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Supplemental Data

Loss of SUFU Function in Familial Multiple Meningioma

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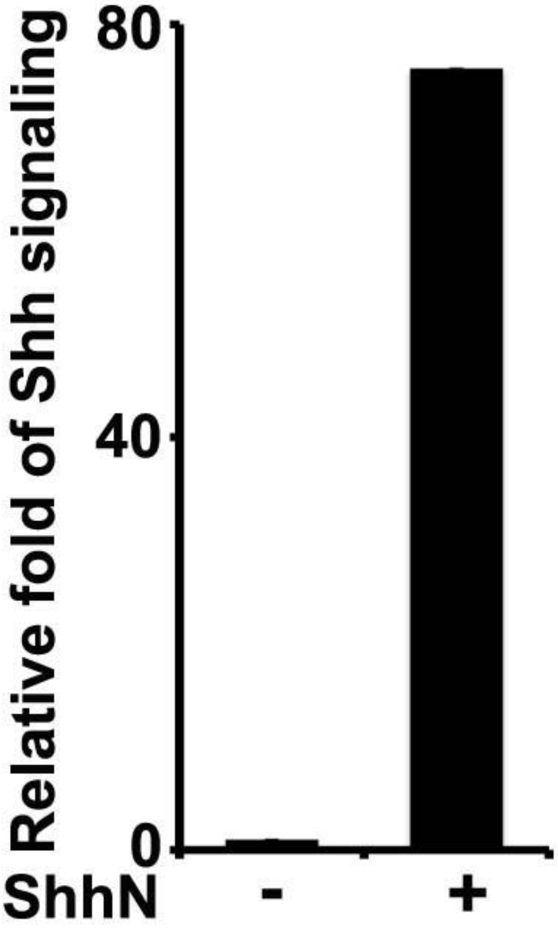

Figure S1. Efficiency of ShhN Conditioned Medium

The biological activity of the ShhN conditioned medium was tested by transfecting Hh pathway specific reporter and control reporter to C3H10T1/2 cells, and incubating the cells with ShhN conditioned medium for two days. Note that ShhN conditioned medium treated cells display much higher luciferase activity than untreated cells. Error bars indicate one standard deviation (duplicate samples).

Table S1. Linked Regions with Positive LOD Scores in Meningioma Family 1

Chr	Start Marker	End Marker	Start bp	End bp	Min LOD	Max LOD	Average LOD	Length cM	Length bp
1	rs7545940	rs1475629	2299627	59608025	0.095	0.432	0.267	83.964	57308398
1	rs7555023	rs6704311	225854495	249210707	0.102	0.432	0.338	46.711	23356212
1	rs1200082	rs659580	169160726	170633896	0.007	0.195	0.187	2.241	1473170
1	rs1887467	rs4847031	102407313	105582135	0.011	0.197	0.190	2.036	3174822
1	rs429201	rs856099	158194899	158891391	0.004	0.195	0.176	1.253	696492
1	rs3934593	rs10800409	161358828	162260715	0.020	0.212	0.193	1.081	901887
1	rs10916197	rs1340865	224230307	225631404	0.012	0.195	0.191	1.018	1401097
1	rs6428606	rs12125484	91480823	92812196	0.009	0.195	0.191	0.948	1331373
1	rs1487492	rs4589114	188162030	188683442	0.045	0.195	0.170	0.369	521412
1	rs2421809	rs2206542	171371998	171788782	0.062	0.195	0.182	0.311	416784
1	rs10801032	rs6659757	188901145	189846235	0.057	0.258	0.225	0.306	945090
1	rs2206510	rs982875	176513537	177208980	0.001	0.019	0.017	0.290	695443
1	rs1840246	rs2029768	77835507	78014042	0.001	0.112	0.095	0.093	178535
2	rs6721317	rs7587759	151574522	199657020	0.029	0.432	0.214	36.234	48082498
2	rs3115376	rs12469535	231845762	243044147	0.036	0.195	0.195	24.769	11198385
2	rs4852700	rs10496388	70921539	105549404	0.049	0.432	0.252	24.694	34627865
2	rs2216174	rs1872603	7992985	8561739	0.009	0.195	0.184	2.259	568754
2	rs1384741	rs1393810	67453172	68178609	0.008	0.195	0.182	1.740	725437
2	rs1975305	rs6713772	122207005	123216847	0.003	0.195	0.186	1.448	1009842
2	rs7580611	rs1458281	209467044	211258344	0.048	0.195	0.186	0.918	1791300
2	rs765253	rs1965391	33708491	34237472	0.061	0.196	0.184	0.914	528981
2	rs2287059	rs4669646	10717806	11061715	0.020	0.195	0.182	0.815	343909
2	rs7588415	rs2879163	21123661	21816746	0.003	0.195	0.180	0.788	693085
2	rs6712836	rs840976	65425014	65707760	0.017	0.148	0.133	0.573	282746
2	rs950233	rs1208081	201594185	202501448	0.009	0.154	0.130	0.519	907263
2	rs2581087	rs4669803	12057524	12198305	0.007	0.139	0.115	0.399	140781

