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Supplemental Data Table S1. VAF (%) and coverage depth of HRR genomic variants identified with the FoundationOne CDx and Oncomine Comprehensive assays

Sample No.	Variant_ Class	Variant_Effect	Gene	Transcript	HGVSc	HGVSp	Allelic frequency (%)		Coverage depth		HRRm status	
							FoundationOne CDx	Oncomine Comprehensive	FoundationOne CDx	Oncomine Comprehensive	FoundationOne CDx	Oncomine Comprehensive
FFPE_1	Indel	Frameshift	*RAD54L*	NM_001142548.1	c.316delC	p.Arg106AlafsTer21	45.78	50.26	1,018	3,898	Positive	Positive
FFPE_2	Indel	Frameshift	*BRCA2*	NM_000059.3	c.5351dup	p.Asn1784Lysfs*3	16.89	17.75	2,362	1,865	Positive	Positive
FFPE_4	SNV	Nonsense	*BRCA2*	NM_000059.3	c.6715G>T	p.Glu2239Ter	12.19	10.94	1,075	2,743	Positive	Positive
FFPE_4	SNV	Missense	*BRCA2*	NM_000059.3	c.398C>G	p.Pro133Arg	12.03	12.54	806	2,281	Negative	Negative
FFPE_7	Indel	Frameshift	*CDK12*	NM_016507.3	c.2597_2598insT	p.Leu866PhefsTer4	7.34	6.02	1,036	1,147	Positive	Positive
FFPE_7	SNV	Missense	*CDK12*	NM_016507.3	c.2219A>C	p.Gln740Pro	8.59	6.78	1,094	958	Negative	Negative
FFPE_9	SNV	Nonsense	*BRCA2*	NM_000059.3	c.8084C>G	p.Ser2695Ter	90.66	92.7	792	1,685	Positive	Positive
FFPE_9	SNV	Missense	*BRCA1*	NM_007294.3	c.5576C>G	p.Pro1859Arg	66.23	65.21	1,063	3,998	Negative	Negative
FFPE_11	SNV	Splicing variant	*BRCA2*	NM_000059.3	c.8953+1G>T	p?	54.58	51.61	590	837	Positive	Positive
FFPE_12	Indel	Frameshift	*ATM*	NM_000051.3	c.1903delC	p.His635ThrfsTer14	44.39	63.05	588	433	Positive	Positive
FFPE_16	SNV	Nonsense	*BRCA1*	NM_007294.3	c.2800C>T	p.Gln934Ter	48.64	49.39	1,032	2,553	Positive	Positive
FFPE_16	SNV	Missense	*PALB2*	NM_024675.3	c.1379A>G	p.Gln460Arg	48.62	47.43	1,047	2,338	Negative	Negative
FFPE_17	Indel	Frameshift	*CHEK2*	NM_007194.4	c.461del	p.Asn154Thrfs*7	31.5	24.86	1,233	1,947	Positive	Positive
FFPE_17	SNV	Missense	*ATM*	NM_000051.3	c.3797A>T	p.Asp1266Val	30.38	31.53	1,241	1,998	Negative	Negative
