Next generation sequencing approach for detecting 491 fusion genes from human cancer

Kenichi URAKAMI¹, Yuji SHIMODA², Keiichi OHSHIMA³, Takeshi NAGASHIMA², Masakuni SERIZAWA⁴, Tomoe TANABE², Junko SAITO⁴, Tamiko USUI¹, Yuko WATANABE³, Akane NARUOKA⁴, Sumiko OHNAMI¹, Shumpei OHNAMI¹, Tohru MOCHIZUKI³, Masatoshi KUSUHARA^{4,5}, and Ken YAMAGUCHI⁶

¹Cancer Diagnostics Research Division, Shizuoka Cancer Center Research Institute, Shizuoka, Japan; ²SRL Inc., Tokyo, Japan; ³Medical Genetics Division, Shizuoka Cancer Center Research Institute, Shizuoka, Japan; ⁴Drug Discovery and Development Division, Shizuoka Cancer Center Research Institute, Shizuoka, Japan; ⁵Regional Resources Division, Shizuoka Cancer Center Research Institute, Shizuoka, Japan; and ⁶Shizuoka Cancer Center, Shizuoka, Japan

(Received 9 December 2015; and accepted 18 December 2015)

ABSTRACT

Next-generation DNA sequencing (NGS) of the genomes of cancer cells is contributing to new discoveries that illuminate the mechanisms of tumorigenesis. To this end, the International Cancer Genome Consortium and The Cancer Genome Atlas are investigating novel alterations of genes that will define the pathways and mechanisms of the development and growth of cancers. These efforts contribute to the development of innovative pharmaceuticals as well as to the introduction of genome sequencing as a component of personalized medicine. In particular, chromosomal translocations that fuse coding sequences serve as important pharmaceutical targets and diagnostic markers given their association with tumorigenesis. Although increasing numbers of fusion genes are being discovered using NGS, the methodology used to identify such fusion genes is complicated, expensive, and requires relatively large samples. Here, to address these problems, we describe the design and development of a panel of 491 fusion genes that performed well in the analysis of cultured human cancer cell lines and 600 clinical tumor specimens.

In late January 2014, the Shizuoka Cancer Center started Project HOPE—High-tech Omics-based Patient Evaluation—with the goal of advancing cancer medicine (26). Specifically, this project's goal is to evaluate the biological characteristics of tumor and diathesis of each patient using multiomics analyses that integrate genomics, transcriptomics, proteomics, and metabolomics. The use of next-generation DNA sequencing techniques (NGS) to analyze the genomes of cancer cells identified numerous gene alterations, including single-base substitutions, small insertions

and deletions, gene amplification, gene deletions and fusions as well as epigenetic modifications (5, 22). In particular, fusion genes that contribute to tumorigenesis are attractive targets for developing new drugs and identifying diagnostic markers (13).

Although the use of NGS led to the discovery of numerous fusion genes (1), the method is complicated, expensive, and a large sample is required (14, 25). To address these impediments facing efforts to advance the prevention, diagnosis, and treatment of cancer, we designed a panel of PCR primers that amplify 491 fusion transcripts, termed the “HOPE fusion panel,” that can detect fusion transcripts in one experiment.

MATERIALS AND METHODS

Ethical statement. The Institutional Review Boards

Address correspondence to: Kenichi Urakami, Cancer Diagnostics Research Division, Shizuoka Cancer Center Research Institute, 1007 Shimonagakubo, Nagaizumi-cho, Sunto-gun, Shizuoka 411-8777, Japan
Tel: +81-55-989-5222, Fax: +81-55-989-6085
E-mail: K.Urakami@scchr.jp

of Shizuoka Cancer Center approved this study.

Design of the fusion panel. Fusion gene data were obtained from the website of the Sanger Institute COSMIC (Catalogue Of Somatic Mutations In Cancer) (2). The COSMIC database v71 includes more than 600 fusion genes. We selected as much of the sequence of the target fusion gene as possible and excluded multiple fusion genes with complex structures (e.g. inversions) with the same breakpoint, ultimately resulting in a selection of 491 fusion genes (Table 1). Primers for detecting fusion transcripts and their 5' and 3' partners were designed using the Ion AmpliSeq Designer website (Thermo Fisher Scientific, Wilmington, DE, USA) (Table 2).

Fig. 1 shows the strategy used to design the primer sets. The PCR reaction mixture was divided into two tubes to prevent interference between the primer sets. One tube contained 452 primer pairs designed to amplify the fusion transcript, and 131 primer pairs designed to amplify the 5' and 3' partners. Another tube contained 39 primer pairs designed to amplify the fusion transcript and 127 primer pairs designed to amplify the 5' and 3' partners. The Ion AmpliSeq primer master mix was purchased from Thermo Fisher Scientific.

Preparation of total RNA from cultured cell lines. We purchased the human cancer cell lines HCC38, HCC1395, NCI-H2228, DU145, NCI-H508, HCC1187, BT-20, SW78, SK-ES-1, and RD-ES from the American Type Culture Collection (ATCC; Rockville, MD, USA) and cultured them in accordance with the instructions provided by the ATCC. Total RNA from the cultured cells was isolated using the microRNAeasy Mini Kit (QIAGEN, Hilden, Germany) and quantified using a Bioanalyzer (Agilent, Santa Clara, CA, USA) in accordance with the manufacturer's instructions.

Preparation of total RNA from clinical samples. Six hundred resected flash-frozen tissue samples were acquired from the HOPE study. Fresh tissue was soaked in the QIAzol Lysis Reagent (QIAGEN), disrupted using a TissueLyser (QIAGEN), and total RNA was isolated using the microRNAeasy Mini Kit and quantified using a Bioanalyzer.

Library preparation and sequencing. Total RNAs (10 ng) were used as templates to prepare cDNAs using the SuperScript VILO cDNA Synthesis Kit (Thermo Fisher Scientific). The Ion AmpliSeq Library Kit 2.0 (Thermo Fisher Scientific) was used to

construct an Ion Torrent adapter-ligated library in accordance with the manufacturer's instructions, and the Ion Proton Sequencing 200 Kit (Thermo Fisher Scientific) was used for nucleotide sequencing in accordance with the manufacturer's protocol.

Detection of ERO1L-FERMT2 transcript by RT-PCR. Total RNA of HCC1395 was used for the reverse transcription with the SuperScript III (Thermo Fisher Scientific), following the manufacturer's instructions. PCR reaction was performed by HotStarTaq Master Mix (QIAGEN) with the forward primer 5'-TGAAGAGGCCGTGTCCTTTC-3' and reverse primer 5'-AGGGCTGCAAACATCATCATTT-3'. The amplification profile of the PCR consisted of 35 cycles of denaturation at 94°C for 1 min, annealing at 60°C for 1 min, and extension at 72°C for 1 min. The PCR products were analysed by QIAxcel Advanced (QIAGEN).

Data analysis. All data were analyzed using the Ion Reporter server. The Ion AmpliSeq RNA Fusion workflow (Thermo Fisher Scientific) was used to detect fusion transcripts targeted by the HOPE fusion panel. The reference file for this workflow was constructed from all fusion variants in the HOPE fusion gene panel. The workflow used a related BED file that describes the breakpoints between the two genes that are associated with each fusion. The reference and BED files are included in the Ion Reporter Software.

RESULTS AND DISCUSSION

Detection of fusion transcripts using immunostaining, FISH, RT-PCR, and RNA-seq is not convenient, as these techniques are time-consuming and generate artifacts (14, 20, 21). Therefore, NGS is used increasingly frequently as an alternative diagnostic tool (9, 16). To take advantage of NGS, we constructed a novel HOPE fusion panel for the detection of fusion transcripts that recur in cancer cells.

We first evaluated the sensitivity of our approach using 10 human cell lines harboring fusion transcripts. All of the expected fusion transcripts except for *ERO1L-FERMT2* were detected in each respective cell line (Table 3). We confirmed *ERO1L-FERMT2* transcript by RT-PCR with different primers. The failure to detect *ERO1L-FERMT2* mRNA might be explained by technical problems such as inappropriate primer design or synthesis.

We next analyzed 600 resected cancer tissues acquired by the HOPE study. The sequence coverage

Table 1 *Fusion genes detected using the fusion panel*

ACBD6-RRP15	COL1A1-PDGFβ	EML4-ALK	EWSR1-NFATC2	FUS-CREB3L2
1 COSF687	43 COSF1285	101 COSF1064	154 COSF1180	196 COSF325
ACSL3-ETV1	44 COSF1289	102 COSF1065	EWSR1-NR4A3	197 COSF330
2 COSF1125	45 COSF1291	103 COSF1127	155 COSF352	198 COSF331
ACTB-GLI1	46 COSF1293	104 COSF1296	156 COSF353	199 COSF332
3 COSF1378	47 COSF531	105 COSF408	157 COSF358	200 COSF334
4 COSF1379	48 COSF533	106 COSF409	158 COSF359	201 COSF335
5 COSF1380	49 COSF535	107 COSF411	159 COSF364	202 COSF336
6 COSF1384	50 COSF539	108 COSF413	160 COSF367	203 COSF337
AGPAT5-MCPH1	51 COSF541	109 COSF475	161 COSF381	204 COSF338
7 COSF695	52 COSF543	110 COSF478	EWSR1-PATZ1	205 COSF339
AGTRAP-BRAF	53 COSF545	111 COSF487	162 COSF283	206 COSF340
8 COSF828	54 COSF547	EPC1-PHF1	EWSR1-PBX1	207 COSF341
9 COSF829	55 COSF550	112 COSF1452	163 COSF349	208 COSF389
AKAP9-BRAF	56 COSF552	ERC1-ELKS-RET	164 COSF350	209 COSF390
10 COSF1013	57 COSF556	113 COSF1507	EWSR1-SMARCA5	210 COSF845
ASPSR1-TFE3	58 COSF562	ERO1L-FERMT2	165 COSF1208	211 COSF846
11 COSF393	59 COSF564	114 COSF667	EWSR1-SP3	212 COSF852
12 COSF395	60 COSF591	ESRP1-RAFI	166 COSF278	213 COSF856
ATF1-EWSR1	61 COSF593	115 COSF826	167 COSF279	214 COSF858
13 COSF259	62 COSF595	ETV6-ITPR2	EWSR1-YY1	215 COSF863
ATG4C-FBXO38	63 COSF596	116 COSF679	168 COSF1421	216 COSF918
14 COSF711	64 COSF597	ETV6-JAK2	EWSR1-ZNF384	217 COSF922
ATIC-ALK	65 COSF599	117 COSF989	169 COSF345	218 COSF925
15 COSF444	66 COSF601	118 COSF993	170 COSF346	219 COSF927
BBS9-PKD1L1	67 COSF603	119 COSF994	171 COSF347	220 COSF930
16 COSF724	68 COSF605	120 COSF995	EWSR1-ZNF444	221 COSF944
BCR-JAK2	69 COSF607	EWSR1-ATF1	172 COSF1342	222 COSF945
17 COSF752	70 COSF626	121 COSF217	173 COSF1343	223 COSF948
18 COSF757	71 COSF634	122 COSF219	EZR-ROS1	224 COSF950
19 COSF987	72 COSF638	123 COSF223	174 COSF1267	225 COSF952
BRAF-AKAP9	73 COSF642	124 COSF224	FAM131B-BRAF	FUS-DDIT3
20 COSF1015	74 COSF644	125 COSF299	175 COSF1189	226 COSF1018
BRD3-C15orf55	75 COSF646	EWSR1-CREB1	176 COSF1191	227 COSF291
21 COSF973	76 COSF648	126 COSF264	177 COSF1193	228 COSF293
BRD4-C15orf55	77 COSF650	EWSR1-DDIT3	FCHSD1-BRAF	229 COSF294
22 COSF780	78 COSF652	127 COSF269	178 COSF403	230 COSF300
23 COSF972	79 COSF654	128 COSF271	FGFR1-PLAG1	231 COSF301
CANT1-ETV4	80 COSF817	129 COSF273	179 COSF1108	232 COSF303
24 COSF1155	81 COSF819	130 COSF281	180 COSF1110	233 COSF304
CARS-ALK	COL1A1-USP6	EWSR1-ERG	181 COSF1111	234 COSF867
25 COSF437	82 COSF1397	131 COSF145	182 COSF1113	FUS-ERG
CCDC6-RET	83 COSF1414	132 COSF146	FGFR1-TACC1	235 COSF309
26 COSF1271	84 COSF1415	133 COSF149	183 COSF1362	236 COSF311
27 COSF1515	COL1A2-PLAG1	134 COSF150	FGFR1-ZNF703	237 COSF314
CD74-ROS1	85 COSF1097	135 COSF152	184 COSF720	238 COSF316
28 COSF1200	86 COSF1098	136 COSF156	FGFR3-BAIAP2L1	239 COSF318
29 COSF1202	CREB3L2-FUS	EWSR1-ETV1	185 COSF1346	240 COSF319
30 COSF1478	87 COSF842	137 COSF163	FGFR3-TACC3	241 COSF624
CDH11-USP6	88 COSF847	EWSR1-ETV4	186 COSF1348	FUS-FEV
31 COSF1399	89 COSF848	138 COSF208	187 COSF1353	242 COSF295
32 COSF1401	90 COSF860	EWSR1-FEV	188 COSF1434	GLI1-ACTB
33 COSF1403	91 COSF861	139 COSF195	FHIT-HMGA2	243 COSF1387
34 COSF1405	CRTC1-MAML2	140 COSF275	189 COSF1024	GMDS-PDE8B
CHCHD7-PLAG1	92 COSF1102	EWSR1-FLI1	FOXO1-PAX3	244 COSF713
35 COSF1087	CRTC3-MAML2	141 COSF1302	190 COSF387	GNAI1-BRAF
36 COSF1088	93 COSF1104	142 COSF165	FUS-ATF1	245 COSF1442
CIC-DUX4	CTAGE5-GEMIN2	143 COSF167	191 COSF296	GOLGA5_PTC5-RET
37 COSF1374	94 COSF697	144 COSF169	FUS-CREB3L1	246 COSF1503
CLCN6-BRAF	CTNNB1-PLAG1	145 COSF171	192 COSF912	GOPC-ROS1
38 COSF1440	95 COSF1077	146 COSF173	193 COSF913	247 COSF1139
CLTC-ALK	96 COSF1079	147 COSF174	194 COSF942	248 COSF1188
39 COSF434	DDX5-ETV4	148 COSF175	195 COSF943	HEY1-NCOA2
CLTC-TFE3	97 COSF1166	149 COSF176		249 COSF1211
40 COSF799	EIF3E-RSPO2	150 COSF180		HMGA2-ALDH2
CNBP-USP6	98 COSF1307	151 COSF183		250 COSF1038
41 COSF1416	99 COSF1309	152 COSF204		251 COSF1039
42 COSF1417	EIF3K-CYP39A1	153 COSF227		HMGA2-CCNB1IP1
	100 COSF703			252 COSF983

