037879	1	1	0.014493	1	1	1	5.51E-09	1	0.062439
1	21083757	21083774	HP1BP3	3.19E-09	2.32E-08	0.037037	1	1	1	1	1	1	1	1	1	2.69E-05	1	0.040658
12	9220823	9220847	A2M	1.25E-09	6.05E-10	1	0.009434	1	1	0.017544	1	1	1	1	1	1.62E-11	1	0.005476
3	62278076	62278094	PTPRG	4.91E-09	2.31E-13	0.088235	0.036361	1	1	1	1	1	1	1	1	2.7E-05	1	0.144478
12	22354981	22354992	ST8SIA1	0.000497	0.000991	0.076923	1	1	1	1	1	1	1	1	1	0.00016	0.08	1
16	74336247	74336258	PSMD7	9.04E-05	2.38E-11	1	1	1	1	1	1	1	1	1	1	2.37E-09	0.029851	1
17	47076449	47076462	IGF2BP1	1.44E-08	1.68E-12	1	1	1	1	1	0.009804	1	0.111835	0.000673	0.181818	1.02E-11	0.0375	0.072642
11	58385231	58385251	ZFP91-CNTF	0.00046	1.38E-10	0.166667	1	0.137931	1	1	0.005952	1	1	1	1	0.043956	1	0.107543
2	64114398	64114425	UGP2	4.28E-07	2.54E-05	1	1	0.085714	1	1	1	0.029703	1	1	1	0.103448	1	0.114485
1	222835522	222835533	MIA3	2.91E-05	1.01E-08	1	1	1	1	1	1	1	1	1	1	0.002105	1	0.005486
17	49077040	49077050	SPAG9	0.011406	1.26E-08	1	1	0.111111	1	1	1	1	1	1	1	0.00021	1	1
X	108785712	108785723	NXT2	9.19E-05	0.000291	1	1	0.089286	1	1	1	1	1	1	1	3.43E-06	0.035294	1
11	68318688	68318706	PPP6R3	0.000446	0.001422	1	1	1	0.049645	1	1	1	1	1	1	1	0.002096	0.110105
6	17662088	17662099	NUP153	0.001638	2.36E-05	1	1	1	1	1	1	1	0.02	1	1	0.000612	1	0.001364
11	102076586	102076611	YAP1	0.026055	7.5E-05	1	1	1	1	1	1	1	0.088355	1	1	0.000158	1	0.014085
10	120810867	120810878	EIF3A	0.005209	9.42E-06	0.101215	1	1	1	1	1	1	0.137931	1	1	5.78E-07	0.032787	0.089552
9	73479430	73479465	TRPM3	3E-07	0.000247	0.04	1	1	1	1	1	0.024793	1	1	1	0.00057	1	0.000306
6	160200860	160200871	TCP1	4.3E-06	4.12E-11	0.079184	1	1	1	0.021277	1	1	0.058824	1	1	4.58E-07	1	0.080645
15	66821146	66821157	ZWILCH	0.002225	5.55E-07	1	1	1	1	1	1	1	1	1	1	3.48E-09	1	0.008249
1	24180806	24180833	FUCA1	2.1E-05	7.5E-12	0.008737	0.010101	1	0.005559	1	1	1	1	1	1	8.8E-07	1	0.088598
10	91178464	91178475	IFIT5	1.25E-06	2.69E-07	1	1	1	1	1	1	1	0.091916	1	1	0.000155	1	1
9	20948224	20948255	FOCAD	4.07E-05	0.023594	0.054054	1	1	0.032609	1	1	1	1	1	1	2.21E-06	1	0.00621
10	118236575	118236595	PNLIPRP3	6.1E-08	4.81E-10	0.004505	1	1	1	1	1	1	1	0.027027	1	0.001184	1	0.124064
13	50134014	50134026	RCBTB1	1.58E-07	2.34E-12	0.12234	0.01	1	0.027027	1	1	1	1	0.066667	1	8.25E-06	0.064516	0.063158
14	58681903	58681915	ACTR10	1.12E-05	1.58E-09	1	1	1	1	1	1	1	0.002193	1	1	6.31E-12	0.041667	0.003676
4	170028345	170028371	SH3RF1	0.110609	4.71E-06	0.028571	1	1	1	1	1	1	1	1	1	0.044613	1	1
13	114113737	114113748	DCUN1D2	0.060427	1.01E-08	0.001282	1	1	1	1	1	1	1	1	0.190476	4.15E-06	1	1
17	39976721	39976731	FKBP10	1.62E-07	1.69E-08	1	0.010101	1	0.001298	1	1	0.033898	0.000335	1	1	0.00535	1	0.143026
10	118704545	118704556	KIAA1598	6.71E-05	4.84E-13	1	1	1	1	1	1	1	1	1	1	3.21E-09	1	0.003153
4	88048163	88048174	AFF1	0.000783	5.06E-07	0.093023	1	1	1	1	1	1	0.112046	1	0.190476	1.48E-06	1	0.469771
2	179325203	179325214	MIR548N	2.48E-06	3.67E-07	1	1	1	1	1	1	0.009259	1	0.016667	1	0.002489	0.026316	1
1	223984306	223984317	TP53BP2	4.22E-05	5.99E-12	1	1	1	0.117229	1	1	1	1	1	0.277778	0.016323	1	1
3	123338956	123338968	MYLK-AS1	2.27E-06	5.36E-11	1	1	1	0.033784	0.033708	1	1	0.068627	1	1	1.98E-07	0.061058	1
7	6470058	6470069	DAGLB	8.27E-11	1.12E-11	1	1	1	0.027397	1	1	1	1	0.027397	1	1.02E-07	0.035294	1
13	20325367	20325378	PSPC1	1.6E-08	4.9E-13	1	1	0.009398	1	0.049744	1	1	1	0.019231	1	1.29E-05	0.027397	0.125149
4	40144242	40144253	N4BP2	0.00116	3.62E-08	0.061538	1	1	1	1	1	1	0.046512	1	1	1.02E-05	1	0.121953
19	17534169	17534197	MVB12A	0.010684	0.031252	1	1	1	1	1	1	1	1	1	1	0.25	1	1
8	29963198	29963210	MIR548O2	5.14E-06	8.9E-07	0.102564	1	1	1	0.026755	1	0.035088	1	1	1	0.000434	1	0.061526
2	39505509	39505528	MAP4K3	4.12E-07	3.66E-06	0.036364	1	1	1	1	1	1	1	0.016129	1	1.12E-07	1	0.132899
X	23723069	23723080	ACOT9	0.060449	0.006429	1	1	1	1	1	1	1	1	1	1	0.295127	1	1
16	72089943	72089995	HP	0.0016	0.01774	1	1	1	1	1	1	1	1	1	1	6E-05	0.048387	1
12	69646939	69646960	CPSF6	0.000926	1.32E-06	1	1	1	1	1	1	1	1	1	1	0.000311	0.042857	0.188732
13	31035467	31035478	HMGB1	0.00034	0.551938	1	1	1	1	1	1	1	1	1	0.083333	1	1	0.061263
15	100345136	100345147	DNM1P46	1.05E-07	6.44E-07	0.166667	1	0.090994	0.035294	1	1	1	0.303735	0.071429	1	1	1	0.264861
17	6553410	6553422	MED31	1.6E-10	2.46E-07	1	1	1	1	1	1	0.072267	1	1	1	1.37E-13	1	0.198654
17	35538304	35538314	ACACA	0.000145	3.33E-06	0.023256	1	1	0.011236	1	1	1	1	1	1	1.16E-05	1	1
3	185540911	185540922	IGF2BP2	0.000192	0.000139	1	1	1	1	1	1	1	1	0.019231	1	1.88E-09	1	1
17	8166113	8166126	PFAS	2.71E-11	3.74E-08	1	1	1	0.034483	1	1	0.007813	0.000406	0.026316	1	0.00053	1	0.029642
10	96317838	96317849	HELLS	6.74E-08	1.2E-12	0.003796	1	1	1	1	1	1	1	1	0.380435	2.58E-10	1	0.000104
2	32706267	32706279	BIRC6	5.23E-09	1.01E-09	0.067212	1	1	1	1	1	1	1	1	1	4.35E-11	1	4.33E-05
2	183033020	183033033	PDE1A	9.8E-09	9.12E-13	0.007932	1	0.467868	1	0.08649	1	0.082152	1	1	0.272188	9.8E-17	0.021277	6.96E-06
10	70669942	70669958	DDX50	1.79E-11	9.67E-10	1	1	1	1	1	1	0.020548	1	0.000887	1	0.00046	1	0.00523
6	30154350	30154364	TRIM26	5.45E-08	7.81E-12	0.029989	0.058252	0.136168	1	1	1	0.069748	1	1	1	1.26E-08	0.006897	1
1	233225957	233225969	PCNXL2	4.82E-07	5.19E-07	0.00048	1	1	1	1	1	1	0.005657	1	0.235294	0.000522	0.059249	0.007113
20	61299715	61299725	SLCO4A1	1.73E-05	2.34E-10	1	1	1	1	0.051716	1	0.013333	0.022222	1	1	2.98E-06	1	0.009726
21	35209167	35209186	ITSN1	1.82E-07	2.83E-07	0.147313	1	1	1	1	1	1	0.035714	1	1	6.65E-07	1	1
17	41566965	41566977	DHX8	5.01E-08	2.33E-06	1	1	1	1	1	1	1	1	1	1	3.03E-05	1	0.013675
10	102265056	102265097	SEC31B	0.000403	0.000116	0.011364	1	1	1	1	1	1	1	1	1	0.000794	1	0.003446
10	17279211	17279223	VIM	2.29E-10	9.15E-09	0.015152	1	0.028169	1	1	1	1	1	0.035714	1	1.31E-21	1	0.057143
4	102839351	102839362	BANK1	4.39E-05	0.000862	0.047619	1	0.081633	1	0.036697	1	0.012658	1	1	1	0.005496	1	0.01183
13	99461532	99461565	DOCK9	0.240893	1.36E-05	1	1	0.342643	1	0.025078	1	1	0.003805	1	0.214286	0.007236	1	0.307114
19	45911309	45911338	ERCC1	0.080906	0.000186	0.025641	1	1	1	1	1	0.099937	0.309717	1	1	0.323529	1	0.01802
18	29625524	29625546	RNF125	2.9E-06	6.3E-06	1	1	1	1	1	1	1	1	0.035088	1	9.48E-06	0.069549	0.311633
7	135375909	135375932	SLC13A4	1.48E-06	2.51E-05	0.001317	1	0.22248	1	1	1	1	0.12067	1	0.046154	2.68E-05	1	0.002493
14	21876732	21876743	CHD8	8.95E-10	1.62E-07	1	1	1	1	1	1	1	1	0.016129	1	4.55E-08	1	0.045455
7	98630574	98630598	LOC101927550	0.000146	2.78E-07	0.037037	1	1	0.016529	1	1	1	1	1	0.0625	2.67E-07	1	1
1	161326722	161326735	SDHC	7.13E-09	2.56E-08	0.017742	1	1	1	1	1	0.016529	1	1	1	9.44E-10	1	5.41E-06
14	92588155	92588170	CPSF2,NDUFB1	3.02E-07	3.58E-07	0.009231	1	1	0.028907	1	1	1	0.009702	1	0.001786	2.66E-06	1	1
3	42251577	42251608	TRAK1	0.346463	0.009645	1	1	1	1	1	1	1	1	1	0.010989	0.659339	1	0.384846
20	9453901	9453922	PLCB4	1.49E-07	4.15E-10	0.001673	1	1	1	0.119187	1	1	1	0.04878	1	2.39E-17	1	1
5	70805272	70805288	BDP1	0.00325	8.4E-07	0.054054	1	0.199417	0.016446	1	1	1	1	0.112605	0.045455	7.17E-05	1	0.050139
8	87440101	87440114	WWP1	1.41E-11	3.23E-08	1	1	1	1	1	1	1	1	1	1	7.25E-10	1	1
12	48174340	48174368	SLC48A1	0.008258	0.000334	1	1	1	1	1	1	1	1	1	1	0.001205	1	1
7	99796751	99796765	STAG3	6.1E-11	0.080087	0.000466	1	1	1	1	1	1	1	1	1	7.8E-09	0.071408	0.026375
2	189926219	189926240	COL5A2	9.11E-12	7.31E-06	0.037037	1	1	1	1	1	1	0.036036	0.000496	1	5.44E-08	1	0.000246
15	50754453	50754465	USP8	6.93E-11	1.4E-09	0.047619	1	1	0.043478	1	1	1	1	1	1	6.16E-09	0.011628	0.089427
3	142402827	142402838	PLS1	6.65E-09	3.24E-09	0.101215	1	0.091743	0.030151	0.024793	1	1	0.047945	0.013889	1	2.25E-07	1	0.145248
17	72285659	72285679	DNAI2	7.56E-06	7.79E-11	0.066212	1	0.047463	0.084619	1	1	0.051716	0.104082	0.0625	1	1.25E-08	1	0.41535
11	62751721	62751750	SLC22A6	1.11E-05	9.98E-06	1	1	1	0.078621	1	1	1	1	1	1	0.193809	1	1
22	16920145	16920157	OR11H1(dist=470341),CCT8L2(dist=151491)	4.81E-09	2.79E-08	0.222222	0.01227	1	0.035928	1	1	0.019417	1	1	1	0.002747	1	2.77E-06
11	67209167	67209194	CORO1B	0.002037	0.001401	0.133333	1	1	0.014925	1	1	1	1	0.016393	1	0.002501	1	1
13	95227114	95227156	TGDS	1.17E-09	1.86E-05	0.066667	1	1	1	1	1	1	1	1	1	3.68E-05	1	0.072261
17	61829856	61829869	CCDC47	1.95E-11	0.003033	0.126882	1	1	1	1	1	1	0.024096	1	1	1.6E-09	1	0.091509
17	27816599	27816619	TAOK1	5.57E-07	0.001985	1	1	1	1	1	1	1	1	0.015385	1	3.72E-10	0.000294	0.000196
7	44715476	44715493	OGDH	3.56E-06	2.31E-10	0.370779	1	1	1	0.063729	1	1	1	1	1	3.83E-06	0.011905	1
12	109547568	109547595	UNG	0.020356	2.05E-09	1	1	1	1	1	1	1	1	1	1	6.52E-12	1	0.176518
1	110563191	110563202	AHCYL1	0.054851	0.000193	1	1	0.1	1	1	1	1	1	1	1	0.621385	1	0.046296
11	117222647	117222659	CEP164	2.13E-09	3.68E-12	1	0.015504	1	1	0.030303	1	0.007519	1	1	1	8.12E-07	1	5.41E-06
16	3367101	3367133	ZNF75A	7.52E-08	1.59E-10	1	1	1	1	1	1	1	0.063158	0.029851	1	9.38E-07	0.026316	0.016304
6	39926112	39926133	MOCS1(dist=23822),LINC00951(dist=385951)	9.25E-09	4.73E-13	1	1	1	1	1	1	1	0.158774	1	1	0.000171	0.021978	0.103376
X	30726149	30726160	GK	2.31E-05	0.000253	0.006048	1	0.05601	1	1	1	1	1	0.015873	1	4.3E-05	0.059249	1
6	7566735	7566757	DSP	1.37E-11	1.43E-10	0.002449	1	1	1	1	1	0.017699	1	1	1	0.00025	0.014085	0.002346
7	75113378	75113398	POM121C	5.63E-09	0.002399	1	1	1	1	0.028846	1	0.014706	1	1	0.467836	1	1	0.02596
1	183498191	183498202	SMG7	2.63E-07	2.23E-12	1	0.013333	0.102041	0.033333	1	1	1	1	1	1	0.00061	0.015873	0.000736
18	21047278	21047290	RIOK3	1.37E-08	7.17E-07	1	1	1	1	1	1	0.014085	1	1	1	3.06E-05	1	1
1	225155114	225155125	DNAH14	0.023847	0.008171	0.094077	1	1	1	1	1	1	1	1	1	0.00165	1	0.000802
7	38282130	38282151	STARD3NL(dist=11858),TARP(dist=17093)	1.2E-07	3.21E-07	0.010279	1	1	0.284374	0.011433	1	1	1	1	1	0.003341	0.128422	0.006806
14	97026967	97026983	PAPOLA	0.007397	1.89E-07	1	0.015748	1	1	0.02381	1	1	1	0.025641	1	4.39E-09	1	0.059545
15	40062813	40062836	FSIP1	2.36E-10	2.36E-05	0.000171	1	1	1	1	1	1	1	1	1	1.28E-11	0.031746	0.005349
6	119501609	119501620	MAN1A1	2.26E-06	4.42E-09	0.033333	1	1	1	1	1	0.028571	1	1	1	4.43E-08	1	0.000594
11	20485929	20485971	PRMT3	8.48E-10	4.42E-07	0.174825	1	1	1	1	1	1	1	1	1	1.37E-06	0.058824	0.007289
2	110325590	110325602	SEPT10	8.56E-07	1.61E-08	9.16E-05	1	1	1	1	1	1	0.021978	0.037037	0.208333	2.03E-10	1	0.004762
5	39341588	39341599	C9	0.000128	2E-10	0.052632	1	0.237811	1	0.02765	1	1	1	1	1	1.58E-07	0.040816	0.017459
1	154557165	154557194	ADAR	0.015451	2.14E-08	1	1	1	1	1	1	1	1	1	1	9.81E-07	1	1
21	36265302	36265336	RUNX1	0.00025	0.00074	0.057692	1	1	1	1	1	1	1	1	1	3.38E-13	1	1
9	4834291	4834302	RCL1	0.000227	1.72E-06	1	1	0.09434	1	1	1	1	1	1	1	0.107498	1	1
3	131186893	131186917	MRPL3	4.43E-07	1.4E-08	0.042129	1	1	0.126485	0.02857	1	0.004198	1	1	0.166667	1.62E-10	0.138554	0.016037
16	3077698	3077728	THOC6	0.000637	0.222222	1	1	1	1	1	1	1	1	1	1	0.00059	1	0.011791
10	70951558	70951580	SUPV3L1	5.31E-10	0.125	0.0375	1	1	1	1	1	0.014493	1	1	1	4.81E-10	0.035714	0.017795
2	215890346	215890382	ABCA12	0.04558	4.55E-05	0.158163	1	0.352802	4.2E-05	1	1	0.005438	0.019206	1	1	0.000857	1	0.001109
5	179707338	179707349	MAPK9	6.38E-06	0.000205	1	1	1	1	1	1	1	1	1	1	0.000124	0.030769	1
14	68944343	68944358	RAD51B	7.02E-12	6.2E-07	0.16544	1	1	1	1	1	1	1	1	1	6.64E-15	0.024691	3.12E-06
11	89531801	89531817	TRIM49	6.92E-11	0.01758	0.002892	1	1	1	1	1	1	1	0.050949	1	1.32E-14	0.064501	1
14	23794543	23794579	BCL2L2-PABPN1	5.99E-12	2.54E-10	0.006061	1	1	0.022472	1	1	1	1	0.066667	1	6.3E-08	1	0.006864
8	109241196	109241208	EIF3E	3.66E-07	5.45E-05	1	1	1	1	1	1	1	0.039798	1	1	0.000337	1	0.038961
X	117679217	117679255	DOCK11	9.67E-09	0.001168	1	1	0.3724	0.129944	1	1	1	0.068164	1	0.230769	8.68E-07	0.204794	0.018197
8	109247189	109247210	EIF3E	1.29E-10	2.15E-10	0.000109	1	1	1	1	1	1	1	1	0.192308	2.33E-25	0.020202	1
6	116911413	116911425	RWDD1	1.94E-11	1.97E-11	4.52E-05	1	0.056452	1	1	1	1	0.059028	1	1	2.47E-14	1	1
11	93454831	93454868	SCARNA9	0.00058	0.215747	1	1	1	1	1	0.024242	0.086494	1	1	1	1	0.158163	0.040342
19	21493271	21493292	ZNF708	5.83E-07	0.002067	0.146589	1	0.429954	1	1	1	1	0.087333	0.090909	1	8.74E-10	1	0.357076
12	99059316	99059327	APAF1	4.73E-08	6.74E-09	0.052632	1	0.068966	0.103383	1	0.012048	0.021277	0.181818	0.023256	1	4.76E-08	1	0.00061
12	1909656	1909667	CACNA2D4	1E-06	5.62E-09	1	1	1	0.011364	0.111016	1	1	1	0.021277	1	6E-09	0.031746	0.123144
12	27841925	27841938	PPFIBP1	4.92E-11	3.84E-13	0.057971	1	1	0.011095	0.003111	0.016194	1	1	1	0.421053	2.55E-12	0.027397	0.00061
17	17697093	17697133	RAI1	0.54755	0.711643	1	1	1	1	1	1	0.002551	1	0.0625	0.284211	0.286578	1	1
6	138628598	138628611	KIAA1244	2.45E-11	5.11E-08	0.103841	1	1	1	0.16039	1	0.030303	0.00084	1	0.227941	1.39E-08	1	0.000207
1	148890177	148890189	NBPF25P	0.10112	0.003453	0.0625	1	1	1	1	1	1	1	1	1	0.000104	0.042857	0.175996
5	101726829	101726840	SLCO6A1	1.01E-08	0.030215	0.004354	1	1	1	1	1	0.023529	0.028846	1	1	2.32E-06	1	0.172424
11	125472337	125472359	STT3A	1.07E-11	0.07	0.064516	1	1	1	1	1	1	1	1	1	2.36E-06	0.024691	0.003595
16	67315128	67315144	PLEKHG4	0.002483	4.58E-05	0.1	1	1	1	1	1	1	1	1	1	0.007656	1	0.101846
2	176959113	176959146	HOXD13	4.01E-08	0.099405	1	1	1	1	1	1	1	1	1	0.285714	8.56E-05	1	0.094654
2	211444533	211444558	CPS1	8.08E-06	5.01E-05	0.002775	1	1	1	1	1	1	1	1	1	3.99E-06	1	0.069882
19	17366101	17366122	USHBP1	6.61E-07	1.88E-08	1	1	1	0.000544	0.064497	1	1	1	1	1	0.00079	0.166308	0.018877
4	39506997	39507008	MIR1273H	0.003662	0.001807	0.193103	1	0.390688	1	1	1	1	1	1	0.294872	0.016852	1	0.130121
4	59931	59941	ZNF595,ZNF718	0.229108	0.566111	0.076923	1	0.183913	1	1	1	1	1	1	1	1	1	1
5	35068814	35068826	PRLR	2.68E-11	3.84E-13	0.000316	1	1	0.162424	1	1	1	0.1322	1	0.277778	8.56E-18	1	0.019272
7	24329103	24329114	NPY	2.36E-06	5.29E-07	1	1	0.355516	1	1	1	0.016667	1	1	0.210526	0.0084	1	0.170422
6	45333093	45333104	RUNX2,SUPT3H	9.36E-11	4.34E-07	0.003623	1	1	1	1	1	1	1	1	1	0.289132	1	0.005153
2	145161712	145161725	ZEB2	0.236842	0.007294	1	1	0.090909	1	1	1	1	1	1	1	0.1125	1	1

1	151134579	151134590	LYSMD1,TNFAIP8L2-SCNM1	0.000271	1.1E-09	0.001057	1	0.052632	1	1	1	0.047059	1	0.041667	0.090909	6.19E-10	1	0.131327
11	67787366	67787383	ALDH3B1	0.4	0.193277	1	1	1	0.029126	1	1	1	1	1	1	0.003173	1	1
3	113442784	113442795	NAA50	1.1E-05	2.18E-10	4E-06	0.01	1	1	1	1	1	1	1	1	3.42E-08	1	0.077982
2	203676382	203676403	ICA1L	1.1E-09	9.47E-08	6.74E-06	1	1	1	1	1	0.010471	1	0.017241	1	1.03E-28	0.02439	0.00144
4	120423686	120423697	PDE5A	7.16E-06	1.24E-10	1.03E-05	0.012658	1	1	1	1	1	0.007541	1	1	2.32E-09	1	0.257162
1	93687513	93687543	CCDC18	0.000558	0.014166	1.3E-05	1	1	1	1	1	1	1	1	1	1.14E-18	1	0.063694
12	121618278	121618293	P2RX7	3.02E-09	0.000196	1.84E-05	1	1	1	1	1	1	1	0.032258	1	2.77E-14	1	0.000871
21	37706087	37706100	MORC3	4.37E-09	3.54E-09	2.52E-05	1	1	1	1	1	1	0.001639	1	1	2.67E-12	1	0.000769
14	20344373	20344394	OR4K2	6.05E-07	6.44E-11	2.82E-05	1	0.502572	1	1	1	1	1	1	1	1.22E-20	0.036364	0.214628
11	110306734	110306760	FDX1	0.000149	9.4E-09	3.3E-05	0.005814	0.133157	1	1	1	1	1	1	1	9.41E-06	1	0.381472
19	12574740	12574762	ZNF709	0.000228	3.47E-09	3.68E-05	1	0.179182	0.363921	1	1	1	1	0.045455	1	1.25E-09	1	0.001279
12	78594396	78594427	NAV3	4.1E-05	0.008614	4.14E-05	1	1	0.019802	1	1	1	1	0.033898	1	8.96E-05	0.037975	1
20	57569617	57569636	NELFCD	3.55E-09	6.04E-10	4.87E-05	1	1	0.047244	1	1	1	1	1	1	1.68E-17	1	0.010697
14	36096255	36096278	RALGAPA1P	2.6E-05	9.05E-09	6.17E-05	1	1	1	1	1	1	1	1	1	3.6E-25	1	1
4	95508108	95508128	PDLIM5	1.97E-09	0.005477	6.17E-05	1	1	1	1	1	1	1	1	1	1.14E-25	1	0.006152
2	141625834	141625854	LRP1B	4.63E-12	3.38E-07	8.35E-05	0.033898	0.237996	1	1	1	0.016129	1	1	1	1.92E-16	0.038462	0.025361
1	169819526	169819538	C1orf112	1.95E-10	2.96E-05	9.16E-05	1	1	1	1	1	0.007692	1	1	1	8.4E-16	0.021505	0.004726
2	136677957	136677968	DARS	1.18E-07	9.63E-09	9.6E-05	1	1	0.025396	1	1	1	1	0.072054	1	0.000299	0.027778	0.050473
12	66522628	66522660	LLPH	0.001516	0.009435	0.000106	1	0.115173	1	1	1	1	1	1	1	3.7E-18	1	0.021843
8	75157416	75157442	JPH1	6.32E-05	0.056416	0.000137	1	1	1	1	1	1	0.001553	1	1	0.0021	1	0.28672
12	124281419	124281436	DNAH10	3.03E-08	5.25E-13	0.000138	1	1	0.092859	1	1	1	1	0.032258	1	4.33E-06	1	0.003429
12	96694172	96694190	CDK17	9.56E-06	6.45E-06	0.000142	1	1	1	0.093702	1	1	1	1	1	2.77E-07	1	0.282428
16	53913911	53913925	FTO	1.87E-09	2.85E-11	0.000161	1	0.06338	1	1	1	1	1	1	0.333333	2E-09	1	0.145923
5	134011834	134011848	SEC24A	2.54E-07	0.000141	0.000182	1	1	1	0.035292	1	0.018868	1	1	1	5.21E-05	1	0.003393
5	78608348	78608371	JMY	4.42E-08	0.010372	0.000192	1	1	1	1	1	1	1	1	1	1.38E-15	0.054054	0.078903
1	93691855	93691881	CCDC18	2.55E-07	2.43E-10	0.0002	1	1	1	1	1	1	1	0.028169	1	4.7E-22	0.028846	0.004712
9	79835312	79835353	VPS13A	4.79E-11	2.8E-08	0.0002	1	1	1	1	1	0.016529	1	1	1	1.93E-10	1	0.313333
7	21603750	21603765	DNAH11	1.04E-11	1.07E-11	0.000209	0.032609	1	1	1	1	1	0.021739	1	1	8.64E-16	0.107143	0.201345
14	96794877	96794890	ATG2B	6.51E-08	6.71E-11	0.000217	1	0.181818	0.017699	0.022727	1	1	0.053571	1	0.111111	1.28E-08	0.027778	1
17	30267579	30267601	SUZ12	4.91E-05	0.002789	0.000217	1	0.082447	1	1	1	1	1	1	1	2.87E-09	1	0.269427
2	60988862	60988872	PAPOLG	9.82E-05	7.21E-09	0.000231	0.000129	1	0.086915	1	1	1	0.040541	1	1	2.98E-10	0.02439	0.00015
12	43964612	43964623	ADAMTS20(dist=18888),PUS7L(dist=157787)	2.04E-05	2.33E-07	0.000264	1	1	1	1	1	1	0.124228	1	0.003497	0.004933	0.001753	0.059935
3	183558468	183558512	PARL	9.76E-05	0.170732	0.000264	1	1	1	1	1	1	1	1	1	1.07E-15	0.024096	1
8	48732074	48732096	PRKDC	5E-08	4.24E-09	0.000264	1	1	1	1	1	0.007143	1	1	1	6.33E-18	1	0.153274
1	207237233	207237262	PFKFB2	2.12E-06	1.54E-07	0.000282	1	0.113384	1	1	1	1	1	1	1	5.11E-09	1	0.013879
12	112119387	112119420	BRAP	1.98E-09	8.83E-08	0.000284	1	1	1	1	1	1	1	1	0.206897	5.87E-19	1	0.177885
1	245025697	245025717	HNRNPU	1.07E-11	2.31E-13	0.000292	1	0.133746	1	1	1	1	1	0.000301	0.019608	3.21E-20	0.005553	0.158469
16	23457290	23457308	COG7	3.33E-10	3.05E-07	0.000302	1	0.208516	1	1	1	1	1	1	1	3.47E-17	1	0.075752
10	88458996	88459025	LDB3	0.000654	8.14E-11	0.000305	0.044554	0.000792	0.174889	1	1	1	0.311996	1	0.028571	0.009628	1	0.03717
1	175087683	175087694	TNN	2.73E-09	1.96E-10	0.000324	0.030612	0.007747	1	1	1	1	1	0.096721	0.019608	0.000245	1	0.092602
6	36569717	36569737	SRSF3	3.61E-07	7.85E-07	0.000335	1	1	1	0.066231	1	1	1	1	1	1.96E-21	1	0.205427
5	61745737	61745750	IPO11	2.66E-07	1.47E-05	0.000348	1	0.012338	0.365751	1	1	0.084619	0.087004	1	1	2.97E-06	1	0.131416
5	65372793	65372805	ERBB2IP	3.43E-10	1.05E-10	0.000392	1	1	1	1	1	1	1	1	0.083333	1.39E-13	0.049074	0.231787
12	94575162	94575177	PLXNC1	1.88E-10	7.98E-11	0.000399	1	1	1	1	0.020548	1	0.129487	0.04878	1	4.25E-14	0.051282	0.054744
4	119674051	119674062	SEC24D	1.99E-05	2.65E-10	0.000403	1	0.218647	1	1	1	1	1	0.003759	0.008772	4.63E-10	1	0.084149
5	162884074	162884113	NUDCD2	8.35E-08	5.56E-13	0.000414	1	1	0.020202	1	1	1	1	1	1	6.57E-10	1	0.12487
6	75890933	75890959	COL12A1	3.82E-10	4.28E-07	0.000429	1	0.343869	1	0.155545	1	1	0.028646	1	0.078947	1.27E-09	1	0.005831
3	10103903	10103946	FANCD2	1.59E-06	0.000115	0.000452	1	1	1	1	1	1	1	0.017241	1	3.31E-21	0.047059	1
7	77584159	77584171	PHTF2	9.33E-12	1.05E-08	0.00048	1	1	0.049505	1	1	1	0.157325	1	0.333333	5.29E-11	0.025974	0.0329
10	17204246	17204272	TRDMT1	2.68E-05	9.69E-08	0.000495	1	0.444979	1	1	1	1	0.179929	0.038462	1	7.98E-07	0.01638	1
17	1265304	1265326	YWHAE	2.13E-11	1.83E-09	0.00051	1	1	0.136821	1	1	0.019608	1	0.015385	1	1.68E-25	1	0.236613
1	215824195	215824226	USH2A	1.47E-11	2.22E-08	0.00056	1	0.079571	0.021739	1	1	1	1	1	1	4.47E-13	0.033708	0.004052
2	169994021	169994058	LRP2	3.97E-10	7.87E-12	0.000605	1	0.133177	1	0.030151	1	0.016393	1	0.018182	1	2.34E-16	0.04	0.000672
4	170658944	170658956	C4orf27	1.32E-05	0.005234	0.000605	1	0.260204	1	1	1	1	1	1	0.3125	3.41E-09	1	0.275995
X	133511862	133511890	PHF6	0.000103	5.89E-09	0.000627	0.025	0.021581	1	0.017241	1	1	1	0.08	1	6.86E-11	1	0.058824
6	42626564	42626585	UBR2	1.63E-06	1.07E-09	0.000656	1	1	1	1	1	1	1	1	1	2.6E-22	1	0.047444
1	173797451	173797462	DARS2	1.04E-09	5.21E-10	0.000659	1	0.068027	0.004173	0.018868	1	0.046875	0.115602	0.003484	1	2.63E-14	0.002177	0.001836
13	29238622	29238633	POMP	4.66E-12	7.77E-10	0.000754	1	1	1	1	1	1	0.0375	0.035088	1	6.34E-12	1	1
7	149543201	149543232	ZNF862	6.51E-06	7.3E-07	0.000754	1	1	1	1	1	1	1	0.012987	1	5.13E-10	1	0.043243
6	111685185	111685219	REV3L	8.92E-08	2.09E-08	0.000784	1	1	0.00084	1	1	1	1	1	1	5.7E-06	1	0.208672
16	15702117	15702141	KIAA0430	0.066409	4.72E-09	0.000938	1	1	1	1	1	1	1	1	1	3.84E-11	1	0.041667
11	132179950	132179979	NTM	0.00015	4.47E-10	0.000945	1	1	1	0.010753	1	1	1	1	1	3.66E-10	1	0.000778
18	21046255	21046274	RIOK3	1.86E-11	1.02E-07	0.000966	0.019868	1	0.072375	1	1	1	1	0.04	1	4.66E-13	1	0.365854
2	219350358	219350383	USP37	3.13E-06	9.45E-06	0.000982	1	0.050886	1	1	1	0.042662	1	1	0.431034	2.67E-14	0.073708	0.020181
12	30887772	30887832	CAPRIN2	4.68E-06	0.183186	0.00101	1	1	1	1	1	1	0.002452	1	0.117647	0.000104	1	1
9	115060090	115060107	MIR3134	1.03E-06	4.04E-12	0.001012	1	0.590106	0.226235	1	1	0.039022	0.156414	1	1	1.26E-06	0.0375	0.284034
13	42772765	42772789	DGKH	1.04E-09	2.44E-06	0.001025	1	0.029333	1	1	0.020305	1	1	0.066102	1	7.29E-13	1	0.202044
11	35287000	35287014	SLC1A2	1.35E-10	3.39E-13	0.001031	1	0.354566	1	1	1	1	0.216488	0.090909	0.032967	1.22E-10	0.119318	0.00056
1	24973106	24973116	SRRM1	1.27E-05	2.45E-13	0.001107	1	1	1	1	1	1	1	1	0.044118	3.6E-14	0.075472	0.01355
11	108549186	108549200	DDX10	1.21E-07	2.21E-13	0.001174	1	0.160956	0.001496	1	1	1	0.044586	1	1	9.16E-12	1	0.100914
12	124144572	124144584	GTF2H3	4.48E-05	6.58E-07	0.00122	1	1	1	1	1	1	0.001832	1	0.462451	2.51E-10	0.116772	0.199362
2	61462921	61462939	USP34	5.64E-12	6.3E-09	0.001221	1	0.07874	1	1	1	0.03125	1	1	1	2.68E-19	0.030303	0.003457
3	167045701	167045723	ZBBX	3.27E-07	1.57E-10	0.001261	1	1	1	1	1	0.034283	1	1	1	6.8E-16	1	5.77E-06
1	198717210	198717235	PTPRC	1.1E-10	0.000109	0.001263	1	0.397257	1	1	1	1	1	0.057143	0.006494	1.57E-17	0.072267	0.096494
13	111932586	111932617	ARHGEF7	1.84E-06	3.1E-10	0.001279	1	1	0.0017	1	1	1	1	1	1	2.07E-08	0.015625	1
2	208606875	208606908	CCNYL1	0.022778	2.66E-05	0.001317	1	1	1	0.014085	1	1	1	1	1	1.41E-14	1	0.009762
10	102035182	102035193	BLOC1S2	0.001159	1.87E-09	0.00135	1	1	0.027303	0.015	1	1	0.000102	0.012346	1	6.52E-07	1	0.031918
11	76260909	76260924	C11orf30	1.02E-11	2.43E-07	0.001364	1	1	1	1	1	1	1	1	1	8E-08	0.052632	0.030951
17	72791074	72791100	TMEM104	4.7E-09	1.23E-07	0.001399	1	1	1	1	1	1	1	1	0.181818	7.03E-08	1	0.264731
3	77645936	77645960	ROBO2	7.56E-08	7.27E-12	0.001402	1	0.254898	1	1	0.016878	0.027273	0.019511	1	1	3.52E-10	0.133181	0.17915
4	109669319	109669332	ETNPPL	2.18E-08	3.34E-09	0.001412	1	1	1	1	1	0.032787	0.139325	1	0.3	8.58E-13	1	0.096253
3	101177901	101177912	SENP7	2.3E-08	4.72E-13	0.001422	1	1	1	1	1	0.075	1	1	1	7.92E-12	0.046154	0.013965
6	36839451	36839462	PPIL1	0.000502	2.92E-09	0.001422	0.012346	1	1	1	1	1	0.096154	1	1	3.06E-09	1	0.012601
1	197009613	197009644	F13B	5.5E-08	6.74E-09	0.001442	1	0.05303	1	0.013575	1	0.01	1	0.032258	1	1.02E-11	0.02439	0.050445
X	2827794	2827827	ARSD	0.009372	0.010197	0.001442	1	1	1	1	1	1	1	1	1	4.79E-05	1	0.079372
18	74591992	74592019	ZNF236	4.12E-10	0.001425	0.001481	1	1	1	1	1	0.037556	1	1	1	1.73E-09	0.108764	0.092873
15	76576173	76576194	ETFA	2.82E-07	8.37E-07	0.001502	1	1	0.04	1	1	1	1	1	1	8.7E-17	1	1
8	97245316	97245361	UQCRB	2.47E-11	7.5E-12	0.001536	1	1	1	1	0.004219	1	1	1	1	3.19E-05	1	0.214141
1	109349996	109350021	STXBP3	9.23E-09	0.001764	0.001536	1	1	1	0.012658	1	1	0.054348	1	1	2.16E-05	0.050633	0.191986
5	72168575	72168596	TNPO1	1.5E-09	3.08E-09	0.001586	0.007353	1	0.022472	1	1	1	1	1	1	7.73E-20	1	1.66E-05
3	101284008	101284019	TRMT10C	0.000741	0.009004	0.001587	1	1	1	1	1	1	1	1	1	0.004352	1	1
X	48156078	48156097	SSX1(dist=29199),SSX9(dist=4888)	9.22E-10	0.505495	0.001673	1	1	1	1	1	1	1	0.066667	1	9.26E-23	0.16544	0.00016
6	17898423	17898434	KIF13A	0.002213	4.17E-06	0.001681	1	1	1	1	1	1	1	0.044444	1	4.92E-09	1	0.004525
7	14028245	14028266	ETV1	0.077744	0.000138	0.001681	1	1	1	1	1	1	1	1	0.01032	2.19E-08	1	0.142669
20	31292298	31292329	COMMD7	1.85E-07	3.19E-05	0.001695	1	1	1	1	1	1	1	1	1	7.03E-11	1	0.409166
5	156525916	156525949	HAVCR2	0.021164	0.027129	0.001695	1	1	1	1	1	1	0.044944	1	1	0.030301	0.05	0.007243
4	107037538	107037563	TBCK	6.75E-12	7.12E-10	0.001755	1	1	1	1	1	1	1	1	1	1.21E-07	1	1
3	129155547	129155558	MBD4	0.000527	6.93E-09	0.001783	1	1	1	0.000766	1	1	0.076923	0.021277	1	3.17E-08	1	0.137204
11	5775903	5775915	OR52N4	7.99E-07	1.13E-06	0.001815	1	0.37416	0.141787	0.051012	1	0.028069	0.002357	1	0.05848	2.46E-08	1	1
16	23486187	23486201	GGA2	1.59E-07	5.53E-12	0.001815	1	1	1	0.014184	1	1	0.026667	1	0.25	2.59E-09	1	1
13	25073399	25073415	PARP4	2.4E-10	1.92E-07	0.001815	1	1	1	0.230769	1	0.08537	0.133181	0.035088	0.015217	2.01E-21	1	0.025953
9	71849283	71849343	TJP2	3.31E-06	3.04E-05	0.00188	1	0.259293	1	1	1	1	1	0.087879	1	0.002604	1	0.270656
1	100381109	100381123	AGL	5.32E-11	2.19E-06	0.00199	1	1	1	1	1	0.06015	0.023438	0.111111	1	1.82E-10	1	0.031287
18	32917176	32917189	ZNF24	1.19E-09	6.05E-12	0.00202	1	1	1	1	1	1	0.002926	0.023256	1	1.26E-11	1	0.125761
5	76607919	76607947	PDE8B	0.00021	2.85E-05	0.002105	1	1	1	1	1	1	1	1	1	0.019105	1	0.172946
11	125442503	125442516	EI24	1.36E-11	9.53E-06	0.002221	1	1	1	1	1	1	1	1	0.26087	1.15E-05	0.072267	0.029119
9	99233176	99233211	HABP4	0.000784	1	0.002221	1	1	0.058824	1	1	1	1	1	1	2.33E-09	1	0.028704
12	112481732	112481750	NAA25	6.34E-09	6.59E-06	0.002259	1	1	1	1	1	0.026229	1	1	1	0.002386	1	0.020618
10	93784489	93784504	BTAF1	2.31E-09	1.39E-10	0.002262	0.014706	0.066372	1	1	1	1	1	1	0.15	4.1E-10	1	0.000111
1	10478830	10478870	PGD	1.16E-09	2.99E-09	0.002283	1	1	1	1	1	1	1	1	1	7.02E-11	1	0.182175
9	86588185	86588199	HNRNPK	3.11E-09	6.91E-12	0.002347	1	1	0.000769	0.001149	1	1	0.000107	1	0.366667	2.02E-18	1	1
15	43784435	43784447	RNU6-28P	1.31E-08	2.01E-07	0.002353	1	0.223003	0.010426	0.028036	1	0.057132	1	1	0.352381	8.69E-06	0.134158	0.021859
17	65119931	65119982	HELZ	0.059307	1	0.002353	1	1	1	1	1	1	1	1	0.119911	1.08E-05	1	1
3	31710396	31710408	OSBPL10	1.19E-08	8.53E-09	0.002353	1	1	1	1	1	1	1	0.079184	1	1.12E-10	0.025641	0.292494
5	54552380	54552391	DHX29	2.97E-05	1.15E-12	0.002353	1	1	1	0.00495	1	1	0.032	0.017241	1	0.00243	0.013333	0.060109
21	30438952	30438998	CCT8	5.41E-12	0.197917	0.002414	1	1	1	1	1	1	1	1	1	8.3E-11	1	0.003657
4	17964528	17964539	LCORL	6.6E-10	1.92E-10	0.002449	1	0.008097	1	1	1	1	1	1	1	1.2E-13	1	0.017819
7	108524444	108524470	C7orf66	9.4E-05	0.010197	0.002449	1	1	1	1	1	1	1	1	1	2.95E-07	1	0.048855
9	20740346	20740366	FOCAD	4.5E-06	7.03E-11	0.002463	0.028673	1	9.77E-05	1	1	1	1	1	1	1.77E-10	1	0.335453
5	82360938	82360963	TMEM167A	6E-07	2.84E-11	0.002484	0.017582	1	1	1	1	1	1	1	1	2.94E-05	1	0.009236
13	40298620	40298639	COG6	1.38E-05	9.44E-08	0.002543	1	1	0.154595	1	1	0.001174	1	1	0.059289	9.96E-17	1	0.004367
1	52912109	52912134	ZCCHC11	7.1E-10	3.53E-11	0.002551	0.011765	0.277328	1	0.036142	1	0.032258	0.12766	0.016393	1	2.45E-08	1	0.006588
2	73957870	73957891	TPRKB	0.000656	1.22E-07	0.002551	1	1	1	1	1	1	1	1	1	0.028538	1	0.09375
1	100366438	100366470	AGL	0.002273	9.41E-09	0.002634	1	1	0.100422	1	1	1	1	1	0.210526	4.52E-06	1	1
19	37581821	37581861	ZNF420	6.07E-07	0.216667	0.002634	1	1	1	1	1	0.013245	1	1	1	0.00018	1	0.128736
3	27478842	27478865	SLC4A7	3.33E-10	4.7E-09	0.002634	1	1	1	1	1	1	1	1	1	4.01E-10	1	0.022483
1	200550498	200550509	KIF14	4.47E-05	1.16E-09	0.00266	1	1	1	1	1	1	0.036364	1	1	7.5E-05	1	1
3	158399757	158399768	GFM1	6.7E-08	0.000144	0.00266	1	0.352859	0.040521	1	1	1	1	1	0.197059	0.003157	1	0.125282
5	98224945	98224957	CHD1	2.6E-09	1.7E-06	0.00266	0.008475	1	1	1	1	1	1	1	1	4.28E-07	1	0.000305
16	66946894	66946927	CDH16	5.7E-08	3.48E-07	0.002747	1	1	1	1	1	1	1	1	1	0.000549	0.050308	0.02355
3	50155887	50155910	RBM5	0.001407	0.006371	0.002775	1	1	1	1	1	1	1	0.019608	1	0.000175	1	1
16	9934670	9934703	GRIN2A	0.003258	0.047953	0.002797	1	1	1	1	1	1	1	1	1	1.04E-05	1	0.061972
11	74329503	74329522	POLD3	0.020841	3.68E-07	0.002849	1	0.125	1	1	1	1	0.162162	1	1	0.053163	1	0.130695
5	141304305	141304339	KIAA0141	7.67E-11	0.023041	0.002849	1	1	1	1	1	1	1	1	1	0.173913	1	0.060386
10	65357667	65357688	REEP3	8.85E-09	0.181818	0.002885	1	1	1	1	1	1	1	1	1	0.201149	0.034091	0.219344
2	219103313	219103336	ARPC2	6.95E-05	1.89E-11	0.002885	1	1	1	1	1	1	0.027273	1	1	1.82E-14	1	0.09589
14	70496910	70496937	SMOC1	1.81E-10	5.61E-10	0.002899	1	1	0.167427	0.120838	1	1	1	1	0.173913	1.57E-06	1	0.002912
17	75187248	75187259	SEC14L1	0.000301	3.96E-10	0.002899	1	1	1	1	1	1	0.02521	0.015873	1	1.28E-05	1	0.017824
15	50570999	50571024	GABPB1	0.000506	1.08E-08	0.002917	1	1	0.001604	1	1	0.001668	0.003072	1	0.007143	7.75E-12	1	0.013757
12	54646020	54646054	CBX5	0.018099	3.74E-05	0.00303	0.008475	1	1	1	1	0.015152	1	1	1	0.00914	1	1
11	47505869	47505883	CELF1	5E-08	3.51E-13	0.00303	1	1	1	0.047612	1	1	1	1	1	3.37E-06	1	0.062704