FFPE_18	SNV	Nonsense	*BRCA2*	NM_000059.3	c.5635G>T	p.Glu1879Ter	63.24	60.06	389	631	Positive	Positive
FFPE_21	Indel	Frameshift	*BRCA2*	NM_000059.3	c.6627_6634delAGAAGTTT	p.Ile2209MetfsTer13	54.47	59.51	995	1,536	Positive	Positive
FFPE_22	SNV	Nonsense	*ATM*	NM_000051.3	c.5692C>T	p.Arg1898Ter	89.74	91.36	341	579	Positive	Positive
FFPE_23	**SNV**	**Nonsense**	***ATM***	**NM_000051.3**	**c.5188C>T**	**p.Arg1730Ter**	**2.34**	**0.92**	**728**	**1,301**	**Positive**	**Negative**
FFPE_23	**SNV**	**Synonymous**	***ATM***	**NM_000051.3**	**c.2250G>A**	**p.Lys750=**	**(-)**	**25.07**	**(-)**	**730**	**Negative**	**Positive**
FFPE_24	SNV	Missense	*RAD51C*	NM_058216.2	c.406A>T	p.Met136Leu	48.75	47.1	1,081	2,119	Negative	Negative
FFPE_26	Indel	Frameshift	*BRCA2*	NM_000059.3	c.5576_5579delTTAA	p.Ile1859LysfsTer3	46.43	52.7	995	1850	Positive	Positive
FFPE_28	SNV	Splicing variant	*ATM*	NM_000051.3	c.4436+1G>T	p?	7.92	5.59	341	1,520	Positive	Positive
FFPE_34	SNV	Missense	*CHEK2*	NM_007194.4	c.410G>A	p.Arg137Gln	48.33	52.32	989	1,898	Negative	Negative
FFPE_35	SNV	Missense	*BRCA2*	NM_000059.3	c.7052C>G	p.Ala2351Gly	50.49	53.23	1,440	975	Negative	Negative
FFPE_36	SNV	Missense	*BRCA2*	NM_000059.3	c.7052C>G	p.Ala2351Gly	34.28	35.4	1,336	870	Negative	Negative
FFPE_36	SNV	Missense	*BRCA2*	NM_000059.3	c.5785A>G	p.Ile1929Val	62.33	66.26	1,468	827	Negative	Negative
FFPE_37	SNV	Missense	*PALB2*	NM_024675.3	c.3236C>T	p.Ala1079Val	45.54	47.14	1,010	1,625	Negative	Negative
FFPE_38	SNV	Splicing variant	*ATM*	NM_000051.3	c.3994-1G>A	p?	26.92	30.49	509	597	Positive	Positive
FFPE_41	Indel	Nonsense	*CDK12*	NM_016507.3	c.688_701delAGCTCCAAACAAGA	p.Ser230Ter	26.63	29.13	1,397	3,927	Positive	Positive
FFPE_41	Indel	Frameshift	*CDK12*	NM_016507.3	c.711delC	p.Ser238ArgfsTer100	55.78	54.36	1,237	3,957	Positive	Positive
FFPE_44	Indel	Frameshift	*CDK12*	NM_016507.3	c.246delC	p.Phe83SerfsTer9	25.72	29.77	1,143	702	Positive	Positive
FFPE_44	Indel	Splicing variant	*CDK12*	NM_016507.3	c.2836_2846+4delGAACTGATCAGGTAC	p?	26.1	42.86	954	469	Positive	Positive

