Supplementary Tables (1 PDF file)

Identification of Targetable FGFR Gene Fusions in Diverse Cancers

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Supplementary Tables S1-S15 include transcriptome and exome sequencing results for the FGFR fusion positive index cases, and summaries of sequencing cohorts.

Supplementary Table S1. Nonsynonymous somatic mutations in MO_1036 cholangiocarcinoma.

SAMPLE	GENE	LOC (hg18)	REFERENCE	VARIANT	VAR FRAGS TUMOR	TUMOR TOTAL FRAGS	VAR FRAC TUMOR	PROTEIN	BLOSUM SCORE	EXPRESSION LEVEL (RPKM)
MO_1036	***ARID1A***	**chr1:26974022**	**C**	**T**	**38**	**110**	**0.35**	**Q1573***	**-4**	**9.2**
MO_1036	*LRRC24*	chr8:145719484	A	G	112	276	0.41	L242P	-3	9.0
MO_1036	***PBRM1***	**chr3:52618728**	**A**	**T**	**47**	**115**	**0.41**	**C736***	**-4**	**2.4**
MO_1036	*GFRA1*	chr10:117846228	C	T	17	69	0.25	E265K	1	0.7
MO_1036	*MADCAM1*	chr19:452701	G	A	7	28	0.25	D234N	1	0.3
MO_1036	*ROR2*	chr9:93526123	T	A	25	163	0.15	Q825L	-2	0.2
MO_1036	*OR51D1*	chr11:4618548	A	G	95	236	0.40	M318V	1	0.0
MO_1036	*RPL3L*	chr16:1944012	C	T	29	107	0.27	G48S	0	0.0

Supplementary Table S2. Gene copy number changes in MO_1036 cholangiocarcinoma.

Sample	Segment (hg18)	Genes in this region	Span (bp)	Number of exons	Copy number ratio (gains)
MO_1036	chr18:12874154-12938146	*PTPN2, SEH11*	63,992	2	3.74
MO_1036	chr11:63709893-63710241	*STIP1*	348	2	3.10
MO_1036	chr19:4408610-4423383	*UBXN6, HDGF2*	14,773	2	3.08
MO_1036	chr5:10303134-10303443	*CCT5*	309	2	2.40
MO_1036	chr6:26128947-26325246	*HFE, HIST1H3A, HIST1H4A, HIST1H4B*	196,299	35	1.57
MO_1036	chr12:9639140-10265625	*LOC374443, CLEC2D/2B/L1, CD69, KLRF1*	626,485	95	1.56
MO_1036	chr18:16944866-20311136	*RIOK3, ROCK1*	3,366,270	331	1.53
MO_1036	chr13:27417497-30093937	*CDX2, FLT1, FLT3*	2,676,440	142	1.51
MO_1036	chr13:32911844-33438270	*STARD13, RFC3*	526,426	12	1.48
MO_1036	chr12:78680-9468534	*CCND2, DYRK4, KDM5A, WNK1, ZNF384*	9,389,854	1212	1.47

Supplementary Table S3. Gene fusions identified in MO_1036. FGFR2 fusion is in bold.

Sample	5' Gene	3' Gene	Number of Supporting Reads	Type
MO_1036	*CDC42SE2*	*DNMT2 (TRDMT1)*	515	Interchromosomal
MO_1036	***FGFR2***	***BICC1***	**259**	**Intrachromosomal**
MO_1036	*ALS2CR16*	*ALS2CR8*	111	Intrachromosomal
MO_1036	*uc003sbm (MSH5)*	*NFKBIL1*	17	Intrachromosomal
MO_1036	*LPCAT3*	*C1RL*	15	Intrachromosomal
MO_1036	*FAM114A2*	*CDC42SE2*	11	Intrachromosomal
MO_1036	*CDC42SE2*	*TRDMT1*	9	Interchromosomal
MO_1036	*THRAP3*	*STK40*	4	Intrachromosomal

Supplementary Table S4. Gene fusions identified in MO_1039. FGFR2 fusion is in bold.

Sample	5' Gene	3' Gene	Number of Supporting Reads	Type
MO_1039	***FGFR2***	***BICC1***	**83**	**Intrachromosomal**
MO_1039	*LDB1*	*BICC1*	30	Intrachromosomal
MO_1039	*FAM62A*	*LOC728937*	20	Intrachromosomal
MO_1039	*GLG1*	*GRM5*	14	Interchromosomal
MO_1039	*AIFM1*	*FGF13*	3	Intrachromosomal

Supplementary Table S5. Nonsynonymous somatic mutations in MO_1039 cholangiocarcinoma.

SAMPLE	GENE	LOC (hg18)	REFERENCE	VARIANT	VAR FRAGS TUMOR	TUMOR TOTAL FRAGS	VAR FRAC TUMOR	PROTEIN	BLOSUM SCORE	EXPRESSION LEVEL (RPKM)
MO_1039	*EEF1D*	chr8:144743100	C	T	33	175	0.19	A99T	0	105.1
MO_1039	*GNAS*	chr20:56862022	C	T	66	173	0.38	P103S	-1	69.1
MO_1039	*GNAS*	chr20:56862021	G	A	68	175	0.39	M102I	1	69.1
MO_1039	*RNF130*	chr5:179372696	T	A	38	105	0.36	R222W	-3	40.6
MO_1039	*PRPF3*	chr1:148572293	C	A	61	215	0.28	P243T	-1	39.4
MO_1039	*NFE2L2*	chr2:177807205	T	C	38	88	0.43	D29G	-1	30.0
MO_1039	*IRF2BP1*	chr19:51080358	G	A	83	205	0.40	S172F	-2	20.1
MO_1039	*GPT*	chr8:145702753	A	G	33	106	0.31	N398S	1	19.9
MO_1039	***TP53***	**chr17:7517864**	**G**	**A**	**50**	**83**	**0.60**	**R267W**	**-3**	**19.2**
MO_1039	*PRODH2*	chr19:40982805	G	A	17	66	0.26	P529L	-3	9.6
MO_1039	*NASP*	chr1:45852427	A	C	15	61	0.25	I529L	2	8.9
MO_1039	*IPO7*	chr11:9416221	G	A	19	41	0.46	M836I	1	8.6
MO_1039	*ZBTB33*	chrX:119271861	C	A	6	30	0.20	S188Y	-2	7.6
MO_1039	*BCOR*	chrX:39807134	G	C	50	71	0.70	Q1294E	2	6.1
MO_1039	*YARS2*	chr12:32799976	C	A	58	146	0.40	G34C	-3	5.7
MO_1039	*PDE4DIP*	chr1:143626918	G	A	10	35	0.29	R622*	-4	5.0
MO_1039	*EPHB3*	chr3:185773007	G	A	37	99	0.37	D69N	1	4.8
MO_1039	*KIAA1199*	chr15:78968899	A	C	31	68	0.46	K333Q	1	2.2
MO_1039	*RIC8B*	chr12:105778179	A	T	6	25	0.24	D437V	-3	2.2
MO_1039	*SPAG1*	chr8:101275567	G	A	33	53	0.62	E331K	1	1.8
MO_1039	*SHROOM4*	chrX:50394164	G	T	97	146	0.66	T550K	-1	0.5
MO_1039	*CDKL5*	chrX:18532688	G	A	118	184	0.64	E575K	1	0.1
MO_1039	*EMR3*	chr19:14609990	C	T	56	141	0.40	G471S	0	0.1
MO_1039	*KCNA10*	chr1:110861676	C	T	50	171	0.29	M419I	1	0.1
MO_1039	*FAM19A4*	chr3:68884793	C	T	25	104	0.24	R66H	0	0.0
MO_1039	*PRDM9*	chr5:23558241	G	C	7	69	0.10	V194L	1	0.0
MO_1039	*CSRNP1*	chr3:39161733	C	T	11	54	0.20	R75Q	1	NA