13	25467010	25467036	CENPJ	2.01E-10	6.97E-12	0.003072	1	1	0.045839	1	1	1	0.139786	1	0.294118	1.48E-08	1	0.00013
5	58271705	58271734	PDE4D	6.99E-06	0.000286	0.003072	1	1	0.234193	1	1	1	0.013999	0.08	1	5.85E-06	1	0.002806
5	76785406	76785444	WDR41	9.09E-10	8.8E-12	0.003072	1	1	1	1	1	1	1	1	1	4.84E-23	0.028169	0.087067
13	103301601	103301612	TPP2	1.78E-10	6.95E-10	0.003171	0.004831	1	1	1	1	1	1	1	1	2.78E-11	1	1
14	72941317	72941328	RGS6	2.52E-05	8.94E-12	0.003171	1	1	0.055545	1	1	1	1	0.016667	1	6.49E-14	1	0.000147
2	209197957	209197992	PIKFYVE	9.17E-08	0.2	0.003171	1	1	1	1	1	1	1	1	1	0.123871	0.036585	0.011897
5	16763725	16763737	MYO10	3.92E-08	3.06E-12	0.003171	1	1	1	1	1	0.029851	0.067797	1	1	6.39E-15	0.049383	0.196535
20	20003130	20003151	NAA20	4.52E-09	1.18E-07	0.003279	1	1	1	1	1	0.028673	1	1	1	1.87E-07	1	0.13754
5	71500888	71500899	MAP1B	2.43E-10	2.8E-11	0.003322	1	1	1	1	1	1	1	0.016667	1	5.87E-05	1	1
6	149899943	149899954	GINM1	4.15E-08	0.002187	0.003322	1	1	1	1	0.010753	1	0.014286	1	1	0.000779	1	0.000891
4	23816235	23816260	PPARGC1A	4.29E-09	0.002976	0.00339	0.11894	0.270556	1	1	1	1	0.048774	1	1	8.98E-07	1	0.052973
10	35818799	35818815	CCNY	1.51E-11	6.61E-11	0.003454	1	1	1	0.091406	1	1	1	1	0.130435	2.43E-11	1	0.071326
4	75147041	75147074	MTHFD2L	3.23E-07	1.69E-06	0.003454	1	0.193824	1	1	1	1	1	1	1	3.41E-10	1	0.053371
1	185953264	185953293	HMCN1	0.000386	2.71E-07	0.003484	0.014599	1	0.023077	0.024169	1	0.068947	1	1	1	4.96E-08	1	1
4	103553441	103553459	MANBA	1.23E-08	2.51E-08	0.003484	1	0.27535	0.106689	1	1	1	1	1	0.2	0.000379	1	0.015118
7	92855628	92855641	HEPACAM2	1.25E-09	0.000672	0.003484	1	0.176032	1	0.106288	1	0.015267	0.107819	0.04	0.142857	2.63E-06	0.000126	0.015831
1	93584864	93584885	MTF2	2.7E-08	0.000308	0.003488	1	1	1	1	1	1	1	0.029851	0.230769	3.3E-21	1	8.63E-05
16	1657306	1657316	IFT140	0.000409	4.87E-08	0.003507	1	1	1	1	1	1	1	1	1	3.78E-07	1	0.171373
1	109350198	109350216	STXBP3	1E-11	3.39E-07	0.003509	1	1	1	1	1	1	1	1	1	2.46E-14	0.030303	2.39E-05
7	77006092	77006113	GSAP	1.83E-05	5.15E-07	0.003583	1	0.046512	1	1	1	1	1	1	1	2.38E-16	1	1
4	15642515	15642535	FBXL5	6.91E-05	6.36E-06	0.003659	1	1	1	0.008734	1	0.068066	1	1	1	4.64E-09	1	1
5	142662342	142662359	NR3C1	1.93E-10	5.1E-05	0.003661	1	1	1	1	1	1	1	1	1	2.68E-05	1	0.099469
1	11886124	11886137	CLCN6	5.07E-08	3.81E-09	0.00369	1	0.090862	1	1	1	1	1	1	1	5.9E-09	0.038462	0.003191
2	196578306	196578326	SLC39A10	2.41E-08	4.41E-06	0.00369	1	1	1	1	1	1	0.019355	1	1	2.08E-14	0.03125	0.11161
15	43739686	43739739	RNU6-28P	2.3E-09	4.2E-08	0.003702	1	1	1	1	1	0.018868	1	1	1	5.37E-12	1	0.004269
15	44778956	44778975	CTDSPL2	1.05E-05	2.73E-08	0.003702	1	1	1	1	1	0.012422	0.018519	1	1	5.05E-15	1	0.327016
20	31981959	31981984	CDK5RAP1	0.017545	0.001934	0.003702	1	1	1	1	1	0.027874	0.026786	1	1	1.51E-06	1	1
12	62785259	62785270	USP15	4.21E-12	2.88E-07	0.003846	1	1	1	1	1	0.014085	0.001012	1	1	4.66E-09	1	0.023358
11	134054705	134054746	NCAPD3	2.41E-11	3.23E-07	0.00404	1	0.483073	0.280635	1	1	0.000716	1	1	0.07326	0.038314	0.272727	0.328672
2	54163830	54163905	PSME4	0.000225	4.44E-07	0.00404	1	0.07619	0.002754	1	1	1	0.096774	1	1	0.001287	1	0.002661
1	33135035	33135055	RBBP4	1.3E-07	8.51E-12	0.004049	1	1	0.009346	1	1	1	1	1	1	1.02E-05	0.03125	0.105187
22	21968716	21968730	UBE2L3	1.44E-10	8.89E-09	0.004049	0.015	1	0.028984	0.013216	1	1	1	1	1	1.98E-08	1	0.0048
8	87751841	87751867	CNGB3	3.01E-10	3.4E-12	0.004062	1	0.349653	0.096618	1	1	1	1	1	0.49	3.95E-24	1	0.026943
12	49091972	49092009	CCNT1	2.48E-07	3.03E-05	0.004152	1	0.003296	1	0.027027	1	1	1	1	1	7.01E-27	1	0.078089
6	108197860	108197894	SEC63	0.008629	4.64E-05	0.004193	1	1	1	1	1	1	1	1	1	0.000581	1	1
18	33611062	33611092	RPRD1A	1.53E-09	0.048276	0.004263	1	1	1	1	1	1	1	1	1	9.11E-14	1	0.159128
4	95170783	95170794	SMARCAD1	0.000107	1.73E-11	0.004267	1	1	1	1	1	1	1	0.016667	0.26087	1.07E-06	1	1
4	66286113	66286124	EPHA5	0.000141	4.13E-06	0.004354	1	1	1	1	1	1	1	1	0.003008	1.16E-05	1	0.008563
14	77934905	77934925	AHSA1	3.31E-09	0.000227	0.004408	1	0.156414	1	1	1	1	1	1	1	8.5E-20	1	0.16297
1	114963973	114963986	TRIM33	7.04E-08	4.42E-09	0.004416	1	1	1	1	1	1	1	0.00202	1	1.31E-11	1	0.002292
1	158582497	158582509	SPTA1	7.05E-12	2.35E-11	0.004505	1	1	0.040323	1	1	1	1	0.026316	1	7.96E-06	0.04878	1
5	50045960	50045967	PARP8	9.91E-10	2.61E-07	0.004505	1	0.129487	1	1	1	1	1	0.020408	1	4.96E-07	0.031746	0.195665
10	94369023	94369100	KIF11	2.95E-06	0.05767	0.004662	0.024589	0.41883	0.052748	1	1	0.003083	0.257291	1	1	0.031677	1	0.395397
3	142094816	142094843	XRN1	5.85E-06	0.035832	0.004706	1	0.24069	1	1	1	0.076923	0.106219	1	0.190476	8.68E-08	0.118415	0.217746
3	169574462	169574474	LRRC31	4.58E-05	2.09E-11	0.004707	1	1	1	1	1	1	1	0.019231	1	0.002318	1	1
8	67743588	67743599	C8orf44-SGK3,SGK3	0.000211	2.49E-10	0.004762	1	1	1	1	1	1	1	1	1	2.39E-11	1	0.195365
10	61840385	61840397	ANK3	4.12E-07	2.87E-09	0.004762	1	1	1	1	1	1	0.02439	0.045455	1	1.65E-09	1	0.139679
15	92694137	92694158	SLCO3A1	1.39E-05	2.24E-10	0.004898	1	0.081818	1	1	1	1	0.042105	1	1	6.07E-10	1	0.072727
3	160960468	160960478	NMD3	0.002379	4.11E-05	0.004898	0.009009	1	0.056818	1	1	1	1	1	1	5.97E-07	0.022222	0.092437
3	195956726	195956749	SLC51A	1.7E-05	0.007538	0.004898	1	0.095562	1	1	0.014563	1	0.181411	1	0.357143	0.007928	1	1
10	69957322	69957333	MYPN	0.000102	2.27E-06	0.004902	1	1	1	1	1	1	1	1	1	0.004783	1	1
15	85659150	85659167	PDE8A	1.34E-06	4.43E-12	0.004926	1	0.105239	0.273179	0.098467	1	0.031127	1	1	1	0.05943	1	0.040973
3	130447530	130447564	PIK3R4	2.01E-10	2.18E-05	0.004995	1	1	1	1	1	1	0.046506	1	1	3E-13	1	0.205834
6	161469631	161469654	MAP3K4	0.000339	9.01E-12	0.005042	1	0.271429	1	0.023622	1	1	1	1	1	0.195876	1	0.001904
1	155330237	155330253	ASH1L	1.34E-08	2.24E-10	0.005102	1	1	1	1	1	1	1	1	1	3.05E-05	0.003393	0.274944
15	49097732	49097750	CEP152	6.63E-11	4.07E-12	0.005102	1	1	1	1	0.021127	0.033471	0.014456	1	1	5.14E-20	1	0.004161
1	154144673	154144694	TPM3	0.005924	4.8E-05	0.005319	1	1	0.016667	1	1	0.008403	1	1	1	2.86E-08	1	0.070175
15	89009056	89009067	MRPL46	4.24E-06	1.68E-09	0.005348	1	1	1	1	1	1	1	1	1	0.125646	1	0.005763
4	57677780	57677805	SPINK2	0.000126	3.24E-08	0.005348	1	1	1	1	1	1	1	1	1	0.003675	1	1
9	37768286	37768304	TRMT10B	0.000225	9.04E-07	0.005348	1	0.117647	1	1	1	1	1	1	1	0.000375	0.074746	0.001329
5	145851163	145851180	TCERG1	2.2E-11	5.51E-08	0.00538	1	1	1	1	1	1	1	1	1	1.71E-11	1	0.00854
7	110764978	110765002	LRRN3	6.93E-12	2.58E-08	0.005464	1	1	1	1	1	1	1	1	1	1.45E-11	1	0.04461
10	22676732	22676743	SPAG6	4.92E-07	1.6E-09	0.00555	1	0.188269	1	1	1	0.034041	1	1	1	8.16E-05	0.039474	0.140059
13	38171301	38171312	POSTN	1.7E-08	3.65E-13	0.00555	1	1	0.087231	1	1	1	0.054945	1	1	6.62E-13	0.047899	0.000414
5	65073389	65073400	NLN	8.88E-05	3.22E-05	0.00555	1	1	1	1	1	1	1	1	1	3.85E-05	1	0.278116
6	109480681	109480693	CEP57L1	1.24E-07	3.69E-10	0.00555	1	1	1	0.013043	1	1	1	1	1	8.93E-16	0.057143	0.000416
1	37959771	37959782	MEAF6	0.107192	4.27E-05	0.005682	1	1	1	1	1	1	1	1	1	0.000494	0.033898	1
16	14738104	14738127	BFAR	1.21E-05	1.74E-11	0.005682	1	1	1	0.037644	1	1	1	1	0.066667	1.93E-06	1	1
17	30376993	30377020	LRRC37B	0.000442	0.000624	0.005682	1	1	1	1	1	1	0.030769	1	1	0.031693	1	0.074534
2	61187478	61187496	PUS10	6.98E-11	2.54E-11	0.005682	1	1	1	1	1	0.041092	0.026316	1	0.006536	8.23E-09	1	0.000635
22	23634614	23634638	BCR	0.000472	2.75E-06	0.005682	1	1	1	1	1	1	1	1	1	0.005415	1	0.15397
9	19350679	19350691	DENND4C	2.09E-06	4.46E-12	0.005797	1	1	0.073821	1	0.004785	1	1	1	1	0.000145	1	0.137981
16	84121078	84121113	MBTPS1	0.000108	1.75E-07	0.005845	1	0.352825	1	1	1	1	1.63E-05	1	0.005848	5.26E-07	1	0.645021
21	34900917	34900939	GART	0.000471	0.000502	0.005869	1	1	1	1	1	1	1	1	0.321429	4.82E-11	1	0.140727
17	38130038	38130058	GSDMA	0.003339	0.002088	0.006048	1	1	1	1	1	1	1	1	1	9.71E-09	1	1
9	86914709	86914724	SLC28A3	8.65E-08	6.35E-08	0.006048	1	1	1	1	1	1	1	1	1	0.005548	1	0.102058
7	77006696	77006740	GSAP	1.68E-05	6.04E-09	0.006061	1	1	1	1	1	1	1	1	1	0.001008	1	0.000153
15	58891938	58891962	ADAM10	2.92E-07	1.73E-07	0.006209	1	0.203162	0.075523	0.049991	0.017241	0.080612	0.006755	1	0.12	0.041216	1	0.040304
2	58453843	58453856	FANCL	7.33E-07	5.73E-05	0.006446	1	1	1	1	1	1	0.009854	1	0.017857	1.95E-10	1	0.442827
11	71548312	71548339	DEFB108B	5.29E-07	1.24E-06	0.006452	1	0.119293	1	0.001586	1	1	1	0.002775	0.083333	4.62E-10	0.072267	0.002482
4	57220268	57220279	AASDH	1.76E-07	3.03E-12	0.006452	1	1	0.079065	1	1	1	1	1	1	7.14E-11	1	0.057143
8	89198831	89198856	MMP16	0.000215	7.77E-06	0.006494	1	1	1	1	1	1	1	1	1	3.64E-08	1	0.253959
18	59922722	59922773	KIAA1468	2.03E-11	3.16E-07	0.006645	1	0.079137	0.036082	1	1	1	1	1	1	0.003588	1	1
16	64294574	64294585	NONE(dist=NONE),CDH11(dist=686098)	1.09E-08	2.75E-12	0.006734	0.014085	1	1	1	1	1	1	0.03125	1	1.95E-14	0.036585	0.011826
16	67470052	67470095	HSD11B2	6.48E-06	3.45E-06	0.006897	1	0.207959	0.011111	0.072375	0.0125	0.074074	0.006963	0.025	1	0.000234	0.030303	0.107158
6	153292551	153292568	FBXO5	0.000299	1.37E-10	0.006969	1	1	0.074504	1	1	1	1	1	0.025	9.35E-05	1	0.552688
8	95521853	95521874	KIAA1429	0.193838	0.001563	0.007317	1	1	1	0.187124	1	0.018772	1	1	0.128205	0.029199	1	0.521833
2	43931055	43931081	PLEKHH2	1.52E-05	0.002767	0.007389	1	0.058333	1	1	1	1	1	1	1	2.79E-08	1	0.584398
22	27019177	27019188	CRYBA4	0.000117	2.06E-09	0.007389	1	1	1	1	1	1	1	1	1	0.085976	1	1
3	41723151	41723162	ULK4	0.000136	1.45E-08	0.007389	1	0.053152	1	1	1	1	1	0.032787	1	3.99E-08	1	1
4	99339781	99339805	RAP1GDS1	3.93E-10	4.87E-11	0.007541	1	1	0.073273	1	1	1	1	1	1	5.87E-12	0.030769	0.09764
7	66703227	66703263	TYW1	0.000144	6.02E-05	0.007692	1	1	1	1	1	1	1	1	1	5.45E-05	0.025316	0.041998
12	64891393	64891418	TBK1	0.033741	0.013956	0.007742	1	0.00058	1	1	1	1	1	1	1	0.000229	1	0.086137
1	161976272	161976283	OLFML2B	4.9E-08	3.94E-12	0.007843	1	1	1	1	1	1	0.036364	1	1	1.75E-15	1	0.011489
3	167540741	167540753	SERPINI1	0.020481	2.06E-07	0.007863	0.017442	1	1	1	1	1	1	1	0.238095	0.00105	0.025974	0.066885
20	20079251	20079271	CFAP61	0.011845	3.59E-07	0.007932	1	1	1	1	1	1	1	1	1	3.15E-07	1	0.210709
10	13647579	13647603	PRPF18	5.24E-05	3.62E-05	0.007937	1	1	1	1	1	0.032256	1	1	1	6.13E-05	1	0.052469
5	10390428	10390439	MARCH6	0.000137	2.73E-11	0.007937	1	1	0.027397	0.021277	1	1	0.012987	0.046512	1	3.42E-06	0.04918	0.084211
6	38897453	38897469	LOC100131047	3.77E-11	6.96E-08	0.007937	1	1	1	1	1	1	0.080612	1	1	0.017457	0.047619	1
12	120295568	120295581	CIT	6.74E-10	3.8E-11	0.008097	1	1	1	0.017467	1	0.016393	1	1	1	0.001169	1	1
17	65074354	65074364	HELZ	0.010279	3.53E-05	0.008097	1	0.208333	1	0.034783	1	1	1	0.004762	0.230769	4.18E-11	0.054054	0.449644
4	73933671	73933706	COX18	2.95E-10	0.06494	0.008163	1	0.48818	1	0.164384	1	0.170207	1	1	0.001225	1.25E-11	1	0.113677
12	8693215	8693257	CLEC4E	0.448607	0.128424	0.008202	1	1	1	0.030928	1	1	1.32E-06	1	0.2	0.000104	1	0.00442
5	137282031	137282059	FAM13B	2.53E-10	8.52E-13	0.008333	1	1	1	1	1	1	1	1	1	6.62E-22	1	0.008536
8	110334770	110334782	NUDCD1	2.01E-09	1.11E-07	0.008475	1	0.036364	0.004869	0.074051	1	1	1	1	0.294118	1.36E-12	1	0.076923
21	38522344	38522368	TTC3	4.68E-11	2.07E-12	0.008535	1	0.188934	1	0.134937	1	1	1	1	0.039216	7.21E-16	1	0.004166
16	50117828	50117845	HEATR3	6.94E-10	1.15E-12	0.008547	1	1	0.080499	1	1	1	0.105178	1	0.4	1.16E-10	0.098305	0.02637
14	89037482	89037493	ZC3H14	9.44E-06	1.34E-08	0.008564	1	0.06014	0.018119	1	1	0.061728	0.020083	1	0.133333	3.4E-05	0.048387	0.00838
14	102276205	102276217	PPP2R5C	1.57E-09	1.8E-05	0.008737	1	1	1	1	1	1	1	1	1	8.25E-11	0.044118	0.122458
2	88484805	88484815	THNSL2	1.08E-05	4.32E-11	0.008865	0.016667	0.065041	0.000116	0.00641	1	1	0.003105	0.041667	1	3.28E-08	1	1
1	207871320	207871341	CR1L	1.03E-06	0.096682	0.009009	1	1	1	1	1	1	1	1	1	3.7E-05	1	0.085674
3	3194099	3194118	CRBN	1.18E-06	7.53E-06	0.009009	0.029555	0.188135	1	0.126414	1	1	1	1	0.057143	1.09E-07	0.000802	0.50573
2	198257652	198257684	SF3B1	0.002119	1.25E-06	0.009015	1	1	1	1	1	0.0008	1	1	1	3.45E-05	1	1
9	100700505	100700528	HEMGN	8.52E-12	1.82E-09	0.009015	0.018519	0.06087	1	1	1	1	0.012195	1	1	2.56E-15	1	9.71E-07
19	48533847	48533859	CABP5	1.24E-08	3.41E-11	0.009363	1	1	1	1	1	0.031619	0.049185	1	1	6.07E-09	1	0.12487
19	18453807	18453828	PGPEP1	4.5E-07	0.016304	0.009614	1	1	0.115294	1	1	0.049993	1	1	1	9.67E-10	1	0.000297
4	122737487	122737519	EXOSC9	5.07E-05	0.001727	0.009614	1	1	1	1	1	1	1	1	1	4.18E-17	1	0.28653
12	56677664	56677675	CS	5.16E-07	2.15E-12	0.009805	0.0125	1	1	1	1	1	1	1	1	2.24E-08	1	0.075397
9	33960778	33960794	UBAP2	7.27E-12	4.14E-11	0.009805	1	0.150242	1	1	1	1	0.14459	1	1	0.000148	1	1
1	202107422	202107460	ARL8A	0.000463	0.087798	0.009936	1	0.45166	1	1	1	1	1	1	0.034444	0.001362	1	0.012956
4	119609182	119609200	METTL14	2.61E-09	2.86E-06	0.009993	1	1	1	1	1	1	1	1	1	5.91E-12	1	1
12	123103008	123103016	KNTC1	9.31E-08	0.026232	0.01	1	0.272199	0.03125	1	1	0.059249	1	1	0.001976	0.005682	1	0.468418
13	45517486	45517513	NUFIP1	3.76E-07	0.009741	0.01	1	0.24617	1	1	1	1	1	1	1	1.1E-08	1	0.11271
4	7811543	7811554	AFAP1	2.75E-05	3.16E-09	0.010084	1	1	1	1	1	1	1	1	1	0.000397	1	0.060241
8	95793284	95793318	DPY19L4	9.22E-09	2.01E-09	0.010084	0.016293	1	1	1	1	0.018519	1	1	1	7.22E-06	1	0.115919
1	103471456	103471487	COL11A1	0.044337	0.153706	0.010084	1	0.479546	0.003078	0.44147	1	0.044444	0.000392	1	1	0.010708	1	0.011536
17	29563068	29563089	NF1	0.001692	2.53E-05	0.010279	1	0.089008	0.193085	1	0.014286	0.085431	1	0.042553	0.109091	4.07E-10	1	0.000773
3	194168811	194168825	ATP13A3	4.82E-10	2.15E-09	0.010279	1	1	1	0.078095	1	1	1	0.076923	1	0.000416	1	1
9	134067542	134067583	NUP214	6.69E-06	0.019533	0.010571	1	1	1	1	1	1	1	1	1	0.002108	1	0.004333
10	70506892	70506914	CCAR1	3.71E-08	1.57E-05	0.01063	1	1	1	1	1	0.016129	0.306293	0.017857	1	1.3E-06	1	0.022397
5	87494728	87494767	TMEM161B	1.29E-11	2.77E-06	0.01063	0.011236	1	1	1	1	0.039406	1	0.115385	1	6.61E-25	1	1
19	43382540	43382581	PSG1	1.98E-05	0.161121	0.010695	1	0.184689	1	1	1	1	1	1	1	0.297704	0.001399	0.226974
21	30910210	30910231	GRIK1	0.008023	0.000127	0.010788	1	1	1	1	1	0.001894	0.018519	1	1	8.51E-05	1	0.035714
8	38912121	38912142	ADAM9	3.47E-06	5.47E-05	0.010798	1	0.20246	1	1	1	1	1	0.0625	1	2.13E-13	1	0.008104
2	209110161	209110186	IDH1	0.002588	3.65E-06	0.01087	1	1	1	1	0.006289	1	1	1	1	0.00012	1	1
2	56102061	56102072	EFEMP1	0.017211	0.0002	0.011257	1	1	0.002695	1	0.020134	0.076169	1	1	0.127273	3.72E-06	0.161905	0.188086
9	5732520	5732544	RIC1	1.42E-10	2.26E-09	0.011312	1	1	1	0.037468	1	1	1	1	0.171569	2.24E-12	1	1
3	77366425	77366436	ROBO2	3.57E-11	1.45E-12	0.011336	1	1	0.058127	1	1	1	1	1	1	5.77E-07	1	1
X	129354254	129354276	ZNF280C	1.02E-06	1.17E-05	0.011336	1	1	5.65E-05	0.068008	1	1	0.125859	0.032787	1	2.26E-07	0.056604	0.035966
11	110479839	110479852	ARHGAP20	4.36E-10	0.000533	0.011364	1	1	0.134932	1	1	1	1	1	1	9.49E-07	1	0.026458
10	120460751	120460768	CACUL1	8.64E-05	0.189781	0.011614	1	1	1	1	1	1	1	1	1	0.000424	1	0.127204

4	22422407	22422418	GPR125	0.00017	2.37E-09	0.011858	1	1	1	1	1	1	1	1	1	3.13E-05	1	1
4	95561651	95561668	PDLIM5	0.000307	1.74E-10	0.011858	0.050847	1	1	1	1	1	0.024948	1	1	0.004449	1	0.007781
1	75679569	75679580	SLC44A5	0.001185	8.68E-05	0.011927	0.015625	1	1	0.147105	1	1	1	0.074074	0.002101	0.008331	1	0.011073
4	21698939	21698965	KCNIP4	0.000857	0.0009	0.012097	1	1	1	1	1	1	1	1	1	0.000266	1	0.038536
9	15017531	15017545	LOC389705	0.000225	2.34E-09	0.01277	1	0.27734	1	1	1	0.049993	1	1	0.368421	7.15E-15	1	0.312276
1	212969842	212969856	TATDN3	4.18E-10	6.94E-06	0.013151	1	0.261768	1	0.083297	1	1	0.010654	1	0.090909	1.58E-11	0.002885	0.013663
22	45828137	45828148	RIBC2	3.7E-07	6.1E-09	0.013256	1	1	1	1	1	1	1	0.016129	1	5.66E-05	1	1
5	132334609	132334620	ZCCHC10	0.000631	1.37E-09	0.013256	1	1	0.035088	1	1	1	1	1	1	0.001115	0.025641	0.193829
X	16711184	16711203	CTPS2	8.93E-08	4.98E-05	0.013733	1	1	1	1	1	1	1	1	1	9.68E-14	1	0.168134
1	86590509	86590523	COL24A1	9.09E-12	1.94E-09	0.013793	1	1	0.052623	0.013605	1	1	1	1	1	0.000227	1	0.06
19	53277686	53277727	ZNF600	4.05E-11	5.01E-08	0.014286	1	1	0.017241	1	1	1	1	1	1	0.000835	1	0.268407
8	28989764	28989782	KIF13B	0.001452	1.96E-06	0.014286	1	1	1	1	0.006757	1	1	1	1	0.055944	1	7E-05
18	59195580	59195606	CDH20	2.16E-09	2.96E-11	0.014286	1	1	1	1	1	1	1	1	1	0.002457	1	1
2	191941054	191941078	STAT4	0.000116	4.12E-08	0.014286	1	1	1	1	1	1	1	1	1	1.75E-06	1	0.000434
9	27011885	27011896	IFT74	0.000126	2.76E-07	0.014286	1	1	1	0.057143	1	1	1	1	1	1.01E-12	1	0.068063
11	60182851	60182862	MS4A14	3.33E-06	0.004072	0.014381	1	1	1	1	0.004762	1	0.067308	0.016667	1	5.16E-06	1	0.006975
10	32099547	32099559	ARHGAP12	1.78E-06	1.32E-09	0.01482	1	0.033421	1	1	1	0.052632	0.199362	1	1	7.34E-05	0.026667	0.496962
3	97499619	97499630	ARL6	3.8E-06	1.18E-09	0.01482	1	1	1	1	1	1	1	1	1	1.19E-10	1	1
4	39851058	39851077	PDS5A	2.07E-05	1.07E-08	0.014833	1	1	1	1	1	1	1	1	0.521053	1E-26	1	0.054319
10	5498523	5498558	NET1	1.24E-06	6.79E-10	0.014872	1	1	0.024272	1	1	1	1	1	1	6.06E-11	1	0.003968
6	152629772	152629787	SYNE1	2.27E-08	2.36E-08	0.015495	1	1	0.190454	1	1	1	0.279659	1	0.210526	1.78E-13	1	0.00097
6	116427506	116427526	NT5DC1	1.31E-11	0.000415	0.015624	1	1	1	0.046512	1	1	1	1	0.298246	2.08E-19	1	0.008988
1	50663196	50663209	ELAVL4	7.38E-10	3.13E-11	0.015709	1	1	1	0.001004	1	1	0.148678	1	1	9.1E-08	1	0.135318
9	32986030	32986069	APTX	1.29E-07	5.18E-07	0.015789	0.035712	0.064551	0.279659	1	1	1	0.036864	0.016393	0.047619	0.026908	0.065918	0.005021
17	5126838	5126849	LOC100130950	0.000621	0.000248	0.015789	1	1	1	1	1	1	1	1	1	0.000479	1	1
18	50589879	50589917	DCC	9.77E-11	0.014782	0.015838	1	0.406322	1	1	1	1	1	1	1	5.96E-11	1	0.024495
7	106898870	106898925	COG5	3.93E-08	0.00226	0.015873	1	1	0.058394	1	1	1	1	1	1	0.000173	1	0.000998
7	139746599	139746634	PARP12	6.57E-05	0.000799	0.016088	1	1	1	1	1	1	1	1	0.052632	1.48E-14	1	0.201345
19	10097443	10097455	COL5A3	1.45E-08	3.32E-13	0.016158	1	0.399794	0.211549	0.014052	1	1	1	0.04	0.15	3.92E-06	0.044776	0.013198
1	161722036	161722059	DUSP12	9.62E-11	1.35E-07	0.016667	1	1	1	1	1	1	1	0.020408	1	1.23E-16	1	0.001092
4	71024674	71024686	PRR27	1.25E-05	9.68E-12	0.016667	0.065574	1	1	1	1	1	1	1	0.444444	7.18E-12	0.016935	1
11	46665805	46665827	ATG13	2.5E-09	8.14E-12	0.016864	1	1	1	1	1	1	0.000567	1	1	0.000593	1	1
7	78130793	78130817	MAGI2	6.09E-10	0.000738	0.016918	1	1	1	1	1	1	1	0.043478	1	6.35E-11	0.025	0.002067
1	29037240	29037253	GMEB1	2.2E-07	8.35E-09	0.017094	1	1	1	1	1	1	1	1	0.35	5.7E-05	0.127869	0.064217
10	7627788	7627817	ITIH5	3.93E-09	0.001294	0.017094	1	1	0.24487	0.025641	1	1	1	1	0.1	2.08E-13	1	0.113484
3	148885779	148885790	HPS3	2.37E-07	4.25E-07	0.017094	1	1	1	1	1	1	1	0.050847	0.002747	1.68E-11	1	0.025197
14	96998621	96998653	PAPOLA	0.000611	1.8E-05	0.017241	1	1	0.228631	0.064086	1	1	1	1	0.15	0.000406	1	0.223353
17	17772622	17772638	TOM1L2	5.07E-05	1.72E-12	0.017544	1	0.298408	1	0.046625	1	1	1	1	1	0.000147	0.23	0.487808
10	105831698	105831735	COL17A1	0.000236	0.336379	0.017544	1	1	1	1	1	1	0.038961	1	1	2.33E-06	1	0.113783
3	114027065	114027097	TIGIT	0.337662	6.86E-05	0.017544	1	1	1	0.051012	1	1	1	0.333333	1	0.470228	1	0.318563
5	88018305	88018317	MEF2C	5.03E-05	2.97E-07	0.017544	1	1	0.02	1	1	1	1	0.028986	0.142857	0.001019	0.033708	0.016129
X	123184949	123184969	STAG2	4.43E-09	0.032407	0.017632	1	0.479833	1	0.082353	1	1	1	0.036364	1	5.31E-16	1	1
11	61977858	61977881	SCGB2A1	1.4E-07	4.73E-11	0.017742	0.046875	0.027878	1	0.106702	1	0.035292	1	1	1	0.226757	1	0.00254
16	31199604	31199632	FUS	9.17E-06	8.47E-07	0.017742	1	1	0.076894	1	1	1	1	1	1	0.03408	1	0.052632
1	176681165	176681194	PAPPA2	6.28E-10	0.002575	0.017825	0.029412	0.080901	0.296069	0.090307	1	1	0.169427	1	0.154799	7.1E-07	1	0.120474
12	97339669	97339680	NEDD1	1.13E-09	1.13E-05	0.018182	1	1	1	1	1	1	0.001762	0.013699	1	2.77E-05	1	0.014407
1	62350123	62350156	INADL	0.000285	7.2E-10	0.018418	1	1	1	1	1	0.032431	1	1	1	1.18E-09	1	0.160888
5	70797500	70797521	BDP1	6.78E-08	6.03E-09	0.018418	1	1	1	0.010101	1	1	1	1	1	1.67E-19	0.040541	0.153818
10	113915574	113915589	GPAM	1.65E-09	4.54E-06	0.018423	1	0.374527	1	1	1	1	1	0.208081	0.157895	2.5E-11	1	0.021375
3	183677635	183677646	ABCC5	0.000556	1.35E-08	0.018462	1	1	1	1	1	1	0.117647	1	1	1.65E-08	1	0.028686
11	34979160	34979172	PDHX	9.99E-08	8.63E-11	0.018868	1	1	1	1	1	1	1	1	1	8.71E-09	1	0.001494
2	26423951	26423962	HADHA	4.95E-05	2.68E-07	0.019231	1	0.1	0.032787	1	1	1	1	1	1	1.97E-07	0.043478	1
12	89865545	89865562	POC1B	7.52E-06	5.78E-07	0.019285	1	0.084173	1	1	1	1	1	1	1	1.56E-06	1	0.009707
17	31266427	31266441	TMEM98	3.16E-09	0.000406	0.019608	0.058385	0.024691	0.043239	1	1	1	1	1	0.3	4.62E-07	0.0375	0.161338
3	4669375	4669386	ITPR1	0.00026	4.89E-08	0.019608	1	1	1	1	1	0.016949	1	0.016949	0.210526	3.25E-07	1	0.01926
6	118822972	118822995	BRD7P3	0.012767	0.000258	0.019608	1	1	1	1	1	0.101695	0.311808	1	1	0.080857	1	0.035584
5	68662287	68662298	AK6,TAF9	2.05E-07	6.08E-10	0.02	1	1	1	0.000454	1	0.04	0.027053	1	1	2.85E-08	1	1
7	150269192	150269204	GIMAP4	1.97E-11	1.23E-10	0.020197	1	1	1	1	0.00885	0.013072	0.052632	0.04918	0.142857	1.62E-07	1	0.210466
17	40491273	40491291	STAT3	0.002604	1.52E-11	0.020209	1	0.117974	1	1	1	1	1	1	1	4.54E-09	1	0.317814
2	7154826	7154836	RNF144A	5E-05	8.12E-06	0.020209	1	0.25824	1	1	1	0.068966	1	0.01	0.52381	1.46E-07	1	1
6	97339275	97339286	NDUFAF4	7.1E-10	5.97E-09	0.020408	1	1	1	0.261247	1	0.041667	1	1	1	4.94E-10	0.058824	0.224358
12	111651931	111651994	CUX2	0.002193	2.96E-12	0.020449	1	1	1	1	1	1	1	1	1	5.43E-14	1	0.172408
1	68952564	68952605	DEPDC1	6.85E-09	1	0.02081	1	1	1	1	1	1	1	1	0.006536	3.59E-11	1	0.160439
10	75214137	75214149	PPP3CB	3.49E-09	1.32E-11	0.020833	1	1	0.003894	1	1	1	0.001906	1	0.444444	2.7E-10	1	5.33E-06
12	970296	970307	WNK1	0.04	0.000233	0.021277	1	1	1	1	1	1	0.068966	1	1	1.95E-05	1	0.087097
17	47109368	47109378	IGF2BP1	0.002659	1.66E-05	0.021719	1	1	0.096328	1	1	0.003092	0.117543	1	0.060606	6.58E-05	1	0.29821
3	186980285	186980302	MASP1	0.111487	0.034886	0.021739	1	1	1	1	1	1	1	1	1	5.13E-05	1	0.099099
1	39802338	39802351	MACF1	1.84E-09	5.11E-11	0.021739	1	0.133572	1	1	1	1	1	1	1	2.6E-06	0.000766	1
1	11156045	11156061	EXOSC10	5.14E-11	3.3E-10	0.022059	1	0.086538	1	1	1	1	1	1	1	0.000884	1	1
3	39110376	39110396	WDR48	5.34E-05	3.27E-13	0.022222	1	1	1	1	1	0.054545	0.014493	0.09375	0.1	8.8E-08	1	1
9	33338476	33338493	NFX1	1.98E-05	2.75E-09	0.022222	1	1	1	1	1	1	1	1	1	5.15E-06	1	0.077348
15	33915964	33915975	RYR3	2.08E-08	2.86E-09	0.02223	1	0.365537	0.023481	1	1	1	1	0.033333	0.003008	9.27E-05	1	0.208063
10	18940185	18940197	NSUN6	6.92E-08	1.08E-08	0.022267	1	0.054375	1	1	1	1	0.184689	0.025	1	0.000961	1	0.090588
10	115405703	115405714	NRAP	2.4E-07	1.23E-09	0.022727	1	1	1	0.079366	1	1	0.031787	1	0.3	6.57E-05	0.088235	0.042122
12	105464590	105464612	ALDH1L2	5.92E-05	7.82E-08	0.022727	1	1	0.031915	1	1	1	1	1	1	9.1E-05	1	0.072289
2	215812345	215812356	LOC101928103	9.07E-06	2.68E-09	0.022727	1	0.127354	1	0.047619	1	0.03463	1	0.029412	1	5.03E-08	0.00036	0.024391
20	3556397	3556408	ATRN	0.000484	1.1E-10	0.022727	0.026402	0.181818	0.038835	1	1	1	1	0.032258	1	0.020768	1	1
8	25287254	25287265	KCTD9	0.000227	0.000322	0.022727	1	1	1	1	1	1	0.043478	0.035714	1	2.4E-06	1	0.028817
20	47705763	47705776	CSE1L	1.26E-09	1.09E-05	0.022739	1	1	1	1	1	1	1	0.054054	0.090909	1.1E-06	0.006585	0.086458
15	49325304	49325330	SECISBP2L	0.003713	3.96E-07	0.023256	0.014493	1	1	1	1	1	1	1	1	2.56E-06	1	0.146853
15	31293995	31294007	TRPM1	7.91E-10	9.79E-10	0.02381	1	1	1	0.057336	1	1	0.060606	1	0.230769	3.74E-09	0.013699	0.005536
2	223498056	223498068	FARSB	9.68E-06	1.55E-11	0.02381	1	1	1	1	1	1	0.013793	1	1	2.07E-08	0.046154	0.064815
21	47337484	47337499	PCBP3	0.295875	0.000109	0.02381	1	1	1	1	1	1	1	1	1	0.035403	1	0.137931
5	101795499	101795510	SLCO6A1	2.29E-06	7.49E-12	0.02381	1	0.164408	1	0.014493	1	1	1	1	1	1.11E-13	0.017544	0.019914
5	14287248	14287259	TRIO	0.000156	1.45E-06	0.02381	1	1	1	1	1	1	1	1	1	7.22E-06	0.001695	0.059829
9	71538318	71538330	PIP5K1B	1.27E-06	8.79E-10	0.02381	1	1	1	1	1	1	1	1	1	1.99E-13	0.038961	0.000241
3	167762678	167762691	GOLIM4	4E-06	0.01937	0.024066	1	1	0.146154	1	1	1	0.11103	1	0.190476	1.3E-07	1	0.008779
1	202990110	202990128	TMEM183A,TMEM183B	4.18E-09	2.12E-09	0.024066	0.033613	0.149738	0.045839	0.100883	1	0.035926	0.032787	1	0.012821	3.84E-22	1	1.67E-05
19	5714321	5714332	LONP1	6.53E-05	4.66E-06	0.02439	1	1	1	1	1	1	1	0.019608	1	0.000236	1	1
17	7080111	7080136	ASGR1	0.000135	1.84E-05	0.024425	1	0.207035	0.201593	1	1	1	1	1	0.111111	0.000174	1	0.001869
5	13842027	13842047	DNAH5	1.34E-05	1.18E-05	0.024425	1	1	0.137416	1	1	1	1	1	1	3.68E-12	1	0.224919
19	21116763	21116804	ZNF85	7.61E-06	0.005949	0.024957	1	0.103307	1	1	1	1	1	1	1	0.693837	0.053571	0.000302
3	169998240	169998253	PRKCI	1.19E-09	5.91E-07	0.025487	1	1	1	1	1	1	0.032609	1	1	7.78E-07	1	0.00265
15	73409213	73409225	NEO1	3.73E-06	1.32E-09	0.025712	1	0.307819	1	0.139775	1	1	0.076923	1	1	1.16E-05	1	2.6E-05
4	167020771	167020795	TLL1	2.6E-10	8.18E-05	0.025927	0.029303	0.065574	1	0.019737	1	1	1	1	0.142857	6.25E-06	1	0.000597
3	112732286	112732324	C3orf17	5.53E-06	5.38E-06	0.025974	1	1	0.027211	1	1	1	1	1	0.411765	6.08E-05	1	0.005988
5	13885023	13885044	DNAH5	0.084903	0.207707	0.025997	1	0.133192	0.121622	1	1	1	0.21174	1	0.081319	0.09929	1	0.122681
6	117706760	117706773	ROS1	8.47E-08	3.37E-13	0.026316	0.033706	1	0.028249	1	1	0.020202	1	1	1	3.33E-06	1	0.064935
6	89614390	89614408	RNGTT	2.06E-06	1.48E-12	0.026316	1	1	0.015748	1	1	1	1	0.02381	1	4.56E-05	1	0.179497
8	76468309	76468322	HNF4G	4.56E-07	3.87E-05	0.026316	1	1	0.068823	1	1	1	0.147905	1	0.227941	0.000877	0.072054	1
12	66771108	66771126	GRIP1	1.51E-11	1.4E-11	0.026455	1	0.339366	0.028249	1	1	0.06292	0.013088	1	0.005263	1.33E-08	1	0.083518
1	153907278	153907322	DENND4B	0.331314	0.052373	0.027027	1	1	1	1	1	1	1	1	0.000877	0.435484	1	1
19	10260006	10260045	DNMT1	0.002623	1.04E-08	0.027027	1	0.153002	1	0.037733	1	1	1	0.058824	1	0.1375	1	0.067138
15	86188984	86189019	AKAP13	6.23E-08	6.07E-06	0.027451	1	0.011177	1	1	1	1	1	1	0.125	0.00207	1	0.155173
15	22414384	22414414	OR4N3P	4.44E-09	0.002869	0.027778	1	1	1	1	1	1	1	1	1	1.09E-09	1	0.015484
4	151683003	151683021	LRBA	4.32E-09	3.24E-13	0.027778	1	1	0.04023	1	1	0.019608	0.054688	0.014085	1	6.85E-11	1	0.121277
4	49032823	49032834	CWH43	1.88E-05	1.02E-05	0.027778	1	1	1	1	1	1	1	1	1	0.013413	0.030769	0.002866
11	76157922	76157934	C11orf30	3.26E-11	3.47E-12	0.028169	1	1	1	1	1	1	0.000183	1	1	5.64E-05	1	0.009853
5	137589876	137589893	GFRA3	2.1E-10	4.82E-05	0.028169	1	1	1	1	1	1	0.021739	1	1	6.57E-10	1	1
9	112211182	112211199	PTPN3	8.71E-10	0.001577	0.028169	0.02	1	1	1	1	1	1	1	1	1.62E-10	1	0.313645
16	29110397	29110417	RRN3P2	7.78E-11	3.81E-08	0.028571	0.007092	0.147059	1	1	1	1	0.192972	0.04	1	1.83E-06	3.81E-05	0.069767
11	134188851	134188867	GLB1L3	1.21E-10	3.36E-12	0.028733	0.009901	1	0.171001	1	1	1	1	1	1	7.48E-13	1	0.233385
20	5548208	5548239	GPCPD1	6.96E-11	4.18E-07	0.028733	1	1	1	1	1	0.033193	0.063143	0.081967	1	2.05E-07	1	0.633639
11	104879686	104879697	CASP5	3.5E-10	4.86E-13	0.02889	1	1	0.039735	0.010811	1	1	1	0.027778	1	1.27E-09	0.038961	0.01623
7	134925241	134925252	STRA8	4.32E-08	5.22E-10	0.02889	1	1	1	1	1	0.058241	1	0.090909	0.007519	1.39E-06	1	0.003698
12	64867983	64868002	TBK1	0.001431	8.94E-05	0.029412	1	1	1	1	1	1	1	1	1	0.040672	1	0.041667
11	26581382	26581423	MUC15	8.77E-09	1	0.030593	1	0.224795	1	1	1	1	1	0.139373	1	2.89E-08	1	0.012063
16	66757728	66757750	DYNC1LI2	0.000287	1.71E-06	0.030593	1	1	1	1	1	1	0.247948	1	0.269231	7.69E-10	1	0.263477
3	113285185	113285212	SIDT1	2.08E-06	0.009996	0.030749	1	1	1	1	1	0.04878	1	1	0.001471	1.16E-06	1	0.499589
10	78704741	78704790	KCNMA1-AS1	2.13E-05	0.00025	0.030769	1	1	1	1	1	1	1	1	1	0.000177	1	1
20	23476401	23476430	CST8	1.02E-08	3.47E-08	0.030769	0.029851	1	1	0.021127	1	1	1	0.150769	1	8.08E-11	1	0.037349
1	115455634	115455651	SYCP1	0.008869	0.000221	0.03125	1	0.192308	1	1	1	1	1	1	1	0.010175	1	0.116071
14	51716141	51716173	TMX1	9.4E-06	2.82E-07	0.03125	1	1	0.294232	1	1	0.314737	0.146107	1	0.133333	8.64E-07	1	0.028289
2	100035414	100035425	REV1	2.86E-09	1.82E-11	0.03125	1	1	1	1	1	1	1	0.033898	1	6.72E-12	1	0.000165
14	93712634	93712660	BTBD7	5.11E-12	4.92E-08	0.031346	1	1	1	1	1	0.006623	0.093788	0.074074	1	3.4E-07	1	0.00048
2	100081461	100081472	REV1	3.79E-10	1.12E-12	0.031579	1	1	1	1	1	0.032258	1	1	1	9.82E-11	0.04	1
3	154002357	154002370	DHX36	2.39E-09	2.99E-07	0.031591	1	1	1	1	1	1	0.009346	1	0.017857	4.43E-08	0.058824	3E-06
1	150310549	150310566	PRPF3	2.85E-10	1.26E-09	0.031621	1	0.203243	1	1	1	1	0.001389	1	1	9.98E-10	1	0.014555
7	102944812	102944838	PMPCB	3.79E-06	0.007585	0.031746	1	1	1	1	1	1	1	1	1	2.18E-06	1	0.001273
11	5799651	5799662	OR52N5	7.68E-07	1.21E-08	0.032258	1	0.145161	1	1	1	1	0.042105	1	1	5.16E-08	1	1
12	132496182	132496193	EP400	1.81E-05	1.38E-06	0.032258	1	1	1	0.000686	1	1	1	1	1	1.84E-11	1	0.003846
3	195102590	195102608	ACAP2	4.69E-10	3.42E-10	0.032258	1	1	1	1	1	1	1	1	1	2.18E-08	1	0.042169
4	69179759	69179783	YTHDC1	8.4E-06	3.94E-12	0.032258	1	1	1	1	1	1	1	1	1	3.03E-06	1	0.073171
8	124440326	124440339	WDYHV1	3.15E-06	3.72E-07	0.032258	0.013889	1	1	0.017751	1	1	0.030612	1	1	0.166667	1	0.07052
2	136956640	136956653	CXCR4(dist=80915),THSD7B(dist=791809)	5.26E-06	5.66E-10	0.032258	1	0.26671	1	1	1	0.062483	0.10281	1	1	4.53E-07	1	0.105474
1	115276971	115276990	CSDE1	8.8E-07	0.000153	0.032693	0.005845	1	1	1	1	0.018519	1	1	0.008333	3.78E-07	1	0.011678
6	102337480	102337497	GRIK2	5.49E-11	2.88E-12	0.032693	1	1	1	0.000358	1	1	1	1	1	2.01E-15	0.015625	0.01196
12	6705122	6705138	CHD4	6.71E-08	8.06E-09	0.033333	1	1	1	0.043663	1	1	0.147429	1	1	3.48E-09	1	0.035371
2	242312477	242312491	FARP2	5.01E-05	6.18E-12	0.033898	1	1	0.159667	1	1	0.12037	1	0.157895	0.051724	2.34E-15	1	1
11	132306682	132306697	OPCML	0.093728	0.2	0.034483	1	1	1	1	1	1	1	1	1	0.033504	1	1
11	62284179	62284194	AHNAK	0.186744	3.78E-09	0.034483	1	1	0.05245	1	1	1	1	0.035088	1	0.15022	1	0.108392

