Supplementary Tables

Supplementary Table 1. Genotypes of progenies obtained from *Pik3ca*$^{e20mwt/+}$ x *Pik3ca*$^{e20mwt/+}$ intercross

Supplementary Table 2. Samples used for genomic analysis

Supplementary Table 3. Predicted somatic mutations in tumors

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Supplementary Table 5. *Trp53* sequencing primers

Supplementary Table 1 Genotypes of progenies obtained from Pik3ca$^{e20mwt/+}$ x Pik3ca$^{e20mwt/+}$ intercross

Line 1 Intercross: PIK3CA$^{e20mwt/+}$ x PIK3CA$^{e20mwt/+}$

	Genotypes		
	e20mwt/e20mwt	**e20mwt/+**	**+/+**
Observed	22	51	26
Expected	24.75	49.5	24.75

Chi squared equals 0.414 with 2 degrees of freedom. The two-tailed P value equals 0.8130

Line 2 Intercross: PIK3CAe20mwt/+ x PIK3CAe20mwt/+

	Genotypes		
	e20mwt/e20mwt	**e20mwt/+**	**+/+**
Observed	11	20	6
Expected	9.25	18.5	9.25

Chi squared equals 1.595 with 2 degrees of freedom. The two-tailed P value equals 0.4505.

Supplementary Table 2. Samples used for genomic analysis

No	Sample ID	Sample Type	Histology	Exome	Expression	CGH	Sanger Sequencing
1	155	Tumor	Adenocarcinoma	x	x	x	
2	358	Tumor	Adenocarcinoma	x		x	
3	359	Tumor	Adenocarcinoma		x		
4	594	Tumor	Adenocarcinoma	x		x	
5	155-p1-1	Tumor	Adenocarcinoma		x	x	
6	155-p1-3	Tumor	Adenocarcinoma		x	x	
7	357-p1	Tumor	Adenocarcinoma		x	x	
8	145	Tumor	Fibroadenoma	x			
9	196	Tumor	Fibroadenoma	x		x	
10	219	Tumor	Fibroadenoma	x		x	
11	317	Tumor	Fibroadenoma	x	x	x	
12	326	Tumor	Fibroadenoma	x	x	x	
13	352	Tumor	Fibroadenoma	x	x	x	
14	612	Tumor	Fibroadenoma	x		x	
15	357	Tumor	Firboadenoma	x	x	x	
16	628	Tumor	Firboadenoma		x		
17	113	Tumor	spindle cell				x
18	323	Tumor	Spindle Cell	x	x	x	
19	323-p1	Tumor	Spindle Cell		x	x	
20	323-p2	Tumor	Spindle Cell		x	x	
21	323-p3	Tumor	Spindle Cell		x	x	
22	2761	sperm	Normal	x			
23	317_Mg_MC	Normal_Mammary gland	Normal		x		
24	326_Mg_MC	Normal_Mammary gland	Normal		x		
25	460_Mg_C	Normal_Mammary gland	Normal		x		
26	461_Mg_C	Normal_Mammary gland	Normal		x		
27	628_Mg_MC	Normal_Mammary gland	Normal		x		
28	707_Mg_C	Normal_Mammary gland	Normal		x		
29	155_kd_MC	Normal_Kidney	Normal	x			
30	219_kd_MC	Normal_Kidney	normal	x		x	

Supplementary Table 2. Samples used for genomic analysis

No	Sample ID	Sample Type	Histology	Exome	Expression	CGH	Sanger Sequencing
31	2762-21	Normal_Kidney	Normal	x			
32	2762-5	Normal_Kidney	Normal	x			
33	2828-377	Normal_Kidney	Normal	x			
34	357_kd_MC	Normal_Kidney	Normal	x			
35	358_kd_MC	Normal_Kidney	Normal	x		x	
36	SCID1	Normal_Kidney	normal	x			
37	SCID6	Normal_Kidney	Normal	x			
38	317_kd_MC	Normal_Kidney	normal	x		x	
39	326_kd_MC	Normal_Kidney	normal	x		x	

Supplementary Table 3.   Predicted somatic mutations in tumors

Sample Id	Histological type	GeneName	DB	Gene	Transcript	Consequence	Position_in_cDNA	Position_in_protein	Amino_acid_change	Chromosome	Position	Ref	Var	Effect (SIFT)	Score (SIFT)	Median Info (SIFT)	Effect (Polyphen)	Score (Polyphen)
155	Adeno Carcinoma	1700086D15Rik	MGI	ENSMUSG00000020548	ENSMUST00000108696	NON_SYNONYMOUS_CODING	388	113	K/R	chr11	64966116	T	C	No sufficient homology	-	-	benign	0.675
155	Adeno Carcinoma	2210408I21Rik	MGI	ENSMUSG00000071252	ENSMUST00000095588	NON_SYNONYMOUS_CODING	2060	676	R/Q	chr13	77407077	G	A	TOLERATED	0.36	4.32	benign	0.107
155	Adeno Carcinoma	C230081A13Rik	MGI	ENSMUSG00000074305	ENSMUST00000061552	NON_SYNONYMOUS_CODING	733	88	E/D	chr9	56108186	C	G	DELETERIOUS	0	4.32	benign	1.245
155	Adeno Carcinoma	Ccdc36	MGI	ENSMUSG00000047220	ENSMUST00000076592	NON_SYNONYMOUS_CODING	1124	375	H/Y	chr9	108307708	G	A	DELETERIOUS	0	4.32	probably damaging	2.056
155	Adeno Carcinoma	Cmah	MGI	ENSMUSG00000016756	ENSMUST00000050859	NON_SYNONYMOUS_CODING	1197	220	V/I	chr13	24527021	G	A	DELETERIOUS	0.03	3.46	benign	1.204
155	Adeno Carcinoma	Hip1	MGI	ENSMUSG00000039959	ENSMUST00000060311	NON_SYNONYMOUS_CODING	872	284	R/L	chr5	135916147	C	A	DELETERIOUS	0.04	2.85	probably damaging	2.178
155	Adeno Carcinoma	Klhl5	MGI	ENSMUSG00000054920	ENSMUST00000101191	NON_SYNONYMOUS_CODING	1238	358	L/F	chr5	65540002	C	T	DELETERIOUS	0	2.74	probably damaging	2.05
155	Adeno Carcinoma	Krt10	MGI	ENSMUSG00000019761	ENSMUST00000103131	NON_SYNONYMOUS_CODING	43	4	L/R	chr11	99250636	A	C	DELETERIOUS	0	4.32	unknown	-
155	Adeno Carcinoma	L3mbtl	MGI	ENSMUSG00000035576	ENSMUST00000035751	NON_SYNONYMOUS_CODING	1342	367	A/T	chr2	162786773	G	A	TOLERATED	0.27	2.78	benign	1.177
155	Adeno Carcinoma	Med1	MGI	ENSMUSG00000018160	ENSMUST00000107545	NON_SYNONYMOUS_CODING	4253	1348	T/M	chr11	98017240	G	A	TOLERATED	0.52	3.59	unknown	-
155	Adeno Carcinoma	Med24	MGI	ENSMUSG00000017210	ENSMUST00000100500	NON_SYNONYMOUS_CODING	813	234	A/V	chr11	98577755	G	A	TOLERATED	0.38	3.37	benign	1.099
155	Adeno Carcinoma	Plk1	MGI	ENSMUSG00000030867	ENSMUST00000033154	NON_SYNONYMOUS_CODING	1148	364	R/W	chr7	129311164	C	T	DELETERIOUS	0.02	2.74	benign	1.397
155	Adeno Carcinoma	Setd2	MGI	ENSMUSG00000044791	ENSMUST00000153838	NON_SYNONYMOUS_CODING	4114	1358	N/K	chr9	110453696	C	G	DELETERIOUS	0	4.32	possibly damaging	1.611
155	Adeno Carcinoma	Sgca	MGI	ENSMUSG00000001508	ENSMUST00000103162	NON_SYNONYMOUS_CODING	731	160	A/S	chr11	94832661	C	A	TOLERATED	0.49	2.86	benign	0.373
155	Adeno Carcinoma	Smg1	MGI	ENSMUSG00000030655	ENSMUST00000032891	NON_SYNONYMOUS_CODING	1839	498	V/I	chr7	125339345	C	T	DELETERIOUS	0	3.53	benign	0.225
155	Adeno Carcinoma	Tpr	MGI	ENSMUSG00000006005	ENSMUST00000064506	NON_SYNONYMOUS_CODING	5804	1831	E/K	chr1	152283895	G	A	DELETERIOUS	0.04	3.49	possibly damaging	1.507
155	Adeno Carcinoma	Tssk2	MGI	ENSMUSG00000045521	ENSMUST00000055374	NON_SYNONYMOUS_CODING	832	251	R/C	chr16	17899578	C	T	DELETERIOUS	0	2.75	benign	0.891
155	Adeno Carcinoma	Zfc3h1	MGI	ENSMUSG00000034163	ENSMUST00000036044	NON_SYNONYMOUS_CODING	5928	1897	A/S	chr10	114867761	G	T	DELETERIOUS	0	4.32	benign	1.002
155	Adeno Carcinoma	Zp2	MGI	ENSMUSG00000030911	ENSMUST00000033207	NON_SYNONYMOUS_CODING	1676	549	A/V	chr7	127278693	G	A	TOLERATED	0.61	2.79	benign	1.097
358	Adeno Carcinoma	Cacna1g	MGI	ENSMUSG00000020866	ENSMUST00000107789	NON_SYNONYMOUS_CODING	6917	2145	S/F	chr11	94271171	G	A	DELETERIOUS	0	3.43	possibly damaging	1.838
358	Adeno Carcinoma	Olfr1016	MGI	ENSMUSG00000075209	ENSMUST00000099915	NON_SYNONYMOUS_CODING	437	146	A/V	chr2	85639989	G	A	TOLERATED	0.62	2.75	benign	0.171
358	Adeno Carcinoma	Syp	MGI	ENSMUSG00000031144	ENSMUST00000069520	NON_SYNONYMOUS_CODING	508	96	F/I	chrX	7221285	T	A	DELETERIOUS	0.03	2.89	probably damaging	2.031
358	Adeno Carcinoma	Trp53	MGI	ENSMUSG00000059552	ENSMUST00000108658	NON_SYNONYMOUS_CODING	703	192	I/N	chr11	69402152	T	A	DELETERIOUS	0	2.77	probably damaging	2.796
594	Adeno Carcinoma	Lilra6	MGI	ENSMUSG00000030427	ENSMUST00000073970	NON_SYNONYMOUS_CODING	1807	600	D/N	chr7	3863069	C	T	TOLERATED	0.31	2.79	benign	0.161
594	Adeno Carcinoma	Mrps30	MGI	ENSMUSG00000021731	ENSMUST00000022245	NON_SYNONYMOUS_CODING	379	121	A/T	chr13	119175681	C	T	TOLERATED	0.45	2.82	benign	0.201
594	Adeno Carcinoma	Pcdha5	MGI	ENSMUSG00000007440	ENSMUST00000115662	NON_SYNONYMOUS_CODING	64	22	A/T	chr18	37099035	G	A	TOLERATED	0.34	2.84	benign	0.211
594	Adeno Carcinoma	Pcdhb5	MGI	ENSMUSG00000063687	ENSMUST00000078271	NON_SYNONYMOUS_CODING	677	163	S/R	chr18	37480711	C	A	TOLERATED	0.53	2.77	benign	0.238
594	Adeno Carcinoma	Rcn3	MGI	ENSMUSG00000019539	ENSMUST00000117546	NON_SYNONYMOUS_CODING	781	220	V/L	chr7	52340295	C	A	DELETERIOUS	0.02	2.84	benign	0.798
594	Adeno Carcinoma	Rcor3	MGI	ENSMUSG00000037395	ENSMUST00000073279	NON_SYNONYMOUS_CODING	510	133	A/V	chr1	193949859	G	A	TOLERATED	0.1	2.89	benign	1.222
594	Adeno Carcinoma	Spna2	MGI	ENSMUSG00000057738	ENSMUST00000113719	NON_SYNONYMOUS_CODING	1322	365	R/C	chr2	29843861	C	T	DELETERIOUS	0	2.87	probably damaging	2.74
594	Adeno Carcinoma	Usp2	MGI	ENSMUSG00000032010	ENSMUST00000034508	NON_SYNONYMOUS_CODING	733	164	D/E	chr9	43883981	T	G	DELETERIOUS	0	4.32	benign	0.9
155-p1-1	Adeno Carcinoma	1700014B07Rik	MGI	ENSMUSG00000048749	ENSMUST00000056627	NON_SYNONYMOUS_CODING	237	79	M/I	chr2	6243581	C	T	-	-	-	-	-
155-p1-1	Adeno Carcinoma	1700014B07Rik	MGI	ENSMUSG00000048749	ENSMUST00000056627	NON_SYNONYMOUS_CODING	236	79	M/R	chr2	6243582	A	C	-	-	-	-	-
155-p1-1	Adeno Carcinoma	1700081L11Rik	MGI	ENSMUSG00000018412	ENSMUST00000106972	NON_SYNONYMOUS_CODING	3559	970	S/I	chr11	104196924	C	A	TOLERATED	0.12	3.53	possibly damaging	1.989
155-p1-1	Adeno Carcinoma	1700086D15Rik	MGI	ENSMUSG00000020548	ENSMUST00000108696	NON_SYNONYMOUS_CODING	388	113	K/R	chr11	64966116	T	C	-	-	-	benign	0.675
155-p1-1	Adeno Carcinoma	2210408I21Rik	MGI	ENSMUSG00000071252	ENSMUST00000095588	NON_SYNONYMOUS_CODING	2060	676	R/Q	chr13	77407077	G	A	TOLERATED	0.36	4.32	benign	0.107
155-p1-1	Adeno Carcinoma	Abca16	MGI	ENSMUSG00000051900	ENSMUST00000120490	NON_SYNONYMOUS_CODING	870	279	R/W	chr7	127577108	C	T	DELETERIOUS	0	2.81	probably damaging	2.348
155-p1-1	Adeno Carcinoma	Aldh3a1	MGI	ENSMUSG00000019102	ENSMUST00000108716	NON_SYNONYMOUS_CODING	627	154	I/N	chr11	61027753	T	A	DELETERIOUS	0	2.79	probably damaging	2.827
155-p1-1	Adeno Carcinoma	Aldh3a1	MGI	ENSMUSG00000019102	ENSMUST00000108716	NON_SYNONYMOUS_CODING	1080	305	H/R	chr11	61029887	A	G	TOLERATED	0.29	2.79	possibly damaging	1.938
155-p1-1	Adeno Carcinoma	Alox15	MGI	ENSMUSG00000018924	ENSMUST00000019068	NON_SYNONYMOUS_CODING	1730	568	K/N	chr11	70158430	T	G	TOLERATED	1	2.77	benign	0.847
155-p1-1	Adeno Carcinoma	Alox15	MGI	ENSMUSG00000018924	ENSMUST00000019068	NON_SYNONYMOUS_CODING	1729	568	K/T	chr11	70158431	T	G	TOLERATED	1	2.77	benign	0.847
155-p1-1	Adeno Carcinoma	Bpil3	MGI	ENSMUSG00000068009	ENSMUST00000088955	NON_SYNONYMOUS_CODING	765	207	S/P	chr2	153731777	T	C	TOLERATED	0.08	2.77	possibly damaging	1.798
155-p1-1	Adeno Carcinoma	C2cd2	MGI	ENSMUSG00000045975	ENSMUST00000060801	NON_SYNONYMOUS_CODING	521	73	A/G	chr16	98143708	G	C	TOLERATED	0.29	3.05	benign	1.262
155-p1-1	Adeno Carcinoma	Ccdc36	MGI	ENSMUSG00000047220	ENSMUST00000076592	NON_SYNONYMOUS_CODING	1124	375	H/Y	chr9	108307708	G	A	DELETERIOUS	0	4.32	probably damaging	2.056
155-p1-1	Adeno Carcinoma	Cmah	MGI	ENSMUSG00000016756	ENSMUST00000050859	NON_SYNONYMOUS_CODING	1197	220	V/I	chr13	24527021	G	A	DELETERIOUS	0.03	3.46	benign	1.204
155-p1-1	Adeno Carcinoma	Corin	MGI	ENSMUSG00000005220	ENSMUST00000005352	NON_SYNONYMOUS_CODING	2878	940	R/C	chr5	72696309	G	A	TOLERATED	0.17	2.83	probably damaging	2.257
155-p1-1	Adeno Carcinoma	Dock3	MGI	ENSMUSG00000039716	ENSMUST00000044532	NON_SYNONYMOUS_CODING	4438	1363	K/E	chr9	106832371	T	C	TOLERATED	0.1	2.77	benign	1.312
155-p1-1	Adeno Carcinoma	Fam83g	MGI	ENSMUSG00000042377	ENSMUST00000093019	NON_SYNONYMOUS_CODING	1746	544	P/L	chr11	61516774	C	T	DELETERIOUS	0	4.32	probably damaging	2.494
155-p1-1	Adeno Carcinoma	Gm10862	MGI	ENSMUSG00000075554	ENSMUST00000100454	NON_SYNONYMOUS_CODING	215	72	R/L	chr2	4013026	G	T	-	-	-	-	-
155-p1-1	Adeno Carcinoma	Heatr6	MGI	ENSMUSG00000000976	ENSMUST00000001002	NON_SYNONYMOUS_CODING	928	301	P/T	chr11	83578487	C	A	TOLERATED	0.13	3.37	probably damaging	2.061
155-p1-1	Adeno Carcinoma	Helb	MGI	ENSMUSG00000020228	ENSMUST00000020449	NON_SYNONYMOUS_CODING	133	3	R/K	chr10	119549911	C	T	DELETERIOUS	0	4.32	benign	1.128
155-p1-1	Adeno Carcinoma	Hip1	MGI	ENSMUSG00000039959	ENSMUST00000060311	NON_SYNONYMOUS_CODING	872	284	R/L	chr5	135916147	C	A	DELETERIOUS	0.04	2.85	probably damaging	2.178
155-p1-1	Adeno Carcinoma	Il1rn	MGI	ENSMUSG00000026981	ENSMUST00000028358	NON_SYNONYMOUS_CODING	121	31	P/S	chr2	24192500	C	T	-	-	-	-	-
155-p1-1	Adeno Carcinoma	Itih5	MGI	ENSMUSG00000025780	ENSMUST00000026886	NON_SYNONYMOUS_CODING	467	124	D/E	chr2	10108654	T	A	TOLERATED	1	2.81	benign	1.342
155-p1-1	Adeno Carcinoma	Itih5	MGI	ENSMUSG00000025780	ENSMUST00000026886	NON_SYNONYMOUS_CODING	1278	395	D/N	chr2	10160263	G	A	TOLERATED	0.13	2.78	benign	1.231
155-p1-1	Adeno Carcinoma	Klhl5	MGI	ENSMUSG00000054920	ENSMUST00000101191	NON_SYNONYMOUS_CODING	1238	358	L/F	chr5	65540002	C	T	DELETERIOUS	0	2.76	probably damaging	2.05
155-p1-1	Adeno Carcinoma	Krt10	MGI	ENSMUSG00000019761	ENSMUST00000103131	NON_SYNONYMOUS_CODING	43	4	L/R	chr11	99250636	A	C	DELETERIOUS	0	4.32	unknown	-
155-p1-1	Adeno Carcinoma	L3mbtl	MGI	ENSMUSG00000035576	ENSMUST00000035751	NON_SYNONYMOUS_CODING	1342	367	A/T	chr2	162786773	G	A	TOLERATED	0.27	2.78	benign	1.177
155-p1-1	Adeno Carcinoma	Lgals9	MGI	ENSMUSG00000001123	ENSMUST00000108269	NON_SYNONYMOUS_CODING	499	155	H/P	chr11	78783286	T	G	TOLERATED	0.26	3.32	benign	0.431
155-p1-1	Adeno Carcinoma	Med1	MGI	ENSMUSG00000018160	ENSMUST00000107545	NON_SYNONYMOUS_CODING	4253	1348	T/M	chr11	98017240	G	A	TOLERATED	0.52	3.59	unknown	-

