Supplementary Table S2: Non-synonymous somatic mutations identified in synchronous DCIS and IDC-NSTs subjected to whole-exome sequencing or MSK-IMPACT targeted massively parallel sequencing and/or targeted amplicon sequencing.

Sample ID	Gene symbol	Aminoacid change	Chromosome	Genomic position	Reference allele	Alternate allele	Type of mutation	Depth at mutation (x)	Mutant allele fraction	HOTSPOT	Loss of heterozygosity (LOH)	Cancer Cell Fraction (ABSOLUTE)	Probability of mutation being clonal	Upper bound of 95% confidence interval for cancer cell fraction	Lower bound of 95% confidence interval for cancer cell fraction	Clonal status	MutationTaster	CHASM (Breast)	PROVEAN	FATHMM	Pathogenicity	Cancer driver genes (Bailey et al)	Cancer Gene Census	Cancer5000-S genes (Lawrence et al)	Sequencing platform
3DCIS	PTEN	p.F241Lfs*15	10	89717695	CT	C	Frame_Shift_Del	144	54.9%	No	No	100%	1.20E-04	100.0%	94.5%	Clonal	.	.	.	.	likely_pathogenic	Yes	Yes	Yes	MSK-IMPACT
3IDC	PTEN	p.F241Lfs*15	10	89717695	CT	C	Frame_Shift_Del	184	29.9%	No	No	83%	0.33407	97.5%	64.9%	Subclonal	.	.	.	.	likely_pathogenic	Yes	Yes	Yes	MSK-IMPACT
3IDC	MGA	p.F254I	15	41961852	T	A	Missense_Mutation	664	2.9%	No	Yes	8%	0	11.8%	4.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	Yes	No	Yes	MSK-IMPACT
3DCIS	MET	p.W586*	7	116395464	G	A	Nonsense_Mutation	258	4.3%	No	No	25%	0	42.7%	13.4%	Subclonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	MSK-IMPACT
3DCIS	CDKN2A	p.D108N	9	21971036	C	T	Missense_Mutation	323	71.8%	No	No	100%	0	100.0%	98.1%	Clonal	D	Passenger	N	T	passenger	Yes	Yes	Yes	MSK-IMPACT
3IDC	CDKN2A	p.D108N	9	21971036	C	T	Missense_Mutation	630	37.1%	No	No	100%	0.92325	100.0%	89.7%	Clonal	D	Passenger	N	T	passenger	Yes	No	Yes	MSK-IMPACT
3DCIS	ATR	p.X878_splice	3	142272480	A	G	Splice_Site	375	16.0%	No	No	92%	0.70538	100.0%	71.4%	Clonal	D	.	.	.	likely_pathogenic	Yes	No	No	MSK-IMPACT
10DCIS	CR1	p.M2208T	1	207787796	T	C	Missense_Mutation	142	3.5%	No	No	12%	0	25.6%	4.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
10DCIS	SCN3B	p.R78Q	11	123513366	C	T	Missense_Mutation	145	23.4%	No	No	77%	0.28273	96.5%	56.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
10DCIS	KRT4	p.R417*	12	53201525	G	A	Nonsense_Mutation	184	28.3%	No	No	100%	0.88503	100.0%	82.4%	Clonal	A	.	.	.	passenger	No	No	No	WES
10DCIS	ARHGEF25	p.A8T	12	58004021	G	A	Missense_Mutation	135	40.0%	No	No	100%	0.90477	100.0%	89.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
10DCIS	ADAMTS17	p.V831A	15	100589161	A	G	Missense_Mutation	119	31.1%	No	No	100%	0.81258	100.0%	72.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
10DCIS	HYDIN	p.H2700N	16	70942671	G	T	Missense_Mutation	222	33.8%	No	No	100%	0.90403	100.0%	84.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
10DCIS	PER2	p.G256A	2	239179958	C	G	Missense_Mutation	56	32.1%	No	No	100%	0.7684	100.0%	63.3%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
10DCIS	PLXNB1	p.M954L	3	48460421	T	A	Missense_Mutation	139	31.7%	No	No	100%	0.83815	100.0%	75.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
10DCIS	PIK3CA	p.E545D	3	178936093	G	T	Missense_Mutation	150	18.7%	No	No	61%	0.01078	83.5%	42.9%	Subclonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
10DCIS	PIK3CA	p.H1047L	3	178952085	A	T	Missense_Mutation	217	31.3%	Yes	No	100%	0.8629	100.0%	79.7%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
10DCIS	GPRIN3	p.A378V	4	90170129	G	A	Missense_Mutation	138	24.6%	No	Yes	56%	7.00E-05	73.4%	40.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
10DCIS	MED23	p.L338P	6	131931250	A	G	Missense_Mutation	83	60.2%	No	Yes	100%	0.63928	100.0%	87.9%	Clonal	D	Driver	D	T	likely_pathogenic	Yes	No	Yes	WES, Ampliseq
10DCIS	MED23	p.Q337P	6	131931253	T	G	Missense_Mutation	81	60.5%	No	Yes	100%	0.63048	100.0%	87.8%	Clonal	D	Driver	D	T	likely_pathogenic	Yes	No	Yes	WES, Ampliseq
10DCIS	GIMAP1	p.A244V	7	150417823	C	T	Missense_Mutation	54	27.8%	No	No	91%	0.65268	100.0%	54.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
10DCIS	GSDMC	p.R34H	8	130789733	C	T	Missense_Mutation	168	19.6%	No	No	64%	0.01593	85.6%	46.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
10DCIS	FAM47B	p.R165H	X	34961442	G	A	Missense_Mutation	221	34.8%	No	No	100%	0.90976	100.0%	85.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
10IDC	ADAM30	p.L16V	1	120438914	G	C	Missense_Mutation	222	6.3%	No	No	39%	1.60E-04	63.4%	23.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
10IDC	CR1	p.M2208T	1	207787796	T	C	Missense_Mutation	75	6.7%	No	No	41%	0.07777	86.4%	17.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
10IDC	CCDC83	p.E139Q	11	85597314	G	C	Missense_Mutation	134	6.0%	No	No	37%	0.00393	69.7%	18.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
10IDC	SCN3B	p.R78Q	11	123513366	C	T	Missense_Mutation	130	22.3%	No	No	100%	0.85902	100.0%	77.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
10IDC	KRT4	p.R417*	12	53201525	G	A	Nonsense_Mutation	110	19.1%	No	No	100%	0.85721	100.0%	71.5%	Clonal	A	.	.	.	passenger	No	No	No	WES
10IDC	ARHGEF25	p.A8T	12	58004021	G	A	Missense_Mutation	88	19.3%	No	No	100%	0.85255	100.0%	67.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
10IDC	ADAMTS17	p.V831A	15	100589161	A	G	Missense_Mutation	114	24.6%	No	No	100%	0.87096	100.0%	78.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
10IDC	EXOC3L1	p.S70L	16	67222842	G	A	Missense_Mutation	167	5.4%	No	No	33%	3.00E-04	61.0%	17.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
10IDC	HYDIN	p.H2700N	16	70942671	G	T	Missense_Mutation	174	18.4%	No	No	100%	0.86232	100.0%	73.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
10IDC	ZNF286B	p.A49del	17	18576347	GCGC	G	In_Frame_Del	25	8.0%	No	Yes	42%	0.34192	94.8%	11.7%	Subclonal	N	.	none	.	passenger	No	No	No	WES
10IDC	HEATR5B	p.R1281*	2	37255078	G	A	Nonsense_Mutation	153	5.2%	No	No	32%	4.70E-04	61.3%	16.3%	Subclonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
10IDC	PER2	p.G256A	2	239179958	C	G	Missense_Mutation	48	22.9%	No	No	100%	0.83781	100.0%	60.1%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
10IDC	PLXNB1	p.M954L	3	48460421	T	A	Missense_Mutation	121	17.4%	No	No	100%	0.80926	100.0%	64.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
10IDC	PIK3CA	p.E545D	3	178936093	G	T	Missense_Mutation	117	17.1%	No	No	100%	0.79897	100.0%	63.2%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
10IDC	PIK3CA	p.H1047L	3	178952085	A	T	Missense_Mutation	147	19.0%	Yes	No	100%	0.85956	100.0%	72.3%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
10IDC	GPRIN3	p.A378V	4	90170129	G	A	Missense_Mutation	142	14.8%	No	Yes	77%	0.55586	97.8%	50.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
10IDC	MED23	p.L338P	6	131931250	A	G	Missense_Mutation	103	21.4%	No	Yes	100%	0.87236	100.0%	66.9%	Clonal	D	Driver	D	T	likely_pathogenic	Yes	No	Yes	WES, Ampliseq
10IDC	MED23	p.Q337P	6	131931253	T	G	Missense_Mutation	101	20.8%	No	Yes	100%	0.86189	100.0%	65.2%	Clonal	D	Driver	D	T	likely_pathogenic	Yes	No	Yes	WES, Ampliseq
10IDC	GIMAP1	p.A244V	7	150417823	C	T	Missense_Mutation	24	12.5%	No	No	77%	0.54326	98.3%	23.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
10IDC	GSDMC	p.R34H	8	130789733	C	T	Missense_Mutation	179	11.7%	No	No	73%	0.36263	96.8%	47.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
10IDC	FAM47B	p.R165H	X	34961442	G	A	Missense_Mutation	200	15.0%	No	No	93%	0.7433	100.0%	63.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
12DCIS	AKT1	p.E17K	14	105246551	C	T	Missense_Mutation	119	31.1%	Yes	No	100%	0.96924	100.0%	86.1%	Clonal	D	Driver	D	T	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
12IDC	AKT1	p.E17K	14	105246551	C	T	Missense_Mutation	197	24.4%	Yes	No	100%	0.76511	100.0%	84.5%	Clonal	D	Driver	D	T	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
12DCIS	ANKRD28	p.N663T	3	15727600	T	G	Missense_Mutation	238	14.7%	No	No	80%	0.54803	98.0%	58.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
12DCIS	ASB18	p.I444N	2	237103585	A	T	Missense_Mutation	168	35.1%	No	No	100%	0.97549	100.0%	90.6%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
12IDC	ASB18	p.I444N	2	237103585	A	T	Missense_Mutation	206	19.9%	No	No	96%	0.80382	100.0%	69.4%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
12DCIS	COL14A1	p.M1235I	8	121293179	G	A	Missense_Mutation	41	17.1%	No	No	93%	0.71209	98.9%	41.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
12IDC	COL14A1	p.M1235I	8	121293179	G	A	Missense_Mutation	22	13.6%	No	No	65%	0.48677	97.7%	21.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
12DCIS	CPAMD8	p.R1135*	19	17038927	G	A	Nonsense_Mutation	212	33.0%	No	No	100%	0.96431	100.0%	91.4%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
12IDC	CPAMD8	p.R1135*	19	17038927	G	A	Nonsense_Mutation	297	21.2%	No	No	100%	0.8775	100.0%	77.5%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
12DCIS	HIF1AN	p.S11F	10	102295747	C	T	Missense_Mutation	230	37.4%	No	No	100%	0.97973	100.0%	93.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
12IDC	HIF1AN	p.S11F	10	102295747	C	T	Missense_Mutation	321	22.1%	No	No	100%	0.90462	100.0%	80.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
12DCIS	MAP3K1	p.F1149Kfs*3	5	56178470	C	CAAAA	Frame_Shift_Ins	163	6.1%	No	No	34%	1.30E-04	59.2%	18.1%	Subclonal	D	.	.	.	likely_pathogenic	Yes	No	Yes	WES
12IDC	MAP3K1	p.F1149Kfs*3	5	56178470	C	CAAAA	Frame_Shift_Ins	222	16.2%	No	No	78%	0.40548	97.1%	56.7%	Subclonal	D	.	.	.	likely_pathogenic	Yes	No	Yes	WES
12DCIS	MMGT1	p.A64S	X	135049595	C	A	Missense_Mutation	88	27.3%	No	No	100%	0.89418	100.0%	76.2%	Clonal	D	Passenger	N	.	passenger	No	No	No	WES, Ampliseq
12IDC	MMGT1	p.A64S	X	135049595	C	A	Missense_Mutation	141	24.8%	No	No	100%	0.8886	100.0%	76.5%	Clonal	D	Passenger	N	.	passenger	No	No	No	WES, Ampliseq
12DCIS	MYH6	p.R1151W	14	23859547	G	A	Missense_Mutation	95	4.2%	No	No	23%	6.70E-04	55.9%	8.8%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
12DCIS	NDUFV2	p.R143P	18	9122638	G	C	Missense_Mutation	201	2.5%	No	No	14%	0	30.6%	5.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
12IDC	NDUFV2	p.R143P	18	9122638	G	C	Missense_Mutation	249	4.4%	No	No	21%	0	36.7%	11.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
12DCIS	NR1H4	p.Q264Hfs*11	12	100930317	CAG	C	Frame_Shift_Del	141	22.0%	No	No	100%	0.89464	100.0%	74.7%	Clonal	D	.	.	.	passenger	No	No	No	WES
12IDC	NR1H4	p.Q264Hfs*11	12	100930317	CAG	C	Frame_Shift_Del	172	14.5%	No	No	70%	0.22773	94.5%	47.7%	Subclonal	D	.	.	.	passenger	No	No	No	WES
12DCIS	PDE11A	p.L98*	2	178936876	GA	G	Frame_Shift_Del	133	20.3%	No	No	100%	0.87286	100.0%	69.9%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
12IDC	PDE11A	p.L98*	2	178936876	GA	G	Frame_Shift_Del	206	18.9%	No	No	91%	0.74473	100.0%	66.2%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
12DCIS	POLR2E	p.E134K	19	1090936	C	T	Missense_Mutation	161	37.3%	No	No	100%	0.89161	100.0%	91.9%	Clonal	D	Passenger	.	T	passenger	No	No	No	WES, Ampliseq
12IDC	POLR2E	p.E134K	19	1090936	C	T	Missense_Mutation	235	20.9%	No	No	100%	0.90304	100.0%	81.0%	Clonal	D	Passenger	.	T	passenger	No	No	No	WES, Ampliseq
12DCIS	PRRC2C	p.H2402Q	1	171548545	T	A	Missense_Mutation	246	22.8%	No	No	100%	0.64403	100.0%	86.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
12IDC	PRRC2C	p.H2402Q	1	171548545	T	A	Missense_Mutation	297	15.5%	No	No	90%	0.72811	100.0%	67.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
12DCIS	RBMXL3	p.Y504*	X	114425516	C	G	Nonsense_Mutation	421	38.0%	No	No	100%	0.98255	100.0%	96.4%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
12IDC	RBMXL3	p.Y504*	X	114425516	C	G	Nonsense_Mutation	688	19.6%	No	No	94%	0.8211	100.0%	79.6%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
12DCIS	SLC9A8	p.F182C	20	48467309	T	G	Missense_Mutation	58	15.5%	No	No	85%	0.67422	98.7%	42.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
12IDC	SLC9A8	p.F182C	20	48467309	T	G	Missense_Mutation	65	24.6%	No	No	100%	0.83067	100.0%	63.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
12DCIS	TAF1A	p.D204V	1	222744001	T	A	Missense_Mutation	134	20.1%	No	No	100%	0.89744	100.0%	77.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
12IDC	TAF1A	p.D204V	1	222744001	T	A	Missense_Mutation	155	18.7%	No	No	100%	0.85136	100.0%	70.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
12IDC	TTC28	p.A1684T	22	28394597	C	T	Missense_Mutation	181	6.6%	No	No	32%	0	53.5%	18.0%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES, Ampliseq
12DCIS	USP8	p.G664R	15	50782478	G	A	Missense_Mutation	85	37.6%	No	No	100%	0.96753	100.0%	84.9%	Clonal	D	Passenger	N	T	passenger	No	Yes	No	WES
12IDC	USP8	p.G664R	15	50782478	G	A	Missense_Mutation	113	30.1%	No	No	100%	0.826	100.0%	81.1%	Clonal	D	Passenger	N	T	passenger	No	Yes	No	WES
12DCIS	ZNF862	p.Y341F	7	149547332	A	T	Missense_Mutation	239	7.1%	No	No	39%	2.00E-05	60.1%	24.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
12DCIS	ZNF862	p.S443I	7	149557577	G	T	Missense_Mutation	299	34.4%	No	No	100%	0.97706	100.0%	94.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
12IDC	ZNF862	p.Y341F	7	149547332	A	T	Missense_Mutation	331	14.5%	No	No	70%	0.04565	89.0%	52.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
12IDC	ZNF862	p.S443I	7	149557577	G	T	Missense_Mutation	392	22.7%	No	No	100%	0.92404	100.0%	84.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13DCIS	ERRFI1	p.L118Qfs*2	1	8074302	TGTGA	T	Frame_Shift_Del	235	13.2%	No	No	91%	0.71961	100.0%	63.1%	Clonal	D	.	.	.	passenger	No	No	No	WES
13DCIS	HNRNPR	p.G189R	1	23650159	C	T	Missense_Mutation	151	15.9%	No	No	100%	0.82378	100.0%	67.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
13DCIS	DCST1	p.W671R	1	155023234	T	C	Missense_Mutation	237	8.9%	No	No	61%	0.07592	89.3%	40.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
13DCIS	LZTS2	p.S639I	10	102766831	G	T	Missense_Mutation	113	23.9%	No	No	100%	0.89545	100.0%	72.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
13DCIS	TRIM3	p.R28Q	11	6486843	C	T	Missense_Mutation	158	19.0%	No	No	93%	0.80737	100.0%	64.3%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
13DCIS	OR4C16	p.L13F	11	55339640	C	T	Missense_Mutation	238	14.3%	No	No	85%	0.60317	98.7%	60.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
13DCIS	A2ML1	p.A593S	12	9000238	G	T	Missense_Mutation	464	5.6%	No	No	84%	0.592	98.7%	56.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
13DCIS	TMTC1	p.D867N	12	29659829	C	T	Missense_Mutation	328	7.6%	No	No	100%	0.84652	100.0%	71.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13DCIS	KRT4	p.R417Q	12	53201524	C	T	Missense_Mutation	91	30.8%	No	Yes	100%	0.8085	100.0%	79.2%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
13DCIS	DISP2	p.A45T	15	40655839	G	A	Missense_Mutation	277	20.9%	No	No	100%	0.89546	100.0%	83.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
13DCIS	FLYWCH1	p.E19V	16	2979742	A	T	Missense_Mutation	174	27.6%	No	No	100%	0.94795	100.0%	89.2%	Clonal	N	Passenger	D	.	passenger	No	No	No	WES
13DCIS	ZNF500	p.E82Q	16	4815736	C	G	Missense_Mutation	107	17.8%	No	No	100%	0.85641	100.0%	70.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13DCIS	KIFC3	p.E359K	16	57803732	C	T	Missense_Mutation	151	16.6%	No	No	100%	0.83953	100.0%	69.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
13DCIS	TP53	p.V73Wfs*50	17	7579470	CG	C	Frame_Shift_Del	131	44.3%	No	Yes	100%	0.5292	100.0%	92.1%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
13DCIS	LGALS3BP	p.V19M	17	76972236	C	T	Missense_Mutation	96	27.1%	No	Yes	100%	0.90124	100.0%	78.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13DCIS	SLC26A11	p.R498W	17	78222443	C	T	Missense_Mutation	91	19.8%	No	Yes	100%	0.82011	100.0%	64.9%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
13DCIS	ZNF541	p.Y78F	19	48058881	T	A	Missense_Mutation	120	25.0%	No	No	100%	0.93405	100.0%	83.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13DCIS	PTOV1	p.D110N	19	50357927	G	A	Missense_Mutation	231	18.2%	No	No	100%	0.88954	100.0%	84.5%	Clonal	D	Passenger	N	.	passenger	No	No	No	WES, Ampliseq
13DCIS	SBK2	p.A317S	19	56041198	C	A	Missense_Mutation	125	5.6%	No	No	67%	0.42024	97.4%	31.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
13DCIS	HIC2	p.G402S	22	21800388	G	A	Missense_Mutation	115	19.1%	No	No	100%	0.82868	100.0%	67.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13DCIS	FANCD2	p.H1320Q	3	10136044	C	A	Missense_Mutation	47	23.4%	No	No	100%	0.82704	100.0%	55.7%	Clonal	D	Passenger	D	T	passenger	Yes	Yes	No	WES, Ampliseq
13DCIS	GABRA2	p.R94*	4	46314709	G	A	Nonsense_Mutation	81	32.1%	No	No	100%	0.95132	100.0%	81.0%	Clonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
13DCIS	HCN1	p.E2V	5	45696191	T	A	Missense_Mutation	48	16.7%	No	No	99%	0.68723	100.0%	44.9%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
13DCIS	PCSK1	p.R80Q	5	95764963	C	T	Missense_Mutation	185	19.5%	No	Yes	96%	0.83486	100.0%	67.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
13DCIS	TUBB	p.S168I	6	30691342	G	T	Missense_Mutation	213	11.3%	No	No	78%	0.47775	97.9%	52.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
13DCIS	HSPA1L	p.G559S	6	31778075	C	T	Missense_Mutation	459	12.4%	No	No	86%	0.59849	98.7%	66.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13DCIS	PREP	p.N477S	6	105736657	T	C	Missense_Mutation	154	10.4%	No	No	72%	0.39574	97.2%	44.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
13DCIS	TSPYL1	p.E151A	6	116600542	T	G	Missense_Mutation	313	14.4%	No	No	99%	0.82182	100.0%	71.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13DCIS	SYNE1	p.L1321M	6	152763257	G	T	Missense_Mutation	90	20.0%	No	No	100%	0.85132	100.0%	69.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13DCIS	TECPR1	p.V1003M	7	97851755	C	T	Missense_Mutation	131	8.4%	No	No	100%	0.7069	100.0%	50.2%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
13DCIS	AGBL3	p.V400I	7	134719540	G	A	Missense_Mutation	171	17.0%	No	No	83%	0.66665	98.6%	58.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
13DCIS	IMPAD1	p.G96A	8	57905858	C	G	Missense_Mutation	320	10.3%	No	No	92%	0.72767	100.0%	63.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
13DCIS	DCAF8L2	p.V587M	X	27766771	G	A	Missense_Mutation	209	28.2%	No	No	100%	0.96602	100.0%	90.3%	Clonal	.	Passenger	.	.	passenger	No	No	No	WES, Ampliseq
13DCIS	TAF3	p.R58*	10	7866286	C	T	Nonsense_Mutation	383	5.2%	No	No	62%	0.11551	91.4%	40.2%	Subclonal	A	.	.	.	passenger	No	No	No	WES
13IDC	ERRFI1	p.L118Qfs*2	1	8074302	TGTGA	T	Frame_Shift_Del	156	18.6%	No	No	88%	0.62489	100.0%	61.2%	Clonal	D	.	.	.	passenger	No	No	No	WES
13IDC	PTPRF	p.R808G	1	44069168	C	G	Missense_Mutation	258	3.5%	No	No	24%	0	43.4%	12.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13IDC	SLC6A9	p.C293Y	1	44468589	C	T	Missense_Mutation	310	31.0%	No	No	100%	0.96418	100.0%	94.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
13IDC	ZNF281	p.S841L	1	200376312	G	A	Missense_Mutation	283	4.2%	No	No	20%	0	34.0%	11.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13IDC	TAF3	p.R58*	10	7866286	C	T	Nonsense_Mutation	211	15.6%	No	No	90%	0.65141	100.0%	63.4%	Clonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
13IDC	PTEN	p.Y27C	10	89653782	A	G	Missense_Mutation	36	22.2%	No	Yes	61%	0.27111	94.9%	31.7%	Subclonal	D	Driver	D	D	likely_pathogenic	Yes	Yes	Yes	WES
13IDC	PSD	p.E201*	10	104176195	C	A	Nonsense_Mutation	193	5.2%	No	No	25%	0	43.6%	13.1%	Subclonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
13IDC	TRIM3	p.R28Q	11	6486843	C	T	Missense_Mutation	167	23.4%	No	No	88%	0.60651	99.0%	64.7%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
13IDC	WNK1	p.E2068K	12	1005855	G	A	Missense_Mutation	470	13.2%	No	No	100%	0.95663	100.0%	90.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
13IDC	A2ML1	p.A593S	12	9000238	G	T	Missense_Mutation	693	6.1%	No	No	89%	0.63377	100.0%	64.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
13IDC	TMTC1	p.D867N	12	29659829	C	T	Missense_Mutation	285	10.9%	No	No	100%	0.9188	100.0%	80.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13IDC	SENP1	p.D37Y	12	48491803	C	A	Missense_Mutation	119	29.4%	No	Yes	100%	0.83878	100.0%	74.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13IDC	DNAH10	p.M116I	12	124258721	G	T	Missense_Mutation	93	6.5%	No	Yes	50%	0.13979	92.5%	23.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13IDC	RTL1	p.S393R	14	101349947	G	T	Missense_Mutation	195	22.6%	No	Yes	100%	0.83931	100.0%	75.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13IDC	DISP2	p.A45T	15	40655839	G	A	Missense_Mutation	334	24.3%	No	Yes	91%	0.67444	100.0%	73.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13IDC	FLYWCH1	p.E19V	16	2979742	A	T	Missense_Mutation	230	23.5%	No	No	100%	0.78762	100.0%	85.0%	Clonal	N	Passenger	D	.	passenger	No	No	No	WES
13IDC	KIFC3	p.E359K	16	57803732	C	T	Missense_Mutation	213	18.3%	No	No	100%	0.81459	100.0%	73.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
13IDC	TP53	p.V73Wfs*50	17	7579470	CG	C	Frame_Shift_Del	248	60.9%	No	Yes	100%	0.03027	100.0%	97.1%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
13IDC	ACACA	p.P88R	17	35687188	G	C	Missense_Mutation	233	7.3%	No	Yes	49%	0.00421	76.3%	30.7%	Subclonal	D	Passenger	.	T	passenger	No	No	No	WES, Ampliseq
13IDC	FBXO47	p.T238M	17	37101293	G	A	Missense_Mutation	295	15.9%	No	Yes	100%	0.8384	100.0%	76.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
13IDC	ZNF829	p.E486V	19	37382479	T	A	Missense_Mutation	135	5.2%	No	No	51%	0.12122	91.8%	24.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
13IDC	ZNF585B	p.G81V	19	37680613	C	A	Missense_Mutation	450	16.7%	No	No	100%	0.78695	100.0%	90.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
13IDC	ZNF541	p.Y78F	19	48058881	T	A	Missense_Mutation	203	17.7%	No	No	100%	0.84795	100.0%	76.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13IDC	EMILIN3	p.R733C	20	39990012	G	A	Missense_Mutation	174	17.8%	No	No	100%	0.83646	100.0%	74.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
13IDC	C2CD2	p.E87V	21	43373498	T	A	Missense_Mutation	187	4.8%	No	No	23%	0	41.8%	11.7%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
13IDC	HIC2	p.G402S	22	21800388	G	A	Missense_Mutation	219	15.1%	No	No	87%	0.59107	98.9%	61.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13IDC	FANCD2	p.H1320Q	3	10136044	C	A	Missense_Mutation	46	19.6%	No	No	73%	0.42139	97.9%	38.6%	Subclonal	D	Passenger	D	T	passenger	Yes	Yes	No	WES, Ampliseq
13IDC	STAG1	p.R131*	3	136287610	G	A	Nonsense_Mutation	45	17.8%	No	No	84%	0.54772	98.7%	40.9%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
13IDC	GABRA2	p.R94*	4	46314709	G	A	Nonsense_Mutation	36	22.2%	No	No	100%	0.66678	100.0%	47.2%	Clonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
13IDC	C4orf3	p.H120R	4	120221731	T	C	Missense_Mutation	429	6.3%	No	No	30%	0	42.3%	20.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13IDC	HCN1	p.E2V	5	45696191	T	A	Missense_Mutation	83	22.9%	No	Yes	86%	0.58355	98.9%	55.0%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
13IDC	PCSK1	p.R80Q	5	95764963	C	T	Missense_Mutation	146	25.3%	No	Yes	95%	0.73644	100.0%	68.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
13IDC	DNAJC18	p.P155S	5	138761957	G	A	Missense_Mutation	108	25.0%	No	Yes	100%	0.83044	100.0%	72.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13IDC	CDKAL1	p.R241K	6	20846389	G	A	Missense_Mutation	125	4.8%	No	No	23%	0	47.4%	10.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
13IDC	HSPA1L	p.G559S	6	31778075	C	T	Missense_Mutation	392	15.6%	No	No	74%	0.06011	91.7%	58.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
13IDC	RAPGEF5	p.Q364H	7	22197479	T	G	Missense_Mutation	123	9.8%	No	No	46%	0.00716	76.8%	26.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
13IDC	AGBL3	p.V400I	7	134719540	G	A	Missense_Mutation	135	19.3%	No	No	92%	0.66883	100.0%	61.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
13IDC	IMPAD1	p.G96A	8	57905858	C	G	Missense_Mutation	261	10.7%	No	No	51%	1.60E-04	71.2%	35.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
13IDC	INTS8	p.S268L	8	95848801	C	T	Missense_Mutation	388	3.6%	No	No	35%	1.00E-05	57.7%	20.7%	Subclonal	D	Passenger	N	.	passenger	No	No	No	WES, Ampliseq
13IDC	DCAF8L2	p.V587M	X	27766771	G	A	Missense_Mutation	149	19.5%	No	No	93%	0.68634	100.0%	63.5%	Clonal	.	Passenger	.	.	passenger	No	No	No	WES
