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					Green = Consistent Calls (based on Crystal's visual analysis of the reads supporting the variants)														
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Features & Coordinates					BWAmem_0.7.12 + FreeBayes_0.9.21					HCC2218_Tumor					Crystal_1.3.7				
					Benchmark's Variants					Crystal Genetics' Variants									
					BWA (bio-bwa.sourceforge.net) + FreeBayes (wiki.gacrc.uga.edu/wiki/Freebayes)					Crystal Genetics (www.crystalgenetics.com)									
idx	gene	exonic	chr	position	in_vcf	ref	alt	var	filter	in_vcf	ref	alt	var	filter					
1	APC	1	5	112,173,250	1	G	A	0/1	Q>250	1	G	A	0/1	PASS					
2	APC	1	5	112,176,756	1	T	A	0/1	Q>250	1	T	A	0/1	PASS					
3	ATM	1	11	108,119,823	1	T	C	0/1	Q>250	1	T	C	0/1	PASS					
4	ATM	1	11	108,183,167	1	A	G	1/1	Q>250	1	A	G	1/1	PASS					
5	BARD1	1	2	215,590,410	1	G	A	1/1	Q>250	1	G	A	1/1	PASS					
6	BARD1	1	2	215,590,582	1	C	T	1/1	Q>250	1	C	T	1/1	PASS					
7	BARD1	1	2	215,590,609	1	G	C	0/1	Q>250	1	G	C	0/1	PASS					
8	BARD1	1	2	215,590,775	0	-	-	-	-	1	G	AG	0/1	PASS					
9	BARD1	1	2	215,592,290	1	C	G	1/1	Q>250	1	C	G	1/1	PASS					
10	BARD1	1	2	215,593,233	1	T	C	0/1	Q>250	1	T	C	0/1	PASS					
11	BARD1	1	2	215,593,277	0	-	-	-	-	1	G	TG,TTG	1/2	PASS					
12	BARD1	1	2	215,632,254	0	-	-	-	-	1	ACA	ATG	0/1	PASS					
13	BARD1	1	2	215,645,464	1	C	G	1/1	Q>250	1	C	G	1/1	PASS					
14	BARD1	1	2	215,674,224	1	G	A	0/1	Q<=250	1	G	A	0/1	PASS					
15	BARD1	1	2	215,674,323	1	C	G	1/1	Q>250	1	C	G	1/1	PASS					
16	BARD1	1	2	215,674,341	1	A	G	1/1	Q>250	1	A	G	1/1	PASS					
17	BARD1	1	2	215,674,371	1	C	T	1/1	Q>250	1	C	T	1/1	PASS					
18	BMPR1A	1	10	88,683,890	1	T	A	1/1	Q>250	1	T	A	1/1	PASS					
19	BMPR1A	1	10	88,684,280	0	-	-	-	-	1	G	TG	0/1	PASS					
20	BMPR1A	1	10	88,684,362	1	C	T	0/1	Q>250	1	C	T	0/1	PASS					
21	BMPR1A	1	10	88,684,422	0	-	-	-	-	1	A	G	0/1	PASS					
22	BRCA1	1	17	41,196,408	1	G	A	1/1	Q>250	1	G	A	1/1	PASS					
23	BRCA1	1	17	41,196,839	0	-	-	-	-	1	TTG	G	1/1	PASS					
24	BRCA1	1	17	41,197,274	1	C	A	1/1	Q>250	1	C	A	1/1	PASS					
25	BRCA1	1	17	41,223,094	1	T	C	1/1	Q>250	1	T	C	1/1	PASS					
26	BRCA1	1	17	41,234,470	1	A	G	1/1	Q>250	1	A	G	1/1	PASS					
27	BRCA1	1	17	41,244,000	1	T	C	1/1	Q>250	1	T	C	1/1	PASS					
28	BRCA1	1	17	41,244,435	1	T	C	1/1	Q>250	1	T	C	1/1	PASS					
29	BRCA1	1	17	41,244,936	1	G	A	1/1	Q>250	1	G	A	1/1	PASS					
30	BRCA1	1	17	41,245,237	1	A	G	1/1	Q>250	1	A	G	1/1	PASS					
31	BRCA1	1	17	41,245,466	1	G	A	1/1	Q>250	1	G	A	1/1	PASS					
32	BRCA2	1	13	32,913,055	1	A	G	1/1	Q>250	1	A	G	1/1	PASS					
33	BRCA2	1	13	32,915,005	1	G	C	1/1	Q>250	1	G	C	1/1	PASS					
34	BRCA2	1	13	32,929,387	1	T	C	1/1	Q>250	1	T	C	1/1	PASS					
35	BRCA2	1	13	32,973,276	1	A	G	1/1	Q>250	1	A	G	1/1	PASS					
36	BRIP1	1	17	59,757,143	1	A	C	1/1	Q>250	1	A	C	0/1	PASS					
37	BRIP1	1	17	59,757,169	1	T	A	1/1	Q>250	1	T	A	0/1	PASS					