Supplementary Table S6. Gene copy number changes in MO_1039 cholangiocarcinoma.

Sample	**Segment (hg18)**	**Genes in this region**	**Span (bp)**	**Number of exons**	**Copy number ratio (gains)**
MO_1039	chr1:153098887-153716609	*CLK2,MUC1*	617,722	220	3.61
MO_1039	chr1:144963163-145553014	*BCL9*	589851	47	2.89
MO_1039	chr1:153757794-161591884	*DDR2,FCGR2B,INSRR,NTRK1,PRCC,SDHC,UHMK1*	7,834,090	1244	2.89
MO_1039	chr1:148124359-150554432	*ARNT*	2430073	561	2.86
MO_1039	chr1:150649330-152976224	*NPR1,TPM3*	2,326,894	388	2.83
MO_1039	chr1:145554338-145882120	*BCL9*	327,782	17	2.20
MO_1039	chr20:30074126-30126201	*HCK*	52,075	12	2.15
MO_1039	chr1:150589796-150597931	*FLG2*	8,135	12	2.12
MO_1039	chr1:152994932-153061274	*KCNN3*	66,342	5	2.12
MO_1039	chr16:69441206-69754032	*HYDIN*	312,826	72	1.97
MO_1039	chr1:162512589-162795748	*PBX1*	283,159	2	1.96
Sample	**Segment (hg18)**	**Genes in this region**	**Span (bp)**	**Number of exons**	**Copy number ratio (losses)**
MO_1039	chr6:168856780-168857712	--	932	3	0.37
MO_1039	chr8:935432-947796	*ERICH1-AS1*	12,364	2	0.38
MO_1039	chr21:9809235-9815818	--	6,583	3	0.50
MO_1039	chr10:38835211-39184276	*ACTR3BP5*	349,065	3	0.52
MO_1039	chr6:74228416-74285712	*MTO1, EEF1A1*	57,296	18	0.57

Supplementary Table S7. Gene fusions identified in MO_1051. FGFR2 fusion is in bold.

Sample	5' Gene	3' Gene	Number of Supporting Reads	Type
MO_1051	***FGFR2***	***AFF3***	**138**	**Interchromosomal**
MO_1051	*TBCK*	*PPA2*	81	Intrachromosomal
MO_1051	*CMAS*	*PIK3C2G*	73	Intrachromosomal
MO_1051	*GPATCH8*	*MPP2*	24	Intrachromosomal
MO_1051	*IKBKG*	*PLXNB3*	3	Intrachromosomal
MO_1051	*ITFG1*	*NETO2*	53	Read through
MO_1051	*TXNDC11*	*AK126539*	2	Read through

Supplementary Table S8. Nonsynonymous somatic mutations in MO_1051 breast cancer (Part-1).