6	118953826	118953837	CEP85L	0.000119	7.56E-05	0.034483	1	1	0.071089	1	1	1	1	1	1	0.179487	1	1
6	157496153	157496197	ARID1B	0.0119	0.000152	0.034483	1	0.182444	0.000582	0.015038	1	1	0.055936	1	1	2.24E-05	1	0.068493
X	132458578	132458605	GPC4	0.000512	5.74E-11	0.034483	1	1	1	0.340887	1	0.026786	1	1	1	3.48E-10	1	0.002678
2	227967830	227967842	COL4A4	2.91E-06	3.2E-05	0.034483	1	0.413619	0.397541	1	1	0.004056	1	1	0.010989	0.003515	1	0.49436
4	152065328	152065339	SH3D19	0.001181	2.14E-12	0.035088	1	0.263158	1	1	1	1	0.001186	0.034483	1	8.96E-05	0.045455	1
12	64020310	64020330	DPY19L2	0.000452	0.000898	0.035714	1	1	1	1	1	1	1	1	1	5.93E-07	1	1
16	11862364	11862391	ZC3H7A	1.2E-07	1.55E-12	0.035714	1	1	1	1	1	1	1	0.035088	1	2.81E-10	1	0.001531
18	21758169	21758196	OSBPL1A	8.65E-08	2.1E-05	0.035714	1	1	1	1	1	1	0.117974	1	1	0.000374	1	1
2	234178775	234178807	ATG16L1	4.08E-07	0.000853	0.035714	1	1	1	1	1	1	1	1	1	9.35E-09	1	0.011769
5	139817996	139818007	ANKHD1,ANKHD1-EIF4EBP3	4.11E-07	7.03E-12	0.035714	1	0.158007	1	1	1	1	1	1	1	0.000452	1	0.063636
7	16705132	16705155	BZW2	0.000295	0.000412	0.035714	1	0.144352	1	1	1	1	1	1	1	0.000116	1	0.000107
1	115537600	115537611	SYCP1	0.000716	1.07E-09	0.035714	1	1	1	1	1	1	0.023256	1	1	3.05E-06	0.014925	0.09396
17	10596306	10596316	SCO1	7.54E-05	4.85E-06	0.035714	1	1	1	1	1	0.033898	0.104167	0.037037	1	0.000184	1	1
19	14910637	14910648	OR7C1	0.002704	7.2E-07	0.035714	1	1	1	1	1	1	0.206897	1	1	0.00017	1	1
4	95506684	95506702	PDLIM5	0.004041	1.62E-06	0.035714	1	1	1	1	1	1	1	1	1	0.156111	1	1
1	74818936	74818947	FPGT-TNNI3K,TNNI3K	1.69E-06	7.96E-09	0.036364	1	0.000511	1	0.022124	1	1	1	1	1	4.64E-07	1	0.023053
2	182399497	182399529	ITGA4	6.69E-06	0.00035	0.036364	1	0.284472	1	1	1	1	1	1	0.022269	3.02E-06	1	0.267859
11	63663130	63663159	MARK2	4.47E-07	0.00968	0.036437	1	0.147292	1	1	1	1	1	1	1	0.077108	1	0.101174
16	28842257	28842275	ATXN2L	6.86E-08	9.42E-12	0.03693	1	0.04717	0.108015	1	1	1	1	1	1	0.402998	0.012048	0.159029
1	162769510	162769522	HSD17B7	1.62E-06	0.000133	0.037037	1	1	1	1	1	1	1	1	1	1.82E-14	1	0.114679
1	63096855	63096873	DOCK7	0.005056	0.027453	0.037037	1	1	0.009434	1	1	1	1	1	1	0.008923	1	1
11	47310608	47310619	MADD	0.002407	1.72E-06	0.037037	1	1	0.033708	0.032609	1	1	1	0.02	1	0.000551	1	0.012796
12	14947675	14947706	WBP11	6.18E-06	1.96E-07	0.037037	0.028369	1	1	0.054206	1	0.010989	1	1	0.073529	4.14E-08	0.05	0.198182
12	14949720	14949731	WBP11	0.000252	6.9E-09	0.037037	1	1	0.079434	1	1	1	1	1	0.007353	6.94E-05	1	0.311613
12	53573482	53573510	CSAD	0.000182	8.52E-07	0.037037	0.011628	1	0.147885	1	1	1	0.060976	1	1	0.003468	1	0.100481
15	90984702	90984736	IQGAP1	4.19E-10	7.72E-11	0.037037	1	1	0.057592	1	1	1	0.0949	1	1	0.001638	1	0.002842
3	148711906	148711917	GYG1	6.67E-07	2.14E-12	0.037037	1	1	1	1	1	1	1	1	1	0.000409	1	1
8	91929652	91929681	NECAB1	2.49E-05	0.003799	0.037424	1	1	1	1	1	1	1	1	0.294118	9.98E-05	1	0.01114
12	7818348	7818403	APOBEC1	0.036018	1	0.0375	1	1	1	1	1	1	1	1	0.2	0.465421	1	0.016722
7	22190131	22190150	RAPGEF5	8.04E-09	2.58E-10	0.037662	1	1	1	1	1	1	1	0.056604	1	1.13E-05	1	0.154421
1	151492610	151492637	CGN	0.001523	4.12E-05	0.037736	1	0.115385	1	1	1	1	1	1	1	5.46E-05	1	0.047297
11	94602309	94602345	AMOTL1	0.000236	0.005347	0.037736	1	1	1	1	1	1	1	1	1	1.4E-05	1	0.004439
17	29482977	29482998	NF1	9.18E-10	1.55E-12	0.037736	0.010582	1	1	1	1	1	1	1	1	0.003517	1	1
3	122081881	122081893	CCDC58	2.55E-08	2.63E-11	0.037736	0.011364	1	1	1	1	1	1	1	0.24	4.66E-10	1	2.14E-05
6	10989873	10989887	ELOVL2	0.002253	3.51E-06	0.037736	0.028302	1	0.252527	1	1	1	0.070463	1	1	1.21E-06	0.227273	0.000373
9	19350919	19350938	DENND4C	4.24E-06	6.16E-07	0.037736	1	1	1	0.035474	1	1	1	1	1	8.9E-07	1	1
6	126075709	126075734	HEY2	5.04E-11	9.6E-11	0.037836	1	0.439542	0.175413	0.006278	1	0.091206	1	1	1	1.38E-07	1	0.06231
2	183066377	183066403	PDE1A	3.87E-06	1.56E-05	0.037975	1	1	1	1	1	0.005682	0.016949	1	0.2	1.57E-10	1	0.007804
12	113645152	113645163	IQCD	3.62E-06	4.8E-09	0.038462	1	1	1	0.007143	1	0.017544	1	1	1	4.96E-08	1	1
12	22015991	22016016	ABCC9	5.76E-05	8.04E-08	0.038462	0.025157	0.073036	1	1	1	1	1	0.02381	0.166667	0.016034	1	0.067903
14	103425946	103425957	CDC42BPB	0.000496	1.75E-05	0.038462	1	0.103448	1	1	1	1	1	1	1	2.21E-06	1	0.061033
19	43689403	43689434	PSG5	0.000565	0.046027	0.038462	1	1	1	1	1	1	1	1	1	0.17094	1	0.117062
22	26899774	26899785	TFIP11	6.75E-09	5.49E-05	0.038462	0.004695	1	1	1	1	1	0.102823	1	1	1.65E-07	1	0.004476
5	130857217	130857228	RAPGEF6	0.000737	9.47E-09	0.038462	1	1	1	1	1	1	1	1	1	1.56E-07	1	0.183184
1	155556426	155556438	ASH1L-AS1(dist=22691),MSTO1(dist=23523)	3.13E-06	6.92E-12	0.038462	0.01956	1	0.031056	1	1	0.019048	0.074074	1	1	0.001806	1	1
3	122271204	122271215	PARP9	1.05E-05	0.000158	0.038524	1	1	1	1	0.031915	1	1	1	0.176471	0.000184	1	0.32572
3	56605389	56605427	CCDC66	0.034775	8.4E-08	0.038751	1	1	0.1	1	1	1	1	0.1	1	0.000141	1	0.014104
9	85597720	85597749	RASEF	1.04E-10	7.14E-06	0.039161	1	0.017338	1	1	1	1	1	1	0.021978	3.58E-10	1	0.228316
13	79918806	79918816	RBM26	0.004099	8.8E-06	0.039216	1	1	1	1	1	1	1	1	1	7.17E-05	1	0.002484
10	288184	288195	ZMYND11	0.003507	4.91E-07	0.039409	1	1	1	1	1	1	1	1	1	0.037581	0.025974	0.431611
7	131163354	131163376	MKLN1	4.09E-06	5.46E-12	0.039409	1	0.161825	1	0.043122	1	1	1	1	1	0.001144	1	0.02152
12	44142419	44142447	PUS7L	0.016655	4.51E-05	0.04	1	1	1	1	1	1	1	1	1	0.04629	0.018519	1
15	70992003	70992021	UACA	1.66E-05	5.29E-05	0.04	1	0.056604	1	1	1	1	1	1	1	0.000105	1	0.071429
15	78836661	78836676	PSMA4	5.34E-12	9.15E-05	0.04	1	1	1	0.079184	1	1	0.001935	1	1	7.58E-06	1	0.035749
14	81574828	81574852	TSHR	4.93E-08	4.88E-11	0.040178	1	1	1	1	1	1	1	1	1	1.14E-09	1	0.079646
21	15537721	15537732	LIPI	9.81E-05	9.71E-08	0.040816	1	1	1	1	1	1	0.199385	1	1	3.56E-06	1	0.012576
4	13371622	13371645	RAB28	1.27E-11	3.04E-12	0.040816	1	1	0.027778	1	0.004854	0.021277	1	1	1	5.83E-15	0.041667	1
4	186288457	186288489	LRP2BP	7.5E-11	4.28E-07	0.041096	1	1	1	1	1	0.019868	1	1	1	0.017586	1	0.073175
13	32893197	32893208	BRCA2	0.00023	8.22E-13	0.041667	1	1	1	1	1	1	1	1	1	1.74E-06	1	0.11281
2	232320856	232320866	NCL	0.006938	0.004255	0.041667	1	1	1	1	1	1	1	1	0.057143	0.00242	1	1
3	132196805	132196816	DNAJC13	2.52E-05	5.58E-07	0.041667	1	1	1	1	1	1	0.010101	1	1	0.068435	1	0.068376
X	102632390	102632413	NGFRAP1	0.000786	3.39E-08	0.041667	1	0.227755	1	1	1	1	0.166667	1	1	0.23622	1	0.071429
13	30829757	30829777	KATNAL1	2.72E-05	4.91E-07	0.041667	1	0.246199	1	0.112391	1	1	1	0.035088	1	8.6E-06	1	0.005554
2	183806893	183806904	NCKAP1	0.026602	1.43E-11	0.041667	1	0.191176	1	1	0.040984	1	0.277778	1	0.530444	1.23E-10	0.050847	0.053593
22	36872638	36872662	TXN2	7.79E-06	7.71E-10	0.041667	0.008403	1	0.037037	0.015625	1	1	1	1	1	0.014416	1	0.058047
7	99711461	99711472	TAF6	3.13E-10	3.27E-05	0.042146	1	0.076058	1	1	1	0.004158	1	1	0.066667	0.00762	0.059416	0.144448
2	152426973	152427001	NEB	1.46E-08	3.54E-10	0.042254	1	1	0.05102	1	1	1	1	1	1	7.31E-13	1	1
10	12042023	12042048	UPF2	2.71E-05	5.9E-06	0.042553	1	1	1	1	1	1	1	1	1	3.16E-06	1	1
2	47600881	47600892	EPCAM	7.21E-05	3.59E-10	0.042553	1	1	1	1	1	0.011111	1	1	1	1.56E-09	1	0.06422
4	148604871	148604904	PRMT9	0.003462	2.31E-06	0.042553	1	1	1	1	1	1	1	1	1	1.67E-12	1	1
4	52757893	52757921	DCUN1D4	0.014611	2.83E-11	0.042553	1	1	0.028169	1	1	1	1	1	1	1.43E-11	1	1
5	38954825	38954836	RICTOR	3.31E-07	2.96E-11	0.043478	1	1	1	0.000472	1	1	0.002551	0.073375	1	2.63E-08	1	0.246998
5	904395	904409	TRIP13	1.38E-09	2.27E-11	0.043478	1	1	1	1	1	1	1	0.017544	1	5.01E-07	0.051282	0.095449
17	45481414	45481425	EFCAB13	0.000198	2.65E-05	0.043478	1	1	1	1	1	1	1	1	1	0.00106	1	1
1	207828632	207828649	CR1L	4.68E-06	2.04E-06	0.044118	1	1	1	1	1	1	1	1	1	7.55E-12	1	1
11	14539533	14539551	PSMA1	1.77E-05	0.043447	0.044444	1	1	1	1	1	1	1	1	1	9.16E-05	0.039216	1
15	40509618	40509629	PAK6	1.97E-07	1.8E-09	0.044444	1	1	1	1	1	1	1	1	1	1.04E-05	0.001502	0.004159
2	136690414	136690443	DARS	3.89E-09	1.56E-10	0.044444	1	0.006304	1	1	1	1	1	1	1	2.76E-11	1	0.001806
22	39636899	39636965	PDGFB	0.017995	0.030748	0.044444	1	1	0.083009	1	1	1	0.280224	1	0.447368	0.000522	1	0.275817
1	78435686	78435720	FUBP1	3.5E-07	0.000299	0.044776	1	1	1	1	1	1	1	1	1	1.38E-06	1	1
X	47106419	47106440	USP11	4.88E-05	0.005216	0.044776	1	1	1	1	1	1	1	1	1	3.18E-09	1	0.172246
1	43002199	43002216	CCDC30	0.002632	0.010428	0.045455	1	1	1	1	1	1	0.090909	1	1	6.62E-07	1	1
2	187709405	187709425	ZSWIM2	1.21E-07	7.5E-08	0.045455	1	1	1	1	1	1	1	1	1	4.28E-06	1	1
2	99802762	99802773	MRPL30	7.88E-05	0.018189	0.045455	1	1	1	1	1	1	1	1	1	1.44E-07	0.088195	1
22	26957143	26957154	TPST2	0.004229	9.65E-09	0.045455	1	0.31543	1	1	1	1	1	1	1	5.78E-05	1	0.175098
8	121322316	121322352	COL14A1	0.067639	0.043129	0.045455	1	1	1	1	1	1	0.272727	1	1	0.00748	1	0.08
22	31942815	31942840	SFI1	0.000915	2.57E-05	1	5.45E-05	1	1	0.034555	1	1	1	1	1	0.003285	1	1
20	54823684	54823699	MC3R	0.000147	2.68E-06	1	7.21E-05	1	1	1	1	1	0.000871	1	1	1.93E-06	0.064516	1
5	178140630	178140648	ZNF354A	3.31E-06	4.26E-10	0.076923	9.32E-05	1	1	1	1	1	1	1	1	0.033211	1	0.066667
17	80443296	80443308	NARF	0.006617	8.39E-11	1	0.000911	0.330128	0.005913	0.103364	1	1	1	1	0.047619	0.005013	1	0.523841
12	21958998	21959011	ABCC9	1.59E-11	1.54E-11	0.080021	0.00431	1	0.067921	1	0.015564	1	0.000806	1	1	5.74E-11	0.027397	0.01597
21	30433900	30433919	CCT8	0.000556	0.000154	1	0.004348	1	1	0.027451	1	1	0.04	1	1	0.000576	1	0.048257
19	4292947	4292975	TMIGD2	0.01373	2.4E-11	1	0.004525	1	1	1	1	1	1	1	1	0.25	1	1
3	100992404	100992415	IMPG2	4.42E-06	2.86E-08	1	0.005181	1	0.027586	1	1	1	0.098592	1	1	0.172139	0.034884	0.000339
16	15138162	15138182	NTAN1,PDXDC1	0.000135	2.29E-07	1	0.005405	1	1	1	1	1	1	1	1	0.24	0.04	0.098113
11	73753268	73753288	C2CD3	2.39E-10	4.03E-05	0.078125	0.005435	1	1	1	1	1	1	1	1	2.04E-08	1	0.000218
9	33886999	33887011	UBE2R2	1.18E-09	1.85E-11	1	0.005525	1	1	1	1	1	1	0.014925	1	0.00012	1	0.150214
4	56770490	56770501	EXOC1	9.03E-07	2.81E-10	0.108108	0.005587	1	0.056928	0.082644	1	0.057692	0.113543	1	0.066667	5.06E-08	1	0.036997
15	59961570	59961607	BNIP2	1.29E-05	5.09E-11	1	0.005618	0.118415	1	1	1	1	1	0.014925	1	4.33E-08	1	1
17	26653806	26653817	TMEM97	0.001556	2.23E-12	1	0.005848	1	1	1	1	1	1	0.034483	1	4.37E-05	1	0.075472
19	7670033	7670064	CAMSAP3	0.006962	5.58E-05	1	0.005848	0.092437	1	0.038737	1	1	1	1	1	0.002105	1	0.455847
2	238632159	238632170	LRRFIP1	1.84E-08	6.67E-08	0.083333	0.005848	1	1	0.024038	1	1	0.115602	0.08	1	1.96E-05	1	0.00538
15	70961809	70961821	UACA	1.35E-11	2.21E-10	0.074976	0.006098	0.132735	0.001806	1	1	1	0.059912	1	1	1.8E-15	1	0.050179
6	80837242	80837253	BCKDHB	6.4E-10	6.69E-11	0.046512	0.00641	0.01658	1	1	1	1	1	1	0.315789	0.132829	1	0.050369
7	23823176	23823194	STK31	1.18E-07	4.67E-09	1	0.006536	1	1	1	1	1	0.002442	1	1	0.000645	0.0625	0.006165
13	39603371	39603407	PROSER1	0.180482	0.268966	1	0.006667	0.229786	0.032609	1	1	0.024615	1	1	0.004128	6.76E-05	1	0.380204
17	7306338	7306349	TMEM256-PLSCR3	0.000146	8.1E-12	1	0.006803	1	0.026549	1	1	1	0.081967	1	1	5.37E-06	1	0.12067
20	3928832	3928855	RNF24	8.01E-06	8.81E-07	1	0.006897	0.065918	1	1	1	1	1	1	1	2.52E-05	1	0.008298
1	1688823	1688845	NADK	0.000894	6.42E-11	1	0.007143	1	1	1	1	1	1	1	1	0.333333	1	0.056818
12	69107631	69107642	NUP107	0.024531	0.00053	1	0.007194	1	1	1	1	1	1	1	1	0.070403	1	1
14	92562967	92562986	ATXN3	4.71E-06	3.34E-09	0.066667	0.007353	1	0.029046	1	1	1	1	1	1	4.61E-07	1	1
18	63430040	63430078	CDH7	4.99E-05	2.12E-07	0.20392	0.007463	0.162978	1	1	1	1	0.083734	1	1	0.007522	1	0.036182
7	44663890	44663910	OGDH	1.24E-07	4.39E-10	0.077922	0.007463	0.078621	1	1	1	1	1	1	1	7.42E-10	1	0.000165
5	143853686	143853711	KCTD16	6.35E-05	3.98E-06	1	0.007519	1	1	1	1	1	1	1	1	0.041975	1	0.003129
17	38028508	38028519	ZPBP2	0.00614	8.87E-05	0.05	0.008197	1	1	1	1	1	0.16	1	1	0.006597	1	1
8	27637666	27637677	ESCO2	0.004267	2.96E-08	0.05	0.008197	1	1	1	1	1	1	1	1	5.62E-07	1	0.070313
22	36650908	36650919	APOL1	4.76E-05	5.74E-12	1	0.008333	1	1	1	1	1	1	1	1	1.32E-06	1	1
3	50095096	50095119	RBM6	1.57E-05	5.34E-06	1	0.008368	1	1	1	0.007752	1	1	1	1	0.006272	1	0.073505
1	169845236	169845247	SCYL3	6.63E-07	5.68E-06	0.074074	0.008621	1	1	1	1	1	1	1	1	0.00271	0.00028	0.071895
20	42265908	42265920	IFT52	4.47E-07	1.97E-09	1	0.009346	1	1	1	1	0.008621	0.051282	1	1	1.54E-08	1	0.008138
6	111701462	111701475	REV3L	5.09E-08	1.89E-11	1	0.009346	1	1	0.020202	1	1	1	1	1	8.6E-08	1	0.058376
X	107169290	107169321	LOC101928335	2.74E-08	3E-10	1	0.009346	1	1	1	1	1	1	1	1	3.39E-07	1	0.093542
10	12162338	12162351	DHTKD1	2.58E-11	2.02E-07	1	0.00939	1	1	0.013333	1	1	1	1	1	5.53E-08	1	0.004907
1	70654981	70655003	LRRC40	8.29E-10	6.9E-08	0.169173	0.009434	1	1	1	1	1	1	1	1	4.35E-11	1	0.049108
19	53050992	53051013	ZNF808	4.64E-08	2.96E-06	0.166667	0.009434	1	1	1	1	1	1	0.034483	1	0.004329	0.02439	0.009521
3	42602535	42602546	SEC22C	0.015001	7.9E-05	1	0.009524	1	1	1	1	1	1	1	1	7.9E-06	1	1
19	37967219	37967230	ZNF570	8.3E-09	2.32E-12	1	0.009615	1	0.033149	1	0.015075	1	1	1	1	4.38E-12	1	0.066667
16	21138881	21138894	DNAH3	1.7E-08	5.8E-10	1	0.009615	1	1	1	1	1	0.04386	0.02381	1	0.001289	1	0.007293
19	50951721	50951743	MYBPC2	0.002581	0.000378	1	0.009662	1	1	1	1	1	1	1	1	0.285714	1	0.040179
22	44589636	44589647	PARVG	4.08E-08	5.94E-13	0.071429	0.01005	1	1	1	1	1	1	1	1	4.44E-08	0.021277	0.045451
3	51504906	51504917	VPRBP	1.52E-05	2.19E-06	1	0.010101	1	0.041663	1	1	1	1	1	0.304348	4.65E-10	0.012658	1
16	48333493	48333512	MIR548AE2	1.24E-06	8.09E-10	1	0.010256	1	1	0.035997	1	0.014184	1	1	1	2.22E-06	1	0.055556
7	99672649	99672660	ZNF3	6.81E-05	6.29E-11	1	0.010471	1	1	1	1	1	1	0.030303	1	0.077419	0.022222	0.073298
5	122343337	122343374	SNX24	2.11E-09	3.81E-07	0.046154	0.010471	1	1	1	1	1	1	1	0.461538	6.51E-08	1	0.015103
2	172187261	172187296	METTL8	4.04E-11	1.4E-10	0.057971	0.010638	1	1	1	1	1	1	1	1	1.46E-21	1	0.001101
3	186302391	186302439	DNAJB11	0.104127	0.176991	1	0.010638	1	1	1	1	1	1	1	1	1	1	2.33E-05
14	31762500	31762511	HEATR5A	4.98E-09	3.85E-08	1	0.010811	1	0.002452	0.022922	1	1	0.003912	1	1	0.000122	1	0.067073
12	93149720	93149731	PLEKHG7	1.92E-08	1.18E-07	1	0.010989	0.087912	0.02994	0.037644	1	1	0.03065	1	1	7.97E-05	1	0.000963
10	21901247	21901268	MLLT10	1.06E-11	4.96E-10	0.076923	0.011111	1	0.082609	1	1	1	0.043103	1	1	4.51E-07	1	1
2	71645619	71645662	ZNF638	6.55E-11	4.37E-06	1	0.011173	1	1	1	1	1	1	0.06014	1	0.000368	0.024096	0.032146
5	138760853	138760870	DNAJC18	8.17E-06	5.69E-12	0.076923	0.011299	1	1	1	1	1	1	1	1	5.44E-07	1	0.071823

20	37126168	37126180	RALGAPB	8.66E-09	1.33E-11	0.06	0.011494	1	0.015385	0.023392	1	1	1	0.034483	1	4.34E-07	1	0.000362
18	214605	214622	THOC1	0.005219	5.23E-07	1	0.011628	1	1	1	1	1	1	1	1	7.7E-05	1	1
16	4163683	4163694	ADCY9	0.002974	1.35E-10	1	0.011696	1	1	1	1	1	1	1	1	1.61E-08	1	0.059322
6	112937974	112937995	RFPL4B(dist=265476),LOC101927686(dist=1006742)	0.003358	9.94E-10	0.153846	0.011765	0.096774	0.077888	0.027027	1	1	1	0.032787	1	0.219512	0.023529	1
14	76211938	76211949	TTLL5	5.75E-05	4.47E-08	1	0.011834	1	0.03937	1	1	0.073375	1	1	1	1.93E-07	1	0.03285
10	93841262	93841273	CPEB3	2.46E-09	9.02E-08	0.052632	0.012121	0.07	1	0.009662	1	0.025641	0.054348	1	1	1.67E-06	1	0.01358
7	87056260	87056297	ABCB4	0.00638	1	0.206213	0.01227	0.18697	1	1	1	1	1	1	0.47619	0.289124	1	0.000369
10	134628521	134628532	CFAP46	0.002296	1.95E-07	1	0.012579	0.029412	1	1	1	0.009346	1	1	1	4.18E-07	1	0.253664
17	4712563	4712580	PLD2	0.162264	0.000659	1	0.012658	1	1	1	1	1	0.005126	0.017241	1	0.055456	1	0.186966
1	226027067	226027104	EPHX1	0.166211	0.005419	1	0.012903	1	1	1	1	1	1	0.043478	1	0.007984	1	0.192957
3	196532148	196532160	PAK2	2.06E-10	4.47E-11	1	0.013158	0.096098	0.017241	1	1	1	0.000813	1	1	5.55E-12	1	0.00103
14	53522638	53522650	DDHD1	1.8E-06	3.5E-10	1	0.013158	1	1	1	1	1	0.042553	1	1	5.53E-07	0.045455	0.011402
4	120192436	120192448	USP53	0.000458	7.94E-10	1	0.013423	1	1	1	1	1	1	1	1	3.84E-06	1	0.003703
22	36901817	36901832	FOXRED2	0.039097	1.09E-12	0.2	0.013423	1	1	1	1	1	0.026786	1	1	0.006061	1	1
X	18599975	18599996	CDKL5	1.26E-06	0.000538	1	0.013793	1	0.043103	1	1	1	0.093333	0.089852	1	0.06645	0.030769	0.012183
17	61278039	61278050	TANC2	0.027474	3.82E-08	1	0.013889	0.288278	1	1	1	1	0.12037	1	1	0.015217	1	0.024362
5	137464887	137464899	NME5	1.26E-05	1.37E-06	1	0.013986	1	1	1	1	1	1	0.076169	0.447368	0.000116	1	0.003381
3	20212754	20212778	SGOL1	6.52E-06	1.55E-10	0.095188	0.014184	1	0.024194	1	1	1	1	1	1	4.17E-13	1	0.153992
15	94841380	94841419	MCTP2	4.76E-07	2.97E-06	1	0.014388	1	1	0.022989	1	1	1	0.016949	1	0.022989	0.029851	0.071246
9	2097548	2097560	SMARCA2	2.52E-10	3.32E-11	0.202742	0.014493	0.220308	1	1	0.042424	1	0.125899	1	0.35	1.18E-06	1	0.00468
3	175041806	175041870	NAALADL2	3.89E-05	1.89E-05	1	0.014599	1	1	1	1	1	1	1	1	0.002021	1	0.075099
1	153954763	153954831	RAB13	7.59E-07	0.001025	1	0.014706	1	0.139977	1	1	0.027778	1	1	0.028571	6.14E-05	1	0.016304
10	81036869	81036879	ZMIZ1	0.000209	2.3E-07	1	0.014815	1	0.002596	0.001043	1	0.054054	0.015502	1	1	0.216018	0.096721	1
21	37591843	37591854	DOPEY2	4.42E-06	2.08E-09	1	0.015038	1	1	0.016807	1	0.028571	0.093023	1	1	1.63E-05	1	1
6	119628160	119628177	MAN1A1	0.000552	2.72E-07	1	0.015625	1	1	1	1	1	1	1	1	0.009623	1	0.015935
14	36339547	36339564	BRMS1L	0.000863	0.000443	1	0.015748	1	1	1	1	0.018182	0.078947	1	1	0.128811	1	0.08
13	110833751	110833764	COL4A1	1.52E-10	6.76E-06	0.066667	0.016129	0.04878	0.236953	1	1	1	0.018519	1	1	2.81E-11	1	0.151893
1	169797067	169797078	C1orf112	0.000247	2.54E-12	1	0.016393	0.021739	6.57E-05	1	1	1	1	1	1	0.265734	1	0.161874
15	41508829	41508841	EXD1	1.38E-11	0.000633	0.046875	0.016393	1	1	1	1	1	0.011905	1	1	3.43E-07	1	0.001128
17	67092937	67092960	ABCA6	3.21E-05	0.000112	0.058824	0.016393	1	1	1	1	1	1	1	1	0.000529	1	1
2	173337669	173337681	ITGA6	0.00032	2.15E-07	1	0.016529	1	1	1	1	0.022222	1	1	1	9.35E-05	1	0.015385
13	77740448	77740459	MYCBP2	0.001718	1	1	0.016807	1	0.033333	1	1	1	0.032787	1	1	0.02188	1	0.121555
15	68469010	68469021	PIAS1	0.001305	1.14E-06	1	0.017241	1	1	1	1	1	1	1	1	4.07E-05	1	0.001681
8	109247333	109247350	EIF3E	0.000323	7.13E-05	0.083333	0.017391	1	1	1	1	1	1	0.029412	1	3.95E-05	1	1
2	201470233	201470249	AOX1	4.22E-10	4.47E-07	0.148148	0.017544	1	0.04109	1	1	0.014925	0.066646	0.115942	0.2	1.1E-06	1	0.002679
1	21183819	21183838	EIF4G3	9.98E-05	3.04E-06	1	0.017857	1	1	1	1	1	0.12377	1	1	0.025683	1	1
2	88875981	88875993	EIF2AK3	2.38E-11	1.77E-10	1	0.018182	1	1	1	1	0.034884	1	0.000925	0.133333	3.74E-07	0.000496	0.124331
10	32742257	32742268	CCDC7	0.002086	2.14E-08	1	0.018349	1	0.035294	1	1	1	0.034483	0.018182	1	6.63E-09	0.030769	0.002229
18	61067251	61067268	VPS4B	0.000552	0.003098	1	0.018692	1	1	1	1	1	1	1	1	0.178039	1	0.067416
19	45555225	45555237	CLASRP	2.81E-09	7.83E-08	0.111111	0.018868	1	1	1	1	1	1	1	1	0.079936	1	0.103189
22	36662141	36662154	APOL1	5.31E-06	1.17E-09	1	0.019048	1	1	1	1	1	0.040323	1	0.263158	5.77E-12	1	0.011494
5	65029554	65029567	NLN	6.99E-11	1.8E-05	1	0.019048	1	1	1	1	1	1	1	1	6.22E-05	1	1
12	102183695	102183706	GNPTAB	1.98E-07	3.42E-11	1	0.019608	1	0.041096	1	1	1	1	1	1	0.001226	1	0.006662
16	74497442	74497453	GLG1	9.65E-06	9.22E-07	0.054054	0.019753	1	1	1	1	1	1	1	1	0.097973	1	1
18	23836102	23836113	TAF4B	2.48E-05	5.56E-07	1	0.01995	1	1	1	1	1	1	1	1	6.1E-06	0.041096	0.043733
1	220789355	220789373	MARK1	6.16E-09	0.002527	0.08	0.020833	1	1	1	1	0.085714	0.14017	1	0.018182	1	1	0.004642
13	29278253	29278275	SLC46A3	8.47E-11	3.18E-09	1	0.021739	0.250705	0.197668	1	1	1	1	1	0.1	0.003359	1	0.003787
19	20440881	20440924	ZNF486(dist=129582),MIR1270(dist=69157)	0.000109	0.385686	1	0.021798	1	1	1	1	1	1	0.133333	1	0.157974	0.023199	0.006989
1	15890342	15890359	DNAJC16	2.94E-08	0.001047	1	0.021978	1	0.020417	0.069093	1	0.053563	0.007546	1	1	2.57E-05	1	0.001026
17	67270277	67270288	ABCA5	1.44E-06	3.38E-07	0.080782	0.022038	1	1	1	1	1	1	1	1	6.9E-06	1	0.001209
19	41798468	41798491	HNRNPUL1	0.266838	0.00131	1	0.022059	1	1	1	1	1	1	1	0.045455	0.003326	1	0.478211
7	16722392	16722403	BZW2	2.89E-11	6.28E-13	0.0625	0.022408	1	1	1	1	1	1	0.000391	1	1.07E-12	0.0375	0.23487
17	29258846	29258863	ADAP2	1.14E-09	3.02E-10	1	0.022727	0.193569	0.081781	1	1	1	1	1	1	0.000115	1	0.001136
3	159976432	159976443	IFT80	1.54E-05	0.000121	0.133192	0.022857	0.25365	1	1	1	1	0.05042	1	0.035088	0.000192	0.044444	0.065558
21	19628809	19628823	CHODL	0.001314	3.97E-08	0.13219	0.023256	1	1	1	1	1	1	1	0.1875	5.09E-11	1	0.004094
3	33434954	33434968	UBP1	3.33E-10	4.51E-05	0.050633	0.026316	0.057971	1	1	1	1	1	1	1	9.03E-11	1	1
17	43616611	43616622	LRRC37A4P(dist=18722),LOC644172(dist=60870)	4.36E-05	0.0003	1	0.026549	0.352381	1	1	1	1	1	0.054545	0.125	0.000187	1	0.013652
15	42536227	42536238	TMEM87A	7.21E-05	1.22E-09	1	0.026755	1	0.020833	1	1	1	0.008045	1	1	8.52E-13	0.02381	0.024613
6	84290141	84290156	SNAP91	2.2E-05	3.03E-09	1	0.027523	1	0.106307	1	1	1	1	1	1	0.002741	0.146154	0.154023
5	167933673	167933685	RARS	2.61E-08	2.42E-06	0.093702	0.028986	1	0.090172	1	1	1	1	0.020833	1	9.99E-08	0.073148	0.132413
17	19480586	19480604	SLC47A1	0.012608	7.15E-06	1	0.029303	0.289231	1	1	1	1	1	1	0.426471	0.131493	1	0.29675
2	152267709	152267733	RIF1	7.18E-10	0.000136	1	0.029412	0.222061	1	1	1	1	1	1	1	8.32E-14	1	0.04093
1	151665554	151665573	SNX27	1.59E-06	2.54E-07	1	0.030187	0.079365	0.028302	1	1	0.027778	1	1	1	6.25E-05	1	1
1	179989020	179989038	CEP350	0.000618	1.28E-10	0.097561	0.030417	1	1	1	1	0.017857	1	1	1	1.11E-05	0.031746	1
10	120795782	120795808	EIF3A	3.9E-07	3.72E-09	1	0.030417	1	1	1	1	1	0.041667	1	1	0.001792	1	1
2	37599619	37599652	QPCT	0.055411	0.001727	1	0.030769	1	1	1	1	1	1	1	1	0.005065	1	1
2	55900225	55900242	PNPT1	0.00027	6.48E-05	0.096341	0.030887	0.066667	1	1	1	0.03125	1	1	0.058824	0.002451	1	1
7	64004813	64004850	ZNF680	0.001598	0.044118	0.235854	0.031913	0.327771	1	1	1	1	1	1	0.028571	0.000433	1	0.000158
17	27861104	27861129	TAOK1	2.61E-05	0.008274	1	0.033331	1	1	1	1	1	1	1	1	0.004008	0.047619	1
7	114303491	114303502	FOXP2	8.57E-07	7.37E-06	0.115294	0.033557	0.234274	1	1	1	1	0.053684	0.04	0.018182	6.57E-05	1	0.014302
5	177035488	177035500	B4GALT7	1.7E-06	0.04749	1	0.033753	1	0.036036	1	1	1	1	1	0.333333	0.156364	1	0.188619
7	50444181	50444192	IKZF1	0.000101	3.42E-11	0.04878	0.03468	1	1	1	1	1	1	1	1	5.67E-07	0.027778	3.27E-06
11	125618700	125618730	PATE1	0.242116	0.020889	0.05	0.035088	1	1	1	1	0.036145	1	1	1	0.028431	0.173913	0.357836
5	7885782	7885795	MTRR	6.16E-09	1.89E-12	0.189947	0.036361	0.548995	0.007375	1	1	1	0.026626	1	0.133333	1.62E-11	1	0.316902
18	29543667	29543679	TRAPPC8(dist=20576),RNF125(dist=54766)	3.76E-09	2.12E-11	1	0.03661	1	1	1	1	1	1	1	1	0.235165	1	0.014464
1	109535489	109535500	WDR47	0.001992	0.007441	0.142857	0.039212	1	1	0.074045	1	1	1	1	1	0.022222	1	0.001317
1	47571943	47571960	CYP4Z1	4.21E-09	5.93E-10	0.138274	0.039502	0.179367	1	1	1	1	1	1	0.098814	2.24E-17	1	0.263349
8	38705639	38705661	TACC1	7.1E-11	0.000131	1	0.04	1	1	1	1	1	1	1	1	7.56E-08	0.048193	0.065274
12	49397291	49397302	PRKAG1	5.23E-08	2.62E-12	0.118415	0.040323	0.070175	0.055353	1.12E-05	1	1	0.131237	1	0.157895	6.27E-10	0.041667	0.004448
4	107037269	107037282	TBCK	6.05E-06	8.2E-06	0.065574	0.041096	1	1	0.01626	1	1	0.02459	1	1	2.05E-10	1	0.000308
12	105260159	105260194	SLC41A2	3.97E-10	0.02056	0.107843	0.042373	0.210654	0.148985	1	1	1	0.203655	0.015385	0.027778	0.001665	1	0.002942
21	38495253	38495270	TTC3	1	1	1	0.042735	1	1	1	1	1	1	1	1	0.523532	1	0.092957
15	45446084	45446109	DUOX1	0.000935	0.190873	0.16946	0.043902	0.365911	0.008151	1	1	1	0.092355	1	1	0.000523	1	0.48046
14	20666587	20666598	OR11G2	0.000559	1.14E-08	0.35	0.048611	0.032494	1	1	1	1	1	1	1	0.000655	1	1
7	23761159	23761171	STK31	3.19E-09	3.24E-06	1	1	0.000138	1	0.014286	1	0.041322	1	0.01	0.166667	1.47E-05	1	0.001617
3	9102112	9102129	SRGAP3	2.77E-07	0.069234	1	1	0.000155	1	1	1	1	1	0.016667	1	5.87E-06	0.025974	0.002021
17	52991026	52991047	TOM1L1	0.006975	0.01004	0.075472	1	0.000165	0.075092	1	1	1	0.064499	1	0.111111	4.01E-06	1	0.00196
1	206566852	206566872	SRGAP2D	5.38E-07	1.06E-06	0.077647	1	0.001126	1	0.022727	1	1	1	1	1	2.45E-13	1	0.022807
X	131231430	131231468	FRMD7	0.000424	0.001205	1	1	0.001292	1	1	1	1	1	1	1	4.48E-05	1	0.023906
12	124116817	124116847	EIF2B1	0.001268	0.000102	1	1	0.001967	1	1	1	1	0.046667	1	1	1	1	0.004107
1	158224559	158224624	CD1A	0.304267	1	0.076923	1	0.002282	1	1	1	1	1	1	1	0.029197	1	0.047107
15	34654339	34654358	LPCAT4	0.026859	0.068162	1	1	0.002298	0.169207	1	1	0.009727	1	1	1	0.604248	0.042553	0.017982
20	42199704	42199743	SGK2	0.068403	0.369707	1	1	0.002364	1	0.024193	1	1	1	1	0.272727	0.114143	1	1
18	6975847	6975857	LAMA1	0.426471	1.02E-07	1	1	0.002634	1	1	1	0.013158	1	1	1	0.02284	1	1
8	7191539	7191558	FAM66B	0.503512	0.034545	1	1	0.002912	1	1	1	1	1	1	1	1	1	1
1	46650191	46650201	TSPAN1	2.87E-06	3.61E-09	0.076169	0.092543	0.003361	0.000926	0.013414	1	0.017544	0.000642	0.098718	0.162023	1.17E-07	1	0.335897
17	61898129	61898142	FTSJ3	5.58E-05	0.001386	1	1	0.00383	1	1	1	1	1	1	1	0.001305	1	1
7	91509436	91509457	MTERF1	0.005863	0.055923	1	1	0.004898	1	1	1	1	1	1	1	0.000587	1	1
X	21534510	21534521	CNKSR2	6.31E-08	1.29E-08	0.052632	1	0.005797	1	0.063812	1	0.016129	1	1	1	2.83E-06	0.018519	0.051852
15	35083508	35083555	LOC101928174	0.186912	1	1	1	0.006058	1	1	1	1	1	1	1	1	1	0.023498
X	122598635	122598648	GRIA3	3.32E-06	3.45E-08	0.074074	1	0.006143	0.093788	1	1	1	0.001854	1	1	0.001466	1	1
7	33075634	33075645	NT5C3A	0.000185	5.28E-09	1	1	0.006342	1	0.028777	1	1	0.114286	1	1	0.001735	1	0.007129
11	58380192	58380205	ZFP91-CNTF	8.21E-08	1.84E-08	0.07128	1	0.006714	1	1	1	0.080808	1	1	1	0.000164	0.034483	0.42418
16	81051115	81051128	CENPN	9.28E-06	1.41E-06	0.051282	1	0.006858	1	1	1	1	1	0.181818	1	1.59E-10	1	1
2	236706612	236706623	AGAP1	0.003872	2.41E-06	1	1	0.00752	0.132597	1	1	1	1	0.02439	1	0.062218	1	0.087148
X	21544904	21544935	CNKSR2	6E-05	6.96E-08	1	1	0.007692	1	1	1	1	0.033333	1	1	2.23E-05	1	0.135338
5	68413042	68413072	SLC30A5	4E-05	1.76E-08	0.1	1	0.008207	0.002678	0.076923	1	1	0.281567	1	0.10989	1.59E-11	0.04	1
5	68396764	68396793	SLC30A5	0.012034	0.018197	1	1	0.008765	0.026667	1	1	1	0.006993	1	0.285714	1.41E-05	1	0.015063
X	1467519	1467589	IL3RA	1	1	1	1	0.009114	1	1	1	1	0.018868	1	0.060606	1	1	0.000249
19	56329186	56329204	NLRP11	8.12E-11	4.76E-08	0.076923	1	0.009665	1	0.13755	1	1	1	1	1	6.41E-12	1	0.000241
14	51477220	51477231	TRIM9	0.002121	9.24E-10	0.047619	1	0.01	1	1	1	1	0.106383	1	1	0.000522	1	0.129944
14	81574687	81574712	TSHR	0.10902	0.344591	1	1	0.010977	1	1	1	1	0.217856	1	0.045455	1	1	0.000342
14	52981552	52981563	TXNDC16	4.86E-07	9.41E-11	1	1	0.01131	1	1	1	0.041237	1	1	1	0.003121	1	0.052576
12	94818770	94818802	CEP83	0.314815	0.001472	1	1	0.011378	1	1	1	1	1	1	0.24	0.0254	1	1
15	41350749	41350793	INO80	0.000419	1	1	1	0.012091	1	1	1	1	1	1	0.166667	0.128258	1	0.186936
6	152631788	152631821	SYNE1	0.000358	0.001281	0.05	1	0.0122	1	1	1	1	1	1	1	0.000538	1	1
2	63182611	63182622	EHBP1	1.57E-11	2.83E-07	0.047778	1	0.012479	1	0.027027	1	1	1	1	0.136364	1.04E-17	0.128873	0.003636
2	9552383	9552396	ITGB1BP1	3.75E-08	6.21E-12	0.187097	1	0.012576	0.096189	1	1	0.066646	0.043663	1	1	0.003697	1	0.005849
14	50605267	50605280	SOS2	4.3E-06	2.71E-06	0.132086	1	0.013151	1	1	1	1	0.005202	1	0.008621	5.02E-08	0.05	0.25722
6	105405900	105405913	LIN28B	1.68E-11	2.28E-09	0.222222	1	0.013889	1	1	1	0.009174	1	1	1	0.000168	1	0.003626
1	29476535	29476555	SRSF4	0.061748	4.81E-06	1	1	0.015625	0.024691	1	1	1	0.097561	1	1	0.010592	1	1
15	50581627	50581647	GABPB1	0.000302	2.11E-06	1	0.099937	0.016129	1	1	1	1	1	1	0.058824	4.13E-08	0.004152	0.125995
20	10622080	10622091	JAG1	6.43E-05	9.06E-09	1	1	0.018087	0.090044	1	0.013514	0.051948	0.178667	1	0.330882	0.016078	1	0.019202
7	18688019	18688056	HDAC9	5E-08	3.03E-05	1	1	0.018103	0.035928	0.022535	1	1	0.105188	1	1	0.002024	1	0.118073
1	248524799	248524818	OR2T4	0.719187	0.335739	0.133192	1	0.018732	0.068947	1	1	1	1	1	0.285714	0.029111	1	1
9	117783551	117783586	TNC	9.27E-10	1.06E-06	1	1	0.020083	0.149423	1	1	0.022556	1	1	1	0.009042	1	0.233007
1	36888302	36888316	OSCP1	7.13E-07	6.59E-13	1	1	0.02026	0.14788	0.106806	1	0.000654	0.001808	1	0.525692	2.65E-08	1	0.196576
7	20180507	20180526	MACC1	0.597468	0.011401	1	1	0.020579	0.31414	1	1	1	0.423269	1	0.428571	0.098194	1	0.049734
6	51910735	51910747	PKHD1	1.48E-06	1.14E-05	0.055556	1	0.021012	1	1	1	0.02381	0.090862	1	0.000999	4.55E-05	0.047619	0.139783
6	36483295	36483334	STK38	9.66E-06	0.208955	1	1	0.021308	1	1	1	1	1	1	1	0.065728	1	0.415981
3	124998098	124998118	ZNF148	6.68E-06	1.71E-06	0.482966	1	0.022214	1	1	1	1	0.019248	1	1	0.000617	1	0.000403
19	20317771	20317824	ZNF486(dist=6472),MIR1270(dist=192257)	1	1	1	1	0.022222	1	1	1	1	1	1	1	0.366667	1	1
18	56245965	56246014	ALPK2	0.077379	0.311321	1	1	0.023835	1	1	1	1	1	1	1	0.404905	1	0.20309
14	93686568	93686587	UBR7	6.47E-06	3.76E-08	1	1	0.025386	0.014183	1	0.029289	1	0.018477	1	1	5.12E-06	1	0.127451
5	142601811	142601862	ARHGAP26	3.2E-10	0.606383	0.176043	1	0.025725	1	1	1	1	1	1	0.125	0.000871	1	0.003117
5	83550060	83550071	EDIL3	1.28E-10	6.84E-13	0.142683	1	0.025858	1	1	1	1	1	0.041667	1	8.26E-10	1	0.293961
7	102038153	102038199	LOC100630923	2.38E-08	0.001808	1	1	0.028274	0.093688	1	1	0.095175	0.119887	1	1	1.14E-08	1	0.360037
2	215876589	215876603	ABCA12	5.66E-11	1.28E-10	0.252874	0.052623	0.029372	1	0.027778	1	1	1	0.066667	0.006536	4.67E-06	1	0.325743
17	33318204	33318216	LIG3	3.17E-06	1.4E-09	1	1	0.030303	1	1	1	1	1	1	1	2.23E-08	1	0.001627
11	89395303	89395315	FOLH1B	0.003766	4.18E-09	0.195578	1	0.030809	0.118569	0.012327	1	1	0.005581	0.148148	0.25	0.000285	1	0.167623
8	24253166	24253199	LOC101929294	0.007317	0.080942	0.056604	1	0.031465	1	1	1	1	0.083294	1	1	0.112604	1	1

