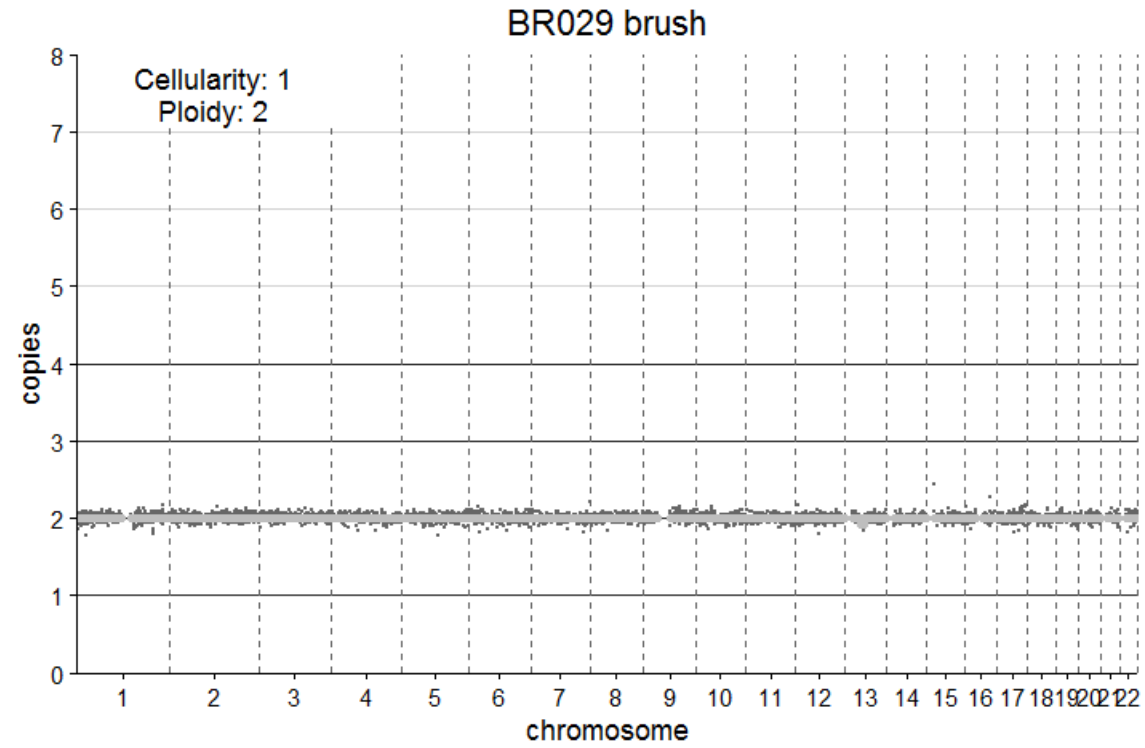
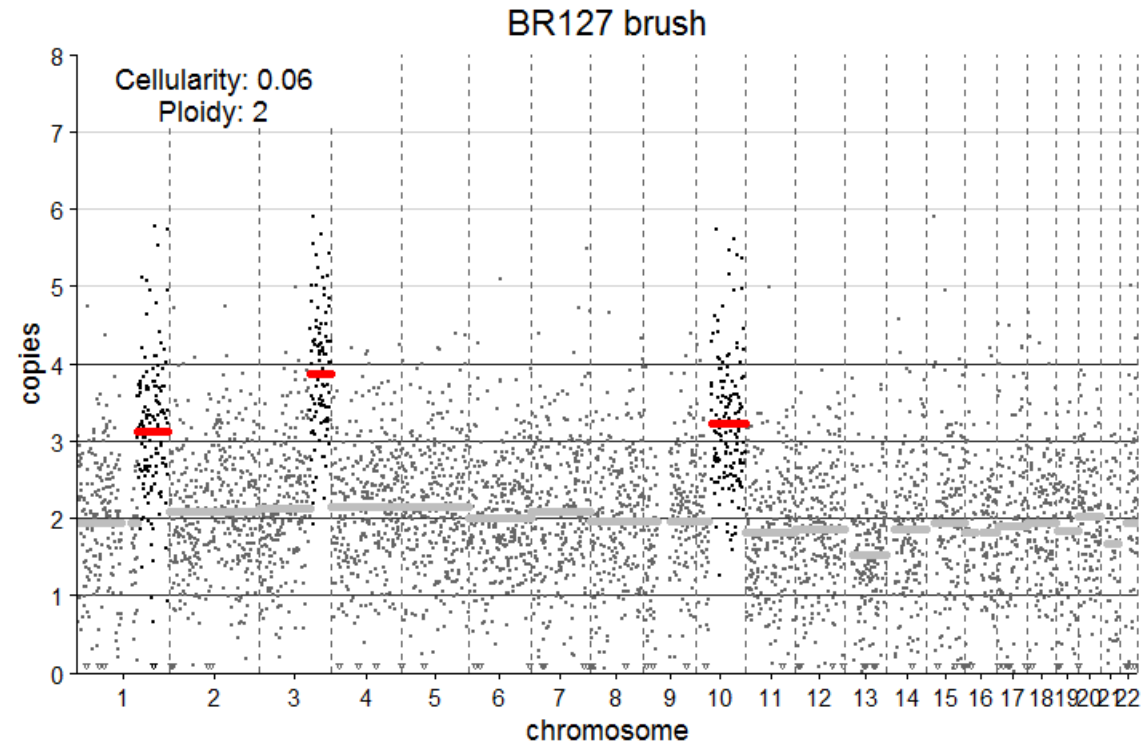


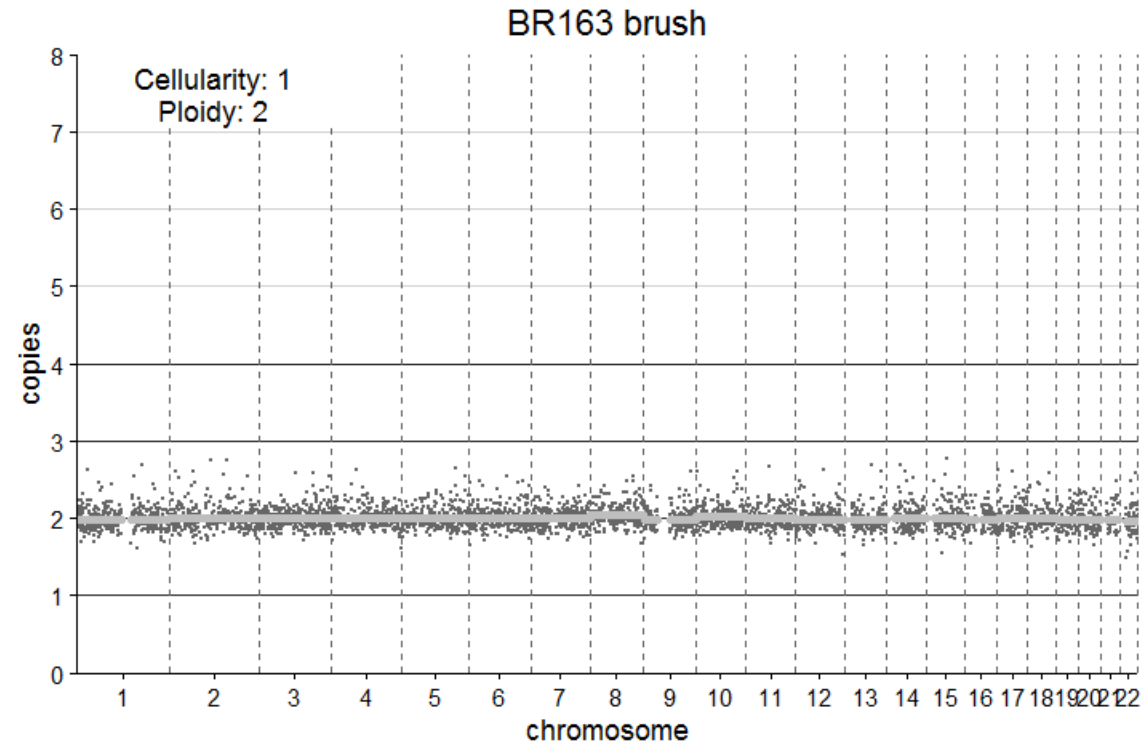
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Sample	Coverage		
												Mean	Max	Min
AU001	chr17	7578526	TP53	C	A	2661	2577	83	3.12	p.Cys135Phe	AU001	2497	3497	432



Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
											Sample	Mean	Max	Min
BR029	chr12	49445156	KMT2D	C..T	C	1724	1380	344	19.95	p.Ser762_Leu770del	BR029	2056	3538	433
BR029	chr12	49445175	KMT2D	T	C	1176	1048	91	7.99	p.Gln764Arg				

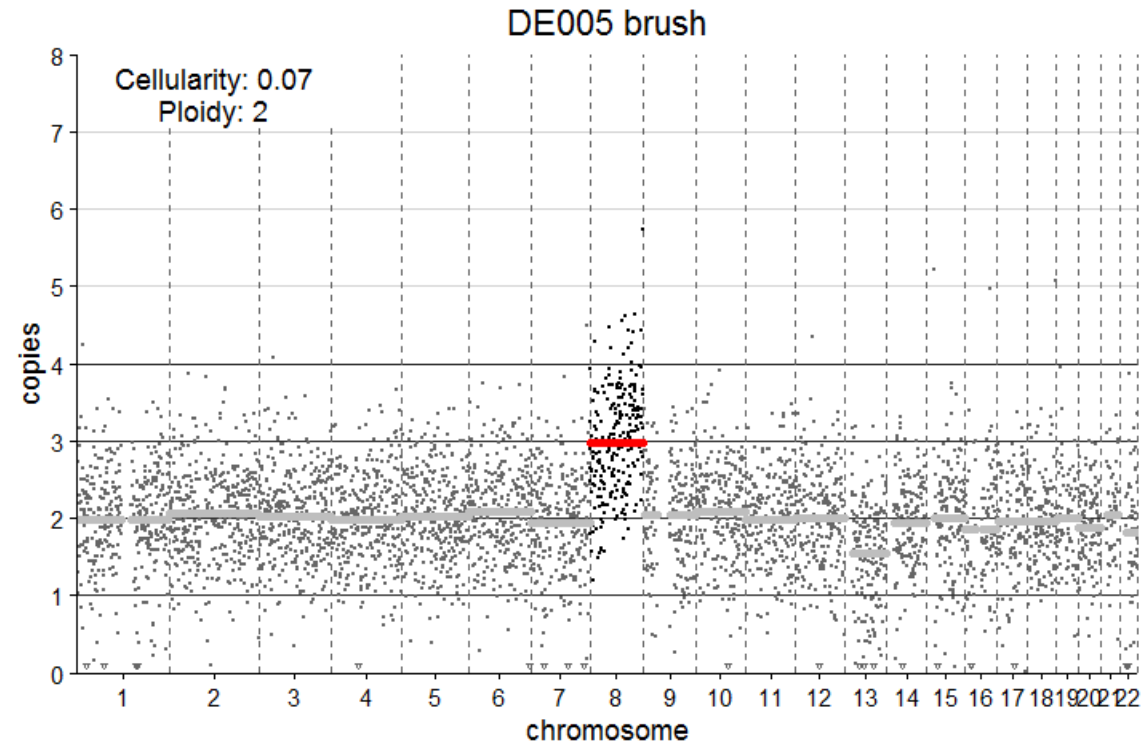


Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Sample	Coverage		
												Mean	Max	Min
BR127	chr12	49426587	KMT2D	T..C	T	1448	1366	83	5.73	p.Phe3966_3967del	BR127	1312	3614	486

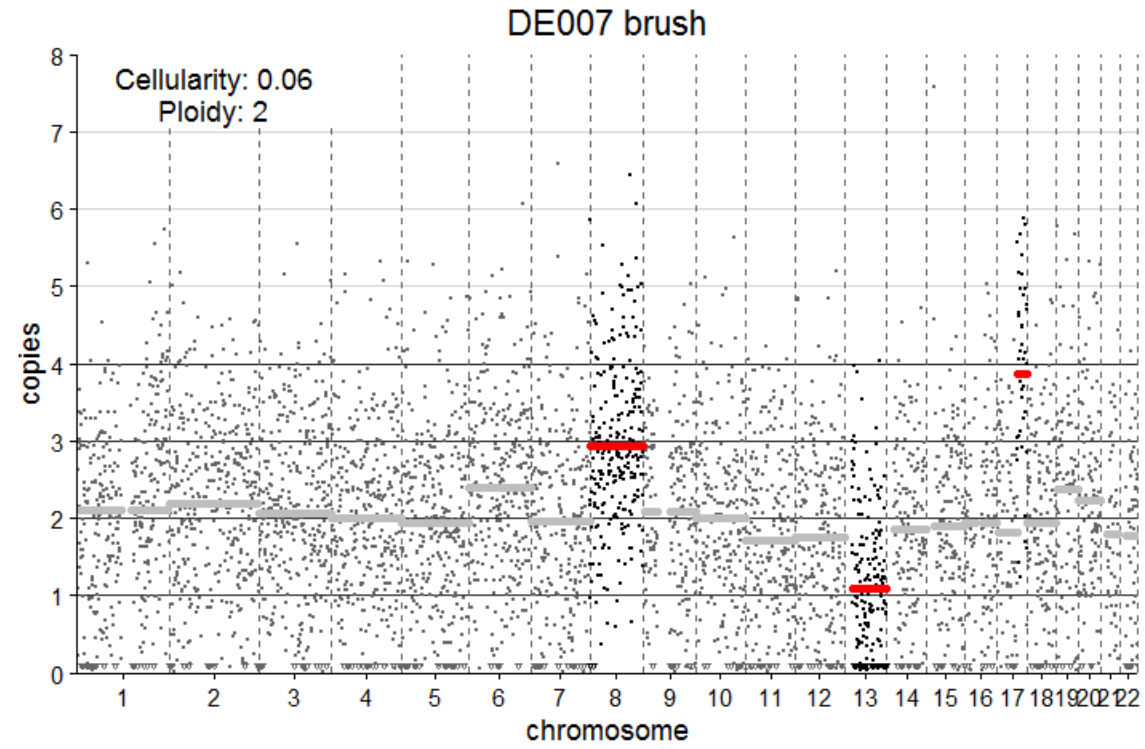


Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change
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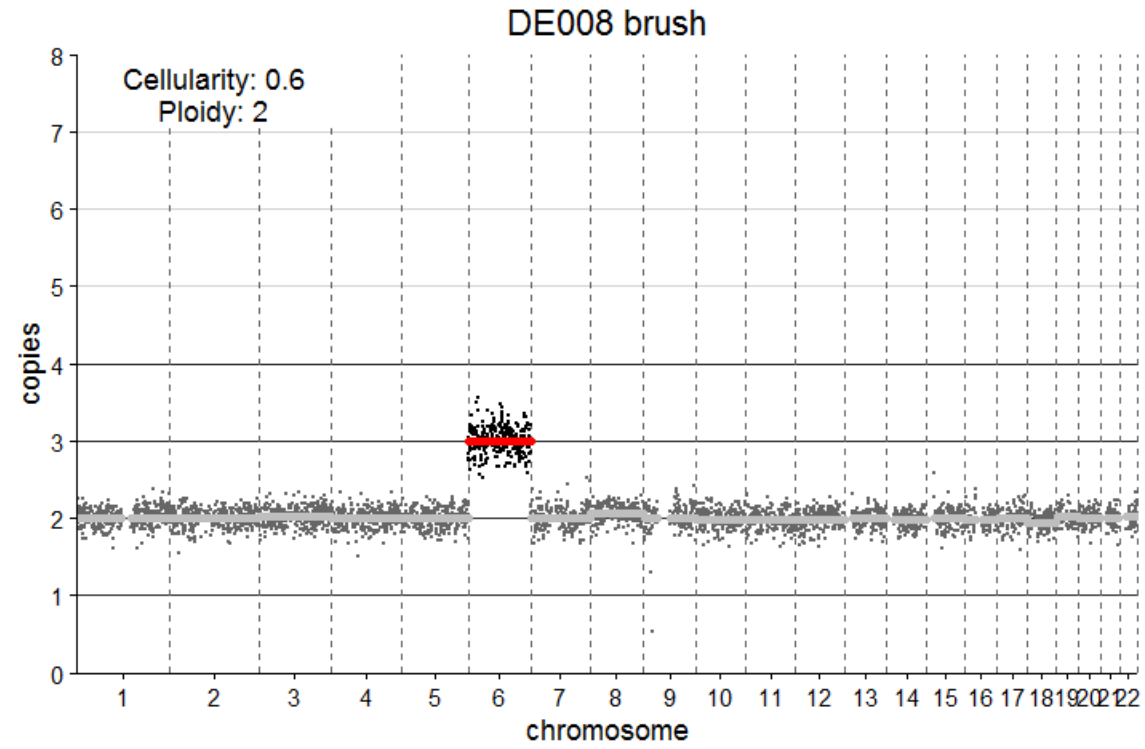
Sample	Coverage		
	Mean	Max	Min
BR163	673	1766	282



Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
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DE005											DE005	2653	4309	387

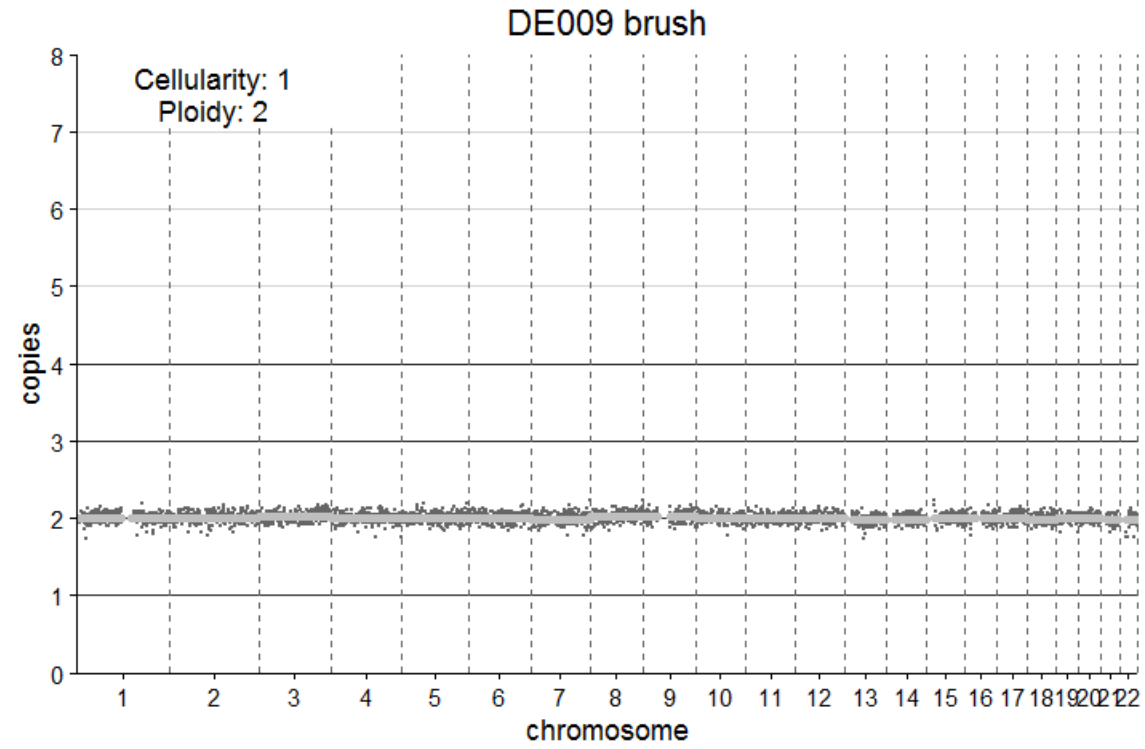


Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage		
											Sample	Mean	Max
DE007											2068	2890	323

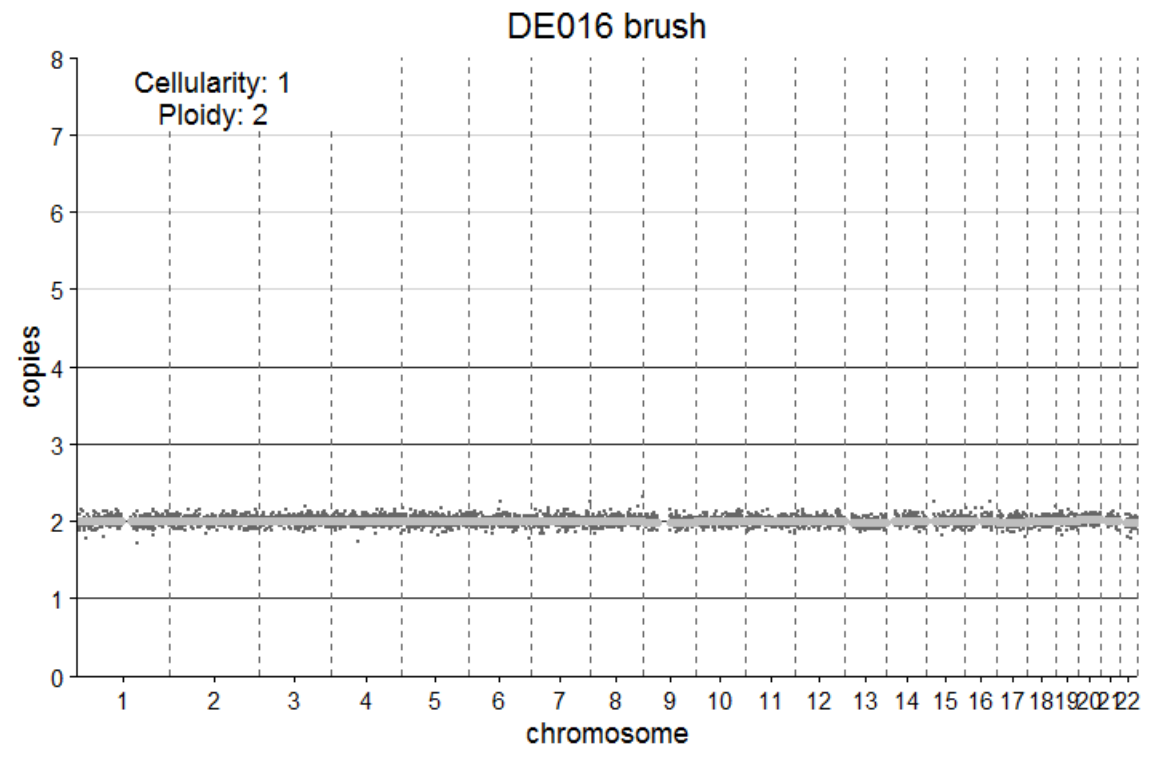


Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VOF (%)	Change
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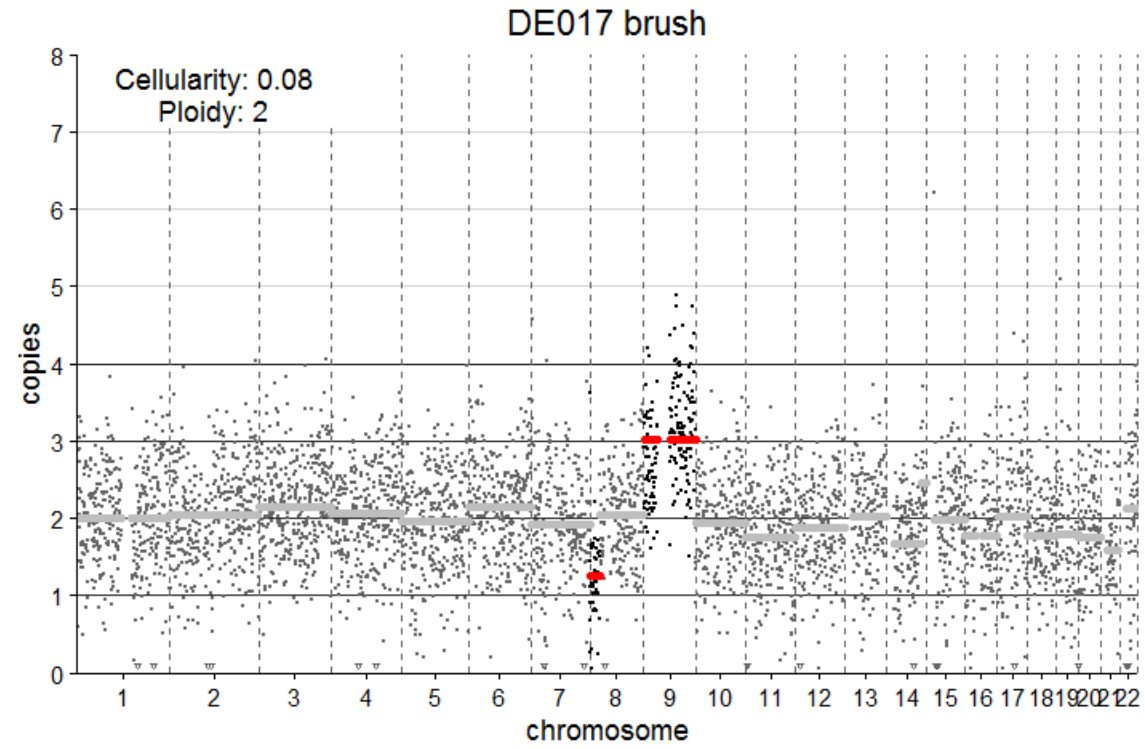
Sample	Coverage		
	Mean	Max	Min
DE008	930	4807	322



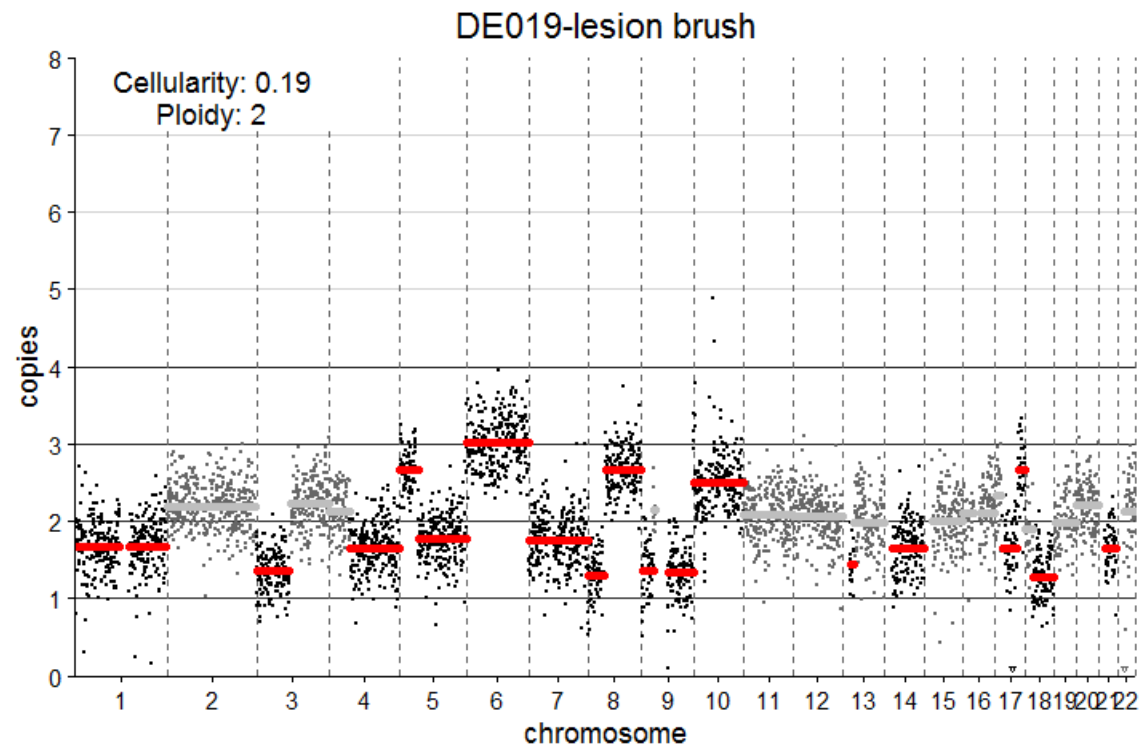
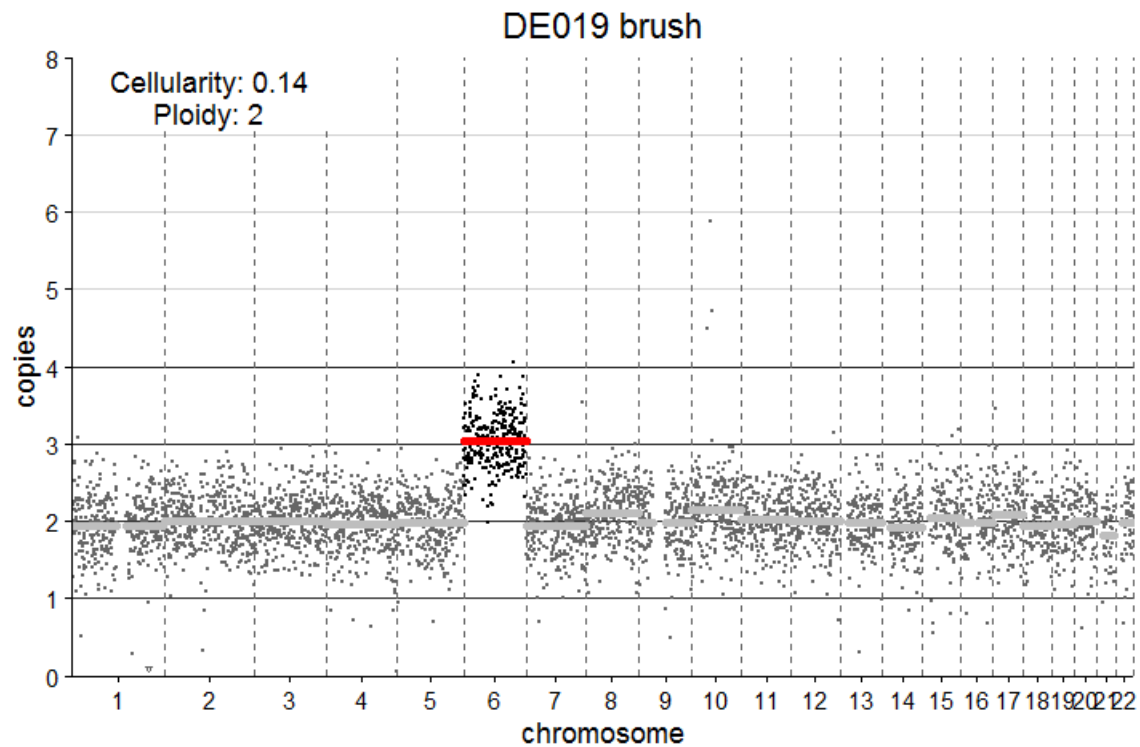
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											Sample	Mean	Max
DE009											2181	3542	372