Table 1 Continued

HMGA2-COX6C	KLC1-ALK	PAX3-NCOA1	SFPQ-TFE3	THRAP3-USP6
253 COSF985	308 COSF1276	354 COSF1042	402 COSF801	450 COSF1410
254 COSF986	KLK2-ETV1	355 COSF289	403 COSF802	451 COSF1411
HMGA2-EBF1	309 COSF1116	PAX3-NCOA2	404 COSF803	TMPRSS2-ERG
255 COSF1020	310 COSF1117	356 COSF1040	405 COSF914	452 COSF116
256 COSF1021	KTNI-RET	PAX5-JAK2	SLC26A6-PRKAR2A	453 COSF123
HMGA2-FHIT	311 COSF1513	357 COSF1071	406 COSF671	454 COSF125
257 COSF1022	LIFR-PLAG1	PAX7-FOXO1	SLC34A2-ROS1	455 COSF127
258 COSF1023	312 COSF1091	358 COSF287	407 COSF1196	456 COSF128
HMGA2-LHFP	313 COSF1092	PAX8-PPARG	408 COSF1198	457 COSF129
259 COSF976	LPP-HMGA2	359 COSF1215	409 COSF1259	458 COSF130
HMGA2-LPP	314 COSF964	360 COSF1217	410 COSF1261	459 COSF135
260 COSF962	315 COSF966	361 COSF1219	SLC45A3-BRAF	460 COSF17
261 COSF969	LRIG3-ROS1	362 COSF1223	411 COSF871	461 COSF18
HMGA2-NFIB	316 COSF1269	PCM1_PTC4-RET	412 COSF872	462 COSF24
262 COSF795	MBOAT2-PRKCE	363 COSF1481	SLC45A3-ELK4	463 COSF26
263 COSF955	317 COSF673	PCM1-JAK2	413 COSF1115	464 COSF36
HMGA2-RAD51B	MBTD1-CXorf67	364 COSF1001	414 COSF1131	465 COSF736
264 COSF981	318 COSF1464	365 COSF1003	SLC45A3-ERG	TMPRSS2-ETV1
HMGA2-WIF1	319 COSF1465	366 COSF1007	415 COSF1137	466 COSF115
265 COSF1026	MEAF6-PHF1	367 COSF1009	SLC45A3-ETV1	467 COSF134
266 COSF1028	320 COSF1450	368 COSF998	416 COSF1119	468 COSF14
267 COSF1029	MKRN1-BRAF	PLAG1-CTNNB1	SLC45A3-ETV5	469 COSF33
268 COSF1030	321 COSF1444	369 COSF1081	417 COSF1157	TMPRSS2-ETV5
269 COSF1031	MSN-ALK	370 COSF1083	SQSTM1-ALK	470 COSF1159
270 COSF1032	322 COSF421	PLXND1-TMCC1	418 COSF1052	471 COSF1160
271 COSF1033	MYB-NFIB	371 COSF689	SRGAP3-RAF1	TPM3-ALK
272 COSF1034	323 COSF784	372 COSF699	419 COSF660	472 COSF439
273 COSF1035	324 COSF786	PPFIBP1-ALK	420 COSF661	TPM3-NTRK1
274 COSF1036	325 COSF876	373 COSF1461	SS18L1-SSX1	473 COSF1329
275 COSF1037	326 COSF877	PRCC-TFE3	421 COSF1123	TPM3-ROS1
HN1-USH1G	327 COSF878	374 COSF805	SS18-SSX1	474 COSF1273
276 COSF691	328 COSF879	375 COSF807	422 COSF499	TPM4-ALK
HNRNP2B1-ETV1	329 COSF880	376 COSF809	423 COSF505	475 COSF441
277 COSF1121	330 COSF883	377 COSF811	424 COSF513	TPR-NTRK1
HOOK3-RET	331 COSF884	PRKARIA-RET	425 COSF514	476 COSF1324
278 COSF1509	332 COSF891	378 COSF1511	426 COSF527	477 COSF1326
IL6R-ATP8B2	NACC2-NTRK2	PTPRK-RSPO3	SS18-SSX4	TRIM24_PTC6-RET
279 COSF705	333 COSF1448	379 COSF1311	427 COSF502	478 COSF1521
INTS4-GAB2	NCOA4_ELE1-RET	380 COSF1313	428 COSF507	TRIM24-RET
280 COSF685	334 COSF1340	QKI-NTRK2	429 COSF525	479 COSF1522
JAK2-ETV6	NCOA4-RET	381 COSF1446	SSBP2-JAK2	TRIM27-RET
281 COSF991	335 COSF1491	RAD51B-HMGA2	430 COSF1045	480 COSF1519
JAK2-PAX5	336 COSF1498	382 COSF978	431 COSF1047	TRIM33_PTC7-RET
282 COSF1073	337 COSF1500	383 COSF980	432 COSF1048	481 COSF1525
283 COSF1074	NDRG1-ERG	RAF1-DAZL	SSH2-SUZ12	UBE2L3-KRAS
284 COSF1075	338 COSF1133	384 COSF675	433 COSF722	482 COSF1298
JAK2-PCMI	339 COSF1135	RAF1-ESRP1	STRN-ALK	VCL-ALK
285 COSF1005	NF1-ASIC2	385 COSF827	434 COSF1430	483 COSF1057
286 COSF996	340 COSF693	RANBP2-ALK	SUSD1-PTBP3	VTI1A-TCF7L2
JAZF1-SUZ12	NFATC2-EWSR1	386 COSF415	435 COSF701	484 COSF1147
287 COSF568	341 COSF1182	RBM14-PAC1	TAF15-NR4A3	485 COSF1149
KIAA1549-BRAF	NFIA-EHF	387 COSF707	436 COSF657	486 COSF1151
288 COSF1226	342 COSF669	RET-GOLGA5	TCEA1-PLAG1	487 COSF1153
289 COSF1283	343 COSF670	388 COSF1505	437 COSF1085	YWHAE-FAM22A
290 COSF1284	NONO-TFE3	RET-NCOA4	TCF12-NR4A3	488 COSF1247
291 COSF1474	344 COSF865	389 COSF1494	438 COSF754	YWHAE-FAM22B
292 COSF481	NOTCH1-GABBR2	390 COSF1496	TCF3-PBX1	489 COSF1249
293 COSF483	345 COSF1178	RET-TRIM33	439 COSF1489	YY1-EWSR1
294 COSF485	NPM1-ALK	391 COSF1527	TECTA-TBCEL	490 COSF1423
295 COSF509	346 COSF198	RGS22-SYCP1	440 COSF718	ZC3H7B-BCOR
296 COSF511	347 COSF200	392 COSF665	TFE3-ASPSR1	491 COSF1469
KIF5B-ALK	NTN1-ACLY	RNF130-BRAF	441 COSF782	
297 COSF1058	348 COSF726	393 COSF1483	442 COSF797	
298 COSF1060	NTRK1-TPM3	SDC4-ROS1	443 COSF798	
299 COSF1257	349 COSF1332	394 COSF1265	TFE3-PRCC	
300 COSF1381	NTRK1-TPR	395 COSF1278	444 COSF839	
KIF5B-RET	350 COSF1336	396 COSF1280	TFG-ALK	
301 COSF1230	NTRK3-ETV6	SEC16A-NOTCH1	445 COSF424	
302 COSF1232	351 COSF825	397 COSF1204	446 COSF426	
303 COSF1234	OMD-USP6	398 COSF1206	447 COSF428	
304 COSF1236	352 COSF1412	SEC31A-JAK2	TFG-NR4A3	
305 COSF1253	PAX3-FOXO1	399 COSF1069	448 COSF1187	
306 COSF1255	353 COSF247	SEC31L1_SEC31A-ALK	TFG-NTRK1	
307 COSF1262		400 COSF459	449 COSF1328	
		401 COSF460		