1	29016705	29016737	GMEB1	0.0012	1	1	1	0.031496	1	1	1	1	1	1	1	0.003166	1	1
16	3117272	3117311	IL32	0.033433	0.185841	1	1	0.032127	1	0.114535	1	1	1	1	1	0.022585	1	0.046488
3	160141137	160141173	SMC4	0.001003	0.011505	1	1	0.032258	1	1	1	0.014184	1	1	1	0.14636	1	0.086957
6	144814625	144814664	UTRN	0.555184	0.006865	1	1	0.032967	1	1	1	1	1	1	1	0.036948	1	0.07183
2	47702411	47702471	MSH2	0.081764	0.241206	0.148148	1	0.033058	1	1	1	1	1	1	1	0.038095	1	1
12	131476665	131476692	GPR133	1.52E-05	0.000269	1	1	0.033464	1	1	1	0.028037	1	1	1	0.203998	1	0.000683
1	16354441	16354448	CLCNKA	0.710243	1	1	1	0.034003	1	0.052623	1	1	0.109015	1	1	0.390688	1	0.155645
2	225035745	225035758	SERPINE2(dist=131709),FAM124B(dist=207657)	1.16E-06	4.82E-10	0.298246	1	0.034783	0.042662	0.025105	1	1	1	1	1	6.68E-07	1	1
2	139308383	139308420	SPOPL	3.16E-07	0.337203	1	1	0.034836	1	1	1	1	1	1	0.017266	0.002271	1	0.114155
10	43671378	43671392	CSGALNACT2	5.63E-06	4.12E-12	0.409944	1	0.035361	0.268822	0.064241	1	0.168354	1	0.108108	1	6.24E-07	0.023256	0.025642
1	66829000	66829011	PDE4B	0.009094	0.001259	0.133333	1	0.035714	1	1	1	1	1	1	1	0.003473	1	1
14	51062236	51062290	ATL1	0.586458	0.012828	0.233343	1	0.036137	1	1	1	1	1	1	1	0.245105	1	1
17	45992566	45992604	SP2-AS1	2.31E-09	4.25E-12	1	1	0.037004	1	1	1	1	1	1	1	3.51E-07	0.034483	0.001734
6	134210497	134210516	TCF21	0.021574	6.31E-09	1	1	0.037553	1	1	1	1	1	1	0.272727	0.000288	1	1
3	38137959	38137970	DLEC1	1.42E-08	5.3E-05	1	1	0.037879	1	1	1	1	0.022556	1	1	0.077291	1	1
2	69420574	69420634	ANTXR1	2.07E-09	0.021611	0.109015	1	0.038462	1	1	1	1	1	1	1	2.21E-05	1	0.235594
1	218578726	218578745	TGFB2	0.024401	0.00018	1	1	0.039798	1	1	1	1	0.041667	1	1	0.322682	1	1
1	155631307	155631342	YY1AP1	2.45E-06	1	0.192993	1	0.040343	1	1	1	1	1	1	0.001538	1.08E-06	1	0.001442
9	123945492	123945515	RAB14	7.58E-06	0.001216	1	1	0.040677	1	0.079967	1	0.039683	1	0.071429	1	0.000511	1	0.316795
19	45781081	45781156	MARK4	0.631693	1	1	1	0.040873	1	1	1	1	1	1	1	0.022989	1	0.016293
19	55452749	55452775	NLRP7	0.182799	0.058708	1	1	0.041237	1	1	1	1	1	1	1	0.243243	1	0.11724
10	6273170	6273182	PFKFB3	0.000824	1.71E-06	1	1	0.04131	0.084767	1	1	0.071408	1	1	1	4.66E-07	1	1
22	26769464	26769477	SEZ6L	0.002161	0.000282	1	1	0.041412	1	1	1	0.015267	0.25276	0.083333	1	2.96E-05	1	1
15	34553225	34553236	SLC12A6	3.78E-05	1.6E-05	1	1	0.041667	0.028249	1	1	1	0.127354	1	1	2.77E-13	0.05	0.009323
7	20180425	20180476	MACC1	0.145235	0.042165	1	1	0.042263	0.000652	1	1	1	1	1	1	0.24	1	0.032212
5	16764255	16764277	MYO10	0.001526	0.01512	1	1	0.042421	0.333321	0.260976	1	1	0.378763	1	0.083333	1	1	0.016147
13	73636910	73636929	KLF5	0.031519	0.096118	0.3	1	0.042779	0.011102	0.215868	1	0.120575	0.228469	1	0.333333	0.303854	1	0.042836
4	7780663	7780674	AFAP1	0.00054	0.000469	0.181818	1	0.042857	1	1	1	1	1	1	1	1	1	0.05625
8	82583104	82583133	IMPA1	0.010358	1	1	1	0.042857	1	1	1	1	1	1	1	2.86E-05	1	1
2	170413815	170413834	FASTKD1	2.18E-10	9.28E-12	0.163647	1	0.042945	1	1	1	1	1	1	1	5.71E-05	0.001207	0.143992
2	84668258	84668269	SUCLG1	3.61E-08	2.51E-11	1	1	0.043478	1	0.029412	1	0.049074	1	1	1	3.57E-10	1	0.007778
20	47268978	47268996	PREX1	0.002281	4.28E-06	0.088235	1	0.044248	1	1	1	1	1	1	1	0.148649	1	1
11	57472141	57472167	MED19	0.614013	0.006603	0.066667	1	0.045045	1	1	1	1	0.032	1	1	0.0004	1	0.056075
10	93695545	93695556	BTAF1	0.006124	0.011434	1	1	0.045455	1	1	1	1	1	1	1	0.007746	1	0.05641
15	53815527	53815550	WDR72	6.64E-05	0.001107	0.145299	1	0.045613	0.188619	1	1	1	0.312431	1	1	0.002223	1	0.044309
7	142139624	142139663	TRY2P(dist=167556),MTRNR2L6(dist=234468)	0.001003	0.102765	1	1	0.046358	1	1	1	1	1	1	1	0.117647	1	1
5	74097328	74097361	FAM169A	0.029969	0.254098	1	1	0.047619	1	1	1	1	1	1	1	0.132215	0.060606	1
12	6657402	6657417	IFFO1	0.00163	0.005516	1	1	0.047619	1	1	1	1	1	1	1	0.009775	1	1
5	54701447	54701491	SKIV2L2	3.68E-06	3.89E-06	0.139373	1	0.047619	0.057851	1	1	0.015873	1	1	1	2.5E-06	1	0.1
11	32852019	32852043	PRRG4	0.000851	3.12E-11	0.197031	1	0.048387	1	1	1	1	0.040404	1	1	0.000326	1	0.016198
4	183600752	183600764	TENM3	2.48E-06	0.000197	0.089852	1	0.048804	0.172494	1	1	1	1	0.132086	0.230769	0.000441	0.013551	1
18	12955439	12955452	SEH1L	2.86E-05	3.76E-07	1	1	0.048979	0.238761	0.013101	1	0.034188	0.010447	1	1	0.031977	1	1
3	7494245	7494274	GRM7	1.43E-07	3.91E-05	0.221484	1	0.049558	1	0.22541	1	1	1	1	1	2.05E-05	1	0.07355
14	67848479	67848493	EIF2S1	1.53E-09	1.11E-05	0.109524	1	0.049587	1	0.045796	1	0.015504	1	1	1	0.116171	1	0.046016
2	46583272	46583283	EPAS1	0.066976	0.210665	1	1	1	2.13E-06	1	1	0.156863	0.307035	1	0.375	0.400724	1	0.420572
18	43314395	43314412	SLC14A1	8.26E-05	1.67E-10	0.05814	1	1	4.24E-05	0.133774	1	1	0.056421	1	0.2	1.58E-06	1	0.199638
X	117883813	117883824	IL13RA1	3.84E-08	1.54E-07	1	1	1	0.000224	0.028571	1	1	0.158163	1	1	0.001579	0.035088	0.074534
1	171511148	171511159	PRRC2C	0.007183	0.165354	1	1	1	0.000474	1	1	1	0.176136	1	1	0.00108	1	0.011285
12	122437594	122437605	WDR66	1.87E-05	1.18E-09	1	1	1	0.000571	1	0.007692	0.015873	1	1	1	0.000637	0.037037	0.038647
12	19475610	19475621	PLEKHA5	8.52E-07	1.25E-12	0.176136	1	1	0.0008	0.023256	1	1	1	0.068966	1	1.16E-06	1	1
6	97615907	97615918	MIR548H3	0.000106	9.26E-10	1	1	1	0.000821	1	1	1	0.086957	1	1	3.99E-10	1	1
15	28427670	28427687	HERC2	0.000398	6.15E-05	0.0625	1	1	0.000942	1	1	1	0.030303	1	1	0.000651	1	0.122389
13	50235208	50235218	EBPL	0.001264	8.42E-06	0.131034	1	0.074074	0.000949	1	1	1	1	1	1	2.69E-07	1	1
4	70280786	70280798	UGT2B28(dist=120018),UGT2B4(dist=65085)	3.52E-06	5.58E-07	0.206349	1	0.431373	0.001094	0.047548	1	1	0.115311	1	0.001225	6.25E-05	1	0.000806
1	160302354	160302365	COPA	0.007242	8.26E-07	0.064516	1	0.110638	0.001221	1	1	0.016529	0.034965	1	1	0.000115	1	1
17	7726648	7726698	DNAH2	0.000443	0.02871	1	1	0.284963	0.001268	0.154999	1	0.061224	0.066863	1	1	0.022323	0.12	0.000745
1	36884530	36884544	OSCP1	1.27E-11	2.29E-13	0.050847	1	1	0.001534	1	1	1	1	0.031746	1	7.54E-16	0.042857	3.16E-05
3	38938299	38938322	SCN11A	6.3E-08	2.95E-06	0.069444	1	0.471529	0.00158	1	0.062176	1	0.029333	0.137931	1	0.002712	1	0.017213
7	56126036	56126047	CCT6A	0.027885	1.17E-06	1	1	0.064516	0.001721	1	1	1	1	1	1	1.53E-05	0.044444	0.144958
5	64084746	64084771	CWC27	0.000355	3.63E-06	0.139373	1	0.536429	0.001762	1	1	1	0.012865	1	0.384615	0.000886	1	0.085224
15	50873112	50873154	TRPM7	0.002047	3.45E-10	1	1	0.061663	0.001858	1	1	1	1	1	1	0.001204	1	0.012539
2	36986088	36986108	VIT	1.29E-06	3.32E-13	1	1	0.172625	0.002457	0.036361	1	1	1	0.017544	1	1.8E-07	0.062004	1
10	64975001	64975012	JMJD1C	9.05E-05	8.72E-09	1	1	1	0.002667	0.05695	1	0.058824	0.002864	1	1	0.000687	1	0.001415
1	45472798	45472829	HECTD3	0.016532	0.002112	1	1	0.064341	0.0027	0.479862	0.104348	1	0.021207	1	1	0.01631	1	0.010119
7	133881908	133881936	LRGUK	0.006086	1	1	1	0.125	0.003222	0.133803	1	0.187342	0.01818	1	1	0.052521	1	0.017962
5	139936680	139936694	SRA1	3.86E-05	3.11E-12	0.35	0.205053	1	0.003544	1	1	1	0.004163	1	1	0.008926	1	0.037681
3	113376110	113376147	KIAA2018	0.373229	0.007721	1	1	0.119898	0.004204	1	1	1	7.97E-05	0.1	0.004902	2.84E-06	1	0.003052
18	18619416	18619428	ROCK1	1.03E-10	1.24E-09	0.056522	1	0.142664	0.004971	1	1	1	1	1	1	4.16E-06	1	7.7E-06
9	32485288	32485313	DDX58	0.003955	2.59E-07	1	1	1	0.00545	0.222209	1	1	0.273364	1	1	0.325593	1	0.007849
19	5739320	5739333	CATSPERD	6.87E-12	2.17E-12	1	1	1	0.005495	1	1	1	0.00949	1	1	0.005037	1	0.003168
10	101731593	101731631	DNMBP	1.61E-10	4.27E-13	0.23	1	1	0.006757	1	1	1	1	0.027778	1	2.21E-05	1	0.003543
8	95750744	95750759	DPY19L4	5.07E-05	4.02E-07	1	1	1	0.006944	1	1	1	1	1	1	1.65E-14	0.021978	0.190919
8	120580546	120580569	ENPP2	1.71E-08	4.63E-12	0.157614	0.083587	0.47607	0.007665	0.075725	1	0.058824	0.020597	0.066102	1	1.18E-07	0.037975	0.041018
4	91549147	91549168	CCSER1	2.65E-06	3.19E-09	0.070175	1	1	0.00824	1	1	1	1	1	0.098039	2.12E-09	1	0.207531
8	139380103	139380130	FAM135B	1.21E-09	9.2E-06	0.078947	1	0.199336	0.008264	1	1	0.055556	0.055556	1	1	6.79E-06	1	1
1	207679180	207679198	CR1	7.54E-05	6.22E-09	1	1	1	0.008475	1	1	1	1	1	1	0.004662	1	0.000445
13	20056698	20056716	TPTE2	0.001158	1.5E-06	1	1	1	0.008929	1	1	1	1	1	1	8.96E-05	1	0.187342
X	40588550	40588561	MED14	7.73E-06	2.6E-06	1	1	1	0.00925	1	1	1	1	1	0.153846	3.97E-10	0.06665	0.197169
20	29623380	29623389	FRG1B	0.214981	1	1	1	1	0.009524	1	1	1	1	1	1	1	1	0.052632
7	86823977	86823988	DMTF1	2.61E-07	5.88E-10	1	1	1	0.009615	1	1	1	1	0.033333	1	5.7E-05	1	0.045802
1	39352116	39352127	RHBDL2	0.002004	0.006484	1	1	1	0.010309	1	1	1	1	1	1	9.35E-05	1	1
7	154745910	154745921	PAXIP1	0.000833	1.43E-10	0.074074	1	1	0.010309	0.042853	1	1	1	1	1	0.000278	1	1
17	12920526	12920549	ELAC2	8.26E-11	9.35E-12	0.057971	1	1	0.010638	0.025861	1	0.006711	1	1	1	2.37E-15	1	0.034934
18	19110456	19110477	ESCO1	0.000234	9.56E-10	0.219457	1	0.426795	0.011378	0.065421	0.052239	0.012303	0.001245	1	0.095238	1.82E-10	0.001107	1
1	168205770	168205781	SFT2D2	2.58E-06	5.03E-10	1	1	1	0.012579	1	1	1	1	1	1	5.82E-08	0.00036	0.110464
2	238925144	238925166	UBE2F-SCLY	2.32E-07	3.27E-09	1	1	1	0.012739	0.004831	1	1	0.048544	1	1	8.86E-05	0.029126	0.003885
9	70993092	70993104	PGM5	2.7E-07	5.4E-12	1	1	0.069265	0.012866	0.136772	1	1	1	1	1	1.9E-09	0.05	0.175298
2	58362150	58362161	VRK2	3.08E-11	5.76E-07	1	1	1	0.012987	0.011765	1	1	1	1	1	0.531921	1	0.003936
11	66618396	66618426	PC	7.01E-05	0.321475	1	1	1	0.013072	1	1	1	1	1	1	0.010948	1	0.110365
14	89878206	89878246	FOXN3	0.086329	0.000204	1	1	1	0.013333	1	1	1	1	0.020408	1	1.74E-07	0.047619	0.055046
19	7707445	7707455	STXBP2	0.002127	4.48E-10	0.0625	1	0.332254	0.013754	0.028267	1	1	1	1	1	0.001064	0.109524	1
1	32119347	32119376	COL16A1	1.25E-08	0.012736	0.349277	1	1	0.014459	1	1	1	1	1	0.00202	0.00657	1	0.074231
9	8338847	8338866	PTPRD	0.407558	0.028573	1	1	0.050832	0.014471	1	1	1	1	1	1	0.041374	1	0.006259
10	111651598	111651609	XPNPEP1	0.005306	0.000528	0.102564	1	1	0.014599	1	1	1	1	1	1	0.02199	1	1
8	124244005	124244016	C8orf76,ZHX1-C8orf76	0.003301	7.13E-12	0.076923	1	1	0.015873	1	1	0.02381	1	1	1	0.031579	1	0.000784
16	67286352	67286366	SLC9A5	4.36E-07	1.75E-11	1	1	1	0.016393	0.024793	1	1	0.002574	1	1	1.03E-05	1	0.009376
17	79176010	79176020	CEP131	0.000713	5.24E-08	1	1	1	0.016949	1	1	1	1	1	1	0.037288	1	0.005795
1	36282435	36282452	AGO4	5.26E-06	7.82E-08	0.065217	1	1	0.017241	1	1	1	1	1	1	0.0523	0.057971	1
1	183873947	183873965	RGL1	0.001612	0.000682	1	1	1	0.017391	1	1	1	1	1	1	3.88E-05	1	0.116772
2	10095014	10095031	GRHL1	0.010888	0.000407	1	1	1	0.017544	1	1	1	1	1	0.071429	0.103185	1	1
2	11317833	11317856	PQLC3	3.39E-06	5.62E-06	0.047619	1	1	0.018349	1	1	1	1	1	1	0.000389	1	0.029218
19	52646629	52646648	ZNF616(dist=3438),ZNF836(dist=11477)	0.002987	6.25E-05	1	1	1	0.018352	1	1	0.047059	0.185855	1	0.210526	8.5E-07	1	0.131216
14	90499389	90499401	TDP1	1.38E-09	2.59E-06	1	1	0.097107	0.018519	1	1	1	0.021978	1	1	2.97E-10	1	1
19	42933173	42933197	LIPE-AS1	1.54E-05	6.48E-12	0.4	1	1	0.018519	0.023077	1	1	0.072727	1	1	0.00233	1	1
5	98208016	98208027	CHD1	1.36E-07	1.44E-05	0.106383	1	1	0.018519	1	1	1	0.019608	1	1	3.5E-06	1	1
20	62163783	62163814	PTK6	0.002836	0.000179	1	1	1	0.019108	1	1	1	1	1	0.464286	0.118132	1	1
13	108518658	108518714	FAM155A	1	0.061894	1	1	1	0.019231	0.031008	1	1	1	1	1	0.416667	1	1
12	27803097	27803114	PPFIBP1	0.200913	0.033443	1	1	1	0.019417	0.046148	1	1	1	1	1	0.030986	1	0.013835
14	69861462	69861490	ERH	5.49E-08	0.004006	1	1	1	0.019608	1	0.016667	0.007937	1	1	1	5.92E-05	1	0.161613
12	57677520	57677531	R3HDM2	5.93E-08	9.68E-12	1	1	0.0625	0.019802	1	1	1	1	1	1	3.28E-11	1	0.096715
3	143551065	143551076	SLC9A9	7.03E-06	1.99E-11	1	1	1	0.019802	1	1	1	0.084746	0.025	1	4.02E-09	1	0.002907
1	100174683	100174709	MIR548AA1,MIR548D1	2.51E-05	2.63E-11	1	1	1	0.02	1	1	1	0.14	0.030769	1	1.07E-05	1	0.137478
18	60034075	60034100	TNFRSF11A	2.07E-05	0.003518	1	1	1	0.02	1	1	1	1	1	1	4.27E-05	1	0.051402
2	101185539	101185550	PDCL3	0.000141	6.77E-06	1	1	1	0.020134	1	1	1	1	1	1	1.32E-08	1	1
3	100569452	100569464	ABI3BP	1.31E-05	8.91E-08	0.053571	1	1	0.020202	1	1	1	0.055046	0.002299	1	9.52E-12	1	0.035321
1	7912944	7912955	UTS2	0.000118	5.86E-13	0.058824	1	0.111111	0.020202	0.014493	1	1	1	1	1	4.34E-08	1	0.019355
4	54319247	54319262	FIP1L1	0.04614	7.36E-06	0.075	1	1	0.020833	1	1	1	0.005994	1	1	0.000279	1	1
12	111701486	111701497	CUX2	0.099456	0.001678	1	1	1	0.020934	0.358547	1	1	0.032127	1	0.044118	0.001498	1	0.018871
9	2088640	2088651	SMARCA2	0.013181	1.74E-09	1	1	1	0.021053	1	0.004255	1	1	0.036364	1	5.15E-07	1	1
1	151010849	151010872	BNIPL	2.71E-08	1.36E-06	1	1	1	0.021277	1	1	1	1	1	1	1.44E-07	0.024096	1
2	45645684	45645695	SRBD1	0.00373	1.09E-07	0.057143	1	1	0.021277	1	1	1	1	0.016393	1	0.001774	1	0.165498
6	144179190	144179202	LTV1	8.08E-08	8.2E-09	0.095238	1	0.090909	0.021277	1	1	0.014706	1	1	1	4.57E-05	1	0.077778
6	54791345	54791356	FAM83B	2.25E-09	5.6E-12	0.052632	1	1	0.021277	1	1	1	0.08	1	1	1.23E-09	0.031746	0.234151
14	53213128	53213140	STYX	2.14E-06	4.36E-12	0.076169	1	1	0.021583	1	1	1	0.168354	1	1	6.53E-11	1	0.004299
16	69687076	69687105	NFAT5	1.17E-11	0.00115	0.065027	1	1	0.021978	0.029703	1	1	1	0.058824	1	2.82E-06	1	1
4	154502520	154502539	KIAA0922	0.030875	1.16E-06	0.05	1	1	0.022222	1	1	1	1	1	1	0.00011	1	1
4	120446868	120446880	PDE5A	6.14E-07	3.26E-11	1	1	0.588281	0.022884	1	1	1	1	1	1	0.004944	0.049911	0.009452
4	85416737	85416758	NKX6-1	0.100812	0.017899	1	1	0.433265	0.023076	1	1	1	0.043973	1	1	0.064663	1	0.15271
17	10543122	10543133	MYH3	2.02E-07	6.9E-09	1	1	1	0.02381	1	1	1	1	0.03125	0.125	1.71E-09	0.026316	0.015838
1	205129466	205129482	DSTYK	2.29E-06	6.23E-11	1	1	1	0.024	1	1	1	0.022901	1	1	1.18E-09	1	2.09E-05
7	146805220	146805232	CNTNAP2	1.66E-05	8.63E-11	1	1	1	0.024194	0.044563	1	1	0.109806	1	0.010989	0.002284	1	0.066005
15	77239728	77239746	RCN2	0.012241	7.68E-08	1	1	1	0.02439	1	1	1	1	1	1	0.007732	1	0.01075
2	99685327	99685344	TSGA10	0.000579	2.37E-06	0.109524	1	1	0.02439	1	1	1	1	0.060606	1	4.38E-07	1	0.002679
14	35592699	35592709	KIAA0391	0.011633	5.27E-05	1	1	1	0.024691	1	1	1	0.026316	1	1	0.000171	1	1
3	64132418	64132433	PRICKLE2	0.005135	1.71E-12	1	1	1	0.025478	1	1	1	1	1	1	0.001997	1	1
2	27660101	27660112	NRBP1	9.95E-05	9.02E-06	1	1	0.070175	0.025641	1	1	1	0.028986	1	1	0.000488	0.02439	1
12	1042252	1042272	RAD52	9.6E-05	5.88E-10	1	1	1	0.026549	0.13054	1	1	0.096774	0.076923	0.00303	0.001674	1	0.039664
17	73519258	73519269	TSEN54	0.000244	6.26E-10	1	1	1	0.026549	1	1	0.023256	0.001086	1	1	0.002258	1	0.059322
15	52439772	52439802	GNB5	3.63E-07	3.52E-12	0.085106	1	1	0.026596	0.022422	1	1	1	1	1	1.13E-07	0.016129	1
6	153603884	153603895	RGS17(dist=151495),OPRM1(dist=727736)	0.051584	2.9E-05	1	1	1	0.026667	1	1	1	0.044944	1	1	0.087719	1	1
19	22255785	22255822	ZNF257	4.24E-06	0.000501	0.075472	1	0.272483	0.026755	1	1	1	1	1	1	0.017995	1	0.051654

1	205594807	205594823	ELK4	1.21E-08	8.58E-08	1	1	1	0.026906	1	1	1	1	1	1	9.43E-07	1	0.024071
1	150998221	150998235	PRUNE	6.98E-07	6.55E-10	0.05	1	0.394884	0.027149	0.21418	1	1	0.142622	1	1	0.000939	1	0.027833
9	74349917	74349938	TMEM2	7.71E-07	2.64E-06	1	0.054412	0.252941	0.027189	0.150972	1	1	1	1	0.04329	0.012726	1	0.240156
12	100994143	100994154	GAS2L3	2.2E-06	2.74E-07	1	1	1	0.027397	0.037736	1	1	0.011364	0.019231	1	0.01069	1	0.174754
3	160156367	160156378	TRIM59	0.003248	5.2E-09	1	1	1	0.027397	1	1	0.0625	1	1	1	7.09E-05	1	1
12	112143465	112143476	ACAD10	2.27E-05	4.71E-08	1	1	1	0.027778	1	1	1	1	0.058824	1	8.6E-13	1	1
17	3846565	3846581	ATP2A3	0.009142	5.22E-13	1	1	1	0.028119	1	1	1	1	1	1	0.114907	0.057692	1
5	50074331	50074342	PARP8	2.9E-05	1.49E-07	1	1	1	0.028169	1	1	1	1	1	1	0.000539	0.046512	0.133175
3	11933140	11933151	TAMM41(dist=44747),SYN2(dist=112683)	0.151724	0.00482	0.119318	1	1	0.028302	1	1	1	1	1	1	0.002096	1	1
12	102159106	102159131	GNPTAB	2.95E-05	1.18E-07	0.075	1	1	0.028571	0.03125	1	1	1	1	1	0.000307	1	0.067797
1	89473441	89473452	GBP3	0.000447	3.37E-08	1	1	0.076923	0.028571	1	1	1	0.138889	1	1	8.33E-08	0.065574	0.01379
8	63985465	63985476	TTPA	2.58E-08	4.74E-11	1	1	1	0.028986	0.043592	1	1	1	1	1	7.44E-06	1	1
20	48467300	48467311	SLC9A8	6.28E-07	2.2E-09	0.068361	1	1	0.028986	0.040319	1	0.031127	0.060811	1	1	1.68E-06	1	3.08E-05
2	179442292	179442314	MIR548N,TTN-AS1	2E-05	6.71E-08	0.05	1	1	0.029126	1	1	1	0.052632	1	0.166667	0.041197	0.001174	0.000672
3	20216049	20216075	SGOL1	3.33E-06	0.001087	0.05	1	1	0.029126	1	1	1	1	1	1	0.001199	1	1
2	192228419	192228444	MYO1B	1.54E-06	2.93E-12	1	1	1	0.029268	0.017021	1	1	1	0.014286	1	0.00914	1	0.003666
17	56688726	56688737	TEX14	1.02E-05	1.51E-10	1	1	1	0.029557	1	1	1	1	1	1	9.14E-05	1	1
2	119748135	119748152	MARCO	0.008906	1.43E-06	0.234274	1	0.216843	0.029568	1	1	1	1	1	0.333333	7.49E-08	1	0.000188
13	110859316	110859336	COL4A1	1.04E-10	5.84E-13	1	1	0.171727	0.030303	1	1	1	1	0.018939	0.031579	5.09E-18	0.06014	0.004841
7	77394978	77395006	RSBN1L	0.502016	0.000811	0.068182	1	1	0.030303	1	1	1	1	1	1	0.20438	1	0.214085
2	37342007	37342019	EIF2AK2	4.4E-05	4.49E-12	0.058824	1	1	0.030303	1	1	1	1	0.030303	1	2.08E-10	1	1
2	271998	272015	ACP1	1.6E-07	6.07E-08	0.090865	0.060962	0.448561	0.030801	0.10097	1	0.091966	0.007548	1	0.011858	6.13E-08	0.059988	0.216545
11	102395831	102395842	MMP7	0.236842	0.002031	0.0625	1	1	0.030928	1	1	1	1	1	1	0.232143	1	0.056604
17	30538050	30538061	RHOT1	1.99E-06	2.17E-07	1	1	1	0.03125	0.020101	1	1	1	0.016667	1	6.59E-05	1	1
2	203807441	203807452	CARF	5.76E-06	0.000596	1	1	0.131001	0.031746	1	1	1	1	1	1	7.65E-06	1	1
11	46666872	46666883	ATG13	3.9E-05	3.91E-11	1	1	1	0.032051	0.010152	1	1	1	1	1	0.000801	1	0.000126
18	31463174	31463185	NOL4	0.009513	4.13E-10	0.052632	0.06865	0.313725	0.032258	1	1	1	1	1	1	0.000562	0.061224	0.194397
4	120241806	120241818	FABP2	2.93E-07	5.36E-10	1	1	1	0.032258	1	1	1	0.057554	1	1	1.52E-06	0.024096	0.190918
6	132270728	132270740	CTGF	0.039452	4.27E-05	0.206897	1	0.216216	0.032361	1	1	1	0.35304	1	0.214286	0.085255	0.223529	0.650209
10	52566432	52566445	A1CF	1.07E-07	3.89E-11	1	1	1	0.03252	0.012422	1	1	1	1	1	3.59E-06	1	0.185148
20	62571412	62571430	UCKL1	5.57E-09	5.89E-07	1	1	1	0.03252	1	1	1	1	1	1	0.088591	1	0.116883
19	5727206	5727218	CATSPERD	9.9E-07	1.41E-06	1	1	1	0.032651	0.015267	1	1	1	1	1	3.6E-08	1	1
22	42997944	42997961	POLDIP3	0.083627	0.011799	1	1	1	0.032787	1	1	1	1	1	1	1	1	1
1	11182261	11182279	MTOR	3.76E-05	6.41E-05	1	1	1	0.033058	1	1	1	1	1	1	0.010546	0.044444	1
5	179665269	179665281	MAPK9	2E-07	1.79E-06	0.069549	1	1	0.033493	1	1	1	0.002095	1	1	3.42E-12	0.027778	0.037461
1	117633133	117633144	TTF2	0.000237	2.63E-06	1	1	1	0.03352	1	0.004854	1	1	1	1	5.7E-08	1	2.24E-05
1	33160254	33160275	SYNC	0.035714	5.34E-08	0.294872	1	1	0.033654	1	1	1	1	1	1	0.003008	1	1
X	151393196	151393224	GABRA3	1.31E-07	7.16E-10	0.143955	1	1	0.033654	1	1	1	1	1	1	1.97E-06	1	0.241513
2	158406601	158406612	ACVR1C	4.9E-09	8.15E-05	0.055556	1	1	0.033708	1	1	0.009709	1	1	1	0.040734	1	0.053476
5	153413451	153413471	FAM114A2	0.000164	0.000261	1	1	1	0.034091	1	1	1	1	1	1	9.77E-09	0.039216	0.016406
11	134055425	134055436	NCAPD3	6.4E-05	5.49E-10	0.054054	1	1	0.034091	1	0.004808	1	1	0.035088	1	0.000415	0.041667	0.158895
10	285473	285500	ZMYND11	0.017474	0.000988	0.051724	1	0.117541	0.034483	1	1	1	1	1	1	0.188235	1	0.16347
10	131755652	131755666	EBF3	2.56E-10	9.56E-07	1	1	1	0.034783	1	1	1	0.009623	0.076923	1	2.1E-06	1	1
4	128751775	128751787	HSPA4L	3.33E-08	6.65E-06	1	1	1	0.035461	1	1	1	1	1	1	8.03E-12	0.042553	0.083333
6	128385949	128385967	LOC101928140	5.17E-05	1.54E-05	0.066667	1	1	0.035714	0.017442	1	1	0.001207	1	1	0.186047	0.044776	0.169878
20	47648454	47648481	ARFGEF2	4.14E-06	2E-10	0.119898	1	1	0.035926	0.06059	0.009479	0.008065	1	1	1	0.06271	1	9.68E-05
6	132190480	132190491	ENPP1	0.002358	1.26E-10	1	1	1	0.035971	1	1	1	1	1	1	0.004727	1	1
15	32716917	32716934	ULK4P1,ULK4P2,ULK4P3	0.041753	0.138392	0.617437	1	0.24694	0.036304	1	1	1	0.31348	1	1	0.007206	1	0.451653
17	66972364	66972375	ABCA9	0.000451	7.47E-07	0.117551	1	0.091916	0.036364	1	1	1	1	1	1	2.33E-06	1	1
2	203680554	203680568	ICA1L	5.55E-09	3.2E-10	0.199507	1	1	0.037034	1	1	1	1	0.02381	1	1.4E-06	1	0.156614
7	99687972	99687988	COPS6	1.09E-11	8.24E-10	1	1	1	0.037556	1	1	1	0.064	1	1	0.001158	0.021978	1
14	75476004	75476015	EIF2B2	1.48E-05	1.84E-08	1	1	0.05	0.037972	1	1	1	1	1	1	4.93E-07	1	0.000375
12	19440358	19440369	PLEKHA5	0.005586	4.55E-05	1	1	1	0.038095	1	1	1	0.122807	1	1	0.039865	1	0.137233
4	94693160	94693173	GRID2	3.7E-10	4.04E-11	0.12	1	1	0.038458	1	1	0.007194	6.94E-05	1	1	9.46E-06	0.043478	0.063604
1	20441896	20441907	PLA2G2D	1.51E-05	0.000852	1	1	1	0.038462	1	1	1	1	0.013699	1	0.004353	1	1
X	135053121	135053154	MMGT1	0.000146	3.12E-07	1	1	1	0.03876	1	1	1	1	1	1	4.07E-08	1	0.000516
13	32814024	32814043	FRY	2.04E-10	1.55E-07	0.065789	1	1	0.039216	1	1	1	1	1	1	6.77E-07	1	0.011851
10	15113934	15113946	OLAH	5.58E-07	6.24E-10	1	1	1	0.040265	1	1	1	1	1	1	9.69E-09	0.000974	5.11E-06
19	43358576	43358613	PSG10P	0.002658	1	1	1	0.060656	0.040265	1	1	1	1	1	0.25	0.092933	1	0.395969
6	132039890	132039901	ENPP3	2.8E-09	1.25E-11	0.15	1	1	0.040462	0.045243	1	0.040198	1	1	1	1.82E-06	1	0.207715
20	3565277	3565289	ATRN	1.07E-11	2.15E-12	0.199417	1	1	0.040609	1	0.004854	0.013605	0.05	0.015385	1	1.85E-06	1	0.003361
17	16137244	16137257	PIGL	2.45E-11	1.8E-09	1	1	1	0.040816	0.051715	1	1	1	0.028571	1	1.02E-09	1	0.000165
2	131883311	131883322	PLEKHB2	8.33E-08	3.86E-05	1	1	1	0.040816	1	1	0.095188	1	1	1	1.04E-07	1	0.141264
16	29375976	29376000	SNX29P2	1.5E-08	4.12E-05	1	1	1	0.041663	1	1	1	0.07573	1	1	2.53E-07	1	0.232592
7	66463195	66463206	TYW1	2.98E-05	0.000224	1	1	1	0.042373	0.181719	1	1	5.5E-06	1	0.000113	0.316483	0.099318	0.007544
2	190603201	190603221	ANKAR	0.005736	3.58E-09	0.053571	1	0.119898	0.042992	0.082439	1	0.113543	0.279755	1	1	0.000521	1	0.128831
6	160430199	160430211	IGF2R	2.33E-09	9.64E-07	1	1	1	0.043243	0.020305	1	1	1	1	1	0.000607	1	0.174214
6	139598061	139598085	TXLNB	0.000213	2.57E-08	0.153627	1	1	0.043478	1	1	1	1	1	0.057143	5.26E-06	0.109524	0.000335
15	32393486	32393502	CHRNA7	1.16E-07	1.09E-12	0.1	1	0.529323	0.043793	0.165032	1	1	7.88E-05	1	0.222222	2.6E-12	1	0.12608
3	180322248	180322260	TTC14	4.14E-11	5.47E-12	1	1	1	0.043956	0.078975	1	0.027586	0.103824	1	1	9.35E-09	1	0.123831
2	110322117	110322127	SEPT10	0.059781	0.002331	1	1	1	0.043956	1	1	1	1	1	1	1	1	1
20	25057191	25057229	VSX1	0.002916	6.72E-11	1	1	1	0.044113	1	1	0.000391	1	1	1	9.08E-10	1	1
2	32366959	32366971	SPAST	9.61E-10	1.08E-12	0.071429	1	1	0.045161	1	1	1	1	0.016129	1	4.42E-19	0.047332	0.001009
2	172943883	172943894	METAP1D	0.005745	4.28E-11	1	1	1	0.045752	1	1	1	1	1	1	0.013994	1	1
2	178357852	178357869	AGPS	0.000249	1.93E-05	0.142857	1	1	0.045752	1	1	1	0.037383	1	1	0.01129	0.044118	0.005965
10	16737156	16737176	RSU1	1.87E-06	0.000132	1	1	0.118294	0.046296	1	1	1	1	1	1	1.53E-05	1	1
6	79695003	79695015	PHIP	6.68E-10	8.41E-13	0.147313	1	0.113113	0.046868	0.040904	1	0.032127	0.189331	1	0.371429	4.41E-17	1	0.012715
20	45878003	45878014	ZMYND8	1.13E-07	4.4E-10	1	1	0.095745	0.047191	1	1	1	1	1	1	0.000256	0.026667	1
12	6777069	6777112	ZNF384	0.29747	0.679559	0.15	1	1	0.047613	0.15468	1	1	1	1	1	0.133738	1	0.05878
5	118865564	118865575	HSD17B4	3.61E-06	4.47E-06	1	1	1	0.047613	1	1	1	1	1	1	0.001558	1	1
19	58445088	58445099	ZNF418	1.47E-06	1.45E-11	1	1	1	0.048041	1	1	1	0.065934	1	1	6.64E-07	1	0.003778
3	37100166	37100183	LRRFIP2	0.001613	1.78E-08	0.25974	1	0.280585	0.048231	1	1	1	1	1	1	0.013257	1	1
2	233271682	233271728	ALPPL2	0.003595	0.095608	1	0.057131	1	0.048851	0.105171	1	1	0.108515	1	0.001471	0.001486	1	0.003688
9	137803188	137803208	FCN1	0.067588	5.71E-05	1	1	1	0.048905	1	1	1	1	0.047619	1	0.129032	0.00135	1
3	121151270	121151281	POLQ	1.57E-05	1.9E-08	0.131034	1	1	0.04902	1	1	1	1	1	1	5.99E-05	1	0.001752
4	165865191	165865202	APELA(dist=46512),TRIM61(dist=10396)	3.08E-07	2.57E-05	1	1	0.1	0.049587	1	1	1	1	1	1	0.00359	1	1
5	140812775	140812788	PCDHGA12	8.18E-08	9.29E-12	0.090865	1	1	1	6.21E-05	1	1	0.00974	1	1	6.99E-06	1	0.000541
1	82187543	82187554	LPHN2	3.02E-05	2.92E-11	1	1	1	1	7.21E-05	1	1	1	1	1	0.071429	0.022989	0.020408
1	92846489	92846501	RPAP2	1.42E-08	8.04E-09	0.058824	1	1	1	0.000164	1	1	0.00813	1	1	0.001458	0.03125	0.003379
21	42598164	42598175	BACE2	0.000319	1.04E-08	0.107143	1	1	1	0.000284	1	1	1	1	1	0.000763	1	1
6	110426583	110426595	WASF1	4.23E-09	5.39E-08	1	1	1	1	0.0005	1	1	0.003301	1	1	1.99E-08	1	0.000568
5	118451836	118451847	DMXL1	1.13E-05	9.16E-07	1	1	1	1	0.000503	1	1	0.057971	1	1	3.3E-06	1	0.000253
17	61958954	61958979	GH2	0.001426	0.000647	1	1	1	1	0.000679	1	1	1	1	0.130435	0.017042	0.019048	0.00487
15	40951461	40951477	CASC5	2.39E-11	1.15E-11	0.05618	1	1	1	0.000717	1	1	1	1	1	1.61E-12	1	0.027857
19	35758789	35758801	LSR	8.26E-09	2.09E-10	0.076923	1	1	1	0.001085	1	1	0.000839	0.013699	1	3.77E-07	1	0.002197
16	19481220	19481235	TMC5	1.91E-05	6.27E-05	1	0.050413	1	1	0.001257	1	1	1	0.107071	1	5.87E-05	1	1
17	39871551	39871566	GAST	1.1E-06	8.76E-09	1	1	0.47133	1	0.001571	1	0.000481	4.78E-07	1	1	0.047343	1	0.056604
14	76524970	76524982	IFT43	0.000182	2.96E-06	0.099879	1	1	0.279197	0.001633	1	0.214555	0.497493	1	1	0.000266	1	0.007395
4	101337123	101337134	EMCN	8.79E-06	4.14E-08	1	1	0.057143	1	0.001843	1	1	1	1	1	3.31E-06	1	0.075682
2	206911191	206911211	INO80D	0.011512	1.75E-08	1	1	1	0.316908	0.002253	1	1	0.188934	1	1	0.070869	0.148148	0.054799
1	234565078	234565090	TARBP1	2.23E-09	6.48E-12	0.127869	1	1	0.083951	0.002836	1	1	1	1	0.357143	2.72E-09	1	0.000672
17	74721967	74721983	JMJD6	5.32E-07	1.24E-12	0.274725	1	1	1	0.003984	1	1	0.01087	1	1	1.08E-05	1	0.112317
1	117911178	117911189	MAN1A2	0.00657	0.021817	1	1	1	1	0.004831	1	1	1	1	1	0.034965	1	1
1	115262366	115262389	CSDE1	2.38E-05	4.95E-11	1	1	0.105651	1	0.005076	1	1	1	1	1	9.94E-06	1	0.187979
X	135630678	135630689	VGLL1	1.76E-06	2.4E-10	0.04878	1	1	1	0.005553	1	1	1	1	1	0.000144	1	0.054422
1	54692854	54692865	SSBP3	0.169565	4.84E-10	1	1	1	0.078146	0.006173	1	1	1	1	0.007353	0.000391	0.052632	1
19	55438923	55438944	NLRP7	0.487734	0.354618	1	1	0.450836	1	0.006369	1	1	1	1	0.038462	0.186047	1	1
3	188242333	188242358	LPP	0.032427	0.022063	1	1	1	1	0.00641	1	0.043478	0.008767	1	1	1	1	1
2	238419543	238419568	MLPH	0.014549	1.42E-12	1	1	1	1	0.00653	1	1	1	1	0.157895	0.005263	1	1
2	54125185	54125196	PSME4	1.55E-07	2.5E-13	1	1	1	1	0.006623	1	0.018182	1	1	1	1.06E-06	1	1
5	131924346	131924374	RAD50	0.000404	8.05E-13	1	1	1	1	0.006897	1	1	1	0.02381	1	1.59E-10	1	0.012783
1	109617803	109617815	TAF13	5.49E-06	1.58E-08	0.166667	1	1	1	0.007042	1	1	1	1	1	0.003291	1	0.014922
5	75858199	75858210	IQGAP2	0.00176	1.04E-07	1	1	1	1	0.007353	1	0.018868	1	1	1	0.003654	1	0.005491
1	179561673	179561709	TDRD5	0.004488	1.6E-05	0.071429	1	1	1	0.007634	1	1	1	1	1	0.04749	1	0.07874
2	111881263	111881275	BCL2L11	0.000203	1.24E-07	0.109015	1	1	1	0.007813	1	0.009804	0.031579	1	0.416667	9.45E-12	1	0.002976
10	93601945	93601955	TNKS2	6.81E-05	1.35E-07	1	1	0.061538	1	0.007874	1	1	1	1	1	2.8E-07	0.095188	1
2	43768233	43768244	THADA	1.62E-09	1.9E-08	0.046512	1	1	1	0.008621	1	1	1	1	1	1.04E-10	1	0.071429
17	37657460	37657471	CDK12	0.005448	0.240352	0.27602	1	1	1	0.008625	1	0.032967	1	1	0.447368	0.00035	0.149747	0.134216
19	34687462	34687485	LSM14A	0.192733	0.000176	0.055556	1	1	1	0.009259	1	1	1	1	1	0.000773	1	0.003506
2	238271786	238271797	COL6A3	0.009625	3.7E-06	0.501478	1	0.124635	0.146789	0.009674	1	0.166667	0.069146	0.170732	0.054545	0.007131	0.136364	0.039362
X	35944077	35944088	CXorf22	0.000263	2.66E-07	0.111111	1	1	1	0.010753	1	1	1	1	1	0.004973	0.010738	1
1	31766005	31766017	SNRNP40	3.42E-08	3.81E-12	1	1	0.119048	1	0.010929	1	1	1	1	1	6.47E-06	1	0.015729
8	38153186	38153199	WHSC1L1	2.52E-08	1.09E-09	1	1	1	1	0.010929	1	1	0.038961	0.045455	1	2.4E-06	1	0.027841
17	16056594	16056626	NCOR1	1.93E-08	7.68E-10	0.053571	1	1	1	0.01105	1	1	4.16E-05	1	1	5.05E-13	1	0.059444
6	28876873	28876904	TRIM27	4.13E-05	2.62E-08	1	1	1	1	0.01145	1	0.016949	1	1	1	1.6E-08	1	0.054374
17	41256074	41256122	BRCA1	0.000131	0.000132	0.077647	1	1	1	0.011469	1	1	1	1	0.054348	0.568708	1	0.007272
15	34434467	34434479	KATNBL1	4.07E-08	0.000628	0.431818	1	1	0.122807	0.011988	1	1	1	1	1	7.15E-05	1	1
6	5000724	5000762	RPP40	0.000267	1.25E-08	1	1	1	1	0.012048	1	1	1	1	1	9.13E-06	1	0.03401
15	43990706	43990741	CKMT1A	1.62E-05	0.030007	1	1	1	1	0.012195	1	1	1	1	1	0.002115	1	6.9E-05
18	3597089	3597100	DLGAP1-AS1	6.24E-05	1.54E-08	1	1	1	1	0.012245	1	1	1	1	1	1	1	1
2	238005446	238005457	COPS8	1.9E-05	1.3E-10	0.105263	1	1	1	0.01227	1	1	1	1	1	3.94E-08	1	0.000308
2	187466921	187466932	ITGAV	1.27E-07	3.23E-07	1	1	0.276292	1	0.0125	1	1	1	1	1	5.67E-13	1	0.017896
9	113449613	113449633	MUSK	0.004078	0.000637	1	1	0.162162	1	0.012579	1	1	1	1	1	0.002142	1	0.107438
21	37425988	37425999	SETD4	2.27E-06	9.45E-11	1	1	1	1	0.012739	1	1	1	1	1	0.000424	1	1
X	103164079	103164090	MIR1256	0.004264	1.11E-10	0.045455	1	1	1	0.012739	1	1	0.058333	1	1	0.001186	1	0.15162
1	16245610	16245621	SPEN	3.94E-05	1.9E-09	1	1	1	1	0.013158	1	0.115602	1	1	1	0.000117	1	1
7	73254451	73254472	WBSCR27	0.001179	1.14E-05	1	1	1	1	0.013333	1	1	1	1	0.25	1	0.04	1
5	108673063	108673074	PJA2	8.02E-05	2.66E-09	1	1	1	1	0.013423	1	1	1	1	1	0.000247	1	0.051852
X	65486260	65486271	HEPH	5.57E-07	7.29E-05	1	1	1	1	0.013605	1	1	1	1	1	1.02E-09	0.04918	0.218268
5	79369202	79369225	CTD-2201I18.1	1.06E-05	0.012996	1	1	1	1	0.014085	1	1	1	1	1	0.072737	1	0.122604
16	66855468	66855480	NAE1	4.69E-07	1.03E-12	1	1	1	1	0.014184	1	0.045796	0.024194	1	1	0.01229	1	0.184239