2	rs6759476	rs208784	230437369	230562414	0.083	0.195	0.185	0.329	125045
3	rs1928565	rs6762405	67580121	133156692	0.008	0.432	0.197	48.324	65576571
3	rs6549924	rs6768998	29357063	43718270	0.014	0.204	0.195	15.006	14361207
3	rs7647261	rs3844057	193938611	196462501	0.019	0.195	0.193	5.312	2523890
3	rs9681213	rs2619566	66894	2624938	0.075	0.195	0.195	5.260	2558044
3	rs7615158	rs899348	140225492	140828801	0.038	0.192	0.169	1.042	603309
3	rs13315015	rs2717302	181515848	182392108	0.017	0.195	0.170	1.026	876260
3	rs696066	rs3774007	189672468	190115611	0.006	0.195	0.180	0.763	443143
3	rs3796343	rs6807359	52324169	53179754	0.024	0.195	0.170	0.693	855585
3	rs250403	rs370477	8920281	9067597	0.024	0.195	0.161	0.452	147316
3	rs12631821	rs2127521	65033653	65382140	0.019	0.195	0.180	0.356	348487
3	rs1995242	rs1983011	177196081	177376886	0.005	0.027	0.020	0.317	180805
3	rs6439563	rs6808137	134928717	135310068	0.012	0.187	0.176	0.299	381351
3	rs7651446	rs10936057	156406997	156758657	0.003	0.160	0.136	0.240	351660
3	rs3732530	rs9826195	47618953	48433635	0.050	0.195	0.188	0.221	814682
3	rs6766822	rs1319985	24778690	24875084	0.001	0.004	0.004	0.080	96394
4	rs4690284	rs524675	73508	13966851	0.002	0.432	0.355	26.993	13893343
4	rs11728123	rs7660745	25983887	38974458	0.055	0.432	0.225	13.676	12990571
4	rs830835	rs13120250	186909596	190927132	0.080	0.432	0.219	10.599	4017536
4	rs7662456	rs10034036	64214915	75629633	0.074	0.432	0.210	8.037	11414718
4	rs2719934	rs1583540	42347473	43115315	0.002	0.386	0.207	0.627	767842
4	rs4618360	rs756334	158039710	158689938	0.005	0.091	0.079	0.530	650228
4	rs4473628	rs7698045	47752554	48240043	0.028	0.195	0.180	0.154	487489
4	rs10029490	rs1032133	19740879	20053908	0.007	0.052	0.046	0.134	313029
4	rs6827817	rs13144424	88330987	88474171	0.099	0.169	0.161	0.109	143184
5	rs186893	rs163129	8473747	78279820	0.028	0.432	0.271	71.957	69806073
5	rs2085448	rs1279912	167885622	180690937	0.191	0.432	0.263	30.485	12805315
5	rs6893150	rs1971335	80509936	81986928	0.056	0.195	0.190	2.255	1476992
5	rs10515889	rs1799542	164546897	165756043	0.003	0.195	0.184	1.843	1209146
5	rs6594693	rs1482377	112516709	113225701	0.025	0.195	0.183	0.492	708992