Table 2 Primer sequences

#	ID	Foward / Reverse Primer	#	ID	Foward / Reverse Primer
1	COSF687	ACATTGACCATAATCAACCAAGGCATCAA / GCTCCCATCATGAAATCATCACGTA	95	COSF1077	TCTGTGGCAGCAGCGTT / GGCAACCTTATTAATAGACCGTCACA
2	COSF1125	CTGTAAACATTGCCACCCTCAGA / GGGCTCATCTCCACTTGT	96	COSF1079	TCTGTGGCAGCAGCGTT / TTGATCTAGCCAGTCCCATGTAC
3	COSF1378	CTCTTCAACAATGAGCTGCGTGT / CAGATTACGGCTCAGCTCTCT	97	COSF1166	GCAAGGAATATACAGTTAGAGGTCACAA / GGAAACAAAGTCTCATCTGTCT
4	COSF1379	CTCCGCACTGTGCAAGG / CACTTGCCAACACGATGT	98	COSF1307	CTCGCATCGCGCACTTTT / AGGGAGACTCGCCACTCA
5	COSF1380	CCTTCTACAATGAGCTGCGTGT / CACTTGCCAACACGATGT	99	COSF1309	CTCGCATCGCGCACTTTT / AACTCTGTGTGACATCGGTACA
6	COSF1384	CCTTCTACAATGAGCTGCGTGT / AGGGCCCTTTTGGTGATCAT	100	COSF703	GTGGGTATCATCTACCAAGCATTT / TGACAGTCCCATTTTCCCTTTC
7	COSF695	GAAGGTACAAGGTATAATCCAGAGCAAA / CAGTGAGGTCACTGTCAITGTGA	101	COSF1064	GGATGTATTAACCTGGAGGAGGGGAAA / CTCAGGGCTCTGCAGCTCC
8	COSF828	CCAGACGATGTGACTCAGCAGA / AAACCTGTGGTGTGATCTCCATC	102	COSF1065	GGATGTATTAACCTGGAGGAGGGGAAA / CTCAGGGCTCTGCAGCTCC
9	COSF829	CCAGACGATGTGACTCAGCAGA / AAACCTGTGGTGTGATCTCCATC	103	COSF1127	GGATGTATTAACCTGGAGGAGGGGAAA / AGGAGGCTCTGCCAGCAAG
10	COSF1013	CTTAGAGCAACTCAACCAAGTGAAATG / AAACCTGTGGTGTGATCTCCATC	104	COSF1296	GTCGAAAATACCTTCAACACCCAATTT / AGGTACACCACAGAGGATCAG
11	COSF393	TCCAAGCCAAGAAAGTCCAAGTC / GCTGACAGTGATGGCTGGT	105	COSF408	GGATGGAGATGTCTTACTGGAGACT / CTCAGGGCTCTGCAGCTCC
12	COSF395	TCCAAGCCAAGAAAGTCCAAGTC / CTGACGATTTCAATGTAACTGGAC	106	COSF409	CATTCCAGTACATACACACCTTT / CTCAGGGCTCTGCAGCTCC
13	COSF259	GGACTCTCCGACAGCATAGG / ACAGGTGGGCTAGATCAAGA	107	COSF411	GTCGAAAATACCTTCAACACCCAATTT / CTCAGGGCTCTGCAGCTCC
14	COSF711	GATCCCACTGTACAATAGGATTTTACT / GGCCAAGAAAGTCCAGTCTCAA	108	COSF413	TCTCTGAAAGAGAAATAGAGGTTCTGTAT / AGGAGGCTTGCCAGCAAG
15	COSF444	GGAAACAGTACAGCAAAAGGTGAT / CTCAGGGCTCTGCAGTCC	109	COSF475	AGGCAGATCAATTTTATAGGACAT / CTCAGGGCTCTGCAGTCC
16	COSF724	CCCAACTTCCCAACATTTCT / CTTCGAAGCCACAGACACTT	110	COSF478	GCGGCTTTGGCTGATGTTTT / CTCAGGGCTCTGCAGTCC
17	COSF752	GCAGATCTGGCCCAACGAT / GATCCCGGCTCTTCAAAGGCA	111	COSF487	TGGATGCAGAAACAGAGATCTAGT / CTCAGGGCTCTGCAGTCC
18	COSF757	GCAGCACTCAAGTGTGTGAAAC / CTGAAGTCTTCTTTGTCCCATCTGA	112	COSF1452	TGGACCCAGACATCTCAGTA / GTCCCAAGGTGAGGAGGCA
19	COSF987	GCAGATCTGGCCCAACGAT / CCAAACTCCATTTGTCTGTGTCC	113	COSF1507	GGCTTAAGACATAGAGATGCTTTG / CAAATTCGCTTCTCTAGTAGT
20	COSF1015	AAATCAATTTGGGCAACGAGACC / GATCCACATGAGTTGAATAAACAGAGAGA	114	COSF667	GAGCTACAAGTATCTGAAGAAGCAAT / GGGCTTCCATCATGAGCATCA
21	COSF973	CTTTGGCGGAAGCTGGAGAGATAT / GTTGTGGGAGAAAGGGGAAGT	115	COSF826	AGCCCTCCACAGGCTACTA / GCGTGTGGGCTCAGATGTT
22	COSF780	GGCTCTCGTCTCAGAGTC / GTTGTGGGAGAAAGGGGAAGT	116	COSF679	ACCTTCATGTTCACGTGCTT / CCAATCACTGGATGGAATGCAAT
23	COSF972	GGCTCTCGTCTCAGAGTC / AGGTTTGGGCACTAATCTGGG	117	COSF989	TCATCGGGAAGACCTGGCTTA / GATCCCGGCTCTCAAAGGCA
24	COSF1155	ACCAGCTGTGAGGAACTT / CTCTCTTGAATCTGGTGGT	118	COSF993	CACCATTCTCCACCTGGA / CCAAACTCATTTGTCTGTGTC
25	COSF437	CACAGTCACTGCCCTACCTTCA / CTCAGGGCTCTGCAGCTCC	119	COSF994	CACCATTCTCCACCTGGA / GGAGGATTTCTGTCTCTGTCT
26	COSF1271	GGAGACCTACAACTGAAGTGCAA / CCAATTCGCTTCTCTAGAGT	120	COSF995	TCATCGGGAAGACCTGGCTTA / CTCTGTAAGTTGTGGAGTTGGTA
27	COSF1515	AGGAGAAAGAAACCTTGTCTGTAAT / CCAATTCGCTTCTCTAGAGT	121	COSF217	GATTTGATCGTGGAGGCTAG / AGAAGTGACACAGCAGAACTC
28	COSF1200	CACCATTTGGCTCTGTTGAAAT / TCAGTGGGATGTAAACACCAAGAAAT	122	COSF219	GATCTACAGCCAAGCTCCAA / TCTGAAGTCTCTGACTCACTG
29	COSF1202	CACCATTTGGCTCTGTTGAAAT / TCAGCTTCTCCCACTGATGTGAATTT	123	COSF223	GACCCATGGATGAAGGACCA / TCTGAAGTCTCTGACTCACTG
30	COSF1478	CACCATTTGGCTCTGTTGAAAT / TCAGCCAACTCTTTGTCTGCTTATA	124	COSF224	GATCTACAGCCAAGCTCCAA / CGGTTTCCAGGCAATTCACATATC
31	COSF1399	CGCCCTGACTGTGGAATG / AGGCACCAAGGCTCTCTGTA	125	COSF299	GACCCATGGATGAAGGACCA / AGAAGTGACAGCAGCAAGAACTC
32	COSF1401	CGCCCTGACTGTGGAATG / TCATAAGTATGCTTCCGCTCTT	126	COSF264	GATCTACAGCCAAGCTCCAA / CCGTACCCCATCGGTACCAT
33	COSF1403	CAATCAGATGGGTGGAGTGTGTA / AGGCACCAAGGCTCTCTGTA	127	COSF269	GATCTACAGCCAAGCTCCAA / TCGAGTGGATCACTGCTGTT
34	COSF1405	CAATCAGATGGGTGGAGTGTGTA / TCATAAGTATGCTTCCGCTCTT	128	COSF271	GGAAGAAGCTCTCAATGACAGTAT / TGCAGTTGGATCAGTCTGCTTT
35	COSF1087	TGACGTGTTTGGAGCTGGAG / TTGATCTTGAAGCAGTCCCATGAC	129	COSF273	GACCCATGGATGAAGGACCA / TGCAGTGGATCAGTCTGCTTT
36	COSF1088	TGACGTGTTTGGAGCTGGAG / GGCAACTTATTAATGACGCTCACA	130	COSF281	GGAAGAAGCTCTCAATGACAGTAT / CTCTGCAAGGCTCTCAATCCA
37	COSF1374	CCCTTGACCAAGCTTCAC / GCTCGCCAGGAGCTCATC	131	COSF145	GATCTACAGCCAAGCTCCAA / GGAATCTGAATCGGATGATC
38	COSF1440	ACAGGAGGAGGAGGATGAGATTC / GCCATCAGGAATCTCCCAAT	132	COSF146	GATCTACAGCCAAGCTCCAA / GTTGAGCAGGTTCTGACTGG
39	COSF434	TGCTTCAGAATCTGAGAAAGAAAGAA / CTCAGGCTCTGCAGCTCC	133	COSF149	CTACCCCATGCAGCCAGT / GGAAGTCCCAAGCTGGATCT
40	COSF799	GGAAAGATTTGTGAGAAAGAGATCCAC / GCTGACAGTGAATGGCTGGT	134	COSF150	GACCCATGGATGAAGGACCA / GTTGAGCAGGTTCTGACTGG
41	COSF1416	ACCTTGGCAGGCGTCTTC / TCATAAGTATGCTTCCGCTCTT	135	COSF152	GATCTACAGCCAAGCTCCAA / GGAATGCCAAAGCTGGATCT
42	COSF1417	ACCTTGGCAGGCGTCTTC / AGGCACCAAGGCTCTCTGTA	136	COSF156	GATCTACAGCCAAGCTCCAA / GGAATGCCAAAGCTGGATCT
43	COSF1285	GGTGAATAATGGAGTCTCTGGT / GGCCTTGGAGATCATCAAAGGA	137	COSF163	GATCTACAGCCAAGCTCCAA / GTGATCTCGGCTGTGTA
44	COSF1289	GAGATGCTACTGGTGACCA / GGCCTTGGAGATCATCAAAGGA	138	COSF208	GATCTACAGCCAAGCTCCAA / CCCTCTGTGGTGAAGTACATTG
45	COSF1291	TTGCTGGCAAGAGTGGTGT / GGCCTTGGAGATCATCAAAGGA	139	COSF195	GACCCATGGATGAAGGACCA / GTTCCGCTGCTTCTGTA
46	COSF1293	TGATGGTCTACTGGTGCTG / GGCCTTGGAGATCATCAAAGGA	140	COSF275	GATCTACAGCCAAGCTCCAA / TGTCTGCTGCTCTCTGAA
47	COSF531	GCTGGCCCTGCTGTAAGA / GGCCTTGGAGATCATCAAAGGA	141	COSF1302	GACCCATGGATGAAGGACCA / ATGTTATGCCCAAGCTCTCT
48	COSF533	GTGGTGCAGAGGCTGGTGTG / GGCCTTGGAGATCATCAAAGGA	142	COSF165	GATCTACAGCCAAGCTCCAA / TGACATCACTGTGAGGATTGG
49	COSF535	CTTCAGGGAATGCCCTGGTGAA / GGCCTTGGAGATCATCAAAGGA	143	COSF167	GATCTACAGCCAAGCTCCAA / GTGAACTTCCCTGAGGTAAGTGA
50	COSF539	GGCCTCTGGTCTCCCAAG / GGCCTTGGAGATCATCAAAGGA	144	COSF169	GACCCATGGATGAAGGACCA / TGACATCACTGTGAGGATTGG
51	COSF541	GGCGAACTGGTGTGATGCT / GGCCTTGGAGATCATCAAAGGA	145	COSF171	GACCCATGGATGAAGGACCA / GTGAACCTTCCCTGAGGTAAGTGA
52	COSF543	CCCAAGGATCTCTGGTGAAG / GGCCTTGGAGATCATCAAAGGA	146	COSF173	GATCTACAGCCAAGCTCCAA / CGGGCCCAAGCTGTGATAC
53	COSF545	CTTGGCCCTTGGTAAATGTT / GGCCTTGGAGATCATCAAAGGA	147	COSF174	GATTGATCTGGAGGCTGAG / AGTTATGGCCCAAGCTCTCT
54	COSF547	TTGCTGGCAAGAGTGGTGT / GGCCTTGGAGATCATCAAAGGA	148	COSF175	GATTGATCTGGAGGCTGAG / ACTCTCTCTGCTTGTGGT
55	COSF550	GTGGTCAAGGCTGGTGTGAT / GGCCTTGGAGATCATCAAAGGA	149	COSF176	GACCCATGGATGAAGGACCA / CGGGCCCAAGCTGTGATAC
56	COSF552	GAGCTGTGTGTGCAAGG / GGCCTTGGAGATCATCAAAGGA	150	COSF180	GATCTACAGCCAAGCTCCAA / ATGTTATGCCCAAGCTCTCT
57	COSF556	CTCCAGGTGAAGCAGGCA / GGCCTTGGAGATCATCAAAGGA	151	COSF183	GATTGATCTGGAGGCTGAG / AGTTATGGCCCAAGCTCTCT
58	COSF562	TGGTCCCTTGGTGCTA / GGCCTTGGAGATCATCAAAGGA	152	COSF204	GATTGATCTGGAGGCTGAG / TGACATCAATCTGAGGATTGG
59	COSF564	GGTCTCTGGTCTCTCTCT / GGCCTTGGAGATCATCAAAGGA	153	COSF227	GATCTACAGCCAAGCTCCAA / CGGGCCCAAGCTGTGATAC
60	COSF591	TTTGTCTCCCAAGCTGTCTTA / GGCCTTGGAGATCATCAAAGGA	154	COSF1180	GATTGATCTGGAGGCTGAG / AGAGCTGACTGACTGGACA
61	COSF593	GGTGCAAGGAGATGCT / GGCCTTGGAGATCATCAAAGGA	155	COSF352	GATGCCAAGTGTCTATGAAGA / TTGCTGGCCGCACTAAT
62	COSF595	TGATGGTGTACTGGTGCTG / GGCCTTGGAGATCATCAAAGGA	156	COSF353	GATCTACAGCCAAGCTCCAA / GCACCGCTAAGGGTCCAG
63	COSF596	TGATGGTGTACTGGTGCTG / GGCCTTGGAGATCATCAAAGGA	157	COSF358	GACAACAGTGAATTTATGACAAGAT / GCACCGCTAAGGGTCCAG
64	COSF597	GCCCGGAGGCTCTGAAG / GGCCTTGGAGATCATCAAAGGA	158	COSF359	GACAACAGTGAATTTATGACAAGAT / GCACCGCTAAGGGTCCAG
65	COSF599	CCCTCGATTTGGCTGGAC / GGCCTTGGAGATCATCAAAGGA	159	COSF364	TAAAGTGAACCAAGAGAACTGGGCA / TTGCTGGCCGCAATACT
66	COSF601	CTCTGGTCAAGGCTGAAAGT / GGCCTTGGAGATCATCAAAGGA	160	COSF367	GGAAGAAGCTCCATGAACAGTAT / TGCTGGCCGCACTAAT
67	COSF603	CCCTCTGGAAGAATGGAGATG / GGCCTTGGAGATCATCAAAGGA	161	COSF381	GATGCCAAGTGTCTATGAAGA / GCACCGCTAAGGGTCCAG
68	COSF605	CTCAGGGTCTGAGGATTG / GGCCTTGGAGATCATCAAAGGA	162	COSF283	GATTGATCTGGAGGCTGAG / AGGTTGGCTTCTCTTGGG
69	COSF607	TCGCTCTGCTGGCAAGG / GGCCTTGGAGATCATCAAAGGA	163	COSF349	GATTGATCTGGAGGCTGAG / GTAAGGGTGTGAGATGGGAATAG
70	COSF626	GGCTCTGCTGTCTGACT / GGCCTTGGAGATCATCAAAGGA	164	COSF350	GATCTACAGCCAAGCTCCAA / GTAAGGGTGTGAGATGGGAATAG
71	COSF634	ACGCTCTGGTGAAGTGTGTC / GGCCTTGGAGATCATCAAAGGA	165	COSF1208	GATCTACAGCCAAGCTCCAA / ACCATTTAGGCACTTCTATCAAAAGA
72	COSF638	CCCTCGATTTGGCTGGAC / GGCCTTGGAGATCATCAAAGGA	166	COSF278	GATCTACAGCCAAGCTCCAA / CAGTGAACAAAGAGGGGCTTCT
73	COSF642	GGTGACAAGGCTGAGACAGG / GGCCTTGGAGATCATCAAAGGA	167	COSF279	GATTGATCTGGAGGCTGAG / CCAATGACTTTACCAATCTGCT
74	COSF644	TCTTGCTCTCTCTGGTGAA / GGCCTTGGAGATCATCAAAGGA	168	COSF1421	GATCTACAGCCAAGCTCCAA / AGTTCTCTCAATGATCTGTCTCAAC
75	COSF646	CAAAGATGGACTAACGGTCTC / GGCCTTGGAGATCATCAAAGGA	169	COSF345	GATCTACAGCCAAGCTCCAA / GAGATTTCTCCATCTACCTCTCTCT
76	COSF648	TTGCTGGACAGCGTGGT / GGCCTTGGAGATCATCAAAGGA	170	COSF346	GATCTACAGCCAAGCTCCAA / GGAGTGGCTTCAAGAGGCAAA
77	COSF650	CTGGTTCGGCGAGAGCAT / GGCCTTGGAGATCATCAAAGGA	171	COSF347	GATCTACAGCCAAGCTCCAA / TTGTTCTGATCTGACCTGAGACT
78	COSF652	CTCCAGGTGAAGCAGGCA / GGCCTTGGAGATCATCAAAGGA	172	COSF1342	GATTGATCTGGAGGCTGAG / TGCTCTTGGCCGCAAA
79	COSF654	GGTCTCTGCTGTCTCTCT / GGCCTTGGAGATCATCAAAGGA	173	COSF1343	GATTGATCTGGAGGCTGAG / GGGCTCTGCTGTGTAGGG
80	COSF817	CACCTGCCGTGACCTCAA / GGCCTTGGAGATCATCAAAGGA	174	COSF1267	GCTGCAGGATATGAGGAGAGA / TCAGTGGATTTGTAACACCAAGAAAT
81	COSF819	GGCTCTGCTGCTCCCAAG / GGCCTTGGAGATCATCAAAGGA	175	COSF1189	GGCTGAAGGATGTGCTATCAA / AAACCTTGGTGTGATCTCCATC
82	COSF1397	CGGCTCTGCTCTCTTTAG / TCATAAGTATGCTTCCGCTCTT	176	COSF1191	GGCCGAGTCCGGTAG / CAGTTAGTTAGTGAAGCAGTAAT
83	COSF1414	CGGCTCTGCTCTCTTTAG / AGGCACCAAGAGTCTCTGTA	177	COSF1193	GGCTGAAGGATGTGCTATCAA / AAACCTTGGTGTGATCTCCATC
84	COSF1415	CGGCTCTGCTCTCTTTAG / CACATAGGATGGAGGGAAGTG	178	COSF403	AGGATGAGGTGGAGCAGGA / AAACCTTGGTGTGATCTCCATC
85	COSF1097	AGACATGCTCAGCTTTGGGATAC / TTGATCTTAGCCAGTCCCATGTAC	179	COSF1108	GGCAGCGGCACTCTC / GGCAACCTTATTAATAGACGCTGACA
86	COSF1098	AGACATGCTCAGCTTTGGGATAC / GGCAACCTTATTAATAGACGCTGACA	180	COSF1110	GGCAGCGGCACTCTC / TTGATCTTAGCCATGACCTTAC
87	COSF842	TGTGGACGCAAGCTGA / GTTGCTGTAATATCTGTTCCGAGT	181	COSF1111	TGCTGGTACAGCCACAC / GGCAACCTTATTAATAGACGCTGACA
88	COSF847	CCATGGACCACTGCATTT / GTTGCTGTAATATCTGTTCCGAGT	182	COSF1113	TGCTGGTACAGCCACAC / TTGATCTTAGCCATGACCTTAC
89	COSF848	CTCGCTCAGACCCACAG / GTTGCTGTAATATCTGTTCCGAGT	183	COSF1362	CCCTCACAGAGACCACTT / CTCACCTCCACAGGACACC
90	COSF860	CCAGTGGACCACTGCATTT / ACTGCTGCGGTTGTAAACCA	184	COSF720	GGCAATGTGATGAGGAGCTAG / GATCTGGAGAGGCTGTA
91	COSF861	CTCGCTCAGACCCACAG / ACTCCACCACTCTGGTCTT	185	COSF1346	GGACCTGGACCTGTGCTCTTA / TGCCAGGATCATAGGCTTACAG
92	COSF1102	TCCAGTCTCAGAAATCCAGTA / AAATGAGTTGTCCCAAAAGCCATTG	186	COSF1348	GGACCTGGACCTGTGCTCTTA / TCAATGATCTTCCCACTTCA
93	COSF1104	AGAAGATCGCGCTGCACA / AAATGAGTTGTCCCAAAAGCCATTG	187	COSF1353	GGACCTGGACCTGTGCTCTTA / GTGCTACAGGAGCTGCTCT
94	COSF697	CCTCTGACACTGGGTCTCTGT / CTCTATCCCTGAGAGATCAGCTACAT	188	COSF1434	GGACCTGGACCTGTGCTCTTA / CTGGAGAGGCTCCATATAGGT