SAMPLE	GENE	LOC (hg18)	REFERENCE	VARIANT	VAR FRAGS TUMOR	TUMOR TOTAL FRAGS	VAR FRAC TUMOR	PROTEIN	BLOSUM SCORE	EXPRESSION LEVEL (RPKM)
MO_1051	*B4GALT3*	chr1:159410453	C	T	32	145	0.22	G167E	-2	125.1
MO_1051	*GANAB*	chr11:62154735	C	T	38	144	0.26	D434N	1	106.4
MO_1051	*EFHD1*	chr2:233206867	C	T	13	27	0.48	A70V	0	106.2
MO_1051	*NTN4*	chr12:94655867	C	T	24	96	0.25	V258I	3	94.6
MO_1051	*SF1*	chr11:64291716	G	C	16	61	0.26	H415Q	0	84.1
MO_1051	*QARS*	chr3:49113864	G	C	19	82	0.23	F268L	0	68.8
MO_1051	*ZNF296*	chr19:50267617	C	T	17	87	0.20	W170*	-4	59.6
MO_1051	*ZNF296*	chr19:50267290	C	G	26	100	0.26	K279N	0	59.6
MO_1051	*PLXNB1*	chr3:48431630	C	T	28	98	0.29	E1309K	1	55.9
MO_1051	*HDAC7*	chr12:46475778	G	A	18	51	0.35	R277W	-3	50.0
MO_1051	*TMEM214*	chr2:27116434	C	T	15	69	0.22	S552F	-2	48.9
MO_1051	*DAG1*	chr3:49545538	C	A	17	57	0.30	Q864K	1	44.0
MO_1051	*DAG1*	chr3:49545403	C	G	17	76	0.22	L819V	1	44.0
MO_1051	*DAG1*	chr3:49545024	C	G	30	124	0.24	F692L	0	44.0
MO_1051	*DAG1*	chr3:49545321	C	A	34	100	0.34	F791L	0	44.0
MO_1051	*PLEKHA6*	chr1:202486311	C	T	11	66	0.17	E527K	1	40.9
MO_1051	*ZFP36L2*	chr2:43306032	G	A	34	127	0.27	Q139*	-4	37.5
MO_1051	*COMTD1*	chr10:76665477	C	T	37	109	0.34	R42Q	1	35.1
MO_1051	*NACC1*	chr19:13107913	C	T	24	80	0.30	R298W	-3	34.9
MO_1051	*TOP1*	chr20:39160281	G	A	15	73	0.21	E289K	1	34.8
MO_1051	*TOP1*	chr20:39160379	G	C	14	93	0.15	K321N	0	34.8
MO_1051	*MGRN1*	chr16:4615042	C	A	20	71	0.28	P27Q	-1	34.1
MO_1051	*TUBA1B*	chr12:47809566	C	G	15	69	0.22	L70F	0	34.1
MO_1051	*THBS2*	chr6:169390445	G	A	32	97	0.33	H201Y	2	33.4
MO_1051	*RAVER1*	chr19:10290021	C	T	7	37	0.19	E642K	1	31.7
MO_1051	*LUC7L2*	chr7:138733981	G	C	11	48	0.23	D85H	-1	30.5
MO_1051	*PSMD1*	chr2:231645346	G	A	12	62	0.19	G285D	-1	29.8
MO_1051	*DHX30*	chr3:47862272	G	A	25	101	0.25	E340K	1	26.4
MO_1051	*DYNC1H1*	chr14:101536124	G	A	10	34	0.29	E1284K	1	25.9
MO_1051	*ZFAND6*	chr15:78201199	C	T	21	71	0.30	S82F	-2	25.9
MO_1051	*ZNF213*	chr16:3131032	C	T	28	114	0.25	R355C	-3	25.5
MO_1051	*TRIM26*	chr6:30262081	C	G	43	158	0.27	E391Q	2	25.4
MO_1051	*SLC35B1*	chr17:45135284	G	T	19	61	0.31	S284Y	-2	24.4
MO_1051	*PIN1*	chr19:9810216	G	A	6	29	0.21	V55I	3	23.8
MO_1051	*SLC38A10*	chr17:76840980	C	G	26	115	0.23	E519Q	2	23.8
MO_1051	*ANKRD30A*	chr10:37548514	G	A	11	53	0.21	E1234K	1	23.3

Supplementary Table S8. Nonsynonymous somatic mutations in MO_1051 breast cancer (Part-2).

SAMPLE	GENE	LOC (hg18)	REFERENCE	VARIANT	VAR FRAGS TUMOR	TUMOR TOTAL FRAGS	VAR FRAC TUMOR	PROTEIN	BLOSUM SCORE	EXPRESSION LEVEL (RPKM)
MO_1051	*USP22*	chr17:20856759	G	A	15	56	0.27	S307L	-2	23.2
MO_1051	*SLC15A3*	chr11:60466117	G	C	21	87	0.24	S358C	-1	22.3
MO_1051	*LRPPRC*	chr2:44024438	C	G	45	154	0.29	R799T	-1	20.5
MO_1051	*SKI*	chr1:2225661	C	G	29	102	0.28	S515C	-1	20.4
MO_1051	*CC2D1A*	chr19:13899076	G	C	32	86	0.37	E772Q	2	20.1
MO_1051	*RAP1GAP*	chr1:21801938	G	C	27	104	0.26	S495C	-1	18.9
MO_1051	*HTATSF1*	chrX:135421575	G	C	17	94	0.18	D669H	-1	18.7
MO_1051	*TRIM41*	chr5:180593353	C	G	33	126	0.26	F425L	0	18.7
MO_1051	*GATAD2B*	chr1:152067127	C	G	36	152	0.24	M107I	1	18.7
MO_1051	*LSS*	chr21:46435568	C	A	27	79	0.34	A693S	1	18.5
MO_1051	*LFNG*	chr7:2533058	C	G	11	50	0.22	F350L	0	18.2
MO_1051	*ABCG1*	chr21:42570107	G	A	26	115	0.23	E191K	1	16.9
MO_1051	***TP53***	**chr17:7518978**	**C**	**T**	**28**	**81**	**0.35**	**G199E**	**-2**	**14.9**
MO_1051	*SHROOM3*	chr4:77879341	C	T	39	132	0.30	Q330*	-4	14.9
MO_1051	*HOXB7*	chr17:44040370	T	C	19	116	0.16	T163A	0	13.8
MO_1051	*IMPAD1*	chr8:58041381	G	A	21	93	0.23	S244F	-2	13.8
MO_1051	*MAN2A1*	chr5:109218851	G	A	32	108	0.30	E1030K	1	13.3
MO_1051	*SEC63*	chr6:108321444	T	C	7	49	0.14	T537A	0	13.0
MO_1051	*KIAA0562*	chr1:3751724	C	T	16	57	0.28	E160K	1	13.0
MO_1051	*DYRK1A*	chr21:37784455	C	G	27	119	0.23	S258C	-1	12.7
MO_1051	*FAM8A1*	chr6:17708899	G	C	28	79	0.35	E94Q	2	12.6
MO_1051	*KLHL17*	chr1:886979	G	A	24	95	0.25	E159K	1	12.4
MO_1051	*BAZ1A*	chr14:34322801	C	G	9	46	0.20	D639H	-1	12.0
MO_1051	*ZNF747*	chr16:30453456	G	C	25	97	0.26	L16V	1	11.6
MO_1051	*ZNF646*	chr16:30996797	G	A	42	148	0.28	D551N	1	11.4
MO_1051	*GMNN*	chr6:24893986	G	A	35	117	0.30	D204N	1	11.4
MO_1051	*NUP205*	chr7:134965696	G	T	14	43	0.33	S1666I	-2	11.3
MO_1051	*MANBA*	chr4:103776138	C	G	16	86	0.19	E697Q	2	10.9
MO_1051	*DHX29*	chr5:54594505	C	G	11	58	0.19	E1180Q	2	10.8
MO_1051	*TRAPPC4*	chr11:118396114	C	T	41	120	0.34	S132L	-2	10.7
MO_1051	*PTPRT*	chr20:40818629	G	A	19	78	0.24	S249L	-2	10.5
MO_1051	*PLEKHG5*	chr1:6453505	C	G	15	42	0.36	Q473H	0	10.3
MO_1051	*USP36*	chr17:74315271	C	T	28	120	0.23	E484K	1	9.5
MO_1051	*C5orf51*	chr5:41940308	G	A	20	85	0.24	E28K	1	9.5
MO_1051	*NUFIP2*	chr17:24637332	C	G	33	122	0.27	Q602H	0	9.0
MO_1051	*NUFIP2*	chr17:24638225	C	A	33	112	0.29	D305Y	-3	9.0

Supplementary Table S8. Nonsynonymous somatic mutations in MO_1051 breast cancer (Part-3).