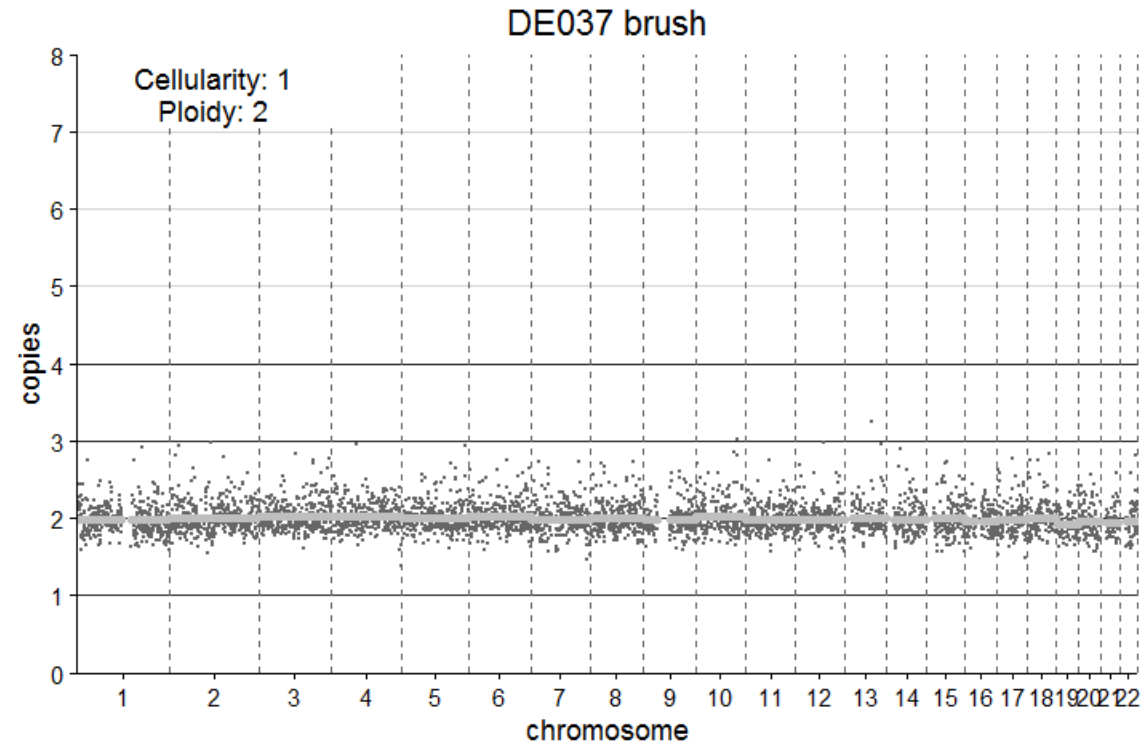
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DE016											923	1376	147



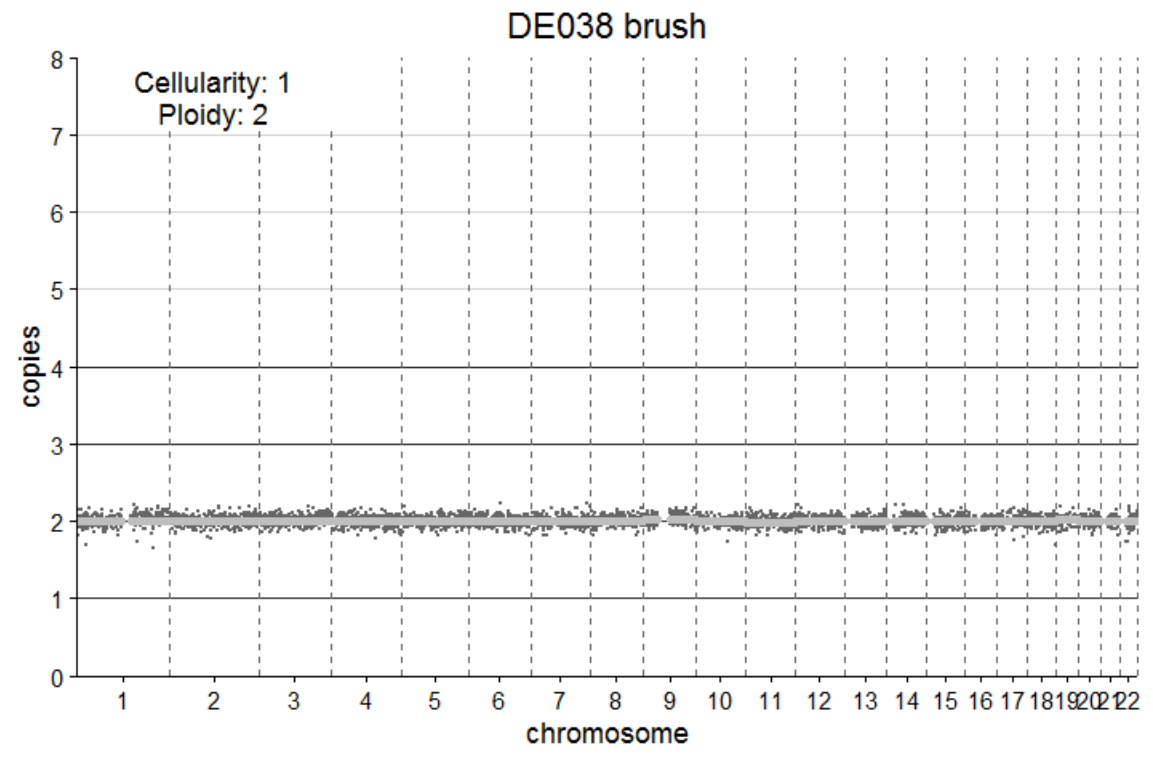
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											Sample	Mean	Max	Min
DE017												2541	6356	865



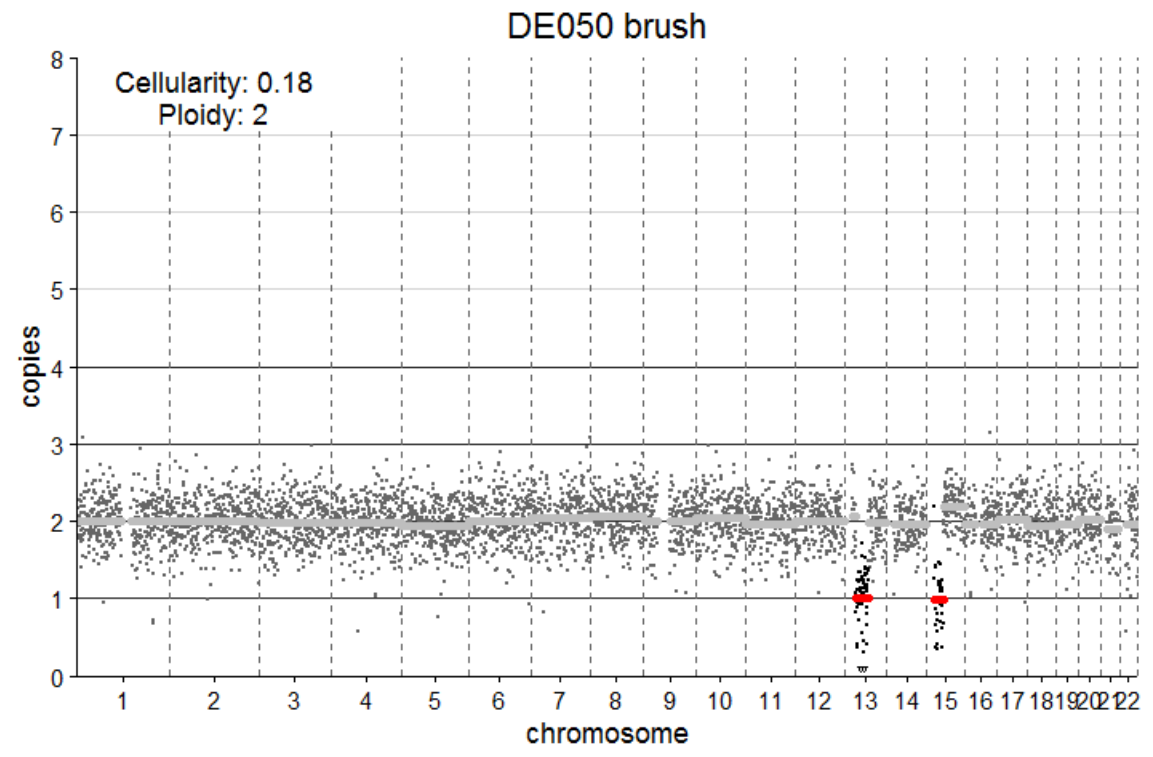
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
											Sample	Mean	Max	Min
DE019	chr9	139412350	NOTCH1	G	A	2785	2679	106	3.81	p.Thr432Met	DE019	3187	5572	547
DE019-lesion	chr4	187549878	FAT1	G	A	5062	4887	175	3.46	p.Gln1455*	DE019-lesion	5667	8211	553
DE019-lesion	chr9	21971108	CDKN2A	C	T	2881	2551	329	11.42	p.Asp84Asn				
DE019-lesion	chr9	21971186	CDKN2A	G	A	1764	1658	105	5.96	p.Arg58*				
DE019-lesion	chr9	139412350	NOTCH1	G	A	4330	3801	529	12.22	p.Thr432Met				
DE019-lesion	chr17	7578200	TP53	CCA	C	5490	4853	638	11.62	p.Val216fs				



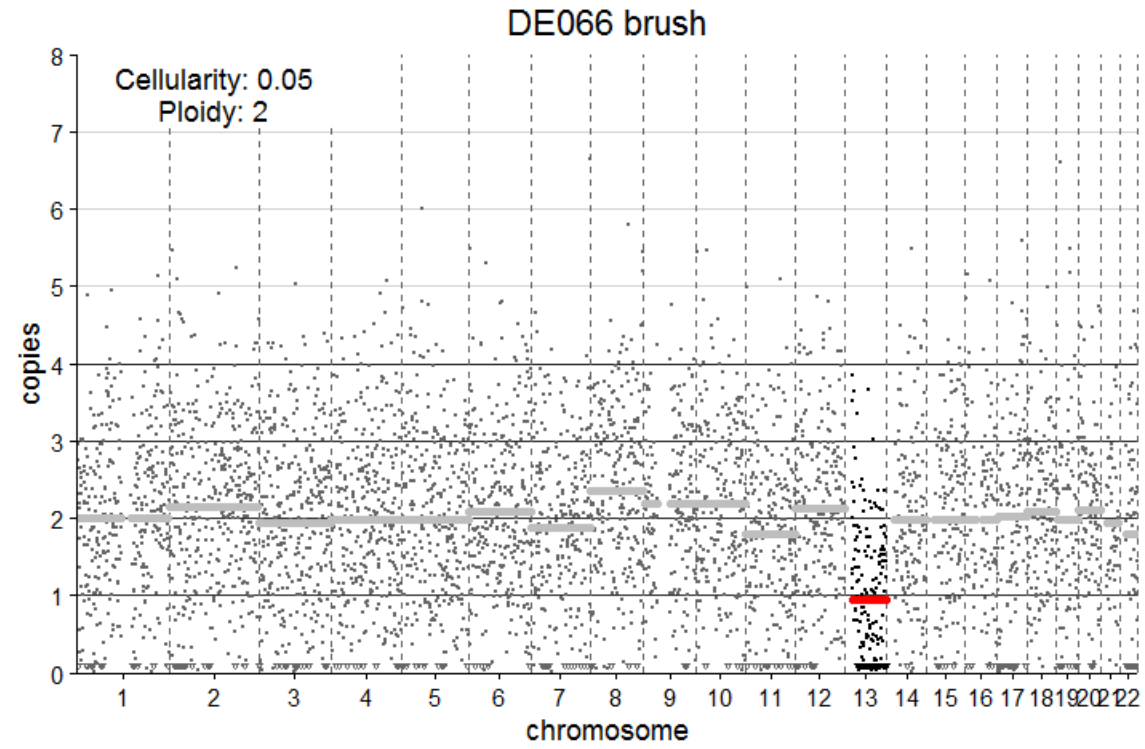
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage		
											Mean	Max	Min
DE037											1234	2860	248



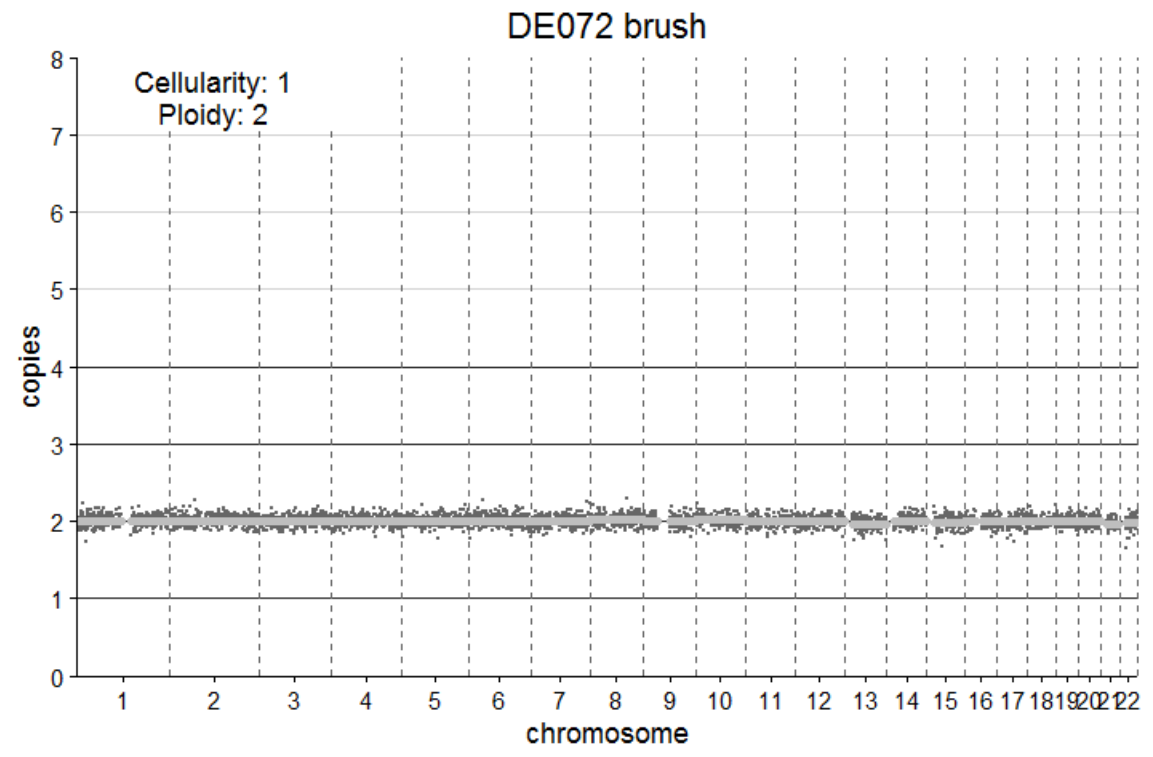
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DE038											6645	9475	526