Supplementary Table 3. Predicted somatic mutations in tumors

Sample Id	Histological type	GeneName	DB	Gene	Transcript	Consequence	Position_in_cDNA	Position_in_protein	Amino_acid_change	Chromosome	Position	Ref	Var	Effect (SIFT)	Score (SIFT)	Median Info (SIFT)	Effect (Polyphen)	Score (Polyphen)
155-p1-1	Adeno Carcinoma	Med24	MGI	ENSMUSG00000017210	ENSMUST00000100500	NON_SYNONYMOUS_CODING	813	234	A/V	chr11	98577755	G	A	TOLERATED	0.38	3.37	benign	1.099
155-p1-1	Adeno Carcinoma	Megf10	MGI	ENSMUSG00000024593	ENSMUST00000075770	NON_SYNONYMOUS_CODING	3420	921	N/T	chr18	57448970	A	C	TOLERATED	0.24	3.36	benign	1.455
155-p1-1	Adeno Carcinoma	Mgl2	MGI	ENSMUSG00000040950	ENSMUST00000108584	NON_SYNONYMOUS_CODING	752	238	R/Q	chr11	69950242	G	A	TOLERATED	0.41	2.75	benign	1.269
155-p1-1	Adeno Carcinoma	Myh13	MGI	ENSMUSG00000060180	ENSMUST00000108684	STOP_GAINED	4851	1564	R/*	chr11	67177997	C	T	-	-	-	unknown	-
155-p1-1	Adeno Carcinoma	Nbr1	MGI	ENSMUSG00000017119	ENSMUST00000103099	NON_SYNONYMOUS_CODING	1411	261	R/Q	chr11	101428492	G	A	DELETERIOUS	0.04	3.55	possibly damaging	1.595
155-p1-1	Adeno Carcinoma	Necab3	MGI	ENSMUSG00000027489	ENSMUST00000000895	STOP_GAINED	136	37	R/*	chr2	154382811	G	A	-	-	-	unknown	-
155-p1-1	Adeno Carcinoma	Nlrp1a	MGI	ENSMUSG00000069830	ENSMUST00000108519	NON_SYNONYMOUS_CODING	3903	1202	S/P	chr11	70906037	A	G	TOLERATED	1	4.32	benign	0.517
155-p1-1	Adeno Carcinoma	Nos2	MGI	ENSMUSG00000020826	ENSMUST00000018610	NON_SYNONYMOUS_CODING	989	245	S/T	chr11	78751092	G	C	TOLERATED	1	2.78	benign	0.633
155-p1-1	Adeno Carcinoma	Plk1	MGI	ENSMUSG00000030867	ENSMUST00000033154	NON_SYNONYMOUS_CODING	1148	364	R/W	chr7	129311164	C	T	DELETERIOUS	0.02	2.79	benign	1.397
155-p1-1	Adeno Carcinoma	Rbbp5	MGI	ENSMUSG00000026439	ENSMUST00000027700	NON_SYNONYMOUS_CODING	1401	420	P/L	chr1	134393468	C	T	TOLERATED	0.08	3.1	probably damaging	2.106
155-p1-1	Adeno Carcinoma	Rpain	MGI	ENSMUSG00000018449	ENSMUST00000018593	NON_SYNONYMOUS_CODING	905	204	S/T	chr11	70788523	G	C	TOLERATED	0.17	2.97	possibly damaging	1.595
155-p1-1	Adeno Carcinoma	Sarm1	MGI	ENSMUSG00000050132	ENSMUST00000108287	NON_SYNONYMOUS_CODING	1720	574	L/F	chr11	78297069	G	A	DELETERIOUS	0	4.32	benign	1.047
155-p1-1	Adeno Carcinoma	Setd2	MGI	ENSMUSG00000044791	ENSMUST00000153838	NON_SYNONYMOUS_CODING	4114	1358	N/K	chr9	110453696	C	G	DELETERIOUS	0	4.32	possibly damaging	1.611
155-p1-1	Adeno Carcinoma	Sgca	MGI	ENSMUSG00000001508	ENSMUST00000103162	NON_SYNONYMOUS_CODING	731	160	A/S	chr11	94832661	C	A	TOLERATED	0.49	2.86	benign	0.373
155-p1-1	Adeno Carcinoma	Tbc1d23	MGI	ENSMUSG00000022749	ENSMUST00000023431	ESSENTIAL_SPLICE_SITE	0	0	-	chr16	57218535	T	A	-	-	-	-	-
155-p1-1	Adeno Carcinoma	Thnsl1	MGI	ENSMUSG00000048550	ENSMUST00000054591	NON_SYNONYMOUS_CODING	366	14	A/T	chr2	21133103	G	A	TOLERATED	1	4.32	benign	0.724
155-p1-1	Adeno Carcinoma	Thnsl1	MGI	ENSMUSG00000048550	ENSMUST00000054591	NON_SYNONYMOUS_CODING	1866	514	V/M	chr2	21134603	G	A	DELETERIOUS	0	2.75	benign	0.927
155-p1-1	Adeno Carcinoma	Tnfrsf13b	MGI	ENSMUSG00000010142	ENSMUST00000010286	NON_SYNONYMOUS_CODING	599	175	R/S	chr11	60960519	C	A	TOLERATED	0.66	4.32	benign	1.093
155-p1-1	Adeno Carcinoma	Tpr	MGI	ENSMUSG00000006005	ENSMUST00000064506	NON_SYNONYMOUS_CODING	5804	1831	E/K	chr1	152283895	G	A	DELETERIOUS	0.04	3.49	possibly damaging	1.507
155-p1-1	Adeno Carcinoma	Tssk2	MGI	ENSMUSG00000045521	ENSMUST00000055374	NON_SYNONYMOUS_CODING	832	251	R/C	chr16	17899578	C	T	DELETERIOUS	0	2.82	benign	0.891
155-p1-1	Adeno Carcinoma	Ugt1a10	MGI	ENSMUSG00000090165	ENSMUST00000113142	ESSENTIAL_SPLICE_SITE	0	0	-	chr1	90114701	G	C	-	-	-	-	-
155-p1-1	Adeno Carcinoma	Unc13c	MGI	ENSMUSG00000062151	ENSMUST00000075245	NON_SYNONYMOUS_CODING	4168	1390	W/R	chr9	73541100	A	G	DELETERIOUS	0	3.7	probably damaging	4.029
155-p1-1	Adeno Carcinoma	Usp43	MGI	ENSMUSG00000020905	ENSMUST00000021288	NON_SYNONYMOUS_CODING	3110	1002	D/G	chr11	67669377	T	C	TOLERATED	0.26	4.32	benign	0.748
155-p1-1	Adeno Carcinoma	Usp43	MGI	ENSMUSG00000020905	ENSMUST00000021288	NON_SYNONYMOUS_CODING	2383	760	M/V	chr11	67688822	T	C	TOLERATED	0.21	3.32	benign	0.696
155-p1-1	Adeno Carcinoma	Zfc3h1	MGI	ENSMUSG00000034163	ENSMUST00000036044	NON_SYNONYMOUS_CODING	5928	1897	A/S	chr10	114867761	G	T	DELETERIOUS	0	4.32	benign	1.002
155-p1-1	Adeno Carcinoma	Zfp106	MGI	ENSMUSG00000027288	ENSMUST00000055241	NON_SYNONYMOUS_CODING	2478	776	N/D	chr2	120359404	T	C	DELETERIOUS	0	3.5	possibly damaging	1.699
155-p1-1	Adeno Carcinoma	Zp2	MGI	ENSMUSG00000030911	ENSMUST00000033207	NON_SYNONYMOUS_CODING	1676	549	A/V	chr7	127278693	G	A	TOLERATED	0.61	2.79	benign	1.097
155-p1-2	Adeno Carcinoma	14-Sep	MGI	ENSMUSG00000032300	ENSMUST00000034846	NON_SYNONYMOUS_CODING	2050	618	E/K	chr9	57105045	C	T	TOLERATED	0.4	3.73	benign	1.372
155-p1-2	Adeno Carcinoma	1700017B05Rik	MGI	ENSMUSG00000032300	ENSMUST00000034846	NON_SYNONYMOUS_CODING	2050	618	E/K	chr9	57105045	C	T	TOLERATED	0.4	3.73	benign	1.372
155-p1-2	Adeno Carcinoma	1700023E05Rik	MGI	ENSMUSG00000029248	ENSMUST00000031161	NON_SYNONYMOUS_CODING	1494	455	E/D	chr5	77490322	A	C	TOLERATED	0.17	3.75	benign	0.675
155-p1-2	Adeno Carcinoma	1700086D15Rik	MGI	ENSMUSG00000020548	ENSMUST00000108696	NON_SYNONYMOUS_CODING	388	113	K/R	chr11	64966116	T	C	-	-	-	benign	0.675
155-p1-2	Adeno Carcinoma	2210408I21Rik	MGI	ENSMUSG00000071252	ENSMUST00000095588	NON_SYNONYMOUS_CODING	2060	676	R/Q	chr13	77407077	G	A	TOLERATED	0.36	4.32	benign	0.107
155-p1-2	Adeno Carcinoma	Abca16	MGI	ENSMUSG00000051900	ENSMUST00000120490	NON_SYNONYMOUS_CODING	870	279	R/W	chr7	127577108	C	T	DELETERIOUS	0	2.81	probably damaging	2.348
155-p1-2	Adeno Carcinoma	AI848100	MGI	ENSMUSG00000040297	ENSMUST00000048377	NON_SYNONYMOUS_CODING	177	59	C/W	chr1	163806552	G	C	DELETERIOUS	0.03	4.32	probably damaging	2.471
155-p1-2	Adeno Carcinoma	Aldh3a1	MGI	ENSMUSG00000019102	ENSMUST00000108716	NON_SYNONYMOUS_CODING	627	154	I/N	chr11	61027753	T	A	DELETERIOUS	0	2.79	probably damaging	2.827
155-p1-2	Adeno Carcinoma	Aldh3a1	MGI	ENSMUSG00000019102	ENSMUST00000108716	NON_SYNONYMOUS_CODING	1080	305	H/R	chr11	61029887	A	G	TOLERATED	0.29	2.79	possibly damaging	1.938
155-p1-2	Adeno Carcinoma	Alox15	MGI	ENSMUSG00000018924	ENSMUST00000019068	NON_SYNONYMOUS_CODING	1730	568	K/N	chr11	70158430	T	G	TOLERATED	1	2.77	benign	0.847
155-p1-2	Adeno Carcinoma	Alox15	MGI	ENSMUSG00000018924	ENSMUST00000019068	NON_SYNONYMOUS_CODING	1729	568	K/T	chr11	70158431	T	G	TOLERATED	1	2.77	benign	0.847
155-p1-2	Adeno Carcinoma	Ankib1	MGI	ENSMUSG00000040351	ENSMUST00000043551	NON_SYNONYMOUS_CODING	1659	418	N/S	chr5	3727642	T	C	TOLERATED	0.56	3.39	benign	0.054
155-p1-2	Adeno Carcinoma	Brwd1	MGI	ENSMUSG00000022914	ENSMUST00000153398	NON_SYNONYMOUS_CODING	3006	954	R/Q	chr16	96255409	C	T	DELETERIOUS	0	3.5	possibly damaging	1.892
155-p1-2	Adeno Carcinoma	C2cd2	MGI	ENSMUSG00000045975	ENSMUST00000060801	NON_SYNONYMOUS_CODING	521	73	A/G	chr16	98143708	G	C	TOLERATED	0.29	3.05	benign	1.262
155-p1-2	Adeno Carcinoma	Ccdc36	MGI	ENSMUSG00000047220	ENSMUST00000076592	NON_SYNONYMOUS_CODING	1124	375	H/Y	chr9	108307708	G	A	DELETERIOUS	0	4.32	probably damaging	2.056
155-p1-2	Adeno Carcinoma	Chpf	MGI	ENSMUSG00000032997	ENSMUST00000079205	NON_SYNONYMOUS_CODING	582	139	R/Q	chr1	75474292	C	T	DELETERIOUS	0.05	2.88	possibly damaging	1.737
155-p1-2	Adeno Carcinoma	Cmah	MGI	ENSMUSG00000016756	ENSMUST00000050859	NON_SYNONYMOUS_CODING	1197	220	V/I	chr13	24527021	G	A	DELETERIOUS	0.03	3.46	benign	1.204
155-p1-2	Adeno Carcinoma	Fam83g	MGI	ENSMUSG00000042377	ENSMUST00000093019	NON_SYNONYMOUS_CODING	1746	544	P/L	chr11	61516774	C	T	DELETERIOUS	0	4.32	probably damaging	2.494
155-p1-2	Adeno Carcinoma	Gm10862	MGI	ENSMUSG00000075554	ENSMUST00000100454	NON_SYNONYMOUS_CODING	215	72	R/L	chr2	4013026	G	T	-	-	-	-	-
155-p1-2	Adeno Carcinoma	Heatr6	MGI	ENSMUSG00000000976	ENSMUST00000001002	NON_SYNONYMOUS_CODING	928	301	P/T	chr11	83578487	C	A	TOLERATED	0.13	3.37	probably damaging	2.061
155-p1-2	Adeno Carcinoma	Hip1	MGI	ENSMUSG00000039959	ENSMUST00000060311	NON_SYNONYMOUS_CODING	872	284	R/L	chr5	135916147	C	A	DELETERIOUS	0.04	2.85	probably damaging	2.178
155-p1-2	Adeno Carcinoma	Hsdl2	MGI	ENSMUSG00000028383	ENSMUST00000030078	NON_SYNONYMOUS_CODING	1193	333	E/Q	chr4	59623513	G	C	TOLERATED	0.17	4.32	unknown	-
155-p1-2	Adeno Carcinoma	Htr2a	MGI	ENSMUSG00000034997	ENSMUST00000036653	NON_SYNONYMOUS_CODING	1541	150	V/I	chr14	75044830	G	A	TOLERATED	0.82	2.75	benign	0.144
155-p1-2	Adeno Carcinoma	Ifrd2	MGI	ENSMUSG00000010048	ENSMUST00000010192	NON_SYNONYMOUS_CODING	1099	310	R/C	chr9	107493944	C	T	DELETERIOUS	0	2.78	probably damaging	2.311
155-p1-2	Adeno Carcinoma	Il1rn	MGI	ENSMUSG00000026981	ENSMUST00000028358	NON_SYNONYMOUS_CODING	121	31	P/S	chr2	24192500	C	T	-	-	-	-	-
155-p1-2	Adeno Carcinoma	Itih5	MGI	ENSMUSG00000025780	ENSMUST00000026886	NON_SYNONYMOUS_CODING	467	124	D/E	chr2	10108654	T	A	TOLERATED	1	2.81	benign	1.342
155-p1-2	Adeno Carcinoma	Itih5	MGI	ENSMUSG00000025780	ENSMUST00000026886	NON_SYNONYMOUS_CODING	1278	395	D/N	chr2	10160263	G	A	TOLERATED	0.13	2.78	benign	1.231
155-p1-2	Adeno Carcinoma	Klhl5	MGI	ENSMUSG00000054920	ENSMUST00000101191	NON_SYNONYMOUS_CODING	1238	358	L/F	chr5	65540002	C	T	DELETERIOUS	0	2.76	probably damaging	2.05
155-p1-2	Adeno Carcinoma	Krt10	MGI	ENSMUSG00000019761	ENSMUST00000103131	NON_SYNONYMOUS_CODING	43	4	L/R	chr11	99250636	A	C	DELETERIOUS	0	4.32	unknown	-
155-p1-2	Adeno Carcinoma	L3mbtl	MGI	ENSMUSG00000035576	ENSMUST00000035751	NON_SYNONYMOUS_CODING	1342	367	A/T	chr2	162786773	G	A	TOLERATED	0.27	2.78	benign	1.177
155-p1-2	Adeno Carcinoma	Lgals9	MGI	ENSMUSG00000001123	ENSMUST00000108269	NON_SYNONYMOUS_CODING	576	181	N/D	chr11	78781529	T	C	TOLERATED	0.2	3	benign	0.874
155-p1-2	Adeno Carcinoma	Lgals9	MGI	ENSMUSG00000001123	ENSMUST00000108269	NON_SYNONYMOUS_CODING	499	155	H/P	chr11	78783286	T	G	TOLERATED	0.26	3.32	benign	0.431
155-p1-2	Adeno Carcinoma	Med1	MGI	ENSMUSG00000018160	ENSMUST00000107545	NON_SYNONYMOUS_CODING	4253	1348	T/M	chr11	98017240	G	A	TOLERATED	0.52	3.59	unknown	-

Supplementary Table 3. Predicted somatic mutations in tumors

Sample Id	Histological type	GeneName	DB	Gene	Transcript	Consequence	Position_in_cDNA	Position_in_protein	Amino_acid_change	Chromosome	Position	Ref	Var	Effect (SIFT)	Score (SIFT)	Median Info (SIFT)	Effect (Polyphen)	Score (Polyphen)
155-p1-2	Adeno Carcinoma	Med24	MGI	ENSMUSG00000017210	ENSMUST00000100500	NON_SYNONYMOUS_CODING	813	234	A/V	chr11	98577755	G	A	TOLERATED	0.38	3.37	benign	1.099
155-p1-2	Adeno Carcinoma	Mgl2	MGI	ENSMUSG00000040950	ENSMUST00000108584	NON_SYNONYMOUS_CODING	752	238	R/Q	chr11	69950242	G	A	TOLERATED	0.41	2.75	benign	1.269
155-p1-2	Adeno Carcinoma	Mrpl24	MGI	ENSMUSG00000019710	ENSMUST00000019854	NON_SYNONYMOUS_CODING	506	86	V/A	chr3	87726126	T	C	DELETERIOUS	0.01	2.77	possibly damaging	1.952
155-p1-2	Adeno Carcinoma	Myh13	MGI	ENSMUSG00000060180	ENSMUST00000108684	STOP_GAINED	4851	1564	R/*	chr11	67177997	C	T	-	-	-	unknown	-
155-p1-2	Adeno Carcinoma	Nfkbiz	MGI	ENSMUSG00000035356	ENSMUST00000036273	NON_SYNONYMOUS_CODING	1271	233	T/I	chr16	55818511	G	A	DELETERIOUS	0	4.32	possibly damaging	1.912
155-p1-2	Adeno Carcinoma	Nos2	MGI	ENSMUSG00000020826	ENSMUST00000018610	NON_SYNONYMOUS_CODING	989	245	S/T	chr11	78751092	G	C	TOLERATED	1	2.78	benign	0.633
155-p1-2	Adeno Carcinoma	Ocm	MGI	ENSMUSG00000029618	ENSMUST00000085704	NON_SYNONYMOUS_CODING	250	41	A/P	chr5	144785370	C	G	TOLERATED	0.16	3.35	benign	0.436
155-p1-2	Adeno Carcinoma	Pfkfb4	MGI	ENSMUSG00000025648	ENSMUST00000051873	NON_SYNONYMOUS_CODING	122	24	P/A	chr9	108894130	C	G	TOLERATED	0.14	3.54	probably damaging	2.023
155-p1-2	Adeno Carcinoma	Plk1	MGI	ENSMUSG00000030867	ENSMUST00000033154	NON_SYNONYMOUS_CODING	1148	364	R/W	chr7	129311164	C	T	DELETERIOUS	0.02	2.79	benign	1.397
155-p1-2	Adeno Carcinoma	Rpain	MGI	ENSMUSG00000018449	ENSMUST00000018593	NON_SYNONYMOUS_CODING	905	204	S/T	chr11	70788523	G	C	TOLERATED	0.17	2.97	possibly damaging	1.595
155-p1-2	Adeno Carcinoma	Sarm1	MGI	ENSMUSG00000050132	ENSMUST00000108287	NON_SYNONYMOUS_CODING	1720	574	L/F	chr11	78297069	G	A	DELETERIOUS	0	4.32	benign	1.047
155-p1-2	Adeno Carcinoma	Setd2	MGI	ENSMUSG00000044791	ENSMUST00000153838	NON_SYNONYMOUS_CODING	4114	1358	N/K	chr9	110453696	C	G	DELETERIOUS	0	4.32	possibly damaging	1.611
155-p1-2	Adeno Carcinoma	Sgca	MGI	ENSMUSG00000001508	ENSMUST00000103162	NON_SYNONYMOUS_CODING	731	160	A/S	chr11	94832661	C	A	TOLERATED	0.49	2.86	benign	0.373
155-p1-2	Adeno Carcinoma	Smg1	MGI	ENSMUSG00000030655	ENSMUST00000032891	NON_SYNONYMOUS_CODING	1839	498	V/I	chr7	125339345	C	T	DELETERIOUS	0	3.53	benign	0.225
155-p1-2	Adeno Carcinoma	Spna1	MGI	ENSMUSG00000026532	ENSMUST00000027817	NON_SYNONYMOUS_CODING	7184	2340	I/S	chr1	176176646	T	G	DELETERIOUS	0	3.17	probably damaging	2.434
155-p1-2	Adeno Carcinoma	St8sia3	MGI	ENSMUSG00000056812	ENSMUST00000025477	NON_SYNONYMOUS_CODING	1183	132	S/P	chr18	64429171	T	C	DELETERIOUS	0.01	2.75	possibly damaging	1.632
155-p1-2	Adeno Carcinoma	Thnsl1	MGI	ENSMUSG00000048550	ENSMUST00000054591	NON_SYNONYMOUS_CODING	366	14	A/T	chr2	21133103	G	A	TOLERATED	1	4.32	benign	0.724
155-p1-2	Adeno Carcinoma	Thnsl1	MGI	ENSMUSG00000048550	ENSMUST00000054591	NON_SYNONYMOUS_CODING	1866	514	V/M	chr2	21134603	G	A	DELETERIOUS	0	2.75	benign	0.927
155-p1-2	Adeno Carcinoma	Tnfrsf13b	MGI	ENSMUSG00000010142	ENSMUST00000010286	NON_SYNONYMOUS_CODING	599	175	R/S	chr11	60960519	C	A	TOLERATED	0.66	4.32	benign	1.093
155-p1-2	Adeno Carcinoma	Tpm2	MGI	ENSMUSG00000028464	ENSMUST00000034926	NON_SYNONYMOUS_CODING	907	266	I/T	chr4	43531717	A	G	TOLERATED	1	4.32	unknown	-
155-p1-2	Adeno Carcinoma	Tpr	MGI	ENSMUSG00000006005	ENSMUST00000064506	NON_SYNONYMOUS_CODING	5804	1831	E/K	chr1	152283895	G	A	DELETERIOUS	0.04	3.49	possibly damaging	1.507
155-p1-2	Adeno Carcinoma	Tssk2	MGI	ENSMUSG00000045521	ENSMUST00000055374	NON_SYNONYMOUS_CODING	832	251	R/C	chr16	17899578	C	T	DELETERIOUS	0	2.82	benign	0.891
155-p1-2	Adeno Carcinoma	Ugt1a10	MGI	ENSMUSG00000090165	ENSMUST00000113142	ESSENTIAL_SPLICE_SITE	0	0	-	chr1	90114701	G	C	-	-	-	-	-
155-p1-2	Adeno Carcinoma	Ugt1a7c	MGI	ENSMUSG00000090124	ENSMUST00000058237	NON_SYNONYMOUS_CODING	448	131	D/N	chr1	89992086	G	A	TOLERATED	1	2.77	benign	0.278
155-p1-2	Adeno Carcinoma	Usp43	MGI	ENSMUSG00000020905	ENSMUST00000021288	NON_SYNONYMOUS_CODING	3110	1002	D/G	chr11	67669377	T	C	TOLERATED	0.26	4.32	benign	0.748
155-p1-2	Adeno Carcinoma	Usp43	MGI	ENSMUSG00000020905	ENSMUST00000021288	NON_SYNONYMOUS_CODING	2383	760	M/V	chr11	67688822	T	C	TOLERATED	0.21	3.32	benign	0.696
155-p1-2	Adeno Carcinoma	Zfc3h1	MGI	ENSMUSG00000034163	ENSMUST00000036044	NON_SYNONYMOUS_CODING	5928	1897	A/S	chr10	114867761	G	T	DELETERIOUS	0	4.32	benign	1.002
155-p1-2	Adeno Carcinoma	Zp2	MGI	ENSMUSG00000030911	ENSMUST00000033207	NON_SYNONYMOUS_CODING	1676	549	A/V	chr7	127278693	G	A	TOLERATED	0.61	2.79	benign	1.097
145	Fibroadenoma	4933415A04Rik	MGI	ENSMUSG00000045877	ENSMUST00000056256	NON_SYNONYMOUS_CODING	377	39	C/Y	chr11	43400918	G	A	-	-	-	unknown	-
145	Fibroadenoma	Arcn1	MGI	ENSMUSG00000032096	ENSMUST00000034607	STOP_GAINED	341	56	Y/*	chr9	44568144	A	C	-	-	-	unknown	-
145	Fibroadenoma	Chd9	MGI	ENSMUSG00000056608	ENSMUST00000109614	ESSENTIAL_SPLICE_SITE	0	0	-	chr8	93457763	T	G	-	-	-	-	-
145	Fibroadenoma	Chrnb2	MGI	ENSMUSG00000027950	ENSMUST00000029562	NON_SYNONYMOUS_CODING	1618	480	P/H	chr3	89561089	G	T	DELETERIOUS	0	2.77	probably damaging	2.643
145	Fibroadenoma	Eif2b1	MGI	ENSMUSG00000029388	ENSMUST00000031334	NON_SYNONYMOUS_CODING	563	149	S/G	chr5	125024644	T	C	TOLERATED	0.18	2.78	possibly damaging	1.716
145	Fibroadenoma	Fam184a	MGI	ENSMUSG00000019856	ENSMUST00000020003	NON_SYNONYMOUS_CODING	1574	515	L/F	chr10	53404159	C	A	DELETERIOUS	0.05	2.98	possibly damaging	1.575
145	Fibroadenoma	Lrrc8c	MGI	ENSMUSG00000054720	ENSMUST00000067924	NON_SYNONYMOUS_CODING	1342	342	F/V	chr5	106036403	T	G	-	-	-	possibly damaging	1.952
145	Fibroadenoma	Lypd6b	MGI	ENSMUSG00000026765	ENSMUST00000028103	NON_SYNONYMOUS_CODING	758	102	T/P	chr2	49801632	A	C	TOLERATED	0.12	3.57	possibly damaging	1.527
145	Fibroadenoma	Pcsk5	MGI	ENSMUSG00000024713	ENSMUST00000025618	STOP_GAINED	1999	644	E/*	chr19	17650375	C	A	-	-	-	unknown	-
145	Fibroadenoma	Sgk1	MGI	ENSMUSG00000019970	ENSMUST00000120509	NON_SYNONYMOUS_CODING	2025	524	L/I	chr10	21718628	C	A	DELETERIOUS	0.01	3.47	benign	1.229
145	Fibroadenoma	Smtn	MGI	ENSMUSG00000020439	ENSMUST00000110011	NON_SYNONYMOUS_CODING	2127	701	S/T	chr11	3424711	C	G	TOLERATED	0.47	3.68	benign	1.019
145	Fibroadenoma	Tns1	MGI	ENSMUSG00000055322	ENSMUST00000068832	NON_SYNONYMOUS_CODING	728	243	A/V	chr1	73972104	G	A	TOLERATED	1	3.17	benign	0.11
145	Fibroadenoma	Wdtc1	MGI	ENSMUSG00000037622	ENSMUST00000043305	NON_SYNONYMOUS_CODING	1189	254	H/P	chr4	132859578	T	G	DELETERIOUS	0.01	2.9	probably damaging	3.496
196	Fibroadenoma	2700073G19Rik	MGI	ENSMUSG00000021041	ENSMUST00000091090	NON_SYNONYMOUS_CODING	432	111	D/E	chr12	88784536	G	C	Not Scored	-	-	benign	0.9
196	Fibroadenoma	Cth	MGI	ENSMUSG00000028179	ENSMUST00000118539	NON_SYNONYMOUS_CODING	703	219	V/G	chr3	157571928	A	C	DELETERIOUS	0	2.79	probably damaging	1.759
196	Fibroadenoma	Gm10165	MGI	ENSMUSG00000066507	ENSMUST00000085433	NON_SYNONYMOUS_CODING	1176	69	T/A	chr12	44912734	T	C	-	-	-	-	-
196	Fibroadenoma	Gm10914	MGI	ENSMUSG00000078102	ENSMUST00000104901	NON_SYNONYMOUS_CODING	176	59	V/E	chr16	4869230	A	T	-	-	-	-	-
196	Fibroadenoma	Gm6306	MGI	ENSMUSG00000060975	ENSMUST00000079069	NON_SYNONYMOUS_CODING	248	83	E/G	chr2	104552079	A	G	-	-	-	-	-
196	Fibroadenoma	Klra10	MGI	ENSMUSG00000072718	ENSMUST00000112020	NON_SYNONYMOUS_CODING	209	68	I/N	chr6	130229505	A	T	DELETERIOUS	0	2.81	probably damaging	2.779
196	Fibroadenoma	Klrb1b	MGI	ENSMUSG00000079298	ENSMUST00000032472	NON_SYNONYMOUS_CODING	607	183	V/D	chr6	128765319	A	T	TOLERATED	0.95	2.78	benign	0.667
196	Fibroadenoma	Krtap4-9	MGI	ENSMUSG00000078262	ENSMUST00000105059	NON_SYNONYMOUS_CODING	161	36	R/S	chr11	99646674	C	A	TOLERATED	0.56	2.82	unknown	-
196	Fibroadenoma	Net1	MGI	ENSMUSG00000021215	ENSMUST00000091853	NON_SYNONYMOUS_CODING	1644	497	R/C	chr13	3883615	G	A	DELETERIOUS	0.01	2.79	probably damaging	2.679
196	Fibroadenoma	Pax6	MGI	ENSMUSG00000027168	ENSMUST00000111087	NON_SYNONYMOUS_CODING	668	128	N/S	chr2	105525243	A	G	TOLERATED	0.43	2.97	benign	0.89
196	Fibroadenoma	Pcif1	MGI	ENSMUSG00000039849	ENSMUST00000041643	NON_SYNONYMOUS_CODING	565	84	S/L	chr2	164710860	C	T	DELETERIOUS	0.01	3.39	possibly damaging	1.745
196	Fibroadenoma	Pdlim5	MGI	ENSMUSG00000028273	ENSMUST00000029941	NON_SYNONYMOUS_CODING	1177	362	W/L	chr3	141940801	C	A	TOLERATED	0.66	2.84	probably damaging	2.896
196	Fibroadenoma	Pla2g4e	MGI	ENSMUSG00000050211	ENSMUST00000090071	NON_SYNONYMOUS_CODING	627	67	S/P	chr2	120070445	A	G	Not Scored	-	-	benign	0.225
219	Fibroadenoma	Foxp2	MGI	ENSMUSG00000029563	ENSMUST00000115474	NON_SYNONYMOUS_CODING	2254	644	S/R	chr6	15365890	C	A	DELETERIOUS	0.02	3.27	possibly damaging	1.57
219	Fibroadenoma	G6pc2	MGI	ENSMUSG00000005232	ENSMUST00000005364	NON_SYNONYMOUS_CODING	696	212	V/I	chr2	69064702	G	A	TOLERATED	0.21	2.88	benign	0.331
219	Fibroadenoma	Olfr419	MGI	ENSMUSG00000050788	ENSMUST00000061990	NON_SYNONYMOUS_CODING	691	231	A/T	chr1	176180366	C	T	TOLERATED	0.13	2.72	benign	0.253
219	Fibroadenoma	Piwil1	MGI	ENSMUSG00000029423	ENSMUST00000086056	NON_SYNONYMOUS_CODING	1028	280	V/F	chr5	129249755	G	T	DELETERIOUS	0.01	2.82	probably damaging	2.235
219	Fibroadenoma	Plekhh2	MGI	ENSMUSG00000040852	ENSMUST00000047206	NON_SYNONYMOUS_CODING	921	282	S/C	chr17	84965472	A	T	DELETERIOUS	0	3.55	benign	1.488
317	Fibroadenoma	Map3k15	MGI	ENSMUSG00000031303	ENSMUST00000033665	NON_SYNONYMOUS_CODING	313	105	V/I	chrX	156426677	G	A	TOLERATED	0.47	2.9	benign	0.045