5	rs1835919	rs157350	155613491	156139569	0.049	0.195	0.184	0.353	526078
6	rs9389549	rs12213906	138343019	170909002	0.168	0.414	0.204	48.700	32565983
6	rs1267514	rs10485346	14691612	33866059	0.194	0.432	0.205	19.972	19174447
6	rs1149305	rs9372110	105745814	106317196	0.007	0.195	0.171	0.804	571382
6	rs913533	rs10458159	3376492	3658852	0.106	0.195	0.187	0.730	282360
6	rs4945909	rs11153496	112999076	115005346	0.038	0.195	0.186	0.701	2006270
6	rs6915644	rs851854	65816812	67098218	0.033	0.195	0.186	0.647	1281406
6	rs9396386	rs17467260	57580780	63223191	0.029	0.109	0.103	0.489	5642411
7	rs6593113	rs1052990	54087762	116148370	0.022	0.432	0.212	46.789	62060608
7	rs7788285	rs4726774	116867295	145566532	0.009	0.417	0.204	30.291	28699237
7	rs4988515	rs917131	45932600	48868672	0.019	0.375	0.195	2.187	2936072
7	rs7793793	rs12111597	33070175	34870001	0.029	0.195	0.192	1.046	1799826
7	rs1035147	rs886890	12094966	12665739	0.043	0.194	0.172	0.896	570773
7	rs217556	rs6461170	14908792	15397643	0.025	0.195	0.180	0.774	488851
7	rs255112	rs12670991	30737133	31089447	0.008	0.170	0.146	0.754	352314
7	rs10951453	rs10848	35994201	36339126	0.022	0.195	0.179	0.662	344925
7	rs2391415	rs739898	27359793	27913060	0.023	0.195	0.167	0.604	553267
7	rs1362363	rs1641215	29511689	29661486	0.017	0.164	0.147	0.347	149797
7	rs10486480	rs6968828	26872652	27223563	0.044	0.195	0.177	0.254	350911
7	rs17135206	rs6974056	52655552	52952144	0.010	0.184	0.164	0.233	296592
7	rs7806592	rs12718123	53998	200682	0.188	0.195	0.194	0.215	146684
7	rs1476689	rs10499549	22265585	22390479	0.024	0.067	0.057	0.140	124894
8	rs11136463	rs7842063	2020224	83738448	0.015	0.432	0.263	90.265	81718224
8	rs7841283	rs7822726	131668278	146274708	0.028	0.207	0.195	26.002	14606430
8	rs7823009	rs12548836	125199582	125529355	0.055	0.156	0.144	0.579	329773
8	rs4397371	rs6470816	130701417	131349715	0.003	0.100	0.091	0.351	648298
9	rs7856900	rs10512124	19475651	84950712	0.006	0.432	0.199	40.554	65475061
9	rs2361093	rs2475335	606676	10260263	0.071	0.369	0.198	22.514	9653587
9	rs4978532	rs7048129	110416006	115245875	0.010	0.364	0.203	6.283	4829869
9	rs7043796	rs7037313	133070040	134164493	0.007	0.195	0.188	1.771	1094453