6	39047035	39047052	GLP1R	0.127097	0.452319	0.098718	1	1	1	0.014925	1	1	0.114846	1	1	0.212121	1	0.246155
X	108924091	108924121	ACSL4	0.001219	5.57E-06	1	1	0.178473	1	0.014925	1	1	1	1	1	0.002153	1	0.177063
17	29206408	29206439	ATAD5	2.27E-10	4.43E-10	0.059524	1	0.127032	1	0.015209	1	1	1	1	0.133333	2.23E-10	1	0.254039
14	35255287	35255316	BAZ1A	0.023469	0.027158	0.053571	1	1	1	0.015267	1	1	1	1	1	0.005344	1	1
1	36297998	36298033	AGO4	1.3E-09	4.23E-06	0.09434	1	1	1	0.015385	1	1	1	1	1	7.16E-11	1	0.003323
6	34831755	34831773	UHRF1BP1	1.28E-07	3.05E-11	1	1	1	1	0.015464	1	1	0.042735	1	1	8.07E-10	1	0.004993
3	196236651	196236664	SMCO1	6.19E-08	1.22E-10	1	1	1	1	0.015504	1	1	0.038645	1	1	2.03E-06	1	0.008191
12	48880078	48880089	C12orf54	5.49E-06	3.79E-06	1	1	1	1	0.015625	1	1	1	0.043478	0.166667	9.45E-10	0.038462	0.055375
1	200544650	200544673	KIF14	0.005644	0.000815	1	1	1	1	0.015655	1	0.041022	0.199362	1	0.318182	0.00035	0.153573	0.095672
3	150906314	150906344	MED12L	0.012192	6.36E-09	1	1	1	1	0.015873	1	1	1	1	0.26087	8.32E-05	1	0.140967
8	53455013	53455024	FAM150A	0.010311	0.001617	1	1	1	1	0.015957	1	1	1	1	1	0.001384	1	0.003893
2	24521686	24521697	ITSN2	3.42E-07	5.97E-07	1	1	1	0.058955	0.01626	1	1	1	0.015625	1	3.01E-05	1	0.104728
12	101779979	101780006	UTP20	0.002119	5.02E-05	0.054054	1	0.194662	1	0.016461	1	1	1	1	1	1.4E-07	1	0.044335
3	32933344	32933365	TRIM71	0.073855	0.377278	1	1	1	1	0.016517	1	1	0.322902	1	0.22619	0.203683	1	0.000432
10	16911550	16911567	CUBN	0.035182	1.07E-06	1	1	1	1	0.016575	1	1	1	1	1	0.252991	1	5.61E-06
9	79852893	79852911	VPS13A	0.000146	1.01E-05	1	1	1	1	0.016667	1	0.020408	0.12	1	1	0.000733	1	0.097902
11	73765552	73765578	C2CD3	0.056693	0.457971	1	1	1	1	0.016667	1	1	1	1	1	3.74E-07	1	1
17	34937714	34937725	GGNBP2	0.008608	0.000141	1	1	1	1	0.016949	1	1	1	1	1	8.39E-06	0.04918	1
20	30354257	30354300	TPX2	1.95E-06	0.025701	0.086957	1	1	1	0.017094	1	1	1	1	1	0.152285	1	0.037462
2	8917110	8917121	KIDINS220	1.55E-05	2.15E-05	1	1	1	1	0.017241	1	1	1	0.035714	1	0.000231	1	0.003126
1	176012466	176012478	RFWD2	1.17E-11	4.03E-13	0.071429	1	1	1	0.017241	0.004292	1	0.019608	1	1	0.000427	0.000605	0.009764
7	157046584	157046595	UBE3C	2.28E-05	0.000899	1	1	1	1	0.017391	1	1	1	0.035088	1	9.29E-09	0.039474	0.048773
2	233392012	233392045	CHRND	0.002423	3.54E-05	1	1	1	1	0.017621	1	0.016129	1	1	1	0.044161	1	0.053254
12	101598350	101598362	SLC5A8	3.95E-08	3.3E-13	1	1	1	1	0.017964	1	1	0.007843	0.014925	1	8.05E-08	1	0.000379
4	89772341	89772364	FAM13A	0.004932	5.47E-06	1	1	1	1	0.018018	1	1	0.003086	1	1	0.005479	1	0.083969
6	26501598	26501613	BTN1A1	0.036765	6.35E-06	1	1	1	1	0.018519	1	1	1	1	1	6.52E-08	0.000496	0.096154
6	130425540	130425551	L3MBTL3	1.18E-06	5.76E-13	1	1	1	1	0.018519	1	1	1	0.045455	1	9.82E-07	0.044118	0.198224
22	35661543	35661561	HMGXB4	0.358974	0.00885	1	1	1	1	0.018605	1	1	1	1	1	0.185185	1	0.059761
X	70608756	70608784	BCYRN1	4.44E-07	6.33E-09	1	1	1	1	0.018605	1	1	1	1	1	1.26E-07	1	1
1	183481943	183481964	SMG7	3.25E-09	1.35E-07	0.075	1	1	1	0.01875	1	0.012048	1	0.024096	1	1.26E-27	1	0.000825
X	15443970	15443993	PIR-FIGF	4.8E-05	0.085348	0.080782	1	1	1	0.018868	1	1	0.034483	1	1	0.005188	1	0.068878
3	119199099	119199113	POGLUT1	9.98E-12	1.96E-08	1	1	1	1	0.019048	1	0.038213	1	1	1	0.002046	1	0.150733
7	74129126	74129143	LOC101926943	0.000154	0.005818	1	1	1	1	0.019048	1	1	0.138961	1	1	0.071292	1	1
14	56107823	56107834	KTN1	0.020443	0.061869	1	1	1	1	0.019231	1	1	1	1	1	0.031818	1	1
1	161293492	161293504	SDHC	0.000117	4.37E-08	1	1	1	1	0.020134	1	1	1	1	1	1.62E-05	1	0.060914
7	26251417	26251429	CBX3	3.85E-11	2.18E-10	1	1	1	1	0.020134	1	1	1	1	1	8.05E-15	1	0.06383
5	14607339	14607351	FAM105A	5.33E-12	1.77E-08	0.067797	1	1	1	0.021097	1	1	1	0.014286	1	0.000139	1	0.05679
21	34882121	34882132	GART	2.91E-05	8.14E-11	1	1	1	1	0.021127	1	1	1	1	1	0.000261	1	0.215384
12	116418759	116418783	MED13L	0.001332	0.001811	1	1	1	1	0.021739	1	1	1	1	1	0.004919	1	1
5	41840434	41840445	OXCT1	0.000207	2.09E-07	1	1	0.107448	1	0.022599	1	1	0.010101	1	1	1.5E-06	1	0.064246
5	647896	647907	CEP72	0.008552	3.28E-10	0.055556	1	1	1	0.022727	1	1	1	1	1	9.47E-10	1	0.042735
9	103035114	103035125	INVS	0.015468	1.18E-07	1	1	1	1	0.022727	1	1	1	0.020408	1	0.019653	0.047619	1
4	119644815	119644826	SEC24D	1.83E-05	3.36E-07	0.179402	1	1	1	0.022727	1	1	1	1	1	0.000114	0.113384	0.393738
8	23292044	23292067	ENTPD4	0.007071	0.000157	1	1	1	1	0.022901	1	1	1	1	0.388889	0.042505	1	0.020939
15	56720549	56720560	TEX9	3.57E-06	1.99E-07	0.083333	1	0.058824	1	0.023077	1	1	1	1	1	1.08E-06	1	0.001809
17	74625858	74625883	ST6GALNAC1	1	0.140187	0.060606	1	1	1	0.023077	0.010417	1	1	1	1	0.000277	1	1
6	51497344	51497355	PKHD1	6.69E-06	3.41E-06	1	1	0.105263	1	0.023256	1	1	1	1	1	1.99E-05	1	0.133178
1	210414859	210414894	SERTAD4	0.000549	2.43E-06	0.128422	1	1	1	0.023999	1	0.014388	0.205044	1	0.291667	1.12E-07	1	1
2	27592090	27592102	EIF2B4	3.1E-10	9.09E-12	1	1	0.079365	0.069424	0.024038	1	1	0.096774	1	1	1.16E-10	1	1
5	167944013	167944039	RARS	1.57E-05	1.52E-05	0.113384	1	1	1	0.02439	1	1	1	1	1	0.009489	1	0.064426
12	124172760	124172779	TCTN2	5.31E-05	7.26E-07	1	1	1	1	0.024752	1	1	1	1	1	3.13E-05	1	1
18	44682613	44682624	IER3IP1	0.043697	0.002228	1	1	1	1	0.024845	1	1	1	1	1	0.010835	1	0.090909
22	35659262	35659272	HMGXB4	2.14E-08	7.01E-06	0.065217	1	1	1	0.025	1	1	1	0.037037	1	3.21E-12	1	0.046875
22	25151880	25151901	PIWIL3	0.175863	0.000369	0.058824	1	0.290559	0.051606	0.025424	1	1	0.086207	1	0.285714	0.078673	0.281263	0.003825
8	90796369	90796393	RIPK2	0.000107	2.09E-05	1	1	1	1	0.026316	1	1	1	0.025974	1	6.18E-12	1	1
17	78263391	78263408	RNF213	0.000509	1.1E-06	1	1	1	1	0.027778	1	1	1	1	0.206897	3.08E-06	1	0.208208
6	122737314	122737337	HSF2	6.55E-06	0.004233	1	1	0.12049	1	0.028169	1	1	1	1	1	0.039969	1	0.033814
10	25883344	25883370	GPR158	1.54E-09	3.28E-09	0.054054	1	1	1	0.028249	1	1	1	1	1	0.000136	1	0.015906
15	64972760	64972789	ZNF609	7.92E-07	1.95E-11	0.263306	1	1	1	0.02941	1	1	1	1	1	0.004552	1	0.089465
2	70131320	70131332	SNRNP27	2.92E-09	7.04E-12	0.229809	1	1	1	0.029851	1	0.051282	1	1	1	4.24E-16	1	0.017215
19	23545530	23545549	ZNF91	2.1E-09	2.07E-08	1	1	1	1	0.029961	1	1	0.008621	1	1	1.8E-07	1	0.201667
8	95182984	95182995	CDH17	0.003869	1.48E-09	1	1	1	1	0.031248	1	1	1	1	1	7.76E-07	0.029851	1
14	57113890	57113916	TMEM260	0.00305	3.23E-12	0.121212	1	1	1	0.03125	1	1	0.016129	1	1	2.28E-05	1	1
2	170127380	170127401	LRP2	1.12E-05	0.001394	0.074074	1	1	1	0.031577	1	0.030928	1	1	0.444444	8.17E-08	1	1
1	215345245	215345313	KCNK2	0.002313	0.275528	1	1	1	1	0.032258	1	1	1	1	0.058824	0.000817	1	0.000499
7	55004033	55004044	LOC100996654(dist=131377),EGFR(dist=82681)	2.21E-06	8.1E-05	1	1	1	1	0.033058	1	1	1	1	1	5.01E-05	1	0.084034
8	6756875	6756886	DEFB1(dist=21346),DEFA6(dist=25330)	0.017138	1.59E-10	0.166667	1	0.166355	1	0.033968	1	1	0.070588	0.029851	1	0.054545	1	0.05
1	167382399	167382426	POU2F1	0.153527	0.117454	1	1	0.366271	0.288054	0.034089	1	1	0.048487	1	1	0.001828	1	0.031495
9	5988325	5988333	KIAA2026	0.002118	3.19E-08	1	1	1	1	0.034483	1	1	1	1	1	0.046252	1	1
5	137451361	137451372	NME5	4.2E-05	2.45E-08	1	1	1	1	0.036232	1	1	1	0.001502	1	2.53E-06	1	1
3	122447512	122447523	PARP14	6.57E-05	1.61E-09	1	1	1	1	0.037037	1	0.027397	0.063291	1	1	0.005897	1	1
2	175318387	175318411	GPR155	2.77E-08	2.08E-07	0.089852	1	1	1	0.038183	1	1	1	0.105263	1	0.000613	1	1
11	18111872	18111889	SAAL1	1.49E-08	5.59E-11	0.069444	1	1	1	0.038462	1	1	1	1	1	7.01E-21	0.026316	0.049005
12	77421978	77421991	E2F7	1.61E-09	1.08E-12	0.145299	1	0.10084	1	0.039735	1	0.014286	1	1	0.090909	8.67E-06	1	0.00027
1	118623681	118623714	SPAG17	1.64E-08	5.48E-08	0.237011	1	0.117091	0.084129	0.040338	1	0.007407	1	1	0.018351	9.27E-07	1	0.154068
15	72455833	72455844	GRAMD2	2.76E-06	3.02E-07	0.068182	1	1	1	0.041447	1	1	1	1	1	0.030422	1	1
12	56096600	56096619	ITGA7	0.556627	0.132215	1	1	1	1	0.043356	1	1	1	1	0.55	0.000987	1	0.060086
5	170395218	170395229	RANBP17	2.09E-06	1.76E-10	1	1	1	1	0.043831	1	1	0.056338	1	1	0.000462	1	0.110464
3	77542380	77542391	ROBO2	3.83E-07	2.53E-10	1	1	0.380422	1	0.045455	1	1	1	1	1	5.34E-05	0.030769	0.011702
6	44115860	44115874	TMEM63B	1.76E-07	1.37E-11	1	1	1	1	0.046371	1	0.081186	1	1	1	7.96E-05	1	0.021277
7	98548682	98548726	TRRAP	0.000733	0.572591	0.056818	1	0.073009	1	0.046504	1	1	1	1	1	0.006182	1	0.013744
19	39412756	39412767	SARS2	9.15E-07	0.000668	0.079184	1	1	1	0.047113	1	1	0.173482	1	0.057143	1.67E-11	0.00058	0.06934
6	73102522	73102533	RIMS1	1.18E-05	8.13E-05	1	1	1	1	0.047238	1	0.078125	1	1	0.1875	6.29E-06	1	0.36038
4	110884220	110884238	EGF	4.4E-12	6.19E-11	0.146154	1	1	1	0.047331	1	1	0.200965	1	1	1.52E-09	1	0.101712
9	136629256	136629277	VAV2	0.027332	0.032434	0.105263	1	1	1	0.047619	1	1	1	1	0.25	0.128653	1	0.271009
5	127122029	127122040	CTXN3(dist=127707),LINC01184(dist=235204)	4.94E-06	1.91E-10	0.057143	1	1	1	1	1	1	1	1	1	0.000131	1	0.068
4	96035796	96035838	BMPR1B	0.021177	0.036074	0.255865	1	1	1	1	1	1	1	1	0.041353	6.6E-05	1	0.297864
19	1364472	1364496	MUM1	0.000126	0.00304	1	1	1	1	1	1	1	1	0.016667	1	0.073101	1	0.054217
19	10288056	10288083	DNMT1	1.58E-05	4.77E-07	1	1	1	1	1	1	1	1	1	1	5.8E-07	0.040541	0.000274
X	122757873	122757909	THOC2	1.98E-06	1.38E-11	1	1	1	1	1	1	1	1	1	1	3.27E-07	1	0.044548
14	35072491	35072521	SNX6	0.000463	0.01254	1	1	1	1	1	1	1	1	1	1	1.13E-05	1	1
9	130915309	130915346	LCN2	1	0.420886	1	1	1	1	1	1	1	1	1	1	0.178947	1	1
7	72040736	72040777	TYW1B	0.000214	0.000273	1	1	1	1	1	1	1	1	1	1	3.72E-07	1	0.164408
11	43419440	43419514	TTC17	0.00113	1	0.063291	1	1	1	1	1	1	1	1	1	0.028918	1	0.145654
1	112031654	112031690	TMIGD3	1	0.185897	0.066667	1	1	1	1	1	1	1	1	1	0.075081	1	0.258965
20	29449657	29449688	NONE(dist=NONE),FRG1B(dist=162191)	3.49E-07	2.49E-08	0.124863	1	1	1	1	1	1	1	1	0.025974	2.72E-14	1	1
17	29192700	29192715	ATAD5	1.76E-10	7.28E-11	0.099942	1	1	1	1	1	0.021978	1	1	1	2.85E-14	1	0.000162
10	129905111	129905126	MKI67	0.032508	0.106454	1	1	1	1	1	1	1	1	1	1	0.045389	1	0.049367
12	56811583	56811604	TIMELESS	0.072774	0.158476	1	1	1	1	1	1	1	1	1	1	0.006947	1	1
10	36811687	36811723	LINC01452(dist=721839),ANKRD30A(dist=603062)	0.644369	0.341216	1	1	0.159691	1	1	1	1	0.067212	1	1	0.418824	1	1
1	29642688	29642716	PTPRU	0.010294	1	1	1	1	1	1	1	1	1	1	1	0.168	1	0.098522
10	115904180	115904217	CCDC186	0.001058	2.17E-07	1	1	0.052632	1	1	1	0.039216	1	1	0.015152	0.005599	1	0.00974
2	111526069	111526123	ACOXL	0.033464	0.017384	0.046875	1	1	1	1	1	1	1	1	1	0.000624	1	0.169816
21	30400154	30400165	USP16	1.33E-05	0.006738	1	1	0.065041	1	1	1	0.017544	1	1	1	1.85E-06	1	0.117712
X	49030763	49030811	PLP2	0.000744	1	1	1	1	1	1	1	0.016129	1	1	1	0.016343	1	1
22	20918792	20918838	MED15	0.448276	1	1	1	1	1	1	1	1	0.066667	1	1	1	1	1
22	20918896	20918940	MED15	0.014366	0.032464	1	1	1	1	1	1	1	1	1	1	0.02296	1	1
6	117735716	117735728	ROS1	3.05E-06	4.14E-05	1	1	0.103734	0.220566	1	1	1	1	1	1	4.26E-10	1	0.165217
20	25900322	25900353	LOC101926935(dist=65665),LOC101926955(dist=36095)	1.41E-05	0.000621	1	1	1	1	1	1	1	1	1	1	1.79E-06	1	0.170581
12	117768089	117768134	NOS1	0.005291	0.000925	0.217376	1	0.199352	1	1	1	1	1	1	0.00129	0.000154	1	0.103259
9	68427818	68427834	LOC642236	0.502262	1	0.047619	1	1	1	1	1	1	1	1	1	1	1	1
19	16640563	16640599	CHERP	0.363636	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	18474348	18474390	ADAMTSL1	0.192476	1	1	1	1	1	1	1	1	1	1	1	0.100302	1	1
15	76171367	76171423	UBE2Q2	6.52E-05	5.42E-06	1	1	1	1	1	1	1	1	1	1	3.2E-11	1	0.004196
3	100463642	100463670	TFG	0.000525	2.31E-07	1	1	1	1	1	1	1	1	1	1	8.94E-06	1	1
8	39607083	39607120	ADAM2	0.003187	0.23741	1	1	1	1	1	1	1	1	1	0.125	0.016216	1	1
16	87935958	87935971	CA5A	3.77E-10	3.34E-05	1	1	1	1	1	1	1	0.043712	1	0.011858	1.23E-11	1	0.04144
16	72107664	72107726	HPR	0.012077	0.25	1	1	0.061856	1	1	1	0.013158	1	1	1	0.0311	1	0.120346
19	52132524	52132559	SIGLEC5	1.53E-07	0.462495	0.050806	1	1	1	1	1	1	1	1	0.005263	1.85E-07	0.106607	0.015344
14	88651822	88651847	KCNK10	2.08E-05	0.247526	0.262458	1	0.282056	1	1	1	1	1	1	0.008772	0.000145	1	0.637267
16	72831357	72831388	ZFHX3	0.004331	7.75E-05	1	1	1	1	1	1	1	1	1	1	3.43E-07	1	1
7	117188653	117188690	CFTR	0.001925	1	1	1	1	1	1	1	1	1	1	0.066667	8.1E-10	1	0.437034
4	143326312	143326333	INPP4B	0.054578	0.07047	0.171123	1	1	0.480512	1	1	1	1	1	0.00202	0.650822	1	0.054963
7	138950972	138951000	UBN2	0.333333	1	1	1	1	1	1	1	1	1	1	1	5.79E-07	1	1
10	61574357	61574382	CCDC6	0.000957	0.301907	0.213675	1	1	1	1	1	1	1	1	0.142857	3.06E-05	1	0.007019
3	137988855	137988866	ARMC8,NME9	4.85E-07	1.05E-11	1	1	1	1	1	1	0.061211	1	1	1	1.95E-14	0.093702	0.215393
3	65425560	65425591	MAGI1	0.344777	0.029647	1	1	1	1	1	1	0.252906	1	1	0.083333	0.007393	0.103383	0.009785
1	180803992	180804003	XPR1	0.131222	3.78E-05	0.057692	1	1	0.069748	1	1	1	1	1	0.173913	1	1	0.18006
6	138644748	138644783	KIAA1244	1.23E-06	1.41E-07	1	1	1	1	1	1	1	0.029126	1	0.15	5.55E-10	1	1
15	84442240	84442266	ADAMTSL3	3.34E-06	5.97E-06	0.06383	1	1	1	1	1	1	1	0.0625	0.166667	0.00197	0.05	0.000952
7	97599691	97599708	MGC72080	4.29E-09	3.23E-05	1	1	1	1	1	1	0.07474	1	1	0.070949	9.73E-09	1	0.303271
15	43903198	43903237	STRC	6.77E-06	0.010765	1	1	1	1	1	1	1	1	1	0.25	0.005454	1	0.291188
5	68695826	68695863	RAD17	0.000132	0.001681	1	1	1	1	1	1	1	1	1	1	0.000392	0.022989	1
10	32106657	32106676	ARHGAP12	2.66E-07	4.52E-07	0.04878	1	1	1	1	1	1	0.102059	1	1	0.00588	0.028169	0.005706
3	47361074	47361096	KLHL18	0.000112	1.58E-08	0.103841	1	1	1	1	1	1	1	1	1	0.001021	1	1
1	212530651	212530683	PPP2R5A	5.28E-11	3.76E-05	0.059701	1	1	1	1	1	1	1	1	1	1.17E-07	1	0.058824
15	44002670	44002699	CKMT1A(dist=11250),CATSPER2P1(dist=25447)	2E-08	1.88E-07	0.045455	1	0.104167	1	1	1	0.014085	1	1	0.111111	7.64E-09	1	1
12	550911	550929	CCDC77	6.98E-07	2.97E-09	1	1	0.227516	1	1	1	0.131212	0.283557	1	1	0.000103	0.029851	0.005603
17	44324686	44324697	LOC644172(dist=1532),LRRC37A(dist=47800)	0.001625	3.39E-07	1	1	1	1	1	1	1	1	1	1	7.37E-11	1	0.105534
16	50368677	50368692	BRD7	0.343574	0.013864	1	1	1	1	1	0.017241	1	4.18E-05	1	1	0.007989	1	0.063158
11	3742062	3742092	NUP98	4.28E-05	3.24E-06	0.070423	1	1	0.051282	0.076923	1	1	1	1	1	6.82E-15	1	1

7	27147451	27147501	HOXA3	0.030779	6.28E-09	0.090909	1	1	1	1	1	1	1	1	1	1.16E-07	0.037383	0.026087
10	81053094	81053105	ZMIZ1	0.05745	0.000124	1	1	1	1	0.053182	1	1	1	1	1	0.008645	1	1
12	105464316	105464342	ALDH1L2	0.000134	4.3E-05	1	1	0.058824	1	1	1	1	0.00051	1	1	0.000132	1	0.004709
11	108119615	108119666	ATM	0.019525	1	1	1	1	1	1	1	1	1	1	1	1	1	0.030537
3	135806702	135806713	PPP2R3A	0.000227	1.8E-12	0.046512	1	1	1	1	1	1	0.072727	0.000887	1	3.51E-10	1	0.046154
9	5753518	5753530	RIC1	4E-05	3.28E-11	0.04878	1	1	1	1	1	1	0.01	1	1	1.84E-12	0.033898	0.087719
4	65180308	65180357	TECRL	0.004395	1	1	1	0.264991	1	1	1	1	1	1	0.000877	0.000284	1	0.028468
16	258007	258018	LUC7L	2.59E-06	2.09E-07	0.229809	1	1	1	1	1	1	0.025974	1	1	0.005067	1	0.086294
19	45823034	45823067	CKM	2.19E-06	1.36E-05	1	1	1	1	1	1	1	0.047619	1	1	0.000841	1	0.067606
3	100432722	100432769	TFG	0.011723	1	1	1	0.065421	1	1	1	1	1	1	1	0.222222	1	1
17	48266152	48266177	COL1A1	0.02042	0.007764	1	1	1	1	1	1	1	0.009307	1	1	0.02911	1	0.02003
7	158935023	158935043	VIPR2	6.06E-05	1.01E-08	1	1	1	1	1	1	1	1	1	0.105263	2.98E-11	1	0.070026
11	128354631	128354658	ETS1	0.000291	0.038168	1	1	1	1	1	1	0.010638	0.037037	1	1	0.593144	1	1
2	165971883	165971895	SCN3A	1.51E-08	2.48E-08	1	1	1	1	1	1	1	1	0.016949	1	1.01E-10	1	0.001159
10	18828669	18828689	CACNB2	0.000127	1.38E-11	1	1	1	1	1	1	1	1	0.052281	1	2.52E-08	1	1
10	70520707	70520747	CCAR1	8.24E-07	8.25E-10	1	1	1	1	1	1	1	1	1	1	5.78E-09	0.010753	0.003139
11	3789982	3790022	NUP98	0.000491	0.001803	1	1	1	1	1	1	1	1	0.068966	1	0.031991	0.021201	0.359865
16	21396850	21396873	SNX29P1	5.24E-07	3.38E-07	0.106383	1	1	1	1	1	1	1	1	1	2.1E-21	1	1
19	52469526	52469555	ZNF350-AS1	7.85E-05	0.000157	0.218733	1	1	1	1	1	0.025	1	1	1	1.95E-05	1	0.040198
4	151835239	151835258	LRBA	4.47E-12	7.33E-11	0.054054	1	1	1	1	1	0.043791	0.045113	1	1	7.32E-09	1	0.100405
3	197562495	197562534	LRCH3	0.150456	0.004767	1	1	1	1	1	1	1	1	1	1	0.198198	1	1
4	142153856	142153880	ZNF330	9.61E-08	7.45E-08	0.124884	1	1	1	1	1	1	1	1	1	7.78E-20	1	0.12163
10	70696596	70696633	DDX50	1.24E-08	0.003657	1	1	1	1	1	1	1	1	1	1	8.38E-06	1	0.011865
3	40503070	40503094	RPL14	1.1E-07	5.35E-06	1	1	1	1	1	1	1	1	1	1	3.68E-07	1	0.130261
8	113323406	113323417	CSMD3	5.4E-08	1.79E-11	0.139373	1	0.090909	1	1	1	1	1	1	1	0.000687	1	0.039454
1	101440343	101440354	SLC30A7	0.000148	7.12E-06	1	1	1	1	1	1	1	1	0.017544	1	9.11E-08	1	0.096386
19	6176498	6176523	ACSBG2	0.34241	0.379035	1	1	1	1	1	1	1	1	1	1	0.065223	1	1
7	129680648	129680677	ZC3HC1	6.5E-10	7.15E-07	0.045455	1	1	1	1	1	0.050413	0.021739	0.001207	1	0.012217	0.070568	0.322309
2	162279850	162279867	TBR1	1	3.26E-05	1	1	1	0.081933	1	1	1	1	1	1	0.069354	1	1
2	73829294	73829305	ALMS1	0.003348	2.64E-05	1	1	1	1	1	1	1	1	1	1	0.013294	1	1
7	121012196	121012208	FAM3C	4.06E-05	2.25E-07	0.055556	1	1	1	1	1	1	1	1	1	2.24E-12	1	1
6	151779420	151779459	C6orf211	0.347518	0.026759	1	1	1	1	1	1	1	1	1	0.25	0.069355	1	1
17	60865741	60865808	MIR548W	0.075369	1	1	1	1	1	1	1	1	1	1	1	0.178571	1	1
9	35107316	35107350	FAM214B	1	1	1	1	1	1	1	1	1	1	1	1	0.000967	1	1
2	61456592	61456645	USP34	0.000219	0.038026	1	1	1	1	1	1	1	1	1	1	0.547485	1	0.00014
16	71772784	71772795	AP1G1	7.4E-07	3.16E-12	1	1	1	0.059837	1	1	1	1	1	1	2.69E-06	1	1
17	26911647	26911664	SPAG5	7.45E-05	0.000642	0.055556	1	1	1	1	1	1	1	1	1	6.22E-08	1	0.019591
3	58120318	58120335	FLNB	0.070204	0.003261	0.052632	1	1	1	1	1	1	1	0.027027	1	0.000145	0.028169	1
12	22065994	22066028	ABCC9	0.000407	0.000161	1	1	1	1	1	1	0.008772	1	1	1	0.176471	1	0.01795
2	165556062	165556091	COBLL1	0.030011	0.203593	1	1	1	1	1	1	1	1	1	1	0.008923	0.039216	1
6	7575506	7575518	DSP	7.85E-08	4.03E-13	0.120192	1	0.067797	1	1	1	0.015038	1	1	1	6.86E-10	1	0.076023
7	103557648	103557659	RELN	5.84E-05	1.04E-05	1	1	1	1	1	1	1	0.153627	1	1	5.84E-06	1	0.095238
1	232564096	232564118	SIPA1L2	5.12E-07	0.005921	0.058824	1	0.074074	1	1	1	1	1	1	1	8.77E-18	1	0.045404
1	35879555	35879566	ZMYM4	0.00077	0.001269	1	1	1	1	1	1	1	1	1	1	2.58E-06	1	0.236113
17	9503559	9503577	CFAP52	1.01E-05	1.72E-11	1	1	1	1	1	1	1	0.079545	1	1	2.2E-05	1	1
4	178274919	178274938	NEIL3	1.93E-10	1.71E-05	0.061728	1	1	1	1	1	0.013699	1	1	1	6.84E-20	1	0.000975
10	28899815	28899861	WAC	9.03E-06	1.77E-07	0.1	1	0.071429	1	1	1	1	1	1	1	0.248599	0.084472	0.075622
1	21175875	21175896	EIF4G3	4.02E-06	3.81E-08	0.1	1	1	1	1	1	1	1	1	1	3.07E-16	1	0.012288
9	103275649	103275693	MSANTD3-TMEFF1,TMEFF1	0.000217	0.050388	0.056338	1	1	1	1	1	1	1	1	1	0.000112	1	1
5	149583372	149583428	SLC6A7	0.001123	1	1	1	1	1	1	1	1	1	0.076923	0.263158	0.009162	1	1
10	28908452	28908478	WAC	6.97E-05	4.1E-09	1	1	1	1	1	1	1	1	0.029412	1	4.3E-11	0.000974	0.100073
9	77742467	77742478	OSTF1	0.006391	6.27E-06	1	1	1	1	1	1	1	1	1	1	0.003401	1	0.138122
13	76134860	76134871	UCHL3	0.000402	6.79E-05	0.051282	1	1	1	1	1	1	0.001488	1	1	0.000833	0.000452	0.115561
4	56277766	56277777	TMEM165	2.41E-05	1.01E-06	1	1	1	1	1	0.005376	1	0.042105	1	1	0.000288	1	0.069182
2	228401293	228401315	AGFG1	0.001625	1.86E-05	1	1	1	1	1	1	1	1	1	1	5.35E-06	1	1
17	17722581	17722596	SREBF1	0.001811	0.002085	1	1	0.069444	1	0.09472	1	1	1	1	1	0.000772	1	1
8	55050032	55050043	MRPL15	4.21E-08	1.1E-08	1	1	1	1	1	1	1	1	1	1	3.7E-18	1	0.054852
9	5073681	5073692	JAK2	2.1E-06	7.2E-13	1	1	1	1	1	1	1	0.069549	1	1	2.03E-05	1	0.012783
5	36995692	36995703	NIPBL	0.02125	3.62E-05	1	1	1	1	1	1	1	1	1	1	0.020792	0.022727	1
7	73467650	73467689	ELN	0.000567	1	1	0.088355	1	1	1	1	1	1	1	1	0.038994	1	0.080563
5	64933457	64933482	TRAPPC13	9.36E-06	0.60344	0.144731	1	1	1	1	1	1	1	1	1	6.96E-09	1	0.119059
6	128297950	128297976	PTPRK	2.38E-11	3.83E-10	1	1	1	0.137397	1	1	1	0.089127	0.032787	1	2.76E-07	0.071408	0.155945
2	202626550	202626577	ALS2	0.011153	0.000141	1	1	1	1	1	1	0.022472	1	1	1	0.007746	1	0.133733
6	170115957	170115968	PHF10	2.97E-05	6.51E-09	1	1	1	1	1	1	1	1	1	1	2.54E-10	1	0.141116
X	122805622	122805633	THOC2	1.38E-05	2.95E-10	1	1	0.227273	1	1	1	1	0.104167	1	1	2.92E-13	0.046875	0.018634
12	116549320	116549361	MED13L	1.8E-05	1.01E-06	1	1	1	1	1	1	1	1	1	1	0.003767	1	0.011294
6	11192516	11192554	NEDD9	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.000356
1	10479048	10479084	PGD	9.36E-11	2.08E-08	0.070423	1	0.071919	1	1	1	1	1	1	1	7.41E-05	1	0.004516
10	71174636	71174668	TACR2	1	0.000236	1	1	0.05102	1	1	1	1	1	1	1	0.228916	1	1
18	22017875	22017901	IMPACT	3.16E-08	3.3E-07	0.2	1	1	1	1	1	0.038462	1	0.052632	0.153846	7.22E-17	0.001695	0.039799
2	198966091	198966121	PLCL1	1.35E-07	0.000424	1	1	1	1	1	1	1	0.076169	1	1	0.001266	0.084181	0.01078
2	42543020	42543053	EML4	0.011738	0.000123	1	1	1	1	1	1	1	1	1	1	0.000201	0.065217	1
6	97058328	97058345	FHL5	1.23E-06	1.05E-09	0.070175	1	0.056604	1	1	1	1	1	1	1	0.001232	1	0.175793
14	74205925	74205972	ELMSAN1	0.375	0.161972	1	1	1	1	1	1	1	1	1	1	1	1	1
1	32631598	32631676	KPNA6	0.000371	0.003854	0.047619	1	1	1	1	1	1	1	1	1	1.66E-05	1	0.00059
17	59118267	59118278	BCAS3	0.005633	1.92E-08	1	1	1	1	1	1	1	1	1	1	0.00279	1	0.080808
17	39022824	39022842	KRT12	0.324215	9.64E-07	0.064516	1	1	1	1	1	1	1	1	1	0.00055	1	1
15	56736722	56736733	MNS1	1.88E-06	1.16E-12	1	1	1	1	1	1	1	0.113384	0.016667	1	1.47E-10	1	0.001252
8	74890927	74890949	TMEM70	3.15E-06	0.093396	1	1	0.161348	1	1	1	0.020202	0.000565	1	0.2	0.051239	1	0.002368
11	87013273	87013284	TMEM135	2.08E-06	6.76E-06	1	1	1	1	0.067144	1	1	1	0.001442	1	5.1E-05	0.072054	1
8	125531026	125531037	TATDN1	0.000373	1.89E-05	1	1	0.080645	1	1	1	1	1	1	1	1.27E-08	1	0.078767
10	13333922	13333939	PHYH	0.000969	0.000324	0.129032	1	1	1	1	1	1	1	1	0.105263	0.00085	1	0.003231
7	127013339	127013370	ZNF800	1.1E-07	2.71E-08	0.058824	1	0.118644	0.099102	1	1	0.027397	1	1	1	1.85E-06	0.028169	0.067227
7	138713741	138713758	ZC3HAV1L	4.28E-05	6.01E-05	1	1	1	1	1	1	1	1	1	1	0.014277	1	1
6	33262443	33262458	RGL2	0.415094	0.395068	1	1	1	1	1	1	1	1	1	1	0.022474	1	0.058824
1	145581627	145581659	NBPF10,NBPF20,PIAS3	0.000328	0.009237	1	1	1	1	1	1	1	1	1	0.181818	2.27E-06	1	1
1	233489705	233489736	KIAA1804	0.458647	0.2	1	1	1	1	1	1	1	1	1	1	0.001856	1	1
15	64385711	64385743	FAM96A	0.005958	0.001016	1	1	1	1	1	1	1	1	1	1	3.48E-08	1	1
4	120189328	120189360	USP53	0.023365	0.036707	1	1	1	1	1	1	1	1	1	1	2.78E-14	1	1
1	54284760	54284771	NDC1	0.000226	0.00224	0.137931	1	1	1	1	1	1	0.051095	1	1	0.000455	1	1
20	55942168	55942179	MIR5095	1.3E-06	8.86E-11	1	1	0.132086	1	1	1	1	1	1	1	2.71E-10	1	0.030335
5	134670602	134670613	H2AFY	3.83E-05	1.55E-07	1	1	1	1	1	1	1	1	1	1	0.001281	1	0.071895
5	49698977	49699002	EMB	2.68E-05	0.43271	1	1	1	1	1	1	1	1	1	1	0.000205	1	0.006154
8	86386051	86386077	CA2	4.22E-05	1.14E-07	1	1	1	1	1	1	1	1	1	1	0.002567	1	1
11	117034388	117034407	PAFAH1B2	3.92E-07	2.75E-08	1	1	0.100914	0.399138	0.149717	1	0.025641	0.198182	1	0.208333	5.51E-06	1	0.314437
18	74968192	74968207	GALR1	0.031294	0.007336	1	1	1	1	1	1	1	1	1	1	1	1	1
5	37212582	37212612	C5orf42	4.93E-10	0.002046	0.109806	1	1	1	1	1	0.006579	1	1	1	2.33E-13	1	0.173489
4	68530860	68530915	UBA6	0.000575	0.000118	1	1	1	1	1	1	1	1	0.054054	0.3	1.27E-08	1	0.438133
15	89816530	89816565	FANCI	0.061985	0.00028	1	1	0.126963	1	1	1	1	1	1	1	0.02011	1	1
12	72028607	72028621	ZFC3H1	3.6E-10	7.84E-08	0.320313	1	1	1	1	1	1	1	1	0.176471	3.03E-12	0.073171	0.014885
1	118483352	118483396	WDR3	0.253659	1	1	1	1	1	1	1	1	1	1	0.083333	1	1	1
22	30367073	30367092	MTMR3	1E-06	1.6E-10	1	1	0.159981	1	1	1	1	1	1	1	5.45E-08	1	3.42E-05
2	62065615	62065626	FAM161A	0.000153	1.34E-09	1	1	1	1	1	1	1	1	1	1	8.58E-06	0.033898	0.021277
18	12680595	12680617	CEP76,PSMG2	0.026457	2.21E-07	0.195107	1	1	1	1	1	1	1	0.001317	1	6.03E-06	1	0.002244
X	69960653	69960673	TEX11	1.36E-09	0.00156	0.046154	1	1	1	1	1	1	1	1	1	4.41E-13	1	0.010583
18	2922252	2922270	LPIN2	0.001813	8.06E-09	1	1	1	1	1	1	1	1	1	1	0.003599	1	1
19	59068569	59068584	UBE2M	0.039066	0.229167	1	1	1	1	1	1	1	1	1	1	1	1	1
2	218712886	218712914	TNS1	1	0.126126	1	1	1	1	1	1	1	1	1	1	0.029536	1	1
6	144165798	144165823	LTV1	8.53E-07	5.64E-05	1	1	0.11812	1	1	1	1	1	1	0.133333	0.001056	1	0.004297
7	117876250	117876293	ANKRD7	0.00047	0.148148	0.099942	1	1	1	1	1	1	1	1	1	0.000339	1	0.382652
19	16613797	16613832	C19orf44	0.124093	0.008547	1	1	1	1	1	0.006173	1	1	1	0.25	0.24026	1	1
11	65647789	65647810	CTSW	4.51E-06	2.06E-05	1	0.077647	1	1	1	1	1	1	1	1	0.001787	1	0.000456
3	65372849	65372864	MAGI1	0.29408	0.002927	1	1	1	1	1	1	1	1	1	1	3.25E-05	1	0.162388
5	55466397	55466434	ANKRD55	3.34E-05	2.64E-06	0.213523	1	1	1	1	1	1	1	1	1	0.015597	1	1
1	222753050	222753061	TAF1A	6.99E-05	1.54E-06	1	1	1	1	1	1	1	1	1	1	0.000129	0.028571	0.076023
7	26764965	26765008	SKAP2	0.014495	1	1	1	1	1	1	1	1	1	1	1	0.002646	1	1
3	37369771	37369798	GOLGA4	0.004807	0.004447	1	1	0.055069	1	0.096706	1	1	1	1	1	0.025683	1	0.001773
14	75508258	75508303	MLH3	7.79E-05	6.56E-08	1	1	0.05	1	1	0.005263	1	1	1	1	0.001051	0.032967	1
4	77065476	77065492	NUP54	4.14E-10	2.57E-13	0.402904	1	0.595882	0.089835	0.342749	1	1	0.265928	1	0.009524	1.33E-13	0.215673	0.373593
9	113530024	113530036	MUSK	8.78E-08	6.04E-10	0.052768	1	1	1	1	1	1	0.003142	1	0.2	0.000141	1	0.331834
3	49463432	49463445	NICN1	0.452381	1	1	1	1	1	1	1	1	0.043956	1	1	1	1	0.028994
19	12991472	12991502	DNASE2	0.01865	0.051111	0.058824	1	1	1	1	1	0.077647	1	1	1	0.032145	1	1
5	68572902	68572925	CDK7	0.003675	1.93E-05	1	1	1	1	1	1	1	1	1	1	6.64E-05	0.02	0.028169
9	910292	910333	DMRT1	3.66E-05	0.007409	1	1	1	1	1	1	1	1	1	1	7.76E-12	1	1
1	204495586	204495610	MDM4	0.004789	1	1	1	1	1	1	1	1	1	1	0.210526	9.92E-06	1	0.063325
7	134252865	134252876	AKR1B15	4.55E-10	4.34E-13	1	1	1	1	1	1	1	0.05	0.035714	1	2.33E-11	1	0.057292
4	144442567	144442579	SMARCA5	3.76E-07	2.34E-12	1	1	1	1	1	1	0.032258	0.036371	1	1	7.17E-07	1	0.065657
19	20829214	20829239	ZNF626	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.089744
16	71682686	71682711	PHLPP2	0.075797	0.030093	0.051282	1	1	1	1	0.005102	1	1	1	1	0.006946	1	1
17	47696764	47696775	SPOP	0.000338	3.37E-11	0.058824	1	1	1	1	1	1	0.000658	1	1	0.008231	0.064516	0.052632
3	15756039	15756083	ANKRD28	0.000585	0.155925	0.054795	1	1	1	1	1	1	1	1	1	3.82E-18	1	0.038978
14	56104085	56104116	KTN1	1.78E-05	0.011727	0.123912	1	1	1	1	1	1	1	1	1	2.76E-05	1	1
11	48168271	48168302	PTPRJ	0.443548	0.050253	1	1	1	1	1	1	1	1	1	1	0.030566	1	1
13	99970244	99970267	MIR548AN	8.18E-06	1.6E-09	0.076923	1	1	1	1	1	1	1	1	1	5.71E-05	1	0.263138
3	196792356	196792367	DLG1	4.24E-09	3.26E-08	0.212698	1	1	1	1	0.006098	1	1	1	1	2.4E-10	1	1
4	38698666	38698677	KLF3	3.82E-07	5.22E-09	0.051724	1	0.195047	1	1	1	1	1	1	1	7.22E-06	1	1
12	8200557	8200579	FOXJ2	0.423729	1	1	1	1	1	1	1	1	1	1	1	1	1	0.061538
14	19571455	19571478	POTEG	8.12E-08	4.07E-08	0.076169	1	0.144001	1	1	1	1	0.040404	0.086957	1	9.38E-05	0.000611	0.085398
19	46299146	46299180	RSPH6A	1	1	1	1	1	1	1	1	1	8.58E-06	1	1	1	1	1
19	7119636	7119690	INSR	0.018684	0.000677	1	1	1	1	1	1	1	1	1	0.25	0.180687	1	0.000331
3	157820718	157820744	SHOX2	0.147145	1	1	1	1	1	1	1	1	1	1	1	1	1	1