Table 2 Continued

#	ID	Forward / Reverse Primer
189	COSF1024	ACAGACTGTGAAGCACGTTCA / CAGACTCTTGTGAGGATGCTCT
190	COSF387	TCAGAGCGGTGCCCTACTTC / GAGCGGTCCGTGCTACT
191	COSF296	CAGCAAAAGCTATATCCCCCTCA / TCTGAAGTCCCTGTACTTCACTCTG
192	COSF912	GGGTGAGAATGTTTACAATTGAGTCTGT / GTGGAGATGCCCTGGAG
193	COSF913	GGGTGAGAATGTTTACAATTGAGTCTGT / GAGCGTCCGTGCTACT
194	COSF942	GCGGTTATGGCAATCAAGACC / AGGAGCAGTGGCCCTGA
195	COSF943	GGTTACAACCGCAGCAGTG / GAGCGTCCGTGCTACT
196	COSF325	GCGGTTATGGCAATCAAGACC / ATGAGGAGCCGTGAGGAGA
197	COSF330	GCGGTTATGGCAATCAAGACC / ATGAGGAGCCGTGAGGAGA
198	COSF331	GCGGTTATGGCAATCAAGACC / ATGAGGAGCCGTGAGGAGA
199	COSF332	GCGGTTATGGCAATCAAGACC / ATGAGGAGCCGTGAGGAGA
200	COSF334	GCGGTTATGGCAATCAAGACC / ATGAGGAGCCGTGAGGAGA
201	COSF335	GCGGTTATGGCAATCAAGACC / ATGAGGAGCCGTGAGGAGA
202	COSF336	GCGGTTATGGCAATCAAGACC / ATGAGGAGCCGTGAGGAGA
203	COSF337	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
204	COSF338	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
205	COSF339	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
206	COSF340	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
207	COSF341	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
208	COSF389	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
209	COSF390	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
210	COSF845	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
211	COSF846	GGTTACAACCGCAGCAGTG / GTGGCGGCAATGCAG
212	COSF852	GGTTACAACCGCAGCAGTG / GTGGCGGCAATGCAG
213	COSF856	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
214	COSF858	GCGGTTATGGCAATCAAGACC / ATGAGGAGCCGTGAGGAGA
215	COSF863	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
216	COSF918	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
217	COSF922	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
218	COSF925	GCGGTTATGGCAATCAAGACC / ATGAGGAGCCGTGAGGAGA
219	COSF927	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
220	COSF930	CAGCAAAAGCTATATCCCCCTCA / GTGGCGGCAATGCAG
221	COSF944	CAGCAAAAGCTATATCCCCCTCA / GGATAGCCCTCAGCGATCAG
222	COSF945	CAGCAAAAGCTATATCCCCCTCA / GGATAGCCCTCAGCGATCAG
223	COSF948	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
224	COSF950	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
225	COSF952	GGTTACAACCGCAGCAGTG / ATGAGGAGCCGTGAGGAGA
226	COSF1018	CTCGCGGGGAGAGCTTTA / TGCAGTTGGATCAGTCTGCTTT
227	COSF291	GGTTACAACCGCAGCAGTG / TGCAGTTGGATCAGTCTGCTTT
228	COSF293	CGAGTTAAGGCCCTTAACCC / TGCAGTTGGATCAGTCTGCTTT
229	COSF294	CAGAGTTACAGTGGTTATAGCCAGT / TGCAGTTGGATCAGTCTGCTTT
230	COSF300	CAGCAAAAGCTATATCCCCCTCA / TGCAGTTGGATCAGTCTGCTTT
231	COSF301	CCCTCGGGACCAAGGATCA / TGCAGTTGGATCAGTCTGCTTT
232	COSF303	GCGGTTATGGCAATCAAGACC / TGCAGTTGGATCAGTCTGCTTT
233	COSF304	GGTTACAACCGCAGCAGTG / TGCAGTTGGATCAGTCTGCTTT
234	COSF867	GGGTGAGAATGTTTACAATTGAGTCTGT / CTCTGCAGGCTCTCATACCA
235	COSF309	GGTTACAACCGCAGCAGTG / GGAAGTGCCTCAAGTGGATCT
236	COSF311	GGTTACAACCGCAGCAGTG / GGAAGTGCCTCAAGTGGATCT
237	COSF314	GGTTACAACCGCAGCAGTG / GGAAGTGCCTCAAGTGGATCT
238	COSF316	GGTTACAACCGCAGCAGTG / GGAAGTGCCTCAAGTGGATCT
239	COSF318	CCCTCGGGACCAAGGATCA / GGAAGTGCCTCAAGTGGATCT
240	COSF319	GGTTACAACCGCAGCAGTG / GTTGAGCAGTCTTGCAGTGG
241	COSF624	CAGCAAAAGCTATATCCCCCTCA / GTTGAGCAGTCTTGCAGTGG
242	COSF295	AGGGAAATCGCAAGCTGAA / TGTCGCTGCCTTTCTGAA
243	COSF1387	GACATCTGTGTGGCAAGT / CCAGGCGCTACAGGGATAG
244	COSF713	AGGAACGTGGCGCTCATC / TTTGACATTTAGTTCATCTAGTGTCTT
245	COSF1442	GTAAGATGATCAGCCGCAACTC / CAGTTAGTTAGTGAGCCAGTAAT
246	COSF1503	GAGGGAGGAATCAGAGAGCTGATG / CCAATTCGCCTTCTCTAGAGT
247	COSF1139	TGGTGTAGTTTGAAGAAGCAGAA / TCAGGCTCAATCTTGTCTTTTATA
248	COSF1188	CCCTTCGTAGACATAGCTGTCTTC / GGAAGGAGGAAGATTTCAATCTCT
249	COSF1211	GCAGGGATCTCTAAGCTAGAA / AGTTGGGCTTTGCAATGTGAT
250	COSF1038	CTAAAGCAGCTCAAAAGAAAGCAGAA / CATCAATGGCTGAGGGAGGAAG
251	COSF1039	CTAAAGCAGCTCAAAAGAAAGCAGAA / CATCAATGGCTGAGGGAGGAAG
252	COSF983	CGGTGAGGCCCTTCTTAAGA / TCAAGTGGCCCTCAGCTCT
253	COSF985	CTAAAGCAGCTCAAAAGAAAGCAGAA / TTTATGTGTCATAGTCAGGAACACAA
254	COSF986	CTAAAGCAGCTCAAAAGAAAGCAGAA / TTTATGTGTCATAGTCAGGAACACAA
255	COSF1020	CTAAAGCAGCTCAAAAGAAAGCAGAA / CCCATGCTTGGAAATATATGAGCAAA
256	COSF1021	CTAAAGCAGCTCAAAAGAAAGCAGAA / CCCATGCTTGGAAATATATGAGCAAA
257	COSF1022	CTAAAGCAGCTCAAAAGAAAGCAGAA / GGCTTCTGCTGCCATTTCC
258	COSF1023	CTAAAGCAGCTCAAAAGAAAGCAGAA / GGCTTCTGCTGCCATTTCC
259	COSF976	CTAAAGCAGCTCAAAAGAAAGCAGAA / CGTGCACAGCAGCATGG
260	COSF962	CTAAAGCAGCTCAAAAGAAAGCAGAA / CCGGTGGCTCGGAGAT
261	COSF969	CTAAAGCAGCTCAAAAGAAAGCAGAA / GGTGCTCAAGCTCATCTCTG
262	COSF795	CTAAAGCAGCTCAAAAGAAAGCAGAA / CATTTGGCCGGTAAGATGGGT
263	COSF955	CTAAAGCAGCTCAAAAGAAAGCAGAA / CATTTGGCCGGTAAGATGGGT
264	COSF981	CTAAAGCAGCTCAAAAGAAAGCAGAA / CAGCTGGAGACACCAAGCTC
265	COSF1026	CTAAAGCAGCTCAAAAGAAAGCAGAA / GCTCCTCGGCCCTTTTAAAGTGA
266	COSF1028	CTAAAGCAGCTCAAAAGAAAGCAGAA / GACGGTTGGATCTGCCATGAT
267	COSF1029	CTAAAGCAGCTCAAAAGAAAGCAGAA / GACGGTTGGATCTGCCATGAT
268	COSF1030	CTAAAGCAGCTCAAAAGAAAGCAGAA / ATAACAATCACATCCACTTCAATGCTG
269	COSF1031	CTAAAGCAGCTCAAAAGAAAGCAGAA / CAACTTCTTGACATTTGCTTGTG
270	COSF1032	CTAAAGCAGCTCAAAAGAAAGCAGAA / CAACTTCTTGACATTTGCTTGTG
271	COSF1033	CTAAAGCAGCTCAAAAGAAAGCAGAA / CAACTTCTTGACATTTGCTTGTG
272	COSF1034	CTAAAGCAGCTCAAAAGAAAGCAGAA / GCTCCTCGGCCCTTTTAAAGTGA
273	COSF1035	CTAAAGCAGCTCAAAAGAAAGCAGAA / GCTCCTCGGCCCTTTTAAAGTGA
274	COSF1036	GTTCGATTCTTACCTCAGCAGCA / GACGGTTGGATCTGCCATGAT
275	COSF1037	TGATCCCATGTGTTTGTATCTCT / GACGGTTGGATCTGCCATGAT
276	COSF691	CAGCTCACTCCGCTCT / TGGCAATCTGCAATCAATTTGGT
277	COSF1121	GAGTCGGGTTCTGTTCTGT / TCTGAATCATGAGCCAGATCTCTGTTA
278	COSF1509	CAGAATAATGTGCTAGTAGAGGAAGT / CCAATTCGCCTTCTCTAGAGT
279	COSF705	GCACGCCCTTGACAGCAATC / ACTCGCATCTGGAATTTCTCATGTG
280	COSF685	TGTCTCCAGTTTGCAGAGAA / GAGTGATCTGTTTGTAGTATTCAGAA
281	COSF991	AACCAGATTACAGGCTCTTTCA / CCATCGGATGAAGTTTCTGATCC
282	COSF1073	AACCAGATTACAGGCTCTTTCA / TGCTCCGAGGAAGTCTCT

#	ID	Forward / Reverse Primer
283	COSF1074	CAGACAAATGGAGTTTGTGATACC / TGCTTCCGGAGGAAGTCTCT
284	COSF1075	AGACAGGAAATCTCTTCTCATCAAA / TGCTTCCGGAGGAAGTCTCT
285	COSF1005	AAGATCTTTGAATTGTTACCAAGTGA / CTCGAAAGCTTCAAAATGGA
286	COSF996	GCAGGTATACAGACTGGAGCTATGTA / TGTGAGTTTCAAGTGGTAAATCTCAACT
287	COSF568	CCACAGCAGTGGAAAGCTTA / AGACATGAAGTAAGATCTGTGCAAA
288	COSF1226	TCATCACCACAGACAGCGATG / GCCCATCAGGAATCTCCCAAT
289	COSF1283	AGCACCGCAGGTGTAGG / AGTGTTTTCATTCGATTCCTGTTCT
290	COSF1284	AGCACCGCAGGTGTAGG / CAGGTAGTGTAGTACGAGGTAAT
291	COSF1474	GTCCCAAGTAAGATCCAGCTT / AAACCTGTGGTTGATCTCCATC
292	COSF481	AGCACCGCAGGTGTAGG / AAACCTGTGGTTGATCTCCATC
293	COSF483	TCATCACCACAGACAGCGATG / AAACCTGTGGTTGATCTCCATC
294	COSF485	AGCACCGCAGGTGTAGG / GCCCATCAGGAATCTCCCAAT
295	COSF509	GCCTCATTTGCTGCCAGA / CAGCTTATGATGAGCCAGTAAT
296	COSF511	CAGAGGACGAGTATGGG / AAACCTGTGGTTGATCTCCATC
297	COSF1058	ATCGCAAAAGCTATCAGCAA / CTCAGGGCTTCGAGCTCC
298	COSF1060	GAGCAGCTGAGATGATGCA / CTCAGGGCTTCGAGCTCC
299	COSF1257	AAAGAAAAGACAGTTGGAGGAATCTG / CTCAGGGCTTCGAGCTCC
300	COSF1381	GAGCAGCTGAGATGATGCA / CTCAGGGCTTCGAGCTCC
301	COSF1230	GAAGAAAATGAAAGGAGTATGACAGT / CCAATTCGCCTTCTCTAGAGT
302	COSF1232	GAGCAGCTGAGATGATGCA / CCAATTCGCCTTCTCTAGAGT
303	COSF1234	GCCTGTCTCAGAGCAAAA / CCAATTCGCCTTCTCTAGAGT
304	COSF1236	ATCGCAAAAGCTATCAGCAA / CTCAGGGCTTCGAGCTCC
305	COSF1253	AGTGCCAAAAGAACTTCAGACTTTACA / CCAATTCGCCTTCTCTAGAGT
306	COSF1255	GAGCAGCTGAGATGATGCA / CCGGAAGAGGAGTACTGAC
307	COSF1262	ATCGCAAAAGCTATCAGCAA / ACAGCGGCTGCGATCACC
308	COSF1276	CAAGCAGAAAACATGTCAAAAGAGAT / CTCAGGGCTTCGAGCTCC
309	COSF1116	ACAGCTCTGGGTGTGGGA / CTTCGATCTGTCGGCAAG
310	COSF1117	CCCCAACTCACCCTG / CTTCGATCTGTCGGCAAG
311	COSF1513	TGAAGAGGTAGAAAGCCATGC / CCAATTCGCCTTCTCTAGAGT
312	COSF1091	CTGCACTTGAAGAACCATATACAC / TTGATCTAGCCAGTCCCATGAC
313	COSF1092	CTGCACTTGAAGAACCATATACAC / GGCAACCTTATTAATGACCGTCAACA
314	COSF964	CTCCGAGGGCAGCCATT / CAGACTTCTGTGAGGATGCTCT
315	COSF966	CATTCCGGCCAGAGGATGA / CAGACTTCTGTGAGGATGCTCT
316	COSF1269	TCACATCTCAGGTGCTGGATTT / TCAGCAACATCTTGTCTTGTGTTATA
317	COSF673	GCTTGCAGAAATCATGATGGA / CTTCGACATCTCCGAATCA
318	COSF1464	ACCAATCAGCTTATCAAAAACAGAGA / GCTTGGCAGAGATGAC
319	COSF1465	ACCAATCAGCTTATCAAAAACAGAGA / GCTTGGCAGAGATGAC
320	COSF1450	GAAGGCTGCTTCTTACTTCT / GTCCCAAAGTGAAGGAGCA
321	COSF1444	CACCGAGATCTTGTGACATGTG / GCCCATCAGGAATCTCCCAAT
322	COSF421	TTGGAAATGGCAGAGCTGACA / CTCAGGGCTTCGAGCTCC
323	COSF784	CTTGAGAAGGAAAAGCGAATAAAGGAA / TCCCAATGTATCTCTAGGTACT
324	COSF786	CTTGAGAAGGAAAAGCGAATAAAGGAA / CATTGGCCGTAAGATGGGT
325	COSF876	GAATCTGATGAATCTGGAATTTGTTCT / TCCCAATGTATCTCTAGGTACT
326	COSF877	GAATCTGATGAATCTGGAATTTGTTCT / CATTGGCCGTAAGATGGGT
327	COSF878	AGAAAGATGAAGACAATGTTCTCAAGCA / TCGCACTGCATGGGATG
328	COSF879	AGAAAGATGAAGACAATGTTCTCAAGCA / TGTATGGAAGAGATGGGTCTCT
329	COSF880	AGAAAGATGAAGACAATGTTCTCAAGCA / TCCCAATGTATCTCTAGGTACT
330	COSF883	AGAAAGATGAAGACAATGTTCTCAAGCA / GCTGAGGAAGAGATCTTGT
331	COSF884	AGAAAGATGAAGACAATGTTCTCAAGCA / CATTGGCCGTAAGATGGGT
332	COSF891	CTTGAGAAGGAAAAGCGAATAAAGGAA / TCGCACTGCATGGGATG
333	COSF1448	CATCCGCTCGTCCACCAGC / GTGGTGTCCCCAGTGTCAT
334	COSF1340	CAGCAAAATTTGGGCCCTTC / CCAATTCGCCTTCTCTAGAGT
335	COSF1491	CAAGCTCTTACATACCCAGCA / CCAATTCGCCTTCTCTAGAGT
336	COSF1498	CAAGCTCTTACATACCCAGCA / CCAATTCGCCTTCTCTAGAGT
337	COSF1500	CAAGCTCTTACATACCCAGCA / CCGGAAGAGGATGAGTACAG
338	COSF1133	AGGGACATGTTCTGGGAGAT / GTGAGGACACATCAAAACAGCA
339	COSF1135	AGGGACATGTTCTGGGAGAT / GTGAGGACACATCAAAACAGCA
340	COSF693	GTCACAATGATGGGTGATCAAGGA / TGTGACCGTGTGAGCAGA
341	COSF1182	TGCGTCCAGAACTCATCT / CAGGTGGGCTCATGATCAAGA
342	COSF669	GGACAGCAGCAAAATGGCAAT / CTGTGCTACCATAGTTGGTGTCT
343	COSF670	GGACAGCAGCAAAATGGCAAT / CTGTGCTACCATAGTTGGTGTCT
344	COSF865	GCGCCGTGAAGAAGAGATG / GCTGACAGTATGGCTGGT
345	COSF1178	TGACCTGCGCATGTTCT / CGATGCCAAGCAGGATGGT
346	COSF198	GGGCTTTGAATAACACCCAGC / CTCAGGGCTTCGAGCTCC
347	COSF200	GGGCTTTGAATAACACCCAGC / CTCAGGGCTTCGAGCTCC
348	COSF726	CCCTGCATAAAGTCCCTGTA / GACAAGGATGTGACTTCGTGCTC
349	COSF1332	CTCCATCATGGCTGCTTCT / GGGCGTTTCACTCTCAATCAG
350	COSF1336	GCCATGTCCCTGCATTTCT / TTGCAAGAGCAGAAAGTTCATCAG
351	COSF825	GTCATGTGAGAACCCCGAGTACT / CCAATGGATGAAGTTTCTGATCC
352	COSF1412	AGGATTTACAATTCATCAACCTCTGA / AGGCAACAGAGGCTCTGTA
353	COSF247	TTTTCAGCTATACAGACAGCTTGT / GAGCATCAACCAAGAACTTTTCC
354	COSF1042	TTTTCAGCTATACAGACAGCTTGT / GTCTCATATAAGCTGGCAACT
355	COSF289	CGACCTTGCCCAAGTACCA / GGAATCTGATCGCTCTGTCT
356	COSF1040	TTTTCAGCTATACAGACAGCTTGT / TGGCTCTGTCTCGGA
357	COSF1071	CGGCTCGTCTACTCCAT / GATCCCGGTTCTCAAGGCA
358	COSF287	AGCTTCTCCAGTACTCTGACA / GAGCATCAACCAAGAACTTTTCC
359	COSF1215	GCAACTCTCGACTCACA / AGTGGTCTTCCATTCAGGAGAGAT
360	COSF1217	TCCGTGTACGGGAGTTC / AGTGGTCTTCCATTCAGGAGAGAT
361	COSF1219	GGCAGCTATGCTCTCTCTG / ATGGTCTTCCATTCAGGAGAGAT
362	COSF1223	CATTGAGCGGACAGCTACT / AGTGGTCTTCCATTCAGGAGAGAT
363	COSF1481	CAGCTGGACCGGCAAAATTAAG / CCAATTCGCCTTCTCTAGAGT
364	COSF1001	CTGGCATCTAAAGATAAACTCCCAAGT / CTCTGTAATGTGGTGAAGTTGGTA
365	COSF1003	TGTTCAAGCAAAAGTATACAGCAAGG / CCAAACTCCATTTGCTTGTGCT
366	COSF1007	CATCAAACTCAGAACTACTCTAGTGA / GTAATGATGTGATTCGAGTTAATCT
367	COSF1009	TGGTGGAAAGTCTGATACATGAAT / GTAATGATGTGATTCGAGTTAATCT
368	COSF998	TGGTGGAAAGTCTGATACATGAAT / CTGAAGTCTTCTTGTCCACTGA
369	COSF1081	CGTCCAGCCGAAATATGAGAAAA / GGGAGTCCGACGCTCT
370	COSF1083	GAACTGTTTCTTGTGAGGCTCTATA / GGGAGTCCGACGCTCT
371	COSF689	CCGCAAGACCTGGGTCTC / TTGGCAAGGCTGCTTACT
372	COSF699	CCACGGCGTGTGGAT / TTGGCAAGGCTGCTTACT
373	COSF1461	GATCTTCGACAGTGCCTGAACA / CTCAGGGCTTCGAGCTCC
374	COSF805	CTCAATCTGCCCTTCCAAT / GCTCTGCTGAGGTGGTA
375	COSF807	TGGTGGCTACTTCTCTGACA / GCTCTGCTGAGGTGGTA
376	COSF809	CTCAATCTGCCCTTCCAAT / CTGAGCATTTCAATGTAAGTGGAC