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Supplemental Data Table S1. Continued

Sample No.	Variant_ Class	Variant_Effect	Gene	Transcript	HGVSc	HGVSp	Allelic frequency (%)		Coverage depth		HRRm status	
							FoundationOne CDx	Oncomine Comprehensive	FoundationOne CDx	Oncomine Comprehensive	FoundationOne CDx	Oncomine Comprehensive
FFPE_45	Indel	Frameshift	*BRCA2*	NM_000059.3	c.1278delA	p.Asp427ThrfsTer3	52.52	49	775	402	Positive	Positive
FFPE_48	Indel	Frameshift	*BRCA2*	NM_000059.3	c.5946delT	p.Ser1982ArgfsTer22	47.61	48.36	1,151	3,892	Positive	Positive
FFPE_49	SNV	Synonymous	*BRCA2*	NM_000059.3	c.9117G>A	p.Pro3039=	59.74	57.8	775	1,320	Positive	Positive
FFPE_51	Indel	Nonsense	*ATM*	NM_000051.3	c.7705_7706delGA	p.Asp2569Ter	46.73	47.73	1,130	1,980	Positive	Positive
FFPE_51	Indel	Frameshift	*ATM*	NM_000051.3	c.4741dupA	p.Ile1581AsnfsTer5	32.46	31.29	949	1,927	Positive	Positive
FFPE_51	Indel	Nonsense	*ATM*	NM_000051.3	c.7705_7706delGA	p.Asp2569Ter	46.73	47.73	1,130	1,980	Positive	Positive
FFPE_55	Indel	Splicing	*CDK12*	NM_016507.3	c.2342T>G	p.Leu781Ter	41.13	41.88	693	2,827	Positive	Positive
FFPE_55	SNV	Splicing variant	*CDK12*	NM_016507.3	c.3095+1G>A	p?	47.19	41.42	606	2,424	Positive	Positive
FFPE_59	Indel	Splicing variant	*CDK12*	NM_016507.3	c.2769-6_2770delTTCTAGAT	p?	41.36	49.7	856	2,803	Positive	Positive
FFPE_60	SNV	Splicing variant	*CDK12*	NM_016507.3	c.2768+1G>T	p?	21.84	18.79	1,177	1,581	Positive	Positive
FFPE_60	Indel	Frameshift	*CDK12*	NM_016507.3	c.1159delG	p.Val387SerfsTer49	11.93	10.3	1442	1,457	Positive	Positive
FFPE_60	SNV	Missense	*ATM*	NM_000051.3	c.4365T>A	p.Ser1455Arg	53.96	50.63	1,023	2,137	Negative	Negative
FFPE_62	Indel	Frameshift	*BRCA2*	NM_000059.3	c.4471_4474delCTGA	p.Leu1491LysfsTer12	44.5	47.87	1,036	211	Positive	Positive
FFPE_62	Indel	Frameshift	*BRCA2*	NM_000059.3	c.9491delA	p.Asn3164IlefsTer53	8.52	9.47	1,197	676	Positive	Positive
FFPE_64	Indel	Frameshift	*CDK12*	NM_016507.3	c.198delT	p.Ile67SerfsTer25	6.13	6.02	1,224	3,985	Positive	Positive
FFPE_68	SNV	Nonsense	*PPP2R2A*	NM_000059.3	c.1123C>T	p.Arg375Ter	91.93	95.35	719	516	Positive	Positive
FFPE_71	Indel	Frameshift	*CDK12*	NM_016507.3	c.800delG	p.Gly267GlufsTer71	36.97	38.05	1,918	3,958	Positive	Positive
FFPE_71	Indel	Frameshift	*CDK12*	NM_016507.3	c.303_306delATCA	p.Ser102IlefsTer21	30.09	33.56	1,645	2,902	Positive	Positive
FFPE_71	SNV	Missense	*BRCA2*	NM_000059.3	c.8356G>A	p.Ala2786Thr	50.11	48.58	902	4,000	Negative	Negative
FFPE_71	SNV	Missense	*BRCA2*	NM_000059.3	c.1166C>T	p.Pro389Leu	51.1	46.98	1,184	4,000	Negative	Negative
FFPE_72	SNV	Splicing variant	*ATM*	NM_000051.3	c.6572+1G>A	p?	39.71	38.81	486	2,463	Positive	Positive
FFPE_75	**SNV**	**Missense**	***CHEK1***	**NM_001114122.2**	**c.1097C>T**	**p.Ser366Leu**	**(-)**	**6.62**	**(-)**	**272**	**Negative**	**Negative**
FFPE_75	SNV	Nonsense	*BRCA2*	NM_000059.3	c.5645C>A	p.Ser1882Ter	61.66	61.24	519	1,504	Positive	Positive
FFPE_76	Indel	Frameshift	*BRCA2*	NM_000059.3	c.5350_5351delAA	p.Asn1784HisfsTer2	51.86	61.12	1,051	1,970	Positive	Positive
FFPE_76	Indel	Frameshift	*CHEK2*	NM_007194.4	c.591del	p.Val198Phefs*7	45.11	45.79	829	1,755	Positive	Positive
FFPE_77	SNV	Nonsense	*BRCA2*	NM_000059.3	c.3103G>T	p.Glu1035Ter	62.84	65.84	767	1,806	Positive	Positive
FFPE_78	SNV	Nonsense	*ATM*	NM_000051.3	c.5644C>T	p.Arg1882Ter	7.2	2.75	1,097	1,127	Positive	Positive
FFPE_78	SNV	Missense	*BRIP1*	NM_032043.3	c.634G>A	p.Gly212Ser	47.11	42.55	917	2,000	Negative	Negative
FFPE_79	SNV	Missense	*BARD1*	NM_000465.4	c.2306C>T	p.Ser769Phe	51.08	47.47	926	3,303	Negative	Negative
FFPE_80	Indel	Frameshift	*CHEK2*	NM_007194.4	c.1100del	p.Thr367Metfs*15	56.03	66.77	373	1,336	Positive	Positive
FFPE_80	SNV	Missense	*BRCA2*	NM_000059.3	c.4315G>A	p.Ala1439Thr	49.48	44.61	966	955	Negative	Negative
FFPE_83	Indel	Frameshift	*CDK12*	NM_016507.3	c.2698delT	p.Trp900GlyfsTer9	10.9	11.71	954	1,495	Positive	Positive

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Supplemental Data Table S1. Continued