2DCISA	PER3	p.A775S	1	7887336	G	T	Missense_Mutation	401	9.2%	No	No	88%	0.64051	100.0%	63.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
2DCISA	ZSCAN20	p.K381E	1	33956999	A	G	Missense_Mutation	178	25.8%	No	No	100%	0.95332	100.0%	87.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	FAAH	p.A164T	1	46871089	G	A	Missense_Mutation	175	4.0%	No	No	30%	4.30E-04	60.1%	14.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	ZNF644	p.R1026G	1	91403835	T	C	Missense_Mutation	291	7.2%	No	Yes	47%	4.30E-04	70.2%	30.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	HRNR	p.G499*	1	152192610	C	A	Nonsense_Mutation	127	11.0%	No	No	94%	0.66981	100.0%	52.7%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISA	NES	p.T456K	1	156642613	G	T	Missense_Mutation	342	58.2%	No	No	100%	0.05514	100.0%	98.0%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES, Ampliseq
2DCISA	DEGS1	p.H89D	1	224377461	C	G	Missense_Mutation	270	7.4%	No	No	63%	0.11712	92.0%	41.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	ARHGAP12	p.S213C	10	32197146	G	C	Missense_Mutation	110	13.6%	No	No	100%	0.72763	100.0%	57.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	DDX21	p.R702C	10	70742320	C	T	Missense_Mutation	88	5.7%	No	No	43%	0.08981	88.6%	18.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	ADAMTS14	p.T658P	10	72503342	A	C	Missense_Mutation	80	16.3%	No	No	100%	0.77716	100.0%	59.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2DCISA	BAG3	p.G238R	10	121431971	G	C	Missense_Mutation	376	33.0%	No	Yes	100%	0.95091	100.0%	95.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	SCUBE2	p.R211T	11	9090928	C	G	Missense_Mutation	101	21.8%	No	No	100%	0.84594	100.0%	73.3%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	ANO3	p.G668A	11	26656577	G	C	Missense_Mutation	269	4.5%	No	No	34%	2.00E-05	57.2%	19.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	GYLTL1B	p.R451G	11	45948891	A	G	Missense_Mutation	86	27.9%	No	No	100%	0.93148	100.0%	80.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	F2	p.P326T	11	46748149	C	A	Missense_Mutation	244	12.3%	No	No	93%	0.70753	100.0%	63.4%	Clonal	N	Passenger	D	D	passenger	No	No	No	WES, Ampliseq
2DCISA	MYRF	p.X1006_splice	11	61550969	G	T	Splice_Site	277	13.4%	No	No	100%	0.79481	100.0%	70.0%	Clonal	N	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISA	CCDC82	p.E66Q	11	96117716	C	G	Missense_Mutation	343	9.6%	No	No	73%	0.21515	95.3%	51.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
2DCISA	NPAT	p.D6E	11	108093246	G	C	Missense_Mutation	174	17.2%	No	Yes	96%	0.79801	100.0%	65.3%	Clonal	D	Passenger	N	T	passenger	No	No	Yes	WES, Ampliseq
2DCISA	KMT2A	p.P2547T	11	118374246	C	A	Missense_Mutation	188	15.4%	No	Yes	86%	0.67229	98.9%	59.4%	Clonal	N	Passenger	N	T	passenger	Yes	Yes	Yes	WES, Ampliseq
2DCISA	TBRG1	p.S224Qfs*48	11	124496873	ATGCCAGCATGAAG	A	Frame_Shift_Del	151	11.3%	No	Yes	63%	0.16353	92.2%	39.2%	Subclonal	D	.	.	.	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	DENND5B	p.D163E	12	31632938	A	C	Missense_Mutation	119	5.0%	No	No	38%	0.02124	78.4%	17.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	KIF5A	p.T806M	12	57971847	C	T	Missense_Mutation	145	12.4%	No	No	94%	0.68554	100.0%	56.6%	Clonal	D	Driver	N	T	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	FGD6	p.Q366K	12	95603964	G	T	Missense_Mutation	244	14.3%	No	No	94%	0.73226	100.0%	66.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	VEZT	p.L237M	12	95660407	C	A	Missense_Mutation	186	14.0%	No	No	92%	0.68936	100.0%	61.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	UHRF1BP1L	p.D1370E	12	100433539	A	C	Missense_Mutation	152	11.8%	No	No	78%	0.47037	98.1%	48.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
2DCISA	UTP20	p.G886*	12	101711359	G	T	Nonsense_Mutation	199	4.5%	No	No	30%	2.00E-05	54.4%	15.4%	Subclonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISA	TAOK3	p.Q460H	12	118619362	C	G	Missense_Mutation	284	13.0%	No	No	85%	0.58539	98.8%	61.7%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	PXN	p.R75*	12	120661971	G	A	Nonsense_Mutation	281	7.8%	No	No	51%	0.00218	75.3%	33.8%	Subclonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISA	MSI1	p.Y239*	12	120791118	G	T	Nonsense_Mutation	88	20.5%	No	No	100%	0.82738	100.0%	68.3%	Clonal	A	.	.	.	passenger	No	No	No	WES
2DCISA	MLXIP	p.P348H	12	122616881	C	A	Missense_Mutation	272	15.1%	No	No	99%	0.79008	100.0%	70.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	RNF6	p.N613S	13	26788181	T	C	Missense_Mutation	255	7.5%	No	No	56%	0.02825	84.7%	36.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	ABCC4	p.P561A	13	95830007	G	C	Missense_Mutation	99	9.1%	No	No	60%	0.22417	94.9%	31.4%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	TBPL2	p.P191L	14	55903315	G	A	Missense_Mutation	282	16.3%	No	No	100%	0.84921	100.0%	75.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	DYNC1H1	p.R1201T	14	102463409	G	C	Missense_Mutation	182	44.5%	No	Yes	100%	0.27649	100.0%	94.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	SLC12A6	p.P757A	15	34533029	G	C	Missense_Mutation	48	14.6%	No	No	96%	0.63108	99.0%	41.5%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	SLC12A1	p.A521D	15	48539535	C	A	Missense_Mutation	138	15.2%	No	No	100%	0.74441	100.0%	61.6%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	IGF1R	p.P1307L	15	99500487	C	T	Missense_Mutation	220	5.0%	No	No	43%	0.00571	74.0%	23.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	TSC2	p.P1042L	16	2129191	C	T	Missense_Mutation	283	8.8%	No	No	67%	0.13065	92.8%	45.3%	Subclonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	No	WES, Ampliseq
2DCISA	FTO	p.S441W	16	53967979	C	G	Missense_Mutation	138	7.2%	No	No	55%	0.1172	91.3%	29.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	TP53	p.E339Rfs*8	17	7574013	G	GA	Frame_Shift_Ins	120	22.5%	No	Yes	100%	0.84592	100.0%	77.3%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
2DCISA	SHISA6	p.S310I	17	11455246	G	T	Missense_Mutation	95	17.9%	No	Yes	100%	0.79303	100.0%	63.7%	Clonal	D	Passenger	N	.	passenger	No	No	No	WES, Ampliseq
2DCISA	EFCAB5	p.E997V	17	28405485	A	T	Missense_Mutation	47	19.1%	No	Yes	100%	0.75515	100.0%	53.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	TMEM101	p.Y199H	17	42089475	A	G	Missense_Mutation	156	11.5%	No	Yes	87%	0.61985	99.0%	53.6%	Clonal	D	Passenger	N	.	passenger	No	No	No	WES, Ampliseq
2DCISA	GPR142	p.R256C	17	72368116	C	T	Missense_Mutation	354	9.6%	No	Yes	100%	0.82898	100.0%	72.1%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	OTOP3	p.D154Y	17	72937874	G	T	Missense_Mutation	391	4.1%	No	Yes	47%	0.0042	75.0%	28.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	OSBPL1A	p.A132G	18	21914294	G	C	Missense_Mutation	104	14.4%	No	No	95%	0.68244	100.0%	54.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
2DCISA	MRO	p.X96_splice	18	48333073	C	A	Splice_Site	101	18.8%	No	No	100%	0.81543	100.0%	67.1%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISA	PAK4	p.G202D	19	39663958	G	A	Missense_Mutation	158	34.2%	No	Yes	100%	0.92852	100.0%	90.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
2DCISA	SYT3	p.T184P	19	51135667	T	G	Missense_Mutation	188	14.9%	No	Yes	98%	0.75241	100.0%	64.9%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	ADAM17	p.I745V	2	9630548	T	C	Missense_Mutation	175	8.6%	No	No	82%	0.54867	98.6%	48.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	GALNT14	p.R401H	2	31147654	C	T	Missense_Mutation	167	12.6%	No	No	100%	0.77737	100.0%	64.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	YIPF4	p.L178V	2	32526499	C	G	Missense_Mutation	200	12.5%	No	No	100%	0.79123	100.0%	66.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	TTC27	p.T811S	2	33045905	C	G	Missense_Mutation	100	10.0%	No	No	86%	0.58352	98.8%	44.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	SIX3	p.A118V	2	45169596	C	T	Missense_Mutation	261	6.1%	No	No	52%	0.02026	82.3%	32.2%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	SIX2	p.R101L	2	45235948	C	A	Missense_Mutation	392	12.0%	No	No	100%	0.82266	100.0%	73.5%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
2DCISA	TTC7A	p.C229W	2	47205969	T	G	Missense_Mutation	316	12.0%	No	No	100%	0.8076	100.0%	71.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	ADD2	p.D676N	2	70890712	C	T	Missense_Mutation	226	9.7%	No	No	83%	0.56297	98.7%	54.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	DNAH6	p.D2172V	2	84899511	A	T	Missense_Mutation	234	10.7%	No	No	91%	0.67996	100.0%	60.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	7-Mar	p.R45T	2	160585667	G	C	Missense_Mutation	128	6.3%	No	No	47%	0.05899	86.4%	23.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	ABCB11	p.M217T	2	169850354	A	G	Missense_Mutation	105	11.4%	No	No	86%	0.59848	98.9%	47.3%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	FAM117B	p.S426Rfs*76	2	203622105	GTAGC	G	Frame_Shift_Del	176	13.6%	No	No	89%	0.65869	100.0%	58.8%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISA	RSPO4	p.F99L	20	947931	A	G	Missense_Mutation	182	14.3%	No	No	100%	0.80109	100.0%	67.7%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	L3MBTL1	p.G6A	20	42142226	G	C	Missense_Mutation	227	19.8%	No	No	100%	0.94861	100.0%	87.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	ZNF831	p.G604S	20	57767884	G	A	Missense_Mutation	321	21.2%	No	No	100%	0.94398	100.0%	90.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	EWSR1	p.A540P	22	29695246	G	C	Missense_Mutation	185	5.9%	No	Yes	45%	0.01082	77.3%	25.0%	Subclonal	D	Passenger	N	T	passenger	Yes	Yes	No	WES, Ampliseq
2DCISA	LIMCH1	p.E565*	4	41652437	G	T	Nonsense_Mutation	129	8.5%	No	No	56%	0.112	91.0%	31.3%	Subclonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISA	GRID2	p.S983L	4	94693573	C	T	Missense_Mutation	254	10.6%	No	No	91%	0.67791	100.0%	60.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	RAP1GDS1	p.V408G	4	99341215	T	G	Missense_Mutation	142	11.3%	No	No	96%	0.69414	100.0%	55.6%	Clonal	D	Passenger	D	T	passenger	Yes	Yes	No	WES, Ampliseq
2DCISA	EMCN	p.S76*	4	101396227	G	C	Nonsense_Mutation	200	8.5%	No	No	73%	0.37406	97.3%	45.2%	Subclonal	A	.	.	.	passenger	No	No	No	WES
2DCISA	COL25A1	p.G216A	4	109861720	C	G	Missense_Mutation	104	10.6%	No	No	90%	0.62668	99.0%	47.4%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	MYO10	p.D302N	5	16779680	C	T	Missense_Mutation	216	6.9%	No	No	52%	0.02487	83.1%	31.8%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	F2RL1	p.C226S	5	76129109	G	C	Missense_Mutation	208	6.7%	No	Yes	44%	0.0019	71.5%	26.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	PITX1	p.S269W	5	134364608	G	C	Missense_Mutation	143	31.5%	No	Yes	100%	0.95226	100.0%	88.4%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	NRG2	p.C5S	5	139422641	C	G	Missense_Mutation	96	28.1%	No	Yes	100%	0.93822	100.0%	81.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
2DCISA	TENM2	p.P2498R	5	167687348	C	G	Missense_Mutation	113	6.2%	No	Yes	41%	0.02086	78.9%	19.6%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISA	ZNF454	p.G520V	5	178392964	G	T	Missense_Mutation	267	9.7%	No	No	93%	0.69767	100.0%	61.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	PKHD1	p.S1728_S1734del	6	51889405	TTGAGGTGAACACCAGGGCAGA	T	In_Frame_Del	135	8.1%	No	Yes	53%	0.0755	88.6%	29.9%	Subclonal	N	.	D	.	passenger	No	No	No	WES
2DCISA	MYCT1	p.L184Q	6	153043231	T	A	Missense_Mutation	308	16.2%	No	Yes	100%	0.85336	100.0%	76.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	GPER1	p.H247Q	7	1132105	C	A	Missense_Mutation	176	10.2%	No	No	87%	0.62242	99.0%	53.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	SAMD9L	p.K312I	7	92764350	T	A	Missense_Mutation	229	6.1%	No	No	52%	0.03227	84.2%	31.1%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	LHFPL3	p.D215Lfs*28	7	104377313	CGACAA	C	Frame_Shift_Del	183	20.8%	No	No	100%	0.83921	100.0%	83.1%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISA	WNT16	p.A231V	7	120978993	C	T	Missense_Mutation	199	14.1%	No	No	100%	0.83833	100.0%	72.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISA	SLC39A4	p.A333V	8	145639797	G	A	Missense_Mutation	161	40.4%	No	Yes	100%	0.38329	100.0%	92.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	DMRTA1	p.L456R	9	22451762	T	G	Missense_Mutation	185	14.1%	No	Yes	92%	0.69505	100.0%	61.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	ZNF484	p.K785Lfs*9	9	95608718	GCCTTT	G	Frame_Shift_Del	265	15.5%	No	No	100%	0.80988	100.0%	71.7%	Clonal	D	.	.	.	passenger	No	No	No	WES
2DCISA	PRRC2B	p.P454L	9	134334700	C	T	Missense_Mutation	72	19.4%	No	No	100%	0.88184	100.0%	67.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	KDM5C	p.E185Q	X	53246429	C	G	Missense_Mutation	143	16.1%	No	Yes	89%	0.72391	100.0%	58.5%	Clonal	D	Passenger	N	D	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
2DCISA	ATP6AP1	p.A40_A41dup	X	153657133	T	TGGCGGC	In_Frame_Ins	177	5.6%	No	Yes	31%	3.00E-05	55.5%	16.8%	Subclonal	N	.	N	.	passenger	No	No	No	WES
2DCISA	SHE	p.S10C	1	154474474	G	C	Missense_Mutation	58	6.9%	No	No	66%	0.41745	97.7%	24.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
2DCISA	SCN9A	p.R677Sfs*4	2	167138227	GCT	G	Frame_Shift_Del	125	8.8%	No	No	66%	0.31782	96.6%	37.0%	Subclonal	D	.	.	.	passenger	No	No	No	WES
2DCISA	TOP2B	p.K1003*	3	25661394	T	A	Nonsense_Mutation	115	10.4%	No	No	100%	0.68638	100.0%	51.8%	Clonal	D	.	.	.	passenger	No	No	No	WES
2DCISA	DNAH1	p.E2969K	3	52420771	G	A	Missense_Mutation	59	18.6%	No	No	100%	0.76685	100.0%	52.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	IFT122	p.A875T	3	129221648	G	A	Missense_Mutation	191	9.4%	No	No	71%	0.32525	96.8%	45.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISA	PIK3CA	p.H1047L	3	178952085	A	T	Missense_Mutation	246	33.3%	Yes	No	100%	0.41418	100.0%	94.3%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
2DCISA	SOX2	p.D201N	3	181430749	G	A	Missense_Mutation	418	15.1%	No	No	100%	0.58105	100.0%	87.1%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	No	WES, Ampliseq
2DCISA	LMX1B	p.X274_splice	9	129456020	TGCAGATGAAGAAGCTGGCGCGGCG	T	Splice_Site	239	4.6%	No	No	49%	0.03264	83.4%	27.0%	Subclonal	D	.	.	.	likely_pathogenic	No	No	No	WES
2DCISB	ACTRT2	p.I250F	1	2938998	A	T	Missense_Mutation	233	10.7%	No	No	85%	0.66981	98.9%	57.1%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
2DCISB	PER3	p.A775S	1	7887336	G	T	Missense_Mutation	296	13.9%	No	No	100%	0.88341	100.0%	75.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
2DCISB	ZSCAN20	p.K381E	1	33956999	A	G	Missense_Mutation	161	26.1%	No	Yes	100%	0.80474	100.0%	84.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	HRNR	p.G499*	1	152192610	C	A	Nonsense_Mutation	120	16.7%	No	Yes	100%	0.86425	100.0%	69.6%	Clonal	D	.	.	.	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	HRNR	p.X46_splice	1	152195590	A	C	Splice_Site	108	5.6%	No	Yes	44%	0.09881	87.5%	20.3%	Subclonal	D	.	.	.	likely_pathogenic	No	No	No	WES, Ampliseq

2DCISB	SHE	p.S10C	1	154474474	G	C	Missense_Mutation	28	21.4%	No	Yes	100%	0.85592	100.0%	51.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
2DCISB	NES	p.T456K	1	156642613	G	T	Missense_Mutation	337	63.8%	No	Yes	100%	0.21495	100.0%	98.1%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES, Ampliseq
2DCISB	ABL2	p.R1070K	1	179077193	C	T	Missense_Mutation	323	7.4%	No	Yes	74%	0.41663	97.1%	49.6%	Subclonal	D	Passenger	N	D	likely_pathogenic	Yes	Yes	No	WES, Ampliseq
2DCISB	DEGS1	p.H89D	1	224377461	C	G	Missense_Mutation	275	10.5%	No	Yes	95%	0.77881	100.0%	63.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	ARHGAP12	p.S213C	10	32197146	G	C	Missense_Mutation	121	13.2%	No	No	92%	0.73043	100.0%	54.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	CCAR1	p.K315*	10	70509005	CAGAAA	C	Frame_Shift_Del	158	10.8%	No	No	75%	0.49781	97.7%	46.6%	Subclonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISB	DDX21	p.R702C	10	70742320	C	T	Missense_Mutation	85	15.3%	No	No	100%	0.78625	100.0%	55.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	ADAMTS14	p.T658P	10	72503342	A	C	Missense_Mutation	84	16.7%	No	No	100%	0.81786	100.0%	59.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2DCISB	IDE	p.E465del	10	94264585	TCTC	T	In_Frame_Del	126	13.5%	No	No	94%	0.74733	100.0%	56.0%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISB	BAG3	p.G238R	10	121431971	G	C	Missense_Mutation	351	32.2%	No	Yes	100%	0.97024	100.0%	94.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	SCUBE2	p.R211T	11	9090928	C	G	Missense_Mutation	108	15.7%	No	No	94%	0.74913	100.0%	56.2%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	GYLTL1B	p.R451G	11	45948891	A	G	Missense_Mutation	69	44.9%	No	No	100%	0.34565	100.0%	86.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	F2	p.P326T	11	46748149	C	A	Missense_Mutation	236	15.3%	No	No	100%	0.86425	100.0%	71.9%	Clonal	N	Passenger	D	D	passenger	No	No	No	WES, Ampliseq
2DCISB	MYRF	p.X1006_splice	11	61550969	G	T	Splice_Site	225	11.6%	No	No	81%	0.57253	98.3%	54.7%	Clonal	N	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISB	CCDC82	p.E66Q	11	96117716	C	G	Missense_Mutation	270	7.4%	No	No	52%	0.00631	77.2%	33.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
2DCISB	NPAT	p.D6E	11	108093246	G	C	Missense_Mutation	195	22.6%	No	Yes	100%	0.92161	100.0%	77.4%	Clonal	D	Passenger	N	T	passenger	No	No	Yes	WES, Ampliseq
2DCISB	KMT2A	p.P2547T	11	118374246	C	A	Missense_Mutation	118	28.0%	No	Yes	100%	0.88646	100.0%	79.7%	Clonal	N	Passenger	N	T	passenger	Yes	Yes	Yes	WES, Ampliseq
2DCISB	TBRG1	p.S224Qfs*48	11	124496873	ATGCCAGCATGAAG	A	Frame_Shift_Del	154	8.4%	No	Yes	42%	0.00156	68.6%	24.4%	Subclonal	D	.	.	.	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	KIF5A	p.T806M	12	57971847	C	T	Missense_Mutation	140	17.1%	No	No	100%	0.86534	100.0%	70.0%	Clonal	D	Driver	N	T	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	FGD6	p.Q366K	12	95603964	G	T	Missense_Mutation	212	13.2%	No	No	92%	0.7566	100.0%	62.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	VEZT	p.L237M	12	95660407	C	A	Missense_Mutation	162	11.1%	No	No	77%	0.54265	98.1%	48.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	UHRF1BP1L	p.D1370E	12	100433539	A	C	Missense_Mutation	208	14.9%	No	No	100%	0.84411	100.0%	68.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
2DCISB	TAOK3	p.Q460H	12	118619362	C	G	Missense_Mutation	269	11.5%	No	No	69%	0.15079	92.6%	48.7%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	MSI1	p.Y239*	12	120791118	G	T	Nonsense_Mutation	84	17.9%	No	No	100%	0.80097	100.0%	58.6%	Clonal	A	.	.	.	passenger	No	No	No	WES
2DCISB	MLXIP	p.P348H	12	122616881	C	A	Missense_Mutation	270	14.4%	No	No	86%	0.67162	98.9%	62.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	RNF6	p.N613S	13	26788181	T	C	Missense_Mutation	223	14.3%	No	No	100%	0.82677	100.0%	67.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	NBEA	p.G1399E	13	35738609	G	A	Missense_Mutation	191	6.3%	No	No	44%	0.00608	73.7%	25.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
2DCISB	ATP7B	p.V149E	13	52548910	A	T	Missense_Mutation	205	4.4%	No	No	26%	0	48.0%	13.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
2DCISB	DCT	p.P320Q	13	95114348	G	T	Missense_Mutation	102	10.8%	No	No	64%	0.335	95.9%	36.0%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	ABCC4	p.P561A	13	95830007	G	C	Missense_Mutation	100	7.0%	No	No	42%	0.03555	80.6%	20.3%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	MBNL2	p.N4Y	13	97928499	A	T	Missense_Mutation	216	16.2%	No	No	97%	0.8122	100.0%	67.6%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	TBPL2	p.P191L	14	55903315	G	A	Missense_Mutation	262	11.8%	No	No	71%	0.2088	94.0%	50.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	DYNC1H1	p.R1201T	14	102463409	G	C	Missense_Mutation	164	45.1%	No	Yes	100%	0.29592	100.0%	94.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	SLC12A1	p.A521D	15	48539535	C	A	Missense_Mutation	153	16.3%	No	No	97%	0.79764	100.0%	63.5%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	APH1B	p.W226S	15	63597883	G	C	Missense_Mutation	154	14.3%	No	No	85%	0.66895	98.8%	55.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2DCISB	CCDC113	p.K363R	16	58313635	A	G	Missense_Mutation	105	13.3%	No	Yes	80%	0.59569	98.4%	46.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
2DCISB	TP53	p.E339Rfs*8	17	7574013	G	GA	Frame_Shift_Ins	169	28.4%	No	Yes	100%	0.90709	100.0%	87.3%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
2DCISB	WRAP53	p.D180E	17	7592917	C	A	Missense_Mutation	51	7.8%	No	Yes	47%	0.23359	93.4%	18.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
2DCISB	SHISA6	p.S310I	17	11455246	G	T	Missense_Mutation	90	7.8%	No	Yes	46%	0.08901	87.0%	22.5%	Subclonal	D	Passenger	N	.	passenger	No	No	No	WES, Ampliseq
2DCISB	EFCAB5	p.E997V	17	28405485	A	T	Missense_Mutation	47	23.4%	No	Yes	100%	0.88345	100.0%	62.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	TMEM101	p.Y199H	17	42089475	A	G	Missense_Mutation	154	14.3%	No	Yes	100%	0.79852	100.0%	62.2%	Clonal	D	Passenger	N	.	passenger	No	No	No	WES, Ampliseq
2DCISB	ABCA10	p.I363T	17	67197728	A	G	Missense_Mutation	272	6.6%	No	Yes	73%	0.43713	97.3%	45.6%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES, Ampliseq
2DCISB	GPR142	p.R256C	17	72368116	C	T	Missense_Mutation	371	7.8%	No	Yes	86%	0.66913	98.9%	58.7%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	NOTUM	p.L367F	17	79913310	G	A	Missense_Mutation	211	6.6%	No	Yes	73%	0.48092	97.6%	42.8%	Subclonal	D	Passenger	N	.	passenger	No	No	No	WES, Ampliseq
2DCISB	OSBPL1A	p.A132G	18	21914294	G	C	Missense_Mutation	108	15.7%	No	No	94%	0.74913	100.0%	56.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	MRO	p.X96_splice	18	48333073	C	A	Splice_Site	98	15.3%	No	No	91%	0.72313	100.0%	53.2%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISB	ZNF121	p.V63M	19	9677602	C	T	Missense_Mutation	216	7.4%	No	Yes	66%	0.30235	95.5%	40.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	PAK4	p.G202D	19	39663958	G	A	Missense_Mutation	199	56.8%	No	Yes	100%	0.0885	100.0%	96.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
2DCISB	SYT3	p.T184P	19	51135667	T	G	Missense_Mutation	210	13.3%	No	Yes	80%	0.53722	98.1%	55.1%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	ADAM17	p.I745V	2	9630548	T	C	Missense_Mutation	175	10.9%	No	No	97%	0.77207	100.0%	58.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	GALNT14	p.R401H	2	31147654	C	T	Missense_Mutation	141	14.9%	No	No	100%	0.85233	100.0%	67.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	YIPF4	p.L178V	2	32526499	C	G	Missense_Mutation	211	12.8%	No	No	100%	0.82336	100.0%	66.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	TTC27	p.T811S	2	33045905	C	G	Missense_Mutation	105	11.4%	No	No	91%	0.7048	100.0%	49.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	SIX2	p.R101L	2	45235948	C	A	Missense_Mutation	410	14.9%	No	No	100%	0.9151	100.0%	82.3%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
2DCISB	TTC7A	p.C229W	2	47205969	T	G	Missense_Mutation	270	10.7%	No	No	86%	0.66882	98.9%	58.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	ADD2	p.D676N	2	70890712	C	T	Missense_Mutation	219	13.2%	No	No	100%	0.8439	100.0%	68.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	DNAH6	p.D2172V	2	84899511	A	T	Missense_Mutation	230	10.9%	No	No	87%	0.68637	98.9%	57.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	C2orf49	p.H179R	2	105959574	A	G	Missense_Mutation	328	7.9%	No	No	63%	0.07742	89.0%	43.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	SCN9A	p.R677Sfs*4	2	167138227	GCT	G	Frame_Shift_Del	116	10.3%	No	No	72%	0.48506	97.6%	40.9%	Subclonal	D	.	.	.	passenger	No	No	No	WES