9	rs4842136	rs7864699	137489483	137724371	0.021	0.195	0.180	1.308	234888
9	rs1942476	rs1927702	15362057	15986716	0.003	0.150	0.120	1.062	624659
9	rs6479562	rs6479604	97429160	98110248	0.040	0.191	0.180	0.695	681088
9	rs479600	rs2995211	104202803	104709020	0.038	0.194	0.167	0.464	506217
9	rs7869160	rs2382444	13968260	14221591	0.032	0.177	0.159	0.426	253331
9	rs1341062	rs1332712	18519566	18632128	0.007	0.068	0.062	0.294	112562
9	rs10511667	rs2171957	18989696	19086979	0.010	0.035	0.031	0.254	97283
10	rs538037	rs2803804	29441743	119091401	0.011	0.431	0.196	82.768	89649658
10	rs10830183	rs11101905	128774872	135434303	0.087	0.432	0.240	21.123	6659431
10	rs1149975	rs6602387	9341029	10034807	0.062	0.191	0.174	1.217	693778
10	rs3740563	rs10749330	121095400	121711232	0.018	0.195	0.179	0.945	615832
10	rs11251048	rs7079384	2120407	2692656	0.067	0.195	0.187	0.908	572249
10	rs7906287	rs11253471	135853	903950	0.179	0.196	0.195	0.710	768097
10	rs10764124	rs4338432	19963583	20458202	0.003	0.032	0.029	0.344	494619
11	rs2584834	rs7104859	20043439	95824593	0.005	0.432	0.237	64.694	75781154
11	rs4300402	rs4540845	131219868	134930689	0.047	0.430	0.205	9.050	3710821
11	rs2075292	rs7083	116732512	117156552	0.018	0.195	0.187	0.900	424040
11	rs4073915	rs4757788	18796480	19339176	0.037	0.195	0.178	0.753	542696
11	rs4938784	rs10789859	111413465	111960533	0.046	0.194	0.174	0.680	547068
11	rs12281062	rs1176754	113494864	113827650	0.010	0.039	0.034	0.509	332786
11	rs1275097	rs666135	123543428	124208977	0.002	0.023	0.013	0.359	665549
11	rs10892201	rs4938499	117848292	118162496	0.057	0.195	0.184	0.281	314204
11	rs9326314	rs7110790	101433161	101909363	0.107	0.188	0.181	0.090	476202
12	rs1476796	rs7975069	126769933	133778796	0.107	0.195	0.195	22.855	7008863
12	rs1464054	rs35063	26406081	31153037	0.045	0.195	0.195	5.276	4746956
12	rs500037	rs4126012	118139540	119064852	0.053	0.195	0.189	2.093	925312
12	rs1847461	rs7301434	91077508	92856031	0.028	0.195	0.188	2.078	1778523
12	rs6487136	rs10845052	8605216	10295622	0.053	0.195	0.190	1.508	1690406
12	rs10842189	rs3922562	23759406	24358865	0.003	0.195	0.186	1.203	599459
12	rs310796	rs10161149	77453226	78075142	0.020	0.195	0.179	1.163	621916