Sample No.	Variant_ Class	Variant_Effect	Gene	Transcript	HGVSc	HGVSp	Allelic frequency (%)		Coverage depth		HRRm status	
							FoundationOne CDx	Oncomine Comprehensive	FoundationOne CDx	Oncomine Comprehensive	FoundationOne CDx	Oncomine Comprehensive
FFPE_84	Indel	Frameshift	*BRCA2*	NM_000059.3	c.9672_9673insA	p.Tyr3225IlefsTer30	54.87	64.21	924	1,467	Positive	Positive
FFPE_85	Indel	Frameshift	*CDK12*	NM_016507.3	c.215delA	p.Glu72GlyfsTer20	25.52	23.37	905	1,896	Positive	Positive
FFPE_85	Indel	Frameshift	*CDK12*	NM_016507.3	c.2622delA	p.Lys874AsnfsTer2	12.29	9.15	911	852	Positive	Positive
FFPE_87	SNV	Missense	*BRCA2*	NM_000059.3	c.964A>C	p.Lys322Gln	49.84	74.47	642	854	Negative	Negative
FFPE_88	Indel	Frameshift	*BARD1*	NM_000465.4	c.513del	p.Asp172Metfs*40	18.77	20.61	1,188	1,917	Positive	Positive
FFPE_88	Indel	Frameshift	*BRCA2*	NM_000059.3	c.5351del	p.Asn1784Thrfs*7	12.46	15.31	2,794	1,972	Positive	Positive
FFPE_89	SNV	Missense	*BRCA2*	NM_000059.3	c.2908G>A	p.Asp970Asn	49.49	48	1,087	2,000	Negative	Negative
FFPE_92	Indel	Frameshift	*BRCA2*	NM_000059.3	c.4538_4566del	p.Asp1513Glyfs*6	73.52	65.8 (5.75)	506	260 (87)	Positive	Positive
FFPE_93	Indel	Frameshift	*CHEK2*	NM_007194.4	c.1100del	p.Thr367Metfs*15	51.6	49.78	528	679	Positive	Positive
FFPE_94	SNV	Missense	*CDK12*	NM_016507.3	c.2843T>C	p.Ile948Thr	68.6	74.57	551	1,726	Negative	Negative
FFPE_96	SNV	Splicing variant	*ATM*	NM_000051.3	c.2921+1G>T	p?	56.49	56.68	1,055	3,944	Positive	Positive
FFPE_97	SNV	Missense	*BRCA2*	NM_000059.3	c.6325G>A	p.Val2109Ile	64.1	69	844	471	Negative	Negative
FFPE_99	SNV	Nonsense	*CDK12*	NM_016507.3	c.268A>T	p.Lys90Ter	5.73	6.02	890	1,993	Positive	Positive
FFPE_99	SNV	Splicing variant	*CDK12*	NM_016507.3	c.3095+1G>T	p?	5.59	1.95	930	4,532	Positive	Positive
FFPE_99	SNV	Missense	*BRCA2*	NM_000059.3	c.6853A>G	p.Ile2285Val	48.01	48.15	752	1,813	Negative	Negative

Bold denotes discrepancy results between NGS assays.
Abbreviations: SNV, single nucleotide variant; VAF, variant allele frequency; HRR, homologous recombination repair; HRRm, homologous recombination repair mutation; HGVSp, Human Genome Variation Society protein sequence; HGVSc, Human Genome Variation Society coding sequence.

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Supplemental Data Table S2. VAF (%) and coverage depth of HRR genomic alterations in the FoundationOne CDx assay and SureSelect Custom assay