Supplementary Table 3. Predicted somatic mutations in tumors

Sample Id	Histological type	GeneName	DB	Gene	Transcript	Consequence	Position_in_cDNA	Position_in_protein	Amino_acid_change	Chromosome	Position	Ref	Var	Effect (SIFT)	Score (SIFT)	Median Info (SIFT)	Effect (Polyphen)	Score (Polyphen)
317	Fibroadenoma	Rai14	MGI	ENSMUSG00000022246	ENSMUST00000090339	NON_SYNONYMOUS_CODING	1629	463	Q/P	chr15	10505325	T	G	DELETERIOUS	0.01	3.05	possibly damaging	1.593
326	Fibroadenoma	Olfr572	MGI	ENSMUSG00000073963	ENSMUST00000098214	NON_SYNONYMOUS_CODING	93	31	F/L	chr7	110076236	C	A	TOLERATED	0.28	2.78	benign	0.334
326	Fibroadenoma	Rnf112	MGI	ENSMUSG00000010086	ENSMUST00000060255	NON_SYNONYMOUS_CODING	835	227	P/A	chr11	61265622	G	C	TOLERATED	1	3.08	probably damaging	2.117
326	Fibroadenoma	Rps27l	MGI	ENSMUSG00000036781	ENSMUST00000127896	NON_SYNONYMOUS_CODING	158	25	V/G	chr9	66794705	T	G	DELETERIOUS	0	3.33	possibly damaging	1.588
326	Fibroadenoma	Ybx1	MGI	ENSMUSG00000028639	ENSMUST00000079644	NON_SYNONYMOUS_CODING	1151	304	A/T	chr4	118951629	C	T	TOLERATED	0.18	3.11	possibly damaging	1.56
612	Fibroadenoma	A230006K03Rik	MGI	ENSMUSG00000078690	ENSMUST00000107533	NON_SYNONYMOUS_CODING	494	101	Q/R	chr7	68347607	T	C	DELETERIOUS	0.02	2.8	unknown	-
612	Fibroadenoma	Bai1	MGI	ENSMUSG00000034730	ENSMUST00000042035	NON_SYNONYMOUS_CODING	2016	536	V/I	chr15	74372004	G	A	TOLERATED	0.12	2.92	benign	0.875
612	Fibroadenoma	Mllt3	MGI	ENSMUSG00000028496	ENSMUST00000078090	NON_SYNONYMOUS_CODING	1210	314	A/E	chr4	87486773	G	T	DELETERIOUS	0.01	3.35	benign	1.218
612	Fibroadenoma	Ptpre	MGI	ENSMUSG00000041836	ENSMUST00000073961	NON_SYNONYMOUS_CODING	2111	596	E/D	chr7	142870841	G	C	TOLERATED	0.11	2.8	benign	0.349
612	Fibroadenoma	Scd2	MGI	ENSMUSG00000025203	ENSMUST00000026221	NON_SYNONYMOUS_CODING	1393	227	V/I	chr19	44375736	G	A	TOLERATED	1	2.79	benign	0.193
612	Fibroadenoma	Slc4a10	MGI	ENSMUSG00000026904	ENSMUST00000112480	NON_SYNONYMOUS_CODING	136	46	R/W	chr2	62028802	C	T	DELETERIOUS	0.01	3.1	probably damaging	2.637
612	Fibroadenoma	Ston2	MGI	ENSMUSG00000020961	ENSMUST00000052969	NON_SYNONYMOUS_CODING	1226	244	P/L	chr12	92887342	G	A	DELETERIOUS	0	3.58	probably damaging	2.316
113	Spindle Cell	Trp53	MGI	ENSMUSG00000059552	ENSMUST00000108658	NON_SYNONYMOUS_CODING	561	135	A/V	chr11	69402152	A	T	DELETERIOUS				
323	Spindle Cell	5730419I09Rik	MGI	ENSMUSG00000030279	ENSMUST00000111758	NON_SYNONYMOUS_CODING	2063	632	T/S	chr6	142984762	G	C	TOLERATED	0.92	3.38	benign	0.268
323	Spindle Cell	A730018C14Rik	MGI	ENSMUSG00000047828	ENSMUST00000050754	NON_SYNONYMOUS_CODING	593	42	S/P	chr12	113653786	A	G	No sufficient homology	-	-	unknown	-
323	Spindle Cell	B3galt1	MGI	ENSMUSG00000034780	ENSMUST00000042456	STOP_GAINED	1100	273	R/*	chr2	67956816	C	T	Stop codon not handled	-	-	unknown	-
323	Spindle Cell	BC022687	MGI	ENSMUSG00000037594	ENSMUST00000037014	NON_SYNONYMOUS_CODING	844	144	S/C	chr12	114049094	A	T	TOLERATED	0.16	4.32	benign	0.446
323	Spindle Cell	Bcat1	MGI	ENSMUSG00000030268	ENSMUST00000087468	NON_SYNONYMOUS_CODING	762	240	L/P	chr6	144967868	A	G	DELETERIOUS	0	2.8	probably damaging	2.618
323	Spindle Cell	Cacng8	MGI	ENSMUSG00000053395	ENSMUST00000092351	NON_SYNONYMOUS_CODING	568	154	R/G	chr7	3412530	A	G	DELETERIOUS	0.02	2.97	probably damaging	2.087
323	Spindle Cell	Cdca4	MGI	ENSMUSG00000047832	ENSMUST00000062092	NON_SYNONYMOUS_CODING	1134	196	S/T	chr12	114059731	C	G	TOLERATED	0.94	2.93	benign	0.575
323	Spindle Cell	Chd4	MGI	ENSMUSG00000063870	ENSMUST00000112390	NON_SYNONYMOUS_CODING	4976	1600	P/T	chr6	125072159	C	A	DELETERIOUS	0.04	3.32	possibly damaging	1.8
323	Spindle Cell	Chd5	MGI	ENSMUSG00000005045	ENSMUST00000030775	NON_SYNONYMOUS_CODING	4194	1298	R/L	chr4	151751234	G	T	TOLERATED	0.23	2.83	possibly damaging	1.828
323	Spindle Cell	Cntnap4	MGI	ENSMUSG00000031772	ENSMUST00000118171	ESSENTIAL_SPLICE_SITE	0	0	-	chr8	115334642	G	C	-	-	-	-	-
323	Spindle Cell	Col27a1	MGI	ENSMUSG00000045672	ENSMUST00000036300	NON_SYNONYMOUS_CODING	3919	1176	E/D	chr4	62967737	G	C	No sufficient homology	-	-	unknown	-
323	Spindle Cell	E330021D16Rik	MGI	ENSMUSG00000045291	ENSMUST00000058713	NON_SYNONYMOUS_CODING	375	26	V/M	chr6	136351777	C	T	TOLERATED	0.37	3.35	benign	0.669
323	Spindle Cell	Ears2	MGI	ENSMUSG00000030871	ENSMUST00000033159	NON_SYNONYMOUS_CODING	1670	484	V/M	chr7	129183264	C	T	TOLERATED	0.31	2.76	benign	0.202
323	Spindle Cell	Efr3b	MGI	ENSMUSG00000020658	ENSMUST00000111178	NON_SYNONYMOUS_CODING	1733	535	C/S	chr12	3977151	A	T	TOLERATED	0.05	2.99	possibly damaging	1.896
323	Spindle Cell	Gle1	MGI	ENSMUSG00000019715	ENSMUST00000019859	NON_SYNONYMOUS_CODING	1801	576	R/H	chr2	29806199	G	A	DELETERIOUS	0.03	2.81	probably damaging	2.238
323	Spindle Cell	Gm71	MGI	ENSMUSG00000049882	ENSMUST00000058639	NON_SYNONYMOUS_CODING	254	84	M/V	chr12	70683724	T	C	TOLERATED	1	2.76	benign	0.466
323	Spindle Cell	Gm766	MGI	ENSMUSG00000048473	ENSMUST00000111768	NON_SYNONYMOUS_CODING	8	3	C/S	chr6	142752903	C	G	DELETERIOUS	0	4.32	benign	0.426
323	Spindle Cell	Gm900	MGI	ENSMUSG00000076611	ENSMUST00000103413	NON_SYNONYMOUS_CODING	865	289	D/V	chr12	114509971	T	A	DELETERIOUS	0.01	2.8	benign	1.379
323	Spindle Cell	Gsg1	MGI	ENSMUSG00000030206	ENSMUST00000087729	NON_SYNONYMOUS_CODING	983	287	S/N	chr6	135187668	C	T	TOLERATED	0.28	3.57	benign	1.22
323	Spindle Cell	Ighg1	MGI	ENSMUSG00000076614	ENSMUST00000103419	NON_SYNONYMOUS_CODING	846	283	V/I	chr12	114567315	C	T	TOLERATED	0.44	2.8	benign	0.091
323	Spindle Cell	Kif26a	MGI	ENSMUSG00000021294	ENSMUST00000128402	NON_SYNONYMOUS_CODING	4128	1333	T/N	chr12	113415522	C	A	TOLERATED	0.26	3.34	benign	0.13
323	Spindle Cell	Klra12	MGI	ENSMUSG00000079280	ENSMUST00000049314	NON_SYNONYMOUS_CODING	757	28	I/F	chr6	130216483	T	A	TOLERATED	0.97	3.38	unknown	-
323	Spindle Cell	Klra3	MGI	ENSMUSG00000067591	ENSMUST00000111998	NON_SYNONYMOUS_CODING	159	13	L/F	chr6	130285781	G	A	TOLERATED	1	2.84	benign	0.953
323	Spindle Cell	Klrc3	MGI	ENSMUSG00000033027	ENSMUST00000053164	NON_SYNONYMOUS_CODING	773	245	P/T	chr6	129589111	G	T	DELETERIOUS	0	4.32	probably damaging	2.017
323	Spindle Cell	Mgat5b	MGI	ENSMUSG00000043857	ENSMUST00000103027	NON_SYNONYMOUS_CODING	2561	650	L/V	chr11	116846213	C	G	TOLERATED	1	4.32	benign	0.087
323	Spindle Cell	Mid1	MGI	ENSMUSG00000035299	ENSMUST00000112104	NON_SYNONYMOUS_CODING	2109	627	S/A	chrX	166426979	T	G	TOLERATED	0.22	2.83	benign	0.167
323	Spindle Cell	Ocrl	MGI	ENSMUSG00000001173	ENSMUST00000001202	NON_SYNONYMOUS_CODING	1561	432	S/T	chrX	45291529	G	C	TOLERATED	0.32	2.85	benign	0.171
323	Spindle Cell	Palm2	MGI	ENSMUSG00000090053	ENSMUST00000102905	NON_SYNONYMOUS_CODING	474	55	V/I	chr4	57660898	G	A	TOLERATED	0.59	2.86	benign	0.461
323	Spindle Cell	Pde3a	MGI	ENSMUSG00000041741	ENSMUST00000043259	NON_SYNONYMOUS_CODING	1159	387	I/F	chr6	141407730	A	T	TOLERATED	0.07	3.03	benign	1.394
323	Spindle Cell	Pick1	MGI	ENSMUSG00000068206	ENSMUST00000053926	NON_SYNONYMOUS_CODING	1600	461	R/K	chr15	79086314	G	A	DELETERIOUS	0.01	4.32	unknown	-
323	Spindle Cell	Ppfibp1	MGI	ENSMUSG00000016487	ENSMUST00000111623	NON_SYNONYMOUS_CODING	1326	371	L/P	chr6	146954499	T	C	TOLERATED	0.3	2.99	benign	0.114
323	Spindle Cell	Prpmp5	MGI	ENSMUSG00000052262	ENSMUST00000048686	NON_SYNONYMOUS_CODING	581	185	Q/K	chr6	132262325	G	T	TOLERATED	0.36	2.86	unknown	-
323	Spindle Cell	Rusc2	MGI	ENSMUSG00000035969	ENSMUST00000035645	NON_SYNONYMOUS_CODING	2469	728	P/R	chr4	43434636	C	G	TOLERATED	0.54	3.88	benign	1.423
323	Spindle Cell	Slc15a5	MGI	ENSMUSG00000044378	ENSMUST00000050132	NON_SYNONYMOUS_CODING	1135	333	G/S	chr6	137960686	C	T	TOLERATED	0.49	2.81	benign	0.573
323	Spindle Cell	Sv2c	MGI	ENSMUSG00000051111	ENSMUST00000161263	ESSENTIAL_SPLICE_SITE	0	0	-	chr13	96751791	A	C	-	-	-	-	-
323	Spindle Cell	Tdrd9	MGI	ENSMUSG00000054003	ENSMUST00000079009	NON_SYNONYMOUS_CODING	980	104	Y/H	chr12	113261479	T	C	TOLERATED	0.54	2.78	possibly damaging	1.631
323	Spindle Cell	Tex19.2	MGI	ENSMUSG00000039337	ENSMUST00000039146	NON_SYNONYMOUS_CODING	1582	314	D/E	chr11	120977993	A	C	Not Scored	-	-	benign	0.675
323	Spindle Cell	Timm9	MGI	ENSMUSG00000021079	ENSMUST00000021486	NON_SYNONYMOUS_CODING	412	89	R/W	chr12	72224544	G	A	DELETERIOUS	0	4.32	probably damaging	2.257
323	Spindle Cell	Tmem67	MGI	ENSMUSG00000049488	ENSMUST00000108293	NON_SYNONYMOUS_CODING	669	26	Q/P	chr4	12016499	T	G	Not Scored	-	-	benign	1.35
323	Spindle Cell	Trmt61a	MGI	ENSMUSG00000060950	ENSMUST00000084947	NON_SYNONYMOUS_CODING	613	42	V/L	chr12	112916966	G	C	TOLERATED	0.45	2.78	benign	1.43
323	Spindle Cell	Trp53	MGI	ENSMUSG00000059552	ENSMUST00000108658	NON_SYNONYMOUS_CODING	862	245	R/H	chr11	69402713	G	A	DELETERIOUS	0	2.76	probably damaging	2.45
323	Spindle Cell	Zbtb42	MGI	ENSMUSG00000037638	ENSMUST00000037962	NON_SYNONYMOUS_CODING	232	78	T/A	chr12	113917878	A	G	TOLERATED	1	4.32	unknown	-
323	Spindle Cell	Zdhhc4	MGI	ENSMUSG00000001844	ENSMUST00000001900	NON_SYNONYMOUS_CODING	1178	300	R/H	chr5	144078354	C	T	TOLERATED	0.98	2.88	benign	0.867
323	Spindle Cell	Zfp217	MGI	ENSMUSG00000052056	ENSMUST00000109155	NON_SYNONYMOUS_CODING	1927	473	P/H	chr2	169941728	G	T	TOLERATED	0.38	2.99	benign	0.894
323-p1	Spindle Cell	1700023A16Rik	MGI	ENSMUSG00000030292	ENSMUST00000111634	NON_SYNONYMOUS_CODING	659	219	T/N	chr6	146810206	C	A	TOLERATED	0.38	4.32	benign	0.08
323-p1	Spindle Cell	5330439B14Rik	MGI	ENSMUSG00000041614	ENSMUST00000040390	NON_SYNONYMOUS_CODING	626	96	L/V	chr6	142574216	C	G	-	-	-	unknown	-
323-p1	Spindle Cell	Adcy5	MGI	ENSMUSG00000022840	ENSMUST00000023549	NON_SYNONYMOUS_CODING	3992	924	V/M	chr16	35291630	G	A	DELETERIOUS	0	2.77	benign	0.399