5	56231347	56231384	MIER3	9.17E-05	1.06E-08	1	1	1	1	1	1	1	1	1	1	0.001803	1	0.058824
3	10076842	10076853	FANCD2	0.000346	2.17E-10	0.090909	1	0.535039	1	0.163288	1	1	1	1	0.006105	0.00058	0.070779	0.609632
4	81123013	81123030	PRDM8	1	1	1	1	0.240404	1	1	1	1	1	1	1	0.063215	0.038462	0.090275
3	64184677	64184697	PRICKLE2-AS3	1.61E-10	0.000261	0.069767	1	0.095562	1	1	1	1	1	1	1	3.65E-05	1	0.003434
5	96314793	96314804	LNPEP	2.64E-09	3.74E-13	1	1	1	1	1	1	1	1	0.036364	1	4.55E-05	1	0.008572
X	106109272	106109294	TBC1D8B	4.02E-07	5.71E-05	0.053571	1	1	1	1	1	1	1	1	1	3.43E-05	1	0.126681
7	134264233	134264254	AKR1B15	1.39E-08	0.00035	0.171047	1	0.238138	1	1	1	1	1	1	1	5.26E-06	0.079184	0.344046
15	41663884	41663900	NUSAP1	1.83E-10	6.27E-12	1	1	0.190932	1	1	1	1	1	0.012987	1	3.82E-20	0.002387	0.010325
19	15648108	15648133	CYP4F22	0.004423	0.028029	1	1	1	1	1	1	1	0.096154	1	1	0.000188	1	0.087719
11	93170895	93170938	CCDC67	0.006919	0.030896	0.109015	1	1	1	1	1	1	1	1	0.184211	9.4E-06	1	0.057681
6	117753497	117753511	ROS1(dist=6479),DCBLD1(dist=50309)	7.04E-07	2.61E-08	1	1	0.313852	0.071038	1	0.014218	1	0.047606	0.0625	1	6.15E-05	1	0.033923
2	233243528	233243550	ALPP	0.06397	1	1	1	1	1	1	1	1	1	1	1	0.330601	0.03125	1
19	6466368	6466409	CRB3	0.432432	0.210526	1	1	1	1	1	1	1	1	1	1	1	1	1
3	100009610	100009621	TBC1D23	0.00116	4.09E-10	1	1	1	1	1	1	1	0.063492	1	1	5.86E-07	1	1
12	55820958	55820971	OR6C76	2.96E-06	1.07E-09	0.263306	1	0.425032	1	0.063275	0.011236	1	1	1	1	0.00013	1	0.063081
8	104930646	104930658	RIMS2	5.1E-06	3.85E-11	0.066102	1	1	0.110193	0.117517	1	1	0.006439	1	0.333333	9.22E-10	0.086957	0.161505
9	138594012	138594030	KCNT1	1	0.000469	1	1	1	1	1	1	1	1	1	1	1	1	1
7	121942442	121942464	FEZF1	0.008511	2.26E-06	1	1	1	1	1	1	1	0.018182	1	1	0.04045	1	0.027726
1	17354373	17354398	SDHB	0.318841	0.462746	1	1	1	1	1	1	1	1	1	1	0.423926	1	1
X	23724675	23724698	ACOT9	1.89E-08	0.314685	1	1	1	1	1	1	1	1	0.079184	1	1.73E-21	1	0.405212
5	180663941	180663952	GNB2L1	3.62E-06	0.000789	1	1	1	0.228861	1	1	1	0.203862	0.109091	0.005882	2E-14	1	0.018471
15	59970049	59970060	BNIP2	1.53E-05	7.07E-10	1	1	1	1	1	1	1	0.102941	1	1	3.16E-10	1	0.199349
1	155737425	155737454	GON4L	0.032705	0.020729	0.197031	1	0.066641	0.145873	1	1	1	1	1	0.002259	0.001231	1	0.147134
3	100016726	100016752	TBC1D23	0.038268	0.003526	0.080782	1	0.130303	1	1	1	0.052632	1	0.061224	1	0.000246	0.001442	1
10	52502803	52502820	ASAH2B	6.76E-06	0.003115	1	1	0.075924	1	0.056169	1	1	1	1	1	7.1E-05	1	0.000145
20	58415393	58415404	PHACTR3	2.88E-05	2.97E-06	1	1	1	1	1	1	1	1	1	1	0.008542	1	0.561627
17	37580118	37580153	MED1	3.91E-10	0.001401	1	1	1	1	1	1	1	1	1	1	4.28E-09	0.037975	0.004761
22	38259110	38259129	EIF3L	1.48E-08	0.014261	1	1	1	1	1	1	1	1	1	1	1.39E-10	1	0.013309
2	37373976	37373983	EIF2AK2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.513293
X	101804817	101804836	NXF4	1.69E-11	0.171437	0.142651	1	1	1	1	1	1	1	0.039216	0.176471	6.9E-09	0.027397	0.032514
2	74756111	74756122	AUP1	0.003739	1.69E-05	1	1	0.103841	1	1	1	0.022222	1	1	0.018182	0.009296	1	0.368144
1	235301496	235301510	RBM34	5.29E-09	1.56E-07	1	1	0.289576	0.055046	1	1	1	1	1	0.210526	9.97E-15	0.061538	0.017913
X	72433663	72433688	NAP1L2	0.609844	1	1	1	1	1	1	1	1	1	1	1	0.140461	1	0.008201
15	84685118	84685129	ADAMTSL3	0.004356	2.58E-10	1	1	1	1	0.060592	1	1	1	1	1	0.000298	0.057143	0.296942
3	179291295	179291319	ACTL6A	0.000529	4.3E-07	0.053571	1	0.487089	1	0.092728	1	1	1	1	0.071429	3.64E-07	1	1
5	38959431	38959442	RICTOR	0.001362	0.004785	1	1	1	1	1	1	1	1	1	1	0.003502	1	0.107663
9	4701841	4701860	CDC37L1	7.36E-06	0.00124	1	1	1	1	0.077141	1	1	0.458353	0.09375	1	0.000185	1	0.527822
11	107969287	107969319	CUL5	3.01E-05	0.004266	1	1	1	1	1	1	1	1	1	1	1.45E-07	1	1
8	194596	194607	ZNF596	3.01E-07	4.47E-13	0.136213	1	1	1	1	0.010753	1	1	1	0.111111	3.6E-09	1	0.164912
11	17111197	17111227	PIK3C2A	0.147948	1	1	1	0.130435	1	1	1	1	1	0.090909	0.315789	0.016343	1	1
11	124007398	124007486	VWA5A	0.095916	0.163934	1	1	0.080878	1	1	1	1	1	1	1	0.452247	1	0.00979
2	197762941	197762956	PGAP1	2.46E-07	0.001578	0.211144	1	1	1	1	1	0.014493	0.017094	1	0.173913	1.52E-06	0.079184	1
2	38545608	38545626	ATL2	6.65E-06	0.000395	1	1	1	1	1	1	1	1	1	1	8.68E-08	0.000974	1
6	39580887	39580898	KIF6	0.004198	0.001084	1	1	1	1	1	1	0.009259	0.037037	1	1	0.000149	0.046154	0.082748
1	94544805	94544830	ABCA4	0.000671	0.004908	0.066667	1	1	1	1	1	1	0.324331	1	0.022059	1.45E-07	0.027778	0.043316
19	14952706	14952735	OR7A10	2.52E-09	0.006417	0.117647	1	1	1	1	1	1	0.033058	1	1	5.13E-10	1	0.316908
12	58361014	58361034	XRCC6BP1(dist=9962),LOC101927653(dist=598708)	3.75E-10	6.41E-10	0.083333	1	1	1	1	0.004348	1	0.088563	1	1	0.001325	0.027778	0.006402
19	7995974	7996007	TIMM44	6.25E-09	3.31E-10	1	1	1	1	1	0.004348	0.007692	2.86E-05	1	1	2.11E-06	1	0.000415
14	76173952	76173964	TTLL5	1.63E-11	1.73E-08	1	1	0.134168	1	1	0.004425	1	0.035461	1	1	8.15E-05	0.051282	0.000712
9	131721441	131721453	NUP188	2.68E-06	2.93E-09	0.097561	1	0.114754	1	1	0.004587	0.021739	1	0.019231	1	1.46E-06	0.022727	0.067265
8	1844623	1844634	ARHGEF10	0.000361	1.03E-09	1	1	1	1	1	0.004695	1	1	1	1	3.29E-05	1	0.100525
2	114210810	114210837	CBWD2	3.16E-07	7.64E-10	1	1	1	0.05111	1	0.004739	0.108764	0.092543	1	1	1.58E-07	1	0.203844
19	18857939	18857956	CRTC1	5.21E-11	3.32E-05	1	1	1	1	1	0.006993	1	1	1	1	1	1	1
2	166898938	166898948	SCN1A	0.000685	3.32E-11	1	1	1	1	1	0.007194	1	1	1	1	9.52E-13	0.045455	0.006645
17	29528313	29528336	NF1	1.54E-05	2.81E-09	0.06	1	1	1	1	0.007246	1	1	1	1	0.0011	1	1
18	14218568	14218580	ANKRD20A5P	3.45E-06	7.9E-13	1	1	1	1	1	0.008097	1	1	1	1	0.025	1	1
21	37787572	37787585	CHAF1B	5.43E-10	3.18E-06	1	1	0.064103	1	1	0.008299	1	1.52E-05	0.0625	1	1.72E-05	1	0.12487
17	49048274	49048312	SPAG9	2.63E-07	0.005247	1	1	1	1	1	0.009804	1	1	1	1	0.026549	1	0.000965
19	12112120	12112142	ZNF763(dist=20922),ZNF433(dist=13390)	3.96E-06	0.008564	1	1	1	1	1	0.010417	1	1	1	1	0.001254	0.033333	1
16	10851655	10851666	NUBP1	6.24E-05	0.000121	1	1	1	1	1	0.011173	1	0.085714	0.037037	1	0.357143	1	1
1	74575199	74575231	LRRIQ3	4.79E-05	0.002136	0.081081	1	1	0.064499	1	0.011696	1	1	0.08599	1	0.001096	1	0.000537
11	74790486	74790510	NEU3(dist=71743),OR2AT4(dist=9286)	1.63E-07	5.66E-12	0.166667	1	1	1	1	0.01227	1	1	1	1	0.001375	0.052632	0.098305
6	160157277	160157288	WTAP	4.05E-06	3.41E-12	0.061224	1	1	1	1	0.013216	1	0.000949	1	1	3.62E-11	0.036585	0.061538
16	75670529	75670550	KARS	0.002083	5.77E-05	1	1	1	1	1	0.014706	1	1	1	1	0.003623	1	1
12	53823175	53823189	AMHR2	0.002143	5.05E-09	1	1	1	0.096084	1	0.016878	0.002193	0.119076	1	1	0.019317	1	0.146079
2	158283943	158283954	CYTIP	1.33E-07	0.002467	1	1	1	1	1	0.017241	1	1	1	1	0.020483	1	0.118408
15	31220709	31220744	FAN1	1.17E-08	1.67E-09	0.199417	1	0.09909	1	1	0.019324	0.037736	1	1	0.045455	0.118024	1	0.152639
17	16344523	16344534	LRRC75A-AS1	7.62E-08	3.28E-05	1	1	1	1	1	0.019737	0.00768	0.092593	1	0.076923	0.655057	0.04878	0.367699
7	126086436	126086447	GRM8	0.000127	1.41E-08	1	1	1	1	1	0.021622	1	0.108764	1	1	0.03821	1	0.192535
1	70904523	70904552	CTH	4.52E-05	0.103477	1	1	1	1	1	0.026738	1	1	1	0.516484	0.001474	1	0.000278
11	67165932	67165942	PPP1CA	6.18E-10	0.000248	1	0.054414	1	1	1	0.034091	0.001414	1	1	1	1.16E-10	1	1
14	55429897	55429917	WDHD1	5.24E-09	4.82E-08	0.04918	0.069307	1	1	0.278508	0.034483	1	1	1	1	8.16E-18	1	0.100159
15	42111745	42111756	MAPKBP1	0.107558	3.91E-09	1	1	1	0.051224	0.243614	0.035461	1	0.153573	0.068966	1	0.029412	1	0.091891
19	41703604	41703616	CYP2S1	1.14E-09	3.64E-07	0.177489	1	1	0.108594	1	0.042781	1	1	1	1	0.000491	1	0.538778
2	169728069	169728084	SPC25	2.02E-05	2.33E-06	1	1	0.173941	0.100867	1	1	1	1	1	1	1.46E-05	0.019608	0.027877
19	10091541	10091552	COL5A3	3.41E-06	2.24E-05	1	1	1	1	0.054545	1	1	1	1	1	0.000111	1	0.003864
20	3674821	3674864	SIGLEC1	0.009348	0.039995	1	1	1	1	1	1	1	1	1	0.166667	0.231304	1	1
14	20836923	20836952	TEP1	0.006553	1	1	1	1	1	1	1	1	1	1	0.130435	0.000162	0.163043	0.15151
2	203624120	203624131	FAM117B	0.005515	9.25E-05	1	1	1	1	1	1	0.02381	1	0.037037	1	5.46E-05	1	0.012504
4	146297387	146297396	OTUD4(dist=196555),SMAD1(dist=105555)	2.22E-06	0.033265	0.084181	1	1	0.317748	0.099264	1	1	0.30402	1	0.013986	5.6E-08	1	0.073348
17	39021015	39021026	KRT12	0.000673	1.99E-09	0.158163	1	0.349676	1	1	1	0.028037	0.088889	0.183508	0.001786	0.101769	1	0.150142
10	96201821	96201857	TBC1D12	0.012166	0.172242	1	1	1	1	1	1	1	1	1	1	0.008384	1	0.216206
3	38539061	38539118	EXOG	2.7E-10	8.91E-13	1	1	1	1	1	1	1	1	1	1	0.00073	0.053684	0.136013
19	46815969	46815994	HIF3A	0.107261	0.03113	1	1	1	1	0.091778	1	1	1	1	0.006061	1	1	0.077577
3	125313710	125313722	OSBPL11	0.000153	7.34E-08	0.077647	1	1	1	1	1	1	1	1	1	3.1E-07	1	1
5	169507130	169507149	DOCK2	0.017085	4.38E-05	1	1	1	1	1	1	0.019802	1	1	1	3.45E-06	1	1
6	50681660	50681681	TFAP2D	1.5E-08	0.002202	1	1	1	0.076892	1	1	1	1	1	1	0.000155	1	1
1	75688156	75688167	SLC44A5	1.24E-05	1.29E-12	1	1	1	1	1	1	1	1	1	1	5.47E-06	1	0.002549
16	21991811	21991822	UQCRC2	0.025547	8.64E-06	1	1	1	1	1	1	1	1	1	0.006494	0.103685	1	0.015965
15	45430242	45430305	DUOX1	1	0.359204	1	1	1	1	1	1	1	0.025424	1	0.333333	1	1	0.300444
19	17339193	17339204	OCEL1	0.002422	3.58E-06	1	1	1	1	1	1	0.046875	1	1	0.2	0.002228	0.019285	0.387736
7	149589490	149589511	ATP6V0E2(dist=11689),ACTR3C(dist=354790)	0.070534	0.181356	0.094077	1	0.110769	1	1	1	0.061058	1	1	0.015789	0.628678	1	0.042549
10	52610342	52610369	A1CF	0.333136	1	1	1	1	1	1	1	1	1	1	0.019608	0.005251	1	0.176027
3	179448066	179448087	USP13	7.08E-05	3.68E-08	1	1	0.100566	1	0.061335	1	0.126984	0.180317	1	1	0.000804	1	1
14	102496394	102496415	DYNC1H1	0.104211	0.161703	1	1	0.327495	0.184797	1	1	0.0625	0.382956	0.130303	1	0.301044	1	0.080172
7	64852790	64852812	LOC441242	0.025931	0.007687	1	1	1	1	1	1	1	1	1	0.333333	0.023532	1	1
4	17590673	17590702	LAP3	8.48E-08	0.001423	0.076923	1	0.200156	1	1	1	0.041092	0.056452	1	1	0.005701	1	1
1	196642969	196642979	CFH	0.366963	0.000488	1	1	1	1	1	1	1	0.002885	1	0.357143	0.005742	1	0.217308
20	44333326	44333341	WFDC10B,WFDC13	5.12E-08	9.94E-12	0.090909	1	0.337971	1	1	1	1	1	1	1	0.000114	1	0.001011
8	126015400	126015412	SQLE	4.29E-07	8.62E-07	1	1	1	1	0.191837	1	0.028302	1	0.061058	1	1.08E-05	1	0.026274
1	42647536	42647585	FOXJ3	0.002039	0.431727	1	1	0.0625	1	1	1	1	1	1	1	0.001472	0.037736	1
17	4053092	4053109	CYB5D2	0.233927	0.00079	1	1	0.222986	1	1	1	1	1	1	1	0.146362	0.04878	0.152149
7	129028857	129028882	AHCYL2	4.5E-10	9.75E-09	1	1	1	1	1	1	0.085669	0.005255	1	1	9.64E-08	0.097761	1
17	40359505	40359544	STAT5B	0.003597	6.18E-05	0.221369	1	1	1	1	1	1	1	1	0.130435	0.001319	1	0.078965
2	201448283	201448294	SGOL2	4.41E-09	5.64E-07	1	1	1	1	1	1	1	1	0.027027	0.157895	1.09E-05	1	0.002477
10	38647463	38647474	HSD17B7P2	0.000101	0.030685	1	1	1	1	1	1	0.064501	1	1	0.071429	0.005484	1	0.011195
5	130535204	130535217	LYRM7	6.97E-06	1.36E-07	0.13219	1	1	1	1	1	1	1	0.016393	0.047619	4.96E-09	1	0.014499
9	8528534	8528553	PTPRD	8.88E-06	0.004294	0.129944	1	0.249939	0.121484	1	1	1	0.141293	1	0.176471	1.47E-06	1	0.005647
6	87796161	87796171	CGA	4.9E-06	4.02E-06	1	1	1	0.349388	0.056065	1	1	1	0.052632	0.018182	1.34E-09	1	0.183466
17	13399486	13399503	HS3ST3A1	6.25E-06	0.000123	1	1	0.350679	1	1	1	1	1	1	0.001998	0.002915	0.010482	0.2345
7	141536351	141536374	PRSS37	0.003931	0.105262	0.074074	1	0.216181	1	1	1	1	1	1	1	8.08E-08	1	0.063815
7	2985361	2985406	CARD11	0.085578	0.170998	0.252874	1	0.405165	1	1	1	1	1	1	1	8.74E-06	1	0.062937
7	29394220	29394233	CHN2	2.25E-09	0.000142	0.313725	1	1	1	1	1	1	0.242092	1	0.125	0.029286	1	0.052276
4	41648344	41648362	LIMCH1	1.74E-06	0.000743	0.089852	1	1	1	1	1	1	1	1	1	0.002274	1	0.001827
1	76257074	76257089	RABGGTB	1.4E-10	9.56E-09	0.115385	1	1	1	0.131887	1	1	1	1	0.266667	7.34E-14	1	0.052292
2	98872662	98872674	VWA3B	2.25E-07	3.94E-07	0.09375	1	1	0.258166	1	1	0.053089	0.020597	1	1	0.000767	0.045455	0.020824
19	44047493	44047532	XRCC1	9.47E-11	0.057565	0.204678	1	0.370674	0.133511	1	1	1	0.203349	1	1	0.037383	0.038462	0.137636
4	38930985	38930995	FAM114A1	0.008704	0.01265	1	1	1	1	1	1	1	1	0.006061	0.076923	0.018074	1	0.397274
3	154010515	154010550	DHX36	8.78E-09	0.031649	0.231707	1	0.209252	0.134937	1	1	1	0.098704	1	0.015738	5.89E-09	1	0.017645
5	112346416	112346447	DCP2	8.47E-08	2.31E-09	1	1	1	0.198182	1	1	1	1	1	1	8.86E-06	1	0.000193
1	9006088	9006116	CA6	0.072728	0.06998	1	1	1	1	1	1	1	1	1	1	1	1	1
14	22975756	22975775	OR4E2(dist=841518),DAD1(dist=58032)	0.062481	0.034983	1	1	1	1	1	1	1	1	1	1	0.220748	1	1
17	38152373	38152389	PSMD3	7.8E-05	4.09E-07	1	0.067613	1	0.110423	1	1	1	0.047675	1	0.181818	1.28E-06	1	0.125515
15	62201333	62201345	VPS13C	0.000655	0.001187	1	1	1	1	1	1	1	1	1	0.181818	0.000303	1	0.016049
4	170989708	170989719	AADAT	8.16E-12	4.71E-08	1	1	1	1	0.050149	1	0.000219	0.35253	0.142683	0.25	5.72E-08	1	0.034495
6	66115281	66115291	EYS	0.001467	0.00294	0.471719	1	0.098978	1	1	1	1	0.078788	1	0.2	0.059135	1	0.014173
11	118210424	118210457	CD3D	0.037194	1	1	1	0.350146	1	1	1	1	0.111538	1	0.076923	1	1	1
4	41263718	41263729	UCHL1	7.04E-09	6.79E-11	1	1	0.591382	1	1	1	0.013889	0.580825	0.056604	0.257143	8.23E-06	1	0.002479
20	23349607	23349618	GZF1	0.004045	0.002871	1	1	0.422568	1	1	1	1	1	1	0.003953	0.474106	1	0.001813
19	10091267	10091319	COL5A3	0.001782	0.068418	0.305322	1	0.428039	1	0.280769	1	1	1	1	0.153846	0.030389	1	0.186695
4	120107098	120107109	MYOZ2	3.26E-07	0.000681	0.20863	1	0.065027	1	0.097194	1	1	0.147905	1	1	0.016655	1	0.272009
19	21428062	21428087	ZNF431(dist=59257),ZNF708(dist=45875)	9.39E-05	0.002975	1	1	1	1	1	1	1	1	1	1	0.000198	1	0.000736
1	209880508	209880520	HSD11B1	6.05E-12	2.4E-09	0.25946	1	1	1	1	1	1	1	1	0.062951	0.000228	1	0.001766
3	101399910	101399923	RPL24	1.59E-05	2.95E-09	0.240404	1	0.13488	0.258794	0.229152	1	1	1	1	1	5.93E-09	1	0.197466
8	124448907	124448919	WDYHV1	1.08E-06	9.52E-07	1	1	0.512787	1	1	1	0.076892	0.028037	0.084181	1	0.001468	1	0.222867
3	108229437	108229449	MYH15	3.51E-07	1.54E-08	0.147313	1	0.098291	0.231319	1	1	0.044444	1	1	0.3125	0.003216	1	0.003821
5	177676986	177677011	COL23A1	0.028772	0.00046	1	1	1	1	1	1	1	1	1	1	0.10148	1	0.000194
2	86107945	86107963	ST3GAL5	0.151584	3E-07	1	1	1	1	0.100422	1	1	1	1	1	0.125	1	1
4	5630470	5630482	EVC2	0.000206	4.21E-10	1	1	0.417989	1	1	1	0.001852	0.12049	0.015239	0.3125	0.003348	0.325091	0.07182
3	172634021	172634039	SPATA16	8.31E-11	1.01E-11	0.140212	1	0.114656	0.12199	0.050624	1	0.002173	0.167224	1	0.1	2.54E-05	0.061538	0.307498
6	41876911	41876925	MED20	2.41E-06	1.45E-11	1	1	1	0.113004	1	1	0.005598	0.078658	1	1	0.003796	1	1

8	42761230	42761249	HOOK3	7.54E-12	4.93E-06	0.11894	0.055164	1	1	1	1	0.006173	1	1	0.115385	1.05E-18	0.014778	0.048956
15	44024081	44024112	CKMT1A(dist=32661),CATSPER2P1(dist=4034)	1.17E-08	0.000205	1	1	1	1	1	1	0.006494	1	1	1	0.002068	1	0.035987
1	100671860	100671880	DBT	1.36E-10	9.54E-13	0.103383	1	1	1	1	1	0.006849	1	0.019231	1	1.09E-05	1	0.006344
17	17039561	17039595	MPRIP	0.012022	0.457788	1	1	1	0.194976	1	1	0.007368	0.000531	1	0.005882	0.0242	1	0.219981
14	94745068	94745095	PPP4R4	8.01E-09	1.4E-08	1	1	1	1	1	1	0.007463	1	0.098718	1	6.85E-05	1	0.016429
2	136529897	136529910	UBXN4	9.15E-08	4.52E-11	1	0.050308	1	1	1	1	0.007463	1	1	1	4.68E-06	1	0.054393
8	124817605	124817620	FAM91A1	1.15E-11	3.04E-08	0.122024	1	1	0.163647	1	1	0.007752	1	0.056729	1	3.47E-18	0.023256	0.171518
1	36019913	36019925	KIAA0319L	2E-07	2.28E-10	1	1	1	0.063143	1	1	0.007813	0.036585	1	1	5.38E-09	1	0.004167
2	109123970	109124000	GCC2	3.92E-07	1.09E-06	0.058824	1	1	1	1	1	0.008	1	1	0.166667	6.04E-10	0.078919	0.430873
13	50306915	50306932	KPNA3	3.88E-06	0.051282	0.229858	1	1	1	1	1	0.008333	1	0.017857	1	1.93E-05	1	0.116487
12	76453670	76453694	NAP1L1	1.77E-05	0.002042	1	1	1	1	1	1	0.00885	1	1	1	5.42E-05	1	0.03939
16	71718538	71718563	PHLPP2	8.8E-09	0.000222	1	1	1	1	1	1	0.009174	0.025862	0.016949	1	1.08E-08	1	1
8	103664685	103664719	KLF10	0.001576	0.010242	1	1	0.304366	1	1	1	0.011173	1	1	1	6.12E-07	1	0.122017
6	13620380	13620391	NOL7	0.004639	0.00748	1	1	1	1	1	1	0.011364	1	1	1	0.025103	1	1
6	44081957	44081968	MRPL14	0.000317	1.1E-11	0.047619	1	1	1	1	1	0.011364	1	1	1	0.000745	1	1
14	56104386	56104405	KTN1	3.21E-10	8.85E-10	1	1	1	1	1	1	0.012195	0.000342	1	1	7.89E-11	0.033898	0.049107
X	135767763	135767792	ARHGEF6	1.8E-08	0.000278	0.067212	1	1	1	1	1	0.012346	1	1	1	0.000181	1	0.013201
10	93752074	93752105	BTAF1	2.79E-11	1.03E-09	0.058824	1	1	0.052941	1	1	0.012821	1	0.06298	1	1.38E-09	0.004146	0.150857
11	77672189	77672229	INTS4	3.08E-09	1.57E-08	0.185616	1	1	1	1	1	0.012821	1	1	1	3.24E-13	1	0.280456
2	15676456	15676468	NBAS	3.75E-10	2.4E-11	0.068966	1	1	1	1	1	0.012987	1	1	1	6.51E-05	1	0.217062
10	62544391	62544411	CDK1	2.25E-05	4.16E-05	1	1	0.062857	1	1	1	0.013072	0.02439	1	1	0.000136	0.043478	0.059226
10	69961537	69961564	MYPN	2.48E-06	0.002541	1	1	1	1	1	1	0.013245	0.033557	1	1	0.055135	1	0.171309
2	108999483	108999515	SULT1C4	1.99E-07	7.04E-07	0.057971	1	0.064516	1	1	1	0.013245	1	1	1	3.34E-07	1	1
1	148594259	148594272	NBPF25P	9.82E-05	8.71E-09	0.066667	1	1	1	1	1	0.013514	0.022989	1	1	0.000397	1	0.061856
1	185951573	185951589	HMCN1	8.88E-10	4.86E-09	0.098305	1	0.105984	1	1	1	0.013605	1	1	1	2.79E-10	1	0.050481
20	47734948	47734972	STAU1	1.13E-05	6.62E-05	1	1	1	1	1	1	0.013699	1	1	1	0.0004	0.000974	1
7	5780521	5780558	RNF216	0.003038	5.5E-07	1	1	1	1	1	1	0.013793	1	1	1	0.00053	1	0.172854
11	102575512	102575536	MMP27	9.73E-05	1.97E-07	1	1	1	1	1	1	0.013889	1	1	1	8.54E-11	0.019231	9.59E-05
15	78839102	78839127	PSMA4	0.136346	0.034429	1	1	1	1	1	1	0.013986	1	1	0.02	0.662112	1	0.03501
16	4861103	4861130	GLYR1	2.01E-10	6.5E-07	1	1	1	1	1	1	0.014286	0.038217	1	1	7.62E-06	1	0.070225
3	108102580	108102602	MYH15	0.000951	9.06E-07	0.122024	1	0.246467	1	1	1	0.014493	1	1	0.05	0.008854	1	0.00553
8	39114668	39114704	ADAM32	2.13E-11	0.018946	0.082447	1	1	1	1	1	0.014599	1	1	1	1.64E-09	0.001947	1
6	117859721	117859732	DCBLD1	1.39E-05	0.016335	1	1	1	1	1	1	0.015152	1	1	1	2.86E-05	1	0.005641
X	106396617	106396641	NUP62CL	6.99E-12	3.02E-13	0.085106	1	1	1	1	1	0.015267	1	1	1	5.63E-11	0.00084	0.063291
13	21373161	21373193	XPO4	1.84E-06	5.95E-07	1	1	1	1	1	1	0.015625	1	1	1	0.025837	1	0.058201
17	57128711	57128722	TRIM37	4.07E-05	4.76E-06	1	1	1	1	1	1	0.015625	1	0.035088	1	0.000438	1	0.029095
16	53721713	53721724	RPGRIP1L	1.53E-06	1.07E-10	1	1	1	1	1	1	0.015873	0.031008	1	1	0.000102	1	0.221703
7	105108955	105108983	PUS7	3.03E-05	0.008274	0.072727	1	1	1	1	1	0.015873	1	1	1	0.005414	1	1
3	17418001	17418012	TBC1D5	4.56E-06	5.52E-06	1	1	1	1	1	1	0.015873	0.214701	1	1	2.81E-09	0.030303	0.085714
10	71055448	71055460	HK1	4.42E-07	5.72E-10	0.053571	1	1	1	1	1	0.017544	1	0.000649	1	0.000154	1	0.020376
2	225710433	225710459	DOCK10	1.08E-05	4.18E-11	1	1	1	1	1	1	0.017699	0.108515	1	1	0.055468	1	0.097898
2	224760359	224760376	WDFY1	0.11619	0.482587	1	1	1	1	1	1	0.018349	1	1	1	0.058401	1	1
3	171455451	171455462	PLD1	3.29E-07	4.07E-08	1	1	1	1	1	1	0.019231	0.054348	1	0.142857	4.36E-09	0.047619	0.000386
19	12981477	12981503	MAST1	8.72E-08	1.36E-09	1	1	1	1	1	1	0.019417	1	1	1	0.022059	1	1
7	87323209	87323220	ABCB1,RUNDC3B	1.58E-05	4.07E-09	1	1	0.096774	1	0.06865	1	0.019608	1	0.022727	1	0.102337	1	0.063492
14	68126414	68126425	VTI1B	3.85E-06	1.82E-06	1	1	1	1	1	1	0.020833	1	1	1	0.009922	1	0.00269
18	44444219	44444231	PIAS2	1.29E-09	2.21E-07	1	1	1	1	1	1	0.022222	1	1	1	2.59E-12	1	0.072727
5	16474764	16474795	FAM134B	7.8E-08	4.53E-11	0.096774	1	1	1	1	1	0.022222	1	0.072267	1	2.54E-10	1	1.35E-05
11	18231188	18231224	LOC494141	0.000847	0.030834	1	1	1	0.071726	1	1	0.022556	1	1	1	9.68E-07	1	1
17	27614746	27614770	NUFIP2	2.84E-07	0.000282	1	1	1	1	1	1	0.022727	1	1	0.002597	9.48E-06	1	0.224377
1	114123141	114123159	MAGI3	1.06E-07	1.59E-09	1	1	1	1	1	1	0.022727	1	1	1	1.74E-06	1	0.007154
12	7170167	7170178	C1S	6.8E-07	4.25E-11	1	1	1	1	1	1	0.023256	0.010279	1	1	1.11E-07	1	0.069307
21	17135361	17135372	USP25	0.000107	3.78E-07	0.076923	1	1	1	1	1	0.023529	1	0.0625	1	0.000461	0.000816	1
17	43226461	43226506	HEXIM1	0.154267	0.007636	1	1	1	1	1	1	0.024096	1	1	1	1	0.002347	0.203537
19	53952582	53952595	ZNF761	2E-06	2.14E-09	1	1	1	1	1	1	0.024096	1	1	1	0.018182	1	0.111021
15	30003291	30003303	TJP1	2.04E-09	1.03E-09	0.047619	1	1	1	1	1	0.02439	0.012658	1	1	2.63E-05	1	0.003761
7	22206774	22206785	RAPGEF5	0.000848	0.177419	0.083333	1	0.082569	1	1	1	0.02459	1	1	1	6.66E-07	1	1
10	131639306	131639325	EBF3	1.53E-06	2.08E-09	1	1	0.081967	1	1	1	0.025	1	0.062004	1	0.002202	0.073148	0.131956
8	2017705	2017719	MYOM2	5.74E-09	7.65E-08	1	1	1	1	1	1	0.025236	1	1	1	8.42E-09	1	0.108636
15	30033645	30033656	TJP1	0.001211	0.002883	1	1	1	1	1	1	0.025641	1	1	0.065934	0.000341	0.00303	1
15	90999351	90999362	IQGAP1	0.000151	2.78E-05	0.25974	1	1	1	1	1	0.025974	1	1	1	0.005877	1	0.007968
21	15306554	15306584	CYP4F29P(dist=85869),ANKRD20A11P(dist=9512)	0.000276	9.95E-08	0.4	1	0.377966	0.365016	0.117541	1	0.025974	1	0.130435	1	1	1	1
13	25363466	25363477	RNF17	6.05E-07	7.3E-11	1	1	1	1	1	1	0.026316	1	1	1	2.3E-07	1	0.095745
6	13652915	13652932	RANBP9	0.000156	2.49E-07	1	1	1	1	1	1	0.026667	1	1	1	1.5E-08	1	1
9	111903890	111903901	FRRS1L	0.00066	0.012813	0.054054	1	1	1	1	1	0.026667	0.138961	1	1	0.00066	0.090909	0.018881
16	3558262	3558286	CLUAP1	4.32E-08	2.88E-13	1	1	1	1	1	1	0.026755	1	1	1	4.57E-09	1	0.000159
12	1890035	1890046	ADIPOR2	0.000446	1.84E-09	1	1	1	1	1	1	0.027027	0.052632	1	1	7.8E-07	1	0.074074
2	190670539	190670551	PMS1	1.25E-07	0.002508	0.210521	1	1	1	1	1	0.027523	0.026316	1	0.304348	4.54E-08	0.037975	0.076847
13	26959325	26959336	CDK8	1.93E-07	1.82E-08	0.076923	1	1	1	1	1	0.027778	1	1	1	2.45E-06	1	1
11	33078624	33078650	TCP11L1	0.01087	6.07E-12	1	1	0.107143	0.072375	1	1	0.027778	0.18136	1	0.214286	0.000537	1	0.157974
8	135533265	135533276	ZFAT	2.08E-08	1.67E-07	1	1	1	1	1	1	0.028037	1	1	1	2.02E-08	1	0.076046
2	203142654	203142665	NOP58	0.000105	6.3E-11	0.047619	1	1	1	1	1	0.029412	0.240404	1	1	8.24E-08	1	1
12	90147633	90147660	LINC00936(dist=41904),LINC00615(dist=1164140)	0.00657	1.84E-10	1	1	1	1	1	1	0.029703	1	1	1	0.086957	1	0.026667
19	49339682	49339697	HSD17B14	0.243697	0.000773	1	1	1	1	1	1	0.030303	1	1	1	0.028067	0.035088	1
14	50584990	50585017	SOS2	0.0055	0.000637	1	1	1	1	1	1	0.030769	1	1	0.153846	1	1	1
7	18688075	18688086	HDAC9	0.000367	9.61E-10	1	1	1	1	1	1	0.030928	1	1	1	0.00017	1	0.11996
19	9582078	9582102	ZNF560	0.000479	0.000104	0.115013	1	0.387578	1	1	1	0.031371	1	0.065574	0.217391	0.016953	1	0.142643
3	124460895	124460940	UMPS	5.71E-07	1.36E-10	0.064516	1	1	1	1	1	0.031746	0.112189	1	1	0.001563	0.038462	0.096813
2	15601269	15601293	NBAS	0.557397	1	1	1	1	0.084463	1	1	0.03252	0.044944	1	0.2	1	1	0.00641
10	17747108	17747119	STAM	1.84E-09	4.8E-07	1	1	0.379294	1	1	1	0.032787	1	1	0.210526	4.65E-05	1	0.068532
4	10027509	10027520	SLC2A9	0.004143	1.54E-07	1	1	0.246467	1	0.149719	1	0.032787	1	1	0.004128	0.004562	1	0.000498
13	19415628	19415644	ANKRD20A9P	0.002617	2.38E-10	1	1	1	0.126126	1	1	0.032967	1	1	1	0.01	0.134977	0.074468
10	33196108	33196119	ITGB1	0.000403	0.001744	1	1	1	1	1	1	0.033898	0.009307	1	1	0.000101	1	0.512516
10	116920034	116920045	ATRNL1	9.32E-06	1.72E-09	0.109524	1	1	1	1	1	0.034483	0.042553	0.094077	1	2.84E-08	1	0.001195
14	95670804	95670838	CLMN	0.113755	2.26E-05	0.05	1	1	1	1	1	0.034483	1	1	0.181818	0.02172	1	0.000827
X	100608058	100608084	BTK	1.78E-10	1.38E-06	1	1	1	1	1	1	0.036197	1	1	1	0.044444	0.068947	1
12	100478156	100478205	UHRF1BP1L	7.32E-12	1	0.255746	1	1	1	1	1	0.036583	1	1	0.12	0.00103	1	0.129184
15	99482380	99482391	IGF1R	0.017168	3.06E-05	1	1	1	1	1	1	0.037207	1	1	1	0.028667	1	1
15	71633455	71633466	THSD4	5.22E-06	2.07E-11	1	1	1	1	1	1	0.0375	1	1	1	0.000334	0.065201	1
4	108603095	108603105	PAPSS1	2.78E-06	0.000133	1	1	1	1	1	1	0.037736	1	1	1	0.000966	1	0.076023
19	43529312	43529337	PSG11	5.59E-06	0.070309	0.1	1	1	1	1	1	0.037879	1	1	1	0.00214	1	0.073993
5	127507307	127507351	SLC12A2	0.000153	0.016837	1	1	0.591546	1	1	1	0.038462	0.123156	1	1	0.016972	1	0.548081
6	155566889	155566913	TIAM2	0.00877	1.25E-08	1	1	1	1	1	1	0.038706	1	1	1	2.43E-07	1	1
1	109952506	109952527	PSMA5	0.000127	5.49E-10	1	1	1	1	1	1	0.04	0.081967	1	1	1.03E-06	1	0.009905
1	43664319	43664330	CFAP57	0.001833	9.05E-11	0.071429	0.058394	1	1	0.237617	1	0.04	0.389754	1	0.002597	2.72E-05	1	0.220228
16	47252866	47252877	ITFG1	5.73E-06	0.000401	1	1	1	1	1	1	0.040198	1	1	1	0.000209	1	0.020469
2	216296730	216296742	FN1	1.12E-08	2.64E-08	1	1	0.29519	1	1	1	0.040265	1	0.02	0.227273	1.58E-06	1	0.00237
15	60748719	60748828	ICE2	0.044106	0.000863	0.108108	1	1	1	1	1	0.041322	1	1	1	0.002475	1	5.02E-05
11	121348741	121348762	SORL1	1.77E-05	9.95E-05	1	1	1	0.18379	1	1	0.041663	0.075441	1	1	0.095191	1	0.553842
8	18413893	18413904	PSD3	1.7E-07	2.6E-06	0.103841	1	0.472576	1	1	1	0.042105	0.369933	1	1	9.96E-05	1	0.1183
12	111351963	111351982	MYL2	0.084261	0.261002	1	1	1	1	1	1	0.042553	1	1	1	0.160305	1	1
19	13338173	13338205	CACNA1A	1	0.024612	1	1	1	1	1	1	0.042857	1	1	1	0.032769	1	0.073958
7	79828450	79828462	GNAI1	7.15E-12	2.57E-09	0.058824	1	1	1	0.066667	1	0.043161	0.064516	1	0.065934	1.18E-14	0.030303	0.212008
10	96100257	96100284	NOC3L	0.000132	7.9E-07	1	1	0.059394	1	0.139718	1	0.044776	0.138961	1	0.333333	0.000608	0.051282	0.036018
20	57828914	57828934	ZNF831	0.026212	4.5E-09	0.054054	1	1	0.232656	1	1	0.045455	1	1	1	0.009498	1	0.077373
17	2888249	2888260	RAP1GAP2	0.003059	1.27E-07	1	1	1	1	1	1	0.046512	1	1	0.154799	0.010546	0.146154	1
9	114124456	114124509	KIAA0368	2.42E-05	0.000512	1	1	1	1	1	1	0.046512	1	1	0.166667	2.21E-07	0.0625	0.00471
2	24306107	24306124	FAM228B,TP53I3	0.067162	0.000353	1	1	1	1	1	1	0.046875	1	1	1	0.073969	1	0.011494
19	12543765	12543777	ZNF443	5.21E-08	4.89E-12	1	1	0.143742	1	1	1	0.048	0.127223	0.117647	0.230769	1.44E-07	0.050847	0.000289
17	36352408	36352420	LOC440434	5.87E-07	2.34E-07	0.231061	1	0.579614	0.16215	1	1	0.048193	0.169886	0.069767	0.060606	1.04E-10	0.136591	0.030456
20	30060720	30060741	DEFB124	0.041919	0.006075	1	1	1	1	1	1	0.048774	1	1	0.175824	0.152752	1	0.473997
6	32824975	32824999	PSMB9	0.000165	1.11E-09	1	1	1	1	1	1	0.04958	1	1	1	3.77E-08	1	1
8	133740259	133740296	TMEM71	0.009699	0.311672	0.234274	1	0.162973	1	0.164578	1	0.049587	1	1	0.063235	0.113061	1	0.138931
X	76972553	76972573	ATRX	2.25E-06	1.25E-08	0.052632	1	1	1	1	1	1	1	0.071429	1	1.8E-10	0.033333	0.001753
22	35726271	35726283	TOM1	2.18E-05	7.23E-07	0.060606	1	1	1	1	1	1	0.04023	1	1	0.018872	1	0.009651
4	8415928	8415939	ACOX3	4.97E-08	4.21E-08	1	1	0.080808	1	1	1	1	0.054054	1	1	0.003431	0.049383	1
8	101164032	101164044	POLR2K	0.000575	1.2E-08	1	1	1	1	1	1	1	1	1	1	4.6E-06	1	1
1	35879693	35879704	ZMYM4	2.01E-09	2E-09	0.086957	1	1	1	1	1	1	1	1	1	4.11E-10	1	1
1	205687332	205687377	NUCKS1	4.13E-07	0.002147	0.149798	1	0.289159	1	1	1	1	0.187678	1	1	0.000327	1	0.043204
6	122001462	122001492	GJA1(dist=230572),HSF2(dist=719204)	1.83E-10	9.76E-13	0.1	1	1	1	1	1	0.078919	1	1	1	0.163043	0.046779	0.008772
9	376186	376197	DOCK8	0.00296	5.61E-09	1	1	1	1	1	1	1	1	0.000673	1	0.006429	1	0.21583
11	64011554	64011590	FKBP2	0.003818	1.1E-12	1	1	1	1	1	1	1	1	1	1	1.43E-05	1	1
11	108014662	108014674	ACAT1	6.2E-12	3.08E-13	1	1	0.399957	1	1	1	1	0.235318	0.095238	1	3.04E-13	0.042857	0.005144
6	90338816	90338828	ANKRD6	6.86E-08	5.41E-11	1	1	1	1	1	1	1	0.017264	1	1	5.07E-10	1	0.288009
2	209110006	209110017	IDH1	7.96E-05	1.01E-09	0.066667	1	1	1	1	1	1	0.2	0.017857	0.153846	1.18E-07	1	0.231496
12	104995800	104995813	CHST11	6.27E-11	5.31E-10	0.409703	1	1	1	0.224377	1	0.110149	2.69E-05	1	1	2.22E-07	1	0.217661
21	43770926	43770938	TFF2	0.009413	0.391935	0.075	1	0.321386	0.063291	1	1	1	0.00101	1	0.153846	0.030612	1	0.075254
12	62261077	62261088	FAM19A2	4.64E-07	2.17E-09	1	1	1	1	1	1	1	0.000257	1	1	4.45E-05	1	1.04E-06
17	8052506	8052542	PER1	0.780478	7.45E-06	1	1	0.434227	0.48894	1	1	1	0.457027	1	1	0.270469	0.099318	0.474006
7	99161319	99161332	ZNF655	1.55E-09	1.78E-10	0.16	1	1	1	1	1	1	1	1	1	0.000222	1	0.020588
1	59004989	59005000	OMA1	0.000768	6.27E-06	1	1	1	1	1	1	1	1	1	1	0.003474	1	1
12	96408594	96408611	LTA4H	4.01E-09	3.1E-09	1	1	1	1	1	1	1	1	1	1	3.38E-06	0.030769	0.078014
9	36198871	36198890	CLTA	0.001175	9.25E-12	0.133333	1	0.076528	1	1	1	1	1	1	0.1	3.48E-06	1	0.134292
17	59999191	59999209	INTS2	1.4E-06	0.000267	0.064516	1	1	1	1	1	1	1	1	1	0.000356	1	1
19	14755137	14755150	EMR3	3.89E-07	1.24E-07	1	1	1	1	1	1	1	1	1	1	0.000139	1	0.027273
1	51937328	51937339	EPS15	0.00053	3.05E-06	1	1	1	1	1	1	1	0.013462	1	1	2.39E-06	1	0.147327
2	9607820	9607831	CPSF3	1.64E-06	8.1E-13	1	1	1	1	1	1	1	0.044025	0.029412	1	1.87E-16	0.022989	0.034483
11	20083832	20083843	NAV2	2.5E-11	8.29E-07	0.052632	1	0.091603	1	1	1	1	1	1	1	4.46E-05	1	0.091594
11	117163561	117163572	BACE1	0.001865	2.97E-11	1	1	1	1	1	1	1	1	1	1	0.208333	1	0.001025
16	4057345	4057364	ADCY9	0.003128	1.09E-11	1	1	1	1	1	1	1	1	1	1	0.027526	1	1
10	70156582	70156592	RUFY2	0.615699	5.37E-05	0.045455	1	1	1	1	1	1	1	1	1	1.16E-06	1	0.007834