2DCISB	ABCB11	p.M217T	2	169850354	A	G	Missense_Mutation	100	16.0%	No	No	100%	0.84555	100.0%	64.5%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	FAM117B	p.S426Rfs*76	2	203622105	GTAGC	G	Frame_Shift_Del	187	13.4%	No	No	80%	0.55737	98.2%	54.0%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISB	RQCD1	p.T106N	2	219447806	C	A	Missense_Mutation	236	3.4%	No	No	24%	0	45.1%	11.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	RSPO4	p.F99L	20	947931	A	G	Missense_Mutation	158	11.4%	No	No	79%	0.58006	98.3%	49.7%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	L3MBTL1	p.G6A	20	42142226	G	C	Missense_Mutation	227	18.5%	No	No	100%	0.90017	100.0%	84.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	OCSTAMP	p.A286E	20	45174156	G	T	Missense_Mutation	182	6.6%	No	No	59%	0.20176	93.1%	33.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	ZNF831	p.G604S	20	57767884	G	A	Missense_Mutation	260	23.5%	No	No	100%	0.95608	100.0%	90.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	DNMT3L	p.P215S	21	45674550	G	A	Missense_Mutation	214	8.9%	No	No	62%	0.12585	90.9%	39.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	CPNE9	p.T276S	3	9757661	A	T	Missense_Mutation	77	6.5%	No	No	65%	0.46717	97.5%	26.8%	Subclonal	D	Driver	N	T	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	TOP2B	p.K1003*	3	25661394	T	A	Nonsense_Mutation	103	10.7%	No	No	96%	0.72496	100.0%	49.1%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISB	DNAH1	p.E2969K	3	52420771	G	A	Missense_Mutation	51	15.7%	No	Yes	78%	0.65479	98.4%	38.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	IFT122	p.A875T	3	129221648	G	A	Missense_Mutation	157	15.9%	No	No	100%	0.8522	100.0%	68.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	PIK3CA	p.H1047L	3	178952085	A	T	Missense_Mutation	200	41.5%	Yes	No	100%	0.21704	100.0%	94.6%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
2DCISB	SOX2	p.D201N	3	181430749	G	A	Missense_Mutation	365	12.1%	No	No	96%	0.81502	100.0%	69.7%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	No	WES, Ampliseq
2DCISB	LIMCH1	p.E565*	4	41652437	G	T	Nonsense_Mutation	83	16.9%	No	No	100%	0.77274	100.0%	55.5%	Clonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISB	KIAA1211	p.K1171Yfs*60	4	57190399	AAAAAGGCC	A	Frame_Shift_Del	160	8.8%	No	No	70%	0.41362	96.9%	41.3%	Subclonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2DCISB	GRID2	p.S983L	4	94693573	C	T	Missense_Mutation	267	10.5%	No	No	84%	0.63261	98.7%	57.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	RAP1GDS1	p.V408G	4	99341215	T	G	Missense_Mutation	149	15.4%	No	No	100%	0.86443	100.0%	69.9%	Clonal	D	Passenger	D	T	passenger	Yes	Yes	No	WES, Ampliseq
2DCISB	EMCN	p.S76*	4	101396227	G	C	Nonsense_Mutation	166	11.4%	No	No	91%	0.72972	100.0%	56.2%	Clonal	A	.	.	.	passenger	No	No	No	WES
2DCISB	COL25A1	p.G216A	4	109861720	C	G	Missense_Mutation	86	10.5%	No	No	83%	0.63619	98.7%	41.7%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	MYO10	p.D302N	5	16779680	C	T	Missense_Mutation	204	10.8%	No	No	75%	0.45991	97.4%	49.6%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	F2RL1	p.C226S	5	76129109	G	C	Missense_Mutation	199	17.1%	No	Yes	100%	0.84402	100.0%	69.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	PITX1	p.S269W	5	134364608	G	C	Missense_Mutation	142	36.6%	No	Yes	100%	0.94492	100.0%	90.3%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	NRG2	p.C5S	5	139422641	C	G	Missense_Mutation	80	28.8%	No	Yes	100%	0.92479	100.0%	77.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
2DCISB	SLC26A2	p.D652A	5	149361111	A	C	Missense_Mutation	240	10.0%	No	Yes	70%	0.2698	95.1%	46.9%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	TENM2	p.P2498R	5	167687348	C	G	Missense_Mutation	149	16.8%	No	Yes	83%	0.69573	98.6%	56.4%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	ZNF454	p.G520V	5	178392964	G	T	Missense_Mutation	234	14.5%	No	No	100%	0.88361	100.0%	77.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	PKHD1	p.S1728_S1734del	6	51889405	TTGAGGTGAACACCAGGGCAGA	T	In_Frame_Del	140	6.4%	No	Yes	38%	0.00369	69.7%	20.1%	Subclonal	N	.	D	.	passenger	No	No	No	WES
2DCISB	MYB	p.V117L	6	135511307	G	C	Missense_Mutation	170	18.8%	No	Yes	100%	0.87586	100.0%	72.7%	Clonal	D	Passenger	N	T	passenger	Yes	Yes	No	WES, Ampliseq
2DCISB	MYCT1	p.L184Q	6	153043231	T	A	Missense_Mutation	269	16.0%	No	Yes	95%	0.81156	100.0%	69.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	GPER1	p.H247Q	7	1132105	C	A	Missense_Mutation	170	17.1%	No	No	100%	0.87496	100.0%	76.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	EPHB4	p.G252D	7	100419946	C	T	Missense_Mutation	126	11.9%	No	Yes	83%	0.63948	98.7%	49.2%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	LHFPL3	p.D215Lfs*28	7	104377313	CGACAA	C	Frame_Shift_Del	177	27.1%	No	Yes	100%	0.94501	100.0%	89.1%	Clonal	D	.	.	.	likely_pathogenic	No	No	No	WES, Ampliseq
2DCISB	WNT16	p.A231V	7	120978993	C	T	Missense_Mutation	233	8.2%	No	Yes	73%	0.43922	97.3%	46.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2DCISB	SLC39A4	p.A333V	8	145639797	G	A	Missense_Mutation	142	31.0%	No	Yes	100%	0.95154	100.0%	87.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	DMRTA1	p.L456R	9	22451762	T	G	Missense_Mutation	148	20.9%	No	Yes	100%	0.88714	100.0%	75.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	ZNF484	p.K785Lfs*9	9	95608718	GCCTTT	G	Frame_Shift_Del	186	10.2%	No	No	61%	0.10086	89.8%	39.2%	Subclonal	D	.	.	.	passenger	No	No	No	WES
2DCISB	NUP188	p.D1571V	9	131767784	A	T	Missense_Mutation	366	10.1%	No	Yes	81%	0.52726	98.0%	58.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	PRRC2B	p.P454L	9	134334700	C	T	Missense_Mutation	66	7.6%	No	Yes	60%	0.41231	96.8%	25.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2DCISB	KDM5C	p.E185Q	X	53246429	C	G	Missense_Mutation	133	20.3%	No	Yes	100%	0.86279	100.0%	66.4%	Clonal	D	Passenger	N	D	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
2DCISB	LMX1B	p.X274_splice	9	129456020	TGCAGATGAAGAAGCTGGCGCGGCG	T	Splice_Site	201	4.0%	No	No	40%	0.01477	75.4%	20.0%	Subclonal	D	.	.	.	likely_pathogenic	No	No	No	WES
2IDCA	ZSCAN20	p.K381E	1	33956999	A	G	Missense_Mutation	217	25.8%	No	No	96%	0.82213	100.0%	73.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	SHE	p.S10C	1	154474474	G	C	Missense_Mutation	67	19.4%	No	Yes	91%	0.70114	100.0%	51.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
2IDCA	NES	p.T456K	1	156642613	G	T	Missense_Mutation	379	67.3%	No	Yes	100%	0.35908	100.0%	98.1%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES, Ampliseq
2IDCA	SEC16B	p.K155M	1	177934251	T	A	Missense_Mutation	87	19.5%	No	No	92%	0.72123	100.0%	55.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	ZBTB41	p.P809L	1	197128793	G	A	Missense_Mutation	202	15.3%	No	No	88%	0.68598	100.0%	61.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	CCSAP	p.Y187D	1	229462562	A	C	Missense_Mutation	218	17.0%	No	No	97%	0.8047	100.0%	68.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	ARHGAP12	p.S213C	10	32197146	G	C	Missense_Mutation	75	30.7%	No	No	100%	0.86199	100.0%	75.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	CCAR1	p.K315*	10	70509005	CAGAAA	C	Frame_Shift_Del	82	13.4%	No	No	63%	0.27879	95.2%	35.5%	Subclonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2IDCA	ADAMTS14	p.T658P	10	72503342	A	C	Missense_Mutation	97	26.8%	No	No	100%	0.87237	100.0%	74.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCA	BAG3	p.G238R	10	121431971	G	C	Missense_Mutation	553	59.1%	No	Yes	100%	0.76018	100.0%	98.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	OR51L1	p.H183Q	11	5020761	C	A	Missense_Mutation	247	17.0%	No	No	63%	0.00434	81.9%	47.2%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	SCUBE2	p.R211T	11	9090928	C	G	Missense_Mutation	133	24.8%	No	No	92%	0.75539	100.0%	65.5%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	ABTB2	p.G338R	11	34226109	C	G	Missense_Mutation	146	15.1%	No	No	56%	0.00877	80.3%	37.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	GYLTL1B	p.R451G	11	45948891	A	G	Missense_Mutation	110	47.3%	No	No	100%	0.92367	100.0%	89.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	F2	p.P326T	11	46748149	C	A	Missense_Mutation	368	20.1%	No	No	75%	0.04209	90.4%	60.2%	Subclonal	N	Passenger	D	D	passenger	No	No	No	WES, Ampliseq
2IDCA	PLA2G16	p.E114Q	11	63357619	C	G	Missense_Mutation	187	16.0%	No	No	76%	0.36485	96.7%	53.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCA	TENM4	p.H703N	11	78516409	G	T	Missense_Mutation	223	8.5%	No	No	40%	1.00E-05	60.5%	25.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCA	NPAT	p.D6E	11	108093246	G	C	Missense_Mutation	183	56.3%	No	Yes	100%	1.50E-04	100.0%	94.0%	Clonal	D	Passenger	N	T	passenger	No	No	Yes	WES, Ampliseq
2IDCA	KMT2A	p.P2547T	11	118374246	C	A	Missense_Mutation	82	43.9%	No	Yes	100%	0.92439	100.0%	79.3%	Clonal	N	Passenger	N	T	passenger	Yes	Yes	Yes	WES, Ampliseq
2IDCA	TBRG1	p.S224Qfs*48	11	124496873	ATGCCAGCATGAAG	A	Frame_Shift_Del	81	23.5%	No	Yes	64%	0.11543	90.0%	41.7%	Subclonal	D	.	.	.	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	IQSEC3	p.E768K	12	266719	G	A	Missense_Mutation	277	27.4%	No	Yes	100%	0.89055	100.0%	80.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	TULP3	p.M20I	12	3018713	G	A	Missense_Mutation	40	25.0%	No	Yes	93%	0.69903	100.0%	48.2%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
2IDCA	LTBR	p.H55Q	12	6493822	C	A	Missense_Mutation	383	6.8%	No	No	32%	0	45.5%	21.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	RNF41	p.X201_splice	12	56601429	C	T	Splice_Site	86	22.1%	No	No	100%	0.80225	100.0%	62.4%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2IDCA	KIF5A	p.T806M	12	57971847	C	T	Missense_Mutation	176	18.2%	No	No	86%	0.64788	98.8%	60.8%	Clonal	D	Driver	N	T	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	PPP1R12A	p.S336Y	12	80214661	G	T	Missense_Mutation	94	26.6%	No	No	99%	0.801	100.0%	65.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	VEZT	p.L237M	12	95660407	C	A	Missense_Mutation	95	20.0%	No	No	74%	0.41682	97.2%	48.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	UHRF1BP1L	p.D1370E	12	100433539	A	C	Missense_Mutation	114	25.4%	No	No	94%	0.77567	100.0%	65.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
2IDCA	MSI1	p.Y239*	12	120791118	G	T	Nonsense_Mutation	126	22.2%	No	No	83%	0.57991	98.5%	57.8%	Clonal	A	.	.	.	passenger	No	No	No	WES
2IDCA	MLXIP	p.P348H	12	122616881	C	A	Missense_Mutation	382	20.4%	No	No	76%	0.05483	91.2%	61.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	GALNT9	p.Q224*	12	132681696	G	A	Nonsense_Mutation	307	9.1%	No	No	34%	0	47.3%	23.2%	Subclonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2IDCA	RNF6	p.N613S	13	26788181	T	C	Missense_Mutation	172	25.0%	No	No	100%	0.89793	100.0%	79.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	COL4A1	p.Q1563H	13	110807696	C	A	Missense_Mutation	151	26.5%	No	No	98%	0.82862	100.0%	71.3%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	ZFHX2	p.P294T	14	24003655	G	T	Missense_Mutation	269	7.4%	No	No	35%	0	52.3%	22.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
2IDCA	TBPL2	p.P191L	14	55903315	G	A	Missense_Mutation	188	29.8%	No	Yes	100%	0.90713	100.0%	80.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	DYNC1H1	p.R1201T	14	102463409	G	C	Missense_Mutation	218	72.9%	No	Yes	100%	0.262	100.0%	97.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCA	ZBTB42	p.L93R	14	105267812	T	G	Missense_Mutation	595	17.6%	No	Yes	100%	0.89319	100.0%	81.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	NPAP1	p.P111H	15	24921346	C	A	Missense_Mutation	178	8.4%	No	No	31%	0	49.4%	18.8%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	SQRDL	p.K344N	15	45974843	G	C	Missense_Mutation	26	34.6%	No	No	100%	0.80526	100.0%	55.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCA	SLC12A1	p.A521D	15	48539535	C	A	Missense_Mutation	98	28.6%	No	No	100%	0.84725	100.0%	69.9%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	ISL2	p.Q259H	15	76632882	G	T	Missense_Mutation	176	26.1%	No	No	97%	0.82526	100.0%	72.2%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
2IDCA	SMG1	p.H2161Y	16	18853102	G	A	Missense_Mutation	111	36.0%	No	No	100%	0.90947	100.0%	85.8%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	FBXL19	p.G64V	16	30937206	G	T	Missense_Mutation	54	13.0%	No	No	61%	0.33631	96.1%	29.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	TP53	p.E339Rfs*8	17	7574013	G	GA	Frame_Shift_Ins	175	45.1%	No	Yes	100%	0.73445	100.0%	92.4%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
2IDCA	EFCAB5	p.E997V	17	28405485	A	T	Missense_Mutation	29	27.6%	No	Yes	100%	0.72768	100.0%	47.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	SMURF2	p.D546Y	17	62551086	C	A	Missense_Mutation	138	10.9%	No	Yes	84%	0.62978	98.8%	49.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	QRICH2	p.A45V	17	74300569	G	A	Missense_Mutation	454	14.3%	No	Yes	100%	0.90409	100.0%	80.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	THOC1	p.D608E	18	214776	G	C	Missense_Mutation	171	18.1%	No	No	85%	0.64395	98.8%	60.3%	Clonal	N	Passenger	N	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	OSBPL1A	p.A132G	18	21914294	G	C	Missense_Mutation	69	30.4%	No	No	100%	0.84607	100.0%	67.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
2IDCA	MRO	p.X96_splice	18	48333073	C	A	Splice_Site	84	26.2%	No	No	97%	0.78197	100.0%	62.7%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2IDCA	MUC16	p.T4363I	19	9074358	G	A	Missense_Mutation	97	27.8%	No	Yes	100%	0.83262	100.0%	68.3%	Clonal	.	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	LDLR	p.G37E	19	11210941	G	A	Missense_Mutation	289	28.4%	No	Yes	100%	0.91182	100.0%	82.4%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	GDF1	p.G84E	19	18980866	C	T	Missense_Mutation	360	36.4%	No	Yes	100%	0.97013	100.0%	95.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
2IDCA	ZFP14	p.C373F	19	36831610	C	A	Missense_Mutation	138	23.9%	No	Yes	100%	0.86328	100.0%	79.0%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	PAK4	p.G202D	19	39663958	G	A	Missense_Mutation	167	44.9%	No	Yes	100%	0.92597	100.0%	88.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
2IDCA	SLC17A7	p.A218V	19	49937288	G	A	Missense_Mutation	126	19.0%	No	Yes	71%	0.24437	94.9%	48.3%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	SYT3	p.T184P	19	51135667	T	G	Missense_Mutation	328	29.3%	No	Yes	100%	0.9293	100.0%	85.3%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	GALNT14	p.R401H	2	31147654	C	T	Missense_Mutation	183	19.1%	No	No	90%	0.72665	100.0%	64.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	YIPF4	p.L178V	2	32526499	C	G	Missense_Mutation	107	21.5%	No	No	100%	0.80416	100.0%	64.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	TTC27	p.T811S	2	33045905	C	G	Missense_Mutation	48	33.3%	No	No	100%	0.88717	100.0%	70.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	SIX2	p.R101L	2	45235948	C	A	Missense_Mutation	576	21.4%	No	No	100%	0.90177	100.0%	83.1%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
2IDCA	ADD2	p.D676N	2	70890712	C	T	Missense_Mutation	342	30.7%	No	No	100%	0.90254	100.0%	93.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	SMYD5	p.P388T	2	73452979	C	A	Missense_Mutation	340	14.4%	No	No	82%	0.509	98.0%	62.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCA	DNAH6	p.D2172V	2	84899511	A	T	Missense_Mutation	165	20.6%	No	No	100%	0.88073	100.0%	75.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	NCK2	p.A186T	2	106498113	G	A	Missense_Mutation	415	18.8%	No	No	100%	0.90939	100.0%	81.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	SCN9A	p.R677Sfs*4	2	167138227	GCT	G	Frame_Shift_Del	85	18.8%	No	No	89%	0.68757	100.0%	53.4%	Clonal	D	.	.	.	passenger	No	No	No	WES
2IDCA	ABCB11	p.M217T	2	169850354	A	G	Missense_Mutation	62	25.8%	No	No	100%	0.83378	100.0%	64.5%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	FAM117B	p.S426Rfs*76	2	203622105	GTAGC	G	Frame_Shift_Del	170	45.3%	No	No	100%	0.76277	100.0%	92.2%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2IDCA	HDLBP	p.E657Q	2	242182075	C	G	Missense_Mutation	135	4.4%	No	Yes	12%	0	24.9%	5.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	SIGLEC1	p.I119Mfs*2	20	3687021	CATCTGACCAGCGGTTGACCTCACTG	C	Frame_Shift_Del	453	7.1%	No	No	33%	0	45.7%	23.3%	Subclonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2IDCA	GNAS	p.F226L	20	57428996	T	C	Missense_Mutation	416	9.4%	No	Yes	44%	0	58.7%	32.2%	Subclonal	D	Passenger	N	D	likely_pathogenic	Yes	No	No	WES
2IDCA	DNAH1	p.E2969K	3	52420771	G	A	Missense_Mutation	53	37.7%	No	Yes	100%	0.8549	100.0%	64.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	IFT122	p.A875T	3	129221648	G	A	Missense_Mutation	290	21.4%	No	No	100%	0.86737	100.0%	76.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	COL6A5	p.L2039F	3	130159297	C	T	Missense_Mutation	104	25.0%	No	Yes	93%	0.75376	100.0%	62.9%	Clonal	N	Passenger	.	T	passenger	No	No	No	WES
2IDCA	PIK3CA	p.H1047L	3	178952085	A	T	Missense_Mutation	154	39.0%	Yes	No	100%	0.93553	100.0%	91.6%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
2IDCA	SOX2	p.L186H	3	181430705	T	A	Missense_Mutation	438	20.8%	No	No	98%	0.86341	100.0%	79.0%	Clonal	D	Passenger	N	D	likely_pathogenic	Yes	Yes	No	WES
2IDCA	MAEA	p.G281E	4	1330725	G	A	Missense_Mutation	312	14.4%	No	No	68%	0.03184	87.7%	51.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	CCDC158	p.Q138E	4	77305555	G	C	Missense_Mutation	115	9.6%	No	No	55%	0.10774	89.6%	30.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
2IDCA	RAP1GDS1	p.V408G	4	99341215	T	G	Missense_Mutation	52	28.8%	No	No	100%	0.80012	100.0%	60.2%	Clonal	D	Passenger	D	T	passenger	Yes	Yes	No	WES
2IDCA	COL25A1	p.G216A	4	109861720	C	G	Missense_Mutation	61	37.7%	No	No	100%	0.85979	100.0%	75.5%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	CCRN4L	p.N409I	4	139966558	A	T	Missense_Mutation	269	22.7%	No	No	84%	0.51939	98.1%	66.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCA	RNF150	p.K36R	4	142053856	T	C	Missense_Mutation	168	26.2%	No	No	97%	0.8247	100.0%	71.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
2IDCA	CASP3	p.S198T	4	185552203	A	T	Missense_Mutation	34	55.9%	No	Yes	100%	0.83292	100.0%	75.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCA	MYO10	p.D302N	5	16779680	C	T	Missense_Mutation	100	17.0%	No	No	63%	0.13846	91.8%	40.0%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	DROSHA	p.P683L	5	31483684	G	A	Missense_Mutation	51	23.5%	No	No	87%	0.66708	98.9%	49.0%	Clonal	D	Passenger	D	T	passenger	No	Yes	No	WES, Ampliseq
2IDCA	PITX1	p.S269W	5	134364608	G	C	Missense_Mutation	150	47.3%	No	Yes	100%	0.84196	100.0%	88.8%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	WNT8A	p.G153A	5	137424706	G	C	Missense_Mutation	27	33.3%	No	Yes	100%	0.79581	100.0%	54.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	NRG2	p.C5S	5	139422641	C	G	Missense_Mutation	156	47.4%	No	Yes	100%	0.91149	100.0%	92.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
2IDCA	FBXO38	p.S93R	5	147781561	T	G	Missense_Mutation	78	25.6%	No	Yes	95%	0.76068	100.0%	60.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCA	TENM2	p.Q2698L	5	167689583	A	T	Missense_Mutation	212	9.0%	No	Yes	33%	0	49.9%	21.1%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
2IDCA	VWA7	p.R137H	6	31743844	C	T	Missense_Mutation	321	19.0%	No	No	100%	0.89929	100.0%	79.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	PNPLA1	p.E70Q	6	36259099	G	C	Missense_Mutation	264	3.0%	No	No	11%	0	21.3%	5.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	PKHD1	p.S1728_S1734del	6	51889405	TTGAGGTGAACACCAGGGCAGA	T	In_Frame_Del	119	15.1%	No	Yes	56%	0.02431	83.4%	35.9%	Subclonal	N	.	D	.	passenger	No	No	No	WES
2IDCA	MYCT1	p.L184Q	6	153043231	T	A	Missense_Mutation	200	30.0%	No	Yes	100%	0.9124	100.0%	81.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	TIAM2	p.L998V	6	155504562	C	G	Missense_Mutation	117	25.6%	No	Yes	95%	0.78466	100.0%	66.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	URGCP	p.L192F	7	43918488	G	A	Missense_Mutation	519	13.7%	No	No	78%	0.19669	94.8%	62.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	ABCA13	p.L4494R	7	48547602	T	G	Missense_Mutation	137	24.1%	No	No	100%	0.87526	100.0%	74.1%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	AKAP9	p.M942I	7	91632057	G	C	Missense_Mutation	148	10.1%	No	No	68%	0.33418	96.2%	41.3%	Subclonal	D	Passenger	N	T	passenger	Yes	No	No	WES
2IDCA	PILRB	p.L12M	7	99955959	C	A	Missense_Mutation	646	15.3%	No	Yes	88%	0.60367	98.6%	72.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	LHFPL3	p.D215Lfs*28	7	104377313	CGACAA	C	Frame_Shift_Del	106	27.4%	No	No	100%	0.87693	100.0%	76.2%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2IDCA	WNT16	p.A231V	7	120978993	C	T	Missense_Mutation	126	16.7%	No	No	95%	0.75583	100.0%	60.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	SLC39A4	p.A333V	8	145639797	G	A	Missense_Mutation	265	60.8%	No	Yes	100%	0.79374	100.0%	97.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	DMRTA1	p.L456R	9	22451762	T	G	Missense_Mutation	54	31.5%	No	Yes	85%	0.71404	98.8%	54.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCA	LMX1B	p.X274_splice	9	129456020	TGCAGATGAAGAAGCTGGCGCGGCG	T	Splice_Site	367	7.4%	No	No	49%	2.00E-04	70.0%	33.8%	Subclonal	D	.	.	.	likely_pathogenic	No	No	No	WES
2IDCA	PRRC2B	p.P454L	9	134334700	C	T	Missense_Mutation	107	18.7%	No	No	100%	0.84999	100.0%	68.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCA	ANAPC2	p.Q722E	9	140069781	G	C	Missense_Mutation	501	7.8%	No	No	37%	0	48.8%	26.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	CNKSR2	p.V411I	X	21550113	G	A	Missense_Mutation	73	8.2%	No	No	63%	0.41056	97.1%	28.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCA	RSPO4	p.F99L	20	947931	A	G	Missense_Mutation	274	2.9%	No	No	14%	0	26.1%	6.6%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCA	ZBED4	p.E233V	22	50278008	A	T	Missense_Mutation	382	2.1%	No	No	8%	0	14.7%	3.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
2IDCB	ZSCAN20	p.K381E	1	33956999	A	G	Missense_Mutation	188	32.4%	No	No	100%	0.92106	100.0%	82.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	DENND2C	p.R663Q	1	115142942	C	T	Missense_Mutation	28	39.3%	No	Yes	99%	0.76224	100.0%	53.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	S100A13	p.T15I	1	153598905	G	A	Missense_Mutation	273	21.2%	No	Yes	96%	0.8286	100.0%	73.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCB	SHE	p.S10C	1	154474474	G	C	Missense_Mutation	78	26.9%	No	Yes	100%	0.86173	100.0%	69.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
2IDCB	NES	p.T456K	1	156642613	G	T	Missense_Mutation	385	71.9%	No	Yes	100%	0.21141	100.0%	98.2%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES, Ampliseq
2IDCB	CD244	p.T262N	1	160808305	G	T	Missense_Mutation	113	19.5%	No	No	100%	0.83113	100.0%	65.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	SEC16B	p.K155M	1	177934251	T	A	Missense_Mutation	117	17.9%	No	No	99%	0.79031	100.0%	61.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	CCSAP	p.Y187D	1	229462562	A	C	Missense_Mutation	214	16.8%	No	No	93%	0.77091	100.0%	66.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	ARHGAP12	p.S213C	10	32197146	G	C	Missense_Mutation	79	19.0%	No	No	86%	0.66581	98.9%	51.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	RBP3	p.L1230H	10	48381960	A	T	Missense_Mutation	254	20.5%	No	No	92%	0.7789	100.0%	70.3%	Clonal	D	Passenger	.	T	passenger	No	No	No	WES
2IDCB	CCAR1	p.K315*	10	70509005	CAGAAA	C	Frame_Shift_Del	99	14.1%	No	No	64%	0.23472	94.2%	38.4%	Subclonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2IDCB	ADAMTS14	p.T658P	10	72503342	A	C	Missense_Mutation	101	23.8%	No	No	100%	0.84155	100.0%	67.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCB	BAG3	p.G238R	10	121431971	G	C	Missense_Mutation	534	61.6%	No	Yes	100%	0.87961	100.0%	98.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	SCUBE2	p.R211T	11	9090928	C	G	Missense_Mutation	118	23.7%	No	No	83%	0.61033	98.6%	58.4%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCB	ABTB2	p.G338R	11	34226109	C	G	Missense_Mutation	163	21.5%	No	No	97%	0.81273	100.0%	68.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	GYLTL1B	p.R451G	11	45948891	A	G	Missense_Mutation	118	60.2%	No	No	100%	0.43292	100.0%	93.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	F2	p.P326T	11	46748149	C	A	Missense_Mutation	360	24.7%	No	No	100%	0.93089	100.0%	85.1%	Clonal	N	Passenger	D	D	passenger	No	No	No	WES, Ampliseq