12	rs1587458	rs9325144	33252638	39018673	0.013	0.195	0.180	0.675	5766035
12	rs1482434	rs9943826	84589672	84945039	0.006	0.018	0.014	0.240	355367
12	rs2370405	rs17045250	78614718	78782912	0.005	0.037	0.030	0.219	168194
12	rs7137869	rs708893	119989646	119991312	0.195	0.195	0.195	0.005	1666
13	rs9316335	rs10492715	21958918	108133693	0.003	0.432	0.218	111.026	86174775
13	rs7996418	rs9549575	112882015	113512331	0.034	0.195	0.182	2.228	630316
13	rs406801	rs331974	109487337	110319113	0.008	0.195	0.190	1.486	831776
13	rs7989816	rs9805752	114070793	114876429	0.059	0.195	0.184	1.338	805636
13	rs3936159	rs4907674	112535799	112852673	0.031	0.195	0.187	0.743	316874
14	rs1540427	rs1544317	87762614	107281980	0.068	0.197	0.195	39.308	19519366
14	rs2319870	rs1950231	22034624	40659684	0.071	0.432	0.209	30.017	18625060
14	rs2215837	rs7146567	78856784	79032690	0.004	0.040	0.034	0.298	175906
15	rs7175950	rs7181323	78236353	95113239	0.001	0.260	0.196	29.266	16876886
15	rs631864	rs7164165	70376441	71784536	0.033	0.195	0.189	2.416	1408095
15	rs7169915	rs4966036	98892286	99429749	0.045	0.112	0.104	1.945	537463
15	rs11632769	rs1913426	33215074	33555802	0.005	0.195	0.177	1.633	340728
15	rs2077422	rs6495662	34191286	34630582	0.006	0.195	0.174	0.964	439296
15	rs892775	rs951442	33824530	33917942	0.022	0.083	0.077	0.262	93412
16	rs7193424	rs11645438	25887889	48493721	0.012	0.411	0.218	8.069	22605832
16	rs8466	rs2269911	97354	3065924	0.016	0.366	0.209	7.796	2968570
16	rs6540278	rs11646219	85620902	87096577	0.018	0.197	0.194	5.236	1475675
16	rs8056635	rs1468609	5234055	6428783	0.004	0.431	0.232	4.074	1194728
16	rs2035247	rs6500936	7069056	7270582	0.006	0.195	0.184	0.441	201526
16	rs1364230	rs198017	62628710	63131263	0.017	0.054	0.046	0.164	502553
17	rs6502246	rs2165894	13183901	19489796	0.192	0.394	0.205	11.915	6305895
17	rs2188729	rs938299	59669134	63148473	0.004	0.195	0.184	3.093	3479339
17	rs9303193	rs8079279	5432405	5993315	0.019	0.196	0.181	2.890	560910
17	rs3785602	rs756944	66356883	67531235	0.004	0.195	0.184	1.796	1174352
17	rs7405782	rs658591	21490090	26610769	0.045	0.195	0.190	1.544	5120679
17	rs17728713	rs17635849	52000506	52848767	0.004	0.167	0.146	0.497	848261

18	rs12457331	rs11662742	277763	10676435	0.004	0.432	0.262	34.936	10398672
18	rs592921	rs12960632	74089533	78015180	0.101	0.195	0.195	9.645	3925647
18	rs4334403	rs11151425	64898303	65808846	0.081	0.195	0.192	1.499	910543
18	rs1791520	rs1668852	22118315	22516866	0.073	0.168	0.161	0.755	398551
18	rs10502537	rs1442998	27502730	28066601	0.007	0.195	0.178	0.359	563871
19	rs791464	rs917649	1489080	56924761	0.010	0.432	0.257	106.684	55435681
19	rs4801531	rs931258	58401560	58808709	0.026	0.195	0.180	0.403	407149
20	rs1418258	rs6037988	63799	4830412	0.014	0.204	0.195	14.146	4766613
20	rs6069788	rs864184	55149352	58326432	0.092	0.195	0.194	8.711	3177080
20	rs6125111	rs6127552	36092914	36879360	0.004	0.195	0.180	1.658	786446
20	rs1884034	rs6072705	40608629	40999761	0.054	0.185	0.155	1.050	391132
20	rs6106154	rs6046790	19883823	20303376	0.048	0.195	0.186	0.982	419553
20	rs1204759	rs761685	49757406	49940226	0.069	0.146	0.134	0.759	182820
20	rs6141319	rs853849	31144807	31439355	0.078	0.195	0.182	0.327	294548
20	rs6058224	rs6087733	33881774	34298628	0.071	0.194	0.179	0.027	416854
21	rs3787751	rs2839378	38160163	48084989	0.162	0.432	0.221	34.781	9924826
21	rs2510527	rs2833092	31577206	32168483	0.043	0.195	0.175	0.755	591277
21	rs2834426	rs11701051	35631938	35839963	0.030	0.135	0.114	0.561	208025
21	rs2192160	rs1153304	15588213	15660539	0.036	0.067	0.062	0.258	72326
22	rs2226691	rs929020	26789849	47971041	0.025	0.201	0.195	39.819	21181192
22	rs6004814	rs137183	26290588	26670085	0.106	0.194	0.189	1.163	379497
22	rs137916	rs2272843	50491713	50599466	0.005	0.124	0.099	0.433	107753
X	rs2240584	rs2704838	7883894	24179042	0.153	0.467	0.465	26.838	16295148
X	rs2404538	rs204332	110242674	126158857	0.007	0.467	0.463	24.337	15916183
X	rs5987005	rs557132	153892867	154929412	0.283	0.402	0.384	2.031	1036545
X	rs12557174	rs5953334	48117763	49443185	0.074	0.467	0.419	1.375	1325422
X	rs221406	rs3850163	27555758	28445637	0.193	0.383	0.352	0.591	889879
X	rs5970389	rs6526155	152021096	152226542	0.030	0.230	0.208	0.403	205446