Table 2 Continued

#	ID	Forward / Reverse Primer	#	ID	Forward / Reverse Primer
377	COSF811	CGGAGTTGCAATAGGGAAGTTCAG / GCTGACAGTGATGGCTGGT	471	COSF1160	GGTCTGACGAGGCTTC / CACTTTGAGAGGTTTCAGCATTGAG
378	COSF1511	GCAGCCACTGTCAAAGCAAGA / CATTCTTCAGGCTCTCTAGAGT	472	COSF439	CAGAGACCCGTGCTGAGTT / CTCAGGGCTCTGCAGCTCC
379	COSF1311	CTTTTGTGGCGCTCTTGCTC / TGGGCTTACATGACAAACATCCATT	473	COSF1329	CAGAGACCCGTGCTGAGTT / CGAGACCCCAAGAGGTGTTTC
380	COSF1313	GCTCCAGGACCTCCACTA / TGGGCTTACATGACAAACATCCATT	474	COSF1273	CAGAGACCCGTGCTGAGTT / TCAGCCAACTCTTTGCTCTGTTATA
381	COSF1446	ACACCTCATGAGTACCCCTACAC / GTGGGCTGGCAGAGTCAT	475	COSF441	CTGACAACTGAAAGAGGCTGAGA / CTCAGGGCTCTGCAGCTCC
382	COSF978	GAACAAAGTCTTGCAAGAGAGG / CTTTGTAGCTGCTTAGAGGGACT	476	COSF1324	TGTTAAGTATCGAGAAAAACGCTTGA / AGTATGTGGGTCTTCGATGATG
383	COSF980	GAACAAAGTCTTGCAAGAGAGG / CATTCTTCAGGCTCTCTAGAGT	477	COSF1326	CACCTCAGTAATATGGAAGTCCAAGTT / CGAGACCCCAAGAGGTGTTTC
384	COSF675	AGAGGTGCAGATCCACACCTAAT / TGGTGTGACGCTGATGAGGAC	478	COSF1521	CAACACAGATCAGCTAGCTCAA / CCAATTCGCTCTCTCTAGAGT
385	COSF827	AGAGGTGCAGATCCACACCTAAT / TGTGGAGGGACACCGCTAA	479	COSF1522	TGGGTTTACCAAAACCTAGAATGC / CCAATTCGCTCTCTCTAGAGT
386	COSF415	CATCGTTGGCCACAGAGAATTA / CTCAGGGCTCTGCAGCTCC	480	COSF1519	CGCTCAGTAGAAGAGAGA / CCAATTCGCTCTCTCTAGAGT
387	COSF707	CGCCCTATGAGGCTACCC / CACAGTGGCCTTCATTAG	481	COSF1525	GGAAAGCCAGAAGTTGAATATGATTG / CCAATTCGCTCTCTCTAGAGT
388	COSF1505	CGGTGAGTCTCTCTCTCC / TTTCTGCCAGCTATTTGGTCAT	482	COSF1298	CAGGTCTGTCTGCCAGTAATAGT / CTCTTGCTCAGCCACCA
389	COSF1494	CGGTGAGTCTCTCTCTCC / GGAGCTTGATAACCACTGGCA	483	COSF1057	CTGTGAAAGCTGCTCTGATGA / CTCAGGGCTCTGCAGCTCC
390	COSF1496	CGGTGAGTCTCTCTCTCC / ATTTTCTACTCTTGAGGAGCCAGTT	484	COSF1147	CCGCTGATGAAAGAAACAGATG / CTGTACGTGATAAGAGCGCTGAG
391	COSF1527	CGGTGAGTCTCTCTCTCC / GTAGTTGGTATCGAAGCAAGAA	485	COSF1149	GTGAGGAGGTATGACAGCAACA / CTGTACGTGATAAGAGCGCTGAG
392	COSF665	GCAAGCCAGAAGATTATGAACAC / GTGTCTGTGATTCTCCAAATTTCTGTT	486	COSF1151	AGGTACGGATCGCCTACA / CTGTACGTGATAAGAGCGCTGAG
393	COSF1483	GCATGGCTCAATTTACTTCAATCAGA / AAACCTGTGGTGTGATCTCCATC	487	COSF1153	GTGAGGGATGACAGCAACA / GGGCATCTTGAGGGCTT
394	COSF1265	CGGCAGGAATCTGATGACTTT / TCAGCTTTCTCCACTGTATGAAITTT	488	COSF1247	GGACTCTACATTTATCATGCAATGTTA / GGTGTGGTGAAGGCGAGAG
395	COSF1278	GGTGTCAATGTCAGCACTGT / TCAGCTTTCTCCACTGTATGAAITTT	489	COSF1249	GGACTCTACATTTATCATGCAATGTTA / GGTGTGGTGAAGGCGAGAG
396	COSF1280	GGTGTCAATGTCAGCACTGT / TCAGTGGGATGTAAACACCAAGAA	490	COSF1423	CAGAAGCAGGTGCAGATCA / ACAGTGGGCTCTAGATCAAGA
397	COSF1204	ATGCACTTGTGCAAGGGTTCA / GTGGCACTCTGGAAGCACT	491	COSF1469	CTGCTGCCATCTCCGA / CCACAAGTACTTCTCCACAGGAA
398	COSF1206	ATGCACTTGTGCAAGGGTTCA / CGCGCCACGATCACTGA	492	HMB5	CCAGCTCCCTGCGAAGAG / AGGATGAGGCACTGAACTCC
399	COSF1069	GCTCCACATCATCTTCAGCTT / CCAAACTCCTATTTGCTGTTGCC	493	TBP	GACTCCCATGACCCCATC / ACAGAAGTCAATGGCTTTAGGT
400	COSF459	GCTCCACATCATCTTCAGCTT / CTCAGGGCTCTGCAGCTCC	494	ITGB7	CTATCTTGAGATGGCTGGTGCAAG / CGTGGCTGCTGCTCCCTTTCTTG
401	COSF460	CAAATGCTGCTGGTCACTT / CTCAGGGCTCTGCAGCTCC	495	MYC	CTGTGCTGCTTACGAGGAGA / GTGATCCAGCTCTGCACTTTTGCCA
402	COSF801	TCAACGTGAGTGAAGAAACAATGA / CTGAGCAATTCATCTGTAATGGAC	496	LMNA	CTGAGAAGCGCTGACAGCATGAA / ACTACGCTCTTCCCATGTCAA
403	COSF802	TCAACGTGAGTGAAGAAACAATGA / CTGAGCAATTCATCTGTAATGGAC	497	ALK	AGTGAAACCCGCACTGT / GCTGGAGGACTGTCCCAITC
404	COSF803	TGGTGTGGTCAATAGGTATGAA / CTGAGCAATTCATCTGTAATGGAC	498	ALK	AAACTGCTCTTGACCTGTC / ACTTAAGTGGCAGCATGGA
405	COSF914	GTGGTGGTGGCAIAGGTATGAA / GCTGACGTGATGGCTGGT	499	RET	CTGCCAGTACTACTCTCCCT / CACGAGGAATGACAGCTGTGA
406	COSF671	CATTAATGTCACACACCGCTTGAA / GGAAGATATCTTGCAAGCTTCTTGAA	500	RET	GGACAAAAGGCGGCTGTTG / CTGAGAGGCGCTGCTCATATAAT
407	COSF1196	CGTGTGCTCTGGATATCTTAGTA / TCAGCTTTCTCCACTGTATGAAITTT	501	ROS1	ACTGCTCAAACTGAGGAAATTA / GGTGACGGAAGTGTGCTCTATAAATG
408	COSF1198	CGTGTGCTCTGGATATCTTAGTA / TCAGTGGGATGTAAACACAGAAAT	502	ROS1	ATGAACCCCAATACATTAATCTGGA / TCTACACAGGCTCTACAAAGTCAA
409	COSF1259	GGCTCTCAAGTATGTATAACATAAC / TCAGCTTTCTCCACTGTATGAAITTT	503	NRK1	CTTGGGACACCATGAGCTT / CTCTACAGTGGTGAAGTTTCTCA
410	COSF1261	GGCTCTGAGACCTTTGATAACATAAC / TCAGTGGGATGTAAACACAGAAAT	504	NRK1	TGCTCTGGGAGATCTTCACTTA / CATGATGGCTGAGACCTCTGG
411	COSF871	CTGGCTCGGGTGACAGC / AAACCTGTGGTGTGATCTCCATC	505	CXorf67	CCACTCAGTCAGACATGAGAA / GGAGATGCTTGGCTGGAGAC
412	COSF872	CTGGCTCGGGTGACAGC / TCGGAAGGCTGTGGAAATG	506	DUX4	GCAACCTCTCTCAGAAACGGA / CGCGGTGTGGAGTCTCT
413	COSF1115	CTGGCTCGGGTGACAGC / ATCATTAGAGGTCCAACAGATCATGTG	507	FAM22B_NUTM2B	CTTCTCCCAAGCTCTGACA / TGCTCGTGTGCTGCCATT
414	COSF1131	CTGCAGATCTGCCCTACA / ATCATTAGAGGTCCAACAGATCATGTG	508	SEPT8	TTGATCCGGGTGAACATGGA / CTGCGCTGATGATCTTGT
415	COSF1137	CTGGCTCGGGTGACAGC / CTGAGGCACTCAAAACAGA	509	ACLY	GCTTGTGGCTGGATGAGA / ATCTCAGGATGGGTGAAGTACAAGT
416	COSF1119	CTGGCTCGGGTGACAGC / CTGATTCTGGAACATGGACTGTGG	510	ACSL3	CTTGGGAAGTGAAGGACAGCTT / CTTTAAAGTCTTTCTTGAGCTAGTT
417	COSF1157	CTGGCTCGGGTGACAGC / GCTGACGGGACATAGGTT	511	ACTB	CCAGGTCTACCATCTGGCAAT / CTGACAGGCTTCTGCGGATGT
418	COSF1052	CTTCTCGGCTCATGGAGGAT / CTCAGGGCTCTGCAGCTCC	512	AFB4	TTCCAGTGACAGTGAAGGCA / GGGATGTTACTGCTCCAGTGAAG
419	COSF660	CAAGACAGGATTAACCAAGCA / GCCTGTGGGCTCAGATGTT	513	AGRAP	GGCTGCATTTGATCTCAGGCT / GTGCAGCATGTCAGGAAGAT
420	COSF661	CTCTCTCAAGTATAGCCATAAATCT / ACTTCAAGCTCTTCTATTTCCATAAT	514	AKAP9	CGAGAGGCTGAAGTATACAACTGA / CTGGTAAATGAGAGCTTTTGAAAC
421	COSF1123	GGCAGACATGCGGAAGCTA / CTCTGACACTCCCTTGAATCAT	515	ALDH2	CGGAGACTTCTCAAGCTACACA / GTGCTGCTCAGTCACTTCACTA
422	COSF499	GATATAGACCAACACAGCTGGA / CTCTGACACTCCCTTGAATCAT	516	ALK	CTTGGAAGAGTACGATGCT / CACTCATGCGCTCTCTGTT
423	COSF505	ACCTCCACCAACAGGATATCCA / CTCTGACACTCCCTTGAATCAT	517	ARFIP1	GCATTCATTACCACTGAGCTTGT / GCAACCTCTGATGAGAGACA
424	COSF1513	GATATAGACCAACACAGCTGGA / CTCTGACACTCCCTTGAATCAT	518	ARID1A	CTTTGCACTGCTGATTCCAA / ATCTTGAGAGTGGTGGCTTGA
425	COSF514	GATATAGACCAACACAGCTGGA / CTCTGACACTCCCTTGAATCAT	519	ASIC2	GGTGAAGATCCCAAGCAAGA / ACTTCAAGCGCTCTTCTGTCTAAT
426	COSF527	ACCTCCACCAACAGGATATCCA / GGTCAATATCAAAATCATCCCTGGAA	520	ASPSR1	CGGAGCTGCTGATGAGTTC / CGCCTCAAGCTTCTCTTTAT
427	COSF502	GATATAGACCAACACAGCTGGA / CCCATCATTTTGTGGCCAGAT	521	ATG4C	GTGATTCCTCTTGGCTCTTT / CTGTAAATCAGGATGCTTGTCT
428	COSF507	GATATAGACCAACACAGCTGGA / GATTTCTCTCGAGGATTCATCTTTCC	522	ATIC	TGACGTGAAGTGAAGGCAAGT / TGGTATCATCAAAAGCATGGCAAT
429	COSF525	GATATAGACCAACACAGCTGGA / CAGGGCTGCTGATCTTCTATAAA	523	ATP8B2	GACAGGCTGGCTGAGTCAAT / GTCTCCGGTATGATACCCAAA
430	COSF1045	TCCGAGTCCAGTGTAGGAA / CTGAAGTTCTCTTTTGCTCCACTGA	524	BAIAP2L1	GCTTTGACAGGAGGATGACA / CGGTCACTGCTTCTGTCTCAT
431	COSF1047	ACACTCAAGTGACGAAAGAGCT / CTGAAGTTCTCTTTTGCTCCACTGA	525	BBS9	CCCAACTTCCCAACTCTCT / AGATTGAAGCTTTGAGCTTGA
432	COSF1048	GGGAACACCAGGATTTCTACA / CTGAAGTTCTCTTTTGCTCCACTGA	526	BCOR	CCCCTGTATGGGAAGCTTCA / AGTGTGGTTCAGAGGATCTC
433	COSF722	GGTCCAGGCTCACTA / CCCATCTCAGGATTTGTT	527	BCR	CGAGATCTGGCCCAACGAT / GAGGGGAGTCAATGATGG
434	COSF1430	AGGAAGAGGCCAATACCAAGT / CTCAGGGCTCTGCAGCTCC	528	BRD3	CTTTGGGGAGCTGGAAGATAT / CAITCTCGAGAGCTTTTTC
435	COSF701	AGAGCTGAGGAGGAAGATCA / CGTTAATGATGCCAAGAAAGAAAG	529	BRD4	CCCCAGATGTCAAGTTGCA / GATGATGGGTGAGTGATCTCT
436	COSF657	CGAGTCAAAATATGATCAGAGCAT / TGCTGCGCGCAATACT	530	C15orf55	TGAGGCTGAGGAGATGAGAT / AGGCTGCTTCTCTCGGAATG
437	COSF1085	CCATGTGAGGACGAAGTGT / TTGATCTTAGCAGATCCCATGAC	531	CANT1	GGGTGATGTGGTGAAGCAGA / AGGCAGGTGAGGTGATGAGTA
438	COSF754	TGACAGTCGATAGGAGCCCAT / TGCTGCGCGCAATACT	532	CARS	ATTCACAGCATGGCAGAT / TCTGCTGGGACAGTGA
439	COSF1489	CACAGGCTCATGCAACAAC / GTTGTCCAGCGCATCAG	533	CNNB1IP1	GTTCAGTCTGGACCTCTTGG / TCGAATATCAAAAGCAGATGTTCA
440	COSF718	TCTCAGTGGAGGTGAATGGCTA / GTCTTAGGTCTCATTTGCTCCAAA	534	CDH11	GCTGGCTCAACATCACTGT / CTGATCACTCTCAGAGTGAACCTT
441	COSF782	GCTCACCATCGGGTCCA / TCAAGAATCATCAGGACGCTC	535	CHCHD7	TGACGTGTTGGAGATGAGT / CATTTCAATCTCTTTCTCCGGATT
442	COSF797	CCAGTTACAATGATGAATGCTCAGTCA / TCAAGAATCATCAGGACGCTC	536	CIC	GACATCTTCACTTTGAGCTGAC / GGAATGAGGCTGAGCTCTGAAAGA
443	COSF798	CTCAAGGTGACAGACCATCT / TCAAGAATCATCAGGACGCTC	537	CLCN6	CGAGTCCCAATGAGATCACTA / CCACTCTGTCTCCCAITCC
444	COSF839	GTGGTTGGCTCTCTGCT / AGACAAACAGTCCCTCACT	538	CLTC	GAGCGAGCTCACTGGGAAT / TGCCCAAGATGAGCTTGTCT
445	COSF424	GTAGTAATGTTTATGGATAGTTGGAA / CTCAGGGCTCTGCAGCTCC	539	CNBP	CATGCAGATGAGCAAGATGAT / GCCACAGCGGTAAACAGTTG
446	COSF426	AAAATGTTATGTCAGGCTTTGGCTTAA / CTCAGGGCTCTGCAGCTCC	540	COL1A1	CTGGTTCCGGGAGAGCAAT / ACCTGTTCTTTCAGTGTTA
447	COSF428	CTCTCTCAGCAGCTCAC / CTCAGGGCTCTGCAGCTCC	541	COL1A2	GCAACAGCAGGTTCACTTACAT / GTGCAACACACCGATGTC
448	COSF1187	CGGCTAGGTGACAGCA / TGCTGCGCCGCAATCT	542	C0X6C	GCTCCCAAGTTTGGCA / TCTGCGTATGCTCTTCTTTTGA
449	COSF1328	AAAATGTTATGTCAGGCTTTGGCTTAA / CGAGACCCCAAGAGGTGTTTC	543	CREB1	ATCCTCCCAAGCACTTCTTA / TCAAGCACTGCCACTCTGTT
450	COSF1410	AGGTTGGGCTGGTGTGTC / AGGCACCAAGAGTCTCTGTA	544	CREB3L1	CGACTCTCCCACTCCAAGGA / GCGGATCCGGGTATGTA
451	COSF1411	AGGTTGGGCTGGTGTGTC / CACATAGGAGTGGAGGGAAGTG	545	CREB3L2	TGTGCTTGGCGTGTGAT / GTTCTCGTATGATCAGCAGGTTTC
452	COSF116	GTACCTTGATCAACCCCTCTAA / CGTAGGCACACTCAAAACAGA	546	CRTC1	CACAGTGGCATCCCAACA / GGTGATCTTGATGTTGCTCA
453	COSF123	TGAGGCGCGAGCTAAGCA / GTGAGTCAATTTGCTTGTGTTTGGT	547	CRTC3	GGCTCATCTTTGACCACTTCT / GGAATACGGGCTTGGTCTCA
454	COSF125	TGAGGCGCGAGCTAAGCA / CGTAGGCACACTCAAAACAGA	548	CTNNB1	GTGTACCGCTGGGACCTT / GGTGTGGAGAGTGTGATGGCAT
455	COSF127	CAGGTCAATGTGAACATTCAGACACT / GTGAGTCAATTTGCTTGTGTTTGGT	549	CYP39A1	TGCTGAGGATGACTGGAGAA / CATCAACAGTCCCAAGGAAGT
456	COSF128	CAGGTCAATGTGAACATTCAGACACT / CGTAGGCACACTCAAAACAGA	550	DAZL	CGGTGGTATCTGTCTGTTAATCA / GTAACATAGTAAGCAGGAGGATCAAA
457	COSF129	CAGGTCAATGTGAACATTCAGACACT / GGGCTGCCACCATCTTC	551	DDX5	TTCTGCTCAATGTGAGTCA / AAGTAGACTTCAAGCGACATCT
458	COSF130	GCTTCTGACGAGGCTTC / CGTAGGCACACTCAAAACAGA	552	EBF1	TCAACGAACCCACCATGAT / GGTGTGTTGTTGGCATCCCAAT
459	COSF135	GGTCTTACGCGAGGCTTC / GTGATCAATTTGCTTGTGTTTGGT	553	EHF	TTCTTCCAAGTGTTCGACATA / GGAACAGGTCACTAGTCACT
460	COSF17	CTGTGCATCACCCTGACCTT / GGGCTGCCACCATCTTC	554	EHF3E	CCAGTACGAATGTGGGAATTCTCA / CCATGGCTGCATCCCAATCT
461	COSF18	CTGTGCATCACCCTGACCTT / CGTAGGCACACTCAAAACAGA	555	EHF3K	AGTCATGGGATGTTGAGCA / CCAGGTGGCTTCCAGATGAT
462	COSF24	TGAGGCGCGAGCTAAGCA / GACAGTCTGAATCATGCTTCACT	556	ELK4	CATCTCTCCCTACAGTCTTCTTACA / TGTAGCACTTCTGAGTCTGG
463	COSF26	TGAGGCGCGAGCTAAGCA / GGGCTGCCACCATCTTC	557	EML4	TGCCACACATCCCTTCAAGGAT / CCACTGTGCCACTTGGATGA
464	COSF36	TGAGGCGCGAGCTAAGCA / TCTGGAAGGCCATATCTTTTACC	558	EPC1	GCCAAAGCAGCTCATACACA / GGGGCTCAATCATCTCTCTAAA
465	COSF376	CAGGTCAATGTGAACATTCAGACACT / GACAGTCTGAATCATGCTTTCAGT	559	ERC1	GCTCAATGGGAGGAGTGAA / CTGTTTACTTACTGAGAACTGGTITTC
466	COSF115	CAGGTCAATGTGAACATTCAGACACT / TCAGCTGTGATGCTGTGTAACAACT	560	EROL1	CAGGTGATGGTACTTGGATGATTG / GAAAGGACCCGAGGCTTGA
467	COSF134	CAGGTCAATGTGAACATTCAGACACT / CTGATTTCTGAACATGGAGCTGTGG	561	ESRP1	AGGCCAGGACTCTACCCAAA / AGACAACCTTCCCTGAAITTTGCT
468	COSF14	TGAGGCGCGAGCTAAGCA / TCAGCTGTGATGCTGTGACAACT	562	ETV1	GAGGGAAGTTTGTGACGCTT / GCTGGTCAATAAATCCATCATGCT
469	COSF33	TGAGGCGCGAGCTAAGCA / CTGATTTCTGAACATGGAGCTGTGG	563	ETV4	ATGGCGAGCAGTGCCTTAA / GGAGGTGCCAGAGGATCTCA
470	COSF1159	TGAGGCGCGAGCTAAGCA / CACTTTGAGAGGTTTTCAGATTGAG	564	EWSR1	GCCTCTATGACAGCTCAGTC / GTTGAACCCCTGTGCTAGAT