SAMPLE	GENE	LOC (hg18)	REFERENCE	VARIANT	VAR FRAGS TUMOR	TUMOR TOTAL FRAGS	VAR FRAC TUMOR	PROTEIN	BLOSUM SCORE	EXPRESSION LEVEL (RPKM)
MO_1051	*NUFIP2*	chr17:24638363	C	G	33	119	0.28	E259Q	2	9.0
MO_1051	*NUFIP2*	chr17:24637377	C	G	27	114	0.24	E587D	2	9.0
MO_1051	*NUFIP2*	chr17:24637206	C	G	35	119	0.29	Q644H	0	9.0
MO_1051	*NUFIP2*	chr17:24638147	C	G	35	113	0.31	E331Q	2	9.0
MO_1051	*AFF4*	chr5:132260052	C	G	32	131	0.24	L723F	0	8.9
MO_1051	*SIN3A*	chr15:73451408	G	A	42	127	0.33	R1263C	-3	8.9
MO_1051	*C3orf63*	chr3:56650564	G	C	27	93	0.29	D428E	2	8.4
MO_1051	*GBP2*	chr1:89355953	G	C	16	67	0.24	P174A	-1	8.4
MO_1051	*USP48*	chr1:21902699	C	G	10	37	0.27	Splice acceptor		8.2
MO_1051	*USP48*	chr1:21900628	C	T	8	38	0.21	D893N	1	8.2
MO_1051	*USP48*	chr1:21902642	C	T	29	83	0.35	E858K	1	8.2
MO_1051	*MCM2*	chr3:128807680	G	A	34	110	0.31	E235K	1	8.0
MO_1051	*PTK2B*	chr8:27350634	G	A	24	76	0.32	E474K	1	7.8
MO_1051	*GPATCH8*	chr17:39832348	C	T	56	142	0.39	D875N	1	7.6
MO_1051	*NT5DC1*	chr6:116528847	C	G	13	40	0.33	L21V	1	7.6
MO_1051	*PANX1*	chr11:93502171	C	G	24	77	0.31	F15L	0	7.4
MO_1051	*NOL8*	chr9:94116453	C	T	35	111	0.32	E759K	1	6.7
MO_1051	*SRR*	chr17:2171641	G	T	10	40	0.25	G192V	-3	6.6
MO_1051	*IGF1R*	chr15:97273886	G	C	11	70	0.16	K560N	0	6.2
MO_1051	*C12orf35*	chr12:32029593	G	A	24	100	0.24	M1479I	1	5.8
MO_1051	*TRMT12*	chr8:125533520	G	A	36	127	0.28	E391K	1	5.6
MO_1051	*ZNF770*	chr15:33062510	C	T	51	139	0.37	A140T	0	5.6
MO_1051	*HSPA13*	chr21:14668314	G	C	34	129	0.26	S304C	-1	5.5
MO_1051	*GTF2E1*	chr3:121982852	G	A	49	150	0.33	E389K	1	4.8
MO_1051	*ITSN1*	chr21:34091656	G	A	10	50	0.20	E686K	1	4.7
MO_1051	*PGLYRP2*	chr19:15443755	C	T	28	99	0.28	R430H	0	4.7
MO_1051	*ZKSCAN1*	chr7:99469022	G	C	10	35	0.29	E320Q	2	4.4
MO_1051	*C2orf69*	chr2:200484591	G	A	32	100	0.32	G62E	-2	4.4
MO_1051	*MASP1*	chr3:188463101	G	C	20	59	0.34	F113L	0	4.4
MO_1051	*RANBP6*	chr9:6003154	C	G	31	118	0.26	L818F	0	4.3
MO_1051	*CD52*	chr1:26519322	G	A	43	131	0.33	G43E	-2	4.2
MO_1051	*CD97*	chr19:14378256	C	G	32	119	0.27	F645L	0	4.2
MO_1051	*NFATC1*	chr18:75388521	G	A	11	79	0.14	E917K	1	4.1
MO_1051	*PPP1R12B*	chr1:200678203	C	T	13	85	0.15	S516L	-2	3.8
MO_1051	*PPTC7*	chr12:109474148	C	T	17	101	0.17	D78N	1	3.8
MO_1051	*MYST3*	chr8:41953913	G	A	37	96	0.39	S378L	-2	3.8

Supplementary Table S8. Nonsynonymous somatic mutations in MO_1051 breast cancer (Part-4).