Supplementary Table 3. Predicted somatic mutations in tumors

Sample Id	Histological type	GeneName	DB	Gene	Transcript	Consequence	Position_in_cDNA	Position_in_protein	Amino_acid_change	Chromosome	Position	Ref	Var	Effect (SIFT)	Score (SIFT)	Median Info (SIFT)	Effect (Polyphen)	Score (Polyphen)
323-p1	Spindle Cell	Akap14	MGI	ENSMUSG00000036551	ENSMUST00000046557	NON_SYNONYMOUS_CODING	827	248	A/V	chrX	34703333	G	A	TOLERATED	0.12	3.14	unknown	-
323-p1	Spindle Cell	Atf7ip	MGI	ENSMUSG00000030213	ENSMUST00000032335	NON_SYNONYMOUS_CODING	981	287	D/E	chr6	136509152	T	A	TOLERATED	1	2.91	benign	0.073
323-p1	Spindle Cell	Atf7ip	MGI	ENSMUSG00000030213	ENSMUST00000032335	NON_SYNONYMOUS_CODING	1760	547	A/V	chr6	136509931	C	T	TOLERATED	0.65	2.91	benign	0.572
323-p1	Spindle Cell	B3galt1	MGI	ENSMUSG00000034780	ENSMUST00000042456	STOP_GAINED	1100	273	R/*	chr2	67956816	C	T	-	-	-	unknown	-
323-p1	Spindle Cell	BC049715	MGI	ENSMUSG00000047515	ENSMUST00000052702	NON_SYNONYMOUS_CODING	675	110	A/T	chr6	136788612	G	A	DELETERIOUS	0	3.67	benign	0.242
323-p1	Spindle Cell	BC049715	MGI	ENSMUSG00000047515	ENSMUST00000052702	NON_SYNONYMOUS_CODING	1008	221	E/K	chr6	136788945	G	A	TOLERATED	0.35	3.67	benign	0.309
323-p1	Spindle Cell	Bcat1	MGI	ENSMUSG00000030268	ENSMUST00000087468	NON_SYNONYMOUS_CODING	762	240	L/P	chr6	144967868	A	G	DELETERIOUS	0	2.8	probably damaging	2.618
323-p1	Spindle Cell	Bcl2l14	MGI	ENSMUSG00000030200	ENSMUST00000032321	NON_SYNONYMOUS_CODING	1065	269	R/Q	chr6	134382288	G	A	TOLERATED	1	3.71	benign	0.614
323-p1	Spindle Cell	Chd4	MGI	ENSMUSG00000063870	ENSMUST00000112390	NON_SYNONYMOUS_CODING	4976	1600	P/T	chr6	125072159	C	A	DELETERIOUS	0.04	3.32	possibly damaging	1.8
323-p1	Spindle Cell	Chd5	MGI	ENSMUSG00000005045	ENSMUST00000030775	NON_SYNONYMOUS_CODING	4194	1298	R/L	chr4	151751234	G	T	TOLERATED	0.23	2.82	possibly damaging	1.828
323-p1	Spindle Cell	Cntnap4	MGI	ENSMUSG00000031772	ENSMUST00000118171	ESSENTIAL_SPLICE_SITE	0	0	-	chr8	115334642	G	C	-	-	-	-	-
323-p1	Spindle Cell	E030037K03Rik	MGI	ENSMUSG00000073491	ENSMUST00000150649	NON_SYNONYMOUS_CODING	1418	452	H/R	chr1	175512313	T	C	DELETERIOUS	0	4.32	possibly damaging	1.8
323-p1	Spindle Cell	E030037K03Rik	MGI	ENSMUSG00000073491	ENSMUST00000150649	NON_SYNONYMOUS_CODING	1407	448	R/S	chr1	175512324	C	A	DELETERIOUS	0.01	4.32	benign	0.45
323-p1	Spindle Cell	E330021D16Rik	MGI	ENSMUSG00000045291	ENSMUST00000058713	NON_SYNONYMOUS_CODING	375	26	V/M	chr6	136351777	C	T	TOLERATED	0.37	3.35	benign	0.669
323-p1	Spindle Cell	Ears2	MGI	ENSMUSG00000030871	ENSMUST00000033159	NON_SYNONYMOUS_CODING	1670	484	V/M	chr7	129183264	C	T	TOLERATED	0.31	2.78	benign	0.202
323-p1	Spindle Cell	Eef2	MGI	ENSMUSG00000034994	ENSMUST00000047864	NON_SYNONYMOUS_CODING	458	126	L/P	chr10	80640956	T	C	DELETERIOUS	0	2.79	probably damaging	2.531
323-p1	Spindle Cell	Epn3	MGI	ENSMUSG00000010080	ENSMUST00000127305	NON_SYNONYMOUS_CODING	842	141	R/W	chr11	94357436	G	A	DELETERIOUS	0	2.78	probably damaging	2.596
323-p1	Spindle Cell	Fcrl6	MGI	ENSMUSG00000070504	ENSMUST00000094303	NON_SYNONYMOUS_CODING	33	11	E/D	chr1	174530187	C	A	TOLERATED	0.36	3.33	benign	0.069
323-p1	Spindle Cell	Gle1	MGI	ENSMUSG00000019715	ENSMUST00000019859	NON_SYNONYMOUS_CODING	1801	576	R/H	chr2	29806199	G	A	DELETERIOUS	0.03	2.77	probably damaging	2.238
323-p1	Spindle Cell	Gm10010	MGI	ENSMUSG00000056771	ENSMUST00000071101	NON_SYNONYMOUS_CODING	202	68	E/K	chr6	128150440	C	T	-	-	-	unknown	-
323-p1	Spindle Cell	Gm2399	MGI	ENSMUSG00000005397	ENSMUST00000005532	NON_SYNONYMOUS_CODING	249	80	G/S	chr13	13556001	G	A	DELETERIOUS	0	2.89	possibly damaging	1.917
323-p1	Spindle Cell	Gm766	MGI	ENSMUSG00000048473	ENSMUST00000111768	NON_SYNONYMOUS_CODING	8	3	C/S	chr6	142752903	C	G	DELETERIOUS	0	4.32	benign	0.426
323-p1	Spindle Cell	Gsg1	MGI	ENSMUSG00000030206	ENSMUST00000087729	NON_SYNONYMOUS_CODING	983	287	S/N	chr6	135187668	C	T	TOLERATED	0.28	3.57	benign	1.22
323-p1	Spindle Cell	Hsdl2	MGI	ENSMUSG00000028383	ENSMUST00000030078	NON_SYNONYMOUS_CODING	1193	333	E/Q	chr4	59623513	G	C	TOLERATED	0.17	4.32	unknown	-
323-p1	Spindle Cell	Itgb4	MGI	ENSMUSG00000020758	ENSMUST00000106461	NON_SYNONYMOUS_CODING	3069	877	T/A	chr11	115853213	A	G	TOLERATED	1	3.55	benign	0.224
323-p1	Spindle Cell	Klrc3	MGI	ENSMUSG00000033027	ENSMUST00000053164	NON_SYNONYMOUS_CODING	773	245	P/T	chr6	129589111	G	T	DELETERIOUS	0	3.47	probably damaging	2.017
323-p1	Spindle Cell	Map3k15	MGI	ENSMUSG00000031303	ENSMUST00000033665	STOP_GAINED	3817	1273	Q/*	chrX	156560365	C	T	-	-	-	unknown	-
323-p1	Spindle Cell	Mei1	MGI	ENSMUSG00000068117	ENSMUST00000089178	NON_SYNONYMOUS_CODING	2834	825	L/R	chr15	81955359	T	G	DELETERIOUS	0	4.32	possibly damaging	1.873
323-p1	Spindle Cell	Mgat5b	MGI	ENSMUSG00000043857	ENSMUST00000103027	NON_SYNONYMOUS_CODING	2561	650	L/V	chr11	116846213	C	G	TOLERATED	1	4.32	benign	0.087
323-p1	Spindle Cell	Mgst1	MGI	ENSMUSG00000008540	ENSMUST00000118091	NON_SYNONYMOUS_CODING	206	34	R/G	chr6	138090312	A	G	Not Scored	-	-	unknown	-
323-p1	Spindle Cell	Mid1	MGI	ENSMUSG00000035299	ENSMUST00000112104	NON_SYNONYMOUS_CODING	2109	627	S/A	chrX	166426979	T	G	TOLERATED	0.22	2.83	benign	0.167
323-p1	Spindle Cell	Nid1	MGI	ENSMUSG00000005397	ENSMUST00000005532	NON_SYNONYMOUS_CODING	249	80	G/S	chr13	13556001	G	A	DELETERIOUS	0	2.89	possibly damaging	1.917
323-p1	Spindle Cell	Nipal2	MGI	ENSMUSG00000038879	ENSMUST00000040791	NON_SYNONYMOUS_CODING	1395	292	I/F	chr15	34512482	T	A	DELETERIOUS	0.04	2.81	possibly damaging	1.523
323-p1	Spindle Cell	Nrip2	MGI	ENSMUSG00000001520	ENSMUST00000120405	NON_SYNONYMOUS_CODING	615	158	P/S	chr6	128357421	C	T	TOLERATED	0.2	3.09	benign	0.739
323-p1	Spindle Cell	Obscn	MGI	ENSMUSG00000061462	ENSMUST00000020732	NON_SYNONYMOUS_CODING	2608	861	L/M	chr11	58943339	G	T	TOLERATED	0.13	2.84	unknown	-
323-p1	Spindle Cell	Ocm	MGI	ENSMUSG00000029618	ENSMUST00000085704	NON_SYNONYMOUS_CODING	250	41	A/P	chr5	144785370	C	G	TOLERATED	0.16	3.35	benign	0.436
323-p1	Spindle Cell	Ocrl	MGI	ENSMUSG00000001173	ENSMUST00000001202	NON_SYNONYMOUS_CODING	1561	432	S/T	chrX	45291529	G	C	TOLERATED	0.3	2.87	benign	0.171
323-p1	Spindle Cell	Odz1	MGI	ENSMUSG00000016150	ENSMUST00000115059	NON_SYNONYMOUS_CODING	7913	2610	T/I	chrX	39886009	G	A	DELETERIOUS	0	3.05	probably damaging	2.098
323-p1	Spindle Cell	Palm2	MGI	ENSMUSG00000090053	ENSMUST00000102905	NON_SYNONYMOUS_CODING	474	55	V/I	chr4	57660898	G	A	TOLERATED	0.59	2.86	benign	0.461
323-p1	Spindle Cell	Pde3a	MGI	ENSMUSG00000041741	ENSMUST00000043259	NON_SYNONYMOUS_CODING	1159	387	I/F	chr6	141407730	A	T	TOLERATED	0.07	3.03	benign	1.394
323-p1	Spindle Cell	Pick1	MGI	ENSMUSG00000068206	ENSMUST00000053926	NON_SYNONYMOUS_CODING	1600	461	R/K	chr15	79086314	G	A	DELETERIOUS	0.01	4.32	unknown	-
323-p1	Spindle Cell	Ppfibp1	MGI	ENSMUSG00000016487	ENSMUST00000111623	NON_SYNONYMOUS_CODING	1326	371	L/P	chr6	146954499	T	C	TOLERATED	0.3	2.99	benign	0.114
323-p1	Spindle Cell	Prpmp5	MGI	ENSMUSG00000052262	ENSMUST00000048686	NON_SYNONYMOUS_CODING	581	185	Q/K	chr6	132262325	G	T	TOLERATED	0.36	2.86	unknown	-
323-p1	Spindle Cell	Sectm1b	MGI	ENSMUSG00000039364	ENSMUST00000039309	NON_SYNONYMOUS_CODING	571	114	E/K	chr11	120917042	C	T	TOLERATED	0.83	3.36	benign	1.311
323-p1	Spindle Cell	Slco1c1	MGI	ENSMUSG00000030235	ENSMUST00000111837	NON_SYNONYMOUS_CODING	1309	311	N/D	chr6	141495341	A	G	TOLERATED	0.94	2.81	benign	0.53
323-p1	Spindle Cell	St6galnac1	MGI	ENSMUSG00000009588	ENSMUST00000009732	NON_SYNONYMOUS_CODING	207	34	R/S	chr11	116636615	C	A	TOLERATED	0.49	4.32	benign	0.237
323-p1	Spindle Cell	Tex19.2	MGI	ENSMUSG00000039337	ENSMUST00000039146	NON_SYNONYMOUS_CODING	1582	314	D/E	chr11	120977993	A	C	Not Scored	-	-	benign	0.675
323-p1	Spindle Cell	Timm9	MGI	ENSMUSG00000021079	ENSMUST00000021486	NON_SYNONYMOUS_CODING	412	89	R/W	chr12	72224544	G	A	DELETERIOUS	0	4.32	probably damaging	2.257
323-p1	Spindle Cell	Tmem67	MGI	ENSMUSG00000049488	ENSMUST00000108293	NON_SYNONYMOUS_CODING	669	26	Q/P	chr4	12016499	T	G	Not Scored	-	-	benign	1.35
323-p1	Spindle Cell	Tpm2	MGI	ENSMUSG00000028464	ENSMUST00000034926	NON_SYNONYMOUS_CODING	907	266	I/T	chr4	43531717	A	G	TOLERATED	1	4.32	unknown	-
323-p1	Spindle Cell	Tro	MGI	ENSMUSG00000025272	ENSMUST00000087258	NON_SYNONYMOUS_CODING	1283	406	N/S	chrX	147088986	T	C	TOLERATED	0.74	3.45	benign	1.125
323-p1	Spindle Cell	Tro	MGI	ENSMUSG00000025272	ENSMUST00000087258	NON_SYNONYMOUS_CODING	1275	403	D/E	chrX	147088994	A	C	TOLERATED	1	3.45	benign	0.9
323-p1	Spindle Cell	Trp53	MGI	ENSMUSG00000059552	ENSMUST00000108658	NON_SYNONYMOUS_CODING	862	245	R/H	chr11	69402713	G	A	DELETERIOUS	0	2.77	probably damaging	2.45
323-p1	Spindle Cell	Tubb3	MGI	ENSMUSG00000062380	ENSMUST00000071134	NON_SYNONYMOUS_CODING	1009	276	R/Q	chr8	125945056	G	A	DELETERIOUS	0	4.2	probably damaging	1.773
323-p1	Spindle Cell	Wwtr1	MGI	ENSMUSG00000027803	ENSMUST00000120977	NON_SYNONYMOUS_CODING	976	316	A/S	chr3	57267480	C	A	DELETERIOUS	0.02	3.12	benign	1.259
323-p1	Spindle Cell	Zdhhc4	MGI	ENSMUSG00000001844	ENSMUST00000001900	NON_SYNONYMOUS_CODING	1178	300	R/H	chr5	144078354	C	T	TOLERATED	0.98	2.88	benign	0.867
323-p1	Spindle Cell	Zfp217	MGI	ENSMUSG00000052056	ENSMUST00000109155	NON_SYNONYMOUS_CODING	1927	473	P/H	chr2	169941728	G	T	TOLERATED	0.38	2.99	benign	0.894
323-p1	Spindle Cell	Zkscan16	MGI	ENSMUSG00000038630	ENSMUST00000107554	NON_SYNONYMOUS_CODING	166	3	G/A	chr4	58959006	G	C	TOLERATED	1	4.32	benign	0.039
323-p2	Spindle Cell	1700023A16Rik	MGI	ENSMUSG00000030292	ENSMUST00000111634	NON_SYNONYMOUS_CODING	659	219	T/N	chr6	146810206	C	A	TOLERATED	0.38	4.32	benign	0.08
323-p2	Spindle Cell	2310022A10Rik	MGI	ENSMUSG00000049643	ENSMUST00000067386	NON_SYNONYMOUS_CODING	313	105	A/P	chr7	28350678	G	C	TOLERATED	0.28	3.21	benign	0.071

Supplementary Table 3. Predicted somatic mutations in tumors

Sample Id	Histological type	GeneName	DB	Gene	Transcript	Consequence	Position_in_cDNA	Position_in_protein	Amino_acid_change	Chromosome	Position	Ref	Var	Effect (SIFT)	Score (SIFT)	Median Info (SIFT)	Effect (Polyphen)	Score (Polyphen)
323-p2	Spindle Cell	5330439B14Rik	MGI	ENSMUSG00000041614	ENSMUST00000040390	NON_SYNONYMOUS_CODING	626	96	L/V	chr6	142574216	C	G	-	-	-	unknown	-
323-p2	Spindle Cell	Adcy5	MGI	ENSMUSG00000022840	ENSMUST00000023549	NON_SYNONYMOUS_CODING	3992	924	V/M	chr16	35291630	G	A	DELETERIOUS	0	2.77	benign	0.399
323-p2	Spindle Cell	Akap14	MGI	ENSMUSG00000036551	ENSMUST00000046557	NON_SYNONYMOUS_CODING	827	248	A/V	chrX	34703333	G	A	TOLERATED	0.12	3.14	unknown	-
323-p2	Spindle Cell	Atf7ip	MGI	ENSMUSG00000030213	ENSMUST00000032335	NON_SYNONYMOUS_CODING	981	287	D/E	chr6	136509152	T	A	TOLERATED	1	2.91	benign	0.073
323-p2	Spindle Cell	B3galt1	MGI	ENSMUSG00000034780	ENSMUST00000042456	STOP_GAINED	1100	273	R/*	chr2	67956816	C	T	-	-	-	unknown	-
323-p2	Spindle Cell	BC049715	MGI	ENSMUSG00000047515	ENSMUST00000052702	NON_SYNONYMOUS_CODING	1008	221	E/K	chr6	136788945	G	A	TOLERATED	0.35	3.67	benign	0.309
323-p2	Spindle Cell	Bcat1	MGI	ENSMUSG00000030268	ENSMUST00000087468	NON_SYNONYMOUS_CODING	762	240	L/P	chr6	144967868	A	G	DELETERIOUS	0	2.8	probably damaging	2.618
323-p2	Spindle Cell	Bcl2l14	MGI	ENSMUSG00000030200	ENSMUST00000032321	NON_SYNONYMOUS_CODING	1065	269	R/Q	chr6	134382288	G	A	TOLERATED	1	3.71	benign	0.614
323-p2	Spindle Cell	Cfhr2	MGI	ENSMUSG00000033898	ENSMUST00000094484	NON_SYNONYMOUS_CODING	96	12	I/L	chr1	141915392	T	G	TOLERATED	0.11	3.42	unknown	-
323-p2	Spindle Cell	Chd4	MGI	ENSMUSG00000063870	ENSMUST00000112390	NON_SYNONYMOUS_CODING	4976	1600	P/T	chr6	125072159	C	A	DELETERIOUS	0.04	3.32	possibly damaging	1.8
323-p2	Spindle Cell	Chd5	MGI	ENSMUSG00000005045	ENSMUST00000030775	NON_SYNONYMOUS_CODING	4194	1298	R/L	chr4	151751234	G	T	TOLERATED	0.23	2.82	possibly damaging	1.828
323-p2	Spindle Cell	Cntnap4	MGI	ENSMUSG00000031772	ENSMUST00000118171	ESSENTIAL_SPLICE_SITE	0	0	-	chr8	115334642	G	C	-	-	-	-	-
323-p2	Spindle Cell	Col27a1	MGI	ENSMUSG00000045672	ENSMUST00000036300	NON_SYNONYMOUS_CODING	3919	1176	E/D	chr4	62967737	G	C	-	-	-	unknown	-
323-p2	Spindle Cell	E030037K03Rik	MGI	ENSMUSG00000073491	ENSMUST00000150649	NON_SYNONYMOUS_CODING	1058	332	T/I	chr1	175519981	G	A	DELETERIOUS	0	4.32	possibly damaging	1.711
323-p2	Spindle Cell	Ears2	MGI	ENSMUSG00000030871	ENSMUST00000033159	NON_SYNONYMOUS_CODING	1670	484	V/M	chr7	129183264	C	T	TOLERATED	0.31	2.78	benign	0.202
323-p2	Spindle Cell	Eef2	MGI	ENSMUSG00000034994	ENSMUST00000047864	NON_SYNONYMOUS_CODING	458	126	L/P	chr10	80640956	T	C	DELETERIOUS	0	2.79	probably damaging	2.531
323-p2	Spindle Cell	Eef2	MGI	ENSMUSG00000034994	ENSMUST00000047864	ESSENTIAL_SPLICE_SITE	0	0	-	chr10	80641824	A	T	-	-	-	-	-
323-p2	Spindle Cell	Gle1	MGI	ENSMUSG00000019715	ENSMUST00000019859	NON_SYNONYMOUS_CODING	1801	576	R/H	chr2	29806199	G	A	DELETERIOUS	0.03	2.77	probably damaging	2.238
323-p2	Spindle Cell	Gm10010	MGI	ENSMUSG00000056771	ENSMUST00000071101	NON_SYNONYMOUS_CODING	202	68	E/K	chr6	128150440	C	T	-	-	-	unknown	-
323-p2	Spindle Cell	Gm2399	MGI	ENSMUSG00000005397	ENSMUST00000005532	NON_SYNONYMOUS_CODING	249	80	G/S	chr13	13556001	G	A	DELETERIOUS	0	2.89	possibly damaging	1.917
323-p2	Spindle Cell	Gna15	MGI	ENSMUSG00000034792	ENSMUST00000043709	NON_SYNONYMOUS_CODING	506	79	R/W	chr10	80977077	G	A	DELETERIOUS	0	2.88	probably damaging	2.506
323-p2	Spindle Cell	Gsg1	MGI	ENSMUSG00000030206	ENSMUST00000087729	NON_SYNONYMOUS_CODING	983	287	S/N	chr6	135187668	C	T	TOLERATED	0.28	3.57	benign	1.22
323-p2	Spindle Cell	Hsdl2	MGI	ENSMUSG00000028383	ENSMUST00000030078	NON_SYNONYMOUS_CODING	1193	333	E/Q	chr4	59623513	G	C	TOLERATED	0.17	4.32	unknown	-
323-p2	Spindle Cell	Itgb4	MGI	ENSMUSG00000020758	ENSMUST00000106461	NON_SYNONYMOUS_CODING	3069	877	T/A	chr11	115853213	A	G	TOLERATED	1	3.55	benign	0.224
323-p2	Spindle Cell	Klra11	MGI	ENSMUSG00000033024	ENSMUST00000088019	NON_SYNONYMOUS_CODING	193	13	L/F	chr6	130141283	G	A	TOLERATED	1	2.78	benign	0.953
323-p2	Spindle Cell	Klra21	MGI	ENSMUSG00000033024	ENSMUST00000088019	NON_SYNONYMOUS_CODING	193	13	L/F	chr6	130141283	G	A	TOLERATED	1	2.78	benign	0.953
323-p2	Spindle Cell	Klra9	MGI	ENSMUSG00000033024	ENSMUST00000088019	NON_SYNONYMOUS_CODING	193	13	L/F	chr6	130141283	G	A	TOLERATED	1	2.78	benign	0.953
323-p2	Spindle Cell	Megf10	MGI	ENSMUSG00000024593	ENSMUST00000075770	NON_SYNONYMOUS_CODING	3420	921	N/T	chr18	57448970	A	C	TOLERATED	0.24	3.36	benign	1.455
323-p2	Spindle Cell	Mgat5b	MGI	ENSMUSG00000043857	ENSMUST00000103027	NON_SYNONYMOUS_CODING	2561	650	L/V	chr11	116846213	C	G	TOLERATED	1	4.32	benign	0.087
323-p2	Spindle Cell	Mgst1	MGI	ENSMUSG00000008540	ENSMUST00000118091	NON_SYNONYMOUS_CODING	206	34	R/G	chr6	138090312	A	G	Not Scored	-	-	unknown	-
323-p2	Spindle Cell	Mid1	MGI	ENSMUSG00000035299	ENSMUST00000112104	NON_SYNONYMOUS_CODING	2109	627	S/A	chrX	166426979	T	G	TOLERATED	0.22	2.83	benign	0.167
323-p2	Spindle Cell	Nid1	MGI	ENSMUSG00000005397	ENSMUST00000005532	NON_SYNONYMOUS_CODING	249	80	G/S	chr13	13556001	G	A	DELETERIOUS	0	2.89	possibly damaging	1.917
323-p2	Spindle Cell	Nipal2	MGI	ENSMUSG00000038879	ENSMUST00000040791	NON_SYNONYMOUS_CODING	1395	292	I/F	chr15	34512482	T	A	DELETERIOUS	0.04	2.81	possibly damaging	1.523
323-p2	Spindle Cell	Nrip2	MGI	ENSMUSG00000001520	ENSMUST00000120405	NON_SYNONYMOUS_CODING	615	158	P/S	chr6	128357421	C	T	TOLERATED	0.2	3.09	benign	0.739
323-p2	Spindle Cell	Obscn	MGI	ENSMUSG00000061462	ENSMUST00000020732	NON_SYNONYMOUS_CODING	2608	861	L/M	chr11	58943339	G	T	TOLERATED	0.13	2.84	unknown	-
323-p2	Spindle Cell	Ocrl	MGI	ENSMUSG00000001173	ENSMUST00000001202	NON_SYNONYMOUS_CODING	1561	432	S/T	chrX	45291529	G	C	TOLERATED	0.3	2.87	benign	0.171
323-p2	Spindle Cell	Palm2	MGI	ENSMUSG00000090053	ENSMUST00000102905	NON_SYNONYMOUS_CODING	474	55	V/I	chr4	57660898	G	A	TOLERATED	0.59	2.86	benign	0.461
323-p2	Spindle Cell	Pde3a	MGI	ENSMUSG00000041741	ENSMUST00000043259	NON_SYNONYMOUS_CODING	1159	387	I/F	chr6	141407730	A	T	TOLERATED	0.07	3.03	benign	1.394
323-p2	Spindle Cell	Pick1	MGI	ENSMUSG00000068206	ENSMUST00000053926	NON_SYNONYMOUS_CODING	1600	461	R/K	chr15	79086314	G	A	DELETERIOUS	0.01	4.32	unknown	-
323-p2	Spindle Cell	Ppfibp1	MGI	ENSMUSG00000016487	ENSMUST00000111623	NON_SYNONYMOUS_CODING	1326	371	L/P	chr6	146954499	T	C	TOLERATED	0.3	2.99	benign	0.114
323-p2	Spindle Cell	Prpmp5	MGI	ENSMUSG00000052262	ENSMUST00000048686	NON_SYNONYMOUS_CODING	581	185	Q/K	chr6	132262325	G	T	TOLERATED	0.36	2.86	unknown	-
323-p2	Spindle Cell	Slco1c1	MGI	ENSMUSG00000030235	ENSMUST00000111837	NON_SYNONYMOUS_CODING	1309	311	N/D	chr6	141495341	A	G	TOLERATED	0.94	2.81	benign	0.53
323-p2	Spindle Cell	St6galnac1	MGI	ENSMUSG00000009588	ENSMUST00000009732	NON_SYNONYMOUS_CODING	207	34	R/S	chr11	116636615	C	A	TOLERATED	0.49	4.32	benign	0.237
323-p2	Spindle Cell	Tex19.2	MGI	ENSMUSG00000039337	ENSMUST00000039146	NON_SYNONYMOUS_CODING	1582	314	D/E	chr11	120977993	A	C	Not Scored	-	-	benign	0.675
323-p2	Spindle Cell	Timm9	MGI	ENSMUSG00000021079	ENSMUST00000021486	NON_SYNONYMOUS_CODING	412	89	R/W	chr12	72224544	G	A	DELETERIOUS	0	4.32	probably damaging	2.257
323-p2	Spindle Cell	Tmem67	MGI	ENSMUSG00000049488	ENSMUST00000108293	NON_SYNONYMOUS_CODING	669	26	Q/P	chr4	12016499	T	G	Not Scored	-	-	benign	1.35
323-p2	Spindle Cell	Tpm2	MGI	ENSMUSG00000028464	ENSMUST00000034926	NON_SYNONYMOUS_CODING	907	266	I/T	chr4	43531717	A	G	TOLERATED	1	4.32	unknown	-
323-p2	Spindle Cell	Tro	MGI	ENSMUSG00000025272	ENSMUST00000087258	NON_SYNONYMOUS_CODING	1283	406	N/S	chrX	147088986	T	C	TOLERATED	0.74	3.45	benign	1.125
323-p2	Spindle Cell	Tro	MGI	ENSMUSG00000025272	ENSMUST00000087258	NON_SYNONYMOUS_CODING	1275	403	D/E	chrX	147088994	A	C	TOLERATED	1	3.45	benign	0.9
323-p2	Spindle Cell	Trp53	MGI	ENSMUSG00000059552	ENSMUST00000108658	NON_SYNONYMOUS_CODING	862	245	R/H	chr11	69402713	G	A	DELETERIOUS	0	2.77	probably damaging	2.45
323-p2	Spindle Cell	Tubb3	MGI	ENSMUSG00000062380	ENSMUST00000071134	NON_SYNONYMOUS_CODING	1009	276	R/Q	chr8	125945056	G	A	DELETERIOUS	0	4.2	probably damaging	1.773
323-p2	Spindle Cell	Zdhhc4	MGI	ENSMUSG00000001844	ENSMUST00000001900	NON_SYNONYMOUS_CODING	1178	300	R/H	chr5	144078354	C	T	TOLERATED	0.98	2.88	benign	0.867
323-p2	Spindle Cell	Zfp217	MGI	ENSMUSG00000052056	ENSMUST00000109155	NON_SYNONYMOUS_CODING	1927	473	P/H	chr2	169941728	G	T	TOLERATED	0.38	2.99	benign	0.894
323-p2	Spindle Cell	Zkscan16	MGI	ENSMUSG00000038630	ENSMUST00000107554	NON_SYNONYMOUS_CODING	166	3	G/A	chr4	58959006	G	C	TOLERATED	1	4.32	benign	0.039
323-p3	Spindle Cell	1700023A16Rik	MGI	ENSMUSG00000030292	ENSMUST00000111634	NON_SYNONYMOUS_CODING	659	219	T/N	chr6	146810206	C	A	TOLERATED	0.38	4.32	benign	0.08
323-p3	Spindle Cell	2310022A10Rik	MGI	ENSMUSG00000049643	ENSMUST00000067386	NON_SYNONYMOUS_CODING	313	105	A/P	chr7	28350678	G	C	TOLERATED	0.28	3.21	benign	0.071
323-p3	Spindle Cell	4930433I11Rik	MGI	ENSMUSG00000049062	ENSMUST00000056767	NON_SYNONYMOUS_CODING	694	232	P/A	chr7	48248972	C	G	-	-	-	-	-
323-p3	Spindle Cell	4930433I11Rik	MGI	ENSMUSG00000049062	ENSMUST00000056767	NON_SYNONYMOUS_CODING	706	236	L/M	chr7	48248984	C	A	-	-	-	-	-
323-p3	Spindle Cell	4930433I11Rik	MGI	ENSMUSG00000049062	ENSMUST00000056767	NON_SYNONYMOUS_CODING	1007	336	L/H	chr7	48249285	T	A	-	-	-	-	-
323-p3	Spindle Cell	5330439B14Rik	MGI	ENSMUSG00000041614	ENSMUST00000040390	NON_SYNONYMOUS_CODING	626	96	L/V	chr6	142574216	C	G	-	-	-	unknown	-