Table 2 Continued

#	ID	Forward / Reverse Primer
565	EZR	CTGAGACTGCCGTGCTCT / CCATGGTCCCTGGTAAGTTT
566	FAM131B	GCTGCAACTAGATGACAACTC / GGGACTGATCGCTGGCTTC
567	FAM22A	CATTCATCCCCAATTCCTGGAAGA / ATGCTGTTTCTCTTCAAGGGTAG
568	FBXL18	GTCCACAGCAGATCTGATT / CTTCACAGCTGCTCATCT
569	FBXO38	GGTCCCTACCCCTATCACATCT / CGATGGCTTCAAGGGAAGAA
570	FCHSD1	TCTCGGACAGCTCCAGAAA / TGGCAGTTCTCTCGGTAGTAAT
571	FERM12	TGCTCCGATTCAGATTATACAGCTTT / GCAGGGCTGCAAACTCATC
572	FGFR3	GACGGCACCCTACGTT / TCGGCCACGCTATGAAAT
573	FHDC1	AGGCAGAACTGCACCTGCT / TGGAGCTCTGTTCAGCAT
574	FHIT	TCAGATTGGCCAACTCTCATCA / CAGGACGACAGGTCTAGGAA
575	FN1	GGATGACAAGGAAGTGTCCCT / GTGATGCGGTACCAATAATGTT
576	GABBR2	CATGGCCAGTGTCTTCTCTTC / ACAAGGATCATCAAGGCCAAA
577	GEMIN2	CGAAGCAGCTCAATGTCCAGAT / CCATCTGTGCTGTGCCATT
578	GLI1	CTCTGAGACGCGATGTTCACT / GAGGTAGCTTGGTGGCAGA
579	GMD5	GAGCGGAGGACTTCGTT / GTGAACCTTCCGGTCTCTTTAC
580	GNAI1	ACTGCAGAACTTCTGGAGTT / CGGAGTGAATTTGGTTAGCTATTCT
581	HAS2	CGCAATGGTCTGTCCAACAAA / ATGAGGCTGGGTCAAGCATAG
582	HN1	TGGTGGATCCAATTTTCATAGGTTT / CCTGCCACCACTAGACTTG
583	HNRNP2B1	CATACCATCAATGGTCAATATGACAGAA / TCTGGTCTGGTCTGAAA
584	HOOK3	GAATATGCTCAAGATGCCATGAAT / CCTTCTCTCTGCTGGACTGTTA
585	IL6R	GCCCTCATGCAATGTGT / AACTTCTGGGACTCTGGGAATA
586	INTS4	GAGCATGTGACGATCTCTCA / GGTGTGGGAGAGATAAATCTGAT
587	ITPR2	AGAAGGCAATTTCTCTGGCATT / CTATTTCTTCTGAGCAGCTCTATTC
588	JAK2	GATAACCTCTAAGTCTGAGTTCTC / GGCTCTGAAAGAGGCTGAAAT
589	JAZF1	GAAGCATCTCTCAGTCTCAT / TGGCGACAGGAATCTGTGT
590	KLC1	TCACGTGGAGCTGGTCAA / TCTGCTGCTGGTCTCAATGG
591	KLK2	GTGGCTGTGTACAGTCTAGGAT / CCTCTGGCTGTGTCTTCAG
592	KRAS	GTGCAATGAGGGACCACTACA / CTACTAGGACCATAGGTACATCTTCA
593	KTNI	AGTTGAGAGCAAGACTAATGCACTTA / GGGCTGTATCTTGGAAATGG
594	LGR5	ACCTCTCTGTGCTTTTCTTAATACT / TGCACAGCATGGTAAGCATATA
595	LHPF	CGAAGAAAGACAGCAAGTGTGTG / CCACAGTTCGTAATGCAGATAA
596	LRI3	TGGGTGGCGGAAAACAATCT / TGTITCTGGCTGAACCGTGT
597	MAM12	GTCAAGGCCCTCCAGATTAT / GGAGTTAAATGGTGTGTGTGAACT
598	MAST2	GGTGTGGAGCTGGACGAGCTT / GCAGCCATCTCTCACTACTT
599	MBOAT2	GCTCTGTGGCCAAACAAGAT / CCAGCGAGCTGTCTCAATT
600	MBTD1	GGTGTGGAGCTTCTGGTCAATAT / GGCACCAAGTAAGTCTTCACT
601	MCPII	GGCCTATGTGAAGTGTGGTCT / CAAGTGTCTGGTAGGCACTTT
602	MEAF6	CCAACTATGGCGATGCACAA / CAGGTAGCTTCTCTCAAAAGCA
603	MKRN1	GTGAGTACTGGGTGGAGGAGAA / GGTGATCCAGTCTTGTAAAACA
604	MSN	GGCTGAGGACGATCGAGGAA / TGGCTCTCTCAGCTTCTTGAC
605	MYB	CCAGGGCACCATTCTGGATA / CTTGTGTGATGTGGCTAGGT
606	NACC2	GATACCGCTGGCATCCCAA / CTTCCGACGCAAGACCTTAT
607	NCOA1	GGTGAGCAGAGGCGATGACA / AGCTCCAGGGCTTAGAGAT
608	NCOA2	CAGAGTCCCATTGATGCAACAT / CATGCTGGTGTGTGCTGTCT
609	NCOA4	CTTTGGGCGTAGGTAGTGT / CCCATTCACGCTAGACCTC
610	NDRG1	GAGCAGGACATCGAGACTTTACAT / CTGATCTCTGCTAGTGTGAAGA
611	NF1	CACCTGACGAGCAGCTAGT / GCGGAGTCTGCTCACTGTT
612	NFATC2	GCACAAACAAAGTCTGGAGATA / GTTCAACCCGCTGTGTTCT
613	NFIA	CACCCAGCCATCCGCTAT / GGTGGGAAGGAATGGGTGTGT
614	NONO	TCTTCTCCCGATCACTGA / TCCAGCTCCATCTTGGCAAT
615	NOTCH1	CCGAGCCACAAGGTGTCTT / GTCGGCTGTGAGTTGATGA
616	NR4A3	TGTCGAGCTTTAAGACAGCTCAAC / GCCAGCTCTTGGATATCATCAAT
617	NTN1	CTCATTGCAAGGCTCCAAAG / CTTGCTTATACAGGAGATGATT
618	NTRK1	CAGGAGCTGGTGTCAAGATT / CGCTCTCGGTGTGAACTT
619	NTRK2	CCGAGTCTGTGCTATTTGGAATG / CCTTCCGCTAGCTCCCTTTT
620	NTRK3	CTGGAATCAACCTTCTCTGAT / ACCTGAGGCTGAAGCAATT
621	NUPI07	CTTTGTCTGCAATGTGTGTTTCT / CAGCAACTTCTTACGCTTCTCTT
622	OMD	AGAAGCTCAGTGTGGACACAA / GTTAAATGGTGTGATGTGGGTCAA
623	HMSB	CCAGCTCTGCTGCGAAGAT / AGGATGATGCGCTGAACCT
624	TBP	GACTCCCATGACCCCATC / ACAGAGTGAATGGCTTGTAGTT
625	ITGB7	CTCTATTTGATGATGGCTGGTCAAG / CGTGTGGTCTGCTCTTCTCTTG
626	MYC	CCTGGTGTCTCATGAGGAGACA / GTGATCCAGACTTGACCTTTTGCCA
627	LMNA	CTGAGAACAGGCTGCAGACCATGA / ACTCAGCTGCTTCCATTTGTCAA
628	ALK_3P	AGTGGAAACCCGAGCTTGT / CTGTGAGGACTGTGCCATTCT
629	ALK_3P	AAACTGCTCTTGACCTGTCC / ACTTAACCTGGACGATGGCA
630	RET_3P	CTGCCCATTCTACTCTCT / CACCAGAGGAATGCAGCTTGTA
631	RET_3P	GGACAAAAGGCGGCTGTGTG / CTGAGAGGCGCTGCTCAATAAT
632	ROS1_5P	ACTGCTCAAACTGAGGAAATTAAT / GGATACAGGAAGGTCTGCTATATAAATG
633	ROS1_3P	ATGAACCCCAATCATATCTGGAA / TCTACACACAGGCTACAAAGGTCAA
634	NTRK1_5P	CTCTGGGACCAATGACAGT / CTTCAGATGGTGTGAGTTTCTCA
635	NTRK1_3P	TGCTTGGGAGATCTTCACTA / CATGATGGCGTAGACCTCTGG
636	CDC6	GCTGGAGACCTCAAACTGAAGTG / CCTTCTGCAAAAGCTGAAATTTCTT
637	BRAF	CGGAGCTGAGGTGATGATGG / CTGAGGTGTAGGTGCTGTCA
638	ETV6	GCTGCTGACCAAGAGGACTT / TCCGGCTGTGTGTATAGAGT
639	ZNF703	GTCTTCCACTCCCTGTCAG / CGCGACCGAGTTGAGTTT
640	IACC3	CCAAGCTTGTGGAGTTCGATT / CACTGATCCAGGCTCTTCTG
641	ROS1	GCTTGGCTAATGCTGCTAT / TGTCTACTGCTGTCTTCTCATC
642	KIAA1549	GGAGCTCAGCCAGTGGAAA / ACCTGAAATAGCGGTGAAGAAGATAC
643	KIF5B	ACACAACTTGCACCAACTCT / TGCATTTAGTGAGCTGTCAAGAT
644	ERG	ACTACTTCTTGTGTCAGAGAAGCAATA / GCGTTCGGTAGGCACT
645	RNF130	TGGCTCTCTAGTCTCTGTGCTAT / TGGCTTCTTCTGGCTGCACT
646	SEC31A	ACCACAGATGCCAAGAGTTC / GTGGTACTGGGTGTGCAAT
647	ETV5	GATGATGCTGAAAACCAATGATCA / GCTCGAGGACAAATAGGTTCT
648	TRIM24	CAGCACTGTGGGTATACCA / GTTGTGAGGATGAGGAGGAAGAAC
649	ACBD6	TGGTGGGCGAGTTATAGTTCTTATA / TCTTCAATCTTCAATTCACATCCACAT
650	APAT5	CGCAGTGCCAAATTAACGAGAA / GCAATGGCTGACTAGTGAAG
651	TFE3	GAATCTGCTGTGATGTGACAGTAGTCA / TGTCTTCTTCTGCGCGTCTCTT
652	ATF1	TGTGATCTCACTCTCAGACA / CCAGAGCTGCAACTCGGTTT
653	FEV	CTGATCAACATGTAACCTGCCAGAT / GCTCCAGCAGAACTGCCA
654	FLJ1	CGAGAACTGTGAGGACAGA / CGGTGTGGGAGGTTGATATATAGG
655	FUS	AAACGGGACAGCCCATGATT / CTTGATAGGATTTCCGGAGAAATCTT
656	LPP	CATTCGCCAGAGGATGA / CTTGATCCATGGCAGTGCAT
657	GAB2	GAAATCGCTCCCGAGAGAA / TTCAGTGTGATGATCCGAGAG