SAMPLE	GENE	LOC (hg18)	REFERENCE	VARIANT	VAR FRAGS TUMOR	TUMOR TOTAL FRAGS	VAR FRAC TUMOR	PROTEIN	BLOSUM SCORE	EXPRESSION LEVEL (RPKM)
MO_1051	*FLT4*	chr5:179980613	C	G	20	77	0.26	G723A	0	3.8
MO_1051	*XDH*	chr2:31426198	G	A	27	88	0.31	R943W	-3	3.7
MO_1051	*FYN*	chr6:112089807	C	T	24	113	0.21	R481Q	1	3.6
MO_1051	*HIVEP1*	chr6:12233605	C	T	40	148	0.27	S1864F	-2	3.5
MO_1051	*CYP4F2*	chr19:15858055	C	G	8	46	0.17	E328Q	2	3.5
MO_1051	*TTC30A*	chr2:178190124	C	T	14	53	0.26	E518K	1	3.4
MO_1051	*CCDC99*	chr5:168953832	G	A	33	124	0.27	E213K	1	3.3
MO_1051	***PIK3CA***	**chr3:180434779**	**A**	**G**	**27**	**88**	**0.31**	**H1047R**	**0**	**3.2**
MO_1051	*TBC1D7*	chr6:13413319	G	A	18	73	0.25	S292L	-2	3.1
MO_1051	*VPS13C*	chr15:59948176	C	T	19	88	0.22	E3613K	1	3.0
MO_1051	*EPDR1*	chr7:37956359	G	C	21	69	0.30	D291H	-1	2.9
MO_1051	*TACC1*	chr8:38764331	G	A	21	54	0.39	G25E	-2	2.7
MO_1051	*FGD6*	chr12:93999456	C	G	17	78	0.22	E1422Q	2	2.7
MO_1051	*C14orf126*	chr14:30987094	C	T	22	88	0.25	E167K	1	2.6
MO_1051	*CD22*	chr19:40523821	G	A	14	81	0.17	A483T	0	2.5
MO_1051	*FAM83D*	chr20:36988686	G	A	29	113	0.26	D93N	1	2.5
MO_1051	*FAM83D*	chr20:36988515	G	A	37	138	0.27	E36K	1	2.5
MO_1051	*INTS2*	chr17:57339654	C	G	35	122	0.29	E368Q	2	2.5
MO_1051	*C3orf15*	chr3:120910127	G	C	21	84	0.25	Splice acceptor		2.5
MO_1051	*AVIL*	chr12:56489676	C	G	47	131	0.36	E304Q	2	2.5
MO_1051	*MAP1B*	chr5:71526970	G	C	7	39	0.18	E678Q	2	2.2
MO_1051	*FJX1*	chr11:35597631	G	C	34	135	0.25	D291H	-1	2.2
MO_1051	*AR*	chrX:66681775	G	C	30	77	0.39	G21A	0	2.1
MO_1051	*ZNF546*	chr19:45212726	C	G	28	101	0.28	S570*	-4	2.1
MO_1051	*KIAA1549*	chr7:138254176	G	C	43	120	0.36	P196A	-1	2.0
MO_1051	*LYST*	chr1:233987317	G	C	21	115	0.18	L2316V	1	2.0
MO_1051	*ELOVL2*	chr6:11097983	A	T	27	113	0.24	L235H	-3	2.0
MO_1051	*C2orf67*	chr2:210648720	G	A	11	83	0.13	S519L	-2	1.9
MO_1051	*SEMA5B*	chr3:124114940	C	G	39	139	0.28	E768Q	2	1.7
MO_1051	*GRIN2D*	chr19:53637221	G	T	15	74	0.20	E815*	-4	1.6
MO_1051	*PCNXL2*	chr1:231227606	A	G	15	127	0.12	I1505T	-1	1.3
MO_1051	*RABGAP1L*	chr1:172455004	C	T	9	79	0.11	P29L	-3	1.3
MO_1051	*P2RX7*	chr12:120106623	G	A	37	103	0.36	V475I	3	1.1
MO_1051	*MYBL1*	chr8:67641733	C	T	18	64	0.28	E593K	1	1.0
MO_1051	*KIAA1524*	chr3:109755239	C	T	20	87	0.23	E785K	1	0.9
MO_1051	*FEZ1*	chr11:124835703	C	G	18	51	0.35	E190Q	2	0.9

Supplementary Table S8. Nonsynonymous somatic mutations in MO_1051 breast cancer (Part-5).

SAMPLE	GENE	LOC (hg18)	REFERENCE	VARIANT	VAR FRAGS TUMOR	TUMOR TOTAL FRAGS	VAR FRAC TUMOR	PROTEIN	BLOSUM SCORE	EXPRESSION LEVEL (RPKM)
MO_1051	*KIF21B*	chr1:199215290	G	A	18	94	0.19	L1373F	0	0.8
MO_1051	*LINGO4*	chr1:150040235	G	A	35	145	0.24	P524S	-1	0.7
MO_1051	*ST8SIA4*	chr5:100250047	C	T	42	138	0.30	M134I	1	0.6
MO_1051	*FAM124B*	chr2:224952709	G	C	11	82	0.13	S398C	-1	0.6
MO_1051	*ATOH8*	chr2:85835449	C	T	38	121	0.31	S209L	-2	0.6
MO_1051	*PNMA3*	chrX:151976633	G	A	28	134	0.21	E189K	1	0.5
MO_1051	*BRIP1*	chr17:57115738	C	T	43	142	0.30	E1151K	1	0.5
MO_1051	*MAML2*	chr11:95465186	G	A	39	128	0.30	Q553*	-4	0.4
MO_1051	*PLXNA4*	chr7:131562861	C	T	22	62	0.35	V591I	3	0.4
MO_1051	*PHOSPHO1*	chr17:44657062	C	G	11	70	0.16	E117Q	2	0.4
MO_1051	*MADCAM1*	chr19:452701	G	A	6	15	0.40	D234N	1	0.3
MO_1051	*ABCA10*	chr17:64700956	C	T	29	94	0.31	G557E	-2	0.3
MO_1051	*ANKLE1*	chr19:17255720	T	G	54	155	0.35	F383V	-1	0.3
MO_1051	*FAT4*	chr4:126459294	C	T	31	129	0.24	Q760*	-4	0.2
MO_1051	*FHOD3*	chr18:32552148	G	C	14	68	0.21	K788N	0	0.2
MO_1051	*KIRREL2*	chr19:41049157	C	G	30	127	0.24	L684V	1	0.2
MO_1051	*FCAMR*	chr1:205207606	C	T	41	162	0.25	R18K	2	0.2
MO_1051	*CDH7*	chr18:61642928	G	A	15	61	0.25	D288N	1	0.2
MO_1051	*DNAH7*	chr2:196560129	C	T	7	37	0.19	E554K	1	0.2
MO_1051	*ADCY10*	chr1:166137634	C	T	43	176	0.24	R109Q	1	0.2
MO_1051	*CCDC36*	chr3:49268748	C	T	42	134	0.31	Q262*	-4	0.1
MO_1051	*FBXO15*	chr18:69941604	G	A	11	34	0.32	R297C	-3	0.1
MO_1051	*HOXA2*	chr7:27107247	G	A	23	118	0.19	Q252*	-4	0.1
MO_1051	*PAPPA2*	chr1:175005504	C	T	23	72	0.32	R1488C	-3	0.1
MO_1051	*PI16*	chr6:37034898	G	A	19	58	0.33	Splice acceptor		0.1
MO_1051	*SHANK1*	chr19:55909256	G	A	15	54	0.28	S212L	-2	0.1
MO_1051	*C9orf131*	chr9:35033137	C	G	28	137	0.20	Q171E	2	0.1
MO_1051	*ZPLD1*	chr3:103678980	C	T	39	140	0.28	S375F	-2	0.1
MO_1051	*CUBN*	chr10:16995929	G	A	11	61	0.18	H2474Y	2	0.1
MO_1051	*C9orf153*	chr9:88032614	C	G	35	126	0.28	R73T	-1	0.1
MO_1051	*BNC1*	chr15:81723220	C	G	39	148	0.26	G596A	0	0.1
MO_1051	*ODZ1*	chrX:123382210	C	T	32	120	0.27	M1531I	1	0.0
MO_1051	*CNKSR2*	chrX:21459906	G	A	21	70	0.30	G368E	-2	0.0
MO_1051	*DNAH6*	chr2:84775044	G	T	16	92	0.17	D2485Y	-3	0.0
MO_1051	*FCRLA*	chr1:159948581	G	A	28	136	0.21	E262K	1	0.0
MO_1051	*GCK*	chr7:44153904	C	T	14	60	0.23	E246K	1	0.0