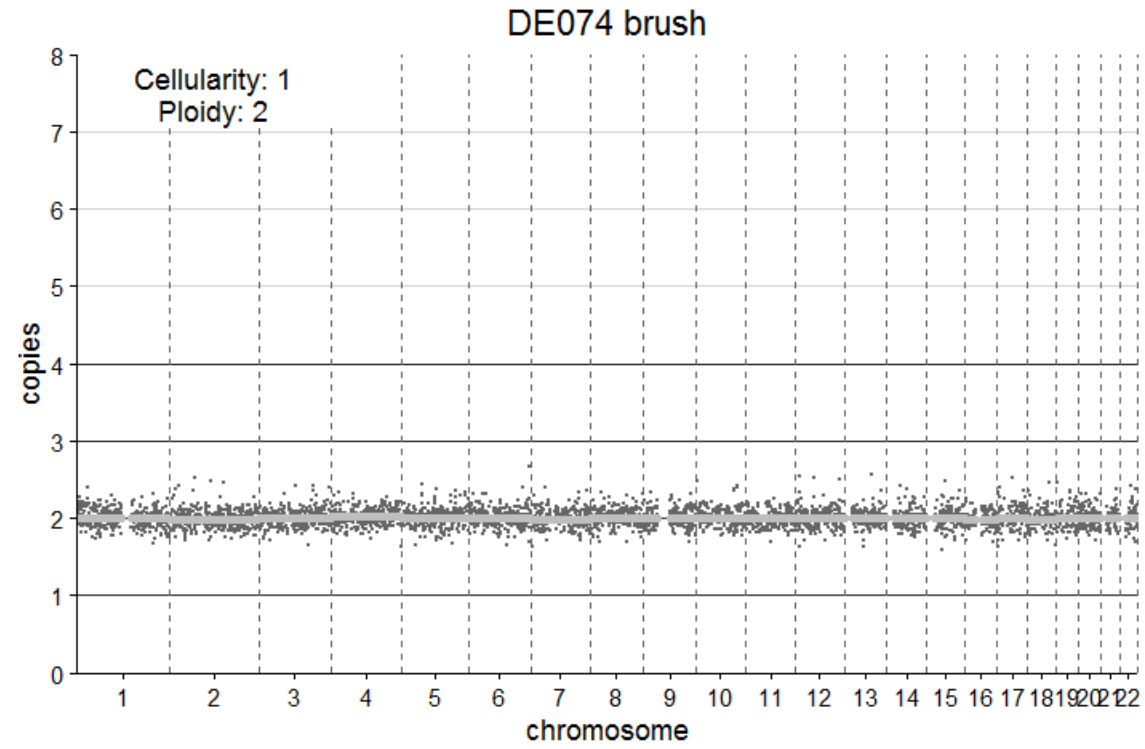
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
											Sample	Mean	Max	Min
DE050											DE050	2699	3737	514



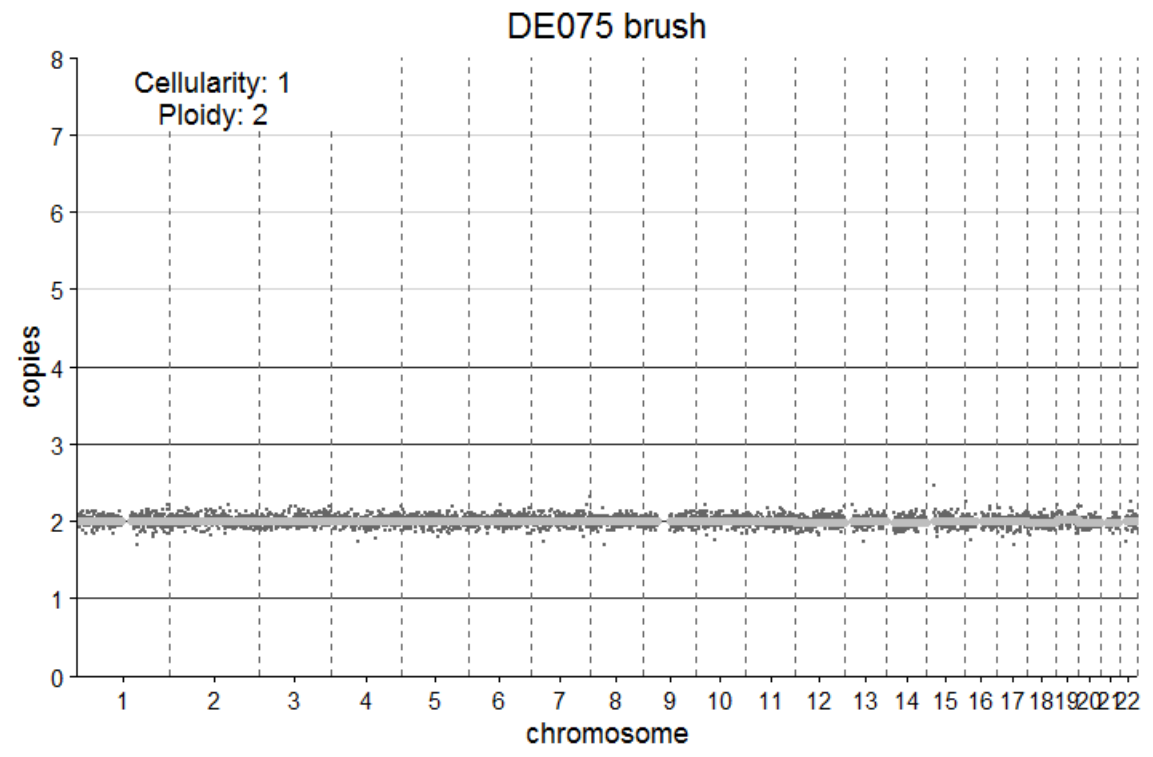
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
											Sample	Mean	Max	Min
DE066											DE066	2821	4680	459



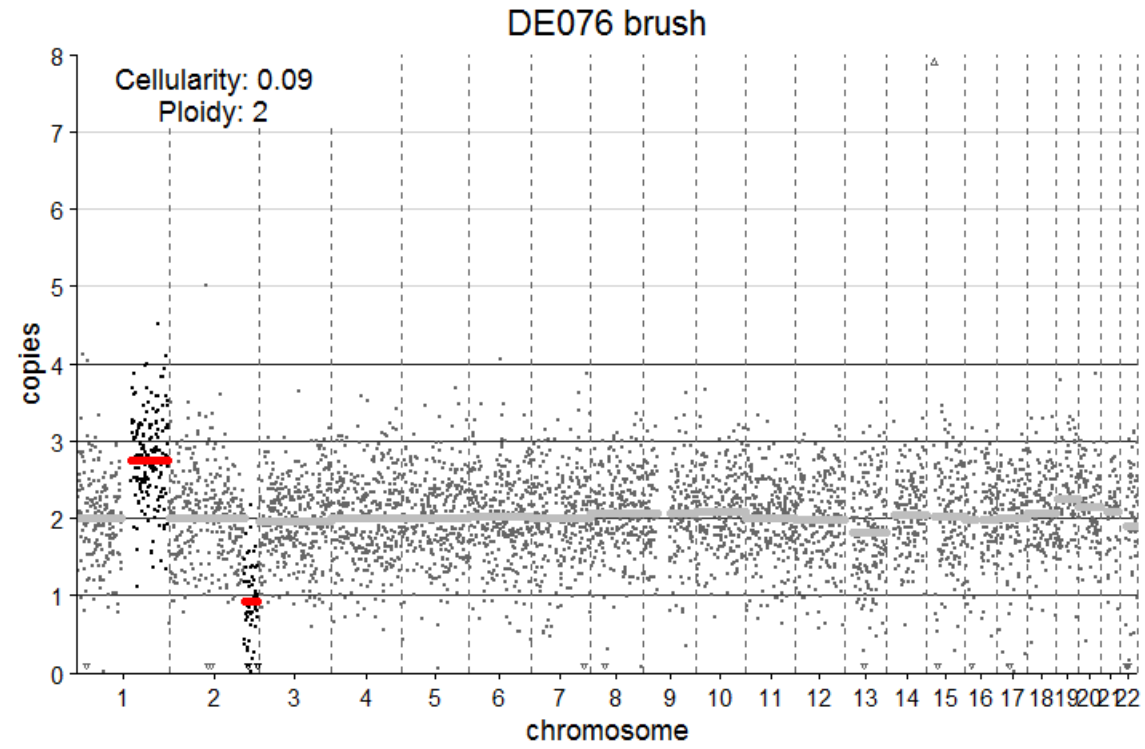
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Sample	Coverage		
												Mean	Max	Min
DE072											DE072	3751	5385	473



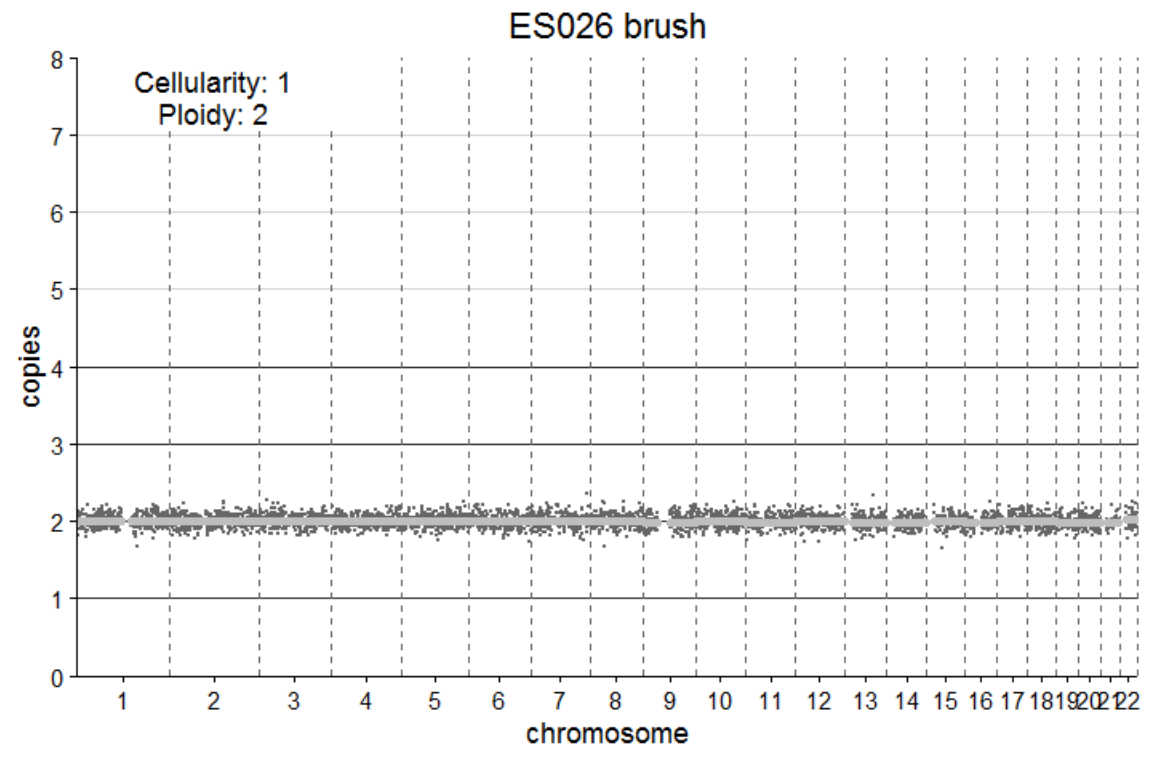
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
											Sample	Mean	Max	Min
DE074											DE074	672	2468	192



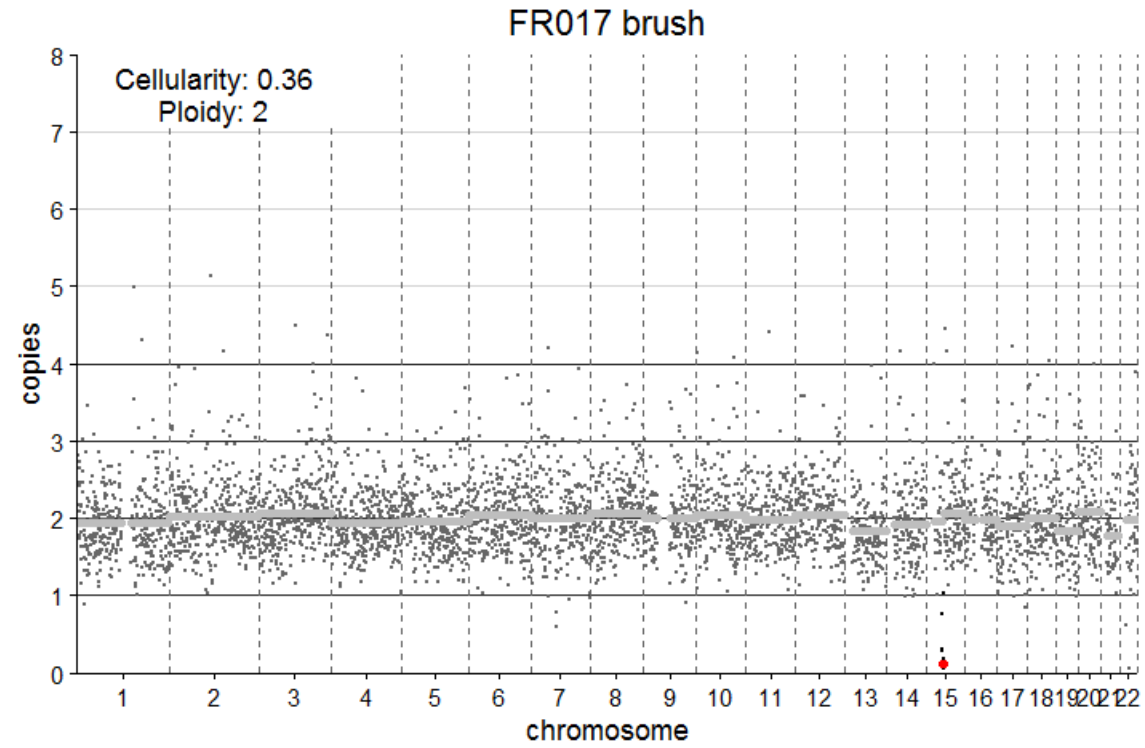
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DE075											DE075	1073	1904	293



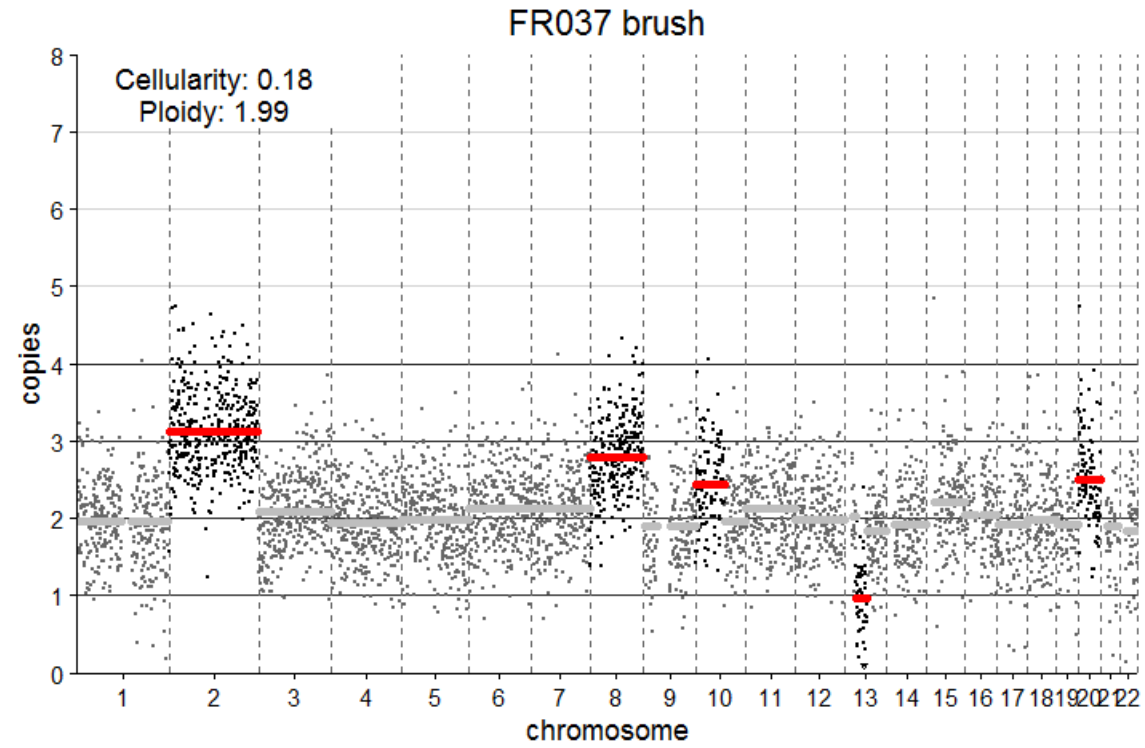
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Sample	Coverage		
												Mean	Max	Min
DE076											DE076	5857	9655	832