Sample No.	Variant_ Class	Variant_Effect	Gene	Transcript	HGVSc	HGVSp	Allelic frequency (%)		Coverage depth		HRRm status	
							Foundation-One CDx	SureSelect Custom	Foundation-One CDx	SureSelect Custom	FoundatioOne CDx	SureSelect Custom
FFPE_1	Indel	Frameshift	*RAD54L*	NM_001142548.1	c.316delC	p.Arg106AlafsTer21	45.8	47.7	1,018	1,778	Positive	Positive
FFPE_2	Indel	Frameshift	*BRCA2*	NM_000059.3	c.5351dup	p.Asn1784Lysfs*3	16.9	20.1	2,362	3,036	Positive	Positive
FFPE_4	SNV	Nonsense	*BRCA2*	NM_000059.3	c.6715G>T	p.Glu2239Ter	12.2	12.9	1,075	1,935	Positive	Positive
FFPE_4	SNV	Missense	*BRCA2*	NM_000059.3	c.398C>G	p.Pro133Arg	12	12.1	806	1,488	Negative	Negative
FFPE_7	Indel	Frameshift	*CDK12*	NM_016507.3	c.2597dup	p.Leu866Phefs*4	7.3	7.5	1,036	1,034	Positive	Positive
FFPE_7	SNV	Missense	*CDK12*	NM_016507.3	c.2219A>C	p.Gln740Pro	8.6	5.9	1,094	627	Negative	Negative
FFPE_9	SNV	Nonsense	*BRCA2*	NM_000059.3	c.8084C>G	p.Ser2695Ter	90.7	92.4	792	1,019	Positive	Positive
FFPE_9	SNV	Missense	*BRCA1*	NM_007294.3	c.5576C>G	p.Pro1859Arg	66.2	66.2	1,063	1,645	Negative	Negative
FFPE_11	SNV	Splicing variant	*BRCA2*	NM_000059.3	c.8953+1G>T	p?	54.6	52.6	590	420	Positive	Positive
FFPE_12	Indel	Frameshift	*ATM*	NM_000051.3	c.1903delC	p.His635ThrfsTer14	44.4	43.8	588	176	Positive	Positive
FFPE_16	SNV	Nonsense	*BRCA1*	NM_007294.3	c.2800C>T	p.Gln934Ter	48.6	47.5	1,032	1,421	Positive	Positive
FFPE_16	SNV	Missense	*PALB2*	NM_024675.3	c.1379A>G	p.Gln460Arg	48.6	46.2	1,047	796	Negative	Negative
FFPE_17	Indel	Frameshift	*CHEK2*	NM_007194.4	c.461del	p.(Asn154Thrfs*7)	25.1	28.9	1,233	823	Positive	Positive
FFPE_17	SNV	Missense	*ATM*	NM_000051.3	c.3797A>T	p.Asp1266Val	30.4	30.6		566	Negative	Negative
FFPE_21	Indel	Frameshift	*BRCA2*	NM_000059.3	c.6627_6634delAGAAGTTT	p.Ile2209MetfsTer13	54.5	52.3	995	733	Positive	Positive
FFPE_22	SNV	Nonsense	*ATM*	NM_000051.3	c.5692C>T	p.Arg1898Ter	89.7	87.8	341	401	Positive	Positive
FFPE_23	SNV	Nonsense	*ATM*	NM_000051.3	c.5188C>T	p.Arg1730Ter	2.3	1.9	728	736	Positive	Positive
FFPE_23	**SNV**	**Synonymous**	***ATM***	**NM_000051.3**	**c.2250G>A**	**p.Lys750=**	**(-)**	**24.2**	**(-)**	**310**	**Negative**	**Positive**
FFPE_24	SNV	Missense	*RAD51C*	NM_058216.2	c.406A>T	p.Met136Leu	48.8	46.5	1,081	1,027	Negative	Negative
FFPE_25	Indel	Frameshift	*BRCA2*	NM_000059.3	c.5576_5579delTTAA	p.Ile1859LysfsTer3	47.4	54.3	667	243	Positive	Positive
FFPE_25	SNV	Missense	*BRCA2*	NM_000059.3	c.9218A>C	p.Asp3073Ala	13.5	11.7	1,085	429	Negative	Negative
FFPE_26	Indel	Frameshift	*BRCA2*	NM_000059.3	c.5576_5579delTTAA	p.Ile1859LysfsTer3	46.4	43.9	995	786	Positive	Positive
FFPE_28	SNV	Splicing variant	*ATM*	NM_000051.3	c.4436+1G>T	p?	7.9	5	341	220	Positive	Positive
FFPE_32	SNV	Nonsense	*CDK12*	NM_016507.3	c.2662G>T	p.Glu888Ter	9.4	3.9	983	412	Positive	Positive
FFPE_32	Indel	Frameshift	*CDK12*	NM_016507.3	c.198dup	p.(Ile67Tyrfs*8)	10	11	1,259	889	Positive	Positive
FFPE_34	SNV	Missense	*CHEK2*	NM_007194.4	c.410G>A	p.Arg137Gln	48.3	52.6	989	842	Negative	Negative
FFPE_35	SNV	Missense	*BRCA2*	NM_000059.3	c.7052C>G	p.Ala2351Gly	50.5	45.7	1,440	801	Negative	Negative
FFPE_36	SNV	Missense	*BRCA2*	NM_000059.3	c.7052C>G	p.Ala2351Gly	34.3	28.3	1,336	2,204	Negative	Negative
FFPE_36	SNV	Missense	*BRCA2*	NM_000059.3	c.5785A>G	p.Ile1929Val	62.3	63.2	1,468	2,164	Negative	Negative
FFPE_37	SNV	Missense	*PALB2*	NM_024675.3	c.3236C>T	p.Ala1079Val	45.5	42.9	1,010	940	Negative	Negative
FFPE_38	SNV	Splicing variant	*ATM*	NM_000051.3	c.3994-1G>A	p?	26.9	22.2	509	239	Positive	Positive
FFPE_41	Indel	Nonsense	*CDK12*	NM_016507.3	c.688_701delAGCTCCAAACAAGA	p.Ser230Ter	26.6	23.4	1,397	852	Positive	Positive