Supplementary Table S8. Nonsynonymous somatic mutations in MO_1051 breast cancer (Part-6).

SAMPLE	GENE	LOC (hg18)	REFERENCE	VARIANT	VAR FRAGS TUMOR	TUMOR TOTAL FRAGS	VAR FRAC TUMOR	PROTEIN	BLOSUM SCORE	EXPRESSION LEVEL (RPKM)
MO_1051	*TYRP1*	chr9:12699141	G	A	40	151	0.26	E525K	1	0.0
MO_1051	*RHAG*	chr6:49694882	G	T	8	28	0.29	Q104K	1	0.0
MO_1051	*RPH3A*	chr12:111818909	G	C	16	60	0.27	D672H	-1	0.0
MO_1051	*POU6F2*	chr7:39213708	G	A	34	102	0.33	G159R	-2	0.0
MO_1051	*MYT1L*	chr2:1905497	G	A	54	169	0.32	P351S	-1	0.0
MO_1051	*LRRTM4*	chr2:77600343	C	A	57	180	0.32	D54Y	-3	0.0
MO_1051	*ALK*	chr2:29310018	C	T	32	109	0.29	E802K	1	0.0
MO_1051	*CIB4*	chr2:26717641	C	G	25	93	0.27	E16Q	2	0.0
MO_1051	*A2ML1*	chr12:8912114	C	T	40	91	0.44	L1319F	0	0.0
MO_1051	*GABRR1*	chr6:89945354	C	T	42	127	0.33	E426K	1	0.0
MO_1051	*POU6F2*	chr7:39213709	G	A	35	106	0.33	G159E	-2	0.0
MO_1051	*NKX2-3*	chr10:101285073	G	C	11	44	0.25	D234H	-1	0.0
MO_1051	*ATP12A*	chr13:24181895	C	G	15	83	0.18	L898V	1	0.0
MO_1051	*CBLN4*	chr20:54009229	G	A	11	66	0.17	H125Y	2	0.0
MO_1051	*SLC1A6*	chr19:14944567	G	C	28	101	0.28	F52L	0	0.0
MO_1051	*FOXI2*	chr10:129425568	C	T	13	27	0.48	P14L	-3	0.0
MO_1051	*OR5K3*	chr3:99592974	C	T	17	64	0.27	R259*	-4	0.0
MO_1051	*SPINT4*	chr20:43786011	G	T	18	84	0.21	R65I	-3	0.0
MO_1051	*SI*	chr3:166209775	C	G	13	80	0.16	D1389H	-1	0.0
MO_1051	*TMEM202*	chr15:70487239	C	G	6	37	0.16	S258C	-1	0.0
MO_1051	*HELQ*	chr4:84569908	C	G	10	47	0.21	D771H	-1	NA
MO_1051	*AKR1E2*	chr10:4867919	C	A	20	62	0.32	S126*	-4	NA
MO_1051	*EPG5*	chr18:41714088	C	T	12	33	0.36	E1873K	1	NA
MO_1051	*BRAT1*	chr7:2549466	G	A	10	42	0.24	S274F	-2	NA

Supplementary Table S9. Gene copy number changes in MO_1051 breast cancer.

Sample	Segment (hg18)	Genes in this region	Span (bp)	Number of exons	Copy number ratio (gains)
MO_1051	chr12:44407518-44410034	*LOC400027,ARID2*	2,516	2	3.01
MO_1051	chr6:114285600-114288048	*MARCKS*	2448	2	2.94
MO_1051	chr1:150750710-151082749	*KPRP*,*C1orf68*, Late envelope proteins	332,039	19	2.34
MO_1051	chr11:6188000-6189418	*C11orf42,FAM160A2*	1418	3	2.07
MO_1051	chr20:60909386-60938896	*OGFR,COL9A3*	29,510	32	1.82
MO_1051	chrX:34058471-34871964	*TMEM47*	813,493	10	1.66
MO_1051	chrX:107291498-107822692	*COL4A6,COL4A5*	531,194	87	1.61
MO_1051	chr1:151123700-225910130	*ABL2,CAMK1G,CDC42BPA,CLK2,DDR2DYRK3,ELK4,FCGR2B,IKBKE,INSRRMAPKAPK2,MARK1,MDM4,MUC1,NEK2NEK7,NPR1,NTRK1,NUAK2,PBX1PRCC,PTGS2,RNASEL,RPS6KC1,SCYL3SDHC,SLC45A3,TPM3,TPR,UHMK1*	74,786,430	6263	1.59

Sample	Segment (hg18)	Genes in this region	Span (bp)	Number of exons	Copy number ratio (losses)
MO_1051	chr8:935432-947796	*ERICH1-AS1*	12,364	2	0.13
MO_1051	chr16:87826705-87827520	*ENSG00000205014*	815	2	0.15
MO_1051	chr10:2787544-2920752	--	133,208	2	0.18
MO_1051	chr7:157748520-157812260	*PTPRN2*	63,740	5	0.21
MO_1051	chr12:48557874-48559872	*FAIM2*	1,998	3	0.22
MO_1051	chr12:131422038-131542490	--	120,452	5	0.24
MO_1051	chr4:88754446-88756667	*DSPP*	2,221	3	0.31
MO_1051	chr6:168856780-168857712	--	932	3	0.31
MO_1051	chr9:95464514-95465753	*PHF2*	1,239	3	0.35
MO_1051	chr7:141566309-141567246	--	937	3	0.36
MO_1051	chr9:138860132-138861212	*C9orf172*	1,080	4	0.41
MO_1051	chr17:11085763-11939730	*SHISA6,DNAH9,ZNF18,MAP2K4*	853,967	88	0.41

Supplementary Table S10. Gene fusions identified in MO_1081. FGFR2 fusion is in bold.