7	142157724	142157754	TRY2P(dist=185656),MTRNR2L6(dist=216377)	1	0.2	1	1	1	1	1	1	1	1	1	1	1	1	1
3	197702875	197702887	LMLN	7.83E-09	1.27E-07	1	1	1	1	1	1	1	1.49E-05	0.018519	1	6.18E-08	0.04	0.063492
1	116268178	116268202	CASQ2	0.000777	0.028783	1	1	1	1	1	1	1	1	1	1	0.007229	1	1
17	79894106	79894120	PYCR1	2.87E-10	8.18E-10	1	1	0.166387	1	1	1	1	1	1	1	1.1E-09	0.066102	0.011658
7	129681029	129681046	ZC3HC1	0.000617	3.95E-07	1	1	0.066667	1	1	1	1	1	1	1	0.000531	1	0.006621
12	18534672	18534687	PIK3C2G	0.077573	0.379404	1	1	0.117647	1	1	1	1	1	1	1	0.00694	1	0.152306
17	42962709	42962720	EFTUD2	2.04E-08	5.73E-09	0.103448	1	1	1	1	1	1	1	1	1	2.64E-06	1	0.021642
6	35810383	35810394	SRPK1	1.07E-09	1.45E-08	1	1	1	1	1	1	1	0.027033	0.029412	1	3.31E-08	1	0.009502
10	75564660	75564677	NDST2	6.49E-11	7.67E-09	1	1	1	1	1	1	1	1	1	1	2.19E-15	1	0.117142
3	57846577	57846588	SLMAP	5.16E-05	0.000223	0.047619	1	1	1	1	1	1	1	1	1	0.001803	1	1
5	140953001	140953024	DIAPH1	0.602597	0.007858	1	1	1	1	1	1	1	1	1	1	0.031602	1	1
3	41860984	41860995	ULK4	0.000163	1.91E-06	1	1	1	1	1	1	1	1	1	1	2.67E-07	1	0.006446
12	122181461	122181473	TMEM120B	0.004152	6.62E-13	1	1	1	1	1	1	1	0.1	1	1	0.098039	1	1
8	110591950	110591968	SYBU	0.006302	5.8E-08	0.057143	1	1	1	1	1	1	1	1	1	0.010389	1	0.06087
14	31625994	31626011	HECTD1	6.79E-11	1.31E-06	0.090865	0.125	1	1	0.101846	1	1	1	1	0.217391	1.6E-14	1	0.014409
16	53480931	53480950	RBL2	3.78E-05	1.3E-10	1	1	0.122956	1	1	1	1	1	0.040816	1	0.007349	0.029851	0.00868
14	58795071	58795082	ARID4A	0.00018	5.25E-07	1	1	1	1	1	1	1	1	0.037037	1	0.000147	1	0.007117
16	2342074	2342086	ABCA3	3.24E-11	2.04E-09	1	1	1	1	1	1	1	1	1	1	5.31E-09	1	0.005914
4	148886159	148886170	ARHGAP10	6.4E-07	4.07E-05	0.045614	1	1	1	1	1	1	1	0.03125	1	4.6E-05	1	1
4	20884202	20884222	KCNIP4	2.71E-08	2.25E-09	1	1	1	1	1	1	1	1	1	1	1.33E-07	0.034483	0.116646
4	113347609	113347620	ALPK1	5.88E-06	4.18E-08	1	1	0.192423	0.151988	1	1	1	1	0.035714	0.2	1.7E-08	1	1
8	62555482	62555493	ASPH	4.97E-06	2.64E-06	1	1	1	1	1	1	1	1	1	1	2.63E-08	0.026667	1
19	2733501	2733518	SLC39A3	1	0.012363	1	1	1	1	1	1	1	1	1	1	0.007317	1	1
19	57746489	57746504	AURKC	0.425676	1	1	1	1	1	1	1	1	1	1	1	0.192308	1	0.127454
18	21422554	21422569	LAMA3	0.003665	0.020011	1	1	1	1	1	1	1	0.030242	1	1	0.009622	1	1
7	41740041	41740093	INHBA-AS1	4.45E-06	5.64E-09	1	1	0.051546	1	1	1	1	1	0.032258	1	0.125	1	1
4	185340725	185340746	IRF2	0.074275	0.00071	1	1	0.243614	1	1	1	1	1	1	1	0.002033	1	0.287053
2	201362423	201362434	KCTD18	6.22E-05	4.18E-08	1	1	1	1	1	1	1	0.125	1	1	0.001396	1	1
2	138727858	138727884	HNMT	9.29E-06	0.00033	0.096721	1	1	1	1	1	1	1	1	1	1.24E-10	1	0.063776
12	51392897	51392918	SLC11A2	6.64E-11	2.08E-12	0.122024	1	1	1	1	1	1	1	0.034483	1	7.38E-11	1	0.064103
3	98031433	98031444	OR5H2(dist=28757),OR5K4(dist=41254)	0.000545	9.71E-08	1	1	1	1	1	1	1	1	1	1	0.004398	1	0.005536
10	127526735	127526746	BCCIP,DHX32	0.00019	8.82E-10	1	1	1	1	1	1	1	1	1	1	0.008938	1	1
14	96178148	96178161	TCL1A	1	0.461219	1	1	1	1	1	1	1	1	1	1	0.302326	1	1
12	110342657	110342668	TCHP	6.34E-05	1.47E-06	1	1	1	1	1	1	1	1	1	1	0.000131	1	0.097826
11	125505493	125505515	CHEK1	0.008167	1.87E-05	0.0625	1	1	1	1	1	1	1	1	1	0.034627	1	1
6	118024705	118024722	NUS1	0.289136	0.417061	1	1	1	1	1	1	1	1	1	1	0.03219	1	1
10	48980563	48980577	GLUD1P7	7.58E-10	0.002042	1	1	1	1	1	1	1	1	0.016667	1	0.019608	3.08E-05	1
X	77393375	77393394	TAF9B	0.001166	4.92E-11	0.074074	1	1	1	1	1	1	1	1	1	1.06E-06	0.002262	0.157599
2	242643983	242643994	ING5	1.58E-07	3.97E-07	1	1	1	1	1	1	1	1	1	1	1.3E-06	0.052281	0.001918
21	35183099	35183110	ITSN1	0.000799	1.09E-07	1	1	0.095238	1	1	1	1	1	1	1	0.013793	0.101846	1
1	65830283	65830313	DNAJC6	7.91E-05	0.003924	0.090909	1	0.066176	1	1	1	1	1	1	1	0.110823	1	1
9	12972768	12972779	LURAP1L(dist=149709),MPDZ(dist=132924)	0.044156	1.93E-10	1	1	1	1	1	1	1	1	1	1	0.004857	1	1
1	43828861	43828872	CDC20	1.49E-05	0.002863	0.088235	1	1	1	1	1	1	1	1	1	2.29E-07	1	1
1	63836738	63836761	ALG6	4.88E-08	8.39E-05	1	1	1	1	1	1	1	0.3	0.020833	1	9.23E-07	0.071429	2.33E-05
17	28011501	28011522	SSH2	0.000143	2.78E-06	0.055556	1	1	1	1	1	1	1	1	1	6.67E-08	1	1
1	100624000	100624012	LRRC39	6.94E-07	1.37E-06	1	1	1	1	1	1	1	1	1	1	9.19E-05	1	0.000269
12	58142484	58142507	CDK4	0.003754	0.00941	1	1	1	1	1	1	1	1	1	1	0.130417	1	0.010645
X	54471045	54471056	TSR2	1.68E-07	0.000115	1	1	1	1	1	1	1	1	1	1	4.27E-12	1	1
3	128292318	128292337	LINC01565	0.000973	0.000898	1	1	1	1	0.056996	1	1	1	1	1	0.002652	1	1
1	11140610	11140663	EXOSC10	0.02212	8.49E-05	1	1	1	1	1	1	1	1	1	0.16	0.004018	1	0.509727
12	121444018	121444039	C12orf43	1.66E-08	1.96E-05	0.056338	1	1	1	1	1	1	1	1	0.25	9.75E-05	1	0.031504
15	31202787	31202806	FAN1	2.42E-05	4.02E-09	0.127536	1	1	1	1	1	1	1	1	1	0.008031	1	0.061404
2	231065503	231065514	SP110	0.002542	0.000136	0.064516	1	1	1	1	1	1	1	1	1	0.015018	1	1
4	174219176	174219187	GALNT7	0.003094	2.69E-05	0.111111	1	1	1	1	1	1	1	1	1	0.424086	1	1
8	77690727	77690761	ZFHX4	0.012219	1	1	1	1	1	1	1	1	1	1	1	0.011139	1	1
6	52643165	52643176	GSTA2(dist=14804),GSTA1(dist=13002)	0.000275	4.7E-07	1	1	1	1	1	1	1	1	1	1	0.001474	0.0375	1
21	48063387	48063405	PRMT2	0.004175	8.91E-13	1	1	1	1	1	1	1	0.139786	0.285714	1	4.99E-12	0.09375	0.0375
1	89618472	89618489	GBP7	3.7E-09	3.85E-05	1	1	1	1	1	1	1	1	0.071429	1	0.056484	0.0625	0.057436
22	20920813	20920850	MED15	0.000269	0.058304	1	1	1	0.069848	1	1	1	1	1	1	0.084082	1	0.58336
7	65599239	65599262	CRCP	3.76E-06	6.72E-11	1	1	1	1	1	1	1	1	1	0.25	1.4E-05	1	0.009472
12	104732900	104732910	TXNRD1	2.57E-05	0.038054	1	1	1	1	1	1	1	1	1	1	9.48E-06	0.051724	0.023887
17	57721884	57721911	CLTC	0.002231	0.289474	0.121212	1	1	1	1	1	1	1	1	1	0.15625	1	0.013717
11	94349639	94349651	PIWIL4	0.003946	2.62E-13	0.090909	1	1	1	1	1	1	0.073529	1	1	2.46E-07	1	1
22	41195142	41195154	SLC25A17	0.001015	4.41E-06	1	1	1	1	1	1	1	1	1	1	3.12E-06	1	0.001433
20	16352234	16352260	KIF16B	6.8E-05	0.049659	0.163647	1	0.147893	1	1	1	1	1	1	1	1.72E-06	1	1
3	25792762	25792774	NGLY1	1.8E-11	7.16E-06	1	1	1	1	1	1	1	1	0.125	1	9.17E-19	1	1
9	33364821	33364833	NFX1	1.06E-09	3.35E-07	0.098039	1	1	1	1	1	1	1	0.015873	1	2.2E-05	1	0.018861
7	23347410	23347421	MALSU1	4.67E-10	5.42E-09	1	1	1	1	1	1	1	1	0.016949	1	1.78E-07	1	0.012856
15	50152754	50152776	ATP8B4	0.00055	5.59E-12	1	1	1	0.057336	1	1	1	1	1	1	0.009736	1	0.000699
11	46685495	46685514	ATG13	0.003122	1.6E-07	0.111111	1	1	1	0.072434	1	1	1	1	1	1	1	1
1	46165875	46165886	IPP	6.98E-07	1.06E-06	0.135468	1	1	0.088838	1	1	1	0.104572	1	0.166667	1.49E-06	1	0.071339
8	86163230	86163250	CA13	0.122515	3.82E-08	1	1	1	1	1	1	1	0.017442	1	1	8.31E-08	1	1
2	55490745	55490761	MTIF2	4.77E-10	9.78E-06	0.502498	1	1	1	1	1	1	1	0.020833	1	4.72E-05	1	0.018187
X	107829820	107829831	COL4A5	0.000593	0.001281	1	1	1	1	1	1	1	1	1	1	0.017532	1	0.208829
9	111679747	111679766	IKBKAP	9.72E-06	3.82E-12	0.187022	1	0.173473	1	1	1	1	1	1	1	9.27E-14	0.054045	0.013
17	53124546	53124579	STXBP4	2.8E-05	0.418955	0.271068	1	1	0.303567	1	1	1	1	1	0.019608	3.26E-05	1	0.070159
2	20130970	20130984	WDR35	6.79E-12	5.39E-08	0.064516	1	1	1	1	1	1	1	0.030303	1	8.14E-09	0.02439	1
1	103354939	103354966	COL11A1	1.75E-11	0.018611	1	1	0.261538	1	1	1	1	1	1	1	0.041564	0.159261	0.073469
19	2514966	2515003	GNG7	0.180088	0.00056	1	1	1	1	1	1	1	1	1	1	0.033613	1	0.293543
20	45797749	45797770	EYA2	6.86E-06	1.28E-05	0.069767	1	1	0.056911	1	1	1	0.094287	1	1	3.54E-05	1	1
7	142247455	142247474	TRY2P(dist=275387),MTRNR2L6(dist=126657)	0.004677	0.000104	1	1	0.542319	1	1	1	0.061728	1	1	1	0.490909	1	0.187043
5	14481270	14481282	TRIO	0.070413	1.11E-06	1	1	1	1	0.158774	1	0.088889	0.000202	0.006536	0.05848	0.000675	0.298246	0.008024
13	39618366	39618405	NHLRC3	0.018399	0.002448	1	1	1	1	1	1	1	1	1	1	0.055344	1	0.008651
19	19989267	19989282	ZNF253	0.217639	0.035061	1	1	1	1	1	1	1	1	1	0.071429	0.037288	0.028571	1
9	84248203	84248240	TLE1	0.20902	0.003403	1	1	1	1	1	1	1	1	1	0.4	0.029362	1	0.54724
5	65310477	65310488	ERBB2IP	4.91E-08	0.000256	1	1	0.079208	1	1	1	1	1	1	1	8.93E-09	1	1
5	76707435	76707447	PDE8B	2.74E-11	1.32E-12	0.058824	1	1	1	1	1	1	0.002236	1	1	3.51E-09	0.054795	0.000142
5	137682312	137682324	FAM53C	0.007641	0.007738	1	1	1	1	1	1	1	1	1	1	0.130142	1	1
8	17882845	17882857	PCM1	9.16E-08	3.81E-11	0.074074	1	1	1	1	1	1	4.47E-05	1	1	6.81E-07	1	1
16	75665791	75665803	KARS	4.49E-08	6.1E-09	1	1	0.071429	0.078146	1	1	1	5.87E-05	1	1	0.003766	1	0.005302
6	31624922	31624937	APOM	1.72E-06	2.18E-11	1	1	1	1	1	1	1	6.45E-05	1	1	1.82E-05	1	1
4	184570723	184570735	RWDD4	1.42E-06	4.44E-06	0.3769	0.061728	1	0.245264	1	1	1	0.000123	0.143955	0.307692	1.97E-06	1	0.081032
4	128724672	128724734	HSPA4L	0.005096	3.06E-10	1	1	1	1	1	1	1	0.000198	1	1	3.25E-05	1	1
1	206904644	206904665	MAPKAPK2	0.000576	0.001668	0.065217	1	1	1	0.141614	1	1	0.000244	1	0.157895	0.00047	1	0.395335
13	37602245	37602257	SUPT20H	6.61E-12	9.26E-13	0.058824	1	1	1	1	1	1	0.000273	1	1	3E-11	1	1
11	1944050	1944071	TNNT3	0.000102	2.83E-05	1	1	1	1	1	1	1	0.000392	1	1	2.84E-05	1	1
1	204234196	204234213	PLEKHA6	0.010476	0.192182	1	1	0.322325	1	1	1	1	0.000398	1	0.0625	0.015278	1	0.048365
5	56546749	56546777	GPBP1	4.15E-05	2.01E-05	1	1	1	1	1	1	1	0.000746	0.060606	0.086957	0.000424	0.001642	0.292845
6	31646746	31646758	LY6G5C	0.004499	2.3E-08	0.245161	1	1	1	1	1	1	0.000747	1	1	9.32E-07	1	1
6	131999103	131999115	ENPP3	4.92E-11	3.8E-09	0.113122	1	1	1	1	1	1	0.001101	1	1	5.33E-11	1	3.96E-07
5	147475501	147475520	SPINK5	0.440678	1	1	1	0.189905	0.152786	1	1	1	0.001319	1	0.133333	0.334012	1	0.017203
15	50935484	50935496	TRPM7	0.002207	5.81E-05	1	1	0.143955	0.120618	1	1	1	0.001415	1	1	0.105263	1	0.234438
12	53685372	53685383	ESPL1	0.00769	9.72E-11	0.181818	1	1	1	1	1	1	0.002016	1	1	0.474747	1	0.018868
13	114514907	114514927	TMEM255B	0.004575	2.06E-09	1	1	1	1	1	1	1	0.002467	1	1	0.003331	0.039474	1
16	58200464	58200481	CSNK2A2	0.073191	0.03928	1	1	1	0.056928	1	1	1	0.002645	1	1	0.001458	1	1
16	4835778	4835794	SEPT12	2.03E-08	2.53E-10	1	1	1	1	1	1	1	0.002722	1	0.227273	3.01E-05	1	0.049925
1	227218085	227218097	CDC42BPA	5.28E-09	6.2E-07	0.268571	1	1	1	1	1	1	0.002757	1	0.333333	0.000155	0.12037	0.069241
3	113955055	113955069	ZNF80	1.58E-05	3.81E-11	0.071429	1	1	0.212566	1	1	1	0.002965	1	1	0.000319	1	0.092799
2	38527397	38527412	ATL2	0.40329	0.172414	1	1	1	1	1	1	1	0.003042	1	1	1	1	0.254178
13	101727043	101727094	NALCN	0.000369	0.000452	0.15	1	1	0.13772	1	1	0.07619	0.003058	1	1	0.041456	1	0.088921
8	7217010	7217023	ZNF705G	1.03E-08	4.22E-05	0.403313	1	0.45273	1	1	1	0.121555	0.003851	1	0.087719	1.65E-05	0.054348	0.00184
15	86278759	86278785	AKAP13	4.67E-10	1.74E-11	0.115294	1	1	1	1	1	1	0.004058	0.016949	1	7.41E-17	1	0.343075
19	16101139	16101166	OR10H4(dist=40371),LINC00661(dist=25278)	6.55E-05	0.060085	1	1	0.509752	0.282089	1	1	1	0.004618	1	1	0.086961	1	0.11535
1	224318148	224318164	FBXO28	1	0.338898	0.271429	1	0.405554	0.184542	1	1	1	0.005079	1	1	1	1	0.307781
10	99118165	99118176	RRP12	0.008024	3.71E-08	1	1	1	1	1	1	1	0.005202	1	1	7.81E-05	1	1
1	150201305	150201316	ANP32E	0.027967	0.031729	1	1	0.155102	0.063815	1	1	0.078788	0.005889	1	1	0.001878	1	0.439159
1	9770690	9770741	PIK3CD	0.000409	0.057876	1	1	1	1	1	1	1	0.006478	1	0.025974	0.000706	1	0.006872
17	31324395	31324414	SPACA3	0.016295	0.00769	1	1	1	1	1	1	1	0.007485	1	1	9.6E-05	1	0.071429
15	33256195	33256250	FMN1	0.000562	0.159297	1	1	0.161841	1	1	1	1	0.009091	1	0.031621	0.000376	1	0.003975
16	29809634	29809669	KIF22	0.359289	0.002291	0.395604	1	0.120704	1	1	1	1	0.00922	1	1	0.660313	1	0.056375
3	158537409	158537442	MFSD1	3.41E-08	1	1	1	1	1	0.162252	1	0.066646	0.011204	1	1	0.181818	1	1
11	114398627	114398638	NXPE1	0.000784	0.000742	0.193103	1	1	1	1	1	1	0.011282	1	0.007703	0.000375	0.365517	0.161376
15	52656713	52656733	MYO5A	0.005834	1.48E-09	0.079184	1	1	1	1	1	1	0.011765	1	1	0.004049	1	0.010106
18	196523	196552	USP14	2.03E-08	0.034783	0.083333	1	1	1	1	1	1	0.012987	1	1	0.009383	1	0.13115
13	25670801	25670809	PABPC3	1	1	1	1	0.198575	1	0.172252	1	1	0.014085	1	0.363636	0.282376	1	0.004114
10	105108810	105108824	PCGF6	2.88E-06	4.09E-08	0.068361	1	1	1	1	1	1	0.015152	1	1	4.67E-05	1	1
6	131211616	131211641	EPB41L2	5.12E-12	1.39E-09	1	1	0.402343	1	1	1	1	0.016055	1	1	7.58E-11	0.000821	0.019234
6	93967249	93967261	EPHA7	9.01E-06	1.39E-05	1	1	1	1	1	1	1	0.016529	1	1	1.05E-06	1	0.099936
11	10789205	10789217	CTR9	0.000226	2.07E-11	1	1	0.158976	1	1	1	1	0.017241	1	1	0.000182	1	0.059795
3	149613232	149613251	RNF13	3.12E-08	2.85E-07	0.130303	1	1	1	1	1	1	0.017472	1	1	2.12E-19	1	0.305042
12	21457514	21457525	SLCO1A2	0.000758	0.000268	1	1	1	0.177329	0.090275	1	1	0.017836	1	1	0.000218	1	0.375375
16	70350114	70350130	LOC100506083	0.000206	3.97E-07	1	1	1	1	1	1	1	0.019231	1	1	5.38E-06	1	0.072727
18	12963146	12963157	SEH1L	0.000225	0.000212	1	1	1	1	1	1	1	0.020209	1	1	0.124601	1	0.070203
11	63965534	63965549	STIP1	7.73E-06	1.48E-07	1	1	0.05814	1	1	1	1	0.020833	0.081081	1	5.64E-13	1	0.020148
4	6050724	6050736	JAKMIP1	6.4E-12	0.000499	0.093023	1	1	1	1	1	1	0.022727	0.06014	1	0.01796	1	1
7	140434574	140434645	BRAF	0.188327	0.000915	1	0.061762	1	0.111538	1	1	0.071406	0.022727	1	1	0.15579	1	0.09189
2	113310197	113310210	POLR1B	9.59E-10	6.36E-08	1	1	0.082819	1	1	1	0.099318	0.022797	1	0.003497	0.0015	1	0.011284
X	23930070	23930087	CXorf58	3.94E-07	6.57E-07	0.108764	1	1	1	1	1	1	0.02381	1	1	4.88E-08	1	0.369844
4	20555358	20555405	SLIT2	2.83E-08	0.001502	1	1	0.092965	1	1	1	1	0.02459	1	1	0.006335	0.084181	0.350902
8	42012568	42012580	AP3M2	3.49E-06	5.4E-08	1	1	1	1	1	1	1	0.025	1	1	1.45E-07	1	0.089841
3	196215451	196215463	RNF168	3.76E-05	8.8E-06	1	1	0.588446	1	1	1	1	0.027908	0.003659	0.117647	0.001984	0.149321	0.16947

1	42966090	42966103	PPCS(dist=27041),CCDC30(dist=34457)	5.91E-07	2.3E-07	1	1	1	1	1	1	1	0.028069	1	1	2.56E-07	1	1
3	179094712	179094723	MFN1	0.001871	1.5E-07	1	1	1	1	1	1	1	0.028571	1	1	5.7E-09	1	0.054348
4	185634171	185634196	CENPU	4.86E-11	2.74E-12	1	1	0.114391	0.106417	1	1	1	0.028986	0.071429	1	5.16E-13	1	0.011091
1	20005322	20005337	HTR6	0.421488	0.025815	1	1	1	0.076894	1	1	1	0.029412	1	1	1	1	0.121884
10	123996879	123996899	TACC2	0.000142	8.53E-08	1	1	1	1	1	1	1	0.029412	1	1	0.003438	1	0.002555
13	45589547	45589558	GPALPP1	1.34E-08	1.05E-12	0.074074	1	1	1	1	1	1	0.030864	1	1	8.84E-06	1	0.034351
2	152267897	152267923	RIF1	5.56E-06	3.11E-05	0.14976	0.064918	1	1	1	1	1	0.031371	1	0.090909	2.12E-14	1	1
11	8494831	8494856	STK33	8.94E-10	1.48E-08	1	1	1	1	1	1	1	0.032258	1	1	0.000362	1	1.37E-06
3	37369724	37369761	GOLGA4	0.000997	0.046002	0.187805	1	0.302725	1	1	1	1	0.03252	1	1	0.003036	1	0.133921
20	29614290	29614296	FRG1B	0.467532	1	1	1	0.262912	1	1	1	1	0.033708	1	1	1	1	1
10	79491504	79491535	KCNMA1(dist=93927),DLG5(dist=59014)	0.038274	0.006766	1	1	1	1	1	1	1	0.033898	1	1	0.090909	1	1
3	183493743	183493771	YEATS2	0.476209	1	1	1	1	1	1	1	1	0.034212	1	0.011905	0.083388	1	0.310159
1	205740426	205740441	RAB29	0.003626	2.5E-06	0.235294	1	1	1	1	1	0.091783	0.034783	1	1	0.249012	1	0.014401
1	236708022	236708034	LGALS8	0.000245	7.19E-10	0.222222	1	0.584073	0.248642	0.257165	1	1	0.035505	0.035714	1	0.012756	1	0.012469
1	92944314	92944351	GFI1	0.000954	1	1	1	1	1	1	1	1	0.036496	1	0.004449	0.049204	1	0.00043
7	94047903	94047914	COL1A2	1.96E-07	4.54E-06	0.142683	1	0.116883	0.178128	1	1	0.225015	0.037037	0.284058	0.066667	0.003319	1	0.02182
2	70070184	70070208	GMCL1	9.93E-11	0.015444	1	1	1	1	1	1	1	0.038462	1	1	2.91E-10	1	0.114032
16	58557209	58557220	CNOT1	1.63E-05	0.001961	0.051724	1	1	0.115484	0.123564	1	1	0.040323	0.054545	0.370779	4.63E-06	1	0.084719
6	90491071	90491082	MDN1	1.14E-05	1.73E-08	1	1	1	1	1	1	1	0.040404	1	1	0.002935	1	0.065693
3	53531142	53531165	CACNA1D	0.050219	2.99E-07	1	1	1	1	1	1	1	0.040816	1	1	1.07E-07	1	0.027778
7	72667735	72667760	NCF1B(dist=17756),NSUN5(dist=48753)	2.28E-08	0.044392	0.57247	1	1	1	1	1	1	0.041881	1	1	0.26697	1	0.000955
22	32841691	32841723	BPIFC	0.046059	1	1	1	1	1	1	1	1	0.041958	1	1	0.127483	1	1
2	198264715	198264732	SF3B1	0.014936	0.00012	0.083333	1	1	1	1	1	1	0.042857	1	1	5.41E-05	1	0.094508
2	170678569	170678588	METTL5	0.000928	5.23E-05	1	1	1	1	1	1	1	0.043478	1	1	0.263158	0.051724	1
11	85421989	85422001	SYTL2	1.09E-10	2.55E-12	0.057143	1	1	1	1	1	1	0.044248	1	1	0.009561	0.052632	0.04318
22	38917543	38917608	DMC1	0.16314	1	1	1	1	1	1	1	0.06473	0.045455	1	1	0.186441	1	0.238061
3	5022981	5022992	BHLHE40	0.568895	0.656805	1	1	1	1	1	1	1	0.045726	1	0.047619	1	1	0.088314
12	9007492	9007509	A2ML1	1.52E-05	0.000964	0.103158	1	1	1	1	1	1	0.046296	1	1	2.07E-08	0.044776	0.02066
13	113908908	113908936	CUL4A	6.68E-05	0.000245	0.075	1	1	1	1	1	1	0.046667	1	1	9.21E-06	1	0.122953
6	30545853	30545864	ABCF1	1.39E-09	7.15E-13	0.178197	1	1	1	1	1	1	0.047619	1	1	1.12E-06	1	0.066667
12	72023336	72023373	ZFC3H1	2.31E-06	0.168339	1	1	1	1	1	1	1	0.048041	1	1	0.056215	1	0.012911
6	83842074	83842105	DOPEY1	0.168536	0.00433	1	1	1	1	1	1	1	0.04902	1	0.3125	0.241935	1	1
5	74226391	74226403	FAM169A(dist=63728),GCNT4(dist=96886)	6.86E-05	1.13E-12	1	1	1	1	1	1	1	1	0.000452	1	5.85E-05	0.033333	1
16	3350676	3350699	TIGD7	5.2E-09	1.19E-11	0.153627	1	1	1	1	1	1	1	0.000673	1	1.46E-12	0.035294	1
10	112211000	112211025	SMNDC1(dist=146293),DUSP5(dist=46600)	2.05E-07	9.23E-08	0.1	1	1	1	1	1	1	1	0.002449	1	0.006536	1	0.051606
2	230705516	230705530	TRIP12	2.66E-10	5.89E-10	1	1	1	0.084472	1	1	1	0.055036	0.010101	0.238095	6.6E-15	1	0.012519
12	108104315	108104351	PWP1	0.1901	0.241379	1	1	1	1	1	1	1	1	0.0125	1	0.192308	1	0.0625
15	76191743	76191755	UBE2Q2	1.47E-10	1.1E-05	0.112605	1	1	1	1	1	1	1	0.012821	1	1.57E-06	1	1
3	93754080	93754099	ARL13B	1.36E-09	0.000103	0.071429	1	1	1	1	1	1	1	0.013333	1	9.06E-15	0.021739	1
7	155099925	155099936	INSIG1	2.45E-05	9.15E-11	1	1	1	1	1	1	1	1	0.013889	1	0.000102	1	1
10	104449572	104449619	ARL3	2.02E-09	0.008969	1	1	1	1	1	1	1	1	0.014085	1	3.31E-05	1	0.070988
20	29449706	29449717	NONE(dist=NONE),FRG1B(dist=162162)	2.23E-06	1	1	1	1	1	1	1	1	1	0.014706	1	0.000287	1	0.008534
13	45781539	45781550	GTF2F2	8.04E-12	3.95E-09	1	1	1	1	1	1	1	1	0.014925	1	1.95E-07	0.022727	0.005836
7	120590802	120590830	ING3	2.78E-07	1.92E-05	1	1	1	1	1	1	1	1	0.015152	1	9.91E-08	0.041096	1
11	27412757	27412806	LGR4	0.000123	0.415653	0.157591	1	1	1	1	1	1	1	0.015625	1	1.44E-06	0.08216	0.037211
20	7976762	7976773	TMX4	1.1E-08	8.24E-07	0.057143	1	1	1	1	1	1	1	0.015625	1	1.17E-09	1	0.008333
10	88753099	88753110	AGAP11	2.38E-05	1.66E-07	1	1	0.166667	1	1	1	1	0.078947	0.015873	1	0.24	1	1
2	37152389	37152408	STRN	1.41E-06	1.89E-09	0.052632	1	1	1	1	1	1	1	0.016129	1	0.000107	1	1
9	123886190	123886202	CNTRL	1.16E-06	2.55E-05	0.065217	1	0.240285	1	1	1	1	1	0.016129	1	5.07E-08	1	0.024342
16	15141966	15141977	NTAN1,PDXDC1	0.288196	0.000478	1	1	1	1	1	1	1	0.25	0.016949	1	0.00362	1	1
7	56052489	56052500	GBAS	0.004762	0.004516	0.051724	1	1	1	1	1	1	1	0.016949	1	0.024085	1	0.246825
5	72795055	72795066	BTF3	5.57E-07	3.48E-07	1	1	1	1	1	1	1	1	0.017241	0.294118	8.13E-09	0.007974	0.071642
1	86241399	86241410	COL24A1	0.000262	9.31E-07	1	1	1	1	1	1	1	1	0.018182	1	0.000982	1	1
13	37579999	37580023	EXOSC8	2.59E-05	0.004449	1	1	1	1	1	1	1	1	0.018182	0.230769	1.68E-09	1	0.005111
2	211521401	211521434	CPS1	9.1E-06	0.063879	0.051282	1	1	1	1	1	1	1	0.019231	1	1.5E-11	1	1
21	30319921	30319949	LTN1	0.000611	2.78E-06	1	1	1	1	1	1	1	1	0.019608	1	0.000259	1	1
1	223980973	223980985	TP53BP2	6.64E-06	8.27E-12	1	1	1	1	1	1	1	1	0.02	1	4.49E-09	1	0.089655
1	23664147	23664161	HNRNPR	3.04E-10	4.25E-09	0.08951	1	1	1	0.066646	1	1	1	0.021277	1	5.54E-09	1	1
16	76555005	76555027	CNTNAP4	0.044132	0.00037	0.157895	1	1	1	1	1	1	1	0.021277	1	0.297872	1	0.049628
19	20500444	20500464	ZNF486(dist=189145),MIR1270(dist=9617)	0.186885	0.287027	1	1	0.143955	1	1	1	1	1	0.021277	1	1	1	0.05618
1	223962513	223962524	CAPN2	0.034028	1.8E-11	1	1	1	1	1	1	1	1	0.021739	1	2.14E-06	1	1
3	160137363	160137375	SMC4	5.2E-05	7.43E-06	0.243742	1	1	0.108015	1	1	1	1	0.021739	1	1.84E-05	1	0.168026
7	35288458	35288475	TBX20	0.184839	0.000171	1	1	1	1	1	1	1	1	0.022222	1	0.035048	1	1
12	107393931	107393943	CRY1	5.27E-10	2.12E-09	1	1	1	1	1	1	1	1	0.022727	1	1.46E-11	1	0.061224
19	19650372	19650398	CILP2	0.292399	1.61E-05	1	1	1	1	1	1	1	1	0.023256	1	0.444444	1	1
3	140675348	140675367	SLC25A36	4.08E-06	7.22E-13	1	1	0.093242	1	1	1	0.060388	1	0.023529	1	7.92E-08	1	0.265865
1	93159821	93159835	EVI5	4.8E-09	4.47E-09	1	1	1	1	1	1	1	0.065359	0.02439	1	5.58E-11	1	8.33E-06
8	32505909	32505926	NRG1	0.01718	0.284958	1	1	1	1	1	1	1	1	0.02439	1	0.002066	1	0.013198
1	121116638	121116657	SRGAP2-AS1,SRGAP2D	1.31E-06	0.077154	0.055556	1	1	1	1	1	1	1	0.025	1	1.14E-05	0.05	0.067511
13	37580343	37580361	EXOSC8	9.9E-08	7.51E-05	0.114286	1	1	1	1	1	1	1	0.025316	1	0.004068	0.022222	1
5	63802636	63802672	RGS7BP	0.001447	0.035522	1	1	1	1	1	1	1	1	0.025641	1	0.000215	1	1
1	150203082	150203098	ANP32E	9.31E-10	5.42E-12	0.166387	1	1	1	1	1	1	1	0.026316	1	0.025641	1	0.00554
10	18803851	18803862	CACNB2	1.7E-10	4.82E-07	1	1	1	1	1	1	1	1	0.026316	1	2.63E-11	1	0.080717
8	68062171	68062207	CSPP1	0.002884	6.26E-05	1	1	1	1	1	1	1	1	0.027397	1	0.000608	1	1
15	35185808	35185855	AQR	0.059486	0.360804	0.061538	1	1	1	1	1	1	1	0.027778	1	0.059707	1	0.005639
8	22175821	22175848	PIWIL2	1.14E-05	0.003571	1	1	1	1	1	1	1	1	0.028571	1	0.012861	0.000224	0.10032
4	74442242	74442253	RASSF6	0.000494	6.54E-09	1	1	1	1	1	1	1	1	0.028571	1	0.002751	1	1
9	85607951	85607962	RASEF	0.002493	3.23E-06	1	1	0.218033	1	1	1	1	1	0.028986	1	0.000113	1	0.135292
5	150051068	150051088	MYOZ3	0.00012	0.0049	1	1	1	1	1	1	1	1	0.029412	1	1	1	1
21	37626051	37626062	DOPEY2	0.000274	7.18E-06	1	1	1	1	1	1	1	0.071408	0.029851	1	1	1	0.131266
9	36671219	36671230	MELK	1.78E-10	1.33E-08	1	1	1	1	1	1	1	1	0.029851	1	8.56E-12	1	0.057627
1	213341188	213341199	RPS6KC1	1.39E-06	1.43E-06	1	1	0.081967	1	1	1	1	1	0.030303	1	8.48E-07	1	0.022401
19	16472811	16472822	EPS15L1	6.24E-06	0.282784	0.204678	1	1	1	1	1	1	1	0.030303	1	0.026316	0.036145	1
3	137907220	137907259	ARMC8	1.77E-07	0.000234	1	1	1	1	1	1	1	1	0.030303	1	2.65E-05	0.0125	1
6	4052172	4052184	PRPF4B	2.48E-07	2.59E-10	0.103841	1	1	1	1	1	1	1	0.030769	0.154412	1.61E-10	0.108345	0.017956
4	85647941	85647967	WDFY3	0.01358	1.27E-06	1	1	1	1	1	1	1	1	0.03125	1	2.78E-14	1	0.386479
1	35486072	35486084	ZMYM6	0.007049	2.17E-08	0.124884	1	0.156667	0.075269	0.097969	1	1	0.154743	0.031746	0.333333	4.18E-07	0.098305	0.003288
10	123310733	123310744	FGFR2	0.000113	5.57E-13	1	1	1	1	1	1	1	1	0.032258	1	9.38E-06	1	0.000518
2	87127887	87127910	ANAPC1P1(dist=5722),RGPD2(dist=13025)	7.82E-07	0.005029	0.066667	1	1	1	1	1	1	1	0.033333	1	0.001665	1	0.061947
12	117365809	117365820	FBXW8	0.000276	1.8E-10	0.052632	1	1	1	1	1	1	1	0.033333	0.142857	3.72E-10	1	0.018669
8	101105741	101105760	RGS22	1.61E-06	2.89E-06	0.199507	1	1	1	1	1	0.052973	1	0.033333	1	3.9E-07	1	1
X	70767658	70767687	BCYRN1	8.42E-10	7.15E-08	1	1	1	1	1	1	1	1	0.033898	1	0.027282	0.043011	0.010481
1	121306721	121306745	EMBP1	3.49E-07	5.4E-05	0.125	1	1	1	1	1	1	1	0.034483	1	0.021408	1	0.07109
2	190323461	190323472	WDR75	2.36E-06	3.29E-07	1	1	1	1	1	1	1	1	0.035714	1	2.01E-07	0.028169	0.051546
X	15822390	15822409	ZRSR2	0.000333	5.38E-13	0.058824	1	1	1	1	1	1	1	0.035714	1	1.03E-07	1	1
16	56704955	56704966	MT1H	5.3E-05	7.61E-06	1	1	1	1	1	1	1	1	0.037736	1	0.000373	0.042857	0.028431
7	36580178	36580209	AOAH	0.028127	1	1	1	1	1	1	1	1	1	0.037736	1	0.026718	1	0.137981
7	87516629	87516640	DBF4	5.45E-09	3.63E-08	1	1	1	1	1	1	1	1	0.037736	1	1.12E-13	1	0.000237
5	40767498	40767510	PRKAA1	3.3E-10	1.18E-07	0.068966	1	0.072072	1	0.138319	1	1	1	0.038462	1	3.75E-08	0.046512	1
7	116381108	116381138	MET	4.46E-07	0.077279	0.061538	1	0.0625	1	1	1	1	1	0.04	1	1.45E-07	1	0.121831
3	125651602	125651614	ALG1L	3.07E-10	8.61E-07	0.124884	1	1	1	1	1	1	1	0.042857	0.019608	1.42E-09	1	0.020603
5	89977095	89977106	GPR98	2.6E-06	2.08E-07	0.076923	1	0.098592	1	1	1	1	0.069444	0.043478	1	0.000125	0.002221	0.031054
9	114905936	114905962	MIR3134	0.001183	0.003704	0.058824	1	1	1	1	1	1	1	0.045455	1	0.001553	1	1
8	11994625	11994638	FAM66D	1	0.026437	1	1	1	1	1	1	1	1	0.047619	1	1	1	1
5	128359297	128359309	SLC27A6	1.85E-10	5.11E-10	0.061265	1	0.271596	0.078095	1	1	1	0.319745	0.047619	1	0.002651	1	0.062758
9	78907125	78907145	PCSK5	0.036474	4.8E-07	0.052632	1	0.566081	0.055118	1	1	0.087879	1	0.048387	1	0.000148	1	0.014286
12	54963479	54963504	PDE1B	2.82E-10	0.000517	0.057143	1	1	1	1	1	1	1	0.05	1	3.91E-10	1	0.000131
3	47814184	47814204	SMARCC1	0.000607	0.069265	1	1	1	1	1	1	1	1	0.05	1	4.17E-05	1	0.022395
3	189690816	189690828	LEPREL1	1.93E-06	2.75E-08	0.138274	1	1	1	0.118312	1	1	1	1	0.001471	2.14E-09	0.085678	0.093083
12	122097043	122097074	MORN3	0.002887	0.003335	1	1	0.321573	1	1	1	1	1	1	0.001634	0.002633	0.096774	1
X	52706249	52706291	SSX7(dist=22299),SSX2B(dist=19655)	0.000453	1	0.054054	1	0.322853	1	1	1	1	1	1	0.003096	0.000733	1	1.04E-06
2	112725684	112725699	MERTK	0.005408	0.024027	1	1	1	1	1	1	1	1	1	0.005882	0.016076	1	1
11	26692594	26692629	SLC5A12	0.007128	0.001926	1	1	1	1	1	1	0.080612	1	1	0.006303	6.57E-05	1	0.551777
17	28811658	28811669	GOSR1	2.9E-09	0.000163	0.146154	1	0.172078	0.134649	1	1	1	1	1	0.006993	1.94E-12	0.155102	0.142111
4	88231324	88231350	HSD17B13	1.45E-05	1.77E-08	0.079758	1	0.057362	1	1	1	1	1	1	0.008599	1.12E-05	1	0.006591
1	236703817	236703841	LGALS8	1.85E-05	0.003286	1	1	1	0.368277	1	1	1	0.188934	1	0.009524	0.000438	1	0.260696
10	21177138	21177164	NEBL	0.096852	0.012303	1	1	1	0.170071	1	1	0.163265	0.335354	1	0.009524	0.001193	0.11103	0.174933
5	157180930	157180952	LSM11	2.81E-08	0.000392	1	1	0.067212	1	1	1	1	0.053684	1	0.012987	9.39E-07	1	0.144141
5	122359502	122359533	PPIC	3.96E-09	1.6E-10	0.050851	1	0.306011	1	1	1	1	1	1	0.013932	1.57E-06	1	0.001515
12	76461257	76461268	NAP1L1	5.58E-06	5.87E-09	1	1	1	1	0.270163	1	1	0.158676	1	0.015152	0.005035	0.335227	0.168368
4	110606384	110606404	CCDC109B	0.06572	0.004992	1	1	1	1	0.061289	1	1	0.166667	0.119048	0.015152	0.017702	1	0.162315
4	155469959	155469971	PLRG1	4.71E-05	8.5E-09	1	1	1	0.299605	1	1	1	1	1	0.015152	0.037918	1	0.046169
3	47143087	47143124	SETD2	0.000117	1	1	1	1	1	1	1	1	1	1	0.015217	0.053197	1	0.0245
3	66434357	66434397	LRIG1	0.038061	0.156219	1	1	1	1	1	1	1	1	1	0.017094	0.180765	1	1
1	111059812	111059831	KCNA10	0.042645	1	0.176136	1	0.170071	1	1	1	1	0.211051	1	0.017544	0.009288	1	0.128819
11	60778650	60778677	CD6	0.428703	0.177778	1	1	0.384729	1	1	1	1	1	1	0.018462	0.005441	1	0.092429
12	8807982	8807993	MFAP5	2.37E-06	1.15E-09	1	1	1	1	1	1	1	1	0.074074	0.019608	9.76E-13	1	0.068674
2	15319070	15319084	NBAS	4.18E-05	8.19E-09	0.237011	0.056486	1	1	1	1	1	0.264117	1	0.021978	1E-09	1	1
20	52188386	52188410	ZNF217	0.004767	2.16E-06	0.221538	1	1	1	1	1	1	1	1	0.022059	0.001458	1	0.149967
17	15643372	15643392	TBC1D26	1	9.8E-05	1	1	0.547847	0.272809	1	0.061404	1	0.39709	1	0.024242	0.037971	0.016667	0.054083
3	170857167	170857204	TNIK	0.003627	0.11769	1	1	1	1	1	1	1	1	1	0.025974	0.051371	1	0.503909
4	88532182	88532215	DSPP	0.062586	0.383607	0.393987	1	1	1	0.061211	1	1	1	1	0.025974	6.45E-11	1	0.362219
10	106974123	106974140	SORCS3	0.03113	0.000316	1	1	0.260729	0.152709	1	1	0.060364	1	1	0.028571	0.099819	1	0.046283
1	50956053	50956192	FAF1	0.025998	0.227012	1	1	0.257449	0.37385	1	1	1	1	1	0.030702	0.129171	1	0.043431
12	9021018	9021072	A2ML1	0.214886	0.008322	0.319611	1	1	1	1	1	1	1	1	0.031992	0.084687	1	0.055674
19	21558015	21558037	ZNF738	0.003569	0.001028	0.311594	1	0.38447	0.233715	1	1	0.173514	1	1	0.032967	0.00706	1	0.030385
4	110268615	110268631	COL25A1(dist=44816),SEC24B-AS1(dist=82488)	2.4E-11	4.45E-09	0.166317	1	0.235065	1	1	1	1	1	1	0.033333	8.62E-14	1	0.02034
8	73983976	73984004	SBSPON	1.18E-06	0.000112	1	1	1	1	1	1	1	1	0.1	0.039216	7.46E-07	1	0.439757
9	79897218	79897232	VPS13A	7.12E-07	2.16E-12	0.068493	1	0.148264	1	1	1	1	1	0.077647	0.039216	2.11E-09	1	1
9	117803175	117803204	TNC	2.39E-05	0.073708	1	1	0.135505	0.354245	1	1	1	0.131508	1	0.042735	0.00296	1	0.057683
20	44512744	44512783	ZSWIM1	0.077973	0.131313	0.046512	1	1	1	1	1	1	1	1	0.047619	0.000291	1	1