#	ID	Forward / Reverse Primer
658	PRKCE	TCTATGCTGCAGAGGTACATC / ATTCAAGATCCCTTCTTGCACAT
659	FOXO1	TCAAGAGCGTCCCTACTTC / GATTGAGCATCCCAAGAACTTTT
660	PRCC	CAAGATGGCAGCAGGTCTCAAG / TCTGTGACGATAGTAGCCA
661	SFPQ	GGTGTGGTGGCATAGGTTA / AGGCCCATCTCTCTAGGAC
662	CD74	CAGGCACTCTTGGAGCAA / GCATGGAGTGGCAGATAGT
663	DDIT3	GTATCTTCATACATCACCACACTGAA / TGGAAAAGCAATCTGCAGGA
664	GOPC	GCGAGACTAGCTGCCAAGT / CACAGTTTGTGACGATGCAAAATGA
665	HEY1	GGATCACTGAAAATGCTGCAATC / TCAGAGGCACTAGTCTTCTCAATGA
666	LIFR	GGAGCCTCTGCAGCTCAT / AATGTGTATAACAGCCACTGGAAATTTG
667	NFIB	TCGAGTACTTTTCTCATCAACAATC / GCCAGGCACTTTCCTTACT
668	NPM1	GGTTCAGGGCCAGTGCA / GTGGAACCTTGTACCACTTC
669	QK1	CACCTATGAGTACCCCTACACA / GGCTCGCGGTACACATCTT
670	RSPO2	CCTTTTCTCTTTTGGCTCTCAT / CGGTATACACCAATGTCTCT
671	SDC4	GGCAGCAACATCTTGGAGAGAA / GGGTTTCTTGGCCAGGTCTATA
672	TPM4	TGGAAGAACAATGTAGACTGGAA / GCTCCAGAGTTTCTTGGGAACAA
673	FGFR1	CTGCTATCTACCAGACACTGT / GAGCTGATCTCTCTTTTCAAACT
674	TAI15	CGAGTCAATATGATCAGCAGCAT / TGTGACCCGCAATCTCTCTA
675	USP6	ACCGAGTTCACATCCACAT / CACTTCAATGATGTCTTCCGCTCT
676	PHF1	CTCACTTTGGGACCCAGCTT / CCAGACACACTCTCTTAGCA
677	CTAGE5	GGTCACTCAGACTCTCACTT / AGTGTCAAGGAGGAGCCCTATG
678	PDGFB	GGAGTCGGCATGAATGCT / GGGTTGGAGATCATCAAGGA
679	PACS1	TCTTAAGCGAGATGCCAACAA / CACCGATGGCGCTTCTATTAG
680	PAI21	AAGCAGGTGCACACTTCTGA / GTTGGTGTGCCCGCAAGT
681	PAX3	GACCTTGCACACGTACA / GTCTGGTTGGGAAGATGCT
682	PAX5	GCCACTCCCGATGTAGTC / GGCTGTAGTCTTCTGCTCATATAA
683	PAX7	GGCGACTCGGATGATAGA / CGCGGCTAATCGAATCACTAA
684	PAX8	GGCTCCACTACTCCATCAAT / TCCGTGCGAAGGTGCTT
685	PBX1	GAGCGTGCAGTCACTCAAT / CCTCGCGACTGTACATCT
686	PCM1	CTCACTGCTGGAGAGATGAT / CATCTTCAATCTTCTTCACTTCTCTT
687	PDE8B	GGTCAAGGACACCAATGCAA / GGCTGTGTGATGTGTTCACA
688	KDIL1	ATGACATCTCTCATGTGCTT / CACCGACTCAGCGATGTCT
689	PLAG1	GGCCCTACAAGTGCATACAA / GATTCTTCAGATGATCTTCCGGTGA
690	PLXND1	TGTGGCATGGCAGAGATT / CACTCGTAGTGTGTCTTCTT
691	PPARG	GCCTTCACTACTGTTGACTTCT / GGAGATCAGAGGCTCCACTTT
692	PPFBP1	GATGCAATTGGCTCCCTCAATA / GACTGTGATGGCTCTTTGAT
693	PRKAR1A	TGCTACAAGTCTGGTGCAGAA / GGTCAGCTTAACGCACTTCAA
694	PRKAR2A	TTTCTCAAGTCTCTGATCGGAT / CAACAGAGCGGTTTGATTAATCTT
695	PTBP3	TCAGATGGCGATGCAATAA / TCTTATGTCAGACTTGGTCTTCTT
696	PTPRK	TGGTGAATCAAGTAACGTGTGT / TGGTAGGCACTCACTGAT
697	RAD51B	CTTCACTCATTTGTCTACACATA / TGGTGGCACTGATGGTCTCTA
698	RAF1	CACAGATCTTCTAAGCAAGCAAA / ACTGACACAGCACTTGGTT
699	RANBP2	CCTCGGACTGCTGAGAACT / ATAAATGAGTCTTCCGCTGTT
700	RBM14	CGCCCTATGAGCGTACCC / ACAGAAAGCTGCGACTTGTATAA
701	RGS22	AGCAGCTTGATGCACTGTT / AGAGCTTCTGCTATGCTTTTCACT
702	RNF215	GCTTGGCTACAGATGAATGAAGA / TGGGCAATCTGATGAGACACTT
703	RRP16	GCTATGGTAAAGTCTCAACAAAGAA / CATTTCCACTGAGCCCTTTTATC
704	RSPO3	TTGACAATTGCCAGAGAGGT / CCGGTCTTTCAGTCTCTTCT
705	SEC16A	CTGGCGGCTACTACTACTA / GCACCATATAGGCGTGTAT
706	SLC26A6	CCTTGGGCTCAGTAACCTTAT / TGACATATGAGGAGGATGAAAAGG
707	SLC34A2	CATTGAGAGGCTTATCCACTCA / AAGATGCGGAGATGTTGAAGAAA
708	SLC45A3	CTGCAGATCTGCCCTACA / GAAGGGAGTCCAGGCTTAG
709	SMARCA5	TGATGATGCGTCACTTGGAAA / TCTGAGCAGCAGGTGAATGAAA
710	SP3	TGAGGTGGCTTAAACACACTATG / CACCGTTTCCGTTGCTGTTG
711	SQSTM1	AAGTGCCTTGTACCCACAT / GAGCGCTCCGATGTGATA
712	SRGAP3	TCAATCTGGCAGCCACCA / GAGAGGCTCTGAGTGTGATTTCAG
713	SS18	GCACTGCACTACAGATGATGA / GCTTCCCTGTGGCATATTGT
714	SS18L1	GCGACAGTACGGAAGCTA / TGGATGAACACGCTACACAA
715	SSBP2	GGGCACCTCAAGGGATGAT / GTAGTCTGTGGAAGGGGTGACTC
716	SSH2	CCTGGCTAGTGGATGAGA / CGGTCCAGATCCAGCAGTATTC
717	SSX1	TCACCACTGTGCACTT / GCTTCTCTTCTGATGCTTTAGCA
718	SSX2	GGGAAAACCAACTACCTCTGAGAA / GCACCAATGAAGTGGACAAACTG
719	SSX4	CACGCCGATTTGCCCTTTT / CTTCGTAACTTCTCTGATATTGAGCATC
720	STRN	GCCTTACGTTGGCCAAATGA / AAACAGGCTCAATGGGATGAA
721	SUSD1	CGTCCGGTACCAACTACAT / CAGCTTCCGTTGCTGTTG
722	SUZ12	GCCATATGTTGAAGTCTTACTGTT / CCCCATCTCAGGATTTCTGTT
723	SYCP1	TCTGTTGCCCTATAGACGTT / GCTGCTGTATCTCGGTGGTA
724	TACC1	GTTGGTGAAGGTGAAGAAGCA / ACATGACCTGATGCGAGTTT
725	TBCE1	TGGGAGACGCTCCACATGA / CCAGTCTTGGAGTTATTTGCTGT
726	TCEA1	CATCAGATGGCAGAGCTGTT / TCGATTCCACATTTATACAGACAA
727	TCF12	GCCTGTGGTCAAGTGA / CTGACAGAGTCTTCCCGATGAG
728	TCF3	TGTGCGAGATGCACCTCAAG / TTTCTCTTCTGCGGCTTTCAA
729	TCF7L2	AAAGAAGTGTGGGCACTGT / GAGGCGAATCTAGTAAGCTTCCA
730	TECTA	CTGGACTGTGTGAGGACAT / CGTCCAGACTTGAAGTTCATGAA
731	TGF	GTTGGTGCAGCGGATG / TCTTCCCAAGTTGAGCTTTG
732	THRAP3	CAAGTCTGGATCTCGTCTTCT / GTGGGAAATATGATCGGAACGA
733	TMCC1	CCCAGGTCTTATCCCAACTG / TGGGCAAGGCTGCTTACT
734	TPMRSS2	GTCAGAACGCTCCAGTGT / GGCTCCATAGAACATGAAGATTGTC
735	TPM3	CCGGGCTTAAAGATGAAGAAAGAT / CGTCTCTCTGTGCGTTCCA
736	TPR	GAATAGAAAAGAGGTTGTCCACAGT / GCGATCTGAGCAATTTCAAGTT
737	TRIM27	CTGAAGCTGACTGCGAGGA / CTTTTAAATGTTGAGCTGGTCTGT
738	TRIM33	GAAAGTTGTCAAGTTTATGACAGACA / AACTTGGCAAGGTGGCA
739	UBE2L3	TGACTTGGCAAGGGCTTATGT / CTTTCTGCTGATTTGGGTGATA
740	USH1G	CAGCATCAGGCTCCCACT / TGCAACATGATATCAATTTTGGT
741	VCL	CCATCAATCAGCCGCTCAA / TCTTACCAGCCGAGACATCTCA
742	VH1IA	GCACATCTGCTGATAACACAGA / TTCAGTCTGCTGCTGATCTT
743	WIF1	GGACCTGTTTCACTTGGAAAT / GGCTTCTCTGTAAGCTTTGG
744	WT1	TGACCGTTCGCACTGAGA / CAGTCTTGAAGTACACATGTA
745	WVHA	GCTAACACTGGCAGTCCAA / GCTTCTATATCACTAGCAGCTTGA
746	YY1	GTTGCAAGCTTTTGTGAGAGT / CTCGGGATGATTCGCACAT
747	ZC3H7B	ACCTTGTGCTGAGATGAGT / GGCTTGGACATACCCAGAG
748	ZNF384	GGCATCAGTATGGACACAGAGT / CCTTCTCTCTTCACTCTGA
749	ZNF444	CGAGCTTTTGGGCACTGT / TCCGAGGGATCTCAAGTCAG

Fig. 1 Design of the primer set. Fusion-specific amplicons contain the nucleotide sequence of the junction joining two genes. The AmpliSeq Designer was used to design the sequences of primer sets to amplify the region across the breakpoint.