Table S2. Candidate Variants in the Linked Regions Shared by Individuals III-1, III-2, and III-4

Gene	RefSeq	Chr	Variation	dbSNP ID	Segregation[a]	In Unaffected Family Members	In Healthy Controls	In Silico Predictions[b]	LOH[c] in Tumors
CTRC	NM_007272.2	1	c.674A>C (p.Glu225Ala)	rs201486613	yes	yes	0/187	-	-
SSFA2	NM_006751.5	2	c.2393C>T (p.Ser798Leu)	rs201543593	no	-	-	-	-
METAP1D	NM_199227.1	2	c.653T>C (p.Ile218Thr)	rs200008075	no	-	-	-	-
ZNF80	NM_007136.3	3	c.169G>A (p.Val57Met)	rs146464395	yes	yes	0/182	-	-
PDCD2	NM_002598.3	6	c.725A>G (p.Gln242Arg)	rs202247759	no	-	-	-	-
TNXB	NM_019105.6	6	c.12716C>T (p.Ala4239Val)	rs202247763	no	-	-	-	-
AASS	NM_005763.3	7	c.1990T>C (p.Ser664Pro)	rs202247760	yes	no	0/174	tolerated	0/7
POLR1E	NM_022490.1	9	c.994A>G (p.Met332Val)	rs144866314	no	-	-	-	-
IFIT2	NM_001547.4	10	c.1334A>G (p.Lys445Arg)	rs138979563	yes	-	3/69	-	-
SUFU	NM_016169.3	10	c.367C>T (p.Arg123Cys)	rs202247756	yes	no	0/180	damaging	7/7
ACAD8	NM_014384.2	11	c.1007C>T (p.Ala336Val)	rs202247761	no	-	-	-	-
NCAPD3	NM_015261.2	11	c.4342C>T	rs140724102	no	-	-	-	-

			(p.Arg1448Trp)						
KL	NM_004795.3	13	c.1160G>A (p.Arg387His)	rs200112661	yes	-	1/90	-	-
SERPINA12	NM_173850.2	14	c.1118C>T (p.Arg373Val)	rs138209155	yes	-	1/89	-	-
C14orf102	NM_017970.2	14	c.1924C>T (p.Gln642*)	rs200542150	no	-	-	-	-
ARNT2	NM_014862.3	15	c.1707G>T (p.Gln569>His)	rs145379118	no	-	-	-	-
ZNF491	NM_152356.3	19	c.695G>T (p.Arg232Met)	rs142223398	no	-	-	-	-
ARHGAP33	NM_052948.3	19	c.1511C>T (p.Thr504Ile)	rs140445323	no	-	-	-	-
PHEX	NM_000444.4	X	c.901A>C (p.Asn301His)	rs199893153	no	-	-	-	-
KLHL15	NM_030624.2	X	c.1528C>T (p.Pro510Ser)	rs202247762	no	-	-	-	-

a) With the meningiomas in Family 1.

b) With Polyphen2 and SIFT.

c) Loss of Heterozygosity.