Supplementary Table 3. Predicted somatic mutations in tumors

Sample Id	Histological type	GeneName	DB	Gene	Transcript	Consequence	Position_in_cDNA	Position_in_protein	Amino_acid_change	Chromosome	Position	Ref	Var	Effect (SIFT)	Score (SIFT)	Median Info (SIFT)	Effect (Polyphen)	Score (Polyphen)
323-p3	Spindle Cell	Adcy5	MGI	ENSMUSG00000022840	ENSMUST00000023549	NON_SYNONYMOUS_CODING	3992	924	V/M	chr16	35291630	G	A	DELETERIOUS	0	2.77	benign	0.399
323-p3	Spindle Cell	Akap14	MGI	ENSMUSG00000036551	ENSMUST00000046557	NON_SYNONYMOUS_CODING	827	248	A/V	chrX	34703333	G	A	TOLERATED	0.12	3.14	unknown	-
323-p3	Spindle Cell	Atf7ip	MGI	ENSMUSG00000030213	ENSMUST00000032335	NON_SYNONYMOUS_CODING	981	287	D/E	chr6	136509152	T	A	TOLERATED	1	2.91	benign	0.073
323-p3	Spindle Cell	Atf7ip	MGI	ENSMUSG00000030213	ENSMUST00000032335	NON_SYNONYMOUS_CODING	1760	547	A/V	chr6	136509931	C	T	TOLERATED	0.65	2.91	benign	0.572
323-p3	Spindle Cell	Atp11a	MGI	ENSMUSG00000031441	ENSMUST00000091237	NON_SYNONYMOUS_CODING	2625	776	D/G	chr8	12846118	A	G	TOLERATED	0.06	3.5	benign	1.329
323-p3	Spindle Cell	B3galt1	MGI	ENSMUSG00000034780	ENSMUST00000042456	STOP_GAINED	1100	273	R/*	chr2	67956816	C	T	-	-	-	unknown	-
323-p3	Spindle Cell	BC049715	MGI	ENSMUSG00000047515	ENSMUST00000052702	NON_SYNONYMOUS_CODING	675	110	A/T	chr6	136788612	G	A	DELETERIOUS	0	3.67	benign	0.242
323-p3	Spindle Cell	BC049715	MGI	ENSMUSG00000047515	ENSMUST00000052702	NON_SYNONYMOUS_CODING	1008	221	E/K	chr6	136788945	G	A	TOLERATED	0.35	3.67	benign	0.309
323-p3	Spindle Cell	Bcat1	MGI	ENSMUSG00000030268	ENSMUST00000087468	NON_SYNONYMOUS_CODING	762	240	L/P	chr6	144967868	A	G	DELETERIOUS	0	2.8	probably damaging	2.618
323-p3	Spindle Cell	Bcl2l14	MGI	ENSMUSG00000030200	ENSMUST00000032321	NON_SYNONYMOUS_CODING	1065	269	R/Q	chr6	134382288	G	A	TOLERATED	1	3.71	benign	0.614
323-p3	Spindle Cell	Blzf1	MGI	ENSMUSG00000026577	ENSMUST00000027866	NON_SYNONYMOUS_CODING	401	38	E/K	chr1	166232801	C	T	TOLERATED	0.13	3.84	benign	0.488
323-p3	Spindle Cell	Butr1	MGI	ENSMUSG00000020490	ENSMUST00000069941	NON_SYNONYMOUS_CODING	1484	399	K/N	chr11	58737194	G	C	TOLERATED	1	2.78	benign	0.858
323-p3	Spindle Cell	Cd244	MGI	ENSMUSG00000004709	ENSMUST00000004829	NON_SYNONYMOUS_CODING	182	17	H/P	chr1	173489505	A	C	TOLERATED	0.18	2.88	probably damaging	2.656
323-p3	Spindle Cell	Cep68	MGI	ENSMUSG00000044066	ENSMUST00000050611	NON_SYNONYMOUS_CODING	832	227	P/A	chr11	20140335	G	C	TOLERATED	0.26	3.44	possibly damaging	1.951
323-p3	Spindle Cell	Cfhr2	MGI	ENSMUSG00000033898	ENSMUST00000094484	NON_SYNONYMOUS_CODING	96	12	I/L	chr1	141915392	T	G	TOLERATED	0.11	3.42	unknown	-
323-p3	Spindle Cell	Chd4	MGI	ENSMUSG00000063870	ENSMUST00000112390	NON_SYNONYMOUS_CODING	4976	1600	P/T	chr6	125072159	C	A	DELETERIOUS	0.04	3.32	possibly damaging	1.8
323-p3	Spindle Cell	Chd5	MGI	ENSMUSG00000005045	ENSMUST00000030775	NON_SYNONYMOUS_CODING	4194	1298	R/L	chr4	151751234	G	T	TOLERATED	0.23	2.82	possibly damaging	1.828
323-p3	Spindle Cell	Cntnap4	MGI	ENSMUSG00000031772	ENSMUST00000118171	ESSENTIAL_SPLICE_SITE	0	0	-	chr8	115334642	G	C	-	-	-	-	-
323-p3	Spindle Cell	Col27a1	MGI	ENSMUSG00000045672	ENSMUST00000036300	NON_SYNONYMOUS_CODING	3919	1176	E/D	chr4	62967737	G	C	-	-	-	unknown	-
323-p3	Spindle Cell	Cpne1	MGI	ENSMUSG00000074643	ENSMUST00000109608	NON_SYNONYMOUS_CODING	1171	322	V/M	chr2	155903320	C	T	DELETERIOUS	0	2.77	probably damaging	2.133
323-p3	Spindle Cell	E030037K03Rik	MGI	ENSMUSG00000073491	ENSMUST00000150649	NON_SYNONYMOUS_CODING	1058	332	T/I	chr1	175519981	G	A	DELETERIOUS	0	4.32	possibly damaging	1.711
323-p3	Spindle Cell	E330021D16Rik	MGI	ENSMUSG00000045291	ENSMUST00000058713	NON_SYNONYMOUS_CODING	375	26	V/M	chr6	136351777	C	T	TOLERATED	0.37	3.35	benign	0.669
323-p3	Spindle Cell	Ears2	MGI	ENSMUSG00000030871	ENSMUST00000033159	NON_SYNONYMOUS_CODING	1670	484	V/M	chr7	129183264	C	T	TOLERATED	0.31	2.78	benign	0.202
323-p3	Spindle Cell	Epn3	MGI	ENSMUSG00000010080	ENSMUST00000127305	NON_SYNONYMOUS_CODING	842	141	R/W	chr11	94357436	G	A	DELETERIOUS	0	2.78	probably damaging	2.596
323-p3	Spindle Cell	Esrrb	MGI	ENSMUSG00000021255	ENSMUST00000116402	NON_SYNONYMOUS_CODING	605	202	N/T	chr12	87846843	A	C	TOLERATED	0.57	2.8	benign	0.496
323-p3	Spindle Cell	Fam190a	MGI	ENSMUSG00000039578	ENSMUST00000126214	NON_SYNONYMOUS_CODING	1980	537	S/P	chr6	61372965	T	C	DELETERIOUS	0.01	3.78	possibly damaging	1.773
323-p3	Spindle Cell	Fat1	MGI	ENSMUSG00000070047	ENSMUST00000098796	NON_SYNONYMOUS_CODING	13051	4351	S/P	chr8	46130441	T	C	TOLERATED	0.16	3.16	unknown	-
323-p3	Spindle Cell	Gle1	MGI	ENSMUSG00000019715	ENSMUST00000019859	NON_SYNONYMOUS_CODING	1801	576	R/H	chr2	29806199	G	A	DELETERIOUS	0.03	2.77	probably damaging	2.238
323-p3	Spindle Cell	Gm10010	MGI	ENSMUSG00000056771	ENSMUST00000071101	NON_SYNONYMOUS_CODING	202	68	E/K	chr6	128150440	C	T	-	-	-	unknown	-
323-p3	Spindle Cell	Gm10101	MGI	ENSMUSG00000061510	ENSMUST00000074862	NON_SYNONYMOUS_CODING	62	21	T/I	chr14	47450104	G	A	-	-	-	benign	0.675
323-p3	Spindle Cell	Gm10101	MGI	ENSMUSG00000061510	ENSMUST00000074862	NON_SYNONYMOUS_CODING	31	11	L/F	chr14	47450135	G	A	-	-	-	benign	0.837
323-p3	Spindle Cell	Gm2399	MGI	ENSMUSG00000005397	ENSMUST00000005532	NON_SYNONYMOUS_CODING	249	80	G/S	chr13	13556001	G	A	DELETERIOUS	0	2.89	possibly damaging	1.917
323-p3	Spindle Cell	Gm766	MGI	ENSMUSG00000048473	ENSMUST00000111768	NON_SYNONYMOUS_CODING	8	3	C/S	chr6	142752903	C	G	DELETERIOUS	0	4.32	benign	0.426
323-p3	Spindle Cell	Gna15	MGI	ENSMUSG00000034792	ENSMUST00000043709	NON_SYNONYMOUS_CODING	506	79	R/W	chr10	80977077	G	A	DELETERIOUS	0	2.88	probably damaging	2.506
323-p3	Spindle Cell	Gsg1	MGI	ENSMUSG00000030206	ENSMUST00000087729	NON_SYNONYMOUS_CODING	983	287	S/N	chr6	135187668	C	T	TOLERATED	0.28	3.57	benign	1.22
323-p3	Spindle Cell	Gsr	MGI	ENSMUSG00000031584	ENSMUST00000033992	NON_SYNONYMOUS_CODING	810	170	T/A	chr8	34784640	A	G	DELETERIOUS	0.01	2.77	possibly damaging	1.502
323-p3	Spindle Cell	Hsdl2	MGI	ENSMUSG00000028383	ENSMUST00000030078	NON_SYNONYMOUS_CODING	1193	333	E/Q	chr4	59623513	G	C	TOLERATED	0.17	4.32	unknown	-
323-p3	Spindle Cell	Ifi27l2b	MGI	ENSMUSG00000021208	ENSMUST00000044687	NON_SYNONYMOUS_CODING	689	209	A/P	chr12	104689512	C	G	TOLERATED	0.1	3.11	unknown	-
323-p3	Spindle Cell	Irf2bp1	MGI	ENSMUSG00000044030	ENSMUST00000053713	NON_SYNONYMOUS_CODING	1687	439	D/N	chr7	19591100	G	A	TOLERATED	0.19	2.99	benign	1.415
323-p3	Spindle Cell	Itgb4	MGI	ENSMUSG00000020758	ENSMUST00000106461	NON_SYNONYMOUS_CODING	3069	877	T/A	chr11	115853213	A	G	TOLERATED	1	3.55	benign	0.224
323-p3	Spindle Cell	Klra11	MGI	ENSMUSG00000033024	ENSMUST00000088019	NON_SYNONYMOUS_CODING	193	13	L/F	chr6	130141283	G	A	TOLERATED	1	2.78	benign	0.953
323-p3	Spindle Cell	Klra21	MGI	ENSMUSG00000033024	ENSMUST00000088019	NON_SYNONYMOUS_CODING	193	13	L/F	chr6	130141283	G	A	TOLERATED	1	2.78	benign	0.953
323-p3	Spindle Cell	Klra5	MGI	ENSMUSG00000030173	ENSMUST00000014683	NON_SYNONYMOUS_CODING	118	4	P/A	chr6	129861470	G	C	DELETERIOUS	0	2.83	benign	1.316
323-p3	Spindle Cell	Klra9	MGI	ENSMUSG00000033024	ENSMUST00000088019	NON_SYNONYMOUS_CODING	193	13	L/F	chr6	130141283	G	A	TOLERATED	1	2.78	benign	0.953
323-p3	Spindle Cell	Map3k15	MGI	ENSMUSG00000031303	ENSMUST00000033665	STOP_GAINED	3817	1273	Q/*	chrX	156560365	C	T	-	-	-	unknown	-
323-p3	Spindle Cell	Megf10	MGI	ENSMUSG00000024593	ENSMUST00000075770	NON_SYNONYMOUS_CODING	3420	921	N/T	chr18	57448970	A	C	TOLERATED	0.24	3.36	benign	1.455
323-p3	Spindle Cell	Mgat5b	MGI	ENSMUSG00000043857	ENSMUST00000103027	NON_SYNONYMOUS_CODING	2561	650	L/V	chr11	116846213	C	G	TOLERATED	1	4.32	benign	0.087
323-p3	Spindle Cell	Mgst1	MGI	ENSMUSG00000008540	ENSMUST00000118091	NON_SYNONYMOUS_CODING	206	34	R/G	chr6	138090312	A	G	Not Scored	-	-	unknown	-
323-p3	Spindle Cell	Mgst1	MGI	ENSMUSG00000008540	ENSMUST00000118091	NON_SYNONYMOUS_CODING	296	64	G/S	chr6	138090402	G	A	DELETERIOUS	0.03	4.32	benign	1.35
323-p3	Spindle Cell	Mid1	MGI	ENSMUSG00000035299	ENSMUST00000112104	NON_SYNONYMOUS_CODING	2109	627	S/A	chrX	166426979	T	G	TOLERATED	0.22	2.83	benign	0.167
323-p3	Spindle Cell	Nfrkb	MGI	ENSMUSG00000042185	ENSMUST00000086167	NON_SYNONYMOUS_CODING	3357	1080	K/N	chr9	31222087	A	C	TOLERATED	0.32	3.21	benign	1.497
323-p3	Spindle Cell	Nid1	MGI	ENSMUSG00000005397	ENSMUST00000005532	NON_SYNONYMOUS_CODING	249	80	G/S	chr13	13556001	G	A	DELETERIOUS	0	2.89	possibly damaging	1.917
323-p3	Spindle Cell	Nipal2	MGI	ENSMUSG00000038879	ENSMUST00000040791	NON_SYNONYMOUS_CODING	1395	292	I/F	chr15	34512482	T	A	DELETERIOUS	0.04	2.81	possibly damaging	1.523
323-p3	Spindle Cell	Nlrp1a	MGI	ENSMUSG00000069830	ENSMUST00000108519	NON_SYNONYMOUS_CODING	4041	1248	S/A	chr11	70905899	A	C	TOLERATED	1	3.64	benign	0.435
323-p3	Spindle Cell	Nrip2	MGI	ENSMUSG00000001520	ENSMUST00000120405	NON_SYNONYMOUS_CODING	615	158	P/S	chr6	128357421	C	T	TOLERATED	0.2	3.09	benign	0.739
323-p3	Spindle Cell	Ocm	MGI	ENSMUSG00000029618	ENSMUST00000085704	NON_SYNONYMOUS_CODING	250	41	A/P	chr5	144785370	C	G	TOLERATED	0.16	3.35	benign	0.436
323-p3	Spindle Cell	Ocrl	MGI	ENSMUSG00000001173	ENSMUST00000001202	NON_SYNONYMOUS_CODING	1561	432	S/T	chrX	45291529	G	C	TOLERATED	0.3	2.87	benign	0.171
323-p3	Spindle Cell	Odz1	MGI	ENSMUSG00000016150	ENSMUST00000115059	NON_SYNONYMOUS_CODING	7913	2610	T/I	chrX	39886009	G	A	DELETERIOUS	0	3.05	probably damaging	2.098
323-p3	Spindle Cell	Palm2	MGI	ENSMUSG00000090053	ENSMUST00000102905	NON_SYNONYMOUS_CODING	474	55	V/I	chr4	57660898	G	A	TOLERATED	0.59	2.86	benign	0.461
323-p3	Spindle Cell	Pde3a	MGI	ENSMUSG00000041741	ENSMUST00000043259	NON_SYNONYMOUS_CODING	1159	387	I/F	chr6	141407730	A	T	TOLERATED	0.07	3.03	benign	1.394

Supplementary Table 3. Predicted somatic mutations in tumors

Sample Id	Histological type	GeneName	DB	Gene	Transcript	Consequence	Position_in_cDNA	Position_in_protein	Amino_acid_change	Chromosome	Position	Ref	Var	Effect (SIFT)	Score (SIFT)	Median Info (SIFT)	Effect (Polyphen)	Score (Polyphen)
323-p3	Spindle Cell	Pick1	MGI	ENSMUSG00000068206	ENSMUST00000053926	NON_SYNONYMOUS_CODING	1600	461	R/K	chr15	79086314	G	A	DELETERIOUS	0.01	4.32	unknown	-
323-p3	Spindle Cell	Plod3	MGI	ENSMUSG00000004846	ENSMUST00000004968	NON_SYNONYMOUS_CODING	2760	698	R/H	chr5	137471998	G	A	DELETERIOUS	0	2.99	probably damaging	2.455
323-p3	Spindle Cell	Ppfibp1	MGI	ENSMUSG00000016487	ENSMUST00000111623	NON_SYNONYMOUS_CODING	1326	371	L/P	chr6	146954499	T	C	TOLERATED	0.3	2.99	benign	0.114
323-p3	Spindle Cell	Prpmp5	MGI	ENSMUSG00000052262	ENSMUST00000048686	NON_SYNONYMOUS_CODING	581	185	Q/K	chr6	132262325	G	T	TOLERATED	0.36	2.86	unknown	-
323-p3	Spindle Cell	Ptprm	MGI	ENSMUSG00000033278	ENSMUST00000112708	NON_SYNONYMOUS_CODING	315	89	T/N	chr17	67703413	G	T	-	-	-	-	-
323-p3	Spindle Cell	Sectm1b	MGI	ENSMUSG00000039364	ENSMUST00000039309	NON_SYNONYMOUS_CODING	579	116	W/C	chr11	120917034	C	G	TOLERATED	0.05	3.36	probably damaging	2.734
323-p3	Spindle Cell	Sectm1b	MGI	ENSMUSG00000039364	ENSMUST00000039309	NON_SYNONYMOUS_CODING	571	114	E/K	chr11	120917042	C	T	TOLERATED	0.83	3.36	benign	1.311
323-p3	Spindle Cell	Slco1c1	MGI	ENSMUSG00000030235	ENSMUST00000111837	NON_SYNONYMOUS_CODING	1309	311	N/D	chr6	141495341	A	G	TOLERATED	0.94	2.81	benign	0.53
323-p3	Spindle Cell	Spna1	MGI	ENSMUSG00000026532	ENSMUST00000027817	NON_SYNONYMOUS_CODING	2984	940	E/G	chr1	176133403	A	G	DELETERIOUS	0.01	2.91	probably damaging	2.422
323-p3	Spindle Cell	Spnb4	MGI	ENSMUSG00000011751	ENSMUST00000011895	NON_SYNONYMOUS_CODING	4222	1357	E/G	chr7	28179190	T	C	TOLERATED	0.06	2.88	possibly damaging	1.627
323-p3	Spindle Cell	Tas2r134	MGI	ENSMUSG00000056115	ENSMUST00000070028	NON_SYNONYMOUS_CODING	149	50	C/F	chr2	51483179	G	T	DELETERIOUS	0.02	2.85	probably damaging	3.131
323-p3	Spindle Cell	Tex19.2	MGI	ENSMUSG00000039337	ENSMUST00000039146	NON_SYNONYMOUS_CODING	1582	314	D/E	chr11	120977993	A	C	Not Scored	-	-	benign	0.675
323-p3	Spindle Cell	Timm9	MGI	ENSMUSG00000021079	ENSMUST00000021486	NON_SYNONYMOUS_CODING	412	89	R/W	chr12	72224544	G	A	DELETERIOUS	0	4.32	probably damaging	2.257
323-p3	Spindle Cell	Tmem67	MGI	ENSMUSG00000049488	ENSMUST00000108293	NON_SYNONYMOUS_CODING	669	26	Q/P	chr4	12016499	T	G	Not Scored	-	-	benign	1.35
323-p3	Spindle Cell	Tpm2	MGI	ENSMUSG00000028464	ENSMUST00000034926	NON_SYNONYMOUS_CODING	907	266	I/T	chr4	43531717	A	G	TOLERATED	1	4.32	unknown	-
323-p3	Spindle Cell	Trp53	MGI	ENSMUSG00000059552	ENSMUST00000108658	NON_SYNONYMOUS_CODING	862	245	R/H	chr11	69402713	G	A	DELETERIOUS	0	2.77	probably damaging	2.45
323-p3	Spindle Cell	Tubb3	MGI	ENSMUSG00000062380	ENSMUST00000071134	NON_SYNONYMOUS_CODING	1009	276	R/Q	chr8	125945056	G	A	DELETERIOUS	0	4.2	probably damaging	1.773
323-p3	Spindle Cell	Vwf	MGI	ENSMUSG00000001930	ENSMUST00000112254	NON_SYNONYMOUS_CODING	7183	2314	R/C	chr6	125613551	C	T	TOLERATED	0.07	3.04	probably damaging	2.654
323-p3	Spindle Cell	Wwtr1	MGI	ENSMUSG00000027803	ENSMUST00000120977	NON_SYNONYMOUS_CODING	976	316	A/S	chr3	57267480	C	A	DELETERIOUS	0.02	3.12	benign	1.259
323-p3	Spindle Cell	Zdhhc4	MGI	ENSMUSG00000001844	ENSMUST00000001900	NON_SYNONYMOUS_CODING	1178	300	R/H	chr5	144078354	C	T	TOLERATED	0.98	2.88	benign	0.867
323-p3	Spindle Cell	Zfp217	MGI	ENSMUSG00000052056	ENSMUST00000109155	NON_SYNONYMOUS_CODING	1927	473	P/H	chr2	169941728	G	T	TOLERATED	0.38	2.99	benign	0.894
323-p3	Spindle Cell	Zkscan16	MGI	ENSMUSG00000038630	ENSMUST00000107554	NON_SYNONYMOUS_CODING	166	3	G/A	chr4	58959006	G	C	TOLERATED	1	4.32	benign	0.039