2IDCB	TUT1	p.R573C	11	62343588	G	A	Missense_Mutation	407	15.7%	No	No	87%	0.63993	98.7%	68.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	PLA2G16	p.E114Q	11	63357619	C	G	Missense_Mutation	187	17.1%	No	No	94%	0.7825	100.0%	65.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCB	IGHMBP2	p.V538I	11	68702006	G	A	Missense_Mutation	262	18.7%	No	No	84%	0.58883	98.5%	64.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	FAT3	p.S1574Y	11	92526042	C	A	Missense_Mutation	125	6.4%	No	No	29%	3.00E-05	54.2%	14.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	NPAT	p.D6E	11	108093246	G	C	Missense_Mutation	152	39.5%	No	Yes	99%	0.87473	100.0%	77.7%	Clonal	D	Passenger	N	T	passenger	No	No	Yes	WES, Ampliseq
2IDCB	KMT2A	p.P2547T	11	118374246	C	A	Missense_Mutation	94	38.3%	No	Yes	96%	0.82221	100.0%	70.4%	Clonal	N	Passenger	N	T	passenger	Yes	Yes	Yes	WES, Ampliseq
2IDCB	TBRG1	p.S224Qfs*48	11	124496873	ATGCCAGCATGAAG	A	Frame_Shift_Del	55	16.4%	No	Yes	41%	0.00238	70.6%	21.9%	Subclonal	D	.	.	.	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCB	TULP3	p.M20I	12	3018713	G	A	Missense_Mutation	52	38.5%	No	Yes	100%	0.92987	100.0%	76.4%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
2IDCB	RNF41	p.X201_splice	12	56601429	C	T	Splice_Site	88	30.7%	No	No	100%	0.86633	100.0%	77.0%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2IDCB	KIF5A	p.T806M	12	57971847	C	T	Missense_Mutation	157	17.2%	No	No	78%	0.46742	97.6%	53.8%	Subclonal	D	Driver	N	T	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCB	PPP1R12A	p.S336Y	12	80214661	G	T	Missense_Mutation	129	27.1%	No	No	100%	0.89367	100.0%	77.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	VEZT	p.L237M	12	95660407	C	A	Missense_Mutation	119	22.7%	No	No	100%	0.83042	100.0%	67.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	UHRF1BP1L	p.D1370E	12	100433539	A	C	Missense_Mutation	122	22.1%	No	No	100%	0.81686	100.0%	66.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
2IDCB	GNPTAB	p.N684K	12	102158643	G	C	Missense_Mutation	108	19.4%	No	No	88%	0.69609	100.0%	56.9%	Clonal	N	Passenger	N	D	passenger	Yes	No	Yes	WES, Ampliseq
2IDCB	MSI1	p.Y239*	12	120791118	G	T	Nonsense_Mutation	134	20.9%	No	No	94%	0.77791	100.0%	64.1%	Clonal	A	.	.	.	passenger	No	No	No	WES
2IDCB	MLXIP	p.P348H	12	122616881	C	A	Missense_Mutation	353	22.4%	No	No	100%	0.88841	100.0%	79.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	RNF6	p.N613S	13	26788181	T	C	Missense_Mutation	163	27.0%	No	No	100%	0.90395	100.0%	80.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	TBPL2	p.P191L	14	55903315	G	A	Missense_Mutation	185	30.8%	No	Yes	100%	0.9073	100.0%	80.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	ASB2	p.Y350N	14	94413699	A	T	Missense_Mutation	277	17.0%	No	Yes	77%	0.26617	95.5%	58.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	DYNC1H1	p.R1201T	14	102463409	G	C	Missense_Mutation	196	73.0%	No	Yes	100%	0.39335	100.0%	97.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCB	SLC12A1	p.A521D	15	48539535	C	A	Missense_Mutation	109	29.4%	No	No	100%	0.85158	100.0%	70.8%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCB	CEP152	p.L622Cfs*24	15	49061197	GA	G	Frame_Shift_Del	48	25.0%	No	No	88%	0.68272	98.9%	49.4%	Clonal	D	.	.	.	passenger	No	No	No	WES
2IDCB	SMG1	p.H2161Y	16	18853102	G	A	Missense_Mutation	95	24.2%	No	No	100%	0.84473	100.0%	67.4%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCB	CES5A	p.P80L	16	55907871	G	A	Missense_Mutation	180	31.1%	No	No	100%	0.90914	100.0%	80.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	SGSM2	p.E452G	17	2270631	A	G	Missense_Mutation	155	4.5%	No	Yes	16%	0	31.2%	7.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	TP53	p.E339Rfs*8	17	7574013	G	GA	Frame_Shift_Ins	158	47.5%	No	Yes	100%	0.70611	100.0%	92.1%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
2IDCB	GIT1	p.E705D	17	27901918	C	A	Missense_Mutation	294	18.7%	No	Yes	84%	0.57197	98.4%	65.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	EFCAB5	p.E997V	17	28405485	A	T	Missense_Mutation	26	34.6%	No	Yes	100%	0.80056	100.0%	54.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	QRICH2	p.A45V	17	74300569	G	A	Missense_Mutation	546	11.4%	No	Yes	97%	0.83291	100.0%	73.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	THOC1	p.D608E	18	214776	G	C	Missense_Mutation	191	15.2%	No	No	69%	0.14186	92.4%	48.2%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCB	OSBPL1A	p.A132G	18	21914294	G	C	Missense_Mutation	75	32.0%	No	No	100%	0.86387	100.0%	76.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	MRO	p.X96_splice	18	48333073	C	A	Splice_Site	72	26.4%	No	No	93%	0.74725	100.0%	58.6%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2IDCB	PLVAP	p.D229N	19	17476589	C	T	Missense_Mutation	525	23.2%	No	No	100%	0.92885	100.0%	85.2%	Clonal	D	Passenger	N	.	passenger	No	No	No	WES, Ampliseq
2IDCB	ARRDC2	p.A281T	19	18120840	G	A	Missense_Mutation	250	4.8%	No	No	22%	0	36.5%	12.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
2IDCB	UBA2	p.G40C	19	34919455	G	T	Missense_Mutation	261	4.2%	No	Yes	15%	0	25.5%	7.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCB	PAK4	p.G202D	19	39663958	G	A	Missense_Mutation	264	62.9%	No	Yes	100%	0.89227	100.0%	97.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
2IDCB	SYT3	p.T184P	19	51135667	T	G	Missense_Mutation	320	29.4%	No	Yes	100%	0.91377	100.0%	82.8%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCB	YIPF4	p.L178V	2	32526499	C	G	Missense_Mutation	151	37.1%	No	No	100%	0.96345	100.0%	90.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	TTC27	p.T811S	2	33045905	C	G	Missense_Mutation	65	9.2%	No	No	51%	0.19707	92.6%	23.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	SIX2	p.R101L	2	45235948	C	A	Missense_Mutation	656	20.1%	No	No	100%	0.94222	100.0%	87.9%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
2IDCB	ADD2	p.D676N	2	70890712	C	T	Missense_Mutation	317	17.0%	No	No	94%	0.80001	100.0%	71.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	ZNF638	p.D153E	2	71576543	C	A	Missense_Mutation	166	17.5%	No	No	96%	0.79403	100.0%	65.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	DNAH6	p.D2172V	2	84899511	A	T	Missense_Mutation	185	15.7%	No	No	86%	0.677	98.9%	59.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	SNRNP200	p.W1123L	2	96953293	C	A	Missense_Mutation	230	8.7%	No	No	39%	0	58.4%	25.3%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCB	NCK2	p.A186T	2	106498113	G	A	Missense_Mutation	368	16.6%	No	No	75%	0.10587	92.4%	58.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq

2IDCB	SCN9A	p.R677Sfs*4	2	167138227	GCT	G	Frame_Shift_Del	84	25.0%	No	Yes	88%	0.6978	100.0%	57.5%	Clonal	D	.	.	.	likely_pathogenic	No	No	No	WES
2IDCB	FAM117B	p.S426Rfs*76	2	203622105	GTAGC	G	Frame_Shift_Del	186	24.2%	No	No	85%	0.60897	98.6%	64.4%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
2IDCB	RSPO4	p.F99L	20	947931	A	G	Missense_Mutation	290	15.5%	No	No	86%	0.63831	98.7%	64.0%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCB	NINL	p.E1091*	20	25450709	C	A	Nonsense_Mutation	218	23.9%	No	No	100%	0.86908	100.0%	84.0%	Clonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
2IDCB	L3MBTL1	p.G6A	20	42142226	G	C	Missense_Mutation	406	20.7%	No	No	100%	0.92813	100.0%	85.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	SPATA25	p.A203T	20	44515233	C	T	Missense_Mutation	410	3.4%	No	No	19%	0	30.7%	10.8%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	PTPN1	p.D265E	20	49195797	C	A	Missense_Mutation	179	10.1%	No	No	45%	4.20E-04	68.7%	28.7%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCB	ZNF831	p.G604S	20	57767884	G	A	Missense_Mutation	369	18.4%	No	No	83%	0.46758	97.7%	66.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	CDC45	p.X18_splice	22	19467680	G	A	Splice_Site	138	16.7%	No	No	92%	0.74312	100.0%	59.8%	Clonal	D	.	.	.	passenger	No	No	No	WES
2IDCB	SOX10	p.S464Y	22	38369512	G	T	Missense_Mutation	144	12.5%	No	Yes	44%	1.00E-04	65.9%	27.9%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
2IDCB	ZBED4	p.E233V	22	50278008	A	T	Missense_Mutation	387	24.5%	No	Yes	86%	0.52375	98.1%	71.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	PTH1R	p.E258G	3	46940286	A	G	Missense_Mutation	93	28.0%	No	Yes	70%	0.15689	92.9%	49.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
2IDCB	DNAH1	p.E2969K	3	52420771	G	A	Missense_Mutation	68	38.2%	No	Yes	96%	0.80333	100.0%	66.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	IFT122	p.A875T	3	129221648	G	A	Missense_Mutation	268	24.3%	No	No	100%	0.91287	100.0%	81.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	PLCH1	p.D1324H	3	155199869	C	G	Missense_Mutation	264	14.0%	No	No	100%	0.85747	100.0%	71.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	PIK3CA	p.H1047L	3	178952085	A	T	Missense_Mutation	268	32.5%	Yes	No	100%	0.74538	100.0%	94.1%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
2IDCB	SOX2	p.D201N	3	181430749	G	A	Missense_Mutation	655	20.8%	No	No	94%	0.81293	100.0%	79.4%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	No	WES, Ampliseq
2IDCB	MAEA	p.G281E	4	1330725	G	A	Missense_Mutation	266	22.9%	No	No	100%	0.88849	100.0%	78.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	UTP3	p.E457*	4	71555763	G	T	Nonsense_Mutation	137	26.3%	No	No	100%	0.89382	100.0%	77.0%	Clonal	D	.	.	.	passenger	No	No	No	WES
2IDCB	UTP3	p.E457A	4	71555764	A	C	Missense_Mutation	136	26.5%	No	No	100%	0.8944	100.0%	77.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCB	RAP1GDS1	p.V408G	4	99341215	T	G	Missense_Mutation	61	27.9%	No	No	100%	0.85143	100.0%	66.7%	Clonal	D	Passenger	D	T	passenger	Yes	Yes	No	WES
2IDCB	COL25A1	p.G216A	4	109861720	C	G	Missense_Mutation	71	26.8%	No	No	94%	0.75825	100.0%	59.2%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCB	POU4F2	p.H127Q	4	147561111	C	A	Missense_Mutation	337	32.6%	No	No	100%	0.93867	100.0%	88.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	MYO10	p.D302N	5	16779680	C	T	Missense_Mutation	144	20.1%	No	No	91%	0.74302	100.0%	62.7%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCB	DROSHA	p.P683L	5	31483684	G	A	Missense_Mutation	62	17.7%	No	No	80%	0.59926	98.5%	44.1%	Clonal	D	Passenger	D	T	passenger	No	Yes	No	WES, Ampliseq
2IDCB	PITX1	p.S269W	5	134364608	G	C	Missense_Mutation	138	55.8%	No	Yes	100%	0.10738	100.0%	91.4%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCB	NRG2	p.C5S	5	139422641	C	G	Missense_Mutation	154	62.3%	No	Yes	100%	0.94471	100.0%	95.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
2IDCB	FBXO38	p.S93R	5	147781561	T	G	Missense_Mutation	105	26.7%	No	Yes	94%	0.77568	100.0%	64.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCB	PKHD1	p.S1728_S1734del	6	51889405	TTGAGGTGAACACCAGGGCAGA	T	In_Frame_Del	80	20.0%	No	Yes	70%	0.3514	96.3%	44.0%	Subclonal	N	.	D	.	passenger	No	No	No	WES
2IDCB	MYCT1	p.L184Q	6	153043231	T	A	Missense_Mutation	145	25.5%	No	Yes	90%	0.73026	100.0%	65.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	EZR	p.R40L	6	159208213	C	A	Missense_Mutation	74	6.8%	No	Yes	24%	5.00E-05	51.7%	10.0%	Subclonal	D	Passenger	D	T	passenger	Yes	Yes	No	WES, Ampliseq
2IDCB	AKAP9	p.M942I	7	91632057	G	C	Missense_Mutation	177	23.7%	No	Yes	100%	0.88259	100.0%	81.3%	Clonal	D	Passenger	N	T	passenger	Yes	No	No	WES
2IDCB	PILRB	p.L12M	7	99955959	C	A	Missense_Mutation	679	23.7%	No	Yes	100%	0.01454	100.0%	95.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
2IDCB	LHFPL3	p.D215Lfs*28	7	104377313	CGACAA	C	Frame_Shift_Del	120	12.5%	No	Yes	56%	0.06247	86.9%	34.4%	Subclonal	D	.	.	.	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCB	CSMD1	p.X1662_splice	8	3063024	A	C	Splice_Site	47	10.6%	No	Yes	27%	1.50E-04	56.4%	11.4%	Subclonal	D	.	.	.	likely_pathogenic	No	No	No	WES, Ampliseq
2IDCB	SLC39A4	p.A333V	8	145639797	G	A	Missense_Mutation	196	50.0%	No	Yes	100%	0.72705	100.0%	91.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	DMRTA1	p.L456R	9	22451762	T	G	Missense_Mutation	68	38.2%	No	Yes	96%	0.80333	100.0%	66.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
2IDCB	ALG2	p.G25A	9	101984103	C	G	Missense_Mutation	204	17.6%	No	No	62%	0.00608	81.9%	45.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	LMX1B	p.X274_splice	9	129456020	TGCAGATGAAGAAGCTGGCGCGGCG	T	Splice_Site	533	5.1%	No	No	38%	0	54.1%	25.9%	Subclonal	D	.	.	.	likely_pathogenic	No	No	No	WES
2IDCB	ST6GALNAC4	p.M218I	9	130672295	C	A	Missense_Mutation	631	6.8%	No	No	51%	1.00E-05	67.5%	37.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
2IDCB	CACNA1B	p.A1182D	9	140941852	C	A	Missense_Mutation	95	24.2%	No	No	85%	0.65495	98.8%	57.1%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
2IDCB	ABCB11	p.M217T	2	169850354	A	G	Missense_Mutation	60	6.7%	No	No	23%	3.60E-04	55.5%	9.0%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES, Ampliseq
4DCIS	ADAMTSL4	p.R528C	1	150529102	C	T	Missense_Mutation	288	32.6%	No	No	100%	0.92563	100.0%	86.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4DCIS	SELE	p.K107T	1	169701857	T	G	Missense_Mutation	96	35.4%	No	No	100%	0.87937	100.0%	78.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
4DCIS	GATA3	p.P408Afs*99	10	8115874	C	CA	Frame_Shift_Ins	467	27.4%	No	No	95%	0.81223	100.0%	80.3%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
4DCIS	CCAR1	p.L106*	10	70500411	T	G	Nonsense_Mutation	174	38.5%	No	Yes	95%	0.84901	100.0%	76.1%	Clonal	A	.	.	.	likely_pathogenic	No	No	No	WES
4DCIS	NRG3	p.K675N	10	84745295	A	C	Missense_Mutation	231	28.1%	No	No	97%	0.82812	100.0%	76.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
4DCIS	PTEN	p.E235*	10	89717678	G	T	Nonsense_Mutation	134	34.3%	No	Yes	84%	0.59792	98.3%	65.2%	Clonal	A	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
4DCIS	MCMBP	p.N253I	10	121607194	T	A	Missense_Mutation	53	37.7%	No	Yes	93%	0.78563	100.0%	60.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4DCIS	ST5	p.R312Q	11	8751902	C	T	Missense_Mutation	349	26.1%	No	No	90%	0.68027	100.0%	74.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
4DCIS	C12orf10	p.R253*	12	53700096	C	T	Nonsense_Mutation	42	11.9%	No	No	41%	0.05088	84.1%	17.8%	Subclonal	A	.	.	.	passenger	No	No	No	WES
4DCIS	TCTN1	p.G34V	12	111052088	G	T	Missense_Mutation	254	33.9%	No	No	100%	0.91825	100.0%	87.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
4DCIS	TMEM132B	p.V450F	12	126068466	G	T	Missense_Mutation	174	21.3%	No	No	74%	0.17191	94.3%	54.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4DCIS	LTBP2	p.G1614S	14	74969970	C	T	Missense_Mutation	93	31.2%	No	No	100%	0.84056	100.0%	71.4%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
4DCIS	CYP19A1	p.R457*	15	51503148	G	A	Nonsense_Mutation	135	18.5%	No	No	64%	0.05228	88.6%	44.1%	Subclonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
4DCIS	MMP2	p.V648A	16	55539314	T	C	Missense_Mutation	165	27.9%	No	No	96%	0.79926	100.0%	72.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
4DCIS	GPATCH8	p.P1443S	17	42475118	G	A	Missense_Mutation	32	46.9%	No	Yes	100%	0.86521	100.0%	65.0%	Clonal	D	Passenger	.	T	passenger	No	No	No	WES, Ampliseq
4DCIS	C17orf67	p.P44H	17	54892255	G	T	Missense_Mutation	412	3.6%	No	Yes	38%	7.00E-05	61.4%	22.8%	Subclonal	D	Passenger	.	.	passenger	No	No	No	WES, Ampliseq
4DCIS	SCN4A	p.S682L	17	62034853	G	A	Missense_Mutation	611	14.4%	No	No	100%	0.90064	100.0%	82.6%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
4DCIS	MIF4GD	p.F116L	17	73263950	G	C	Missense_Mutation	301	51.8%	No	No	100%	0.44193	100.0%	97.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4DCIS	RDH13	p.G16S	19	55574355	C	T	Missense_Mutation	93	18.3%	No	No	82%	0.56016	98.6%	50.8%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
4DCIS	TRPM8	p.G913C	2	234891844	G	T	Missense_Mutation	109	15.6%	No	No	54%	0.01252	81.0%	34.1%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
4DCIS	LAMA5	p.C1145S	20	60907623	A	T	Missense_Mutation	406	75.9%	No	No	100%	0.33845	100.0%	98.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4DCIS	PCNT	p.A2292D	21	47836707	C	A	Missense_Mutation	37	21.6%	No	No	75%	0.49181	98.1%	37.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
4DCIS	MYO18B	p.A135V	22	26164287	C	T	Missense_Mutation	203	46.8%	No	Yes	100%	0.94781	100.0%	88.8%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES, Ampliseq
4DCIS	DTX3L	p.V452I	3	122288290	G	A	Missense_Mutation	138	13.0%	No	Yes	45%	1.60E-04	67.7%	28.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
4DCIS	PIK3CA	p.E418K	3	178927974	G	A	Missense_Mutation	93	52.7%	No	Yes	100%	0.95493	100.0%	89.6%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
4DCIS	MAML3	p.S342L	4	140811565	G	A	Missense_Mutation	233	27.0%	No	No	94%	0.77194	100.0%	73.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4DCIS	LIFR	p.R75P	5	38528861	C	G	Missense_Mutation	58	19.0%	No	No	66%	0.28368	95.8%	37.2%	Subclonal	N	Passenger	N	T	passenger	Yes	Yes	No	WES, Ampliseq
4DCIS	APC	p.A1591V	5	112176063	C	T	Missense_Mutation	170	21.8%	No	No	75%	0.2333	95.5%	55.6%	Subclonal	D	Driver	N	D	likely_pathogenic	Yes	Yes	Yes	WES
4DCIS	PCDHA3	p.Q755*	5	140183045	C	T	Nonsense_Mutation	315	4.4%	No	No	15%	0	24.8%	8.7%	Subclonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
4DCIS	HIST1H4B	p.D86H	6	26027225	C	G	Missense_Mutation	188	26.6%	No	No	92%	0.73902	100.0%	70.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4DCIS	RUNX2	p.A180P	6	45399714	G	C	Missense_Mutation	211	32.2%	No	No	100%	0.9095	100.0%	83.2%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
4DCIS	ECT2L	p.I31T	6	139135653	T	C	Missense_Mutation	155	31.6%	No	No	100%	0.88464	100.0%	78.9%	Clonal	D	Passenger	D	T	passenger	Yes	No	No	WES
4DCIS	GLUD2	p.R50W	X	120181686	C	T	Missense_Mutation	136	32.4%	No	No	100%	0.88431	100.0%	78.5%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
4DCIS	SMARCA1	p.E500K	X	128631828	C	T	Missense_Mutation	102	25.5%	No	No	88%	0.66438	100.0%	60.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
4IDC	ADAMTSL4	p.R528C	1	150529102	C	T	Missense_Mutation	399	30.6%	No	No	100%	0.25895	100.0%	94.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4IDC	SELE	p.K107T	1	169701857	T	G	Missense_Mutation	86	27.9%	No	No	100%	0.87469	100.0%	75.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
4IDC	GATA3	p.P408Afs*99	10	8115874	C	CA	Frame_Shift_Ins	611	19.1%	No	No	100%	0.9037	100.0%	82.3%	Clonal	.	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
4IDC	CCAR1	p.L106*	10	70500411	T	G	Nonsense_Mutation	205	32.2%	No	Yes	100%	0.753	100.0%	87.9%	Clonal	A	.	.	.	likely_pathogenic	No	No	No	WES
4IDC	ADAMTS14	p.C1008F	10	72517794	G	T	Missense_Mutation	344	8.4%	No	No	53%	6.90E-04	73.4%	36.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4IDC	NRG3	p.K675N	10	84745295	A	C	Missense_Mutation	192	18.8%	No	No	98%	0.82774	100.0%	69.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
4IDC	PTEN	p.E235*	10	89717678	G	T	Nonsense_Mutation	103	20.4%	No	Yes	86%	0.75449	98.9%	56.3%	Clonal	A	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
4IDC	MCMBP	p.N253I	10	121607194	T	A	Missense_Mutation	32	15.6%	No	Yes	66%	0.56251	97.5%	27.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4IDC	ST5	p.R312Q	11	8751902	C	T	Missense_Mutation	463	16.4%	No	No	86%	0.59587	98.5%	69.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
4IDC	C12orf10	p.R253*	12	53700096	C	T	Nonsense_Mutation	38	21.1%	No	No	100%	0.76355	100.0%	48.0%	Clonal	A	.	.	.	passenger	No	No	No	WES
4IDC	TCTN1	p.G34V	12	111052088	G	T	Missense_Mutation	360	20.0%	No	No	100%	0.90448	100.0%	80.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
4IDC	TMEM132B	p.V450F	12	126068466	G	T	Missense_Mutation	137	13.1%	No	No	69%	0.31697	95.7%	43.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4IDC	LTBP2	p.G1614S	14	74969970	C	T	Missense_Mutation	114	15.8%	No	No	83%	0.63515	98.7%	51.9%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
4IDC	CYP19A1	p.R457*	15	51503148	G	A	Nonsense_Mutation	67	14.9%	No	No	78%	0.58852	98.4%	41.7%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
4IDC	MMP2	p.V648A	16	55539314	T	C	Missense_Mutation	201	15.4%	No	No	81%	0.55451	98.2%	57.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
4IDC	GPATCH8	p.P1443S	17	42475118	G	A	Missense_Mutation	42	23.8%	No	Yes	100%	0.81109	100.0%	50.5%	Clonal	D	Passenger	.	T	passenger	No	No	No	WES, Ampliseq
4IDC	YPEL2	p.K8N	17	57430794	G	C	Missense_Mutation	201	13.9%	No	No	100%	0.87722	100.0%	74.1%	Clonal	D	Passenger	N	.	passenger	No	No	No	WES, Ampliseq
4IDC	SCN4A	p.S682L	17	62034853	G	A	Missense_Mutation	620	11.3%	No	No	100%	0.89426	100.0%	78.7%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
4IDC	MIF4GD	p.F116L	17	73263950	G	C	Missense_Mutation	304	33.6%	No	No	100%	0.72272	100.0%	95.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4IDC	FOXA3	p.R209L	19	46375889	G	T	Missense_Mutation	555	7.9%	No	No	49%	0	64.9%	36.7%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
4IDC	RDH13	p.G16S	19	55574355	C	T	Missense_Mutation	109	16.5%	No	No	86%	0.68603	98.9%	53.8%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
4IDC	DNAH7	p.M2582I	2	196723519	C	A	Missense_Mutation	118	22.9%	No	No	100%	0.8785	100.0%	72.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
4IDC	LAMA5	p.C1145S	20	60907623	A	T	Missense_Mutation	237	26.2%	No	No	100%	0.83845	100.0%	89.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4IDC	RTEL1	p.L670V	20	62320912	C	G	Missense_Mutation	579	9.0%	No	No	65%	0.00734	83.4%	49.6%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
4IDC	PCNT	p.A2292D	21	47836707	C	A	Missense_Mutation	61	21.3%	No	No	100%	0.80698	100.0%	57.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
4IDC	MYO18B	p.A135V	22	26164287	C	T	Missense_Mutation	238	23.1%	No	Yes	98%	0.88982	100.0%	74.3%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES, Ampliseq
4IDC	C3orf72	p.S8F	3	138666229	C	T	Missense_Mutation	115	6.1%	No	Yes	32%	9.80E-04	62.5%	15.3%	Subclonal	N	Passenger	D	.	passenger	No	No	No	WES, Ampliseq
4IDC	PIK3CA	p.E418K	3	178927974	G	A	Missense_Mutation	61	36.1%	No	Yes	100%	0.95102	100.0%	78.7%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
4IDC	FAM184B	p.A118E	4	17711056	G	T	Missense_Mutation	341	20.5%	No	No	100%	0.91252	100.0%	81.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4IDC	MAML3	p.S342L	4	140811565	G	A	Missense_Mutation	217	16.6%	No	No	87%	0.6895	98.9%	62.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4IDC	APC	p.A1591V	5	112176063	C	T	Missense_Mutation	114	21.9%	No	No	100%	0.86612	100.0%	70.1%	Clonal	D	Driver	N	D	likely_pathogenic	Yes	Yes	Yes	WES
4IDC	HIST1H4B	p.D86H	6	26027225	C	G	Missense_Mutation	197	14.7%	No	No	92%	0.75806	100.0%	62.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
4IDC	RUNX2	p.A180P	6	45399714	G	C	Missense_Mutation	132	13.6%	No	No	71%	0.39165	96.7%	45.4%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
4IDC	ECT2L	p.I31T	6	139135653	T	C	Missense_Mutation	82	15.9%	No	No	83%	0.64287	98.7%	47.6%	Clonal	D	Passenger	D	T	passenger	Yes	No	No	WES
4IDC	HAS2	p.I13T	8	122641543	A	G	Missense_Mutation	96	15.6%	No	No	97%	0.76248	100.0%	55.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
4IDC	CDK16	p.E541D	X	47087991	G	C	Missense_Mutation	328	16.8%	No	No	88%	0.69377	99.0%	67.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
4IDC	SLC16A2	p.Q301P	X	73744520	A	C	Missense_Mutation	476	18.5%	No	No	97%	0.85989	100.0%	77.8%	Clonal	D	Passenger	.	T	passenger	No	No	No	WES
4IDC	GLUD2	p.R50W	X	120181686	C	T	Missense_Mutation	184	24.5%	No	No	100%	0.89456	100.0%	81.7%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
4IDC	SMARCA1	p.E500K	X	128631828	C	T	Missense_Mutation	54	11.1%	No	No	58%	0.34001	95.8%	26.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
4IDC	LIFR	p.R75P	5	38528861	C	G	Missense_Mutation	59	16.9%	No	No	89%	0.68656	98.9%	45.9%	Clonal	N	Passenger	N	T	passenger	Yes	Yes	No	WES
5DCISA	PAPPA2	p.V569I	1	176564445	G	A	Missense_Mutation	347	23.6%	No	Yes	69%	1.50E-04	82.2%	56.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5DCISA	TMCC2	p.P448L	1	205238673	C	T	Missense_Mutation	515	6.4%	No	Yes	19%	0	25.4%	12.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5DCISA	PCNXL2	p.A2103D	1	233120156	G	T	Missense_Mutation	423	24.3%	No	No	95%	0.62456	100.0%	78.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5DCISA	GATA3	p.P408Afs*99	10	8115873	T	TC	Frame_Shift_Ins	618	33.2%	No	No	97%	0.70367	100.0%	85.1%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
