

Color Code Description		White = Identical or Equivalent Calls (based on the reported data and Crystal's visual analysis)												
		Green = Consistent Calls (based on Crystal's visual analysis of the reads supporting the variants)												
Features & Coordinates		BWAmem_0.7.12 + FreeBayes_0.9.21						HCC1187_Tumor			Crystal_1.3.7			
		Benchmark's Variants BWA (bio-bwa.sourceforge.net) + FreeBayes (wiki.gacrc.uga.edu/wiki/Freebayes)						Crystal Genetics' Variants 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	112,162,854	1	T	C	1/1	Q>250	1	T	C	1/1	PASS
2	APC	1	5	112,164,561	1	G	A	1/1	Q>250	1	G	A	1/1	PASS
3	APC	1	5	112,175,617	1	T	A	1/1	Q>250	1	T	A	1/1	PASS
4	APC	1	5	112,175,770	1	G	A	1/1	Q>250	1	G	A	1/1	PASS
5	APC	1	5	112,176,325	1	G	A	1/1	Q>250	1	G	A	1/1	PASS
6	APC	1	5	112,176,559	1	T	G	1/1	Q>250	1	T	G	1/1	PASS
7	APC	1	5	112,176,756	1	T	A	1/1	Q>250	1	T	A	1/1	PASS
8	APC	1	5	112,177,171	1	G	A	1/1	Q>250	1	G	A	1/1	PASS
9	APC	1	5	112,180,228	1	CAAAAAAAT	CAAAAAAAT	1/1	Q>250	1	C	CA	1/1	PASS
10	APC	1	5	112,180,921	1	T	C	1/1	Q>250	1	T	C	1/1	PASS
11	APC	1	5	112,181,191	0	-	-	-	-	1	G	T	0/1	PASS
12	APC	1	5	112,181,379	1	C	G	1/1	Q>250	1	C	G	1/1	PASS
13	APC	1	5	112,181,576	1	G	A	1/1	Q>250	1	G	A	1/1	PASS
14	ATM	1	11	108,093,833	1	G	A	0/1	Q>250	1	G	A	0/1	PASS
15	ATM	1	11	108,183,167	1	G	G	1/1	Q>250	1	A	G	1/1	PASS
16	ATM	1	11	108,236,783	1	GTAT	TTAC	0/1	Q>250	1	G	T	0/1	PASS
17	ATM	1	11	108,236,786	0	-	-	-	-	1	T	C	0/1	PASS
18	ATM	1	11	108,237,839	1	C	T	0/1	Q>250	1	C	T	0/1	PASS
19	ATM	1	11	108,239,628	1	G	T	0/1	Q>250	1	G	T	0/1	PASS
20	BARD1	1	2	215,590,410	1	G	A	1/1	Q>250	1	G	A	1/1	PASS
21	BARD1	1	2	215,590,582	1	C	T	1/1	Q>250	1	C	T	1/1	PASS
22	BARD1	1	2	215,590,789	1	T	A	1/1	Q>250	1	T	A	1/1	PASS
23	BARD1	1	2	215,592,290	1	C	G	1/1	Q>250	1	C	G	1/1	PASS
24	BARD1	1	2	215,592,306	1	G	A	1/1	Q>250	1	G	A	1/1	PASS
25	BARD1	1	2	215,592,906	1	T	A	1/1	Q>250	1	T	A	1/1	PASS
26	BARD1	1	2	215,593,233	1	T	C	1/1	Q>250	1	T	C	1/1	PASS
27	BARD1	1	2	215,593,261	1	CTTTTTTTTTTTTG	CTTTTTTTTTTTTTTG	1/1	Q>250	1	C	CTT	1/1	PASS
28	BARD1	1	2	215,593,277	0	-	-	-	-	1	G	TG	0/1	PASS
29	BARD1	1	2	215,632,254	0	-	-	-	-	1	ACA	ATG	1/1	PASS
30	BARD1	1	2	215,632,255	1	CA	TG	1/1	Q>250	0	-	-	-	-
31	BARD1	1	2	215,645,464	1	C	G	1/1	Q>250	1	C	G	1/1	PASS
32	BARD1	1	2	215,674,224	1	G	A	1/1	Q>250	1	G	A	1/1	PASS
33	BARD1	1	2	215,674,323	1	C	G	1/1	Q>250	1	C	G	1/1	PASS
34	BARD1	1	2	215,674,341	1	A	G	1/1	Q>250	1	A	G	1/1	PASS
35	BARD1	1	2	215,674,371	1	C	T	1/1	Q>250	1	C	T	1/1	PASS
36	BMPR1A	1	10	88,516,595	1	T	C	1/1	Q>250	1	T	C	1/1	PASS
37	BMPR1A	1	10	88,684,586	0	-	-	-	-	1	A	G	0/1	PASS
38	CDK4	1	12	58,142,019	0	-	-	-	-	1	G	AG	0/1	PASS
39	MSH6	1	2	48,010,488	1	G	A	1/1	Q>250	1	G	A	1/1	PASS
40	NBN	1	8	90,945,598	1	C	T	0/1	Q>250	1	C	T	0/1	PASS
41	NBN	1	8	90,945,833	1	A	G	0/1	Q>250	1	A	G	0/1	PASS
42	NBN	1	8	90,946,118	1	T	C	0/1	Q>250	1	T	C	0/1	PASS
43	NBN	1	8	90,996,832	0	-	-	-	-	1	A	C	0/1	PASS
44	SMAD4	1	18	48,606,335	1	GTTTTTTTTTTTTTA	GTTTTTTTTTTTTTTA	0/1	Q>250	1	G	GT	0/1	PASS
45	SMAD4	1	18	48,610,382	1	GCACACACACACACACACACACAG	GCACACACACACACACACACACAG	1/1	Q>250	1	GCA	GCACACACAG	1/2	PASS
46	SMAD4	1	18	48,611,260	1	G	C	0/1	Q>250	1	G	C	0/1	PASS
47	STK11	1	19	1,228,191	1	T	C	1/1	Q>250	1	T	C	1/1	PASS
48	STK11	1	19	1,228,412	1	AAAGCTGGGA	AA	0/1	Q>250	1	AAAGCTGGG	A	1/1	PASS
49	TP53	1	17	7,572,154	1	GAAAAAAAAAAAAAAAAAAG	GAAAAAAAAAAAAAAAAAAG	1/1	Q<=250	1	GA	G	1/1	PASS
50	TP53	1	17	7,578,645	1	C	T	1/1	Q>250	1	C	T	1/1	PASS
51	TP53	1	17	7,578,727	0	-	-	-	-	1	TTTG	G	1/1	PASS
52	TP53	1	17	7,579,362	1	AACCG	AG	1/1	Q>250	0	-	-	-	-
53	TP53	1	17	7,579,363	0	-	-	-	-	1	ACCG	G	1/1	PASS
54	TP53	1	17	7,579,472	1	G	C	1/1	Q>250	1	G	C	1/1	PASS
55	TP53	1	17	7,579,801	1	G	C	1/1	Q>250	1	G	C	1/1	PASS