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T155	Adenocarcinoma	1	-0.5832	ENSMUSG00000038209	1	173354798	173371968	Itln1
T155	Adenocarcinoma	1	-0.5832	ENSMUSG00000004709	1	173395868	173420260	Cd244
T155	Adenocarcinoma	2	0.6253	ENSMUSG00000044138	3	15348525	15551793	Sirpb1
T155	Adenocarcinoma	2	0.6253	ENSMUSG00000074677	3	15987305	16040598	Sirpb1
T155	Adenocarcinoma	3	0.8945	ENSMUSG00000049214	4	111470967	111481052	NP_808486.1
T155	Adenocarcinoma	3	0.8945	ENSMUSG00000055960	4	111570571	111665328	NP_848901.1
T155	Adenocarcinoma	3	0.8945	ENSMUSG00000070868	4	111733673	111796139	A430090E18Rik
T155	Adenocarcinoma	3	0.8945	ENSMUSG00000049972	4	111883901	111931917	NP_808532.1
T155	Adenocarcinoma	3	0.8945	ENSMUSG00000034359	4	112055126	112145772	OTTMUSG00000008540
T155	Adenocarcinoma	3	0.8945	ENSMUSG00000065318	4	112088704	112088810	U6
T155	Adenocarcinoma	4	0.7608	ENSMUSG00000060264	4	112453007	112454218	
T155	Adenocarcinoma	4	0.7608	ENSMUSG00000051602	4	112476241	112477763	
T155	Adenocarcinoma	5	-0.6526	ENSMUSG00000066613	5	110247339	110250320	2310001H12Rik
T155	Adenocarcinoma	6	-0.5371	ENSMUSG00000075297	10	21972889	21976663	
T155	Adenocarcinoma	7	-0.9625	ENSMUSG00000070390	11	70988256	71034514	
T155	Adenocarcinoma	7	-0.9625	ENSMUSG00000077340	11	71050002	71050135	SNORA17
T155	Adenocarcinoma	7	-0.9625	ENSMUSG00000040575	11	71058625	71101427	Nlrp1c
T155	Adenocarcinoma	7	-0.9625	ENSMUSG00000077632	11	71104620	71104753	SNORA17
T155	Adenocarcinoma	8	-0.5924	ENSMUSG00000047632	19	36982690	36984743	Fgfbp3
T155	Adenocarcinoma	9	-0.6396	ENSMUSG00000056999	19	37335574	37395757	Ide
T358	Adenocarcinoma	1	-0.5663	ENSMUSG00000038218	1	173351908	173353597	
T358	Adenocarcinoma	1	-0.5663	ENSMUSG00000038209	1	173354798	173371968	Itln1
T358	Adenocarcinoma	1	-0.5663	ENSMUSG00000004709	1	173395868	173420260	Cd244
T358	Adenocarcinoma	2	0.8014	ENSMUSG00000055960	4	111570571	111665328	NP_848901.1
T358	Adenocarcinoma	2	0.8014	ENSMUSG00000070868	4	111733673	111796139	A430090E18Rik
T358	Adenocarcinoma	2	0.8014	ENSMUSG00000049972	4	111883901	111931917	NP_808532.1
T358	Adenocarcinoma	2	0.8014	ENSMUSG00000034359	4	112055126	112145772	OTTMUSG00000008540
T358	Adenocarcinoma	2	0.8014	ENSMUSG00000065318	4	112088704	112088810	U6
T358	Adenocarcinoma	3	0.5772	ENSMUSG00000048766	4	112209079	112272798	A030001H23Rik
T358	Adenocarcinoma	3	0.5772	ENSMUSG00000060264	4	112453007	112454218	
T358	Adenocarcinoma	3	0.5772	ENSMUSG00000051602	4	112476241	112477763	
T358	Adenocarcinoma	4	-0.7548	ENSMUSG00000076466	6	41043174	41043674	TRBV12-1
T358	Adenocarcinoma	4	-0.7548	ENSMUSG00000076467	6	41045643	41046075	TRBV13-1
T358	Adenocarcinoma	4	-0.7548	ENSMUSG00000076468	6	41048471	41048971	TRBV12-2
T358	Adenocarcinoma	4	-0.7548	ENSMUSG00000076469	6	41051003	41051439	TRBV13-2

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T358	Adenocarcinoma	4	-0.7548	ENSMUSG00000076470	6	41059754	41060192	TRBV13-3
T358	Adenocarcinoma	4	-0.7548	ENSMUSG00000076471	6	41064774	41065223	TRBV14
T358	Adenocarcinoma	4	-0.7548	ENSMUSG00000076472	6	41070818	41071265	TRBV15
T358	Adenocarcinoma	4	-0.7548	ENSMUSG00000076473	6	41081398	41081837	TRBV16
T358	Adenocarcinoma	5	0.4481	ENSMUSG00000049556	9	56416612	56483390	Lingo1
T358	Adenocarcinoma	5	0.4481	ENSMUSG00000045620	9	56646796	56650100	Odf3l1
T358	Adenocarcinoma	5	0.4481	ENSMUSG00000032911	9	56663297	56697272	Cspg4
T358	Adenocarcinoma	6	0.4608	ENSMUSG00000034248	14	68195176	68238400	Slc25a37
T358	Adenocarcinoma	6	0.4608	ENSMUSG00000047977	14	68243712	68247629	D930020E02Rik
T358	Adenocarcinoma	6	0.4608	ENSMUSG00000022066	14	68290504	68320600	Entpd4
T358	Adenocarcinoma	6	0.4608	ENSMUSG00000071316	14	68343957	68344433	ENSMUSG00000071316
T358	Adenocarcinoma	6	0.4608	ENSMUSG00000034205	14	68344248	68428800	Loxl2
T358	Adenocarcinoma	6	0.4608	ENSMUSG00000056640	14	68393255	68393578	ENSMUSG00000056640
T358	Adenocarcinoma	7	-0.4542	ENSMUSG00000050982	15	77304302	77318324	9030421J09Rik
T358	Adenocarcinoma	7	-0.4542	ENSMUSG00000044309	15	77352890	77357382	2210421G13Rik
T358	Adenocarcinoma	8	0.5567	ENSMUSG00000054939	16	3762541	3770034	NP_001074686.1
T358	Adenocarcinoma	8	0.5567	ENSMUSG00000039789	16	3776772	3787602	Zfp597
T358	Adenocarcinoma	8	0.5567	ENSMUSG00000005982	16	3799911	3817167	1200013P24Rik
T358	Adenocarcinoma	8	0.5567	ENSMUSG00000005983	16	3810409	3822985	1700037C18Rik
T358	Adenocarcinoma	8	0.5567	ENSMUSG00000071682	16	3824085	3824420	1700016D08Rik
T358	Adenocarcinoma	8	0.5567	ENSMUSG00000014232	16	3824237	3856375	Cluap1
T358	Adenocarcinoma	8	0.5567	ENSMUSG00000049871	16	3860838	3891773	Nlrc3
T358	Adenocarcinoma	8	0.5567	ENSMUSG00000039738	16	3895049	3914580	Btbd12
T358	Adenocarcinoma	8	0.5567	ENSMUSG00000005980	16	3952371	3955247	Dnase1
T358	Adenocarcinoma	8	0.5567	ENSMUSG00000005981	16	3955205	3993038	Trap1
T358	Adenocarcinoma	8	0.5567	ENSMUSG00000075417	16	3997429	3997761	Crebbp
T358	Adenocarcinoma	8	0.5567	ENSMUSG00000022521	16	3999276	4128632	Crebbp
T358	Adenocarcinoma	9	0.6909	ENSMUSG00000022542	16	4902179	4913173	SEPT12
T358	Adenocarcinoma	9	0.6909	ENSMUSG00000022540	16	4924050	4928848	Rogdi
T358	Adenocarcinoma	9	0.6909	ENSMUSG00000022536	16	4929258	4965181	3930401K13Rik
T358	Adenocarcinoma	9	0.6909	ENSMUSG00000039473	16	4970410	5001610	Ubn1
T358	Adenocarcinoma	9	0.6909	ENSMUSG00000077367	16	4976096	4976203	U6
T358	Adenocarcinoma	9	0.6909	ENSMUSG00000039457	16	5002046	5047742	Ppl
T358	Adenocarcinoma	10	0.963	ENSMUSG00000008658	16	6985156	7325300	A2bp1
T358	Adenocarcinoma	11	0.6974	ENSMUSG00000077152	16	8318135	8318266	SNORA17

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T358	Adenocarcinoma	11	0.6974	ENSMUSG00000022715	16	8324597	8340457	4930511J11Rik
T358	Adenocarcinoma	11	0.6974	ENSMUSG00000039345	16	8386134	8405518	BC024814
T358	Adenocarcinoma	11	0.6974	ENSMUSG00000077557	16	8395981	8396062	SNORD86
T358	Adenocarcinoma	11	0.6974	ENSMUSG00000057880	16	8428810	8536889	Abat
T358	Adenocarcinoma	11	0.6974	ENSMUSG00000051226	16	8536068	8536460	ENSMUSG00000051226
T358	Adenocarcinoma	11	0.6974	ENSMUSG00000076039	16	8538484	8538591	
T358	Adenocarcinoma	11	0.6974	ENSMUSG00000052361	16	8538504	8540640	
T358	Adenocarcinoma	11	0.6974	ENSMUSG00000043140	16	8549205	8553032	Tmem186
T358	Adenocarcinoma	11	0.6974	ENSMUSG00000022711	16	8553047	8572870	Pmm2
T358	Adenocarcinoma	11	0.6974	ENSMUSG00000008393	16	8573908	8587474	Carhsp1
T358	Adenocarcinoma	11	0.6974	ENSMUSG00000022710	16	8606101	8672887	Q6A4J8-2
T358	Adenocarcinoma	11	0.6974	ENSMUSG00000065902	16	8682039	8682146	U6
T358	Adenocarcinoma	11	0.6974	ENSMUSG00000022507	16	8745971	8772066	1810013L24Rik
T358	Adenocarcinoma	11	0.6974	ENSMUSG00000068674	16	8835612	8835944	
T358	Adenocarcinoma	12	0.4552	ENSMUSG00000059003	16	9491382	9906111	Grin2a
T358	Adenocarcinoma	12	0.4552	ENSMUSG00000056779	16	9958539	9959308	
T358	Adenocarcinoma	12	0.4552	ENSMUSG00000039209	16	10083806	10088489	Rpl39l
T358	Adenocarcinoma	12	0.4552	ENSMUSG00000039200	16	10106500	10155534	Atf7ip2
T358	Adenocarcinoma	12	0.4552	ENSMUSG00000075406	16	10155598	10156629	Atf7ip2
T358	Adenocarcinoma	13	0.9408	ENSMUSG00000022505	16	10195337	10227546	Emp2
T358	Adenocarcinoma	13	0.9408	ENSMUSG00000039179	16	10271531	10308997	Tekt5
T358	Adenocarcinoma	13	0.9408	ENSMUSG00000022503	16	10325526	10337996	Nubp1
T358	Adenocarcinoma	13	0.9408	ENSMUSG00000050908	16	10337777	10360623	BC068110
T358	Adenocarcinoma	13	0.9408	ENSMUSG00000022504	16	10393637	10441141	Ciita
T358	Adenocarcinoma	13	0.9408	ENSMUSG00000075404	16	10403400	10404635	EG669998
T358	Adenocarcinoma	13	0.9408	ENSMUSG00000038055	16	10443793	10456632	Dexi
T358	Adenocarcinoma	13	0.9408	ENSMUSG00000068663	16	10458965	10658449	4932416N17Rik
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000068663	16	10458965	10658449	4932416N17Rik
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000038037	16	10695821	10699114	Socs1
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000043050	16	10701514	10702238	Tnp2
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000050058	16	10704162	10704467	Prm3
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000038015	16	10704961	10705683	Prm2
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000022501	16	10709905	10710404	Prm1
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000071671	16	10714953	10715294	
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000037991	16	10748668	10799812	A630055G03Rik

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000022500	16	10872437	10906698	Litaf
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000075403	16	10949524	10949943	ENSMUSG00000075403
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000051848	16	10973670	10979700	ENSMUSG00000051848
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000037972	16	10974523	10988561	Snn
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000022498	16	10988489	11048110	Txndc11
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000037965	16	11050181	11089867	Zc3h7a
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000076258	16	11057618	11057726	mmu-mir-689-2
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000064565	16	11080683	11080845	U1
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000005846	16	11106615	11116872	Rsl1d1
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000062203	16	11133733	11167787	Gspt1
T358	Adenocarcinoma	14	0.6053	ENSMUSG00000022496	16	11227390	11233650	Tnfrsf17
T358	Adenocarcinoma	15	1.0013	ENSMUSG00000071669	16	11319226	11669050	4933437K13Rik
T358	Adenocarcinoma	16	0.6367	ENSMUSG00000071669	16	11319226	11669050	4933437K13Rik
T358	Adenocarcinoma	16	0.6367	ENSMUSG00000065979	16	11717299	11823023	C530044N13Rik
T358	Adenocarcinoma	16	0.6367	ENSMUSG00000055015	16	11814942	11844172	ENSMUSG00000055015
T358	Adenocarcinoma	16	0.6367	ENSMUSG00000022494	16	11898036	11898722	2700045P11Rik
T358	Adenocarcinoma	17	0.5849	ENSMUSG00000069321	16	12864339	12865033	XR_003024.1
T358	Adenocarcinoma	17	0.5849	ENSMUSG00000022545	16	13023314	13062312	Ercc4
T358	Adenocarcinoma	17	0.5849	ENSMUSG00000053458	16	13239996	13246499	Gt4-1
T358	Adenocarcinoma	17	0.5849	ENSMUSG00000009569	16	13272217	13326281	Mkl2
T358	Adenocarcinoma	17	0.5849	ENSMUSG00000075401	16	13329075	13329467	ENSMUSG00000075401
T358	Adenocarcinoma	17	0.5849	ENSMUSG00000076972	16	13363098	13363180	
T358	Adenocarcinoma	17	0.5849	ENSMUSG00000065449	16	13367418	13367504	mmu-mir-365-1
T358	Adenocarcinoma	17	0.5849	ENSMUSG00000075400	16	13429804	13432863	2310015D24Rik
T358	Adenocarcinoma	17	0.5849	ENSMUSG00000077488	16	13445006	13445129	SNORA17
T358	Adenocarcinoma	17	0.5849	ENSMUSG00000022685	16	13452428	13581193	Parn
T358	Adenocarcinoma	17	0.5849	ENSMUSG00000022684	16	13585566	13617180	3110001I22Rik
T358	Adenocarcinoma	17	0.5849	ENSMUSG00000022683	16	13628640	13644163	Pla2g10
T358	Adenocarcinoma	18	0.5492	ENSMUSG00000022682	16	13694277	13728419	Rrn3
T358	Adenocarcinoma	18	0.5492	ENSMUSG00000022681	16	13732855	13749028	Ntan1
T358	Adenocarcinoma	18	0.5492	ENSMUSG00000022680	16	13748392	13801348	Pdxdc1
T358	Adenocarcinoma	18	0.5492	ENSMUSG00000022679	16	13854273	13862956	Mpv17l
T358	Adenocarcinoma	18	0.5492	ENSMUSG00000065968	16	13895549	13897387	EG665536
T358	Adenocarcinoma	18	0.5492	ENSMUSG00000044117	16	13900184	14014886	2900011O08Rik
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000026181	16	16816884	16840925	Ppm1f

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000060383	16	16882172	16882634	XR_003211.1
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000063358	16	16896945	16961016	Mapk1
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000022773	16	16983786	17000251	Ypel1
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000055497	16	16995561	16996254	
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000022771	16	17000121	17024795	Ppil2
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000049916	16	17026961	17038669	2610318N02Rik
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000065572	16	17037624	17037705	mmu-mir-130b
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000076288	16	17037963	17038059	mmu-mir-301b
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000022769	16	17043701	17045928	Sdf2l1
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000022768	16	17052627	17060792	Ccdc116
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000041774	16	17060542	17062406	1810015A11Rik
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000038965	16	17065576	17115055	Ube2l3
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000065710	16	17119355	17119461	U6
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000071636	16	17122548	17127484	Gm603
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000050240	16	17147150	17176993	Hic2
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000055692	16	17189905	17192223	D16Bwg1494e
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000041720	16	17194132	17319877	Pik4ca
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000022766	16	17244978	17257137	Serpind1
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000065331	16	17255469	17255575	U6
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000022765	16	17319595	17344389	Snap29
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000006134	16	17365550	17399818	Crkl
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000022763	16	17403254	17421046	Aifm3
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000022761	16	17422531	17439894	Lztr1
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000022760	16	17441542	17444420	Thap7
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000022759	16	17459047	17474787	4930451C15Rik
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000022758	16	17475572	17485574	P2rxl1
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000022756	16	17485581	17490234	Slc7a4
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000005899	16	17532920	17558391	Smpd4
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000041617	16	17560181	17562978	2310015A05Rik
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000012114	16	17564784	17636460	Pcqap
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000022750	16	17673234	17706765	Klhl22
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000012017	16	17710845	17721850	Scarf2
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000053571	16	17746701	17748045	B830017H08Rik
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000003166	16	17748839	17805234	Car15
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000041566	16	17807786	17811485	Tssk1

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000045521	16	17812217	17813587	Tssk2
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000003527	16	17815328	17824904	Es2el
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000022738	16	17826677	17828566	Gscl
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000003528	16	17838786	17841736	Slc25a1
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000059280	16	17893989	17894836	Vpreb2
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000075352	16	17942480	17942680	AA066038
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000003531	16	17978722	17984926	Dgcr6
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000003526	16	17985289	18002720	Prodh
T358	Adenocarcinoma	19	0.4026	ENSMUSG00000043811	16	18064294	18065694	Rtn4r
T358	Adenocarcinoma	20	0.4338	ENSMUSG00000041215	16	20054651	20146116	Yeats2
T358	Adenocarcinoma	20	0.4338	ENSMUSG00000041205	16	20148791	20154863	Map6d1
T358	Adenocarcinoma	20	0.4338	ENSMUSG00000033918	16	20193361	20215905	Parl
T358	Adenocarcinoma	21	0.7767	ENSMUSG00000022818	16	20221930	20236551	EG224044
T358	Adenocarcinoma	21	0.7767	ENSMUSG00000022822	16	20244846	20339937	Abcc5
T358	Adenocarcinoma	21	0.7767	ENSMUSG00000003235	16	20412360	20422866	Eif2b5
T358	Adenocarcinoma	21	0.7767	ENSMUSG00000003233	16	20430525	20445059	Dvl3
T358	Adenocarcinoma	21	0.7767	ENSMUSG00000022841	16	20449047	20457598	Ap2m1
T358	Adenocarcinoma	21	0.7767	ENSMUSG00000075326	16	20459458	20459742	ENSMUSG00000075326
T358	Adenocarcinoma	21	0.7767	ENSMUSG00000003234	16	20462183	20474922	Abcf3
T358	Adenocarcinoma	21	0.7767	ENSMUSG00000046613	16	20503633	20511997	BC052055
T358	Adenocarcinoma	22	0.5713	ENSMUSG00000068492	16	21066845	21067800	NM_025634.2
T358	Adenocarcinoma	22	0.5713	ENSMUSG00000005958	16	21118777	21137287	Ephb3
T594	Adenocarcinoma	1	-0.5548	ENSMUSG00000038218	1	173351908	173353597	
T594	Adenocarcinoma	1	-0.5548	ENSMUSG00000038209	1	173354798	173371968	Itln1
T594	Adenocarcinoma	1	-0.5548	ENSMUSG00000004709	1	173395868	173420260	Cd244
T594	Adenocarcinoma	2	0.8814	ENSMUSG00000055960	4	111570571	111665328	NP_848901.1
T594	Adenocarcinoma	2	0.8814	ENSMUSG00000070868	4	111733673	111796139	A430090E18Rik
T594	Adenocarcinoma	2	0.8814	ENSMUSG00000049972	4	111883901	111931917	NP_808532.1
T594	Adenocarcinoma	2	0.8814	ENSMUSG00000034359	4	112055126	112145772	OTTMUSG00000008540
T594	Adenocarcinoma	2	0.8814	ENSMUSG00000065318	4	112088704	112088810	U6
T594	Adenocarcinoma	3	0.4549	ENSMUSG00000034359	4	112055126	112145772	OTTMUSG00000008540
T594	Adenocarcinoma	3	0.4549	ENSMUSG00000048766	4	112209079	112272798	A030001H23Rik
T594	Adenocarcinoma	3	0.4549	ENSMUSG00000060264	4	112453007	112454218	
T594	Adenocarcinoma	3	0.4549	ENSMUSG00000051602	4	112476241	112477763	
T594	Adenocarcinoma	4	-0.7677	ENSMUSG00000060441	7	104139188	104161960	