38	BRIP1	1	17	59,757,542	1	AAAAAAAAAAAAAAAAAAAAAT	AAAAAAAAAAAAAAAAAAAAAT	1/1	Q>250	0	-	-	-	-					
39	BRIP1	1	17	59,757,563	0	-	-	-	-	1	AT	T	1/1	PASS					
40	BRIP1	1	17	59,758,567	1	C	G	1/1	Q>250	1	CTGGGGACA	GTGGG	1/1	PASS					

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idx	gene	exonic	chr	position	in_vcf	ref	alt	var	filter	in_vcf	ref	alt	var	filter					
41	BRIP1	1	17	59,758,571	1	GGACAT	GT	1/1	Q>250	1	GGACA	G	1/1	PASS					
42	BRIP1	1	17	59,760,174	1	G	A	1/1	Q>250	1	G	A	0/1	PASS					
43	BRIP1	1	17	59,760,499	1	A	G	1/1	Q>250	1	A	G	1/1	PASS					
44	BRIP1	1	17	59,760,996	1	A	G	1/1	Q>250	1	A	G	1/1	PASS					
45	BRIP1	1	17	59,763,347	1	A	G	1/1	Q>250	1	A	G	1/1	PASS					
46	BRIP1	1	17	59,763,465	1	T	C	1/1	Q>250	1	T	C	0/1	PASS					
47	BRIP1	1	17	59,940,819	1	C	T	1/1	Q>250	1	C	T	1/1	PASS					
48	CDH1	1	16	68,857,441	1	T	C	1/1	Q>250	1	T	C	1/1	PASS					
49	CDH1	1	16	68,867,611	1	CTTTTTTTTTTTC	CTTTTTTTTTTTC	1/1	Q>250	1	C	CT	1/1	PASS					
50	CDH1	1	16	68,868,522	1	T	C	1/1	Q>250	1	T	C	1/1	PASS					
51	CDKN2A	1	9	21,968,199	1	C	G	0/1	Q>250	1	C	G	0/1	PASS					
52	CDKN2A	1	9	21,975,017	1	C	T	0/1	Q>250	1	C	T	0/1	PASS					
53	CHEK2	1	22	29,091,840	0	-	-	-	-	1	TGG	CAG	0/1	PASS					
54	EPCAM	1	2	47,601,106	1	T	C	0/1	Q<=250	1	T	C	0/1	PASS					
55	EPCAM	1	2	47,613,870	1	T	C	0/1	Q<=250	1	T	C	0/1	PASS					
56	MLH1	1	3	37,053,568	1	A	G	0/1	Q<=250	1	A	G	0/1	PASS					
57	MSH2	1	2	47,630,213	1	T	C	0/1	Q<=250	1	T	C	0/1	PASS					
58	MSH2	1	2	47,630,231	1	G	A	0/1	Q<=250	1	G	A	0/1	PASS					
59	MSH2	1	2	47,690,182	1	G	A	0/1	Q>250	1	G	A	0/1	PASS					
60	MSH6	1	2	48,023,115	1	T	C	0/1	Q<=250	1	T	C	0/1	PASS					
61	MSH6	1	2	48,025,764	1	C	T	0/1	Q<=250	1	C	T	0/1	PASS					
62	PMS2	1	7	6,026,775	1	T	C	0/1	Q<=250	1	T	C	0/1	PASS					
63	PMS2	1	7	6,026,988	1	G	A	0/1	Q<=250	1	G	A	0/1	PASS					
64	PMS2	1	7	6,036,980	1	G	C	0/1	Q>250	1	G	C	0/1	PASS					
65	PTEN	1	10	89,623,860	1	CTG	CG	1/1	Q>250	0	-	-	-	-					
66	PTEN	1	10	89,623,861	0	-	-	-	-	1	TG	G	1/1	PASS					
67	PTEN	1	10	89,623,901	1	G	C	1/1	Q>250	1	G	C	1/1	PASS					
68	PTEN	1	10	89,726,199	1	C	A	0/1	Q>250	1	C	A	0/1	PASS					
69	PTEN	1	10	89,726,401	0	-	-	-	-	1	C	G	0/1	PASS					
70	PTEN	1	10	89,726,660	0	-	-	-	-	1	TTT	T	1/1	PASS					
71	PTEN	1	10	89,726,745	1	T	C	1/1	Q>250	1	T	C	1/1	PASS					
72	RAD51C	1	17	56,769,979	1	C	T	0/1	Q>250	1	C	T	0/1	PASS					
73	RAD51D	1	17	33,433,453	1	G	A	0/1	Q>250	1	G	A	0/1	PASS					
74	SMAD4	1	18	48,606,016	1	T	C	0/1	Q>250	1	T	C	0/1	PASS					
75	SMAD4	1	18	48,610,372	0	-	-	-	-	1	A	ACG	0/1	PASS					
76	SMAD4	1	18	48,610,382	1	GC	GCGCAC	0/1	Q<=250	1	G	GCGCA	0/1	PASS					
77	TP53	1	17	7,577,091	1	G	A	1/1	Q>250	1	G	A	1/1	PASS					
78	TP53	1	17	7,578,645	1	C	T	1/1	Q>250	1	C	T	1/1	PASS					
79	TP53	1	17	7,579,472	1	G	C	1/1	Q>250	1	G	C	1/1	PASS					
80	TP53	1	17	7,579,801	1	G	C	1/1	Q>250	1	G	C	1/1	PASS					