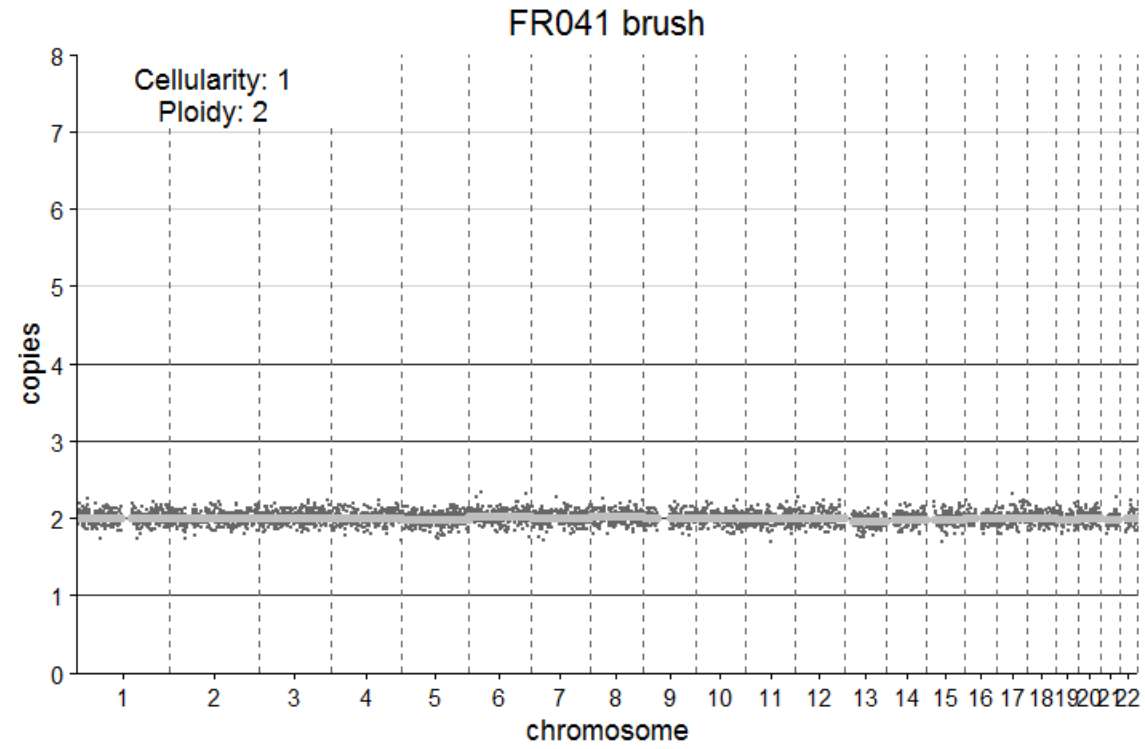
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
											Sample	Mean	Max	Min
ES026											ES026	1017	2142	374



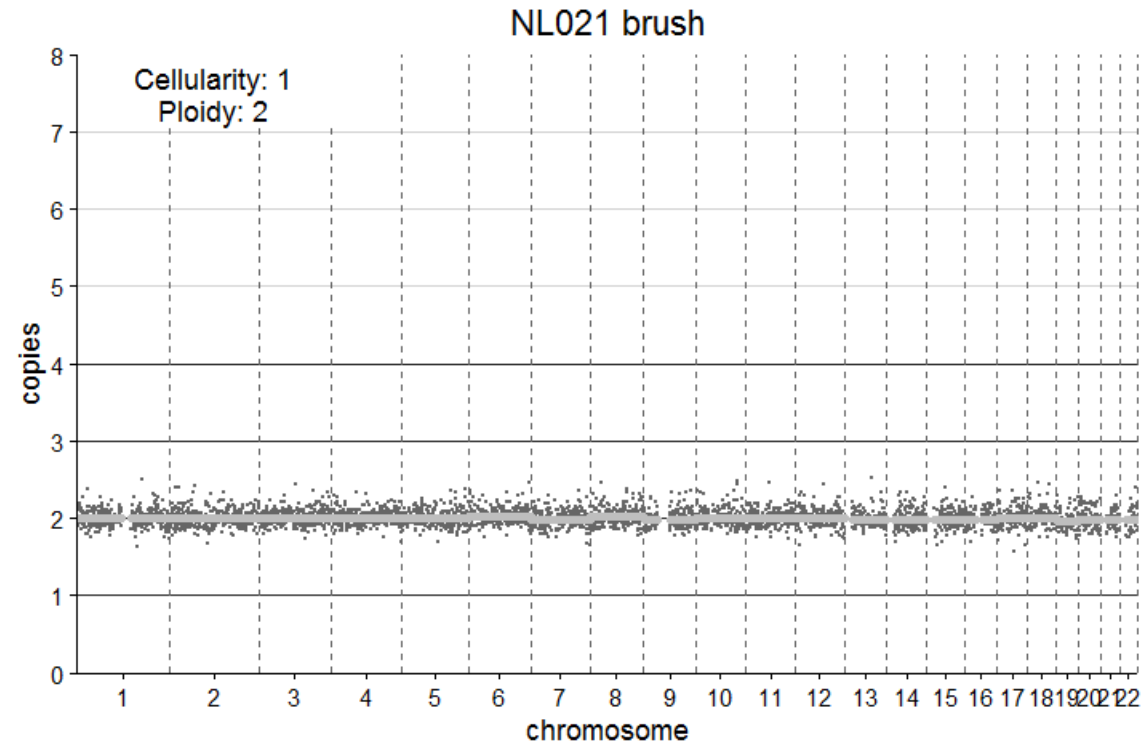
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Sample	Coverage		
												Mean	Max	Min
FR017	chr10	89717672	PTEN	C	T	88	72	16	18.18	p.Arg233*	FR017	280	1136	51
FR017	chr12	49444974	KMT2D	G	A	297	289	8	2.69	p.Ser831Leu				
FR017	chr17	7577139	TP53	G	A	222	214	8	3.6	p.Arg267Trp				
FR017	chr17	7577538	TP53	C	T	216	210	6	2.78	p.Arg248Gln				



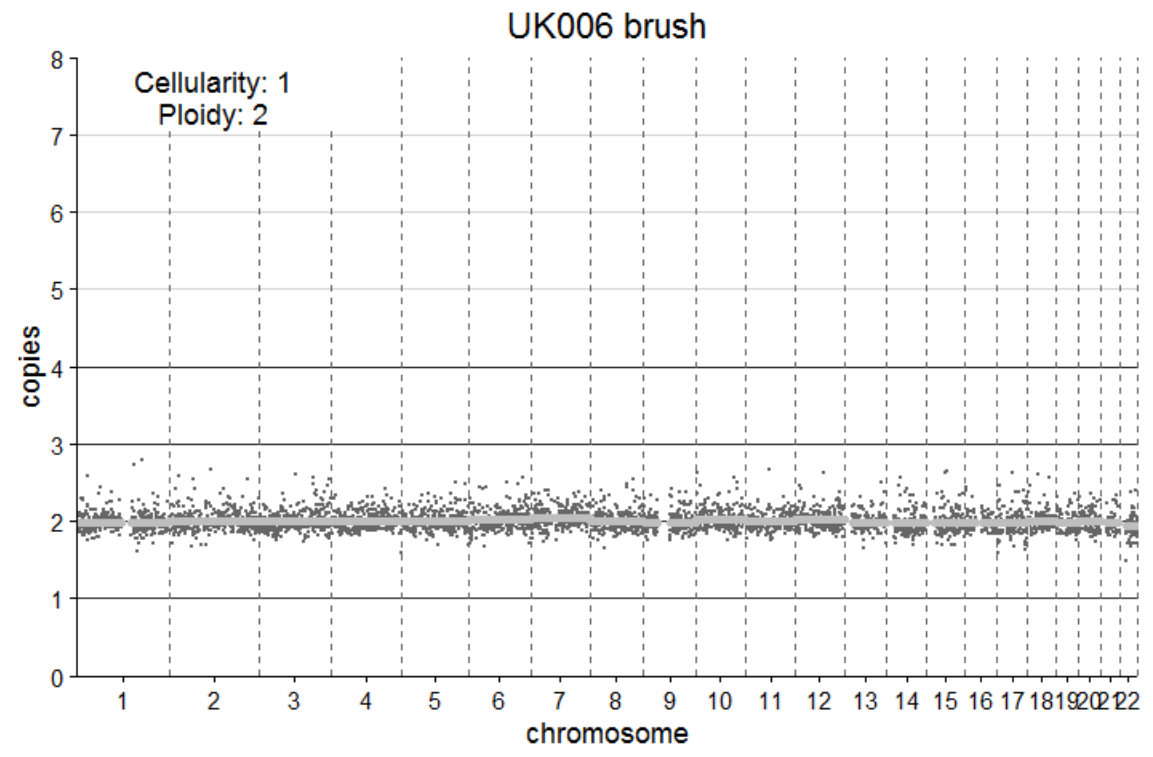
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Sample	Coverage		
												Mean	Max	Min
FR037	chr17	7577547	TP53	C	T	768	747	21	2.73	p.Gly245Asp	FR037	877	1501	314
FR037	chr17	7578406	TP53	C	T	792	759	33	4.17	p.Arg175His				
FR037	chr3	178928079	PIK3CA	G	A	644	626	18	2.8	p.Glu453Lys				
FR037	chr9	21971120	CDKN2A	G	A	583	538	45	7.72	p.Arg80*				



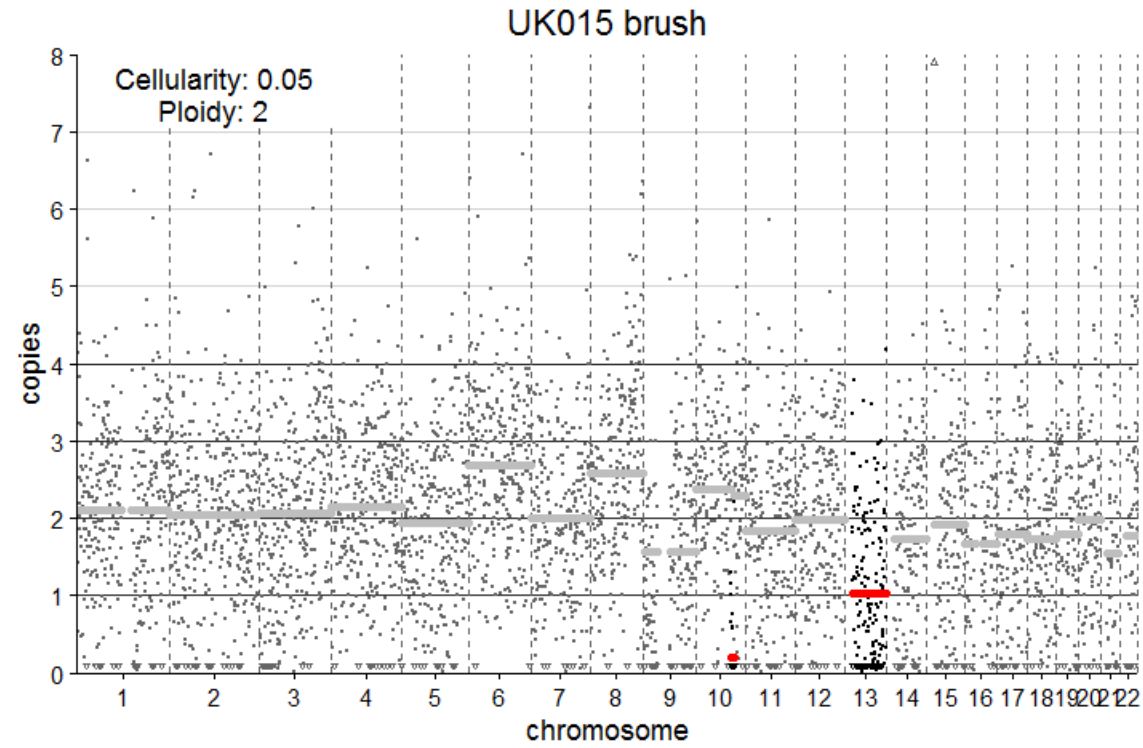
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage		
											Mean	Max	Min
FR041											1074	1679	244



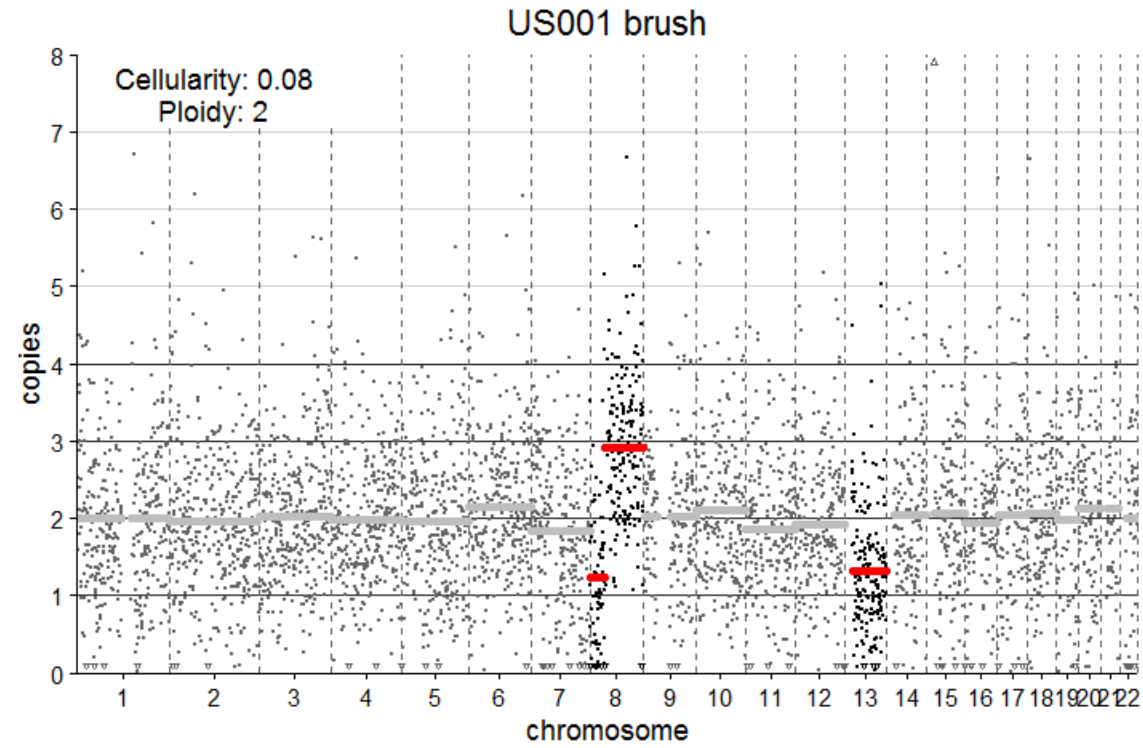
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage		
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NL021											2671	4993	588