5DCISA	ETS1	p.R197H	11	128355987	C	T	Missense_Mutation	129	34.9%	No	No	100%	0.6777	100.0%	75.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5DCISA	ANO2	p.V828L	12	5685139	C	A	Missense_Mutation	98	38.8%	No	No	100%	0.7426	100.0%	77.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5DCISA	MYH7	p.R23P	14	23902874	C	G	Missense_Mutation	74	45.9%	No	Yes	88%	0.49451	98.9%	66.0%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
5DCISA	KCNH5	p.K5Qfs*21	14	63511893	G	GC	Frame_Shift_Ins	77	46.8%	No	Yes	90%	0.53789	100.0%	67.7%	Clonal	D	.	.	.	likely_pathogenic	No	No	No	WES, Ampliseq
5DCISA	LTBP2	p.M962I	14	74983547	C	T	Missense_Mutation	75	8.0%	No	Yes	15%	0	30.9%	6.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
5DCISA	RYR3	p.R402C	15	33858936	C	T	Missense_Mutation	180	7.2%	No	No	28%	0	46.4%	16.3%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
5DCISA	PIK3R5	p.A259V	17	8793325	G	A	Missense_Mutation	111	42.3%	No	Yes	81%	0.1771	96.4%	63.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5DCISA	SRRM5	p.A24V	19	44116344	C	T	Missense_Mutation	608	35.5%	No	No	100%	0.85918	100.0%	89.6%	Clonal	N	Passenger	N	.	passenger	No	No	No	WES, Ampliseq
5DCISA	XPO1	p.X121_splice	2	61729382	A	G	Splice_Site	157	12.1%	No	No	35%	0	52.4%	22.5%	Subclonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
5DCISA	TFPI	p.L44F	2	188361795	C	A	Missense_Mutation	79	19.0%	No	No	55%	0.00935	83.7%	34.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
5DCISA	DBNDD2	p.R117C	20	44037150	C	T	Missense_Mutation	301	39.5%	No	No	100%	0.84741	100.0%	89.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
5DCISA	DNAH12	p.Q2221H	3	57390731	T	A	Missense_Mutation	56	32.1%	No	No	94%	0.49094	100.0%	59.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5DCISA	ZIC4	p.T326M	3	147108895	G	A	Missense_Mutation	377	27.1%	No	No	79%	0.01718	91.9%	66.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
5DCISA	TMEM165	p.M174R	4	56283326	T	G	Missense_Mutation	45	35.6%	No	No	100%	0.56795	100.0%	61.2%	Clonal	D	Driver	D	D	likely_pathogenic	No	No	No	WES
5DCISA	MED23	p.R1093I	6	131914266	C	A	Missense_Mutation	46	39.1%	No	Yes	75%	0.20655	96.6%	49.8%	Subclonal	D	Driver	D	D	likely_pathogenic	Yes	No	Yes	WES, Ampliseq
5DCISA	MLLT4	p.X102_splice	6	168271062	GAAGA	G	Splice_Site	40	75.0%	No	Yes	100%	0.50289	100.0%	84.7%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	No	WES
5DCISA	PIWIL2	p.H528Q	8	22165484	C	G	Missense_Mutation	58	17.2%	No	No	50%	0.01166	83.3%	27.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
5DCISA	BRWD3	p.K906T	X	79960181	T	G	Missense_Mutation	130	5.4%	No	No	16%	0	30.7%	7.3%	Subclonal	D	Driver	N	T	likely_pathogenic	No	No	No	WES
5DCISA	THOC2	p.Q1235K	X	122756691	G	T	Missense_Mutation	69	17.4%	No	No	68%	0.15473	96.5%	39.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
5DCISA	GPAT2	p.R692C	2	96688929	G	A	Missense_Mutation	114	3.5%	No	No	10%	0	24.8%	3.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
5DCISB	HRNR	p.Q526P	1	152192528	T	G	Missense_Mutation	115	7.8%	No	No	41%	0.00472	73.7%	21.5%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
5DCISB	GATA3	p.P424Afs*82	10	8115922	ACC	A	Frame_Shift_Del	526	16.0%	No	No	83%	0.30598	97.5%	67.8%	Subclonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
5DCISB	CUTC	p.V261I	10	101515455	G	A	Missense_Mutation	92	18.5%	No	No	97%	0.65072	100.0%	57.5%	Clonal	D	Passenger	N	.	passenger	No	No	No	WES, Ampliseq
5DCISB	OR5M1	p.S190F	11	56380410	G	A	Missense_Mutation	70	11.4%	No	No	60%	0.19703	95.3%	30.4%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
5DCISB	OR9G1	p.S156*	11	56468330	C	A	Nonsense_Mutation	221	6.3%	No	No	33%	0	53.7%	19.5%	Subclonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
5DCISB	PRKCB	p.R361Q	16	24166021	G	A	Missense_Mutation	273	16.1%	No	No	84%	0.46768	98.5%	63.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5DCISB	TP53	p.X126_splice	17	7578555	CTGTAG	C	Splice_Site	143	16.8%	No	Yes	71%	0.23872	95.3%	48.3%	Subclonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
5DCISB	G6PC3	p.M116I	17	42152070	G	A	Missense_Mutation	205	4.4%	No	Yes	19%	0	33.9%	9.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
5DCISB	EPHX3	p.Q293*	19	15338454	G	A	Nonsense_Mutation	210	23.8%	No	Yes	100%	0.83951	100.0%	74.7%	Clonal	D	.	.	.	likely_pathogenic	No	No	No	WES, Ampliseq
5DCISB	PPFIA3	p.S508C	19	49639038	C	G	Missense_Mutation	247	13.0%	No	No	68%	0.0625	91.1%	48.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
5DCISB	PPFIA3	p.P532S	19	49639109	C	T	Missense_Mutation	183	20.2%	No	No	100%	0.78837	100.0%	72.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5DCISB	CD33	p.D79H	19	51728671	G	C	Missense_Mutation	275	10.9%	No	No	100%	0.80431	100.0%	73.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5DCISB	GPAT2	p.R692C	2	96688929	G	A	Missense_Mutation	78	5.1%	No	No	27%	0.00228	64.5%	10.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
5DCISB	SLC4A3	p.A888T	2	220502348	G	A	Missense_Mutation	403	17.6%	No	No	92%	0.66987	100.0%	72.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5DCISB	GNAS	p.S51C	20	57470679	C	G	Missense_Mutation	33	15.2%	No	Yes	79%	0.45319	98.4%	31.7%	Subclonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	No	WES, Ampliseq
5DCISB	KRTAP12-2	p.C126Y	21	46086427	C	T	Missense_Mutation	332	18.7%	No	No	98%	0.76361	100.0%	75.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
5DCISB	PKD2L2	p.T76S	5	137228262	C	G	Missense_Mutation	144	18.1%	No	No	94%	0.66375	100.0%	62.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
5DCISB	LCA5	p.F519C	6	80197259	A	C	Missense_Mutation	115	8.7%	No	Yes	37%	4.20E-04	64.1%	19.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5DCISB	HUWE1	p.D2504E	X	53587373	G	T	Missense_Mutation	56	17.9%	No	No	93%	0.58358	100.0%	47.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5DCISB	MORC4	p.X419_splice	X	106205241	C	T	Splice_Site	74	17.6%	No	No	92%	0.59133	100.0%	51.3%	Clonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
5IDC	KIF1B	p.A328T	1	10336420	G	A	Missense_Mutation	248	12.9%	No	No	43%	0	58.0%	30.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
5IDC	CASZ1	p.R590*	1	10714546	G	A	Nonsense_Mutation	239	5.0%	No	No	17%	0	27.9%	9.1%	Subclonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
5IDC	SPEN	p.I1300L	1	16256633	A	T	Missense_Mutation	186	5.4%	No	No	18%	0	31.4%	9.3%	Subclonal	N	Passenger	N	T	passenger	Yes	Yes	Yes	WES, Ampliseq
5IDC	PCNXL2	p.A2103D	1	233120156	G	T	Missense_Mutation	315	23.2%	No	No	100%	0.75685	100.0%	78.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5IDC	GATA3	p.P408Afs*99	10	8115873	T	TC	Frame_Shift_Ins	490	28.6%	No	No	95%	0.68937	100.0%	80.9%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
5IDC	ETS1	p.R197H	11	128355987	C	T	Missense_Mutation	108	21.3%	No	No	71%	0.12516	94.9%	48.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5IDC	ANO2	p.V828L	12	5685139	C	A	Missense_Mutation	121	41.3%	No	No	100%	0.64803	100.0%	86.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5IDC	SLCO1A2	p.S32F	12	21471823	G	A	Missense_Mutation	70	7.1%	No	No	24%	2.00E-05	51.5%	10.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
5IDC	IRS2	p.G1279E	13	110434565	C	T	Missense_Mutation	89	5.6%	No	Yes	13%	0	28.4%	5.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
5IDC	MYH7	p.R23P	14	23902874	C	G	Missense_Mutation	82	37.8%	No	Yes	88%	0.57439	98.9%	63.7%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
5IDC	RNF31	p.V109M	14	24617317	G	A	Missense_Mutation	147	8.8%	No	Yes	20%	0	33.2%	11.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5IDC	TINF2	p.K62N	14	24711353	C	G	Missense_Mutation	238	16.0%	No	Yes	37%	0	48.5%	27.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
5IDC	KCNH5	p.K5Qfs*21	14	63511893	G	GC	Frame_Shift_Ins	59	47.5%	No	Yes	100%	0.8244	100.0%	73.9%	Clonal	D	.	.	.	likely_pathogenic	No	No	No	WES, Ampliseq
5IDC	RYR3	p.R402C	15	33858936	C	T	Missense_Mutation	155	6.5%	No	No	28%	0	49.0%	14.9%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
5IDC	TM6SF1	p.R234*	15	83793520	A	T	Nonsense_Mutation	191	9.4%	No	No	41%	1.00E-05	61.7%	25.6%	Subclonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
5IDC	CTRL	p.S233F	16	67963934	G	A	Missense_Mutation	347	4.6%	No	No	20%	0	31.3%	11.9%	Subclonal	D	Driver	.	.	likely_pathogenic	No	No	No	WES, Ampliseq
5IDC	SRRM5	p.A24V	19	44116344	C	T	Missense_Mutation	538	28.3%	No	No	94%	0.64655	100.0%	80.6%	Clonal	N	Passenger	N	.	passenger	No	No	No	WES, Ampliseq
5IDC	XPO1	p.X121_splice	2	61729382	A	G	Splice_Site	185	14.1%	No	No	47%	0	65.2%	32.0%	Subclonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
5IDC	COL6A3	p.V1681F	2	238275789	C	A	Missense_Mutation	151	6.0%	No	No	20%	0	35.8%	10.1%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
5IDC	DBNDD2	p.R117C	20	44037150	C	T	Missense_Mutation	211	34.1%	No	No	100%	0.85409	100.0%	84.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
5IDC	DNAH12	p.Q2221H	3	57390731	T	A	Missense_Mutation	32	21.9%	No	Yes	51%	0.05274	87.5%	25.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
5IDC	FAM193A	p.R873G	4	2698303	A	G	Missense_Mutation	150	9.3%	No	No	31%	0	49.5%	18.3%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES, Ampliseq
5IDC	TMEM165	p.M174R	4	56283326	T	G	Missense_Mutation	57	40.4%	No	No	100%	0.7657	100.0%	75.0%	Clonal	D	Driver	D	D	likely_pathogenic	No	No	No	WES
5IDC	MLLT4	p.X102_splice	6	168271062	GAAGA	G	Splice_Site	43	53.5%	No	Yes	100%	0.83866	100.0%	75.2%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	No	WES
5IDC	THOC2	p.Q1235K	X	122756691	G	T	Missense_Mutation	86	22.1%	No	No	95%	0.58319	100.0%	59.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
5IDC	F8	p.P83S	X	154227772	G	A	Missense_Mutation	103	11.7%	No	No	39%	7.00E-05	63.4%	22.1%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
5IDC	GPAT2	p.R692C	2	96688929	G	A	Missense_Mutation	96	3.1%	No	No	10%	0	28.6%	3.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
6DCIS	USP54	p.E1204*	10	75276574	C	A	Nonsense_Mutation	130	30.0%	No	No	87%	0.43568	98.8%	64.6%	Subclonal	N	.	.	.	passenger	No	No	No	WES, Ampliseq
6DCIS	PPP2R2D	p.S169F	10	133757593	C	T	Missense_Mutation	108	25.9%	No	No	75%	0.15502	96.0%	53.0%	Subclonal	D	Passenger	.	T	passenger	No	No	No	WES, Ampliseq
6DCIS	NRXN3	p.V98M	14	78709728	G	A	Missense_Mutation	428	19.4%	No	Yes	56%	0	67.0%	45.4%	Subclonal	D	Passenger	.	.	passenger	No	No	No	WES
6DCIS	AKT1	p.E17K	14	105246551	C	T	Missense_Mutation	140	77.1%	Yes	Yes	100%	0.84248	100.0%	96.1%	Clonal	D	Driver	D	T	likely_pathogenic	Yes	Yes	Yes	WES
6DCIS	ZNF592	p.E219*	15	85326561	G	T	Nonsense_Mutation	388	15.5%	No	No	45%	0	55.5%	34.7%	Subclonal	A	.	.	.	passenger	No	No	No	WES
6DCIS	CDR2	p.I429T	16	22358365	A	G	Missense_Mutation	224	7.1%	No	No	21%	0	32.1%	12.3%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES, Ampliseq
6DCIS	KRT38	p.E409G	17	39594360	T	C	Missense_Mutation	233	34.8%	No	No	100%	0.77047	100.0%	80.6%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
6DCIS	KIAA1683	p.P448A	19	18377008	G	C	Missense_Mutation	305	3.6%	No	No	10%	0	17.8%	5.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
6DCIS	ZNF536	p.P1187Q	19	31040086	C	A	Missense_Mutation	410	2.9%	No	No	8%	0	14.0%	4.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
6DCIS	VGLL4	p.H190Rfs*21	3	11600851	CGCTGT	C	Frame_Shift_Del	129	33.3%	No	No	96%	0.65414	100.0%	71.8%	Clonal	.	.	.	.	passenger	No	No	No	WES
6DCIS	BBS7	p.L23Q	4	122789170	A	T	Missense_Mutation	88	18.2%	No	No	52%	0.00345	78.8%	32.8%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
6DCIS	PCDH12	p.R707C	5	141335298	G	A	Missense_Mutation	439	10.0%	No	No	29%	0	37.6%	21.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
6DCIS	SOGA3	p.F945S	6	127794436	A	G	Missense_Mutation	69	59.4%	No	Yes	100%	0.87302	100.0%	81.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
6DCIS	GAL3ST4	p.E395K	7	99757829	C	T	Missense_Mutation	642	32.9%	No	No	95%	0.67298	100.0%	83.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
6DCIS	GPIHBP1	p.L172F	8	144297352	C	T	Missense_Mutation	402	5.0%	No	No	14%	0	21.3%	8.9%	Subclonal	N	Passenger	.	D	passenger	No	No	No	WES
6DCIS	NAIF1	p.R62C	9	130829197	G	A	Missense_Mutation	641	4.5%	No	No	13%	0	18.0%	8.6%	Subclonal	D	Passenger	D	.	passenger	No	No	No	WES
6DCIS	WNK3	p.Y325*	X	54334469	A	C	Nonsense_Mutation	136	4.4%	No	No	13%	0	26.3%	5.4%	Subclonal	A	.	.	.	passenger	No	No	No	WES
6DCIS	WNK3	p.H324Q	X	54334472	G	T	Missense_Mutation	136	4.4%	No	No	13%	0	26.3%	5.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
6IDC	CKAP5	p.R1481H	11	46780945	C	T	Missense_Mutation	51	11.8%	No	No	92%	0.66259	98.9%	37.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
6IDC	AKT1	p.E17K	14	105246551	C	T	Missense_Mutation	147	28.6%	Yes	Yes	100%	0.9454	100.0%	88.0%	Clonal	D	Driver	D	T	likely_pathogenic	Yes	Yes	Yes	WES
6IDC	CDR2	p.I429T	16	22358365	A	G	Missense_Mutation	185	15.1%	No	No	100%	0.87209	100.0%	75.1%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES, Ampliseq
6IDC	KRT38	p.E409G	17	39594360	T	C	Missense_Mutation	202	18.3%	No	No	100%	0.84315	100.0%	81.0%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
6IDC	KIAA1683	p.P448A	19	18377008	G	C	Missense_Mutation	223	13.0%	No	No	100%	0.82201	100.0%	66.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
6IDC	VGLL4	p.H190Rfs*21	3	11600851	CGCTGT	C	Frame_Shift_Del	120	14.2%	No	No	100%	0.81342	100.0%	61.6%	Clonal	D	.	.	.	passenger	No	No	No	WES
6IDC	PCDH12	p.R707C	5	141335298	G	A	Missense_Mutation	414	25.8%	No	No	100%	0.92089	100.0%	94.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
6IDC	ZNF92	p.G104E	7	64863338	G	A	Missense_Mutation	69	14.5%	No	No	100%	0.81063	100.0%	55.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
6IDC	GPIHBP1	p.L172F	8	144297352	C	T	Missense_Mutation	343	15.5%	No	No	100%	0.90532	100.0%	81.3%	Clonal	N	Passenger	.	D	passenger	No	No	No	WES
6IDC	NAIF1	p.R62C	9	130829197	G	A	Missense_Mutation	610	13.8%	No	No	100%	0.9142	100.0%	82.2%	Clonal	D	Passenger	D	.	passenger	No	No	No	WES
6IDC	WNK3	p.Y325*	X	54334469	A	C	Nonsense_Mutation	133	11.3%	No	No	88%	0.6856	99.0%	51.4%	Clonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
6IDC	WNK3	p.H324Q	X	54334472	G	T	Missense_Mutation	135	11.1%	No	No	87%	0.67331	98.9%	50.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
6IDC	SOGA3	p.F945S	6	127794436	A	G	Missense_Mutation	99	4.0%	No	No	28%	0.00944	67.0%	10.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
7DCIS	GNAI3	p.N22Kfs*25	1	110091405	C	CA	Frame_Shift_Ins	295	13.2%	No	No	64%	0.00853	85.0%	47.4%	Subclonal	D	.	.	.	passenger	No	No	No	WES
7DCIS	KCTD3	p.Q497*	1	215785190	C	T	Nonsense_Mutation	95	21.1%	No	No	100%	0.66815	100.0%	62.6%	Clonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
7DCIS	TMEM26	p.D187H	10	63188730	C	G	Missense_Mutation	86	12.8%	No	No	62%	0.15037	94.9%	35.0%	Subclonal	D	Passenger	D	.	passenger	No	No	No	WES, Ampliseq
7DCIS	ANAPC16	p.S4*	10	73983683	C	A	Nonsense_Mutation	114	20.2%	No	No	98%	0.65014	100.0%	63.1%	Clonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
7DCIS	OR2AG1	p.P287Q	11	6807128	C	A	Missense_Mutation	136	14.7%	No	Yes	57%	0.01486	83.1%	37.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
7DCIS	SLC6A5	p.L503Nfs*27	11	20652241	ACT	A	Frame_Shift_Del	252	15.9%	No	Yes	61%	0.00204	80.5%	45.5%	Subclonal	D	.	.	.	likely_pathogenic	No	No	No	WES, Ampliseq
7DCIS	PDE2A	p.A483V	11	72295684	G	A	Missense_Mutation	160	21.3%	No	No	100%	0.73279	100.0%	70.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7DCIS	KCNA5	p.V496M	12	5154799	G	A	Missense_Mutation	290	20.0%	No	No	97%	0.72101	100.0%	74.3%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
7DCIS	KIF5A	p.E774K	12	57971515	G	A	Missense_Mutation	93	18.3%	No	No	89%	0.53253	100.0%	54.4%	Clonal	D	Driver	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
7DCIS	LRRC43	p.V383M	12	122677349	G	A	Missense_Mutation	185	18.9%	No	No	92%	0.6082	100.0%	65.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
7DCIS	G2E3	p.Y230C	14	31067742	A	G	Missense_Mutation	110	18.2%	No	No	89%	0.53275	100.0%	56.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
7DCIS	AKAP6	p.L1052V	14	33204870	C	G	Missense_Mutation	80	12.5%	No	No	61%	0.14558	94.7%	33.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
7DCIS	PACS2	p.V62M	14	105814894	G	A	Missense_Mutation	118	14.4%	No	No	70%	0.21074	96.4%	44.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7DCIS	NOX5	p.E193*	15	69324109	G	T	Nonsense_Mutation	43	25.6%	No	No	100%	0.68711	100.0%	57.8%	Clonal	A	.	.	.	passenger	No	No	No	WES
7DCIS	IRX5	p.S19W	16	54965166	C	G	Missense_Mutation	227	29.1%	No	Yes	100%	0.89153	100.0%	83.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
7DCIS	SLC16A11	p.S58W	17	6946732	G	C	Missense_Mutation	105	21.0%	No	Yes	81%	0.48511	98.4%	54.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
7DCIS	TP53	p.P278A	17	7577106	G	C	Missense_Mutation	140	25.7%	Yes	Yes	100%	0.77672	100.0%	70.4%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
7DCIS	ERBB2	p.S310F	17	37868208	C	T	Missense_Mutation	112	42.9%	Yes	No	100%	0.94823	100.0%	89.6%	Clonal	D	Driver	D	T	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
7DCIS	NOG	p.G93Vfs*31	17	54671857	CG	C	Frame_Shift_Del	124	36.3%	No	Yes	100%	0.92264	100.0%	87.5%	Clonal	D	.	.	.	likely_pathogenic	No	No	No	WES
7DCIS	LAMA3	p.G2429E	18	21492802	G	A	Missense_Mutation	135	27.4%	No	No	100%	0.79264	100.0%	80.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
7DCIS	RTBDN	p.T45M	19	12940756	G	A	Missense_Mutation	136	15.4%	No	No	75%	0.28216	97.4%	49.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7DCIS	EPS8L1	p.P90L	19	55591209	C	T	Missense_Mutation	66	22.7%	No	No	100%	0.67644	100.0%	60.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7DCIS	IL36G	p.V114M	2	113742456	G	A	Missense_Mutation	236	14.4%	No	No	70%	0.07652	92.8%	50.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7DCIS	ADAM23	p.S175C	2	207395623	C	G	Missense_Mutation	133	14.3%	No	No	70%	0.17815	95.8%	44.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
7DCIS	TNS1	p.D1702N	2	218669286	C	T	Missense_Mutation	78	17.9%	No	No	87%	0.50617	98.9%	50.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
7DCIS	ADA	p.E128K	20	43254306	C	T	Missense_Mutation	122	20.5%	No	No	100%	0.67156	100.0%	64.9%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
7DCIS	CELSR1	p.K1782N	22	46795680	C	G	Missense_Mutation	86	33.7%	No	Yes	100%	0.84567	100.0%	77.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7DCIS	ATP2B2	p.A327V	3	10426972	G	A	Missense_Mutation	65	13.8%	No	Yes	54%	0.08621	90.0%	28.5%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES, Ampliseq
7DCIS	C3orf20	p.R796H	3	14803014	G	A	Missense_Mutation	127	30.7%	No	Yes	100%	0.86552	100.0%	78.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
7DCIS	PIK3CA	p.H1047R	3	178952085	A	G	Missense_Mutation	176	25.0%	Yes	No	100%	0.82634	100.0%	80.2%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
7DCIS	PTGER4	p.E93K	5	40681372	G	A	Missense_Mutation	236	21.2%	No	No	100%	0.77003	100.0%	75.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7DCIS	ATXN1	p.A92T	6	16328268	C	T	Missense_Mutation	241	25.7%	No	Yes	100%	0.81775	100.0%	76.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7DCIS	TTBK1	p.D505N	6	43230615	G	A	Missense_Mutation	79	24.1%	No	Yes	93%	0.66896	100.0%	58.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
7DCIS	HIVEP2	p.V133I	6	143095479	C	T	Missense_Mutation	331	8.5%	No	No	41%	0	57.8%	28.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7DCIS	NOX3	p.E292K	6	155751994	C	T	Missense_Mutation	153	20.9%	No	No	100%	0.71385	100.0%	69.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7DCIS	ABCB5	p.A498S	7	20691202	G	T	Missense_Mutation	216	6.5%	No	No	64%	0.15035	95.0%	38.0%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES, Ampliseq
7DCIS	FRMD3	p.S289*	9	85924511	G	C	Nonsense_Mutation	84	10.7%	No	No	52%	0.05666	89.3%	27.6%	Subclonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
7DCIS	SCML1	p.E261G	X	17770013	A	G	Missense_Mutation	93	18.3%	No	Yes	71%	0.27484	96.4%	44.8%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
7DCIS	CCNB3	p.L735I	X	50053372	C	A	Missense_Mutation	107	14.0%	No	Yes	54%	0.02236	83.8%	33.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
7DCIS	CAPRIN1	p.Q592E	11	34118094	C	G	Missense_Mutation	199	2.5%	No	No	10%	0	21.7%	3.8%	Subclonal	D	Driver	N	T	likely_pathogenic	No	No	No	WES
7DCIS	MLH3	p.D769Y	14	75514054	C	A	Missense_Mutation	183	2.2%	No	No	11%	0	26.2%	3.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
7DCIS	SI	p.R434Q	3	164776848	C	T	Missense_Mutation	130	3.8%	No	No	19%	0	41.8%	7.8%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
7IDC	KCTD3	p.Q497*	1	215785190	C	T	Nonsense_Mutation	71	9.9%	No	No	61%	0.35054	96.3%	29.5%	Subclonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
7IDC	TRIM67	p.V515I	1	231339621	G	A	Missense_Mutation	135	14.1%	No	No	87%	0.67837	99.0%	54.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7IDC	ITGA8	p.V910G	10	15600110	A	C	Missense_Mutation	94	11.7%	No	No	73%	0.48426	97.8%	40.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7IDC	TMEM26	p.D187H	10	63188730	C	G	Missense_Mutation	73	19.2%	No	No	100%	0.81464	100.0%	60.7%	Clonal	D	Passenger	D	.	passenger	No	No	No	WES, Ampliseq
7IDC	SLC6A5	p.L503Nfs*27	11	20652241	ACT	A	Frame_Shift_Del	258	21.3%	No	Yes	90%	0.72211	100.0%	69.3%	Clonal	D	.	.	.	likely_pathogenic	No	No	No	WES, Ampliseq
7IDC	KIAA1549L	p.E1549K	11	33667358	G	A	Missense_Mutation	224	10.7%	No	No	67%	0.1587	92.8%	44.9%	Subclonal	D	Passenger	D	.	passenger	No	No	No	WES, Ampliseq
7IDC	CAPRIN1	p.Q592E	11	34118094	C	G	Missense_Mutation	171	13.5%	No	No	84%	0.62243	98.7%	55.2%	Clonal	D	Driver	N	T	likely_pathogenic	No	No	No	WES, Ampliseq
7IDC	NUP160	p.K106E	11	47862139	T	C	Missense_Mutation	200	4.5%	No	No	28%	1.00E-05	51.2%	14.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
7IDC	KIF5A	p.E774K	12	57971515	G	A	Missense_Mutation	114	15.8%	No	No	82%	0.60874	98.6%	51.7%	Clonal	D	Driver	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
7IDC	LRRC43	p.V383M	12	122677349	G	A	Missense_Mutation	174	37.4%	No	No	100%	0.96863	100.0%	91.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
7IDC	SOX1	p.A378V	13	112723105	C	T	Missense_Mutation	35	20.0%	No	Yes	84%	0.62204	98.7%	38.9%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES

7IDC	G2E3	p.Y230C	14	31067742	A	G	Missense_Mutation	127	19.7%	No	No	100%	0.86407	100.0%	71.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
7IDC	MLH3	p.D769Y	14	75514054	C	A	Missense_Mutation	187	10.2%	No	No	73%	0.41996	97.2%	46.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7IDC	NPAP1	p.G654W	15	24922974	G	T	Missense_Mutation	290	4.5%	No	Yes	23%	0	38.7%	13.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7IDC	ZNF770	p.E570K	15	35273928	C	T	Missense_Mutation	54	13.0%	No	Yes	55%	0.2062	93.3%	26.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7IDC	IRX5	p.S19W	16	54965166	C	G	Missense_Mutation	215	23.7%	No	Yes	100%	0.85292	100.0%	74.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
7IDC	CLUH	p.E1259K	17	2594043	C	T	Missense_Mutation	108	13.9%	No	Yes	86%	0.66009	98.9%	50.9%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES, Ampliseq
7IDC	SLC16A11	p.S58W	17	6946732	G	C	Missense_Mutation	107	24.3%	No	Yes	100%	0.82242	100.0%	66.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
7IDC	TP53	p.P278A	17	7577106	G	C	Missense_Mutation	113	49.6%	Yes	Yes	100%	0.96588	100.0%	91.2%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
7IDC	ERBB2	p.S310F	17	37868208	C	T	Missense_Mutation	157	31.2%	Yes	No	100%	0.96246	100.0%	88.8%	Clonal	D	Driver	D	T	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
7IDC	KPNB1	p.E691K	17	45754461	G	A	Missense_Mutation	202	16.8%	No	No	100%	0.84524	100.0%	70.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
7IDC	EPN3	p.D262N	17	48616569	G	A	Missense_Mutation	96	14.6%	No	No	91%	0.69669	100.0%	51.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7IDC	NOG	p.G93Vfs*31	17	54671857	CG	C	Frame_Shift_Del	167	13.8%	No	No	86%	0.65514	98.9%	56.3%	Clonal	D	.	.	.	passenger	No	No	No	WES
7IDC	MED13	p.P1678A	17	60040145	G	C	Missense_Mutation	204	14.2%	No	No	88%	0.69686	100.0%	60.8%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