17	4906146	4906166	KIF1C	4.03E-05	8.36E-05	1	1	0.31543	1	1	1	1	1	0.133333	0.047619	0.136785	0.213505	0.370843
15	30875074	30875089	ULK4P1,ULK4P2	4.62E-05	5.72E-13	0.231061	1	1	1	1	1	1	0.176043	1	1	2.23E-26	1	0.322421
9	77457028	77457044	TRPM6	1.56E-08	1.29E-06	1	1	1	1	1	1	1	1	1	1	5.91E-20	1	0.000348
9	88571253	88571273	NAA35	7.47E-09	8.81E-12	0.076923	1	1	1	1	1	1	1	1	1	1.26E-18	1	0.003268
1	36475026	36475037	AGO3	2.8E-10	9.53E-11	1	1	1	1	1	1	1	1	1	1	2.6E-17	0.027027	1
4	3938949	3938968	ADRA2C(dist=168696),FAM86EP(dist=4701)	0.000338	0.031842	1	1	1	1	1	1	1	1	1	1	1.26E-16	1	0.16591
5	74872797	74872809	POLK	1.17E-07	1.59E-09	1	1	0.081818	1	1	1	1	1	1	1	1.56E-16	1	1
5	159839530	159839545	SLU7	8.59E-12	0.041121	0.147905	1	1	1	1	1	1	1	1	1	2.17E-16	1	0.118874
5	68680781	68680799	RAD17	6.04E-07	2.1E-06	0.050633	1	1	1	1	1	1	0.055556	1	1	7.69E-16	1	0.039732
3	122629656	122629675	SEMA5B	0.002974	1.02E-05	1	1	1	1	1	1	1	1	1	1	9.54E-16	1	0.086538
5	68550348	68550367	CDK7	9.99E-08	0.001633	0.096914	1	1	1	1	1	1	1	1	1	1.4E-15	1	1
16	31388634	31388654	ITGAX	2.02E-10	1.83E-09	1	1	1	1	1	1	1	1	1	1	2.66E-15	1	0.153221
20	50286484	50286496	ATP9A	1.2E-11	6.64E-06	1	1	1	0.195707	0.068947	1	1	1	1	0.190476	3.6E-15	1	0.003344
11	102587154	102587179	MMP8	2.62E-08	1.95E-06	0.076923	1	1	1	1	1	1	1	1	1	4.11E-15	1	0.022332
3	186479586	186479604	KNG1(dist=17387),EIF4A2(dist=21757)	0.001335	3.7E-07	1	1	1	1	1	1	1	1	1	1	5.23E-15	1	1
3	129811872	129811898	ALG1L2	0.003344	1	1	1	1	0.0625	1	1	1	1	1	1	9.94E-15	0.030612	1
19	41062902	41062914	SPTBN4	5.38E-09	1.09E-08	0.057692	1	1	1	1	1	1	0.238507	0.1875	1	1.33E-14	0.107306	0.220044
14	50280815	50280836	NEMF	1.83E-07	2.54E-09	0.051948	1	1	1	1	1	1	1	1	1	6.9E-14	1	0.049861
X	153906365	153906401	GAB3	2.41E-10	1.1E-09	0.056338	1	1	1	1	1	1	1	1	1	1.29E-13	1	0.016458
11	9459592	9459625	IPO7	5.17E-05	1.69E-06	1	1	0.297504	1	1	1	1	1	1	1	1.3E-13	1	0.034286
4	103237003	103237014	SLC39A8	2.25E-10	2.06E-09	0.096341	1	1	1	0.051805	1	1	0.077267	1	1	2.5E-13	1	0.001109
17	59001879	59001898	BCAS3	2.68E-11	4.46E-05	0.096914	1	1	1	1	1	1	1	1	1	3.54E-13	1	0.022221
12	121613113	121613133	P2RX7	0.002044	0.000202	0.071429	1	1	1	1	1	1	1	1	1	6.65E-13	0.072054	0.060872
2	202073748	202073787	CASP10	3.2E-10	4.11E-07	1	1	1	1	1	1	1	1	1	1	6.72E-13	1	0.004219
5	64629824	64629864	ADAMTS6	1	1	1	1	1	1	1	1	1	1	1	1	1.93E-12	1	1
5	37392279	37392306	WDR70	0.000165	9.44E-08	1	1	1	1	1	1	1	1	1	1	2.43E-12	1	1
5	125809072	125809084	GRAMD3	1.88E-08	6.51E-09	0.076923	1	0.248712	1	1	1	1	1	1	1	3.6E-12	1	1
20	47770443	47770478	STAU1	2.88E-05	4.54E-06	1	1	1	1	1	1	1	1	1	1	5.2E-12	1	0.00036
1	11187618	11187628	MTOR	0.029057	2.33E-11	0.066667	1	1	1	1	1	1	0.125	1	1	5.5E-12	1	0.113924
X	135958875	135958891	RBMX	0.000318	4.4E-08	0.06	1	1	1	1	1	1	1	1	1	5.94E-12	0.055556	1
11	121175278	121175289	SC5D	9.71E-05	3.44E-11	0.12234	1	0.194524	1	1	1	1	1	1	0.166667	6.78E-12	0.277778	0.407909
12	69119604	69119635	NUP107	7.82E-05	0.00059	0.068493	1	1	1	1	1	1	1	1	1	6.84E-12	0.030303	0.126539
2	43054028	43054051	HAAO(dist=34277),LOC102723854(dist=200941)	0.00033	0.00149	0.122024	1	1	1	1	1	1	1	1	0.310345	1.09E-11	1	0.042175
3	148583231	148583243	CPA3	5.13E-09	1.48E-11	0.092262	1	0.051948	1	1	1	1	0.117196	1	1	1.13E-11	1	0.010962
4	177100754	177100775	WDR17	8.53E-11	2.28E-11	1	1	1	1	1	1	1	1	1	0.190476	1.24E-11	1	1
3	15080602	15080612	NR2C2	1.71E-10	1.69E-06	0.233343	1	1	0.138684	1	1	1	0.072289	1	1	1.48E-11	0.031746	0.030572
X	110406671	110406683	PAK3	2.02E-11	1.66E-09	0.107071	1	0.058824	1	0.05775	1	1	1	1	1	1.97E-11	0.056338	0.001585
13	114240056	114240102	TFDP1	2.03E-10	8.58E-12	1	1	1	1	1	1	1	1	1	0.166667	2.77E-11	0.033333	2.79E-05
1	147411014	147411028	GPR89B	5.36E-08	0.311459	0.132086	1	1	1	1	1	1	1	1	1	3.26E-11	1	0.001425
20	56089869	56089882	CTCFL	0.00016	4.02E-07	1	1	0.052768	0.208791	0.151898	1	1	1	1	0.357143	3.4E-11	0.094077	0.0044
19	49657710	49657753	HRC	0.013264	1	1	1	0.384729	1	1	0.067227	1	1	1	1	3.54E-11	0.339516	0.028122
12	7521563	7521588	CD163L1	5.58E-12	1.39E-07	1	1	1	1	1	1	1	1	1	1	5.43E-11	1	0.117376
5	151784731	151784768	NMUR2	1.01E-09	4.51E-08	0.074627	1	1	1	1	1	1	1	1	1	6.63E-11	1	0.113204
2	209049812	209049831	C2orf80	4.24E-06	2.03E-11	1	1	1	1	1	1	1	1	1	1	6.79E-11	0.068966	0.179905
7	128413997	128414041	OPN1SW	2.88E-06	7.66E-06	1	1	1	1	1	1	1	1	1	1	0.074074	2.8E-05	1
6	100901513	100901552	SIM1	0.000712	0.001909	0.055556	0.056526	1	0.068356	1	1	1	1	1	1	0.148983	0.000446	1
2	158390343	158390363	ACVR1C	1.71E-10	9.54E-06	1	1	1	1	1	1	1	1	1	1	0.011224	0.001316	1
8	42829373	42829384	HOOK3	0.000226	1.56E-10	1	1	1	1	1	1	1	1	1	1	6.02E-07	0.002283	0.084337
5	133707247	133707259	UBE2B	0.160528	0.029629	1	1	1	1	1	1	1	1	1	0.125	0.003122	0.002971	1
1	113196179	113196217	CAPZA1	0.155434	9.6E-08	0.063492	1	1	1	1	1	1	1	1	1	2.57E-08	0.00752	0.120366
3	73440108	73440119	PDZRN3	3.75E-08	9.23E-08	0.321524	1	0.093363	1	0.157582	1	0.121555	1	1	0.125	5.86E-08	0.00895	0.125158
6	31765848	31765875	LSM2	0.000165	0.122915	1	1	1	1	1	1	1	1	1	1	0.002311	0.012195	1
12	39716416	39716427	KIF21A	6.38E-07	2.95E-11	1	1	1	1	1	1	1	1	1	1	0.003045	0.014493	0.004254
1	205589975	205589994	ELK4	1.05E-06	2.39E-07	0.171123	1	0.257464	1	1	1	1	1	1	1	4.45E-08	0.015625	0.067692
8	17137986	17137997	VPS37A	0.000553	0.000922	1	1	1	1	1	1	1	1	1	1	0.004896	0.016393	1
3	193272422	193272477	ATP13A4-AS1	0.048316	1	0.210521	1	1	1	1	1	1	1	1	0.052632	0.002508	0.018868	0.408661
4	108824275	108824292	LOC101929595	0.000803	0.000415	1	1	1	1	1	1	1	1	1	1	0.048123	0.018868	1
1	62175139	62175150	TM2D1	6.32E-05	2.35E-06	0.088889	1	1	1	1	1	1	1	1	1	5.25E-07	0.019231	0.088235
10	115370113	115370147	NRAP	1.3E-05	0.080214	0.092308	1	1	1	1	1	1	1	1	1	1.11E-06	0.019231	1
X	19018109	19018130	GPR64	9.91E-06	8.21E-05	1	1	1	1	1	1	1	1	1	1	1.97E-05	0.020408	1
13	20277278	20277289	PSPC1	0.075731	3.74E-05	1	1	1	1	1	1	1	1	1	1	2.19E-06	0.021739	0.013628
12	42717716	42717746	ZCRB1	1.33E-09	9.09E-05	0.163323	1	1	1	1	1	1	1	1	1	0.000587	0.021978	0.062827
6	43021903	43021943	MRPL2	0.070444	2.96E-05	1	1	1	1	1	1	1	0.054536	1	1	0.176471	0.024691	1
10	104140751	104140763	GBF1	4.77E-05	1.51E-07	1	1	1	1	1	1	1	1	1	1	0.002597	0.025316	1
7	73479946	73479965	ELN	0.000231	0.000198	0.088889	1	1	1	1	1	1	1	1	1	0.003184	0.025974	1
1	33478585	33478604	AK2	0.494382	1	1	1	1	1	1	1	1	1	1	1	1	0.026316	1
1	52306188	52306207	NRD1	7.88E-05	3.11E-06	1	1	1	1	1	1	1	1	1	1	0.080016	0.027027	0.130264
15	50581869	50581882	GABPB1	6.83E-10	1.25E-09	1	1	1	1	1	1	1	1	1	1	7.04E-08	0.027273	0.04712
15	59974525	59974539	BNIP2	1.41E-10	1.35E-09	1	1	1	1	1	1	1	1	1	1	7.17E-09	0.027778	7.62E-06
21	48064203	48064243	PRMT2	0.003054	0.013015	0.15625	1	1	1	1	1	1	0.070175	1	1	0.047408	0.027778	0.102703
7	99447339	99447376	CYP3A43	8.66E-06	0.001167	1	1	1	1	1	1	1	1	1	1	1.6E-08	0.027778	0.001763
4	148574961	148574972	PRMT9	0.000417	4.27E-05	1	1	1	1	1	1	1	1	1	1	1.37E-06	0.028571	0.01359
7	151932761	151932772	KMT2C	5.31E-07	7.04E-09	0.047619	1	0.206931	1	1	1	1	1	1	1	7.44E-06	0.028571	1
12	93195359	93195370	EEA1	0.003191	1.58E-07	1	1	1	1	1	1	1	1	1	1	4.22E-05	0.028986	3.75E-05
1	111890233	111890280	PIFO	2.57E-07	6.01E-07	1	1	0.128431	1	1	1	1	1	1	1	0.023474	0.029126	0.063415
10	5762766	5762777	FAM208B	5.57E-05	0.035784	0.25946	1	1	1	1	1	1	1	1	1	9.46E-05	0.029412	1
X	48661515	48661526	HDAC6	1.17E-05	0.000508	1	1	1	1	1	1	1	1	1	0.210526	7.73E-09	0.029412	0.011808
5	168043288	168043299	PANK3(dist=36674),SLIT3(dist=45439)	7.4E-05	4.04E-07	1	1	1	1	1	1	1	1	1	1	0.023715	0.029851	1
3	101373724	101373737	ZBTB11	2.93E-08	4.69E-10	1	1	1	1	1	1	1	1	1	1	3.16E-05	0.031579	0.056338
10	99197102	99197124	EXOSC1	6.07E-10	1.22E-09	1	1	1	1	1	1	1	1	1	1	9.49E-06	0.031746	0.000238
3	45042934	45042947	EXOSC7	9.24E-12	0.000331	1	1	1	1	0.096607	1	1	1	1	1	0.000117	0.031746	1
16	29906499	29906521	SEZ6L2	0.020743	5.34E-06	1	1	1	1	1	1	1	1	1	1	0.002704	0.031915	0.291778
1	28817355	28817375	PHACTR4	1.95E-05	0.00625	1	1	1	1	1	1	1	1	1	1	1.08E-06	0.033333	0.050378
19	54210878	54210912	MIR520C	1.81E-05	0.033937	1	1	1	1	1	1	1	1	1	1	0.084027	0.033333	0.007449
4	100048344	100048355	LOC100507053	3.89E-05	9.12E-07	0.058824	1	1	1	1	1	1	1	1	1	0.00134	0.033898	0.087379
1	47014813	47014833	MKNK1-AS1	0.005648	1	1	1	1	1	1	1	1	1	1	1	0.367956	0.034483	0.111559
17	67516340	67516373	MAP2K6	2.53E-09	5.44E-05	1	1	1	1	1	1	1	1	1	1	1.78E-05	0.034483	1
6	144837920	144837942	UTRN	4.59E-06	9.72E-06	1	1	1	1	1	1	1	1	1	1	0.00748	0.035714	1
18	14225638	14225666	ANKRD20A5P	1.25E-08	0.000325	1	1	1	1	1	1	1	1	1	1	1	0.036585	1
1	184041946	184041957	TSEN15	2.2E-05	5.91E-07	0.058824	1	1	1	1	1	1	1	1	1	2.08E-08	0.037037	0.145249
16	75652400	75652424	ADAT1	5E-08	0.039829	1	1	1	1	1	1	1	1	1	1	1.44E-10	0.037037	0.016727
22	17127506	17127517	TPTEP1	3.04E-07	7.15E-12	0.181818	1	1	1	1	1	1	1	1	1	0.064171	0.038462	0.025712
19	39232968	39232990	CAPN12	0.000702	0.192308	1	1	1	1	1	1	1	1	1	1	0.026667	0.04	1
2	113138227	113138249	RGPD5,RGPD8	7.25E-08	1	1	1	0.186978	1	1	1	1	1	1	1	0.000562	0.040404	0.032989
17	42141310	42141333	LSM12	0.053984	0.010722	1	1	1	1	1	1	1	1	1	1	0.056943	0.041096	0.1
11	104897111	104897136	CASP1	0.00531	2.04E-05	1	1	1	1	1	1	1	1	1	1	0.002974	0.041667	0.063291
21	43974156	43974167	SLC37A1	0.000125	6.03E-05	1	1	1	1	1	1	1	1	1	1	0.099413	0.041667	1
4	47944029	47944048	LOC101927157	6.04E-08	2.1E-08	0.245161	1	1	1	0.111538	1	1	1	1	0.25	3.65E-05	0.041667	0.059706
2	170393885	170393906	FASTKD1	5.01E-07	1.45E-05	1	1	0.171033	1	1	1	1	1	1	1	0.042042	0.041667	0.044031
3	48423614	48423626	FBXW12	1.44E-09	1.49E-09	1	1	1	1	1	1	1	1	1	1	2.81E-08	0.041667	0.047923
7	48045523	48045534	SUN3	0.00103	7.33E-09	1	1	1	1	1	1	1	1	1	1	3.06E-07	0.041667	0.137285
10	78729785	78729795	KCNMA1	0.000184	5.77E-10	1	1	0.053571	0.076528	1	1	1	1	0.1	1	6.73E-06	0.042553	0.019182
16	46652088	46652108	SHCBP1	9.76E-08	3.45E-08	0.146853	1	1	1	1	1	1	1	0.056729	1	1.04E-07	0.042553	0.10996
17	15535692	15535709	TRIM16	0.002938	0.001238	1	1	1	1	1	1	1	1	1	1	0.226415	0.042857	0.078593
2	29004734	29004745	PPP1CB	0.00098	3.56E-05	1	1	1	1	1	1	1	1	0.051282	1	0.035111	0.043478	6.86E-05
6	82459334	82459360	FAM46A	0.000506	0.000146	0.226335	1	1	1	1	1	1	1	1	1	1.31E-07	0.043478	1
15	79172834	79172845	MORF4L1	0.000487	2.89E-05	0.145299	1	1	1	1	1	1	1	1	1	0.000325	0.044776	0.06993
10	43883374	43883407	HNRNPF	2.94E-05	0.002075	1	1	1	1	1	1	1	1	1	1	1.67E-07	0.045455	1
17	40720379	40720390	MLX	6.53E-05	5.57E-10	1	1	1	1	1	1	1	0.138889	1	1	7.47E-05	0.046875	0.061538
17	37901802	37901817	GRB7	1	1	1	1	1	1	1	1	1	0.133181	1	0.230769	0.29441	0.04918	1
12	132398247	132398264	ULK1	1.06E-08	0.311776	0.047619	1	1	1	1	1	1	1	1	1	1.68E-08	0.049684	1
5	137498739	137498760	BRD8	0.08261	1	1	1	0.062425	1	1	1	1	1	1	1	1	1	4.77E-09
14	56116576	56116587	KTN1	0.01201	0.042054	0.073529	1	0.17074	1	1	1	1	1	1	0.081319	1.74E-05	1	3.48E-07
6	26373465	26373491	BTN3A2	3.82E-07	0.006377	0.199468	1	0.216928	1	0.361643	1	1	1	1	1	4.64E-05	1	3.19E-06
10	102019924	102019955	CWF19L1	9.56E-06	1.91E-06	1	1	1	1	1	1	1	1	1	1	0.006826	1	3.26E-06
17	686296	686309	RNMTL1	0.001467	0.000113	1	1	1	0.521632	1	1	1	0.318548	1	1	0.008559	1	6.72E-06
10	11047207	11047257	CELF2	0.044694	1	1	1	1	1	1	1	1	1	1	1	1	1	9.06E-06
14	64632236	64632249	MIR548AZ	9.42E-07	3.81E-11	1	1	1	1	1	1	1	1	1	1	0.000152	1	9.21E-06
22	40696618	40696645	TNRC6B	4.71E-07	2.48E-08	1	1	1	1	1	1	1	1	1	1	0.000455	0.059249	2.4E-05
7	140125524	140125548	RAB19	0.00332	0.005466	1	1	0.352859	1	1	1	1	0.149738	1	1	0.184211	1	2.56E-05
1	38301478	38301491	MTF1	5.55E-12	2.85E-13	0.090909	1	0.063584	0.081967	1	1	1	1	1	1	2.11E-06	1	2.67E-05
18	21124907	21124917	NPC1	0.000573	0.012414	0.296184	1	1	1	0.092168	1	1	0.062425	1	1	1.57E-05	1	3.72E-05
17	48202125	48202172	SAMD14	0.087246	0.20398	1	1	0.112046	1	1	1	1	1	1	1	1	1	4.48E-05
8	131812577	131812590	ADCY8	3.35E-09	4.24E-13	0.16129	1	0.115779	0.115189	1	1	1	1	1	1	2.59E-06	1	6.68E-05
20	29633958	29633977	FRG1B	0.22908	1	1	1	1	0.075918	1	1	1	1	1	1	0.244644	1	7.29E-05
14	20822853	20822873	PARP2	0.001149	0.00014	1	1	0.1	1	1	1	1	1	1	1	0.620382	1	8E-05
13	33349228	33349251	PDS5B	0.003304	0.046398	1	1	1	1	1	1	1	1	1	1	0.001688	1	9.79E-05
19	42213456	42213487	CEACAM5	4.37E-08	1.15E-06	0.142857	1	1	1	1	1	1	1	1	1	0.001876	0.052632	0.000154
11	104869775	104869786	CASP5	2.13E-07	6.87E-10	0.136213	1	0.371429	1	1	1	1	1	1	1	1.05E-08	0.057545	0.00016
17	65919172	65919190	BPTF	6.74E-09	3.2E-07	1	1	1	1	1	1	1	1	1	1	0.003693	1	0.000161
1	144923886	144923908	NBPF20,NBPF9,PDE4DIP	0.000726	7.76E-08	1	1	1	1	1	1	1	1	1	1	0.000977	1	0.000217
2	206630073	206630104	NRP2	0.41855	0.184489	0.183508	1	0.199335	1	1	1	1	1	1	1	0.120448	1	0.000239
2	114691775	114691788	ACTR3	6.82E-06	8.94E-08	0.261084	1	1	1	1	1	1	1	1	1	2.32E-05	0.055556	0.000268
7	95864044	95864057	SLC25A13	0.006341	9.42E-07	1	1	1	1	1	1	1	1	1	1	2.78E-06	1	0.000296
6	135286438	135286451	HBS1L	1.9E-11	5.71E-08	0.137931	1	1	1	1	1	0.108444	0.324589	0.083333	0.324111	2.47E-07	1	0.000327
6	32123361	32123410	PPT2-EGFL8	4.13E-06	1	1	1	1	1	1	1	1	1	1	1	0.27057	1	0.000402
2	190321967	190321989	WDR75	9.6E-08	0.000119	1	1	1	1	1	1	1	1	1	1	1.42E-07	1	0.000413
5	60982634	60982645	LOC101928651	0.037636	0.00751	1	1	0.099942	1	1	1	1	1	1	0.0625	0.000162	1	0.000444
8	21846488	21846505	XPO7	0.291879	0.203008	1	1	1	1	1	1	1	1	1	1	0.511829	1	0.000484
19	55444906	55444921	NLRP7	0.115568	0.127403	1	1	1	1	1	1	1	1	1	1	0.007028	1	0.000542
1	109773427	109773451	SARS	3.21E-07	0.003122	0.08	1	1	1	1	1	1	1	1	1	6.4E-09	1	0.000554

9	130413851	130413880	STXBP1	0.042475	1	1	1	0.142857	1	1	1	1	1	1	1	0.009157	1	0.000556
9	84267021	84267054	TLE1	1.38E-09	0.001699	1	1	0.357539	1	1	1	1	1	1	0.375	0.00076	1	0.000593
2	152589615	152589626	NEB	1.04E-06	8.83E-05	1	1	1	1	1	1	1	1	1	1	9.24E-06	1	0.000675
2	68772281	68772292	APLF	0.001609	1.27E-05	0.096341	1	1	1	1	1	1	0.312912	1	1	0.003417	1	0.000757
6	160966399	160966420	LPA	2.08E-09	1.7E-05	0.169173	1	0.227705	1	1	1	1	1	1	1	1.94E-05	1	0.000799
7	122769378	122769427	SLC13A1	1.69E-07	1	1	1	1	1	1	1	1	1	1	0.12	2.05E-05	1	0.000803
12	6840126	6840143	COPS7A	0.015396	1	1	1	1	1	1	1	1	1	1	1	0.010369	1	0.001062
17	36474721	36474733	MRPL45	1.53E-07	4.78E-06	1	1	0.149038	1	1	1	1	1	1	1	0.000151	1	0.001065
20	50015289	50015312	NFATC2	1.24E-07	4.27E-08	1	1	1	1	1	1	1	0.205396	1	0.125	1.19E-05	1	0.001069
12	49398554	49398645	PRKAG1	0.00413	0.020601	1	1	0.051095	1	1	1	1	1	1	1	0.008579	1	0.001186
6	63989791	63989802	LGSN	6.41E-06	0.000828	1	1	1	1	1	1	1	1	1	1	0.019426	1	0.001307
11	43413146	43413160	TTC17	1.5E-06	0.101852	0.070779	1	1	1	1	1	1	1	1	1	0.025372	1	0.001317
7	142468336	142468342	PRSS1(dist=7409),PRSS3P2(dist=10415)	0.118993	1	1	1	1	1	0.104167	1	1	0.060606	1	1	1	1	0.001425
17	45669428	45669438	NPEPPS	0.41168	0.045594	1	0.177404	1	1	1	1	1	1	1	0.2	0.005929	1	0.001442
14	71542879	71542890	PCNX	9.62E-09	7.12E-06	1	1	0.076923	1	1	1	1	1	1	1	9.01E-07	1	0.001543
14	73945644	73945662	HEATR4	4.54E-05	3.18E-09	1	1	1	1	1	1	1	1	1	1	6.92E-06	1	0.001593
6	43594565	43594593	GTPBP2	7.38E-09	4.81E-10	1	1	1	1	1	1	1	1	1	1	0.344678	1	0.001617
18	751880	751893	YES1	4.31E-06	2.76E-11	1	1	0.234193	1	1	1	1	1	1	1	0.027629	1	0.00176
1	245180639	245180651	EFCAB2	5.51E-12	1.9E-07	0.12234	1	0.224818	1	0.067774	1	1	1	1	1	1.1E-08	1	0.00221
2	37454907	37454917	CEBPZ	5.88E-05	0.000169	1	1	1	1	1	1	1	0.0625	1	1	0.003286	1	0.00237
12	8982250	8982273	A2ML1	7.6E-06	1.19E-06	0.086957	1	0.152701	1	1	1	1	1	1	1	4.1E-06	1	0.002444
2	37076776	37076800	STRN	0.002356	1.69E-06	1	1	1	1	1	1	1	1	1	1	0.034627	1	0.002484
2	189434711	189434722	GULP1	0.002317	1.97E-05	0.096154	1	1	1	1	1	1	1	1	1	0.006947	1	0.002506
7	56136382	56136415	SUMF2	7.94E-07	0.174603	0.142857	1	1	1	1	1	1	1	1	1	0.039927	1	0.002638
17	73660992	73661024	RECQL5	1.53E-05	1.19E-08	1	1	1	1	1	1	1	1	1	1	0.086957	1	0.002695
17	38548371	38548383	TOP2A	2.34E-07	1.92E-07	1	1	1	1	1	1	1	1	1	0.467836	3.85E-07	1	0.002719
8	102381882	102381893	NACAP1	1.6E-06	6.63E-05	0.075472	1	1	1	1	1	1	1	1	1	6.3E-06	1	0.002849
X	15593697	15593710	ACE2	0.305596	0.042308	1	1	1	1	1	1	1	1	1	1	1	1	0.002951
17	35985897	35985908	DDX52	0.000556	1.42E-05	1	1	0.115385	1	1	1	1	1	1	1	0.000371	1	0.003086
8	131136173	131136212	ASAP1	0.000211	0.01084	0.080645	1	1	1	1	1	1	1	1	1	0.000101	1	0.003104
22	32813176	32813194	BPIFC	0.000448	7.94E-10	1	1	1	1	1	1	1	1	1	1	3.34E-06	1	0.00317
7	72685488	72685511	NCF1B(dist=35509),NSUN5(dist=31002)	0.071068	1	1	1	1	1	1	1	1	1	1	1	0.003983	1	0.003274
5	150663779	150663790	SLC36A3	0.000601	2.27E-11	1	1	1	1	1	1	1	1	1	1	1.56E-06	1	0.003361
10	93776240	93776254	BTAF1	6.12E-11	7.65E-08	0.171717	1	1	1	1	1	0.059985	1	1	1	0.001357	1	0.003391
19	55452194	55452209	NLRP7	1.06E-08	0.031962	1	1	1	0.132174	1	1	0.061538	0.126167	1	1	1.86E-07	0.103448	0.003428
21	34903875	34903903	GART	0.000432	9.29E-07	0.076923	1	1	1	1	1	1	1	1	1	0.000161	1	0.003495
6	151420589	151420603	MTHFD1L	3.19E-09	1.8E-10	1	1	0.129487	1	1	1	1	1	1	1	0.056522	1	0.003703
4	48530069	48530081	FRYL	1.44E-11	1.84E-12	1	1	1	1	1	1	1	1	1	0.071429	9.81E-09	1	0.003746
12	50050142	50050168	FMNL3	0.418079	0.185185	0.05	1	1	1	1	1	1	1	1	0.2	0.001334	1	0.003851
12	27553788	27553807	ARNTL2-AS1	0.000272	0.000347	1	1	0.074766	1	1	1	1	1	1	1	0.000897	1	0.004152
11	75694430	75694441	UVRAG	1.77E-07	2.51E-06	1	1	1	1	1	1	1	1	1	1	1.63E-06	1	0.004164
12	8757509	8757545	AICDA	8.08E-09	8.28E-07	1	1	1	1	0.170198	1	1	0.128045	1	1	3.98E-08	1	0.004194
10	101829686	101829697	CPN1	0.000469	1.28E-07	0.052632	1	1	1	1	1	1	1	1	1	0.001536	1	0.004199
4	152609920	152609934	GATB	0.000143	2.46E-06	1	1	0.319154	1	0.187534	1	0.078228	0.129897	1	0.313725	0.000178	1	0.004288
5	96339092	96339114	LNPEP	3.93E-06	6.72E-05	0.071429	1	0.315011	1	0.065918	1	1	1	1	0.272727	7.36E-06	1	0.004441
17	58147228	58147258	HEATR6	0.006002	0.000671	1	1	1	1	1	1	1	1	1	1	0.010415	1	0.004491
1	161192845	161192884	APOA2	0.009501	0.577367	1	1	1	1	1	1	1	1	1	0.444444	0.204246	0.083333	0.004654
2	208461556	208461574	CREB1	0.010408	0.000476	0.05	1	1	1	1	1	1	1	1	1	1.82E-06	1	0.004762
1	173881163	173881173	SERPINC1	0.0087	3.27E-07	1	1	1	1	1	1	1	1	1	1	0.117944	1	0.004818
7	150384193	150384244	GIMAP2	1	1	1	1	0.058812	1	1	1	1	1	1	1	1	1	0.004856
13	28980036	28980047	FLT1	0.000832	8.41E-07	1	1	1	1	1	1	1	0.169427	1	1	0.431184	1	0.004916
2	74076616	74076633	STAMBP	2.8E-06	3.36E-12	1	1	1	1	1	1	1	1	1	1	0.002578	1	0.005065
17	78349502	78349513	LOC100294362	4.09E-12	7.39E-10	0.068966	1	1	1	1	1	1	1	1	1	0.082107	1	0.005122
18	60110451	60110479	TNFRSF11A(dist=55508),ZCCHC2(dist=80179)	7.75E-07	1.82E-08	1	1	1	1	1	1	1	1	1	1	0.000116	1	0.005168
2	85866565	85866594	USP39	1.83E-06	0.010077	0.313725	1	1	1	1	1	1	1	1	1	0.023377	1	0.005206
7	138768472	138768492	ZC3HAV1	1.54E-05	0.000258	1	1	1	1	1	1	1	1	1	1	6.58E-06	1	0.005211
16	21763589	21763638	OTOA	0.01855	3.3E-05	1	1	1	1	1	1	1	1	1	1	0.000334	1	0.005364
9	86893061	86893072	SLC28A3	0.000425	0.000112	1	1	1	1	1	1	1	1	1	1	0.005644	1	0.005789
16	15892465	15892503	MYH11	0.00024	0.001914	0.154595	1	1	1	1	1	1	1	1	1	0.002336	1	0.005915
3	10382058	10382073	ATP2B2	0.101587	0.083617	0.057143	1	1	1	1	1	1	1	1	1	1.07E-06	1	0.006061
3	121500479	121500528	IQCB1	2.75E-07	0.102315	0.237903	1	0.304366	1	1	1	1	1	1	0.375	0.030392	1	0.006801
4	183522050	183522074	TENM3	1	8.81E-05	1	1	1	1	1	1	1	1	1	1	2.84E-05	1	0.006966
19	15795566	15795609	CYP4F12	0.004867	1	1	1	1	1	1	1	1	1	1	1	0.266074	1	0.007069
10	15883639	15883651	FAM188A	4.18E-11	1.02E-10	1	1	1	1	1	1	1	1	1	1	1.01E-10	1	0.007149
17	29528406	29528423	NF1	3.31E-06	2.36E-08	0.193103	1	1	1	1	1	0.073375	0.102041	1	1	1.04E-08	1	0.007265
6	3077011	3077025	RIPK1	0.00131	0.054934	1	1	1	1	1	1	1	1	1	1	0.013581	1	0.007362
2	130970483	130970495	TUBA3E(dist=14449),CCDC115(dist=125011)	7.39E-05	0.000315	0.338924	1	1	0.245351	1	1	1	0.083333	1	1	0.000837	1	0.007632
12	18854540	18854586	PLCZ1	1	1	1	1	0.08037	1	1	1	1	1	1	1	0.020549	1	0.008084
2	144193145	144193166	ARHGAP15	8.63E-12	0.004524	0.238915	1	1	1	1	1	0.056526	0.059406	1	1	0.002812	1	0.008095
15	84651006	84651018	ADAMTSL3	5.48E-08	3.74E-12	1	1	1	1	1	1	1	1	1	1	9.82E-06	1	0.008433
5	52370822	52370833	ITGA2	0.022532	0.001716	1	1	1	1	1	1	1	1	1	1	0.19	1	0.00851
17	30321556	30321576	SUZ12	8.58E-09	2.46E-08	0.078947	1	1	1	1	1	1	1	1	1	3.95E-05	1	0.008831
6	46661920	46661958	TDRD6	0.046165	0.221277	0.094077	1	0.053763	1	1	1	1	1	1	1	1	1	0.009863
17	60483826	60483837	EFCAB3	9.5E-08	1.21E-08	1	1	1	1	1	1	1	1	1	1	2.64E-06	1	0.010323
14	74444083	74444106	ENTPD5	2E-08	0.000258	0.060606	1	0.178787	1	1	1	1	1	1	1	0.002851	1	0.010792
19	43031656	43031701	LIPE-AS1	1	0.190955	1	1	0.113827	1	1	1	1	1	1	1	0.218487	1	0.011032
11	73806199	73806210	C2CD3	0.000999	0.00153	1	1	1	1	1	1	1	1	1	1	0.001114	1	0.011213
3	169988364	169988385	PRKCI	1.15E-07	0.009728	0.068966	1	1	1	1	1	1	1	1	1	8.96E-05	1	0.011348
X	16871982	16871993	RBBP7	0.000581	1.67E-05	1	1	1	1	1	1	1	1	1	1	0.19697	1	0.011475
12	42729668	42729679	PPHLN1	0.000201	2.65E-10	1	1	0.111111	1	1	1	1	1	1	1	0.06662	1	0.011628
19	13927881	13927892	ZSWIM4	0.007539	0.012694	1	1	1	1	1	1	1	0.072289	1	1	1	1	0.012048
3	40553163	40553190	ZNF620	5.83E-05	0.016006	1	1	1	1	1	1	1	1	1	1	0.033186	1	0.012318
5	31541000	31541024	C5orf22	0.010515	0.000403	1	1	1	1	1	1	1	1	1	1	0.001871	1	0.012465
2	71215869	71215900	TEX261	0.178649	0.001057	1	1	1	1	1	1	1	1	1	1	0.046017	1	0.01319
9	75445632	75445678	TMC1	0.003772	1	1	1	0.064815	1	1	1	1	1	1	1	0.00062	1	0.013306
2	162876813	162876843	DPP4	1.33E-05	0.017924	0.19175	1	1	1	1	1	1	1	1	0.071429	3.76E-06	1	0.013367

Supplemental Table 5. Pairwise Euclidean dissimilarity matrix of tissue-specific informative microsatellite loci based on tissue-scaled p-values

	UCEC	STAD	READ	PRAD	OV	LUSC	LUAD	LGG	KIRC	GBM	ESCA	DLBC	COAD	CESC	BRCA
UCEC	0	10.7	13.8	18.2	17.2	16.6	16.6	20.8	17.4	16.8	17.1	18.9	9.3	15	12.4
STAD	10.7	0	16.1	19.3	19.5	18.7	18.4	22.8	19.3	18.7	19.6	21.8	12.5	18	15.4
READ	13.8	16.1	0	19.9	18.8	18.2	18.6	22.1	19.7	18.9	20.4	19.8	13.1	17.9	15.7
PRAD	18.2	19.3	19.9	0	16	13.7	14.6	18.2	18.7	15	21.2	15.9	19.2	16.2	15.4
OV	17.2	19.5	18.8	16	0	11.6	12.8	16.7	17	13.2	20.3	13	18.3	14.4	13.4
LUSC	16.6	18.7	18.2	13.7	11.6	0	9.9	14.4	15.5	10.4	19.4	10.6	17.8	12.4	11.8
LUAD	16.6	18.4	18.6	14.6	12.8	9.9	0	15.6	16.2	11.2	19.7	12.2	17.9	13.3	12.5
LGG	20.8	22.8	22.1	18.2	16.7	14.4	15.6	0	19.7	15.6	23	15.8	22	17.2	16.8
KIRC	17.4	19.3	19.7	18.7	17	15.5	16.2	19.7	0	16.4	21.9	17	18.8	17.2	15.8
GBM	16.8	18.7	18.9	15	13.2	10.4	11.2	15.6	16.4	0	20	12.4	18.3	13.8	12.6
ESCA	17.1	19.6	20.4	21.2	20.3	19.4	19.7	23	21.9	20	0	20.9	18.3	18.3	18.2
DLBC	18.9	21.8	19.8	15.9	13	10.6	12.2	15.8	17	12.4	20.9	0	19.8	14.3	13.8
COAD	9.3	12.5	13.1	19.2	18.3	17.8	17.9	22	18.8	18.3	18.3	19.8	0	16.5	14
CESC	15	18	17.9	16.2	14.4	12.4	13.3	17.2	17.2	13.8	18.3	14.3	16.5	0	13.1
BRCA	12.4	15.4	15.7	15.4	13.4	11.8	12.5	16.8	15.8	12.6	18.2	13.8	14	13.1	0

Supplemental Table 6. Pairwise Cophenetic dissimilarity matrix of tissue-specific informative microsatellite loci based on tissue-scaled p-values

	UCEC	STAD	READ	PRAD	OV	LUSC	LUAD	LGG	KIRC	GBM	ESCA	DLBC	COAD	CESC	BRCA
UCEC	0	12.5	16.1	23	23	23	23	23	19.7	23	21.9	23	9.3	23	23
STAD	12.5	0	16.1	23	23	23	23	23	19.7	23	21.9	23	12.5	23	23
READ	16.1	16.1	0	23	23	23	23	23	19.7	23	21.9	23	16.1	23	23
PRAD	23	23	23	0	16.2	16.2	16.2	18.2	23	16.2	23	16.2	23	16.2	16.2
OV	23	23	23	16.2	0	13.2	13.2	18.2	23	13.2	23	13.2	23	14.4	14.4
LUSC	23	23	23	16.2	13.2	0	9.9	18.2	23	11.2	23	12.4	23	14.4	14.4
LUAD	23	23	23	16.2	13.2	9.9	0	18.2	23	11.2	23	12.4	23	14.4	14.4
LGG	23	23	23	18.2	18.2	18.2	18.2	0	23	18.2	23	18.2	23	18.2	18.2
KIRC	19.7	19.7	19.7	23	23	23	23	23	0	23	21.9	23	19.7	23	23
GBM	23	23	23	16.2	13.2	11.2	11.2	18.2	23	0	23	12.4	23	14.4	14.4
ESCA	21.9	21.9	21.9	23	23	23	23	23	21.9	23	0	23	21.9	23	23
DLBC	23	23	23	16.2	13.2	12.4	12.4	18.2	23	12.4	23	0	23	14.4	14.4
COAD	9.3	12.5	16.1	23	23	23	23	23	19.7	23	21.9	23	0	23	23
CESC	23	23	23	16.2	14.4	14.4	14.4	18.2	23	14.4	23	14.4	23	0	13.1
BRCA	23	23	23	16.2	14.4	14.4	14.4	18.2	23	14.4	23	14.4	23	13.1	0

Supplemental Table 7. Coordinates of and p values of cross-informative microsatellites for diagnosing MSI in endometrial, colon, rectal, and stomach cancers

Chromosome	Start Position	End Position	Gene(s) or distance to closest genes (dist)	UCEC	STAD	READ	COAD
1	149900985	149901002	MTMR11	1.55E-20	3.34E-19	6.52E-06	3.11E-17
1	222904869	222904881	BROX	6.01E-27	5.06E-33	4.59E-06	4.84E-29
10	112360315	112360333	SMC3	7.66E-28	1.89E-24	8.23E-07	1.18E-37
10	35314130	35314161	CUL2	2.33E-16	9.48E-12	1.23E-06	4.56E-27
10	64022582	64022593	RTKN2	1.14E-13	1.26E-15	5.14E-06	5.43E-17
11	118885668	118885701	CCDC84	3.57E-10	1.68E-16	9.19E-07	1.36E-17
12	110834030	110834049	ANAPC7	1.25E-18	2.99E-14	2.25E-06	1.85E-34
12	125587478	125587491	AACS	1.42E-14	3.9E-35	1.3E-06	3.9E-23
12	85285920	85285938	SLC6A15	1.8E-19	8.25E-19	4.63E-06	2.36E-18
12	89853387	89853405	POC1B	9.49E-13	1.35E-13	4.11E-06	5.25E-30
13	79216356	79216381	RNF219	8.49E-32	1.14E-34	2.53E-06	6.25E-34
15	55841195	55841209	PYGO1	4.8E-19	1.24E-21	4.34E-06	2.55E-26
16	10567751	10567778	ATF7IP2	2.76E-17	2.32E-06	6.14E-06	5.38E-28
16	3808052	3808066	CREBBP	9.43E-24	1.7E-25	9.19E-07	1.29E-25
16	9010826	9010844	USP7	1.28E-12	4.6E-07	3.16E-06	7.6E-23
17	29508819	29508836	NF1	5.07E-19	7.64E-19	3.01E-06	7.41E-39
19	6026288	6026302	RFX2	7.76E-21	2.88E-29	2.86E-06	1.91E-22
2	141294271	141294299	LRP1B	1.04E-25	1.04E-09	6.52E-06	1.86E-13
2	203676382	203676403	ICA1L	1.1E-09	9.47E-08	6.74E-06	1.03E-28
2	32095023	32095056	MEMO1	3.71E-16	3.72E-09	7.87E-06	4.58E-25
2	8998775	8998788	MBOAT2	1.18E-13	4.18E-21	6.14E-06	1.92E-13
3	41877473	41877487	ULK4	5.73E-19	2.07E-18	4.63E-06	3.47E-23
4	146031236	146031253	ABCE1	1.39E-34	1.29E-17	3.16E-06	3.47E-37
5	172578549	172578567	BNIP1	3.33E-35	9.43E-28	4.25E-06	5.33E-35
5	36123065	36123135	LMBRD2	1.78E-36	2.55E-15	1.03E-06	5.76E-29
6	102130410	102130422	GRIK2	1.29E-13	8.04E-15	2.35E-06	8.03E-08
6	122733490	122733508	HSF2	1.08E-16	2.77E-20	1.23E-06	1.46E-14
6	36452603	36452620	KCTD20	1.66E-22	6.6E-29	8.39E-06	2.83E-32
6	46636556	46636581	SLC25A27	1.08E-15	1.69E-19	5.78E-06	3.27E-22
6	49415351	49415368	MUT	3.52E-18	2.84E-22	6.94E-06	8.71E-33
7	97939975	97939988	BAIAP2L1	3.04E-24	6.88E-19	2.05E-06	5.79E-15
8	100160282	100160300	VPS13B	5.77E-32	2.33E-24	5.83E-06	7.54E-28
8	33356825	33356839	MAK16	2.52E-24	8.7E-14	1.79E-06	3.19E-22
9	52625	52641	FAM138C(dist=16761),PGM5P3-AS1(dist=20049)	6.03E-18	5.71E-20	5.15E-06	1.08E-12
9	75420448	75420463	TMC1	2.37E-21	3.03E-18	2.48E-06	1.05E-17
X	106092450	106092473	TBC1D8B	2.06E-35	1.3E-07	3.51E-06	2.91E-36
X	19380975	19380993	MAP3K15	9.58E-29	1.52E-24	9.19E-07	4.16E-21

Supplemental Table 8. Covariates associated with instability of MSI-informative microsatellites

Feature Category	Feature	Coefficient*	97.5% confidence interval			p value
Coding context	Intergenic	Not applicable**				
	Upstream	0.26330362	0.201082791	to	0.32552445	1.1E-16
	Downstream	0.24775092	0.19523743	to	0.3002644	2.32E-20
	Exonic	0.63116873	0.312458773	to	0.94987869	0.000104
	Intronic	0.22357372	0.214076632	to	0.23307081	0
	ncRNA exonic	0.24869416	0.139176607	to	0.35821171	8.56E-06
	ncRNA intronic	0.06674437	0.045628207	to	0.08786053	5.83E-10
	ncRNA splicing	0.80560147	0.355024088	to	1.25617886	0.000458
	Splicing	1.095599	0.889927325	to	1.30127068	1.63E-25
	Upstream and Downstream	0.20875388	-0.103550755	to	0.52105852	0.190162
	3' UTR	0.54949742	0.502719112	to	0.59627574	3.1E-117
	5' UTR	0.64615781	0.442216539	to	0.85009909	5.31E-10
Repeat class	Compound repeat	1.46871369	1.301270946	to	1.63615644	3.18E-66
	Complex repeat	0.92271293	0.751505079	to	1.09392078	4.44E-26
	Mononucleotide repeat	1.44146313	1.272848876	to	1.61007737	5.33E-63
	Dinucleotide repeat	0.15687561	-0.012360733	to	0.32611194	0.069246
	Trinucleotide repeat	-0.118346	-0.4131167	to	0.17642471	0.431342
	Tetranucleotide Repeat	0.24265869	0.054478379	to	0.43083901	0.011492
	Pentanucleotide Repeat	Not applicable**				
Number of repeats	5-11	Not applicable**				
	11-12	0.80031813	0.779980199	to	0.82065606	0
	12-13	1.77745115	1.757111464	to	1.79779084	0
	13-14	1.59183987	1.571499926	to	1.61217982	0
	14-16	1.50008182	1.479731404	to	1.52043224	0
	16-18	0.31325393	0.2920993	to	0.33440855	4.6E-185
	18-21	-0.1869956	-0.211463299	to	-0.162528	1.03E-50
	21-25	-0.2282874	-0.255785148	to	-0.2007896	1.61E-59
	25-32	-0.5444188	-0.572807037	to	-0.5160306	0
	>32	-1.2434585	-1.272243027	to	-1.2146739	0

*Positive coefficients values are associated with microsatellite instability; negative values are associated with microsatellie stability

**Category was used as reference for statistical comparisons