Table 3 Summary of cell lines used as positive controls and the fusion genes expressed

#	Cell line	Primary tissue	Fusion gene	Read Counts	Average Depth
1	HCC38	Breast	<i>ACBD6 - RRP15</i> (COSF687)	26	5,035
			<i>MBOAT2 - PRKCE</i> (COSF673)	1,069	
			<i>SLC26A6 - PRKAR2A</i> (COSF671)	714	
2	HCC1395	Breast	<i>EIF3K - CYP39A1</i> (COSF703)	3,672	3,905
			<i>ERO1L - FERMT2</i> (COSF667)	0	
3	NCI-H2228	Lung	<i>EML4 - ALK</i> (COSF411)	1,756	4,798
4	DU145	Prostate	<i>UBE2L3 - KRAS</i> (COSF1298)	4,054	5,320
5	NCI-H508	Colon	<i>VTI1A - TCF7L2</i> (COSF1147)	1,802	5,207
6	HCC1187	Breast	<i>AGPAT5 - MCPH1</i> (COSF695)	3,742	9,858
			<i>CTAGE5 - GEMIN2</i> (COSF697)	3,996	
			<i>PLXND1 - TMCC1</i> (COSF689)	1,918	
			<i>PLXND1 - TMCC1</i> (COSF699)	831	
			<i>SUSD1 - PTBP3</i> (COSF701)	89	
7	BT-20	Breast	<i>NOTCH1 - GABBR2</i> (COSF1178)	78	7,989
8	SW780	Bladder	<i>FGFR3 - BAIAP2L1</i> (COSF1346)	18,000	9,367
			<i>SLC45A3 - ELK4</i> (COSF1131)	506	
9	SK-ES-1	Sarcoma	<i>EWS - FLI1</i> (COSF165)	8,970	9,667
			<i>EWS - FLI1</i> (COSF180)	435	
			<i>EWS - FLI1</i> (COSF204)	298	
			<i>SLC45A3 - ELK4</i> (COSF1131)	31	
10	RD-ES	Sarcoma	<i>EWSR1 - FLI1</i> (COSF165)	8,038	8,551
			<i>EWSR1 - FLI1</i> (COSF180)	265	

The fusion transcripts detected in the 10 cancer cell lines are written in bold text. Only the *ERO1L-FERMT2* transcript was undetectable.

Table 4 Summary of sequencing statistics

	Average (<i>n</i> = 600)	SD
Number of mapped reads	4,715,303	895,471
Average reads per amplicon	6,425	1,218
Average base coverage depth	6,359	1,349

using NGS was over 6,000, indicating high assay sensitivity (Table 4). The types and numbers of tumor tissues analyzed are listed in Table 5. Table 6 summarizes the fusion transcripts detected in the clinical samples. For example, *FUS-DDIT3* in Case 1 and *COL1A1-PDGFB* in Case 8 occur in patients with round cell liposarcoma and dermatofibrosarcoma protuberans, respectively (6, 23). *FGFR3-TACC3*, which was detected in Case 1, occurs in patients with cervical cancer, bladder cancer, glioblastoma, and lung cancer (8). *PTPRK-RSPO3*, which was detected in Cases 3 and 6, occurs in colorectal cancer (17, 18). *PTPRK-RSPO3* encodes a chimeric protein that potentiates WNT signaling (17), and gene fusions involving R-spondin family members *RSPO2* and *RSPO3* occur in 10% of colon tumors (17). We detected *PTPRK-RSPO3* in two of 172 colorectal cancer tissues. *EML4-ALK*, which was detected in Cases 4 and 6, occurs in patients with non-small cell lung cancer (19), and the frequency of detection of *EML4-ALK* here was consistent with that reported by others (7). Primary synovial sarcoma of the kidney in Case 7 was a rare disease (12) and the detected *SS18-SSX1* was characteristic fusion transcripts in synovial sarcoma (3, 4). Mesenchymal chondrosarcoma in Case 9 is an extremely rare subtype of chondrosarcoma. *HEY1-NCOA2* fusion has been reported to be prevalent in nearly 94% of the mesenchymal chondrosarcoma (15, 24).

The 491 fusion genes contain approximately 80% of the fusion gene which has been registered in the COSMIC database. The COSMIC database is frequently updated, adding the newly discovered fusion genes. It is easily extended by adding primers for new fused genes into this HOPE fusion panel.

In conclusion, we used the HOPE fusion panel to simultaneously detect multiple fusion transcripts with a high depth of sequence coverage and high sensitivity. Further, the data are consistent with the COSMIC fusion database. To our knowledge, this is the first study that reports the analysis of a wide variety of cancer tissues derived from clinical samples for the presence of fusion transcripts. Moreover, our findings indicate that the HOPE fusion panel shows promise for classifying tumors at the molecular lev-

Table 5 Classification of 600 samples according to tissue type

Site	Number
Colon	172
Lung	89
Stomach	58
Liver	44
Breast	43
Liver Metastasis	32
Tongue	19
Pancreas	18
Lung Metastasis	17
Kidney	9
Brain	8
Duodenum	6
Gingiva	6
Parotid Gland	5
Skin	5
Pyriiform Sinus, Hypopharynx	5
Soft Tissue	5
Esophagus	5
Ovary	5
Mouth	4
Cheek	3
Glottis	3
Larynx	2
Intracostal Soft Tissue	2
Thymus	2
Oropharynx	2
Retroperitoneum	2
Thyroid Gland	2
Uterine Body	2
Tonsil	2
Unknown	2
Parathyoid Gland	2
Cervical Lymph Node	2
Others	17
Total	600

The tissues were collected by the HOPE study.

el with greater ease and sensitivity.

Acknowledgment

The authors thank the staff at the Shizuoka Cancer

Table 6 Summary of fusion transcripts detected in tumor tissues

Case	Site	Histology	Fusion Gene	Read Counts	Average Depth
1	Soft tissue (leg)	Round cell liposarcoma	FUS - DDIT3 (COSF300)	577	6,940
2	Lung	Squamous cell carcinoma	FGFR3 - TACC3 (COSF1434)	3,777	2,384
			FGFR3 - TACC3 (COSF1348)	1,874	
3	Colon	Advanced colon cancer	PTPRK - RSPO3 (COSF1311)	15,273	7,331
4	Lung	Invasive adenocarcinoma	EML4 - ALK (COSF411)	832	7,091
5	Lung	Invasive adenocarcinoma	EML4 - ALK (COSF411)	1,276	8,051
6	Rectum	Advanced rectal cancer	PTPRK - RSPO3 (COSF1311)	10,076	7,530
7	Kidney	Synovial sarcoma	SS18 - SSX1 (COSF499)	18,263	6,653
8	Skin (thigh)	Dermatofibrosarcoma protuberans	COL1A1 - PDGFB (COSF541)	72,117	7,571
9	Liver metastasis	Metastatic mesenchymal chondrosarcoma	HEY1 - NCOA2 (COSF1211)	29,359	7,547

A fusion transcript was detected in 9 of 600 samples.

Center Hospital for clinical support and sample preparation.

REFERENCES

- Asmann YW, Necela BM, Kalari KR, Hossain A, Baker TR, Carr JM, Davis C, Getz JE, Hostetter G, Li X, McLaughlin SA, Radisky DC, Schroth GP, Cunliffe HE, Perez EA and Thompson EA (2012) Detection of redundant fusion transcripts as biomarkers or disease-specific therapeutic targets in breast cancer. *Cancer Res* **72**, 1921–1928.
- Bamford S, Dawson E, Forbes S, Clements J, Pettett R, Dogan A, Flanagan A, Teague J, Futreal PA, Stratton MR and Wooster R (2004) The COSMIC (Catalogue of Somatic Mutations in Cancer) database and website. *Br J Cancer* **19**, 355–358.
- Clark J, Rocques PJ, Crew AJ, Gill S, Shipley J, Chan AM, Gusterson BA and Cooper CS (1994) Identification of novel genes, SYT and SSX, involved in the t(X;18)(p11.2;q11.2) translocation found in human synovial sarcoma. *Nat Genet* **7**, 502–508.
- Crew AJ, Clark J, Fisher C, Gill S, Grimer R, Chand A, Shipley J, Gusterson BA and Cooper CS (1995) Fusion of SYT to two genes, SSX1 and SSX2, encoding proteins with homology to the Kruppel-associated box in human synovial sarcoma. *EMBO J* **15**, 2333–2340.
- Garraway LA and Lander ES (2013) Lessons from the cancer genome. *Cell* **28**, 17–37.
- Göransson M, Elias E, Ståhlberg A, Olofsson A, Andersson C and Aman P (2005) Myxoid liposarcoma FUS-DDIT3 fusion oncogene induces C/EBP beta-mediated interleukin 6 expression. *Int J Cancer* **115**, 556–560.
- Inamura K, Takeuchi K, Togashi Y, Nomura K, Ninomiya H, Okui M, Satoh Y, Okumura S, Nakagawa K, Soda M, Choi YL, Niki T, Mano H and Ishikawa Y (2008) EML4-ALK fusion is linked to histological characteristics in a subset of lung cancers. *J Thorac Oncol* **3**, 13–17.
- Kim Y, Hammerman PS, Kim J, Yoon JA, Lee Y, Sun JM, Wilkerson MD, Pedamallu CS, Cibulskis K, Yoo YK, Lawrence MS, Stojanov P, Carter SL, McKenna A, Stewart C, Sivachenko AY, Oh IJ, Kim HK, Choi YS, Kim K, Shim YM, Kim KS, Song SY, Na KJ, Choi YL, Hayes DN, Kim J, Cho S, Kim YC, Ahn JS, Ahn MJ, Getz G, Meyerson M and Park K (2014) Integrative and comparative genomic analysis of lung squamous cell carcinomas in East Asian patients. *J Clin Oncol* **32**, 121–128.
- Luthra R, Chen H, Roy-Chowdhuri S and Singh RR (2015) Next-generation sequencing in clinical molecular diagnostics of cancer: advantages and challenges. *Cancers (Basel)* **7**, 2023–2036.
- Maier CA, Kumar-Sinha C, Cao X, Kalyana-Sundaram S, Han B, Jing X, Sam L, Barrette T, Palanisamy N and Chinnaiyan AM (2009) Transcriptome sequencing to detect gene fusions in cancer. *Nature* **458**, 97–101.
- Maier CA, Palanisamy N, Brenner JC, Cao X, Kalyana-Sundaram S, Luo S, Khrebukova I, Barrette TR, Grasso C, Yu J, Lonigro RJ, Schroth G, Kumar-Sinha C and Chinnaiyan AM (2009) Chimeric transcript discovery by paired-end transcriptome sequencing. *Proc Natl Acad Sci U S A* **28**, 12353–12358.
- Majumder A, Dey S, Khandakar B, Medda S and Chandra Paul P (2014) Primary renal synovial sarcoma: a rare tumor with an atypical presentation. *Arch Iran Med* **17**, 726–728.
- Mertens F, Johansson B, Fioretos T and Mitelman F (2015) The emerging complexity of gene fusions in cancer. *Nat Rev Cancer* **15**, 371–381.
- Mertens F and Tayebwa J (2014) Evolving techniques for gene fusion detection in soft tissue tumours. *Histopathology* **64**, 151–162.
- Nakayama R, Miura Y, Ogino J, Susa M, Watanabe I, Horiuchi K, Anazawa U, Toyama Y, Morioka H, Mukai M and Hasegawa T (2012) Detection of HEY1-NCOA2 fusion by fluorescence in-situ hybridization in formalin-fixed paraffin-embedded tissues as a possible diagnostic tool for mesenchymal chondrosarcoma. *Pathol Int* **62**, 823–826.
- Pekar-Zlotin M, Hirsch FR, Soussan-Gutman L, Ilouze M, Dvir A, Boyle T, Wynes M, Miller VA, Lipson D, Palmer GA, Ali SM, Dekel S, Brenner R, Bunn PA Jr and Peled N (2015) Fluorescence in situ hybridization, immunohistochemistry, and next-generation sequencing for detection of EML4-ALK rearrangement in lung cancer. *Oncologist* **20**, 316–322.
- Seshagiri S, Stawiski EW, Durinck S, Modrusan Z, Storm EE, Conboy CB, Chaudhuri S, Guan Y, Janakiraman V, Jaiswal BS, Guillory J, Ha C, Dijkgraaf GJ, Stinson J, Gnad F, Huntley MA, Degenhardt JD, Haverty PM, Bourgon R, Wang W, Koeppen H, Gentleman R, Starr TK, Zhang Z,

- Largaespada DA, Wu TD and de Sauvage FJ (2012) Recurrent R-spondin fusions in colon cancer. *Nature* **488**, 660–664.
18. Shinmura K, Kahyo T, Kato H, Igarashi H, Matsuura S, Nakamura S, Kurachi K, Nakamura T, Ogawa H, Funai K, Tanahashi M, Niwa H and Sugimura H (2014) RSPO fusion transcripts in colorectal cancer in Japanese population. *Mol Biol Rep* **41**, 5375–5384.
 19. Soda M, Choi YL, Enomoto M, Takada S, Yamashita Y, Ishikawa S, Fujiwara S, Watanabe H, Kurashina K, Hatanaka H, Bando M, Ohno S, Ishikawa Y, Aburatani H, Niki T, Sohara Y, Sugiyama Y and Mano H (2007) Identification of the transforming EML4-ALK fusion gene in non-small-cell lung cancer. *Nature* **448**, 561–566.
 20. Teixidó C, Karachaliou N, Peg V, Gimenez-Capitan A and Rosell R (2014) Concordance of IHC, FISH and RT-PCR for EML4-ALK rearrangements. *Transl Lung Cancer Res* **3**, 70–74.
 21. Van de Rijn M, Guo X, Sweeney RT, Beck AH and West RB (2014) Molecular pathological analysis of sarcomas using paraffin-embedded tissue: current limitations and future possibilities. *Histopathology* **64**, 163–170.
 22. Vogelstein B, Papadopoulos N, Velculescu VE, Zhou S, Diaz LA Jr and Kinzler KW (2013) Cancer genome landscapes. *Science* **29**, 1546–1558.
 23. Wang J, Morimitsu Y, Okamoto S, Hisaoka M, Ishida T, Sheng W and Hashimoto H (2000) COL1A1-PDGFB fusion transcripts in fibrosarcomatous areas of six dermatofibrosarcomas protuberans. *J Mol Diagn* **2**, 47–52.
 24. Wang L, Motoi T, Khanin R, Olshen A, Mertens F, Bridge J, Dal Cin P, Antonescu CR, Singer S, Hameed M, Bovee JV, Hogendoorn PC, Socci N and Ladanyi M (2012) Identification of a novel, recurrent HEY1-NCOA2 fusion in mesenchymal chondrosarcoma based on a genome-wide screen of exon-level expression data. *Genes Chromosomes Cancer* **51**, 127–139.
 25. Wang Q, Xia J, Jia P, Pao W and Zhao Z (2013) Application of next generation sequencing to human gene fusion detection: computational tools, features and perspectives. *Brief Bioinform* **14**, 506–519.
 26. Yamaguchi K, Urakami K, Ohshima K, Mochizuki T, Akiyama Y, Uesaka K, Nakajima T, Takahashi M, Tamai S and Kusuvara M (2014) Implementation of individualized medicine for cancer patients by multiomics-based analyses—the Project HOPE—. *Biomed Res (Tokyo)* **35**, 407–412.