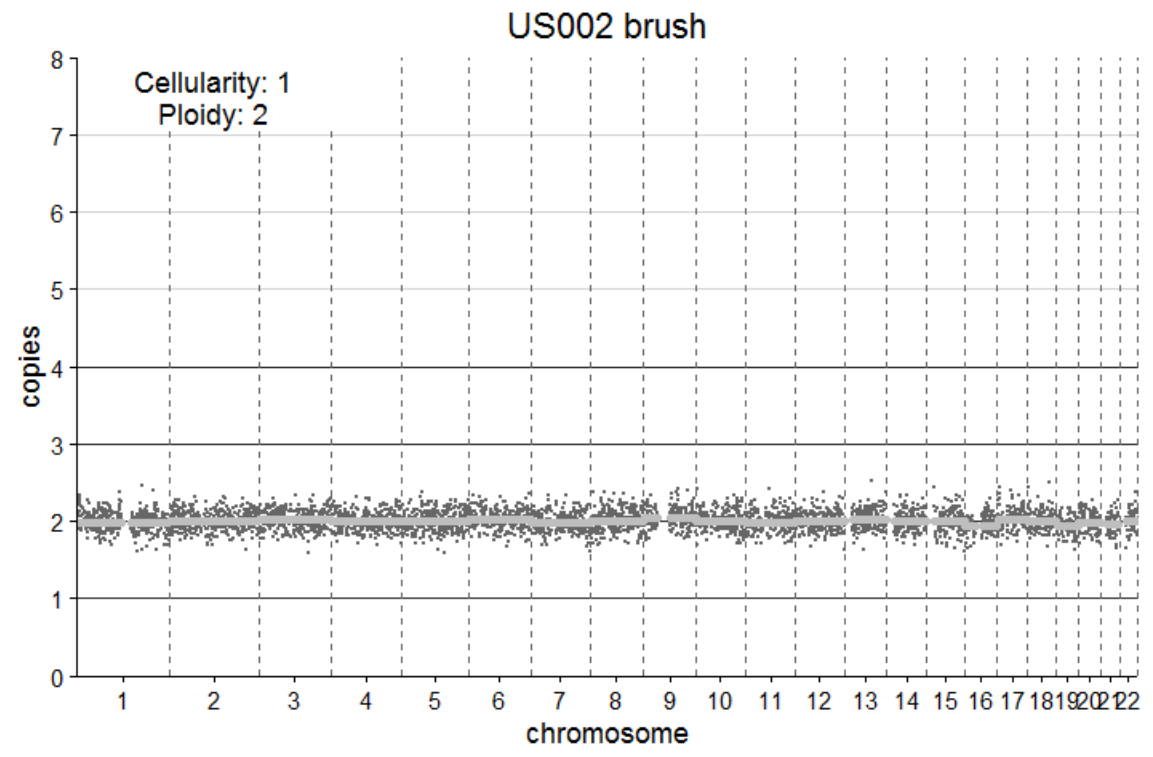
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage		
											Mean	Max	Min
UK006											1015	2153	230



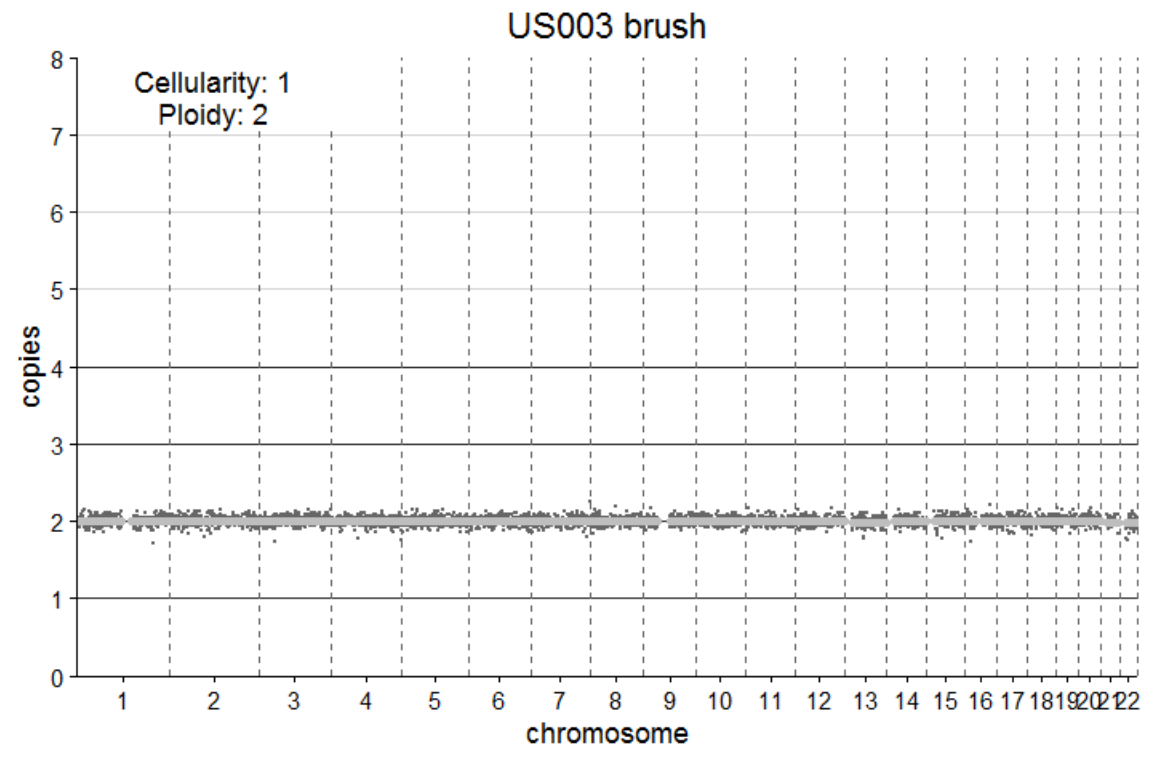
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
											Sample	Mean	Max	Min
UK015											UK015	1295	2794	403



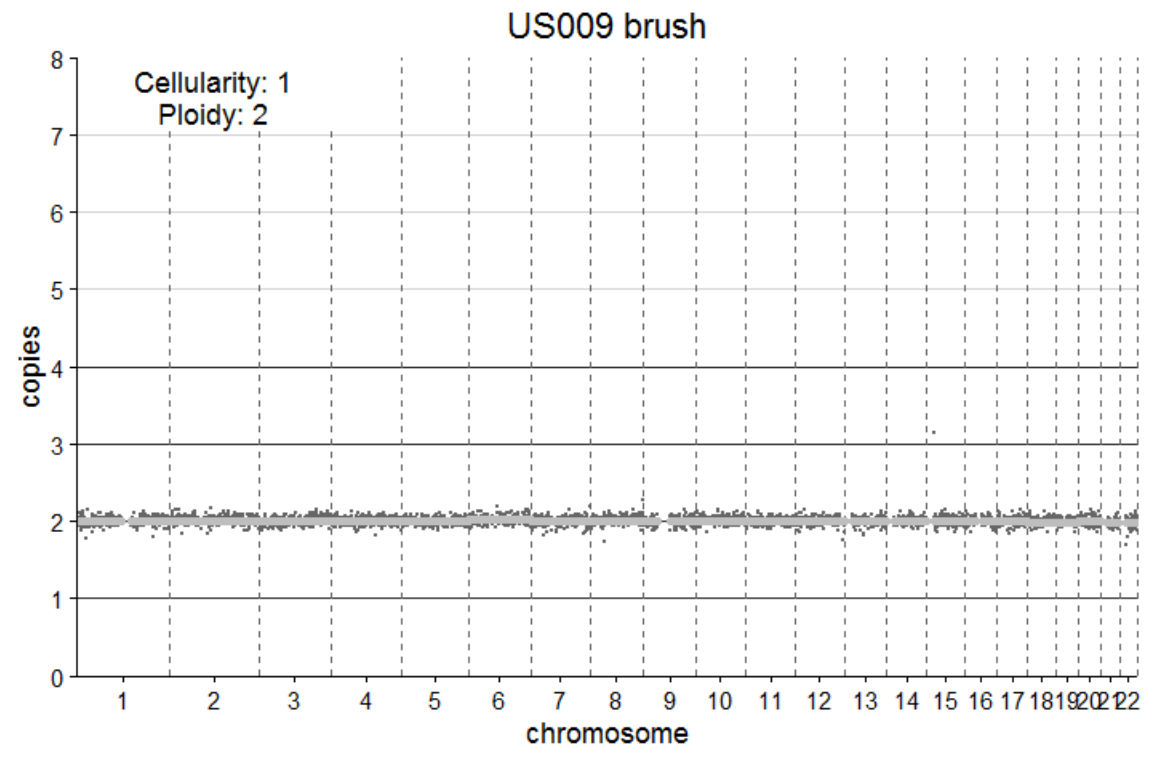
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Sample	Coverage		
												Mean	Max	Min
US001	chr12	49445427	KMT2D	G	A	551	537	14	2.54	p.Thr680Met	US001	671	2321	290
US001	chr2	202137429	CASP8	GAA	G	575	545	29	5.05	p.Lys220fs				
US001	chr4	187628003	FAT1	C	CT	498	459	39	7.83	p.Lys994fs				
US001	chr9	139404331	NOTCH1	GA	G	569	536	33	5.8	p.Phe941fs				



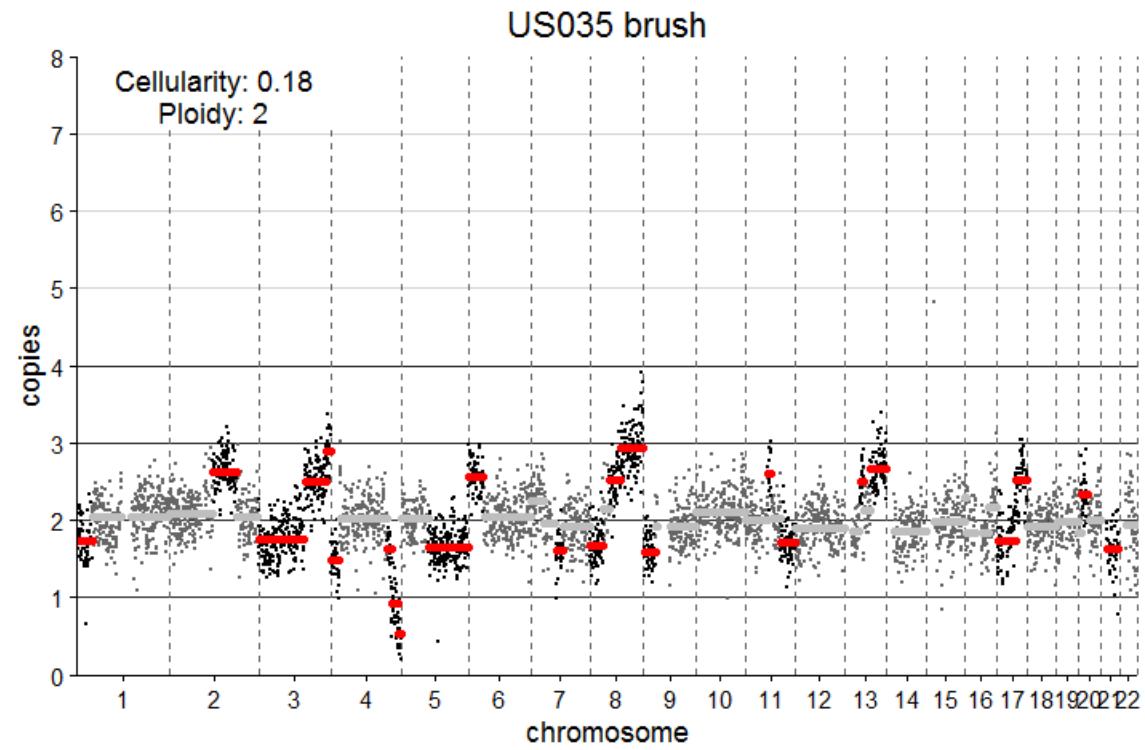
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											Sample	Mean	Max	Min
US002											US002	166	847	47



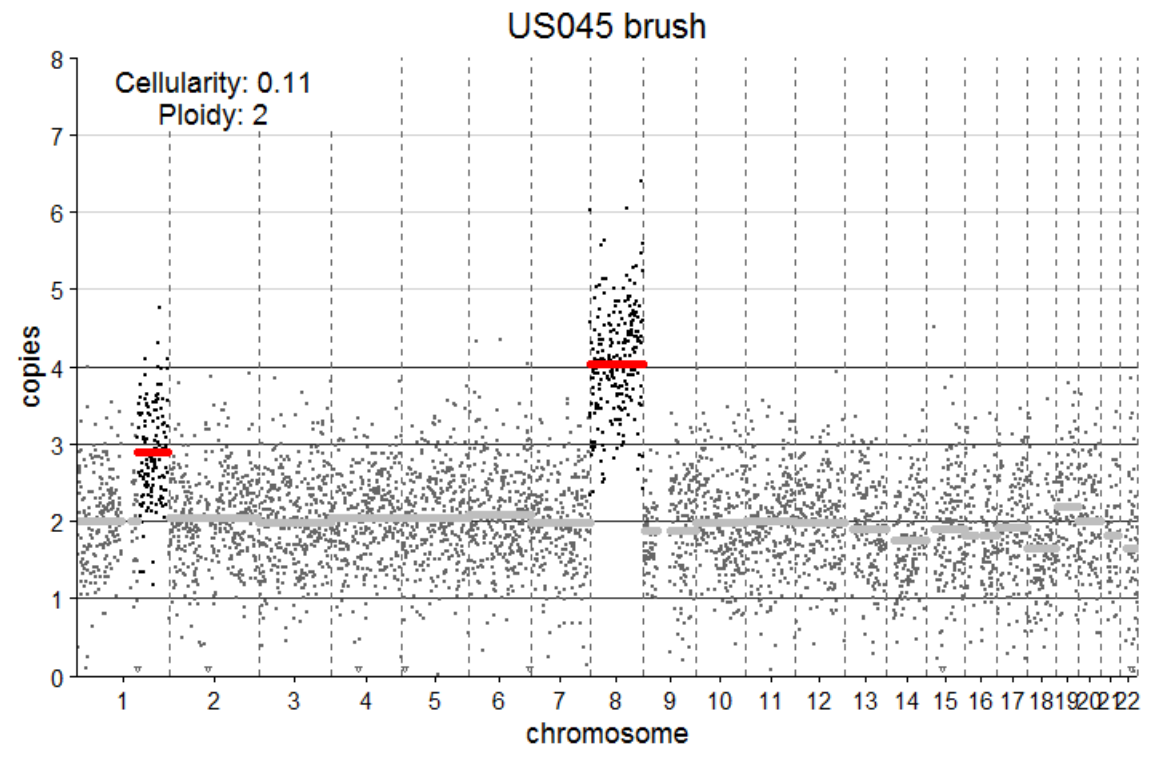
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
											Sample	Mean	Max	Min
US003											US003	3769	5186	469



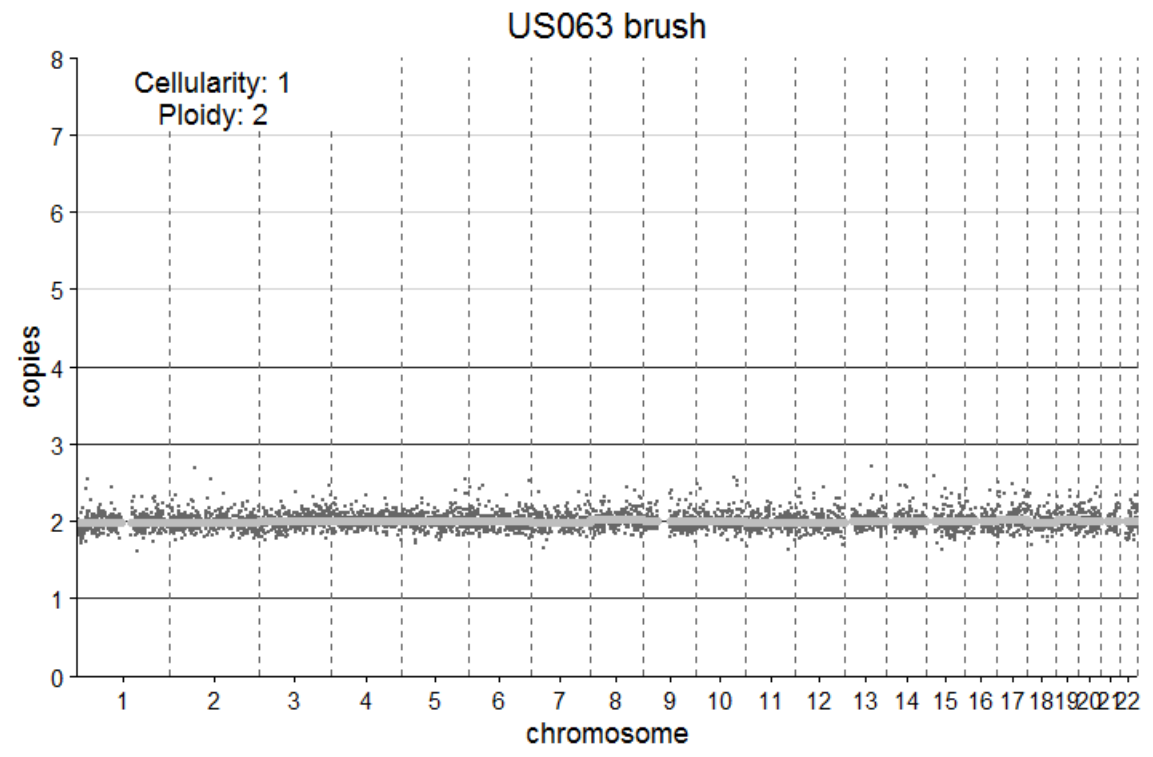
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
											Sample	Mean	Max	Min
US009											US009	1209	2179	366