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T594	Adenocarcinoma	4	-0.7677	ENSMUSG00000066258	7	104173720	104189284	Trim12
T594	Adenocarcinoma	5	-0.7952	ENSMUSG00000057596	7	104345663	104381646	AI451617
T594	Adenocarcinoma	5	-0.7952	ENSMUSG00000073929	7	104406780	104409147	EG625321
T594	Adenocarcinoma	6	-0.5459	ENSMUSG00000050982	15	77304302	77318324	9030421J09Rik
T594	Adenocarcinoma	6	-0.5459	ENSMUSG00000044309	15	77352890	77357382	2210421G13Rik
T594	Adenocarcinoma	7	0.5935	ENSMUSG00000052133	16	35461109	35584353	Sema5b
T594	Adenocarcinoma	8	-0.9475	ENSMUSG00000071562	16	36099373	36204610	Stfa3
T594	Adenocarcinoma	8	-0.9475	ENSMUSG00000051949	16	36172285	36176611	2010005H15Rik
T594	Adenocarcinoma	9	-0.8031	ENSMUSG00000062082	16	44740228	44757396	Cd200r4
T594	Adenocarcinoma	9	-0.8031	ENSMUSG00000057827	16	44786429	44835172	Cd200r2
T196	Fibroadenoma	1	-0.7114	ENSMUSG00000038209	1	173354798	173371968	Itln1
T196	Fibroadenoma	2	0.7634	ENSMUSG00000055960	4	111570571	111665328	NP_848901.1
T196	Fibroadenoma	2	0.7634	ENSMUSG00000070868	4	111733673	111796139	A430090E18Rik
T196	Fibroadenoma	2	0.7634	ENSMUSG00000049972	4	111883901	111931917	NP_808532.1
T196	Fibroadenoma	2	0.7634	ENSMUSG00000034359	4	112055126	112145772	OTTMUSG00000008540
T196	Fibroadenoma	2	0.7634	ENSMUSG00000065318	4	112088704	112088810	U6
T196	Fibroadenoma	3	0.5618	ENSMUSG00000048766	4	112209079	112272798	A030001H23Rik
T196	Fibroadenoma	3	0.5618	ENSMUSG00000060264	4	112453007	112454218	
T196	Fibroadenoma	3	0.5618	ENSMUSG00000051602	4	112476241	112477763	
T196	Fibroadenoma	4	-1.1496	ENSMUSG00000052736	6	129615230	129626382	Klrc2
T196	Fibroadenoma	4	-1.1496	ENSMUSG00000030167	6	129631714	129644629	Klrc1
T196	Fibroadenoma	5	-0.8665	ENSMUSG00000070390	11	70988256	71034514	
T196	Fibroadenoma	5	-0.8665	ENSMUSG00000077340	11	71050002	71050135	SNORA17
T196	Fibroadenoma	5	-0.8665	ENSMUSG00000040575	11	71058625	71101427	Nlrp1c
T196	Fibroadenoma	5	-0.8665	ENSMUSG00000077632	11	71104620	71104753	SNORA17
T196	Fibroadenoma	6	-0.9057	ENSMUSG00000041695	11	110882254	110891741	Kcnj2
T196	Fibroadenoma	7	0.4003	ENSMUSG00000034248	14	68195176	68238400	Slc25a37
T196	Fibroadenoma	7	0.4003	ENSMUSG00000047977	14	68243712	68247629	D930020E02Rik
T196	Fibroadenoma	7	0.4003	ENSMUSG00000022066	14	68290504	68320600	Entpd4
T196	Fibroadenoma	7	0.4003	ENSMUSG00000071316	14	68343957	68344433	ENSMUSG00000071316
T196	Fibroadenoma	7	0.4003	ENSMUSG00000034205	14	68344248	68428800	Loxl2
T196	Fibroadenoma	7	0.4003	ENSMUSG00000056640	14	68393255	68393578	ENSMUSG00000056640
T196	Fibroadenoma	8	0.6755	ENSMUSG00000052133	16	35461109	35584353	Sema5b
T196	Fibroadenoma	9	-1.052	ENSMUSG00000071562	16	36099373	36204610	Stfa3
T219	Fibroadenoma	1	0.5691	ENSMUSG00000038209	1	173354798	173371968	Itln1

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T219	Fibroadenoma	1	0.5691	ENSMUSG00000004709	1	173395868	173420260	Cd244
T219	Fibroadenoma	2	-0.4691	ENSMUSG00000057234	2	108893139	109079129	Mett5d1
T219	Fibroadenoma	2	-0.4691	ENSMUSG00000076987	2	108949428	108949537	
T219	Fibroadenoma	2	-0.4691	ENSMUSG00000027115	2	109081577	109142588	Kif18a
T219	Fibroadenoma	3	0.408	ENSMUSG00000044138	3	15348525	15551793	Sirpb1
T219	Fibroadenoma	3	0.408	ENSMUSG00000074677	3	15987305	16040598	Sirpb1
T219	Fibroadenoma	4	0.9782	ENSMUSG00000055960	4	111570571	111665328	NP_848901.1
T219	Fibroadenoma	4	0.9782	ENSMUSG00000070868	4	111733673	111796139	A430090E18Rik
T219	Fibroadenoma	4	0.9782	ENSMUSG00000049972	4	111883901	111931917	NP_808532.1
T219	Fibroadenoma	4	0.9782	ENSMUSG00000034359	4	112055126	112145772	OTTMUSG00000008540
T219	Fibroadenoma	4	0.9782	ENSMUSG00000065318	4	112088704	112088810	U6
T219	Fibroadenoma	5	0.7212	ENSMUSG00000060264	4	112453007	112454218	
T219	Fibroadenoma	5	0.7212	ENSMUSG00000051602	4	112476241	112477763	
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000037221	5	137826426	137830828	Mospd3
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000075606	5	137831381	137831964	
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000029718	5	137834897	137841156	Pcolce
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000029719	5	137842545	137854376	Fbxo24
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000029720	5	137858971	137870290	Lrch4
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000047182	5	137872820	137875502	Irs3
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000029722	5	137880271	137914405	Hrbl
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000067582	5	137901918	137902225	
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000075603	5	137950457	137951528	Q05D41_MOUSE
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000045348	5	137960736	137971395	6430598A04Rik
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000029723	5	137975784	137998180	Tsc22d4
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000029725	5	138008706	138009895	NP_081518.1
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000029726	5	138011709	138015961	BN3D1_MOUSE
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000037108	5	138017663	138052409	Pilrb2
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000046245	5	138051740	138065977	PILRA_MOUSE
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000066684	5	138084662	138087732	PILRB_MOUSE
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000066682	5	138098362	138101441	Pilrb2
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000029727	5	138122721	138151405	Cyp3a13
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000056966	5	138183597	138192747	Gje1
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000037053	5	138211324	138220018	Azgp1
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000063739	5	138222835	138223212	
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000075599	5	138251064	138264445	NP_001034978.1

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment _id	segment_mean_ ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000075598	5	138267027	138280416	NP_001034978.1
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000060417	5	138294041	138295555	
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000029729	5	138314872	138337610	Zkscan1
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000037017	5	138346743	138364001	Zscan21
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000037007	5	138374455	138382687	Zfp113
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000019494	5	138390885	138393768	Cops6
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000029730	5	138394377	138401650	Mcm7
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000065394	5	138395109	138395192	mmu-mir-25
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000065527	5	138395311	138395398	mmu-mir-93
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000065514	5	138395525	138395606	mmu-mir-106b
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000019518	5	138401809	138408471	Ap4m1
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000036980	5	138408405	138416974	Taf6
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000036968	5	138417267	138423730	2610019P18Rik
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000049285	5	138424102	138425188	BC038925
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000047592	5	138459674	138481432	BC055004
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000050552	5	138485519	138489172	0910001L09Rik
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000036948	5	138489448	138493620	BC037034
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000075593	5	138494713	138502542	Gal3st4
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000029510	5	138503451	138509732	Gpc2
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000036928	5	138510339	138547607	Stag3
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000052024	5	138594048	138595340	EG435427
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000075591	5	138594202	138594606	Q3V0I1_MOUSE
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000064892	5	138608379	138608485	U6
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000036898	5	138671292	138690482	Zfp157
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000029526	5	138791628	138794482	1700123K08Rik
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000058291	5	138834772	138849525	Zfp68
T219	Fibroadenoma	6	-0.4945	ENSMUSG00000056014	5	138852664	138877606	A430033K04Rik
T219	Fibroadenoma	7	-0.7859	ENSMUSG00000052736	6	129615230	129626382	Klrc2
T219	Fibroadenoma	8	-0.4544	ENSMUSG00000035285	7	4525702	4528089	Nat14
T219	Fibroadenoma	8	-0.4544	ENSMUSG00000035279	7	4528931	4547908	A430110N23Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074456	8	19732681	19778305	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000059078	8	19784723	19788967	XR_004244.1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074455	8	19869350	19896121	4930467E23Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000071166	8	20087820	20088673	AY761185
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000071165	8	20114839	20115519	EG574083

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074454	8	20134893	20137404	EG654453
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000065961	8	20145457	20194131	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074453	8	20197458	20204345	ENSMUSG00000074453
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074451	8	20282141	20439218	2610005L07Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000071796	8	20283639	20311823	2610005L07Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074449	8	20353338	20377415	4930467E23Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074447	8	22520296	22521268	Defcr21
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000075842	8	22535008	22535112	U6
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074446	8	22549833	22550673	Defcr23
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000061845	8	22559818	22560669	Defcr5
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000071164	8	22579194	22580037	Defcr25
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000056862	8	22586119	22586601	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000061958	8	22589826	22590802	Defcr-rs1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074444	8	22629415	22630255	Defcr16
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074443	8	22657029	22658001	Defcr22
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000075795	8	22671520	22671624	U6
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074442	8	22686366	22687206	Defcr23
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074441	8	22720158	22745213	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074440	8	22782195	22783035	Defcr3
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074439	8	22792191	22793033	NP_031877.2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074438	8	22810298	22811139	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074437	8	22820640	22821772	Defcr-rs1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074436	8	22910620	22911455	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000065958	8	22974801	22975781	Defcr20
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000065957	8	22994575	23021832	Defcr20
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000075934	8	23013605	23013710	U6
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000065956	8	23030959	23031810	Defcr5
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074434	8	23048572	23049412	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000060070	8	23083728	23084436	Defcr26
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000060208	8	23121346	23122186	Defcr3
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000063206	8	23131342	23132184	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000058618	8	23168062	23169192	AY761184
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000064213	8	23200082	23200922	Defcr24
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000044748	8	23242144	23260730	Defb1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000058568	8	23289084	23296845	Defb50

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000006570	8	23305471	23309027	Defb2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000044743	8	23324446	23327556	Defb10
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000047390	8	23347281	23350966	Defb9
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000045337	8	23370933	23371956	Defb11
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000048500	8	23395358	23398255	Defb15
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000058052	8	23403897	23406348	Defb35
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000044222	8	23412336	23414395	Defb13
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000017049	8	23435320	23439586	Ccdc70
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000006567	8	23459893	23525621	Atp7b
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000063362	8	23526272	23537170	Alg11
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000037738	8	23539161	23590598	Nek5
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031478	8	23593830	23631957	Nek3
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000037725	8	23633994	23651364	Ckap2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031479	8	23658405	23684142	Vps36
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031480	8	23692885	23726867	Thsd1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031481	8	23748986	23836963	Tpte
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031482	8	23841552	23864098	Slc25a15
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074423	8	23874452	23874540	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031533	8	23876927	23895210	Mrps31
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031534	8	23928159	23942400	AI316807
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000037656	8	23942333	24035157	Slc20a2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000008892	8	24042620	24059306	Vdac3
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031535	8	24089588	24093092	Dkk4
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031536	8	24093675	24118966	Polb
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031537	8	24124758	24172108	Ikbkb
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031538	8	24223292	24248389	Plat
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031539	8	24252900	24271172	Ap3m2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000054822	8	24271311	24275082	1700041G16Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031540	8	24325084	24406187	Myst3
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000058567	8	24423749	24423988	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031543	8	24440681	24616041	Ank1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000070084	8	24608100	24608227	mmu-mir-486
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000063672	8	24618816	24624183	Nkx6-3
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031545	8	24638491	24673891	Agpat6
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031546	8	24692170	24703204	Gins4

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000015341	8	24706898	24722600	Golga7
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000047308	8	24722284	24723561	4930518F22Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000077399	8	24755578	24755709	SNORA17
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031548	8	24877063	24915179	Sfrp1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000037492	8	25135208	25528648	Zmat4
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000053979	8	25639449	25651115	A730045E13Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000056313	8	25904121	25904441	1810011O10Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031549	8	25997999	26041878	Indol1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031551	8	26049686	26062554	Indo
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031552	8	26067792	26140300	Adam18
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031553	8	26146263	26191333	Adam3
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031554	8	26192737	26289604	Adam5
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000037437	8	26317781	26414328	Adam32
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031555	8	26415157	26482450	Adam9
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031556	8	26482798	26488803	Tm2d2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000037406	8	26490929	26504426	Htra4
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031557	8	26506385	26567739	Plekha2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000065954	8	26620097	26666830	Tacc1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074412	8	26919798	26920309	NM_024175.2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031565	8	26997826	27039466	Fgfr1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000037363	8	27044040	27063032	Letm2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000043794	8	27062559	27063008	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000054823	8	27067851	27179945	Whsc1l1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031570	8	27185606	27190223	Ppapdc1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000061313	8	27190894	27219954	Ddhd2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000054427	8	27220054	27235249	ENSMUSG00000054427
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000037316	8	27230081	27250754	Bag4
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000037296	8	27251136	27269520	Lsm1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031574	8	27274058	27281527	Star
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031575	8	27281764	27306308	Ash2l
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031576	8	27315201	27403347	Kcnu1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000037260	8	27409999	27442256	Hgsnat
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000037251	8	27446149	27459666	4930444A02Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000015994	8	27464267	27481146	Fnta
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000037234	8	27496216	27584679	Hook3

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000013878	8	27585066	27607163	Rnf170
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000037214	8	27623757	27628579	Thap1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000065951	8	28363721	28446030	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031483	8	28489795	28505373	Erlin2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000045549	8	28508484	28508888	Q9D9Z8_MOUSE
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031485	8	28508534	28522235	Prosc
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031486	8	28551777	28589358	Gpr124
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031487	8	28589300	28594570	Brf2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031488	8	28607894	28640582	Rab11fip1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000039720	8	28663395	28668483	Got1l1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031489	8	28691712	28695524	Adrb3
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031490	8	28726338	28742604	Eif4ebp1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000071138	8	28810330	28815130	Tex24
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031492	8	28834647	28865665	Chrnb3
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031491	8	28869148	28879638	Chrna6
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000065367	8	28887260	28887366	U6
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000063932	8	28913606	28960858	4921537P18Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074404	8	29070287	29086388	Gm1698
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000064882	8	29226945	29227043	U6
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000064019	8	29549260	29550851	XR_001871.1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000063626	8	30118704	30685274	Unc5d
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000053570	8	30552417	30552745	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000043096	8	30752364	30795050	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000071111	8	31647797	31649460	XR_003303.1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000057689	8	32469800	32470254	XR_003324.1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000039661	8	32555597	32562982	Dusp26
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000039328	8	32577781	32597417	Rnf122
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031577	8	32616250	32628598	BC019943
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031578	8	32625403	32634659	Rbm13
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000046152	8	32653313	32727418	Fut10
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000046356	8	32745807	32746796	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031579	8	33202989	33205698	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000062991	8	33283963	33475044	Nrg1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000065950	8	33942818	33943264	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000065949	8	34349452	34350189	

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000043270	8	34657131	34658231	Gtpbp10
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031583	8	34701594	34851407	Wrn
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000049184	8	34851559	34883402	Purg
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000048544	8	34894731	34897949	5930422O12Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000070059	8	34900077	34900777	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000070058	8	34950131	34951102	Hmgb1-rs17
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000009628	8	34983259	35051520	Tex15
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000009630	8	35065560	35085738	Ppp2cb
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000052906	8	35085521	35107911	Ubxd6
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031584	8	35119173	35164097	Gsr
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000049476	8	35196473	35197749	1700104B16Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031585	8	35197977	35243099	Gtf2e2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031586	8	35248579	35395741	Rbpms
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000054618	8	35523139	35525563	ENSMUSG00000054618
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031516	8	35558940	35576975	Dctn6
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000063412	8	35579905	35580219	Erh
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000071113	8	35592261	35593235	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031513	8	35604089	35615256	Leprotl1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031532	8	35623093	35639336	Tmem66
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000062196	8	35775802	35776204	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000060414	8	35790372	35790802	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000060242	8	35796430	35796873	EG546808
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031530	8	36276127	36288411	Dusp4
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000053051	8	36296769	36297101	Tnks
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031529	8	36297696	36434207	Tnks
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000054247	8	36433571	36434726	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000072435	8	36521324	36521900	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000059827	8	36601513	36602016	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000046794	8	36844258	36856662	Ppp1r3b
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031527	8	36935756	36964052	Thex1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000070056	8	37056315	37147964	Mfhas1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000038785	8	37240318	37276208	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000055976	8	37293959	37294849	Cldn23
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000059333	8	37494270	37494653	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000050271	8	37563378	37616061	D8Ertd82e

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000039633	8	37685960	37697772	NP_001074619.1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000062517	8	37841113	37842150	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000039620	8	37926065	37981473	6430573F11Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031523	8	38038050	38201243	Dlc1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000039594	8	38317643	38420953	A730069N07Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074384	8	38462099	38463251	AI429214
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074383	8	38558487	38558696	ENSMUSG00000074383
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000054950	8	38573843	38574520	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000016505	8	38623223	38624331	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000065277	8	38785994	38786095	U6
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000039539	8	38991779	39421574	Sgcz
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000065457	8	39720648	39720721	mmu-mir-383
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000077445	8	40451421	40451552	SNORA17
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000039530	8	40474409	40665143	Tusc3
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000046582	8	40954758	40956013	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000025044	8	41080502	41131646	Msr1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000039505	8	41219059	41219789	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074381	8	41431563	41431820	ENSMUSG00000074381
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031603	8	41777983	41785770	Fgf20
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000039478	8	41834732	41853220	2900075B16Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000039470	8	41922635	41984533	Zdhhc2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031601	8	41991359	42010561	Cnot7
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031600	8	42010620	42043841	Vps37a
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000039431	8	42050368	42107833	Mtmr7
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000046723	8	42173911	42181016	Adam24
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000069864	8	42211576	42212104	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000071937	8	42251025	42254993	Adam25
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000046282	8	42293672	42295954	4930529F22Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000054033	8	42321865	42325678	Adam39
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031596	8	42397761	42415357	Slc7a2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031595	8	42425058	42489599	Pdgfrl
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000052122	8	42489018	42489359	Q8BU63_MOUSE
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000045636	8	42489736	42613484	Mtus1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031594	8	42690254	42713970	Fgl1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031592	8	42738590	42831161	Pcm1

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031591	8	42839468	42873466	Asah1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031590	8	42896276	42915891	Frg1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000077186	8	43021555	43021604	U7
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000071108	8	43156410	43157486	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000058906	8	43580277	43581926	Zfp353
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000053038	8	43745728	43746228	XR_003834.1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000077755	8	44020953	44021020	SNORD95
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031651	8	44628624	44640303	Triml1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000070049	8	44640869	44642973	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000072434	8	44657574	44660408	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000058309	8	44696864	44699207	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000051176	8	44793885	44805797	Zfp42
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000070048	8	44811154	44812725	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000063900	8	45018681	45020780	Adam26b
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000048516	8	45067095	45075524	Adam26a
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000050190	8	45123792	45126002	EG384813
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000062414	8	45149279	45151423	Adam34
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000056818	8	45172637	45174778	EG384814
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000077694	8	46306498	46306546	U7
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000053524	8	46433578	46433884	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000070047	8	46434264	46551072	Fat1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000066158	8	46560884	46561270	AY512931
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000054764	8	46568027	46587323	Mtnr1a
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031645	8	46739987	46760848	F11
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031640	8	46768488	46832013	Cyp4v3
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000070044	8	46835534	46881001	BC035537
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031639	8	46894482	46909356	Tlr3
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000077499	8	47080433	47080564	SNORA17
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031626	8	47157109	47326721	Sorbs2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031636	8	47384302	47418363	Pdlim3
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000071104	8	47433466	47442962	Ccdc110
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000071103	8	47452423	47474069	1700029J07Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031634	8	47474345	47495771	1810047C23Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000050914	8	47495719	47498667	Ankrd37
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031637	8	47498125	47526203	Lrp2bp

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000038291	8	47532089	47615519	Snx25
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031631	8	47662506	47694401	4933411K20Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031633	8	47705991	47709847	Slc25a4
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000042865	8	47728383	47728790	Actb
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000071102	8	47753494	47754495	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000065103	8	47770868	47770964	U6
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000047171	8	47790856	47793488	Helt
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000018796	8	47969859	48034867	Acsl1
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031629	8	48050872	48078824	Mlf1ip
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000038225	8	48074396	48116017	Ccdc111
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031628	8	48116235	48137523	Casp3
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031627	8	48238594	48346283	Irf2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000038173	8	48485742	48593712	Enpp6
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000038143	8	48684773	48788179	Stox2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000060559	8	48911946	48914178	ENSMUSG00000060559
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000064684	8	48939235	48939368	SNORA70
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000038102	8	48988943	49032287	D030016E14Rik
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031568	8	49032509	49049544	Rwdd4a
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000064050	8	49131146	49131581	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000063049	8	49165995	49173975	Ing2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074357	8	49174209	49174535	Q8BND0_MOUSE
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000038069	8	49208265	49212716	Cdkn2aip
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074356	8	49212085	49213128	Q3UPZ6_MOUSE
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000064508	8	49218063	49218186	5S_rRNA
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000061974	8	49320960	49321622	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000038064	8	49322776	49326188	Cldn22
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031563	8	49326412	49489389	Wwc2
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000064519	8	49397999	49398111	5S_rRNA
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000070038	8	49568931	49569445	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031562	8	49608814	49640477	Dctd
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031561	8	49727263	50173458	Odz3
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000059797	8	50483589	50486068	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000074351	8	50557431	50557766	ENSMUSG00000074351
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000050249	8	50680610	50690849	
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000047204	8	50684735	50685091	

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T219	Fibroadenoma	9	-0.4741	ENSMUSG00000031559	8	50962140	51000708	4930555F03Rik
T219	Fibroadenoma	10	-0.4132	ENSMUSG00000065809	8	52062071	52062120	U7
T219	Fibroadenoma	10	-0.4132	ENSMUSG00000065337	8	53577302	53577444	U1
T219	Fibroadenoma	10	-0.4132	ENSMUSG00000052825	8	53694763	53695758	Eif2s2
T219	Fibroadenoma	10	-0.4132	ENSMUSG00000057490	8	53777208	53778173	
T219	Fibroadenoma	10	-0.4132	ENSMUSG00000064682	8	53835617	53835807	U2
T219	Fibroadenoma	10	-0.4132	ENSMUSG00000077508	8	54992473	54992522	U7
T219	Fibroadenoma	10	-0.4132	ENSMUSG00000064847	8	54992563	54992612	U7
T219	Fibroadenoma	10	-0.4132	ENSMUSG00000031521	8	55010424	55022120	Aga
T219	Fibroadenoma	10	-0.4132	ENSMUSG00000039396	8	55085565	55137694	Neil3
T219	Fibroadenoma	10	-0.4132	ENSMUSG00000074349	8	55410437	55411354	
T219	Fibroadenoma	10	-0.4132	ENSMUSG00000031520	8	55576304	55685794	Vegfc
T219	Fibroadenoma	10	-0.4132	ENSMUSG00000054408	8	56019131	56028680	Spcs3
T219	Fibroadenoma	10	-0.4132	ENSMUSG00000031519	8	56049028	56086533	Asb5
T219	Fibroadenoma	10	-0.4132	ENSMUSG00000031518	8	56099478	56108797	Spata4
T219	Fibroadenoma	10	-0.4132	ENSMUSG00000039375	8	56128319	56223065	Wdr17
T219	Fibroadenoma	11	-0.4827	ENSMUSG00000048829	10	18790991	18791733	
T219	Fibroadenoma	12	-0.5405	ENSMUSG00000072600	14	42754735	42755200	
T219	Fibroadenoma	12	-0.5405	ENSMUSG00000072599	14	42802765	42803235	Ear10
T219	Fibroadenoma	12	-0.5405	ENSMUSG00000072319	14	42821125	42821663	XR_004127.1
T219	Fibroadenoma	12	-0.5405	ENSMUSG00000053961	14	42836936	42842939	Ang5
T219	Fibroadenoma	13	0.6738	ENSMUSG00000047222	14	50177212	50178063	Ear11
T219	Fibroadenoma	14	0.4141	ENSMUSG00000054940	17	37912574	37913512	Olfr137
T219	Fibroadenoma	15	-0.6827	ENSMUSG00000047632	19	36982690	36984743	Fgfbp3
T219	Fibroadenoma	16	-0.7667	ENSMUSG00000056999	19	37335574	37395757	Ide
T219	Fibroadenoma	17	-0.6509	ENSMUSG00000035299	X	165223769	165349841	Mid1
T219	Fibroadenoma	17	-0.6509	ENSMUSG00000072844	X	165322483	165322791	G530011O06Rik
T317	Fibroadenoma	1	-0.5963	ENSMUSG00000038209	1	173354798	173371968	Itln1
T317	Fibroadenoma	1	-0.5963	ENSMUSG00000004709	1	173395868	173420260	Cd244
T317	Fibroadenoma	2	0.8753	ENSMUSG00000055960	4	111570571	111665328	NP_848901.1
T317	Fibroadenoma	2	0.8753	ENSMUSG00000070868	4	111733673	111796139	A430090E18Rik
T317	Fibroadenoma	2	0.8753	ENSMUSG00000049972	4	111883901	111931917	NP_808532.1
T317	Fibroadenoma	2	0.8753	ENSMUSG00000034359	4	112055126	112145772	OTTMUSG00000008540
T317	Fibroadenoma	2	0.8753	ENSMUSG00000065318	4	112088704	112088810	U6
T317	Fibroadenoma	3	0.6505	ENSMUSG00000060264	4	112453007	112454218	