7IDC	LAMA3	p.G2429E	18	21492802	G	A	Missense_Mutation	117	28.2%	No	No	100%	0.9386	100.0%	83.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
7IDC	NDUFB7	p.K113R	19	14677021	T	C	Missense_Mutation	296	5.1%	No	No	31%	0	50.4%	18.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7IDC	FAM187B	p.Y52C	19	35719429	T	C	Missense_Mutation	187	17.1%	No	No	89%	0.71204	100.0%	62.7%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
7IDC	OSBPL6	p.Y118H	2	179196312	T	C	Missense_Mutation	181	12.7%	No	No	66%	0.15329	92.6%	44.4%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
7IDC	ADAM23	p.S175C	2	207395623	C	G	Missense_Mutation	119	16.0%	No	No	83%	0.62185	98.7%	52.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
7IDC	SCRT2	p.R97Q	20	644949	C	T	Missense_Mutation	185	20.5%	No	No	100%	0.88559	100.0%	79.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
7IDC	PAX1	p.P255H	20	21687553	C	A	Missense_Mutation	627	3.8%	No	No	24%	0	34.5%	15.6%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
7IDC	BPIFA1	p.G6D	20	31825534	G	A	Missense_Mutation	53	13.2%	No	No	82%	0.60329	98.6%	37.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7IDC	ADA	p.E128K	20	43254306	C	T	Missense_Mutation	155	19.4%	No	No	100%	0.87445	100.0%	74.0%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
7IDC	TSHZ2	p.R101T	20	51870299	G	C	Missense_Mutation	365	14.5%	No	No	90%	0.73114	100.0%	68.6%	Clonal	D	Passenger	N	T	passenger	Yes	No	No	WES, Ampliseq
7IDC	DIP2A	p.T1310A	21	47978265	A	G	Missense_Mutation	224	15.6%	No	No	97%	0.8021	100.0%	67.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
7IDC	TTC28	p.R1946H	22	28379818	C	T	Missense_Mutation	86	10.5%	No	No	65%	0.37373	96.6%	34.1%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
7IDC	NIPSNAP1	p.T189I	22	29957508	G	A	Missense_Mutation	47	17.0%	No	No	100%	0.73091	100.0%	46.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
7IDC	CELSR1	p.K1782N	22	46795680	C	G	Missense_Mutation	52	30.8%	No	Yes	99%	0.82524	100.0%	58.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7IDC	C3orf20	p.R796H	3	14803014	G	A	Missense_Mutation	88	44.3%	No	Yes	100%	0.95874	100.0%	87.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
7IDC	XRN1	p.V1259I	3	142066178	C	T	Missense_Mutation	148	12.2%	No	No	88%	0.67888	99.0%	54.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
7IDC	DHX36	p.G1005R	3	153993974	C	T	Missense_Mutation	133	14.3%	No	No	100%	0.83156	100.0%	65.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7IDC	SI	p.R434Q	3	164776848	C	T	Missense_Mutation	175	19.4%	No	Yes	100%	0.94295	100.0%	83.2%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES, Ampliseq
7IDC	PIK3CA	p.H1047R	3	178952085	A	G	Missense_Mutation	259	64.1%	Yes	Yes	100%	0.1623	100.0%	97.5%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
7IDC	PTGER4	p.E93K	5	40681372	G	A	Missense_Mutation	255	14.5%	No	No	90%	0.72737	100.0%	64.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7IDC	TTBK1	p.D505N	6	43230615	G	A	Missense_Mutation	73	27.4%	No	Yes	100%	0.84455	100.0%	67.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
7IDC	TBX18	p.R422H	6	85446962	C	T	Missense_Mutation	167	17.4%	No	No	91%	0.72826	100.0%	62.3%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES, Ampliseq
7IDC	NOX3	p.E292K	6	155751994	C	T	Missense_Mutation	151	13.9%	No	No	72%	0.36445	96.6%	47.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7IDC	PEG10	p.P273L	7	94293686	C	T	Missense_Mutation	207	16.9%	No	No	100%	0.84939	100.0%	71.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
7IDC	ADRA1A	p.A189V	8	26721921	G	A	Missense_Mutation	161	31.1%	No	Yes	100%	0.8918	100.0%	75.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
7IDC	TRPS1	p.H1143Q	8	116426707	G	C	Missense_Mutation	613	2.9%	No	No	48%	0.00331	73.9%	29.9%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES, Ampliseq
7IDC	COL14A1	p.G1060E	8	121282379	G	A	Missense_Mutation	180	11.1%	No	No	100%	0.82404	100.0%	64.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
7IDC	FRMD3	p.S289*	9	85924511	G	C	Nonsense_Mutation	83	12.0%	No	No	75%	0.52495	98.1%	40.0%	Clonal	A	.	.	.	passenger	No	No	No	WES, Ampliseq
7IDC	PNMA3	p.R408W	X	152226634	C	T	Missense_Mutation	240	16.3%	No	No	85%	0.61573	98.7%	62.1%	Clonal	N	Passenger	.	T	passenger	No	No	No	WES
7IDC	ANAPC16	p.S4*	10	73983683	C	A	Nonsense_Mutation	134	7.5%	No	No	46%	0.02747	80.9%	25.2%	Subclonal	A	.	.	.	passenger	No	No	No	WES
8DCIS	LAPTM5	p.A20T	1	31230535	C	T	Missense_Mutation	80	25.0%	No	No	100%	0.80324	100.0%	66.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
8DCIS	GATA3	p.E262V	10	8105965	A	T	Missense_Mutation	171	22.2%	No	No	100%	0.80587	100.0%	71.5%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
8DCIS	KIAA1377	p.A763T	11	101834053	G	A	Missense_Mutation	321	27.1%	No	No	100%	0.8692	100.0%	88.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
8DCIS	KMT2A	p.P3515Lfs*36	11	118377149	TC	T	Frame_Shift_Del	244	25.0%	No	No	100%	0.89262	100.0%	82.1%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
8DCIS	NOP2	p.P715R	12	6666553	G	C	Missense_Mutation	317	6.0%	No	No	27%	0	41.4%	17.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
8DCIS	A2M	p.V868M	12	9242614	C	T	Missense_Mutation	109	23.9%	No	No	100%	0.81133	100.0%	69.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
8DCIS	PDS5B	p.M875T	13	33320126	T	C	Missense_Mutation	73	24.7%	No	Yes	88%	0.70984	99.0%	55.4%	Clonal	D	Passenger	D	.	passenger	No	No	No	WES, Ampliseq
8DCIS	ATP6V0D1	p.K77M	16	67487519	T	A	Missense_Mutation	147	6.1%	No	No	28%	0	50.8%	14.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
8DCIS	TEKT3	p.R419H	17	15211981	C	T	Missense_Mutation	37	13.5%	No	No	62%	0.34095	96.9%	26.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
8DCIS	COL6A2	p.V812L	21	47546428	G	T	Missense_Mutation	143	21.7%	No	No	99%	0.77145	100.0%	67.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
8DCIS	STAG1	p.K905M	3	136082281	T	A	Missense_Mutation	100	26.0%	No	No	100%	0.83753	100.0%	72.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
8DCIS	IL20RB	p.S311L	3	136729061	C	T	Missense_Mutation	171	27.5%	No	No	100%	0.87442	100.0%	82.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
8DCIS	PIK3CA	p.H1047R	3	178952085	A	G	Missense_Mutation	193	25.9%	Yes	No	100%	0.88445	100.0%	81.1%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
8DCIS	ANKRD33B	p.A274S	5	10649560	G	T	Missense_Mutation	136	22.8%	No	No	100%	0.80503	100.0%	69.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
8DCIS	GET4	p.A13G	7	916320	C	G	Missense_Mutation	64	7.8%	No	No	43%	0.08691	88.6%	18.7%	Subclonal	D	Passenger	N	.	passenger	No	No	No	WES
8DCIS	SCML2	p.R285L	X	18283799	C	A	Missense_Mutation	178	3.9%	No	No	18%	0	35.5%	8.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
8IDC	GJA8	p.L244V	1	147380812	C	G	Missense_Mutation	233	7.7%	No	No	34%	0	52.3%	21.5%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES, Ampliseq
8IDC	C1orf204	p.P157S	1	159810630	G	A	Missense_Mutation	184	5.4%	No	No	24%	0	42.7%	12.8%	Subclonal	N	Passenger	D	.	passenger	No	No	No	WES, Ampliseq
8IDC	DUSP27	p.C782Y	1	167096713	G	A	Missense_Mutation	186	5.9%	No	No	26%	0	45.2%	14.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
8IDC	TBX19	p.S426L	1	168282170	C	T	Missense_Mutation	485	4.7%	No	No	21%	0	30.7%	13.6%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES, Ampliseq
8IDC	OR52M1	p.I128M	11	4566804	C	G	Missense_Mutation	300	8.3%	No	No	37%	0	52.9%	24.9%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
8IDC	TPP1	p.D451H	11	6636476	C	G	Missense_Mutation	406	10.6%	No	No	47%	0	61.6%	34.9%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES, Ampliseq
8IDC	KIAA1377	p.A763T	11	101834053	G	A	Missense_Mutation	273	25.3%	No	No	100%	0.83447	100.0%	82.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
8IDC	KMT2A	p.P3515Lfs*36	11	118377149	TC	T	Frame_Shift_Del	328	23.8%	No	No	100%	0.81234	100.0%	81.6%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
8IDC	CHD4	p.I1247T	12	6696689	A	G	Missense_Mutation	213	5.6%	No	No	25%	0	42.1%	14.1%	Subclonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
8IDC	CHD4	p.R1177C	12	6697052	G	A	Missense_Mutation	293	9.6%	No	No	42%	0	59.4%	29.3%	Subclonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
8IDC	CHD4	p.R957W	12	6701638	G	A	Missense_Mutation	203	4.9%	No	No	22%	0	38.8%	11.6%	Subclonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES, Ampliseq
8IDC	A2M	p.V868M	12	9242614	C	T	Missense_Mutation	101	14.9%	No	No	66%	0.13354	95.0%	40.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
8IDC	PYROXD1	p.E250*	12	21609027	G	T	Nonsense_Mutation	150	4.7%	No	No	21%	0	40.9%	9.8%	Subclonal	D	.	.	.	passenger	No	No	No	WES
8IDC	KIF5A	p.R808Q	12	57971853	G	A	Missense_Mutation	207	10.1%	No	No	45%	3.00E-05	66.3%	29.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES, Ampliseq
8IDC	ACSS3	p.G481V	12	81610767	G	T	Missense_Mutation	161	24.8%	No	No	100%	0.76958	100.0%	75.9%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES, Ampliseq
8IDC	WDR66	p.E670K	12	122396875	G	A	Missense_Mutation	187	8.0%	No	No	36%	0	56.5%	21.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
8IDC	SBNO2	p.G861Afs*29	19	1112231	TCCCCG	T	Frame_Shift_Del	275	9.8%	No	No	53%	6.30E-04	75.3%	36.8%	Subclonal	D	.	.	.	passenger	No	No	No	WES, Ampliseq
8IDC	ZNF527	p.Q229H	19	37879638	G	C	Missense_Mutation	104	7.7%	No	No	42%	0.00827	77.8%	21.2%	Subclonal	N	Passenger	.	.	passenger	No	No	No	WES, Ampliseq
8IDC	CACNB4	p.S441N	2	152695874	C	T	Missense_Mutation	69	13.0%	No	No	58%	0.1047	93.6%	30.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
8IDC	COL6A2	p.V812L	21	47546428	G	T	Missense_Mutation	245	20.8%	No	No	93%	0.59611	100.0%	70.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES, Ampliseq
8IDC	STAG1	p.K905M	3	136082281	T	A	Missense_Mutation	112	23.2%	No	No	100%	0.67367	100.0%	67.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
8IDC	PIK3CA	p.H1047R	3	178952085	A	G	Missense_Mutation	168	20.8%	Yes	No	93%	0.58181	100.0%	66.1%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
8IDC	ANKRD33B	p.A274S	5	10649560	G	T	Missense_Mutation	299	19.1%	No	No	85%	0.36141	98.4%	66.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
8IDC	EBF1	p.S428L	5	158140064	G	A	Missense_Mutation	278	4.7%	No	No	21%	0	34.3%	11.8%	Subclonal	D	Passenger	N	T	passenger	Yes	Yes	No	WES, Ampliseq
8IDC	HRH2	p.R260K	5	175111015	G	A	Missense_Mutation	379	9.8%	No	No	43%	0	58.0%	31.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
8IDC	LANCL3	p.V130M	X	37431511	G	A	Missense_Mutation	130	13.1%	No	No	58%	0.0266	87.2%	36.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
9DCIS	LATS2	p.E282K	13	21563075	C	T	Missense_Mutation	640	18.0%	No	No	100%	0.34486	100.0%	91.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	MSK-IMPACT
9DCIS	TP53	p.K291Rfs*54	17	7577065	CT	C	Frame_Shift_Del	405	72.1%	No	Yes	100%	0	100.0%	98.4%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	MSK-IMPACT, Ampliseq
9DCIS	PARK2	p.G329Afs*106	6	161969982	GC	G	Frame_Shift_Del	594	25.1%	No	Yes	100%	0.97325	100.0%	95.6%	Clonal	D	.	.	.	likely_pathogenic	No	No	No	MSK-IMPACT, Ampliseq
9IDC	TP53	p.K291Rfs*54	17	7577065	CT	C	Frame_Shift_Del	366	20.5%	No	Yes	100%	0.9643	100.0%	92.3%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	MSK-IMPACT
9IDC	PARK2	p.G329Afs*106	6	161969982	GC	G	Frame_Shift_Del	514	7.0%	No	No	72%	0.16058	94.3%	51.6%	Subclonal	D	.	.	.	likely_pathogenic	No	No	No	MSK-IMPACT
14DCIS	SPEN	p.P677Lfs*132	1	16254763	TC	T	Frame_Shift_Del	201	24.4%	No	No	100%	0.84114	100.0%	82.3%	Clonal	.	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
14DCIS	SPEN	p.L2247Cfs*106	1	16259473	TC	T	Frame_Shift_Del	165	17.0%	No	No	87%	0.54507	99.0%	60.1%	Clonal	.	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
14DCIS	PEF1	p.L179V	1	32098186	G	C	Missense_Mutation	51	13.7%	No	No	71%	0.34881	97.8%	33.6%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
14DCIS	PPAP2B	p.S254N	1	56977697	C	T	Missense_Mutation	140	25.7%	No	No	100%	0.81268	100.0%	79.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
14DCIS	AKR1C4	p.G298V	10	5258720	G	T	Missense_Mutation	93	12.9%	No	No	66%	0.22124	96.2%	38.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
14DCIS	LDB3	p.R31Q	10	88428540	G	A	Missense_Mutation	101	27.7%	No	No	100%	0.79581	100.0%	77.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
14DCIS	BTRC	p.L389Ffs*5	10	103294484	C	CT	Frame_Shift_Ins	151	15.2%	No	No	78%	0.36713	98.0%	52.4%	Subclonal	.	.	.	.	passenger	No	No	No	WES
14DCIS	TCF7L2	p.G308Sfs*16	10	114910800	ACGGGCATTCCG	A	Frame_Shift_Del	199	6.5%	No	No	34%	0	55.4%	19.4%	Subclonal	.	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
14DCIS	C11orf1	p.Y53C	11	111753204	A	G	Missense_Mutation	108	17.6%	No	No	91%	0.58143	100.0%	56.6%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
14DCIS	CBFB	p.X55_splice	16	67063717	G	T	Splice_Site	59	30.5%	No	Yes	100%	0.82373	100.0%	68.2%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
14DCIS	CNTROB	p.T195P	17	7838452	A	C	Missense_Mutation	35	25.7%	No	No	100%	0.71394	100.0%	54.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
14DCIS	WIZ	p.R100W	19	15547848	G	A	Missense_Mutation	137	22.6%	No	No	100%	0.80036	100.0%	73.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
14DCIS	ERVV-2	p.A464S	19	53553894	G	T	Missense_Mutation	154	12.3%	No	No	63%	0.08287	91.9%	40.9%	Subclonal	.	Passenger	.	.	passenger	No	No	No	WES
14DCIS	MAPK8IP2	p.G227S	22	51042407	G	A	Missense_Mutation	71	16.9%	No	No	87%	0.52212	98.9%	48.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
14DCIS	COPG1	p.I92V	3	128971749	A	G	Missense_Mutation	186	18.8%	No	No	97%	0.69519	100.0%	68.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
14DCIS	ATP8A1	p.I306V	4	42581914	T	C	Missense_Mutation	150	6.7%	No	No	34%	9.00E-05	60.4%	18.5%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
14DCIS	GK2	p.N92S	4	80329080	T	C	Missense_Mutation	138	15.9%	No	No	82%	0.45071	98.5%	54.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
14DCIS	NAP1L5	p.A22V	4	89618841	G	A	Missense_Mutation	208	8.2%	No	No	42%	7.00E-05	64.9%	26.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
14DCIS	CLTB	NA	5	175819771	GCACC	G	Missense_Mutation	89	6.7%	No	No	35%	0.00428	71.1%	15.9%	Subclonal	.	.	.	.	passenger	No	No	No	WES
14DCIS	SENP6	p.S606R	6	76386942	T	G	Missense_Mutation	127	5.5%	No	No	28%	6.00E-05	55.8%	13.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
14DCIS	VKORC1L1	p.R8S	7	65338382	A	C	Missense_Mutation	87	31.0%	No	No	100%	0.8629	100.0%	79.4%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
14DCIS	TFEC	p.P10S	7	115624468	G	A	Missense_Mutation	112	19.6%	No	No	100%	0.69052	100.0%	63.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
14DCIS	PCMTD1	p.P342S	8	52732961	G	A	Missense_Mutation	23	13.0%	No	No	67%	0.35461	97.8%	21.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
14DCIS	ANP32B	p.G237S	9	100777666	G	A	Missense_Mutation	60	25.0%	No	No	100%	0.75144	100.0%	64.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
14DCIS	GLUD2	p.R76H	X	120181765	G	A	Missense_Mutation	156	5.1%	No	Yes	21%	0	40.1%	10.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
14IDC	SPEN	p.P677Lfs*132	1	16254763	TC	T	Frame_Shift_Del	184	15.2%	No	No	100%	0.78687	100.0%	76.2%	Clonal	.	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
14IDC	MACF1	p.X4015_splice	1	39903682	T	G	Splice_Site	108	4.6%	No	No	43%	0.05758	88.5%	18.2%	Subclonal	D	.	.	.	passenger	No	No	No	WES
14IDC	PPAP2B	p.S254N	1	56977697	C	T	Missense_Mutation	114	10.5%	No	No	97%	0.56458	100.0%	50.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
14IDC	LDB3	p.R31Q	10	88428540	G	A	Missense_Mutation	91	12.1%	No	No	100%	0.6275	100.0%	53.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
14IDC	C11orf1	p.Y53C	11	111753204	A	G	Missense_Mutation	98	11.2%	No	No	100%	0.5922	100.0%	51.3%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
14IDC	SERPINA3	p.M290L	14	95085756	A	C	Missense_Mutation	62	6.5%	No	No	59%	0.25639	97.0%	22.5%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
14IDC	SERPINA3	p.M290K	14	95085757	T	A	Missense_Mutation	60	6.7%	No	No	61%	0.27412	97.2%	23.1%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
14IDC	BCL11B	p.T435I	14	99641869	G	A	Missense_Mutation	147	5.4%	No	No	50%	0.06311	89.7%	25.3%	Subclonal	D	Passenger	D	T	passenger	Yes	Yes	No	WES
14IDC	CBFB	p.X55_splice	16	67063717	G	T	Splice_Site	59	16.9%	No	Yes	100%	0.73605	100.0%	56.9%	Clonal	D	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
14IDC	WIZ	p.R100W	19	15547848	G	A	Missense_Mutation	137	10.9%	No	No	100%	0.6107	100.0%	56.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
14IDC	KLHL26	p.S179L	19	18778743	C	T	Missense_Mutation	112	8.9%	No	No	82%	0.43657	98.6%	42.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
14IDC	SAG	p.R179C	2	234237146	C	T	Missense_Mutation	170	4.1%	No	No	38%	0.00708	74.9%	18.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
14IDC	COPG1	p.I92V	3	128971749	A	G	Missense_Mutation	164	9.8%	No	No	90%	0.5284	100.0%	52.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
14IDC	FAM149A	p.L332I	4	187084738	C	A	Missense_Mutation	140	7.1%	No	No	66%	0.22996	96.7%	35.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
14IDC	FAM174A	p.A31V	5	99871326	C	T	Missense_Mutation	204	4.4%	No	No	41%	0.00495	74.3%	21.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
14IDC	ANP32B	p.G237S	9	100777666	G	A	Missense_Mutation	59	8.5%	No	No	78%	0.39492	98.4%	30.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
14IDC	PHF19	p.R217K	9	123629208	C	T	Missense_Mutation	36	8.3%	No	No	77%	0.38402	98.2%	23.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
14IDC	GLUD2	p.R76H	X	120181765	G	A	Missense_Mutation	202	8.9%	No	Yes	73%	0.34002	97.3%	45.9%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
14IDC	TCF7L2	p.G308Sfs*16	10	114910800	ACGGGCATTCCG	A	Frame_Shift_Del	182	3.8%	No	No	35%	0.0031	70.3%	17.0%	Subclonal	.	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
15DCIS	ADAMTSL4	p.L905P	1	150531592	T	C	Missense_Mutation	240	22.9%	No	No	96%	0.71772	100.0%	73.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
15DCIS	RYR2	p.X3442_splice	1	237880497	G	A	Splice_Site	348	9.5%	No	No	40%	0	53.9%	28.1%	Subclonal	D	.	.	.	passenger	No	No	No	WES
15DCIS	GATA3	p.X308_splice	10	8111432	TCA	T	Splice_Site	269	26.4%	No	No	84%	0.31467	97.7%	67.7%	Subclonal	.	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
15DCIS	ARHGAP22	p.R57C	10	49791063	G	A	Missense_Mutation	243	34.6%	No	No	100%	0.88212	100.0%	85.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
15DCIS	LDB3	p.T527N	10	88476417	C	A	Missense_Mutation	92	38.0%	No	No	100%	0.83446	100.0%	78.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
15DCIS	SIGIRR	p.M410T	11	405900	A	G	Missense_Mutation	336	28.9%	No	No	92%	0.63557	100.0%	76.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
15DCIS	TENM4	p.D1313N	11	78423644	C	T	Missense_Mutation	196	34.2%	No	No	100%	0.86062	100.0%	82.4%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
15DCIS	CBFB	p.Q134*	16	67116116	C	T	Nonsense_Mutation	60	41.7%	No	Yes	91%	0.69225	100.0%	63.5%	Clonal	A	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
15DCIS	KLHL36	p.Q84*	16	84690663	C	T	Nonsense_Mutation	277	47.7%	No	Yes	100%	0.92703	100.0%	87.7%	Clonal	A	.	.	.	likely_pathogenic	No	No	No	WES
15DCIS	EMILIN2	p.G934R	18	2909793	G	A	Missense_Mutation	111	31.5%	No	No	100%	0.74392	100.0%	71.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
15DCIS	FDX1L	p.G87E	19	10426109	C	T	Missense_Mutation	217	9.7%	No	No	31%	0	45.1%	20.0%	Subclonal	D	Passenger	D	.	passenger	No	No	No	WES
15DCIS	MAG	p.N406S	19	35793597	A	G	Missense_Mutation	181	29.3%	No	No	93%	0.67221	100.0%	71.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
15DCIS	ZNF112	p.R791P	19	44831956	C	G	Missense_Mutation	410	30.2%	No	No	96%	0.772	100.0%	81.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
15DCIS	NINL	p.A859S	20	25457352	C	A	Missense_Mutation	279	27.2%	No	No	87%	0.4327	98.5%	70.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
15DCIS	PIK3CA	p.H1047R	3	178952085	A	G	Missense_Mutation	193	34.2%	Yes	No	100%	0.85959	100.0%	82.2%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
15DCIS	LYN	p.L93Wfs*14	8	56860273	TC	T	Frame_Shift_Del	107	33.6%	No	No	100%	0.79551	100.0%	74.4%	Clonal	.	.	.	.	passenger	No	No	No	WES
15IDC	ADAMTSL4	p.L905P	1	150531592	T	C	Missense_Mutation	144	14.6%	No	No	96%	0.61486	100.0%	60.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
15IDC	ZNF496	p.K470N	1	247464175	C	G	Missense_Mutation	220	3.2%	No	No	21%	0	41.6%	9.8%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
15IDC	TAF3	p.R397*	10	8006662	C	T	Nonsense_Mutation	168	7.7%	No	No	35%	1.00E-05	57.9%	20.5%	Subclonal	A	.	.	.	passenger	No	No	No	WES
15IDC	GATA3	p.X308_splice	10	8111432	TCA	T	Splice_Site	164	26.2%	No	No	100%	0.82679	100.0%	79.6%	Clonal	.	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
15IDC	ARHGAP22	p.R57C	10	49791063	G	A	Missense_Mutation	182	15.4%	No	No	70%	0.11177	94.1%	49.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
15IDC	LDB3	p.T527N	10	88476417	C	A	Missense_Mutation	71	25.4%	No	No	100%	0.72254	100.0%	65.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
15IDC	TENM4	p.D1313N	11	78423644	C	T	Missense_Mutation	127	23.6%	No	No	100%	0.75056	100.0%	70.9%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
15IDC	RAD51B	p.S201L	14	68353767	C	T	Missense_Mutation	153	11.8%	No	No	54%	0.0074	80.8%	34.2%	Subclonal	D	Passenger	D	T	passenger	Yes	Yes	No	WES
15IDC	USP8	p.W655R	15	50782070	T	A	Missense_Mutation	81	11.1%	No	No	51%	0.04294	87.5%	26.9%	Subclonal	D	Passenger	D	T	passenger	No	Yes	No	WES
15IDC	CBFB	p.Q134*	16	67116116	C	T	Nonsense_Mutation	59	27.1%	No	Yes	97%	0.69597	100.0%	57.7%	Clonal	A	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
15IDC	TMED6	p.V72G	16	69383553	A	C	Missense_Mutation	34	17.6%	No	Yes	63%	0.31142	96.7%	29.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
15IDC	KLHL36	p.Q84*	16	84690663	C	T	Nonsense_Mutation	246	32.1%	No	Yes	100%	0.90874	100.0%	85.6%	Clonal	A	.	.	.	likely_pathogenic	No	No	No	WES
15IDC	SMTNL2	p.K340N	17	4500185	G	T	Missense_Mutation	32	9.4%	No	No	43%	0.11826	93.0%	14.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
15IDC	EMILIN2	p.G934R	18	2909793	G	A	Missense_Mutation	79	13.9%	No	No	64%	0.1689	95.3%	35.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
15IDC	NINL	p.A859S	20	25457352	C	A	Missense_Mutation	201	16.4%	No	No	75%	0.18662	96.1%	53.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
15IDC	FGD5	p.E63K	3	14860765	G	A	Missense_Mutation	208	3.8%	No	No	18%	0	33.3%	8.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
15IDC	PIK3CA	p.H1047R	3	178952085	A	G	Missense_Mutation	138	15.2%	Yes	No	69%	0.15434	95.2%	45.9%	Subclonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
15IDC	BCKDHB	p.A8T	6	80816432	G	A	Missense_Mutation	41	17.1%	No	No	78%	0.40156	98.4%	36.6%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
15IDC	LYN	p.L93Wfs*14	8	56860273	TC	T	Frame_Shift_Del	71	22.5%	No	No	100%	0.65016	100.0%	59.2%	Clonal	.	.	.	.	passenger	No	No	No	WES
16DCIS	AMPD1	p.R112W	1	115229512	G	A	Missense_Mutation	129	8.5%	No	No	23%	0	38.5%	12.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
16DCIS	CCSAP	p.Q104K	1	229477903	G	T	Missense_Mutation	196	50.0%	No	No	100%	0.80071	100.0%	95.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
16DCIS	ITIH5	p.V402I	10	7621932	C	T	Missense_Mutation	310	7.1%	No	No	19%	0	27.6%	12.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
16DCIS	GATA3	p.R366*	10	8115750	C	T	Nonsense_Mutation	324	37.0%	No	No	99%	0.82025	100.0%	83.2%	Clonal	A	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
16DCIS	ARL14EP	p.D38N	11	30352607	G	A	Missense_Mutation	168	4.8%	No	No	13%	0	23.8%	6.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
16DCIS	IRS2	p.R871W	13	110435790	G	A	Missense_Mutation	135	6.7%	No	No	18%	0	32.0%	9.1%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
16DCIS	SCN4A	p.E452K	17	62041926	C	T	Missense_Mutation	99	22.2%	No	No	59%	0.00815	83.1%	40.0%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