Sample	5' Gene	3' Gene	Number of Supporting Reads	Type
MO_1081	***SLC45A3***	***FGFR2***	**2020**	**Interchromosomal**
MO_1081	*ST7*	*CAV1*	200	Intrachromosomal
MO_1081	*MAP7*	*PERP*	161	Intrachromosomal
MO_1081	*LAS1L*	*OPHN1*	33	Intrachromosomal
MO_1081	*BRE*	*RBKS*	20	Intrachromosomal
MO_1081	*BMPR1B*	*SMARCAD1*	22	Intrachromosomal

Supplementary Table S11. Summary of sequencing datasets analyzed for FGFR fusions.

Cancer type	Data source	Sample number	FGFR Fusion
BRCA (Breast cancer)	TCGA	746	3
LUSC (Lung squamous carcinoma)	TCGA	222	6
BLCA (Bladder Urothelial Carcinoma)	TCGA	85	3
GBM (Glioblastoma multiforme)	TCGA	163	2
HNSC (Head and neck squamous cell carcinoma)	TCGA	284	2
THCA (Papillary thyroid cancer)	TCGA	237	1
LUAD (Lung adenocarcinoma)	TCGA	299	0
LIHC (Liver Hepatocellular Carcinoma)	TCGA	17	0
MI-ONCOSEQ patients	U Michigan	90	4
Research cohorts	U Michigan	232	3
	Total:	2375	24

Research Cohorts from the University of Michgan

Cancer type	Sample number	Cell line	Tissue
Bladder	2	2	0
Breast	93	53	40
Cervical	9	9	0
Colon	9	9	0
Leukemia	4	0	4
Lymphoma	5	5	0
Melanoma	7	7	0
Oral	6	6	0
Pancreas	25	25	0
Prostate	31	0	31
Rare cancer	41	41	0
Total:	232	157	75

Supplementary Table S12. FGFR fusions in human cancers identified by transcriptome sequencing. LUSC, Lung squamous cell carcinoma; THCA, Thyroid carcinoma; GBM, Glioblastoma multiforme; HNSC, Head and Neck squamous cell carcinoma. Inter, interchromosomal; Intra, intrachromosomal.

FGFR2 fusions

5' Gene	3' Gene	Sample ID	Cancer type	Fusion	Predominant isoform	Isoform ratio (major/minor)
FGFR2	*AFF3*	MO_1051 (MI-ONCOSEQ case)	Breast	Inter	IIIc	6.7
FGFR2	*CCDC6*	TCGA-D8-A13Z-01A-11R-A115-07	Breast	Intra	IIIc	72.9
FGFR2	*CASP7*	TCGA-AN-A0AL-01A-11R-A00Z-07	Breast	Intra	IIIc	14.8
FGFR2	*BICC1*	MO_1036 (MI-ONCOSEQ case)	Cholangiocarcinoma	Intra	IIIb	13.5
FGFR2	*BICC1*	MO_1039 (MI-ONCOSEQ case)	Cholangiocarcinoma	Intra	IIIb	5.9
FGFR2	*KIAA1967*	TCGA-66-2765-01A-01R-0851-07	LUSC	Inter	IIIc	24.3
FGFR2	*OFD1*	TCGA-BJ-A0Z0-01A-11R-A10U-07	THCA	Inter	IIIc	67.2
SLC45A3	*FGFR2*	MO_1081 (MI-ONCOSEQ case)	Prostate	Inter	IIIb	1.8

FGFR3 fusions

5' Gene	3' Gene	Sample ID	Cancer type	Fusion	Predominant isoform	Isoform ratio (major/minor)
FGFR3	*BAIAP2L1*	SW780 (Internal collection; cell line)	Bladder	Inter	IIIb	10.2
FGFR3	*TACC3*	RT4 (Internal collection; cell line)	Bladder	Intra	IIIb	7.9
FGFR3	*TACC3*	C9 (Internal collection; cell line)	Oral cancer	Intra	IIIb	12.7
FGFR3	*TACC3*	TCGA-CF-A3MF-01A-12R-A21D-07	Bladder	Intra	IIIc	1.9
FGFR3	*TACC3*	TCGA-CF-A3MG-01A-11R-A20F-07	Bladder	Intra	IIIb	40.6
FGFR3	*TACC3*	TCGA-CF-A3MH-01A-11R-A20F-07	Bladder	Intra	IIIb	12.3
FGFR3	*TACC3*	TCGA-27-1835-01A-01R-1850-01	GBM	Intra	IIIc	8.4
FGFR3	*TACC3*	TCGA-76-4925-01A-01R-1850-01	GBM	Intra	IIIc	28.9
FGFR3	*TACC3*	TCGA-CR-6473-01A-11R-1873-07	HNSC	Intra	IIIb	11.1
FGFR3	*TACC3*	TCGA-CV-7100-01A-11R-2016-07	HNSC	Intra	IIIb	14.5
FGFR3	*TACC3*	TCGA-66-2786-01A-01R-0851-07	LUSC	Intra	IIIb	34.4
FGFR3	*TACC3*	TCGA-39-5024-01A-21R-1820-07	LUSC	Intra	IIIb	10.1
FGFR3	*TACC3*	TCGA-22-4607-01A-01R-1201-07	LUSC	Intra	IIIb	9.5
FGFR3	*TACC3*	TCGA-34-2608-01A-02R-0851-07	LUSC	Intra	IIIb	20.8

FGFR1 fusions

5' Gene	3' Gene	Sample ID	Cancer type	Fusion	Predominant isoform	Isoform ratio (major/minor)
ERLIN2	*FGFR1*	TCGA-D8-A1JC-01A-11R-A13Q-07	Breast	Intra	IIIc	14.5
BAG4	*FGFR1*	TCGA-22-5480-01A-01R-1635-07	LUSC	Intra	IIIc	20.9

Supplementary Table S13. Accession numbers of reference genes.