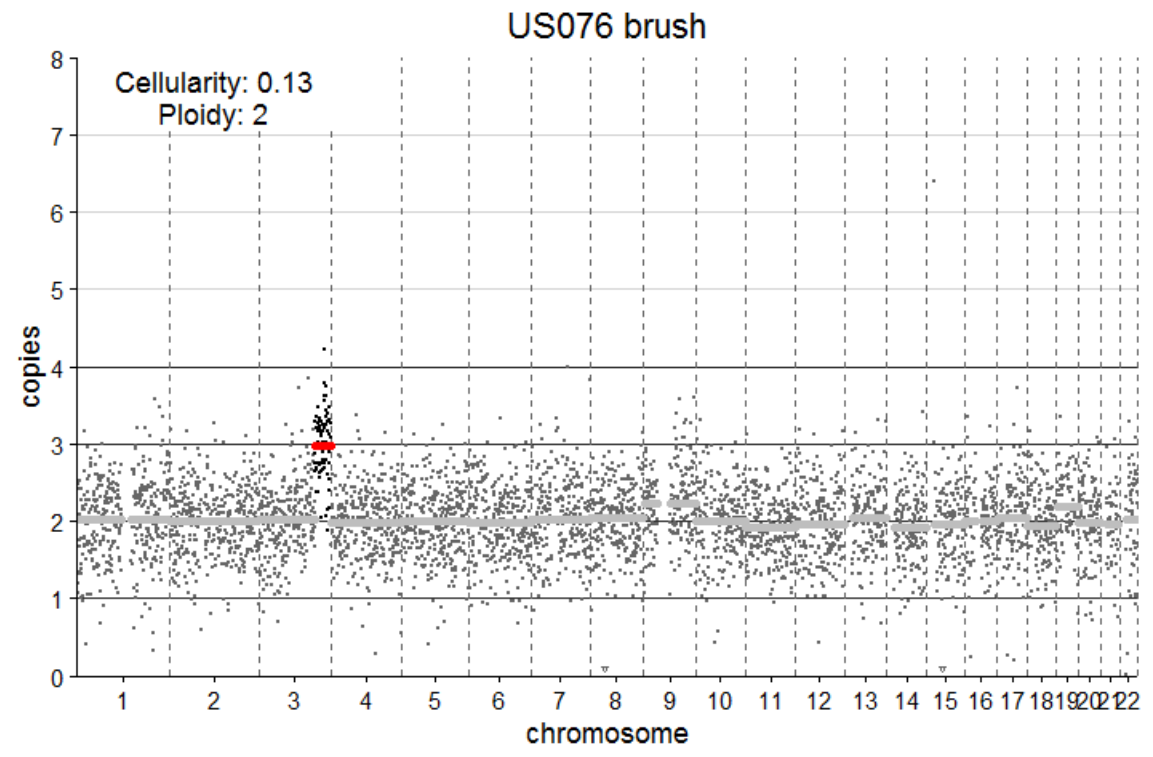
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Sample	Coverage		
												Mean	Max	Min
US035	chr17	7577538	TP53	C	T	2113	2059	54	2.56	p.Arg248Gln	US035	2443	4067	340



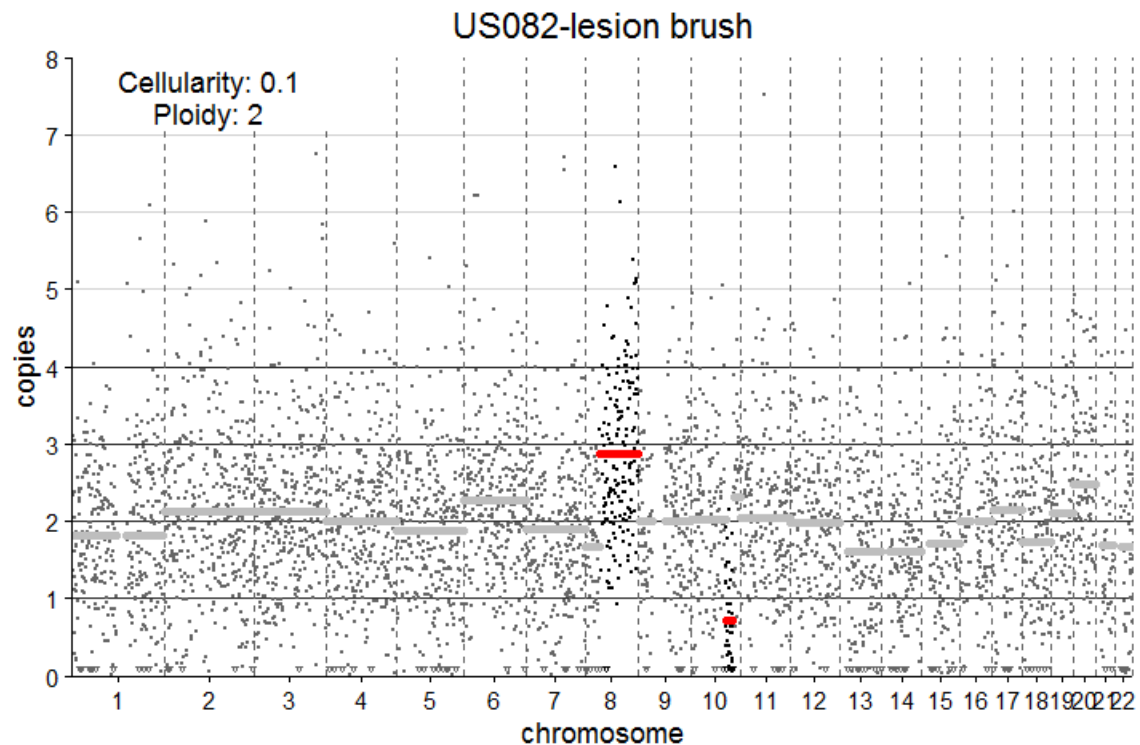
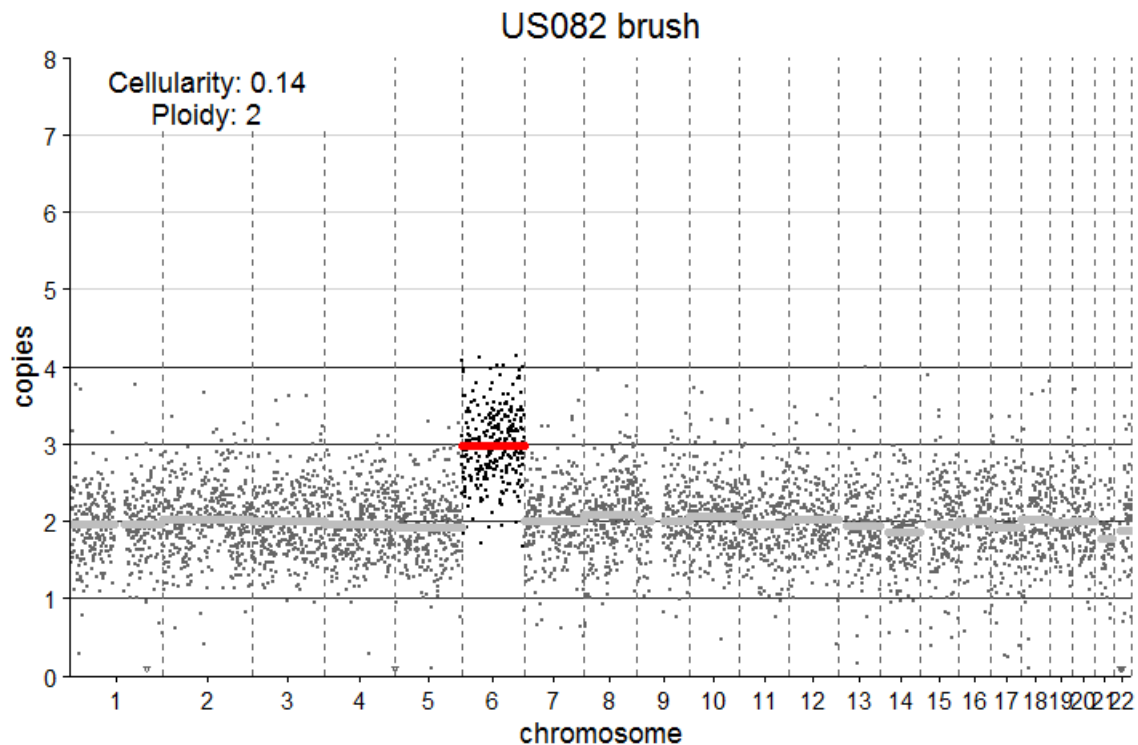
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Sample	Coverage		
												Mean	Max	Min
US045											1649	2721	439	



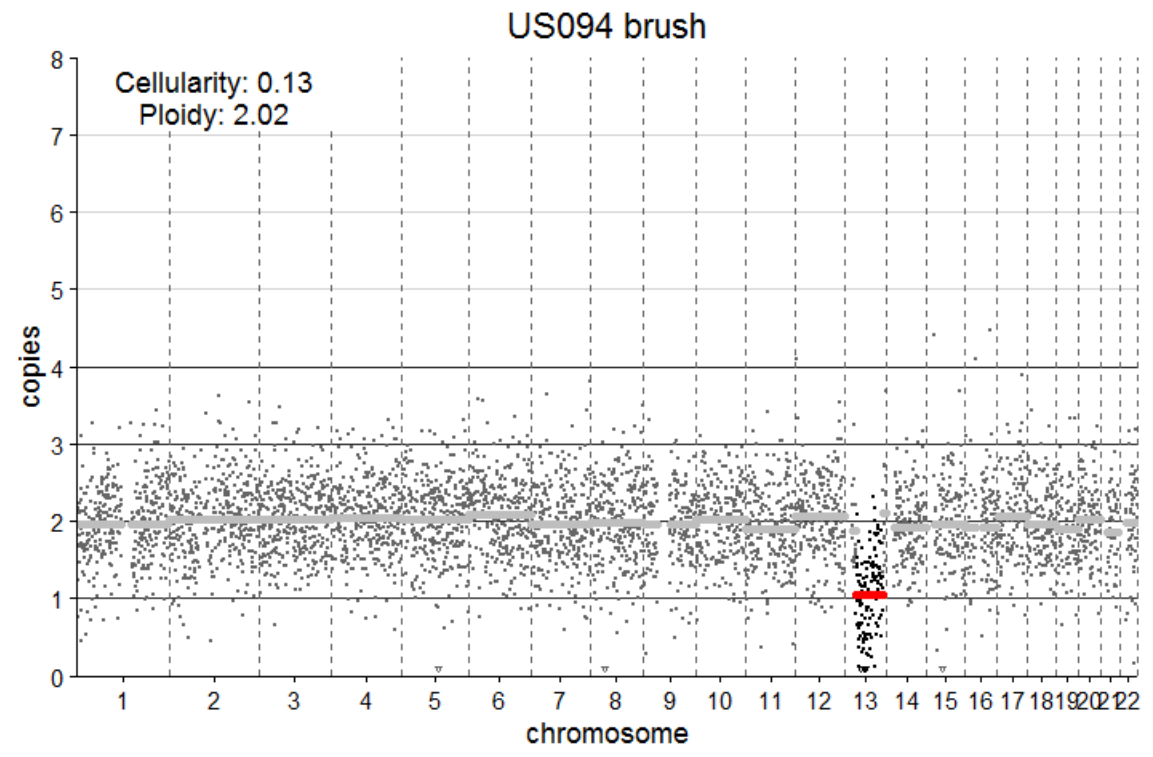
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
											Sample	Mean	Max	Min
US063											US063	923	2465	246



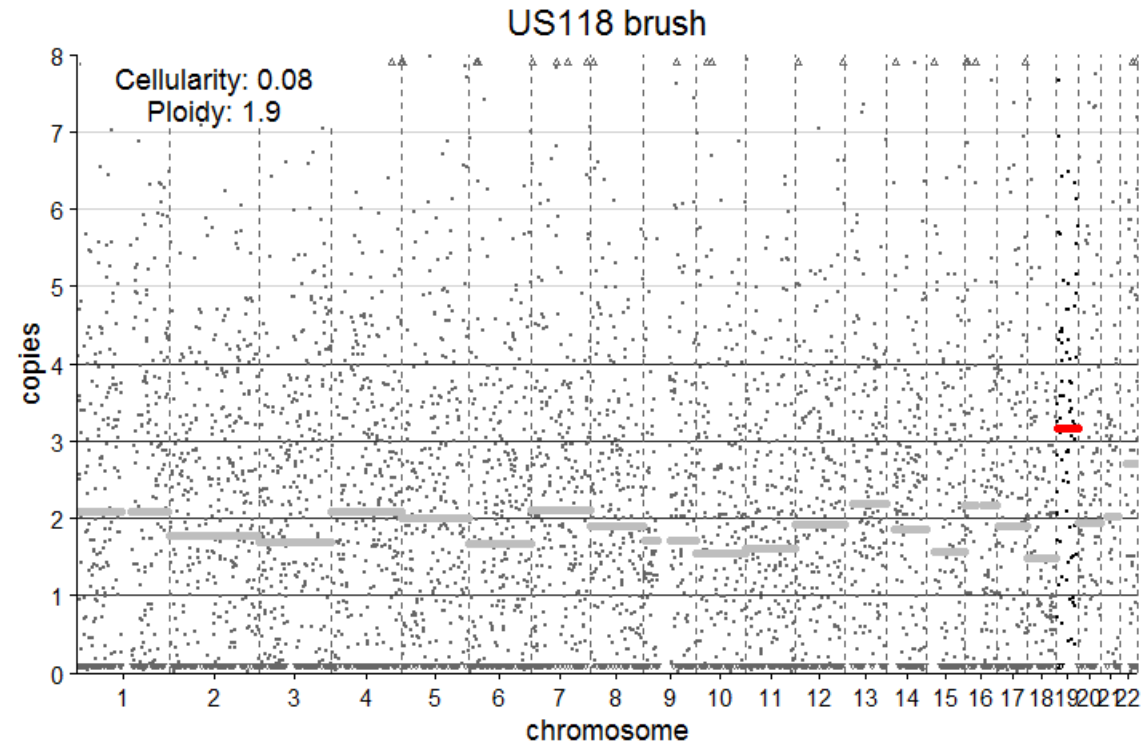
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage		
											Mean	Max	Min
US076											6436	8820	580