16DCIS	MAPK4	p.H147Y	18	48190767	C	T	Missense_Mutation	282	37.2%	No	No	99%	0.81995	100.0%	82.5%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
16DCIS	SSC5D	p.T1321M	19	56029605	C	T	Missense_Mutation	150	7.3%	No	No	20%	0	33.3%	10.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
16DCIS	HOXD4	p.T162Ifs*7	2	177017385	C	CAT	Frame_Shift_Ins	122	39.3%	No	No	100%	0.81283	100.0%	77.9%	Clonal	.	.	.	.	passenger	No	No	No	WES
16DCIS	SSFA2	p.G324E	2	182766751	G	A	Missense_Mutation	176	32.4%	No	No	86%	0.44467	98.6%	68.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
16DCIS	NCKAP1	p.G442S	2	183846007	C	T	Missense_Mutation	266	6.8%	No	No	18%	0	27.4%	11.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
16DCIS	EDN3	p.V179I	20	57896241	G	A	Missense_Mutation	265	10.9%	No	No	29%	0	40.3%	20.1%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
16DCIS	PIK3CA	p.H1047R	3	178952085	A	G	Missense_Mutation	179	36.3%	Yes	No	97%	0.74895	100.0%	76.8%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
16DCIS	AGGF1	p.V202L	5	76332468	G	T	Missense_Mutation	86	4.7%	No	No	12%	0	29.8%	4.5%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
16DCIS	SPINK5	p.A621T	5	147492471	G	A	Missense_Mutation	155	37.4%	No	No	100%	0.78272	100.0%	77.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
16DCIS	RREB1	p.P997Rfs*40	6	7231320	TC	T	Frame_Shift_Del	208	33.7%	No	No	90%	0.55931	100.0%	72.6%	Clonal	.	.	.	.	passenger	No	No	No	WES
16DCIS	SRF	p.V454I	6	43146549	G	A	Missense_Mutation	172	36.6%	No	No	98%	0.76048	100.0%	77.1%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
16DCIS	CPA1	p.R234C	7	130024380	C	T	Missense_Mutation	136	6.6%	No	No	18%	0	31.8%	9.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
16DCIS	MYC	p.V421I	8	128753100	G	A	Missense_Mutation	269	4.1%	No	No	11%	0	18.7%	5.6%	Subclonal	D	Passenger	N	D	likely_pathogenic	Yes	Yes	No	WES
16DCIS	TNC	p.R1843C	9	117798506	G	A	Missense_Mutation	203	4.4%	No	No	12%	0	21.4%	5.8%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
16DCIS	ZNF79	p.V156I	9	130206445	G	A	Missense_Mutation	192	31.8%	No	No	85%	0.35857	98.1%	67.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
16DCIS	GPR101	p.A174V	X	136113313	G	A	Missense_Mutation	173	37.6%	No	No	100%	0.79668	100.0%	78.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
16DCIS	L1CAM	p.R322Q	X	153135537	C	T	Missense_Mutation	314	4.1%	No	No	11%	0	18.0%	6.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
16IDC	FHAD1	p.E1034V	1	15693971	A	T	Missense_Mutation	91	16.5%	No	No	77%	0.36482	98.1%	46.6%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
16IDC	CCSAP	p.Q104K	1	229477903	G	T	Missense_Mutation	131	19.8%	No	No	100%	0.75484	100.0%	69.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
16IDC	GATA3	p.E359Afs*44	10	8115724	AGAAG	A	Frame_Shift_Del	315	16.5%	No	No	77%	0.14191	95.3%	59.2%	Subclonal	.	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
16IDC	CKAP5	p.R1453C	11	46782199	G	A	Missense_Mutation	64	18.8%	No	No	87%	0.51228	98.9%	48.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
16IDC	SCN4A	p.E452K	17	62041926	C	T	Missense_Mutation	142	14.8%	No	No	69%	0.14854	94.9%	45.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
16IDC	MAPK4	p.H147Y	18	48190767	C	T	Missense_Mutation	328	19.8%	No	No	92%	0.64279	100.0%	72.4%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
16IDC	S1PR5	p.S104F	19	10625377	G	A	Missense_Mutation	305	18.0%	No	No	84%	0.38789	98.3%	65.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
16IDC	SSFA2	p.G324E	2	182766751	G	A	Missense_Mutation	240	23.3%	No	No	100%	0.82551	100.0%	79.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
16IDC	SERPINI2	p.E341A	3	167167133	T	G	Missense_Mutation	205	17.1%	No	No	80%	0.31649	97.7%	57.7%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
16IDC	PIK3CA	p.H1047R	3	178952085	A	G	Missense_Mutation	218	22.5%	Yes	No	100%	0.7892	100.0%	76.1%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
16IDC	SPINK5	p.A621T	5	147492471	G	A	Missense_Mutation	219	16.0%	No	No	74%	0.1666	95.6%	54.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
16IDC	RREB1	p.P997Rfs*40	6	7231320	TC	T	Frame_Shift_Del	213	21.1%	No	No	98%	0.72416	100.0%	72.1%	Clonal	.	.	.	.	passenger	No	No	No	WES
16IDC	SRF	p.V454I	6	43146549	G	A	Missense_Mutation	207	21.3%	No	No	99%	0.72896	100.0%	72.1%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
16IDC	ZNF79	p.V156I	9	130206445	G	A	Missense_Mutation	252	27.0%	No	No	100%	0.83095	100.0%	86.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
16IDC	GPR101	p.A174V	X	136113313	G	A	Missense_Mutation	186	21.5%	No	No	100%	0.7322	100.0%	71.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
16IDC	AGGF1	p.V202L	5	76332468	G	T	Missense_Mutation	120	7.5%	No	No	35%	2.70E-04	63.1%	18.3%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
17DCIS	ARHGEF16	p.S627N	1	3396146	G	A	Missense_Mutation	18	16.7%	No	No	100%	0.445	98.8%	27.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
17DCIS	LRP8	p.T744M	1	53723115	G	A	Missense_Mutation	55	9.1%	No	No	58%	0.18057	96.3%	24.6%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
17DCIS	ADAM15	p.R596Q	1	155030787	G	A	Missense_Mutation	82	6.1%	No	No	39%	0.02247	83.1%	16.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
17DCIS	YY1AP1	p.E801Nfs*41	1	155629713	TC	T	Frame_Shift_Del	126	13.5%	No	No	86%	0.43648	98.9%	52.5%	Subclonal	.	.	.	.	passenger	No	No	No	WES
17DCIS	PAQR6	p.P154S	1	156214534	G	A	Missense_Mutation	75	5.3%	No	No	34%	0.01634	80.0%	13.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
17DCIS	GATA3	p.S426Ifs*81	10	8115928	C	CA	Frame_Shift_Ins	193	17.6%	No	No	100%	0.73276	100.0%	73.4%	Clonal	.	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
17DCIS	C10orf71	p.V1247M	10	50534329	G	A	Missense_Mutation	31	45.2%	No	Yes	100%	0.84116	100.0%	73.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
17DCIS	DPYSL4	p.R552*	10	134018369	C	T	Nonsense_Mutation	29	10.3%	No	Yes	56%	0.20486	96.7%	18.6%	Subclonal	D	.	.	.	likely_pathogenic	No	No	No	WES
17DCIS	MUC5AC	p.R476H	11	1161252	G	A	Missense_Mutation	40	10.0%	No	No	74%	0.31736	98.2%	26.7%	Subclonal	.	Passenger	.	T	passenger	No	No	No	WES
17DCIS	OR10A6	p.R293*	11	7949333	G	A	Nonsense_Mutation	122	52.5%	No	No	100%	0.18473	100.0%	93.6%	Clonal	D	.	.	.	passenger	No	No	No	WES
17DCIS	RIN1	p.G573A	11	66101003	C	G	Missense_Mutation	78	10.3%	No	No	65%	0.21068	96.9%	32.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
17DCIS	FEZ1	p.Q166H	11	125333380	C	A	Missense_Mutation	50	14.0%	No	Yes	61%	0.2215	96.1%	29.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
17DCIS	ATXN7L3B	p.G68Efs*37	12	74932090	CA	C	Frame_Shift_Del	160	11.9%	No	No	88%	0.45766	99.0%	54.6%	Subclonal	.	.	.	.	passenger	No	No	No	WES
17DCIS	MLXIP	p.A643S	12	122620108	G	T	Missense_Mutation	101	17.8%	No	No	100%	0.70648	100.0%	67.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
17DCIS	TNFSF11	p.A4T	13	43148449	G	A	Missense_Mutation	19	36.8%	No	No	100%	0.79529	100.0%	55.5%	Clonal	D	Passenger	.	D	likely_pathogenic	No	No	No	WES
17DCIS	ZNF280D	p.R476C	15	56961140	G	A	Missense_Mutation	106	5.7%	No	No	36%	0.00568	74.4%	16.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
17DCIS	GPR114	p.R210H	16	57600593	G	A	Missense_Mutation	27	18.5%	No	No	100%	0.52457	100.0%	39.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
17DCIS	ZFPM1	p.A842V	16	88600891	C	T	Missense_Mutation	12	25.0%	No	No	100%	0.56894	100.0%	32.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
17DCIS	DEF8	p.V17I	16	90015922	G	A	Missense_Mutation	35	11.4%	No	No	73%	0.3123	98.1%	26.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
17DCIS	NCOR1	p.T1566M	17	15971252	G	A	Missense_Mutation	21	52.4%	No	Yes	100%	0.71126	100.0%	69.8%	Clonal	D	Passenger	N	T	passenger	Yes	Yes	Yes	WES
17DCIS	REXO1	p.D57N	19	1828619	C	T	Missense_Mutation	36	19.4%	No	No	100%	0.64509	100.0%	49.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
17DCIS	MYPOP	p.V338M	19	46394069	C	T	Missense_Mutation	69	7.2%	No	No	61%	0.20881	96.9%	25.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
17DCIS	ZNF808	p.R494H	19	53057650	G	A	Missense_Mutation	19	15.8%	No	No	100%	0.4726	98.9%	28.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
17DCIS	SAMHD1	p.A441S	20	35533856	C	A	Missense_Mutation	93	11.8%	No	No	87%	0.43348	98.9%	46.4%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
17DCIS	MED15	p.G114D	22	20909325	G	A	Missense_Mutation	23	13.0%	No	Yes	70%	0.2996	98.0%	22.1%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
17DCIS	MICALL1	p.S447N	22	38321925	G	A	Missense_Mutation	45	8.9%	No	Yes	48%	0.10753	93.8%	18.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
17DCIS	CTDSPL	p.R38K	3	37988581	G	A	Missense_Mutation	34	8.8%	No	Yes	47%	0.13861	95.0%	16.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
17DCIS	IFT80	p.G291E	3	160037633	C	T	Missense_Mutation	147	20.4%	No	No	100%	0.7543	100.0%	76.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
17DCIS	SLC34A2	p.A651V	4	25678250	C	T	Missense_Mutation	53	17.0%	No	No	100%	0.54601	100.0%	49.5%	Clonal	N	Passenger	N	T	passenger	Yes	Yes	No	WES
17DCIS	UCP1	p.W174C	4	141484476	C	A	Missense_Mutation	66	10.6%	No	No	68%	0.24788	97.5%	32.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
17DCIS	SH3TC2	p.R753W	5	148407038	G	A	Missense_Mutation	74	14.9%	No	No	100%	0.57143	100.0%	53.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
17DCIS	AK9	p.Q901H	6	109884848	C	G	Missense_Mutation	197	3.6%	No	No	37%	0.00439	73.4%	17.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
17DCIS	SAP25	p.R126C	7	100170134	G	A	Missense_Mutation	54	7.4%	No	No	55%	0.17436	96.2%	21.1%	Subclonal	N	Passenger	N	.	passenger	No	No	No	WES
17DCIS	SMARCD3	p.Q262Hfs*8	7	150938730	AC	A	Frame_Shift_Del	92	13.0%	No	No	96%	0.50856	100.0%	51.0%	Clonal	.	.	.	.	passenger	No	No	No	WES
17DCIS	ARFGEF1	p.F1614C	8	68117033	A	C	Missense_Mutation	134	14.2%	No	No	90%	0.49421	100.0%	56.2%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
17DCIS	FRMPD4	p.R179C	X	12701668	C	T	Missense_Mutation	81	11.1%	No	No	82%	0.38097	98.6%	41.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
17DCIS	USP9X	p.R2429I	X	41088887	G	T	Missense_Mutation	160	13.8%	No	No	100%	0.60851	100.0%	62.8%	Clonal	D	Passenger	D	T	passenger	Yes	No	No	WES
17IDC	COPA	p.G694E	1	160267459	C	T	Missense_Mutation	161	16.8%	No	No	100%	0.60453	100.0%	65.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
17IDC	GATA3	p.S426Ifs*81	10	8115928	C	CA	Frame_Shift_Ins	317	36.3%	No	No	100%	0.93316	100.0%	95.2%	Clonal	.	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
17IDC	WAC	p.R85G	10	28824665	A	G	Missense_Mutation	75	17.3%	No	No	86%	0.41083	98.9%	48.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
17IDC	C10orf71	p.V1247M	10	50534329	G	A	Missense_Mutation	51	74.5%	No	Yes	100%	0.03417	100.0%	89.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
17IDC	SYT8	p.C120Y	11	1857174	G	A	Missense_Mutation	28	10.7%	No	No	42%	0.0816	92.4%	14.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
17IDC	OR10A6	p.R293*	11	7949333	G	A	Nonsense_Mutation	47	23.4%	No	No	92%	0.46716	100.0%	49.5%	Subclonal	D	.	.	.	passenger	No	No	No	WES
17IDC	LGALS12	p.A94T	11	63276302	G	A	Missense_Mutation	133	4.5%	No	No	18%	0	37.0%	7.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
17IDC	XRRA1	p.R190C	11	74632323	G	A	Missense_Mutation	40	7.5%	No	No	37%	0.04968	89.0%	12.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
17IDC	GDPD4	p.S276L	11	76969468	G	A	Missense_Mutation	55	7.3%	No	No	36%	0.02039	82.5%	14.1%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
17IDC	FOLR4	p.R198Q	11	94040719	G	A	Missense_Mutation	55	7.3%	No	Yes	21%	3.00E-05	50.5%	8.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
17IDC	TINF2	p.F14Gfs*2	14	24711488	CGCGGCGGCGAA	C	Frame_Shift_Del	58	6.9%	No	No	34%	0.01364	79.4%	13.4%	Subclonal	.	.	.	.	passenger	No	No	No	WES
17IDC	AQP9	p.A163P	15	58467227	G	C	Missense_Mutation	110	14.5%	No	No	87%	0.42313	98.9%	52.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
17IDC	CYP11A1	p.R151W	15	74637559	G	A	Missense_Mutation	39	7.7%	No	No	30%	0.0131	78.4%	10.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
17IDC	POLG	p.R42Q	15	89876861	C	T	Missense_Mutation	53	11.3%	No	No	45%	0.02873	86.1%	20.7%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
17IDC	VASN	p.N500K	16	4432378	C	G	Missense_Mutation	235	6.8%	No	No	47%	0.00149	74.4%	29.1%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
17IDC	CAPNS2	p.G118S	16	55601020	G	A	Missense_Mutation	68	5.9%	No	No	23%	1.50E-04	55.5%	9.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
17IDC	ZFPM1	p.A842V	16	88600891	C	T	Missense_Mutation	16	25.0%	No	No	99%	0.42257	98.9%	32.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
17IDC	DNAH2	p.R1448H	17	7674232	G	A	Missense_Mutation	71	5.6%	No	No	28%	0.00205	66.8%	10.8%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
17IDC	NCOR1	p.T1566M	17	15971252	G	A	Missense_Mutation	24	70.8%	No	Yes	100%	0.58	100.0%	79.4%	Clonal	D	Passenger	N	T	passenger	Yes	Yes	Yes	WES
17IDC	REXO1	p.D57N	19	1828619	C	T	Missense_Mutation	32	21.9%	No	No	86%	0.39478	98.8%	39.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
17IDC	CACNA1A	p.S428T	19	13441120	C	G	Missense_Mutation	22	36.4%	No	No	100%	0.66115	100.0%	54.9%	Clonal	N	Passenger	D	D	passenger	No	No	No	WES
17IDC	NPHP1	p.F351L	2	110919249	G	C	Missense_Mutation	61	21.3%	No	No	100%	0.56329	100.0%	56.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
17IDC	KRTAP21-2	p.G52V	21	32119366	C	A	Missense_Mutation	61	24.6%	No	No	100%	0.73427	100.0%	67.1%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
17IDC	NBEAL2	p.H875Y	3	47038510	C	T	Missense_Mutation	80	27.5%	No	Yes	100%	0.65742	100.0%	67.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
17IDC	FLNB	p.P254L	3	58067477	C	T	Missense_Mutation	35	8.6%	No	Yes	34%	0.02691	84.2%	11.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES

17IDC	RP11-503N18.3	p.R203W	4	2460902	C	T	Missense_Mutation	50	34.0%	No	No	100%	0.70378	100.0%	69.0%	Clonal	.	Passenger	D	.	passenger	No	No	No	WES
17IDC	FREM3	p.P112L	4	144621494	G	A	Missense_Mutation	81	4.9%	No	No	24%	4.20E-04	59.0%	9.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
17IDC	ZNF354B	p.I207M	5	178310074	C	G	Missense_Mutation	26	15.4%	No	No	92%	0.39034	98.7%	30.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
17IDC	OR2H2	p.W221*	6	29556383	G	A	Nonsense_Mutation	61	21.3%	No	No	84%	0.39347	98.8%	48.7%	Subclonal	D		.	.	passenger	No	No	No	WES
17IDC	PHIP	p.R1510*	6	79655820	G	A	Nonsense_Mutation	74	8.1%	No	No	40%	0.01312	80.5%	18.5%	Subclonal	A	.	.	.	passenger	No	No	No	WES
17IDC	RSPO3	p.Q254H	6	127517095	G	C	Missense_Mutation	88	13.6%	No	No	54%	0.02356	86.6%	31.1%	Subclonal	D	Passenger	N	T	passenger	Yes	Yes	No	WES
17IDC	ARFGEF1	p.F1614C	8	68117033	A	C	Missense_Mutation	166	16.9%	No	No	100%	0.73304	100.0%	75.4%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
17IDC	EHMT1	p.G1239R	9	140728975	G	A	Missense_Mutation	221	3.2%	No	No	44%	0.02623	85.6%	21.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
17IDC	ZNF157	p.R433Q	X	47272770	G	A	Missense_Mutation	63	6.3%	No	No	31%	0.00675	74.3%	12.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
17IDC	TAF1	p.Q1057*	X	70613208	C	T	Nonsense_Mutation	37	10.8%	No	No	43%	0.05332	89.8%	16.8%	Subclonal	A	.	.	.	likely_pathogenic	Yes	No	No	WES
17IDC	H2BFM	p.Q118H	X	103294897	G	T	Missense_Mutation	103	18.4%	No	No	91%	0.48914	100.0%	57.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
17IDC	F9	p.T205P	X	138633313	A	C	Missense_Mutation	59	16.9%	No	No	84%	0.38518	98.7%	44.2%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
18IDC	NOC2L	p.R213K	1	891363	C	T	Missense_Mutation	112	8.9%	No	Yes	79%	0.66018	98.4%	41.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	NOC2L	p.R213K	1	891363	C	T	Missense_Mutation	179	15.1%	No	Yes	100%	0.82591	100.0%	66.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18IDC	PLCH2	p.F717L	1	2429969	C	A	Missense_Mutation	123	11.4%	No	Yes	100%	0.8404	100.0%	58.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18DCIS	PLCH2	p.F717L	1	2429969	C	A	Missense_Mutation	155	14.8%	No	Yes	100%	0.806	100.0%	63.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18DCIS	HSPG2	p.D3515N	1	22161349	C	T	Missense_Mutation	119	5.9%	No	No	22%	0	43.7%	10.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	PARS2	p.P444R	1	55223504	G	C	Missense_Mutation	113	12.4%	No	No	84%	0.64954	98.8%	48.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18IDC	NUP210L	p.G612R	1	154072605	C	T	Missense_Mutation	86	62.8%	No	Yes	100%	0.11336	100.0%	93.1%	Clonal	N	Passenger	D	T	passenger	No	No	Yes	WES
18DCIS	NUP210L	p.G612R	1	154072605	C	T	Missense_Mutation	151	74.8%	No	Yes	100%	0.21393	100.0%	96.6%	Clonal	N	Passenger	D	T	passenger	No	No	Yes	WES
18IDC	IGFN1	p.D1166N	1	201177517	G	A	Missense_Mutation	135	9.6%	No	Yes	85%	0.71958	98.8%	47.9%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
18DCIS	IGFN1	p.D1166N	1	201177517	G	A	Missense_Mutation	136	12.5%	No	Yes	85%	0.65993	98.8%	51.9%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
18IDC	KDM5B	p.G576R	1	202719882	C	T	Missense_Mutation	69	8.7%	No	Yes	77%	0.64442	98.3%	33.3%	Clonal	D	Driver	D	D	likely_pathogenic	No	No	No	WES
18DCIS	KDM5B	p.G576R	1	202719882	C	T	Missense_Mutation	102	16.7%	No	Yes	100%	0.82519	100.0%	62.5%	Clonal	D	Driver	D	D	likely_pathogenic	No	No	No	WES
18IDC	KCTD3	p.H403Y	1	215777542	C	T	Missense_Mutation	33	39.4%	No	Yes	100%	0.51479	100.0%	73.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18DCIS	KCTD3	p.H403Y	1	215777542	C	T	Missense_Mutation	114	63.2%	No	Yes	100%	0.27496	100.0%	94.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18IDC	FMN2	p.G941A	1	240370934	G	C	Missense_Mutation	497	57.7%	No	Yes	100%	0	100.0%	98.3%	Clonal	P	Passenger	N	T	passenger	No	No	No	WES
18DCIS	FMN2	p.G941A	1	240370934	G	C	Missense_Mutation	428	55.4%	No	Yes	100%	0.26703	100.0%	98.1%	Clonal	P	Passenger	N	T	passenger	No	No	No	WES
18IDC	ZBTB18	p.S145G	1	244217509	A	G	Missense_Mutation	117	12.8%	No	Yes	100%	0.85107	100.0%	59.9%	Clonal	D	Passenger		T	passenger	No	No	No	WES
18DCIS	BMP10	p.W198R	2	69093446	A	G	Missense_Mutation	177	15.3%	No	No	88%	0.71063	100.0%	60.0%	Clonal	D	Driver	D	D	likely_pathogenic	No	No	No	WES
18IDC	TTN	p.I21107L	2	179452815	T	G	Missense_Mutation	64	26.6%	No	No	100%	0.86684	100.0%	76.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18DCIS	TTN	p.I21107L	2	179452815	T	G	Missense_Mutation	91	34.1%	No	No	100%	0.9197	100.0%	85.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18IDC	SLC4A3	p.L747R	2	220500581	T	G	Missense_Mutation	115	13.9%	No	No	100%	0.84818	100.0%	60.0%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
18DCIS	SLC4A3	p.L747R	2	220500581	T	G	Missense_Mutation	155	21.3%	No	No	100%	0.88903	100.0%	76.3%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
18IDC	XPC	p.X207_splice	3	14208668	C	T	Splice_Site	56	14.3%	No	No	100%	0.83489	100.0%	50.1%	Clonal	D				likely_pathogenic	No	Yes	No	WES
18DCIS	KCNH8	p.V1034L	3	19575367	G	C	Missense_Mutation	101	5.0%	No	No	29%	0.00246	63.6%	12.2%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
18IDC	ITGA9	p.E967K	3	37845323	G	A	Missense_Mutation	129	14.7%	No	No	100%	0.88658	100.0%	68.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	ITGA9	p.E967K	3	37845323	G	A	Missense_Mutation	120	15.0%	No	No	87%	0.68559	98.9%	53.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	ZNF445	p.A307D	3	44491016	G	T	Missense_Mutation	64	7.8%	No	No	45%	0.14701	90.3%	19.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
18IDC	OR5H15	p.R143W	3	97887970	C	T	Missense_Mutation	130	3.1%	No	No	27%	0.00903	66.8%	10.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
18DCIS	OR5H15	p.R143W	3	97887970	C	T	Missense_Mutation	204	0.5%	No	No	3%	0	15.1%	0.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
18IDC	MAATS1	p.R419T	3	119452265	G	C	Missense_Mutation	63	6.3%	No	No	56%	0.45559	96.5%	21.5%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
18DCIS	MAATS1	p.R419T	3	119452265	G	C	Missense_Mutation	92	17.4%	No	No	100%	0.78143	100.0%	57.9%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
18IDC	GAK	p.A341T	4	884380	C	T	Missense_Mutation	110	10.0%	No	No	68%	0.57693	97.1%	38.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18DCIS	TMPRSS11D	p.A114V	4	68704024	G	A	Missense_Mutation	92	15.2%	No	No	73%	0.47021	97.5%	43.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	ADAMTS3	p.Q430K	4	73185113	G	T	Missense_Mutation	84	6.0%	No	No	29%	0.00188	62.7%	12.1%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
18IDC	ARHGEF38	p.P179Hfs*29	4	106552080	GC	G	Frame_Shift_Del	43	11.6%	No	No	80%	0.72844	98.4%	31.5%	Clonal					passenger	No	No	No	WES
18DCIS	ARHGEF38	p.P179Hfs*29	4	106552080	GC	G	Frame_Shift_Del	74	39.2%	No	No	100%	0.95337	100.0%	83.0%	Clonal					passenger	No	No	No	WES
18IDC	SEC24B	p.Q496K	4	110416010	C	A	Missense_Mutation	44	25.0%	No	No	100%	0.85501	100.0%	63.2%	Clonal	D	Driver	N	T	likely_pathogenic	No	No	No	WES
18DCIS	SEC24B	p.Q496K	4	110416010	C	A	Missense_Mutation	91	17.6%	No	No	84%	0.65494	98.8%	51.2%	Clonal	D	Driver	N	T	likely_pathogenic	No	No	No	WES
18IDC	GALNTL6	p.E236K	4	173730664	G	A	Missense_Mutation	44	9.1%	No	No	62%	0.6062	97.3%	23.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18DCIS	GALNTL6	p.E236K	4	173730664	G	A	Missense_Mutation	44	38.6%	No	No	100%	0.9397	100.0%	74.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18IDC	FRG1	p.G163E	4	190878608	G	A	Missense_Mutation	168	4.8%	No	No	33%	0.00122	61.9%	16.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	FRG1	p.G163E	4	190878608	G	A	Missense_Mutation	213	11.7%	No	No	56%	0.00747	79.7%	38.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
18IDC	ADAMTS16	p.E67K	5	5146266	G	A	Missense_Mutation	79	15.2%	No	No	100%	0.84854	100.0%	57.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	ADAMTS16	p.E67K	5	5146266	G	A	Missense_Mutation	87	16.1%	No	No	93%	0.72994	100.0%	52.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18IDC	ADAMTS12	p.E1469K	5	33546205	C	T	Missense_Mutation	94	13.8%	No	No	100%	0.83219	100.0%	56.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18DCIS	ADAMTS12	p.E1469K	5	33546205	C	T	Missense_Mutation	143	23.8%	No	No	100%	0.86477	100.0%	79.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18IDC	AGGF1	p.V202L	5	76332468	G	T	Missense_Mutation	71	5.6%	No	No	44%	0.24462	92.2%	17.3%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
18DCIS	AGGF1	p.V202L	5	76332468	G	T	Missense_Mutation	121	2.5%	No	No	14%	0.00001	40.1%	4.7%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
18IDC	DMGDH	p.W606C	5	78324470	C	A	Missense_Mutation	62	8.1%	No	No	63%	0.5206	97.3%	26.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18DCIS	DMGDH	p.W606C	5	78324470	C	A	Missense_Mutation	89	20.2%	No	No	100%	0.84126	100.0%	65.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18DCIS	NR2F1	p.P23T	5	92920796	C	A	Missense_Mutation	65	6.2%	No	No	36%	0.05717	82.4%	14.0%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
18IDC	IRF4	p.Q395H	6	405103	G	T	Missense_Mutation	37	10.8%	No	No	96%	0.72041	98.8%	31.1%	Clonal	D	Passenger	N	D	likely_pathogenic	No	Yes	Yes	WES
18DCIS	IRF4	p.Q395H	6	405103	G	T	Missense_Mutation	41	22.0%	No	No	100%	0.80773	100.0%	53.6%	Clonal	D	Passenger	N	D	likely_pathogenic	No	Yes	Yes	WES
18DCIS	SLC22A23	p.P156R	6	3456327	G	C	Missense_Mutation	229	19.2%	No	No	100%	0.89302	100.0%	76.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18IDC	CDYL	p.Y353Lfs*5	6	4937900	CTTTA	C	Frame_Shift_Del	73	13.7%	No	No	100%	0.83904	100.0%	53.8%	Clonal					passenger	No	No	No	WES
18DCIS	CDYL	p.Y353Lfs*5	6	4937900	CTTTA	C	Frame_Shift_Del	94	12.8%	No	No	74%	0.51217	97.9%	42.0%	Clonal					passenger	No	No	No	WES
18DCIS	RREB1	p.L163Q	6	7211099	T	A	Missense_Mutation	105	6.7%	No	No	32%	0.00088	62.4%	15.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	KIF13A	p.A211V	6	17850639	G	A	Missense_Mutation	100	17.0%	No	No	81%	0.61394	98.5%	50.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18IDC	MICA	p.D249N	6	31379855	G	A	Missense_Mutation	140	2.9%	No	No	NA	0	100.0%	0.0%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