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Supplemental Data Table S2. Continued

Sample No.	Variant_ Class	Variant_Effect	Gene	Transcript	HGVSc	HGVSp	Allelic frequency (%)		Coverage depth		HRRm status	
							Foundation-One CDx	SureSelect Custom	Foundation-One CDx	SureSelect Custom	FoundatioOne CDx	SureSelect Custom
FFPE_41	Indel	Frameshift	*CDK12*	NM_016507.3	c.711delC	p.Ser238ArgfsTer100	55.8	56.8	1,237	764	Positive	Positive
FFPE_41	SNV	Missense	*BRIP1*	NM_032043.3	c.415T>G	p.Ser139Ala	40.4	41.9	1,665	1,021	Negative	Negative
FFPE_43	Indel	Frameshift	*CDK12*	NM_016507.3	c.2305del	p.Ile769Serfs*13	7.4	4.6	1,213	653	Positive	Positive
FFPE_43	Indel	Frameshift	*CDK12*	NM_016507.3	c.505delA	p.Ser169Alafs*22	6.9	6.9	1,250	769	Positive	Positive
FFPE_43	SNV	Missense	*RAD51B*	NM_002877.5	c.203A>G	p.Tyr68Cys	49.9	53.6	798	295	Negative	Negative
FFPE_44	Indel	Frameshift	*CDK12*	NM_016507.3	c.246delC	p.Phe83SerfsTer9	25.7	27.5	1,143	1,002	Positive	Positive
FFPE_44	Indel	Splicing variant	*CDK12*	NM_016507.3	c.2836_2846+4delGAACTGATCAGGTAC	p?	26.1	18.1	954	591	Positive	Positive
FFPE_45	Indel	Frameshift	*BRCA2*	NM_000059.3	c.1278delA	p.Asp427ThrfsTer3	52.5	58.4	775	551	Positive	Positive
FFPE_48	Indel	Frameshift	*BRCA2*	NM_000059.3	c.5946delT	p.Ser1982ArgfsTer22	47.6	46.8	1,151	1,650	Positive	Positive
FFPE_49	SNV	Synonymous	*BRCA2*	NM_000059.3	c.9117G>A	p.Pro3039=	59.7	47	775	460	Positive	Positive
FFPE_51	Indel	Nonsense	*ATM*	NM_000051.3	c.7705_7706delGA	p.Asp2569Ter	46.7	44.9	1,130	1,696	Positive	Positive
FFPE_51	Indel	Frameshift	*ATM*	NM_000051.3	c.4741dupA	p.Ile1581AsnfsTer5	32.5	33.3	949	1,353	Positive	Positive
FFPE_52	SNV	Nonsense	*BRCA2*	NM_000059.3	c.7480C>T	p.Arg2494Ter	37.5	40.7	792	538	Positive	Positive
FFPE_55	Indel	Splicing	*CDK12*	NM_016507.3	c.2342T>G	p.Leu781Ter	41.1	36.8	693	927	Positive	Positive
FFPE_55	SNV	Splicing variant	*CDK12*	NM_016507.3	c.3095+1G>A	p?	47.2	42.3	606	650	Positive	Positive
FFPE_59	Indel	Splicing variant	*CDK12*	NM_016507.3	c.2769-6_2770delTTCTAGAT	p?	41.4	39.5	856	947	Positive	Positive
FFPE_60	SNV	Splicing variant	*CDK12*	NM_016507.3	c.2768+1G>T	p?	21.8	16.8	1,177	512	Positive	Positive
FFPE_60	Indel	Frameshift	*CDK12*	NM_016507.3	c.1159delG	p.Val387SerfsTer49	11.9	9.2	1,442	665	Positive	Positive
FFPE_60	SNV	Missense	*ATM*	NM_000051.3	c.4365T>A	p.Ser1455Arg	54	38.4	1,023	510	Negative	Negative
FFPE_62	Indel	Frameshift	*BRCA2*	NM_000059.3	c.4471_4474delCTGA	p.Leu1491LysfsTer12	44.5	44.4	1,036	358	Positive	Positive
FFPE_62	Indel	Frameshift	*BRCA2*	NM_000059.3	c.9491delA	p.Asn3164IlefsTer53	8.5	10.6	1,197	530	Positive	Positive
FFPE_64	Indel	Frameshift	*CDK12*	NM_016507.3	c.198delT	p.Ile67SerfsTer25	6.1	5.4	1,224	3,894	Positive	Positive
FFPE_68	SNV	Nonsense	*PPP2R2A*	NM_000059.3	c.1123C>T	p.Arg375Ter	91.9	93.7	719	911	Positive	Positive
FFPE_71	Indel	Frameshift	*CDK12*	NM_016507.3	c.800delG	p.Gly267GlufsTer71	37	34.7	1,918	2,525	Positive	Positive
FFPE_71	Indel	Frameshift	*CDK12*	NM_016507.3	c.303_306delATCA	p.Ser102IlefsTer21	30.1	23.6	1,645	2,461	Positive	Positive
FFPE_71	SNV	Missense	*BRCA2*	NM_000059.3	c.8356G>A	p.Ala2786Thr	50.1	43.3	902	876	Negative	Negative
FFPE_71	SNV	Missense	*BRCA2*	NM_000059.3	c.1166C>T	p.Pro389Leu	51.1	49.9	1,184	1,059	Negative	Negative
FFPE_72	SNV	Splicing variant	*ATM*	NM_000051.3	c.6572+1G>A	p?	39.7	31.3	486	1,052	Positive	Positive
FFPE_75	SNV	Nonsense	*BRCA2*	NM_000059.3	c.5645C>A	p.Ser1882Ter	61.7	54.4	519	377	Positive	Positive
FFPE_76	Indel	Frameshift	*BRCA2*	NM_000059.3	c.5350_5351delAA	p.Asn1784HisfsTer2	51.9	57.6	1,051	523	Positive	Positive
FFPE_76	Indel	Frameshift	*CHEK2*	NM_007194.4	c.591del	p.Val198PhefsTer7	45.1	48.9	829	540	Positive	Positive
FFPE_77	SNV	Nonsense	*BRCA2*	NM_000059.3	c.3103G>T	p.Glu1035Ter	62.8	63.2	767	288	Positive	Positive