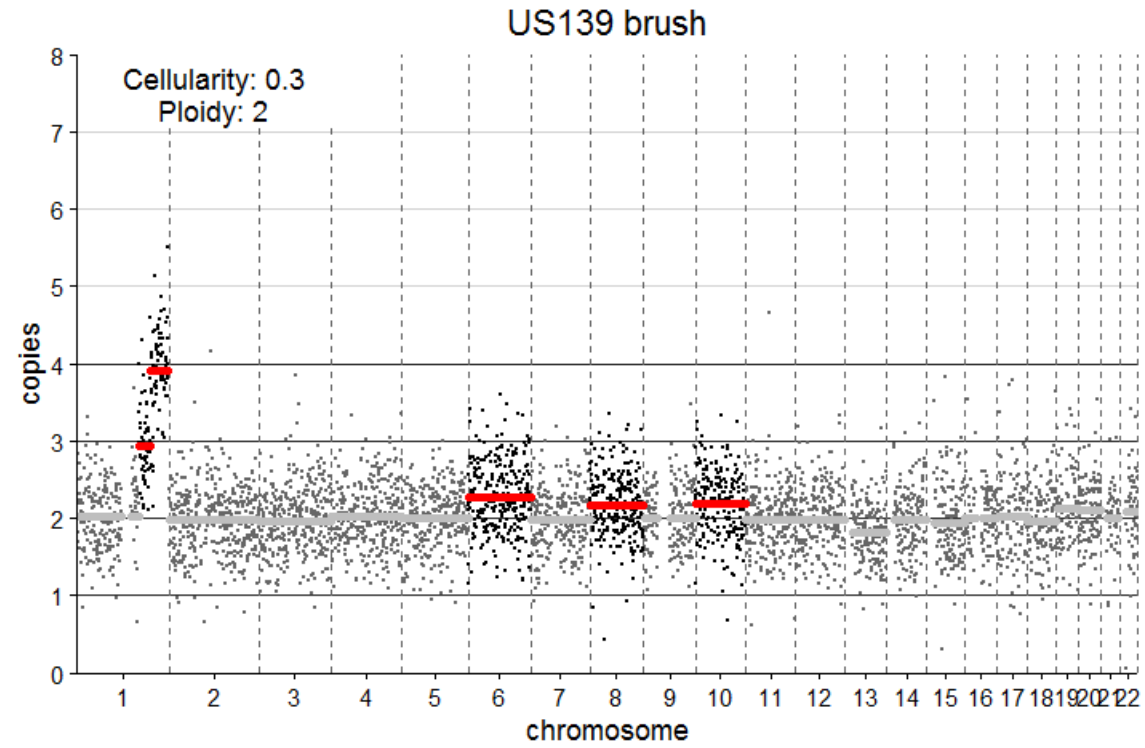
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
											Sample	Mean	Max	Min
US082	chr2	202141586	CASP8	C	T	3475	3361	113	3.25	p.Arg292Trp	US082	3200	5114	124
US082	chr3	178936082	PIK3CA	G	A	3169	2859	310	9.78	p.Glu542Lys				
US082	chr17	7577568	TP53	C	A	3430	3282	148	4.31	p.Cys238Phe				
US082	chr17	7578406	TP53	C	T	2713	2608	105	3.87	p.Arg175His				
US082-lesion	chr2	202141586	CASP8	C	T	466	452	14	3	p.Arg292Trp				
US082-lesion	chr9	139413049	NOTCH1	G	A	341	319	22	6.45	p.Arg365Cys				
US082-lesion	chr12	49426624	KMT2D	A	T	405	374	29	7.2	p.Leu3955Gln				
US082-lesion	chr12	49426669	KMT2D	A	T	289	275	10	3.51	p.Leu3940His				
US082-lesion	chr12	49426696	KMT2D	A	T	246	239	7	2.85	p.Leu3931His				
US082-lesion	chr12	49426711	KMT2D	A	T	231	225	6	2.6	p.Leu3926His				
US082-lesion	chr17	7577085	TP53	C	T	509	463	46	9.04	p.Glu285Lys				



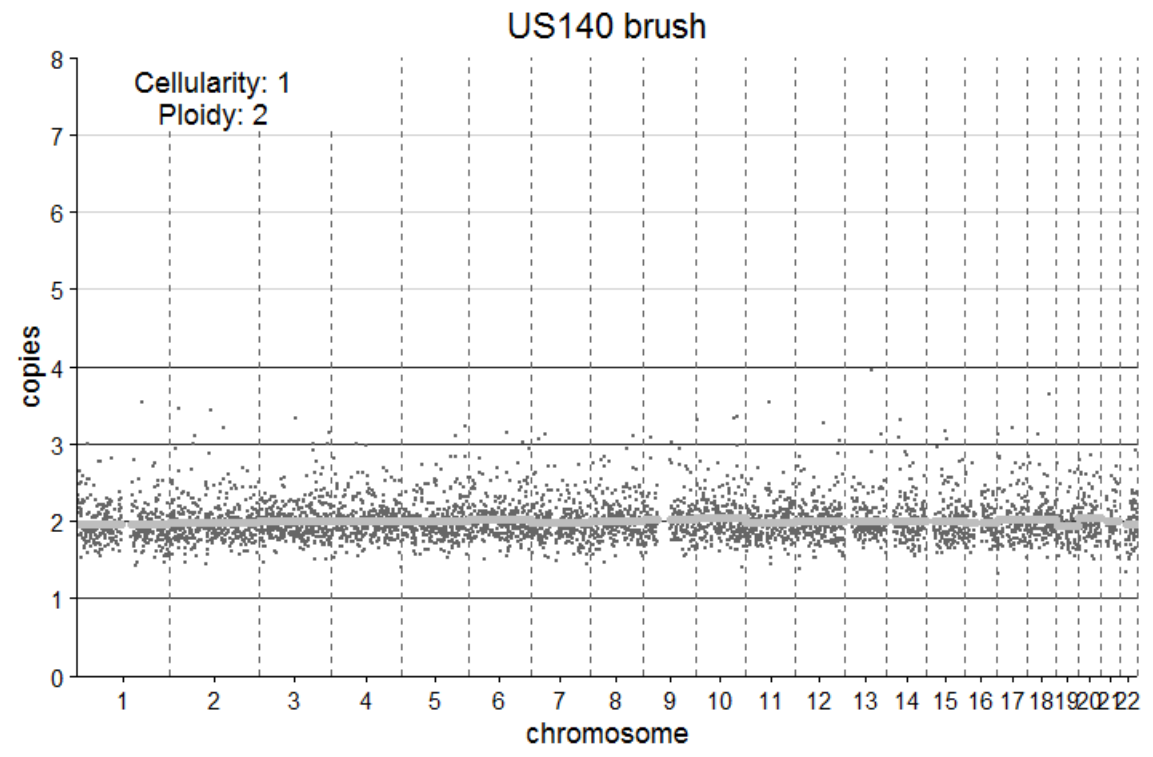
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
											Sample	Mean	Max	Min
US094											US094	1979	2804	404



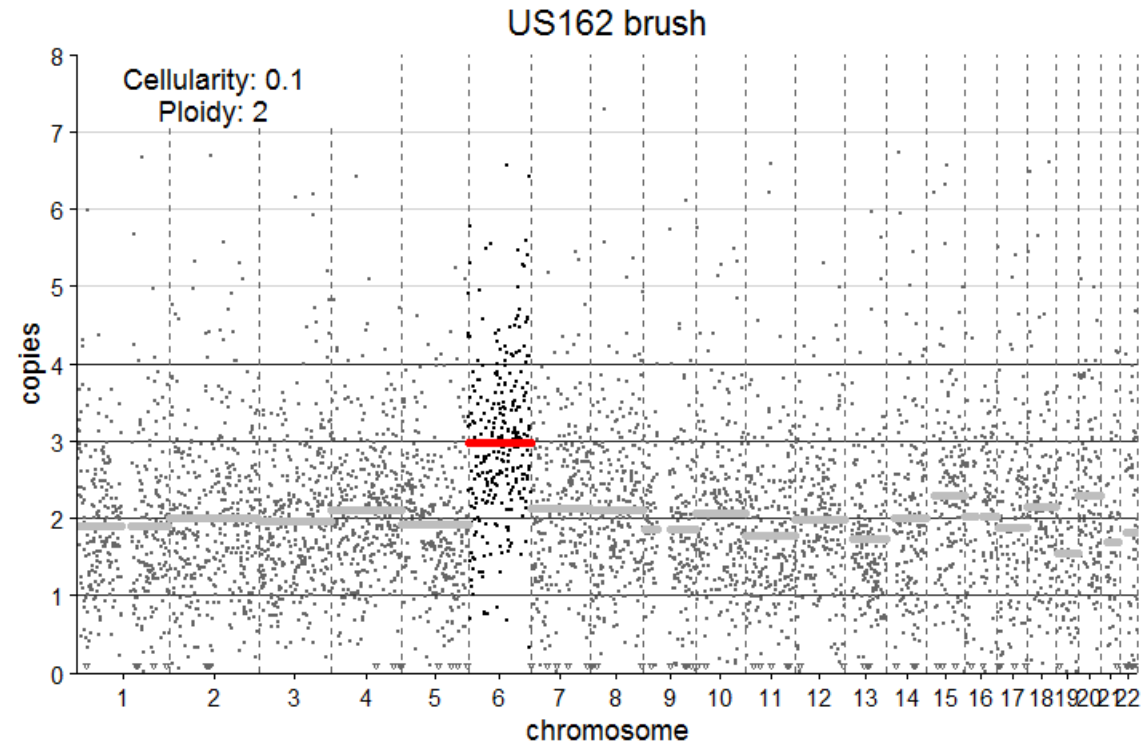
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
											Sample	Mean	Max	Min
US118											US118	1623	3122	628



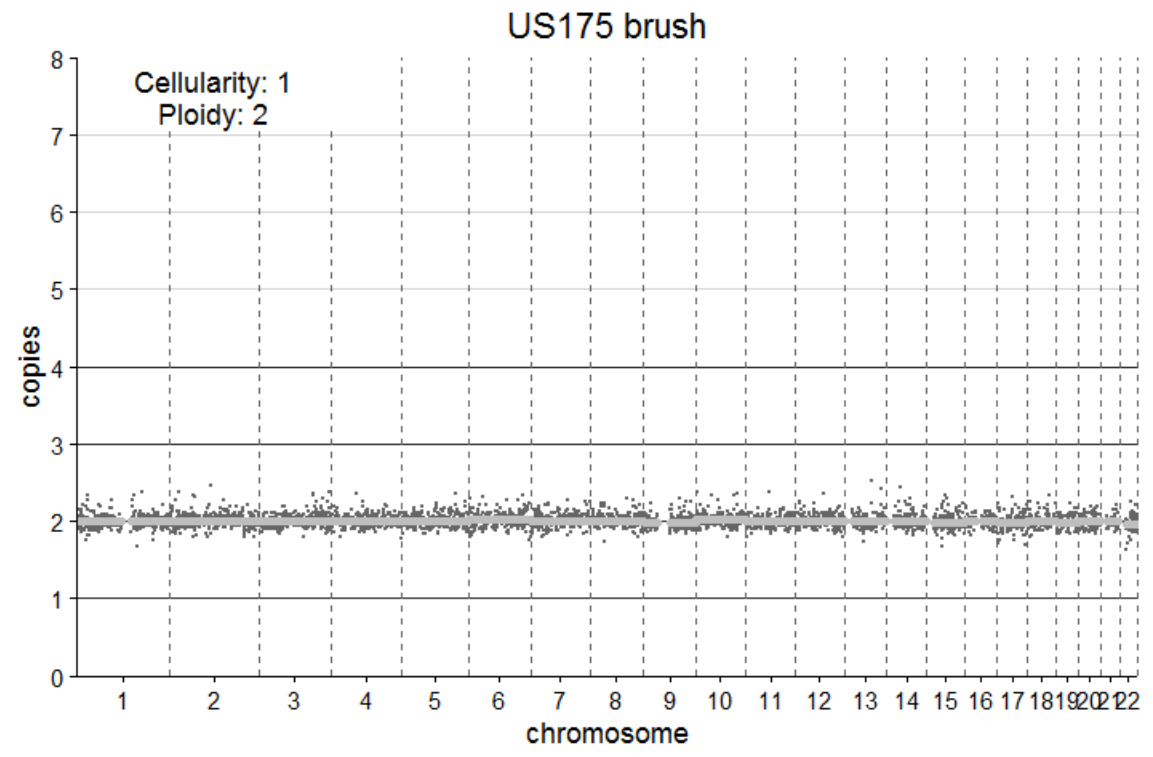
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Sample	Coverage		
												Mean	Max	Min
US139	chr3	178928067	PIK3CA	C	T	310	302	8	2.58	p.Pro449Ser				
US139	chr3	178951957	PIK3CA	G	A	317	307	10	3.15	p.Met1004Ile	US139	286	886	77



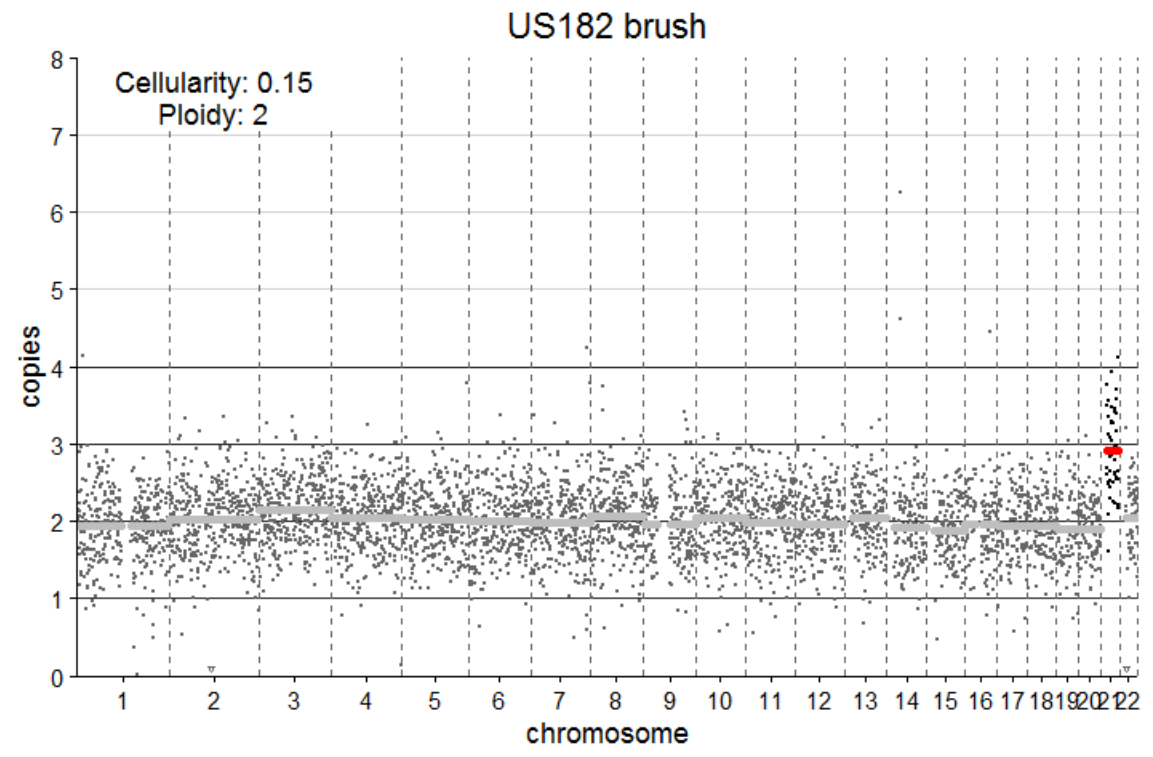
Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
											Sample	Mean	Max	Min
US140											US140	329	1641	76



Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Sample	Coverage		
												Mean	Max	Min
US162	chr14	23450816	AJUBA	C	CA	2613	2358	255	9.76	p.Gly221fs	US162	1695	3366	626



Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage			
											Sample	Mean	Max	Min
US175											US175	2814	5137	717



Sample	Chr	Pos	Gene	REF	ALT	read depth	ref reads	alt reads	VAF (%)	Change	Coverage		
											Mean	Max	Min
US182											2253	3736	378