GENE / ISOFORM	TRANSCRIPT	PROTEIN
FGFR1 IIIc	NM_023110	NP_075598
FGFR2 IIIb	NM_022970	NP_075259
FGFR2 IIIc	NM_000141	NP_000132
FGFR3 IIIb	NM_001163213	NP_001156685
FGFR3 IIIc	NM_000142	NP_000133
AFF3	NM_002285	NP_002276
BAG4	NM_004874	NP_004865
BAIAP2L1	NM_018842	NP_061330
BICC1	NM_001080512	NP_001073981
CASP7	NM_001227	NP_001218
CCDC6	NM_005436	NP_005427
ERLIN2	NM_007175	NP_009106
KIAA1967	NM_021174	NP_066997
OFD1	NM_003611	NP_003602
SLC45A3	NM_033102	NP_149093
TACC3	NM_006342	NP_006333

Supplementary Table S14. Junction sequences of FGFR fusion transcripts.

5' Gene	Junction Sequence	3' Gene
BAG4 exon 2	AGACCAGAATTGCAAGGCCAG | GTCCGTTATGCCACCTGGAGC	*FGFR1* exon 9
ERLIN2 exon 10	CCGCAGAAACTACGAGTTGAT | GGTCAGTTTGAAAAGGAGGAT	*FGFR1* exon 4
FGFR2 exon 19	CTCACTCTCACAACCAATGAG | GAGAGTAGATCTGGAGAAACC	*AFF3* exon 8
FGFR2 exon 19	CTCACTCTCACAACCAATGAG | ATCATGGAGGAAACAAATACG	*BICC1* exon 3
FGFR2 exon 19	CTCACTCTCACAACCAATGAG | ATGGCAGATGATCAGGGCTGT	*CASP7* exon 4
FGFR2 exon 19	CTCACTCTCACAACCAATGAG | CAAGCCAGGGCTGAGCAGGAA	*CCDC6* exon 2
FGFR2 exon 19	CTCACTCTCACAACCAATGAG | GGTGGGGAGAAACAGCGGGTC	*KIAA1967* exon 5
FGFR2 exon 19	CTCACTCTCACAACCAATGAG | ACACAACTTCGAAACCAGCTA	*OFD1* exon 3
SLC45A3 exon 1	ACAGCCGCGCGCCTCGGCCAG | TGACTGCAGCAGCAGCGGCAG	*FGFR2* exon 3b
FGFR3 exon 18	CTTACCGTGACGTCCACCGAC | AATGTTATGGAACAGTTCAAT	*BAIAP2L1* exon 2
FGFR3 exon 18	CTTACCGTGACGTCCACCGAC | GTGCCAGGCCCACCCCCAGGT	*TACC3* exon 10
FGFR3 exon 18	CTTACCGTGACGTCCACCGAC | GTAAAGGCGACACAGGAGGAG	*TACC3* exon 11
FGFR3 intron 18	GCTGAGGTGTGGGGCGGGCCT | TCTGGCCCAGGTGCCCTGGCT	*TACC3* exon 4

Supplementary Table S15. Primer sequences.

Cloning of FGFR fusion alleles	
FGFR2 FL-S	CAACGGTCCGACCATGGTCAGCTGGGGTCGTTTCATC
CCDC6 TAG-AS	GAACGGACCGAAAGGCTGGGAGGAGGGGTG
BICC1 TAG-AS	GAACGGACCGCGGCCACTGACACTAGCAATGT
FGFR3 FL-S	CAACGGTCCGACCATGGGCGCCCCTGCCT
TACC3 TAG-AS	CAACGGACCGATCTTCTCCATCTTGGAGATGAG
BAIAP2L1 TAG-AS	GAACGGACCGCGAATGATGGGTGCCGAGCGAT
Cloning of FGFR fusion partners	
BAIAP2L1 DIM-S	CAACGGTCCGACCATGAATGTTATGGAACAGTTCAATCC
BAIAP2L1 TAG-AS	GAACGGACCGCGAATGATGGGTGCCGAGCGAT
BICC1 DIM-S	GAACGGTCCGACCATGATCATGGAGGAAACAAATACGCAGA
BICC1 TAG-AS	CAACGGACCGCCACTGACACTAGCAATGTCTGA
TACC3 DIM-S	CAACGGTCCGACCATGGTGCCAGGCCCACCCCCAGGTGTT
TACC3 TAG-AS	CAACGGACCGATCTTCTCCATCTTGGAGATGAG
KIAA1967CPO-S	GAACGGTCCGACCATGGGTGGGGAGAAACAGCGGGTCTTCA
KIAA1967 TAG-AS	CTTCGGACCGTTGCTAGGTGCCGGCTCCTCCTT
CCDC6 DIM-S	GAACGGTCCGACCATGCAAGCCAGGGCTGAGCAGGAAGAA
CCDC6 TAG-AS	GAACGGACCGAAAGGCTGGGAGGAGGGGTG
CIT DIM-S	CAACGGTCCGACCATGGCACATAGAGATGAAATCCAGCGCAA
CIT TAG-AS	CAACGGACCGACTGAAGACTGGTCCCAGACCTT
Quantitative RT-PCR primers	
FGFR2-AFF3 QPCR-F	CCAACTGCACCAACGAACTG
FGFR2-AFF3 QPCR-R	GTGGAAGCCAGGTCATCTCC
FGFR2-BICC QPCR-F	GCTGCTGAAGGAAGGACACA
FGFR2-BICC QPCR-R	ATGGCCAAGCAATCTGCGTA
FGFR3-BAIAP2L1 QPCR-F	GACCTGGACCGTGTCCTTAC
FGFR3-BAIAP2L1 QPCR-R	GATCTTGGCCACTCCATCGT