Table S3. Primers for *SUFU* PCR, Sequencing, and Site-Directed Mutagenesis

Exon nro	Primer Sequence (5'-3')	Reverse Primer Sequence (5'-3')	Product Size (bp)	Sample Material
1	GTCAGTGCTCTCCCCGTC	CCACAAATTACTTCGCCCTC	321	DNA[a]
2	TCTGGAGAGATGTGGCCTCT	GGTTCCACGGAGAAGTACCA	388	DNA[a]
3	TTGGATACTGAGGCCACCAT	AAGGCCACTCCACAAACATC	341	DNA[a]
4	CATCCGGAGTGAATGCTTCT	AACCTCCCACTCCCTTCACT	388	DNA[a]
5	CAGAGAGCCTGGGTAGCTGA	CCCCACATGGAGGGTAGTG	242	DNA[a]
6	CAAACAGGGCAGGCTGTAG	CCTCTGTTTTCCCAGGATGA	239	DNA[a]
7	TAAGAGCAGTGGCTGAAAGG	CCCTGCTGGAAGACTTCACT	393	DNA[a]
8	GCTGAGCCAGGTTTCAAGAG	TCTCTCATGCAATCCACAGG	273	DNA[a]
9	TGAGAAGTGCTTGGTGCAGT	CTGGGGAGGCTCTGAAGTG	398	DNA[a]
10	TAGTCCCCACTGTCCCAGAG	CATGAGGCATTCATGACCAG	356	DNA[a]
11	TCCTCCATGGTCAGAAGAGAG	ACATGCATGCACAGACGTG	250	DNA[a]
12	GGCAATCTCTGGAAAGACCA	CGCAGTCTTCCTCACACTTG	283	DNA[a]
2-I	CCAGGATGGGTCCTTTAGGT	AGATCACTCAGGCCGAAGC	210	DNA[b]
2-II	CCAGACCCCTTGGACTATGT	GCTCAGGAAGACCTCAGGAA	182	DNA[b]
3-I	CTGAGGCCACCATAAAAAGG	CCAAGCCCTGCATTAACTCT	214	DNA[b]
3-II	GGCTTTGAGTTGACCTTTCG	AAGGCCACTCCACAAACATC	205	DNA[b]
4-I	AGCCTGGGCTAGTGAGATCC	AACTACCCCAAAGGGTGTCTG	216	DNA[b]
4-II	TTCTGCAGTGGGGACCAT	CTTCACTCCCCCTCCTCAA	220	DNA[b]
5	TGGGTAGCTGACCTTCTTGG	GGAGGGTAGTGGAGGGACTC	225	DNA[b]
6	AAACAGGGCAGGCTGTAGG	CCTCTGTTTTCCCAGGATGA	238	DNA[b]
7-I	AGTGGCTGAAAGGGTGGTC	CTGTGTGCCGATGCAGAT	207	DNA[b]
7-II	TGACAAAGGCATCGAGACAG	CCTGGGGAAAAGGAAGGA	199	DNA[b]
8-I	CTGCTGAGCCAGGTTTCAAG	GGACACTGGGGAACTTACGG	212	DNA[b]
8-II	GGGCAACTTAGTGGTGTCGT	TCTCTCATGCAATCCACAGG	218	DNA[b]
9-II	ACAGCCTGGAAAGTGACAGC	CTGGGGAGGCTCTGAAGTG	206	DNA[b]
10-I	TAGTCCCCACTGTCCCAGAG	GCGTAAGGATGCTCCTCAGT	211	DNA[b]