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T317	Fibroadenoma	3	0.6505	ENSMUSG00000051602	4	112476241	112477763	
T317	Fibroadenoma	4	-0.4109	ENSMUSG00000072826	5	94557031	94560596	XR_004387.1
T317	Fibroadenoma	4	-0.4109	ENSMUSG00000070686	5	94710391	94746621	C87414
T317	Fibroadenoma	5	0.8782	ENSMUSG00000057612	6	66660970	66661878	V1rc10
T317	Fibroadenoma	6	-0.6215	ENSMUSG00000034248	14	68195176	68238400	Slc25a37
T317	Fibroadenoma	6	-0.6215	ENSMUSG00000047977	14	68243712	68247629	D930020E02Rik
T317	Fibroadenoma	6	-0.6215	ENSMUSG00000022066	14	68290504	68320600	Entpd4
T317	Fibroadenoma	6	-0.6215	ENSMUSG00000071316	14	68343957	68344433	ENSMUSG00000071316
T317	Fibroadenoma	6	-0.6215	ENSMUSG00000034205	14	68344248	68428800	Loxl2
T317	Fibroadenoma	6	-0.6215	ENSMUSG00000056640	14	68393255	68393578	ENSMUSG00000056640
T317	Fibroadenoma	7	-0.67	ENSMUSG00000054940	17	37912574	37913512	Olfr137
T317	Fibroadenoma	7	-0.67	ENSMUSG00000062695	17	37943212	37944150	Olfr136
T317	Fibroadenoma	8	0.4457	ENSMUSG00000025431	17	39757236	39782691	Crisp1
T326	Fibroadenoma	1	0.568	ENSMUSG00000038209	1	173354798	173371968	Itln1
T326	Fibroadenoma	1	0.568	ENSMUSG00000004709	1	173395868	173420260	Cd244
T326	Fibroadenoma	2	-2.7798	ENSMUSG00000055960	4	111570571	111665328	NP_848901.1
T326	Fibroadenoma	2	-2.7798	ENSMUSG00000070868	4	111733673	111796139	A430090E18Rik
T326	Fibroadenoma	2	-2.7798	ENSMUSG00000049972	4	111883901	111931917	NP_808532.1
T326	Fibroadenoma	2	-2.7798	ENSMUSG00000034359	4	112055126	112145772	OTTMUSG00000008540
T326	Fibroadenoma	2	-2.7798	ENSMUSG00000065318	4	112088704	112088810	U6
T326	Fibroadenoma	3	-0.5019	ENSMUSG00000034359	4	112055126	112145772	OTTMUSG00000008540
T326	Fibroadenoma	3	-0.5019	ENSMUSG00000048766	4	112209079	112272798	A030001H23Rik
T326	Fibroadenoma	4	-2.4476	ENSMUSG00000060264	4	112453007	112454218	
T326	Fibroadenoma	4	-2.4476	ENSMUSG00000051602	4	112476241	112477763	
T326	Fibroadenoma	5	-0.7625	ENSMUSG00000073763	4	121480811	121493868	A2AGV1_MOUSE
T326	Fibroadenoma	5	-0.7625	ENSMUSG00000073762	4	121583834	121584103	
T326	Fibroadenoma	6	0.4096	ENSMUSG00000034248	14	68195176	68238400	Slc25a37
T326	Fibroadenoma	6	0.4096	ENSMUSG00000047977	14	68243712	68247629	D930020E02Rik
T326	Fibroadenoma	6	0.4096	ENSMUSG00000022066	14	68290504	68320600	Entpd4
T326	Fibroadenoma	6	0.4096	ENSMUSG00000071316	14	68343957	68344433	ENSMUSG00000071316
T326	Fibroadenoma	6	0.4096	ENSMUSG00000034205	14	68344248	68428800	Loxl2
T326	Fibroadenoma	6	0.4096	ENSMUSG00000056640	14	68393255	68393578	ENSMUSG00000056640
T326	Fibroadenoma	7	0.5875	ENSMUSG00000035299	X	165223769	165349841	Mid1
T326	Fibroadenoma	7	0.5875	ENSMUSG00000072844	X	165322483	165322791	G530011O06Rik
T352	Fibroadenoma	1	-0.6384	ENSMUSG00000038209	1	173354798	173371968	Itln1

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T352	Fibroadenoma	1	-0.6384	ENSMUSG00000004709	1	173395868	173420260	Cd244
T352	Fibroadenoma	2	0.5958	ENSMUSG00000044138	3	15348525	15551793	Sirpb1
T352	Fibroadenoma	2	0.5958	ENSMUSG00000074677	3	15987305	16040598	Sirpb1
T352	Fibroadenoma	3	0.4132	ENSMUSG00000049214	4	111470967	111481052	NP_808486.1
T352	Fibroadenoma	3	0.4132	ENSMUSG00000055960	4	111570571	111665328	NP_848901.1
T352	Fibroadenoma	4	0.9591	ENSMUSG00000055960	4	111570571	111665328	NP_848901.1
T352	Fibroadenoma	4	0.9591	ENSMUSG00000070868	4	111733673	111796139	A430090E18Rik
T352	Fibroadenoma	4	0.9591	ENSMUSG00000049972	4	111883901	111931917	NP_808532.1
T352	Fibroadenoma	4	0.9591	ENSMUSG00000034359	4	112055126	112145772	OTTMUSG00000008540
T352	Fibroadenoma	4	0.9591	ENSMUSG00000065318	4	112088704	112088810	U6
T352	Fibroadenoma	5	0.7029	ENSMUSG00000060264	4	112453007	112454218	
T352	Fibroadenoma	5	0.7029	ENSMUSG00000051602	4	112476241	112477763	
T352	Fibroadenoma	6	0.5411	ENSMUSG00000076042	8	67406524	67406633	mmu-mir-710
T352	Fibroadenoma	6	0.5411	ENSMUSG00000037852	8	67484734	67585232	Cpe
T352	Fibroadenoma	6	0.5411	ENSMUSG00000031604	8	67610337	67625770	Sc4mol
T352	Fibroadenoma	7	-0.4475	ENSMUSG00000075297	10	21972889	21976663	
T352	Fibroadenoma	8	-4.2042	ENSMUSG00000070390	11	70988256	71034514	
T352	Fibroadenoma	8	-4.2042	ENSMUSG00000077340	11	71050002	71050135	SNORA17
T352	Fibroadenoma	8	-4.2042	ENSMUSG00000040575	11	71058625	71101427	Nlrp1c
T352	Fibroadenoma	8	-4.2042	ENSMUSG00000077632	11	71104620	71104753	SNORA17
T352	Fibroadenoma	9	-0.6487	ENSMUSG00000054940	17	37912574	37913512	Olfr137
T352	Fibroadenoma	9	-0.6487	ENSMUSG00000062695	17	37943212	37944150	Olfr136
T352	Fibroadenoma	10	0.4689	ENSMUSG00000025431	17	39757236	39782691	Crisp1
T352	Fibroadenoma	11	0.6662	ENSMUSG00000035299	X	165223769	165349841	Mid1
T352	Fibroadenoma	11	0.6662	ENSMUSG00000072844	X	165322483	165322791	G530011O06Rik
T357	Fibroadenoma	1	0.535	ENSMUSG00000038218	1	173351908	173353597	
T357	Fibroadenoma	1	0.535	ENSMUSG00000038209	1	173354798	173371968	Itln1
T357	Fibroadenoma	1	0.535	ENSMUSG00000004709	1	173395868	173420260	Cd244
T357	Fibroadenoma	2	0.5224	ENSMUSG00000044138	3	15348525	15551793	Sirpb1
T357	Fibroadenoma	2	0.5224	ENSMUSG00000074677	3	15987305	16040598	Sirpb1
T357	Fibroadenoma	3	0.8946	ENSMUSG00000055960	4	111570571	111665328	NP_848901.1
T357	Fibroadenoma	3	0.8946	ENSMUSG00000070868	4	111733673	111796139	A430090E18Rik
T357	Fibroadenoma	3	0.8946	ENSMUSG00000049972	4	111883901	111931917	NP_808532.1
T357	Fibroadenoma	3	0.8946	ENSMUSG00000034359	4	112055126	112145772	OTTMUSG00000008540
T357	Fibroadenoma	3	0.8946	ENSMUSG00000065318	4	112088704	112088810	U6

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T357	Fibroadenoma	4	0.7488	ENSMUSG00000060264	4	112453007	112454218	
T357	Fibroadenoma	4	0.7488	ENSMUSG00000051602	4	112476241	112477763	
T357	Fibroadenoma	5	-0.6497	ENSMUSG00000076466	6	41043174	41043674	TRBV12-1
T357	Fibroadenoma	5	-0.6497	ENSMUSG00000076467	6	41045643	41046075	TRBV13-1
T357	Fibroadenoma	5	-0.6497	ENSMUSG00000076468	6	41048471	41048971	TRBV12-2
T357	Fibroadenoma	5	-0.6497	ENSMUSG00000076469	6	41051003	41051439	TRBV13-2
T357	Fibroadenoma	5	-0.6497	ENSMUSG00000076470	6	41059754	41060192	TRBV13-3
T357	Fibroadenoma	5	-0.6497	ENSMUSG00000076471	6	41064774	41065223	TRBV14
T357	Fibroadenoma	5	-0.6497	ENSMUSG00000076472	6	41070818	41071265	TRBV15
T357	Fibroadenoma	5	-0.6497	ENSMUSG00000076473	6	41081398	41081837	TRBV16
T357	Fibroadenoma	6	-0.5394	ENSMUSG00000071521	6	41283787	41287489	Try10
T357	Fibroadenoma	6	-0.5394	ENSMUSG00000071519	6	41303421	41307204	Tcrb-V20
T357	Fibroadenoma	6	-0.5394	ENSMUSG00000058119	6	41321996	41326810	EG436523
T357	Fibroadenoma	6	-0.5394	ENSMUSG00000059014	6	41344917	41430791	EG436523
T357	Fibroadenoma	7	-0.8328	ENSMUSG00000060441	7	104139188	104161960	
T357	Fibroadenoma	7	-0.8328	ENSMUSG00000066258	7	104173720	104189284	Trim12
T357	Fibroadenoma	8	-0.7859	ENSMUSG00000057596	7	104345663	104381646	AI451617
T357	Fibroadenoma	8	-0.7859	ENSMUSG00000073929	7	104406780	104409147	EG625321
T357	Fibroadenoma	9	-0.477	ENSMUSG00000075297	10	21972889	21976663	
T357	Fibroadenoma	10	-0.9597	ENSMUSG00000070390	11	70988256	71034514	
T357	Fibroadenoma	10	-0.9597	ENSMUSG00000077340	11	71050002	71050135	SNORA17
T357	Fibroadenoma	10	-0.9597	ENSMUSG00000040575	11	71058625	71101427	Nlrp1c
T357	Fibroadenoma	10	-0.9597	ENSMUSG00000077632	11	71104620	71104753	SNORA17
T357	Fibroadenoma	11	0.9424	ENSMUSG00000071203	13	101244320	101515245	Birc1-rs1
T357	Fibroadenoma	11	0.9424	ENSMUSG00000021640	13	101508051	101546768	Naip1
T357	Fibroadenoma	12	-0.8369	ENSMUSG00000050982	15	77304302	77318324	9030421J09Rik
T357	Fibroadenoma	12	-0.8369	ENSMUSG00000044309	15	77352890	77357382	2210421G13Rik
T357	Fibroadenoma	13	0.487	ENSMUSG00000052133	16	35461109	35584353	Sema5b
T357	Fibroadenoma	14	-0.8637	ENSMUSG00000071562	16	36099373	36204610	Stfa3
T357	Fibroadenoma	15	-0.7057	ENSMUSG00000062082	16	44740228	44757396	Cd200r4
T357	Fibroadenoma	15	-0.7057	ENSMUSG00000057827	16	44786429	44835172	Cd200r2
T357	Fibroadenoma	16	-2.9937	ENSMUSG00000073402	17	35772665	35776249	EG667977
T357	Fibroadenoma	17	-3.6729	ENSMUSG00000054940	17	37912574	37913512	Olfr137
T357	Fibroadenoma	17	-3.6729	ENSMUSG00000062695	17	37943212	37944150	Olfr136
T357	Fibroadenoma	18	0.8174	ENSMUSG00000025431	17	39757236	39782691	Crisp1

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T357	Fibroadenoma	19	-0.6712	ENSMUSG00000056999	19	37335574	37395757	Ide
T357	Fibroadenoma	20	-1.1078	ENSMUSG00000035299	X	165223769	165349841	Mid1
T357	Fibroadenoma	20	-1.1078	ENSMUSG00000072844	X	165322483	165322791	G530011O06Rik
T612	Fibroadenoma	1	-0.6028	ENSMUSG00000038218	1	173351908	173353597	
T612	Fibroadenoma	1	-0.6028	ENSMUSG00000038209	1	173354798	173371968	Itln1
T612	Fibroadenoma	1	-0.6028	ENSMUSG00000004709	1	173395868	173420260	Cd244
T612	Fibroadenoma	2	0.8351	ENSMUSG00000055960	4	111570571	111665328	NP_848901.1
T612	Fibroadenoma	2	0.8351	ENSMUSG00000070868	4	111733673	111796139	A430090E18Rik
T612	Fibroadenoma	2	0.8351	ENSMUSG00000049972	4	111883901	111931917	NP_808532.1
T612	Fibroadenoma	2	0.8351	ENSMUSG00000034359	4	112055126	112145772	OTTMUSG00000008540
T612	Fibroadenoma	2	0.8351	ENSMUSG00000065318	4	112088704	112088810	U6
T612	Fibroadenoma	3	0.6158	ENSMUSG00000060264	4	112453007	112454218	
T612	Fibroadenoma	3	0.6158	ENSMUSG00000051602	4	112476241	112477763	
T612	Fibroadenoma	4	0.5534	ENSMUSG00000076042	8	67406524	67406633	mmu-mir-710
T612	Fibroadenoma	4	0.5534	ENSMUSG00000037852	8	67484734	67585232	Cpe
T612	Fibroadenoma	4	0.5534	ENSMUSG00000031604	8	67610337	67625770	Sc4mol
T612	Fibroadenoma	5	0.5288	ENSMUSG00000056143	18	88987949	88988281	Socs6
T612	Fibroadenoma	5	0.5288	ENSMUSG00000056153	18	89002071	89028400	Socs6
T612	Fibroadenoma	5	0.5288	ENSMUSG00000023066	18	89105983	89265209	Rttn
T612	Fibroadenoma	5	0.5288	ENSMUSG00000034028	18	89331620	89404520	Cd226
T612	Fibroadenoma	5	0.5288	ENSMUSG00000043498	18	89430063	89430447	
T612	Fibroadenoma	5	0.5288	ENSMUSG00000073514	18	89435328	89903334	Dok6
T323	Spindle Cell	1	0.4875	ENSMUSG00000038218	1	173351908	173353597	
T323	Spindle Cell	1	0.4875	ENSMUSG00000038209	1	173354798	173371968	Itln1
T323	Spindle Cell	1	0.4875	ENSMUSG00000004709	1	173395868	173420260	Cd244
T323	Spindle Cell	2	0.6219	ENSMUSG00000028392	4	61966428	61983659	Bspry
T323	Spindle Cell	2	0.6219	ENSMUSG00000038422	4	61985373	61988575	Hdhd3
T323	Spindle Cell	2	0.6219	ENSMUSG00000028393	4	61995531	62006424	Alad
T323	Spindle Cell	3	0.6511	ENSMUSG00000076042	8	67406524	67406633	mmu-mir-710
T323	Spindle Cell	3	0.6511	ENSMUSG00000037852	8	67484734	67585232	Cpe
T323	Spindle Cell	3	0.6511	ENSMUSG00000031604	8	67610337	67625770	Sc4mol
T323	Spindle Cell	4	-0.5674	ENSMUSG00000075297	10	21972889	21976663	
T323	Spindle Cell	5	-0.6782	ENSMUSG00000055072	11	79112380	79112814	ENSMUSG00000055072
T323	Spindle Cell	5	-0.6782	ENSMUSG00000020716	11	79156087	79397804	Nf1
T323	Spindle Cell	5	-0.6782	ENSMUSG00000049612	11	79317547	79320214	Omg

Supplementary Table 4. Regions showing copy number alterations in the tumor genome

Sample	Histological type	segment_id	segment_mean_ratio	gene_id	chromosome	gene_start	gene_end	gene_symbol
T323	Spindle Cell	5	-0.6782	ENSMUSG00000070354	11	79329580	79346783	Evi2a
T323	Spindle Cell	5	-0.6782	ENSMUSG00000017639	11	79407407	79514217	Rab11fip4
T323	Spindle Cell	5	-0.6782	ENSMUSG00000064486	11	79411363	79411463	U6
T323	Spindle Cell	5	-0.6782	ENSMUSG00000077574	11	79455217	79455323	U6
T323	Spindle Cell	6	-0.6405	ENSMUSG00000020988	12	70609049	70643423	L2hgdh
T323	Spindle Cell	6	-0.6405	ENSMUSG00000054894	12	70643567	70663263	Atp5s
T323	Spindle Cell	6	-0.6405	ENSMUSG00000020990	12	70665453	70709312	Cdkl1
T323	Spindle Cell	6	-0.6405	ENSMUSG00000076065	12	70682440	70682549	mmu-mir-681
T323	Spindle Cell	6	-0.6405	ENSMUSG00000020992	12	70708893	70713116	4930512B01Rik
T323	Spindle Cell	6	-0.6405	ENSMUSG00000034761	12	70722355	70811768	Map4k5
T323	Spindle Cell	6	-0.6405	ENSMUSG00000021066	12	70811874	70882636	Spg3a
T323	Spindle Cell	6	-0.6405	ENSMUSG00000065327	12	70849509	70849810	7SK
T323	Spindle Cell	6	-0.6405	ENSMUSG00000021067	12	70883617	70905607	Sav1
T323	Spindle Cell	7	-0.5698	ENSMUSG00000076708	12	115393758	115394051	IGHV1-43
T323	Spindle Cell	7	-0.5698	ENSMUSG00000076709	12	115438916	115439209	IGHV1-47
T323	Spindle Cell	7	-0.5698	ENSMUSG00000076710	12	115503031	115503324	IGHV1-49
T323	Spindle Cell	8	-0.5084	ENSMUSG00000047632	19	36982690	36984743	Fgfbp3
T323	Spindle Cell	9	-0.5778	ENSMUSG00000056999	19	37335574	37395757	Ide

Trp53 sequencing primers

***Trp53* exon**	**5p outer**	**3p outer**	**5p inner**	**3p inner**
e1a	AAAAGAACTTAGGGGCCCGTG	GATGGTCCCAATGAACTGAAGC	TGTAAAACGACGGCCAGTACTTAGGGGCCCGTGTTGGTT	CAGGAAACAGCTATGACCGGTCCCAATGAACT
e1b	TGCCCTTACTTGTTATGGCGA	CCCCACGGTTTTCTCTAGTTTTATG	TGTAAAACGACGGCCAGTTTGTTATGGCGACTATCCAGCTT	CAGGAAACAGCTATGACCCGGTTTTCTCTAGTT
e2	CCTTTCCTATAAGCCATAGGGGTTT	CCATACCATGTTTGAACACTACTGT	TGTAAAACGACGGCCAGTAAGCCATAGGGGTTTGTTTGTT	CAGGAAACAGCTATGACCGTTTCTCTCAGGCAA
e3	AGGGTCTCAGAAGTTTGAGGTCAT	AAAGAAGAACCCTCAGGACTGTGTT	TGTAAAACGACGGCCAGTGAAGTTTGAGGTCATCATTGACTAC	CAGGAAACAGCTATGACCAACCCTCAGGACTG
e4	CCAGAGCAGAAAGGGACTTGG	GAAGAGGAACCCCCAAATCTAGAC	TGTAAAACGACGGCCAGTGAAAGGGACTTGGGCTTTGGT	CAGGAAACAGCTATGACCGGAACCCCCAAATC
e5	CAATGTGTTTCATTAGTTCCCCAC	CAGGCCTAAGAGCAAGAATAAGTCA	TGTAAAACGACGGCCAGTTCATTAGTTCCCCACCTTGACAC	CAGGAAACAGCTATGACCGCAAGAATAAGTCA
e6	GATGGTAAGCCCTCAACACCG	CGGGTTGCTAGAAAGTCAACATC	TGTAAAACGACGGCCAGTAAGCCCTCAACACCGCCTGTG	CAGGAAACAGCTATGACCGTTGCTAGAAAGTC
e7	GAGGCTATAGCCAGCCATTCC	GCGGGACTCGTGGAACAGAAA	TGTAAAACGACGGCCAGTATAGCCAGCCATTCCCGGCTG	CAGGAAACAGCTATGACCACTCGTGGAACAGA
e8	TGGGGGCCTAGTTTACACACA	GTGAAATACTCTCCATCAAGTGGTT	TGTAAAACGACGGCCAGTCCTAGTTTACACACAGTCAGGATGG	CAGGAAACAGCTATGACCCGCTGTGGAAGGAG
e9	GAGCGCAAAGAGAGGTACGCA	CTGGCAACCTGCTAATAACACTATT	TGTAAAACGACGGCCAGTAAAGAGAGGTACGCAGGCGGG	CAGGAAACAGCTATGACCATTTTATACATGCGA
e10	CCAGCTTAAGTTGGGAACCAA	ATCTTTCACTACAAAGGCTGAG	TGTAAAACGACGGCCAGTGGGAACCAACTTTCAGAAAGAAAG	CAGGAAACAGCTATGACCTCACTACAAAGGCT
e11a	TCCAGCCTAGAGCCTTCCAAG	CAGGCTTTGCAGAATGGAAGG	TGTAAAACGACGGCCAGTAGAGCCTTCCAAGCCTTGATC	CAGGAAACAGCTATGACCGCTTTGCAGAATGG
e11b	CCAGTTGTTGGACCCTGGCAC	GTGGGTACCTCCCAAATTCATC	TGTAAAACGACGGCCAGTGTTGGACCCTGGCACCTACAA	CAGGAAACAGCTATGACCTACCTCCCAAATTCA