(*Continued to the next page*)

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Supplemental Data Table S2. Continued

Sample No.	Variant_ Class	Variant_Effect	Gene	Transcript	HGVSc	HGVSp	Allelic frequency (%)		Coverage depth		HRRm status	
							Foundation-One CDx	SureSelect Custom	Foundation-One CDx	SureSelect Custom	FoundatioOne CDx	SureSelect Custom
FFPE_78	SNV	Nonsense	*ATM*	NM_000051.3	c.5644C>T	p.Arg1882Ter	7.2	3.7	1,097	517	Positive	Positive
FFPE_78	SNV	Missense	*BRIP1*	NM_032043.3	c.634G>A	p.Gly212Ser	47.1	45.8	917	360	Negative	Negative
FFPE_79	SNV	Missense	*BARD1*	NM_000465.4	c.2306C>T	p.Ser769Phe	51.1	46.4	926	869	Negative	Negative
FFPE_80	Indel	Frameshift	*CHEK2*	NM_007194.4	c.1100del	p.Thr367MetfsTer15	56	66.1	373	183	Positive	Positive
FFPE_80	SNV	Missense	*BRCA2*	NM_000059.3	c.4315G>A	p.Ala1439Thr	49.5	35.9	966	284	Negative	Negative
FFPE_83	Indel	Frameshift	*CDK12*	NM_016507.3	c.2698delT	p.Trp900GlyfsTer9	10.9	7.7	954	1,056	Positive	Positive
FFPE_84	Indel	Frameshift	*BRCA2*	NM_000059.3	c.9672dup	p.Tyr3225IlefsTer30	54.9	54.2	924	450	Positive	Positive
FFPE_85	Indel	Frameshift	*CDK12*	NM_016507.3	c.215delA	p.Glu72GlyfsTer20	25.5	22.2	905	1,603	Positive	Positive
FFPE_85	Indel	Frameshift	*CDK12*	NM_016507.3	c.2622delA	p.Lys874AsnfsTer2	12.3	5.8	911	519	Positive	Positive
FFPE_87	SNV	Missense	*BRCA2*	NM_000059.3	c.964A>C	p.Lys322Gln	49.8	54	642	176	Negative	Negative
FFPE_88	Indel	Frameshift	*BARD1*	NM_000465.4	c.513del	p.Asp172MetfsTer40	18.8	22	1,188	980	Positive	Positive
FFPE_88	Indel	Frameshift	*BRCA2*	NM_000059.3	c.5351del	p.Asn1784ThrfsTer7	12.5	14.6	2,794	2,116	Positive	Positive
FFPE_89	SNV	Missense	*BRCA2*	NM_000059.3	c.2908G>A	p.Asp970Asn	49.5	41.7	1,087	470	Negative	Negative
FFPE_93	Indel	Frameshift	*CHEK2*	NM_007194.4	c.1100del	p.Thr367MetfsTer15	42.4	52.5	528	341	Positive	Positive
FFPE_94	SNV	Missense	*CDK12*	NM_016507.3	c.2843T>C	p.Ile948Thr	68.6	69	551	509	Negative	Negative
FFPE_96	SNV	Splicing variant	*ATM*	NM_000051.3	c.2921+1G>T	p?	56.5	54.3	1,055	735	Positive	Positive
FFPE_97	SNV	Missense	*BRCA2*	NM_000059.3	c.6325G>A	p.Val2109Ile	64.1	56.8	844	317	Negative	Negative
FFPE_98	Indel	Frameshift	*CHEK1*	NM_001274.5	c.1336-1delG	p?	5.5	6.3	998	347	Positive	Positive
FFPE_99	SNV	Nonsense	*CDK12*	NM_016507.3	c.268A>T	p.Lys90Ter	5.7	5.3	890	505	Positive	Positive
FFPE_99	SNV	Splicing variant	*CDK12*	NM_016507.3	c.3095+1G>T	p?	5.6	5	930	538	Positive	Positive
FFPE_99	SNV	Missense	*BRCA2*	NM_000059.3	c.6853A>G	p.Ile2285Val	48	40	752	125	Negative	Negative