10-II	GTCTCCATGTTCCCATCTCC	GGTGGGCAAGGAAGTCTATG	211	DNA[b]
11	TTGGTGGTTGGCAAAAAGAT	ACATGCATGCACAGACGTG	216	DNA[b]
12	CTCTGGAAAGACCACGGTGTA	GGAAGTCACTGGGGAGCAG	220	DNA[b]
3	GTTTTGGTGGTTTTGGCTTTGAGTT GACCTTTTGTCTGAAGAG	CTCTTCAGACAAAAGGTCAACTCA AAGCCAAAACCACCAAAAC	215	cDNA clone[c]
1	CCGTAGATGGCGTGCAGT	-	-	cDNA clone[d]
4	-	AACTACCCCAAAGGGTGTCTG	-	cDNA clone[d]
3	GGCTTTGAGTTGACCTTTCG	-	-	cDNA clone[d]
3	TTCTGCAGTGGGGACCAT	-	-	cDNA clone[d]
7	-	CTGTGTGCCGATGCAGAT	-	cDNA clone[d]
7	TGACAAAGGCATCGAGACAG	-	-	cDNA clone[d]
9	ACAGCCTGGAAAGTGACAGC	-	-	cDNA clone[d]
12	-	GGAAGTCACTGGGGAGCAG	-	cDNA clone[d]

a) Primers for Lymphocyte DNA.

b) Primers for FFPE DNA.

c) Primers for site-directed mutagenesis of the human *SUFU* cDNA clone.

d) Primers for sequencing of the human *SUFU* cDNA clone.

Table S4. All *SUFU* Variants Identified in the 162 Individuals with Meningioma

Exon Number	dbSNP ID	Nucleotide Change	Individuals with a Heterozygous Variant[a]	Individuals with a Homozygous Variant[a]
1	rs2274351	c.182+16C>T	16/40	0/40
			47/77	10/77
			1/4	1/4
			nd	nd
2	rs2281879	c.183-49G>C	16/40	0/40
			38/76	4/76
			2/4	0/4
			8/39	5/39
2	rs67595177	c.183-67delG	6/40	0/40
			12/76	0/76
			2/4	0/4
			6/39	0/39
2	rs138784497	c.317+59G>A	0/40	0/40
			1/76	0/76
			0/4	0/4

			nd	nd
3	rs117807100	c.454+45G>T	1/40	0/40
			2/77	0/77
			0/4	0/4
			nd	nd
7	rs202247757	c.910+14C>T	1/40	0/40
			0/76	0/76
			0/4	0/4
			0/40	0/40
8	rs3824756	c.1022+49T>C	5/40	0/40
			10/77	0/77
			3/4	0/4
			2/40	0/40
9	rs202247758	c.1023-28C>T	0/40	0/40
			1/76	0/76
			0/4	0/4
			nd	nd
9	rs117407459	c.1023-23C>G	0/40	0/40

			2/76	0/76
			0/4	0/4
			nd	nd
11	rs12414407	c.1365+19T>C	16/40	18/40
			1/76	0/76
			3/4	0/4
			11/40	10/40
11	rs17114803	c.1299T>C	4/40	1/40
		(p.Ile433=)	1/76	0/76
			2/4	0/4
			3/40	0/40
12	rs4917980	c.1455+20T>G	0/40	0/40
			0/77	77/77
			0/4	3/4
			0/40	23/40

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a) The uppermost numbers denote the UK meningioma cases, the second numbers denote Finnish meningioma cases recruited in the Interphone study group[1], the third numbers denote Finnish *NF2* negative multiple meningioma cases, and the numbers at the bottom denote FFPE meningioma tumors collected through a search into Finnish Cancer Registry.

Reference

1. Bethke, L., Murray, A., Webb, E., Schoemaker, M., Muir, K., McKinney, P., Hepworth, S., Dimitropoulou, P., Lophatananon, A., Feychting, M. et al. (2008). Comprehensive analysis of DNA repair gene variants and risk of meningioma. J. Natl. Cancer Inst. 100, 270-276.