Abbreviations: SNV, single nucleotide variant; VAF, variant allele frequency; HRR, homologous recombination repair; HRRm, homologous recombination repair mutation; HGVSp, Human Genome Variation Society protein sequence; HGVSc, Human Genome Variation Society coding sequence. Bold denotes discrepancy results between NGS assays.

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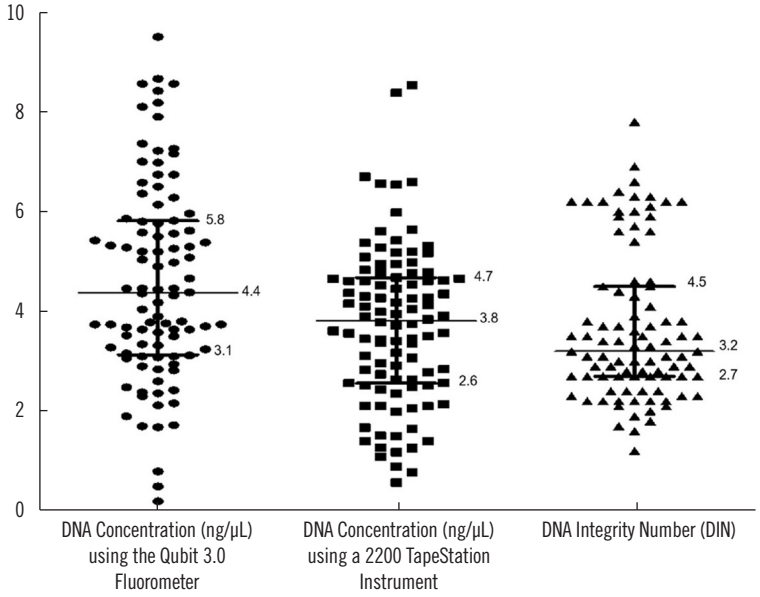
Supplemental Data Table S3. Comparison of the Oncomine Comprehensive and SureSelect Custom assays with the FoundationOne CDx assay for CNV detection

	Case	FoundationOne CDx assay		PPA (%) (95% CI)	NPA (%) (95% CI)	OPA (%) (95% CI)
		Positive	Negative			
Oncomine Comprehensive assay	Positive	3	0	60.0 (23.1–88.2)	100.0 (99.7–100.0)	99.8 (99.4–100.0)
	Negative	2	1,255			
SureSelect Custom assay	Positive	3	0	100.0 (43.9–100.0)	100.0 (99.7–100.0)	100.0 (99.7–100.0)
	Negative	0	1,317			

Abbreviations: CNV, copy number variation; OPA, overall percent agreement; NPA, negative percent agreement; PPA, positive percent agreement; CI, confidence interval.



Supplemental Data Fig. S1. Quality and concentration of DNA sequencing run metrics. The median DNA concentration using the Qubit 3.0 Fluorometer and a 2200 TapeStation Instrument was 4.4 ng/μL and 3.8 ng/μL, respectively. The median DNA integrity number (DIN) was 3.2 using a 2200 TapeStation Instrument.

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