18DCIS	MICA	p.D249N	6	31379855	G	A	Missense_Mutation	112	18.8%	No	No	71%	0.38506	95.8%	47.2%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
18IDC	PRRC2A	p.G1682E	6	31602639	G	A	Missense_Mutation	82	8.5%	No	No	NA	0	100.0%	0.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	PRRC2A	p.G1682E	6	31602639	G	A	Missense_Mutation	81	29.6%	No	No	100%	0.89626	100.0%	69.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18IDC	IBTK	p.I931V	6	82910425	T	C	Missense_Mutation	92	8.7%	No	No	77%	0.64278	98.3%	37.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	IBTK	p.I931V	6	82910425	T	C	Missense_Mutation	143	4.2%	No	No	24%	0.00003	50.7%	10.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
18IDC	TIAM2	p.P579S	6	155465844	C	T	Missense_Mutation	77	6.5%	No	No	64%	0.52514	97.4%	26.5%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
18DCIS	TIAM2	p.P579S	6	155465844	C	T	Missense_Mutation	136	10.3%	No	No	60%	0.1514	91.6%	35.7%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
18IDC	SNX13	p.E515K	7	17873729	C	T	Missense_Mutation	48	8.3%	No	No	74%	0.62328	98.2%	26.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18DCIS	SNX13	p.E515K	7	17873729	C	T	Missense_Mutation	94	26.6%	No	No	100%	0.88401	100.0%	77.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18IDC	SRCRB4D	p.E459Q	7	76021317	C	G	Missense_Mutation	114	14.9%	No	No	100%	0.86742	100.0%	63.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18DCIS	SRCRB4D	p.E459Q	7	76021317	C	G	Missense_Mutation	96	12.5%	No	No	60%	0.19207	92.9%	34.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
18IDC	SMO	p.D786N	7	128852284	G	A	Missense_Mutation	113	15.0%	No	No	100%	0.90009	100.0%	68.7%	Clonal	D	Passenger	N	D	likely_pathogenic	No	Yes	No	WES
18IDC	ATG9B	p.P823S	7	150713569	G	A	Missense_Mutation	99	13.1%	No	No	100%	0.86482	100.0%	60.5%	Clonal		Passenger			passenger	No	No	No	WES
18DCIS	ATG9B	p.P823S	7	150713569	G	A	Missense_Mutation	156	11.5%	No	No	90%	0.71147	100.0%	54.9%	Clonal		Passenger			passenger	No	No	No	WES
18DCIS	SHH	p.A389S	7	155595818	C	A	Missense_Mutation	220	13.2%	No	No	100%	0.82911	100.0%	67.3%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
18IDC	INTS9	p.M519I	8	28633282	C	A	Missense_Mutation	95	15.8%	No	No	NA	0	100.0%	0.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	TEX15	p.P1963S	8	30700647	G	A	Missense_Mutation	130	15.4%	No	No	100%	0.81189	100.0%	62.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18IDC	KIFC2	p.P771L	8	145698628	C	T	Missense_Mutation	137	5.8%	No	No	46%	0.07983	84.6%	23.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
18IDC	TSTD2	p.G364D	9	100367787	C	T	Missense_Mutation	114	21.1%	No	No	100%	0.95011	100.0%	78.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18DCIS	TSTD2	p.G364D	9	100367787	C	T	Missense_Mutation	98	31.6%	No	No	100%	0.91856	100.0%	75.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18IDC	COL27A1	p.G646E	9	116940599	G	A	Missense_Mutation	110	13.6%	No	No	100%	0.86327	100.0%	61.6%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
18DCIS	COL27A1	p.G646E	9	116940599	G	A	Missense_Mutation	89	16.9%	No	No	98%	0.76103	100.0%	55.7%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
18DCIS	PTGS1	p.R60H	9	125140262	G	A	Missense_Mutation	176	13.1%	No	No	76%	0.45769	97.5%	50.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
18DCIS	GTPBP4	p.N5T	10	1034433	A	C	Missense_Mutation	72	6.9%	No	No	40%	0.07137	84.7%	17.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
18IDC	KIAA1462	p.Q893R	10	30316399	T	C	Missense_Mutation	244	19.7%	No	No	100%	0.94321	100.0%	87.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18DCIS	KIAA1462	p.Q893R	10	30316399	T	C	Missense_Mutation	170	27.1%	No	No	100%	0.88776	100.0%	82.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18IDC	PTPN20B	p.L193F	10	48771321	G	A	Missense_Mutation	101	5.9%	No	No	100%	0.78555	100.0%	42.0%	Clonal	D	Passenger		T	passenger	No	No	No	WES
18DCIS	PTPN20B	p.L193F	10	48771321	G	A	Missense_Mutation	155	14.8%	No	No	100%	0.93786	100.0%	77.8%	Clonal	D	Passenger		T	passenger	No	No	No	WES
18DCIS	OIT3	p.G428S	10	74684317	G	A	Missense_Mutation	185	8.1%	No	No	79%	0.58405	98.4%	47.1%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
18IDC	ZFYVE27	p.E148Q	10	99504659	G	C	Missense_Mutation	126	16.7%	No	Yes	100%	0.90835	100.0%	66.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	ZFYVE27	p.E148Q	10	99504659	G	C	Missense_Mutation	113	27.4%	No	Yes	100%	0.88952	100.0%	70.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	CPXM2	p.A118V	10	125639777	G	A	Missense_Mutation	24	16.7%	No	No	63%	0.5338	97.3%	24.2%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
18IDC	GALNT18	p.F92L	11	11470443	G	T	Missense_Mutation	128	17.2%	No	No	100%	0.89473	100.0%	71.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18DCIS	GALNT18	p.F92L	11	11470443	G	T	Missense_Mutation	119	21.8%	No	No	100%	0.84039	100.0%	67.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18IDC	NELL1	p.P628S	11	21581830	C	T	Missense_Mutation	72	20.8%	No	No	100%	0.92087	100.0%	68.6%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
18DCIS	NELL1	p.P628S	11	21581830	C	T	Missense_Mutation	66	36.4%	No	No	100%	0.93559	100.0%	79.3%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
18IDC	OR10AG1	p.V193L	11	55735363	C	A	Missense_Mutation	63	41.3%	No	No	100%	0.45999	100.0%	85.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
18DCIS	OR10AG1	p.V193L	11	55735363	C	A	Missense_Mutation	107	35.5%	No	No	100%	0.95673	100.0%	86.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18IDC	CATSPER1	p.P152H	11	65793396	G	T	Missense_Mutation	94	23.4%	No	No	100%	0.94825	100.0%	77.3%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
18DCIS	CATSPER1	p.P152H	11	65793396	G	T	Missense_Mutation	146	41.1%	No	No	100%	0.86979	100.0%	92.0%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
18IDC	UCP3	p.A231S	11	73715005	C	A	Missense_Mutation	201	7.0%	No	No	76%	0.59726	98.0%	44.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18IDC	KCTD14	p.R157C	11	77727938	G	A	Missense_Mutation	374	3.5%	No	Yes	59%	0.21483	92.5%	34.0%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
18IDC	NPAT	p.S1200Y	11	108032214	G	T	Missense_Mutation	74	6.8%	No	Yes	46%	0.27561	91.4%	19.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
18IDC	SLC6A13	p.Q341E	12	335595	G	C	Missense_Mutation	178	10.1%	No	No	89%	0.76438	100.0%	54.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18DCIS	SLC6A13	p.Q341E	12	335595	G	C	Missense_Mutation	161	21.1%	No	No	100%	0.89047	100.0%	76.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18IDC	TNFRSF1A	p.A357V	12	6438776	G	A	Missense_Mutation	214	9.3%	No	No	73%	0.50191	97.2%	47.3%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
18DCIS	TNFRSF1A	p.A357V	12	6438776	G	A	Missense_Mutation	303	19.1%	No	No	100%	0.908	100.0%	79.9%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
18IDC	ITPR2	p.A445V	12	26834882	G	A	Missense_Mutation	43	9.3%	No	No	82%	0.66982	98.5%	28.5%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
18IDC	DDX11	p.E78K	12	31236834	G	A	Missense_Mutation	133	10.5%	No	No	93%	0.77756	100.0%	52.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18DCIS	DDX11	p.E78K	12	31236834	G	A	Missense_Mutation	123	22.0%	No	No	100%	0.87874	100.0%	74.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18IDC	FREM2	p.A202T	13	39262085	G	A	Missense_Mutation	104	6.7%	No	Yes	46%	0.15008	86.9%	22.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
18IDC	TRIM13	p.E387K	13	50587226	G	A	Missense_Mutation	44	13.6%	No	Yes	93%	0.78989	98.9%	38.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	TRIM13	p.E387K	13	50587226	G	A	Missense_Mutation	82	25.6%	No	Yes	97%	0.83727	100.0%	61.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18IDC	SLITRK5	p.R208W	13	88328265	C	T	Missense_Mutation	62	1.6%	No	No	13%	0.0187	65.5%	2.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
18DCIS	SLITRK5	p.R208W	13	88328265	C	T	Missense_Mutation	105	21.0%	No	No	100%	0.80826	100.0%	63.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18DCIS	OR4K2	p.D175G	14	20344950	A	G	Missense_Mutation	296	3.0%	No	No	18%	0	32.4%	8.9%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
18IDC	SYNE2	p.M3705I	14	64545276	G	C	Missense_Mutation	75	18.7%	No	No	100%	0.89522	100.0%	65.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18DCIS	SYNE2	p.M3705I	14	64545276	G	C	Missense_Mutation	108	0.9%	No	No	4%	0	23.5%	0.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
18IDC	CCDC88C	p.X1371_splice	14	91757429	C	G	Splice_Site	20	15.0%	No	No	100%	0.75839	98.9%	28.8%	Clonal	D				passenger	No	No	No	WES
18DCIS	CCDC88C	p.X1371_splice	14	91757429	C	G	Splice_Site	45	26.7%	No	No	100%	0.83279	100.0%	60.2%	Clonal	D				passenger	No	No	No	WES
18DCIS	SERPINA11	p.A15D	14	94915068	G	T	Missense_Mutation	94	5.3%	No	No	25%	0.00036	56.3%	10.8%	Subclonal	N	Passenger	D	D	passenger	No	No	No	WES
18IDC	USP8	p.A798P	15	50785055	G	C	Missense_Mutation	55	9.1%	No	No	62%	0.58525	97.1%	26.1%	Clonal	D	Passenger	N	T	passenger	No	Yes	No	WES
18DCIS	USP8	p.A798P	15	50785055	G	C	Missense_Mutation	93	2.2%	No	No	10%	0	35.3%	2.6%	Subclonal	D	Passenger	N	T	passenger	No	Yes	No	WES
18IDC	PDCD7	p.A2T	15	65426116	C	T	Missense_Mutation	59	11.9%	No	No	81%	0.74418	98.6%	37.2%	Clonal	N	Passenger	N		passenger	No	No	No	WES
18DCIS	PDCD7	p.A2T	15	65426116	C	T	Missense_Mutation	78	6.4%	No	No	31%	0.00485	67.2%	13.1%	Subclonal	N	Passenger	N		passenger	No	No	No	WES
18IDC	MPG	p.R201W	16	135480	C	T	Missense_Mutation	93	10.8%	No	No	84%	0.70847	98.7%	43.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
18IDC	CCNF	p.D637N	16	2506569	G	A	Missense_Mutation	76	9.2%	No	No	72%	0.60061	98.0%	33.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	CCNF	p.D637N	16	2506569	G	A	Missense_Mutation	62	22.6%	No	No	100%	0.80347	100.0%	58.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18IDC	INO80E	p.K86Sfs*45	16	30012128	CA	C	Frame_Shift_Del	83	16.9%	No	No	100%	0.87641	100.0%	62.9%	Clonal					passenger	No	No	No	WES
18DCIS	INO80E	p.K86Sfs*45	16	30012128	CA	C	Frame_Shift_Del	71	32.4%	No	No	100%	0.88698	100.0%	76.7%	Clonal					passenger	No	No	No	WES
18DCIS	HIC1	p.P265S	17	1960720	C	T	Missense_Mutation	92	5.4%	No	Yes	21%	0.00001	45.4%	8.6%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
18IDC	TP53	p.R273C	17	7577121	G	A	Missense_Mutation	120	34.2%	Yes	Yes	NA	0	100.0%	0.0%	Subclonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
18DCIS	TP53	p.R273C	17	7577121	G	A	Missense_Mutation	95	52.6%	Yes	Yes	100%	0.00005	100.0%	90.3%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
18IDC	CDK5R1	p.R153C	17	30815095	C	T	Missense_Mutation	1494	2.1%	No	No	60%	0.02075	83.1%	41.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
18DCIS	CDK5R1	p.R153C	17	30815095	C	T	Missense_Mutation	2592	2.2%	No	No	58%	0.00012	74.4%	44.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
18IDC	SLFN14	p.S83C	17	33884834	G	C	Missense_Mutation	64	18.8%	No	Yes	100%	0.88953	100.0%	59.4%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
18DCIS	SLFN14	p.S83C	17	33884834	G	C	Missense_Mutation	91	22.0%	No	Yes	100%	0.8229	100.0%	63.6%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
18IDC	ERBB2	p.D769H	17	37880261	G	C	Missense_Mutation	379	16.6%	Yes	Yes	100%	0.33635	100.0%	93.4%	Clonal	D	Driver		D	likely_pathogenic	No	Yes	Yes	WES
18DCIS	ERBB2	p.D769H	17	37880261	G	C	Missense_Mutation	631	16.8%	Yes	Yes	100%	0.33396	100.0%	95.8%	Clonal	D	Driver		D	likely_pathogenic	No	Yes	Yes	WES
18IDC	ERBB2	p.D904N	17	37881640	G	A	Missense_Mutation	996	17.9%	No	Yes	100%	0.37275	100.0%	97.5%	Clonal	D	Passenger		D	likely_pathogenic	No	Yes	Yes	WES
18DCIS	ERBB2	p.D904N	17	37881640	G	A	Missense_Mutation	1440	16.6%	No	Yes	100%	0.20759	100.0%	98.0%	Clonal	D	Passenger		D	likely_pathogenic	No	Yes	Yes	WES
18IDC	KRT15	p.R202C	17	39673194	G	A	Missense_Mutation	166	0.6%	No	Yes	5%	0	25.3%	0.7%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
18DCIS	KRT15	p.R202C	17	39673194	G	A	Missense_Mutation	131	5.3%	No	Yes	20%	0	39.8%	9.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
18IDC	GPATCH8	p.R1023Q	17	42476377	C	T	Missense_Mutation	59	15.3%	No	Yes	NA	0	100.0%	0.0%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
18IDC	HEXDC	p.R327C	17	80397586	C	T	Missense_Mutation	175	14.9%	No	No	100%	0.89302	100.0%	70.3%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
18DCIS	SERPINB13	p.F201L	18	61261717	T	C	Missense_Mutation	103	21.4%	No	No	100%	0.81786	100.0%	64.1%	Clonal	D	Passenger		D	likely_pathogenic	No	No	No	WES
18IDC	ZNF407	p.S586C	18	72344732	C	G	Missense_Mutation	85	14.1%	No	No	100%	0.83196	100.0%	55.2%	Clonal	N	Passenger		T	passenger	No	No	No	WES
18DCIS	ZNF407	p.S586C	18	72344732	C	G	Missense_Mutation	102	19.6%	No	No	94%	0.76054	100.0%	59.1%	Clonal	N	Passenger		T	passenger	No	No	No	WES
18IDC	SPTBN4	p.A2141V	19	41073654	C	T	Missense_Mutation	142	12.0%	No	No	82%	0.75208	98.6%	50.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	SPTBN4	p.A2141V	19	41073654	C	T	Missense_Mutation	202	5.9%	No	No	23%	0	37.8%	12.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
18IDC	PCSK2	p.E90K	20	17240975	G	A	Missense_Mutation	47	8.5%	No	No	75%	0.63296	98.2%	26.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	PCSK2	p.E90K	20	17240975	G	A	Missense_Mutation	59	25.4%	No	No	100%	0.91762	100.0%	69.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	CDH26	p.E267K	20	58560146	G	A	Missense_Mutation	142	5.6%	No	No	38%	0.00762	72.2%	19.3%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
18IDC	HSPA13	p.Q93E	21	15753613	G	C	Missense_Mutation	41	7.3%	No	No	65%	0.5684	97.7%	20.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	HSPA13	p.Q93E	21	15753613	G	C	Missense_Mutation	104	7.7%	No	No	37%	0.00328	68.7%	18.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
18IDC	HSPA13	p.S10L	21	15753861	G	A	Missense_Mutation	43	16.3%	No	No	100%	0.85548	100.0%	49.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	HSPA13	p.S10L	21	15753861	G	A	Missense_Mutation	104	9.6%	No	No	46%	0.02273	79.6%	25.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
18DCIS	ADAMTS5	p.R516C	21	28306928	G	A	Missense_Mutation	251	13.5%	No	No	65%	0.0379	87.1%	46.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
18DCIS	GPR119	p.S6L	23	129519405	G	A	Missense_Mutation	47	29.8%	No	Yes	100%	0.86278	100.0%	60.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18IDC	HCFC1	p.S2025C	23	153214832	G	C	Missense_Mutation	65	18.5%	No	Yes	100%	0.88854	100.0%	59.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
18DCIS	HCFC1	p.S2025C	23	153214832	G	C	Missense_Mutation	48	20.8%	No	Yes	79%	0.6654	98.4%	42.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	VWA5B1	p.P946A	1	20674812	C	G	Missense_Mutation	188	5.3%	No	No	20%	0	34.8%	10.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	PTPRU	p.G365Afs*8	1	29587362	GCACTGGCCGCCCTGGGCCACCCCTC	A	Frame_Shift_Del	140	11.4%	No	Yes	31%	0	47.7%	19.0%	Subclonal					likely_pathogenic	No	No	No	WES
19DCIS	PTPRU	p.G365Afs*8	1	29587362	GCACTGGCCGCCCTGGGCCACCCCTC	A	Frame_Shift_Del	76	25.0%	No	Yes	35%	0	49.3%	22.6%	Subclonal					likely_pathogenic	No	No	No	WES
19IDC	IPP	p.L187F	1	46206736	C	G	Missense_Mutation	100	40.0%	No	No	100%	0.88825	100.0%	88.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19DCIS	IPP	p.L187F	1	46206736	C	G	Missense_Mutation	131	51.1%	No	No	100%	0.92043	100.0%	92.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	IPP	p.L187S	1	46206737	A	G	Missense_Mutation	101	39.6%	No	No	100%	0.89618	100.0%	88.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19DCIS	IPP	p.L187S	1	46206737	A	G	Missense_Mutation	132	51.5%	No	No	100%	0.91159	100.0%	93.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	PRKAA2	p.S519Rfs*20	1	57173280	GCTCTTTGA	G	Frame_Shift_Del	176	8.0%	No	No	45%	0.0018	73.2%	27.0%	Subclonal					passenger	No	No	No	WES
19IDC	SLC25A24	p.L131P	1	108724569	A	G	Missense_Mutation	34	14.7%	No	Yes	40%	0.02259	80.5%	17.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	ANKRD35	p.N678Efs*82	1	145562342	CAAATGAACTGGCCATGG	C	Frame_Shift_Del	245	15.1%	No	No	56%	0.00011	74.2%	40.9%	Subclonal					passenger	No	No	No	WES
19DCIS	ANKRD35	p.N678Efs*82	1	145562342	CAAATGAACTGGCCATGG	C	Frame_Shift_Del	211	27.0%	No	No	65%	0.00019	79.3%	50.8%	Subclonal					passenger	No	No	No	WES
19IDC	SLC27A3	p.S400C	1	153750258	C	G	Missense_Mutation	161	4.3%	No	No	16%	0	31.8%	7.5%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
19IDC	OR6N1	p.G147C	1	158736034	C	A	Missense_Mutation	170	5.3%	No	No	25%	0	45.5%	12.9%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
19IDC	ATP1A2	p.G601C	1	160100361	G	T	Missense_Mutation	281	18.1%	No	No	85%	0.44054	98.6%	65.4%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
19DCIS	ATP1A2	p.G601C	1	160100361	G	T	Missense_Mutation	283	25.8%	No	No	87%	0.59921	98.7%	70.5%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
19IDC	GPR52	p.L102F	1	174417553	C	T	Missense_Mutation	58	41.4%	No	No	100%	0.78603	100.0%	78.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	GPR52	p.L102F	1	174417553	C	T	Missense_Mutation	63	49.2%	No	No	100%	0.88809	100.0%	77.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	RASAL2	p.L964I	1	178427317	C	A	Missense_Mutation	176	4.0%	No	No	15%	0	29.1%	6.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	QSOX1	p.S6G	1	180124058	A	G	Missense_Mutation	121	22.3%	No	No	83%	0.42046	98.5%	57.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	QSOX1	p.S6G	1	180124058	A	G	Missense_Mutation	106	42.5%	No	No	100%	0.85895	100.0%	76.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	KCNT2	p.S572C	1	196309540	T	A	Missense_Mutation	81	28.4%	No	No	100%	0.71191	100.0%	66.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	KCNT2	p.S572C	1	196309540	T	A	Missense_Mutation	66	48.5%	No	No	100%	0.88798	100.0%	77.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	DSTYK	p.K746N	1	205128675	C	A	Missense_Mutation	122	32.8%	No	No	100%	0.82718	100.0%	79.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19DCIS	DSTYK	p.K746N	1	205128675	C	A	Missense_Mutation	121	38.8%	No	No	93%	0.76245	100.0%	71.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	C1orf101	p.L10V	1	244624759	C	G	Missense_Mutation	137	3.6%	No	Yes	14%	0	30.1%	5.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	ADAM17	p.I131V	2	9676022	T	C	Missense_Mutation	94	25.5%	No	No	95%	0.62586	100.0%	62.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	ADAM17	p.I131V	2	9676022	T	C	Missense_Mutation	113	33.6%	No	No	80%	0.38431	97.2%	60.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	NCOA1	p.L483V	2	24929786	C	G	Missense_Mutation	83	13.3%	No	No	49%	0.01306	81.5%	27.7%	Subclonal	N	Passenger	N	T	passenger	No	Yes	No	WES
19IDC	KCNG3	p.M379V	2	42671250	T	C	Missense_Mutation	131	19.1%	No	No	90%	0.56011	100.0%	60.2%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
19DCIS	KCNG3	p.M379V	2	42671250	T	C	Missense_Mutation	139	28.1%	No	No	95%	0.78217	100.0%	69.5%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
19IDC	LHCGR	p.L268F	2	48925818	G	A	Missense_Mutation	102	25.5%	No	No	95%	0.62995	100.0%	63.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19DCIS	LHCGR	p.L268F	2	48925818	G	A	Missense_Mutation	80	41.3%	No	No	99%	0.81664	100.0%	70.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	USP34	p.R2558H	2	61450271	C	T	Missense_Mutation	99	22.2%	No	No	82%	0.42781	98.6%	54.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
19DCIS	USP34	p.R2558H	2	61450271	C	T	Missense_Mutation	101	36.6%	No	No	88%	0.64758	98.9%	65.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	AMMECR1L	p.R291*	2	128622730	G	A	Nonsense_Mutation	82	4.9%	No	Yes	13%	0	31.7%	4.9%	Subclonal	D				likely_pathogenic	No	No	No	WES
19IDC	HNMT	p.D37H	2	138722170	G	C	Missense_Mutation	63	11.1%	No	Yes	30%	0.00005	57.1%	14.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	WDR75	p.W275R	2	190327254	T	C	Missense_Mutation	148	8.8%	No	No	33%	0	53.1%	18.9%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
19IDC	HIBCH	p.R101T	2	191159274	C	G	Missense_Mutation	44	20.5%	No	No	76%	0.3694	98.2%	39.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
19DCIS	HIBCH	p.R101T	2	191159274	C	G	Missense_Mutation	56	42.9%	No	No	100%	0.82031	100.0%	68.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	RBMS3	p.D398H	3	30032585	G	C	Missense_Mutation	78	14.1%	No	Yes	52%	0.02809	85.7%	29.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	RBMS3	p.D398H	3	30032585	G	C	Missense_Mutation	82	37.8%	No	Yes	90%	0.71107	100.0%	65.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	ZNF620	p.L345F	3	40558120	A	C	Missense_Mutation	136	8.8%	No	Yes	24%	0	39.6%	13.4%	Subclonal	N	Passenger	N	T	passenger	No	No	Yes	WES
19DCIS	ZNF620	p.L345F	3	40558120	A	C	Missense_Mutation	131	0.8%	No	Yes	1%	0	5.4%	0.1%	Subclonal	N	Passenger	N	T	passenger	No	No	Yes	WES
19IDC	UQCRC1	p.R442G	3	48637122	G	C	Missense_Mutation	82	29.3%	No	Yes	79%	0.39572	97.9%	54.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
19DCIS	UQCRC1	p.R442G	3	48637122	G	C	Missense_Mutation	45	82.2%	No	Yes	100%	0.94359	100.0%	85.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	TIPARP	p.P102A	3	156395790	C	G	Missense_Mutation	174	0.6%	No	No	3%	0	14.4%	0.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	TIPARP	p.P102A	3	156395790	C	G	Missense_Mutation	232	3.4%	No	No	12%	0	22.0%	5.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	SPATA16	p.X253_splice	3	172766738	C	T	Splice_Site	101	25.7%	No	No	100%	0.78768	100.0%	77.0%	Clonal	D				passenger	No	No	No	WES
19DCIS	SPATA16	p.X253_splice	3	172766738	C	T	Splice_Site	122	27.0%	No	No	100%	0.8751	100.0%	75.9%	Clonal	D				passenger	No	No	No	WES
19DCIS	MUC20	p.A467T	3	195452873	G	A	Missense_Mutation	122	0.8%	No	Yes	1%	0	5.8%	0.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	LGI2	p.A34G	4	25032215	G	C	Missense_Mutation	93	47.3%	No	Yes	100%	0.85647	100.0%	84.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	LGI2	p.A34G	4	25032215	G	C	Missense_Mutation	53	84.9%	No	Yes	100%	0.93206	100.0%	88.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	MAPK10	p.P416L	4	86950355	G	A	Missense_Mutation	54	7.4%	No	No	18%	0	41.5%	6.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	STOX2	p.E908K	4	184938378	G	A	Missense_Mutation	135	4.4%	No	Yes	12%	0	24.9%	5.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	BRD9	p.R311G	5	884088	G	C	Missense_Mutation	277	18.4%	No	No	87%	0.48065	98.8%	66.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	BRD9	p.R311G	5	884088	G	C	Missense_Mutation	257	26.5%	No	No	90%	0.68753	100.0%	71.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	TRIO	p.D2835Y	5	14504593	G	T	Missense_Mutation	223	9.4%	No	Yes	35%	0	51.4%	22.7%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
19IDC	ADAMTS12	p.W545L	5	33641999	C	A	Missense_Mutation	155	3.2%	No	Yes	12%	0	26.7%	4.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	MROH2B	p.L525I	5	41048537	A	T	Missense_Mutation	116	27.6%	No	No	100%	0.72711	100.0%	70.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	MROH2B	p.L525I	5	41048537	A	T	Missense_Mutation	124	43.5%	No	No	100%	0.88616	100.0%	79.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	ZSWIM6	p.X611_splice	5	60822216	AAAAAAAGGTGAATGTG	A	Splice_Site	50	6.0%	No	Yes	16%	0	43.5%	5.4%	Subclonal					likely_pathogenic	No	No	No	WES
19DCIS	ZSWIM6	p.X611_splice	5	60822216	AAAAAAAGGTGAATGTG	A	Splice_Site	27	22.2%	No	Yes	31%	0	56.4%	14.3%	Subclonal					likely_pathogenic	No	No	No	WES
19IDC	ZBED3	p.L133M	5	76373307	G	T	Missense_Mutation	94	5.3%	No	Yes	14%	0	31.6%	5.9%	Subclonal	N	Passenger	N		passenger	No	No	No	WES
19IDC	ACSL6	p.H513Y	5	131303692	G	A	Missense_Mutation	53	24.5%	No	Yes	66%	0.19413	95.0%	39.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	ACSL6	p.H513Y	5	131303692	G	A	Missense_Mutation	51	66.7%	No	Yes	93%	0.79991	100.0%	72.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	SHROOM1	p.P782L	5	132158702	G	A	Missense_Mutation	100	7.0%	No	Yes	10%	0	18.6%	4.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	HNRNPH1	p.N382I	5	179043932	T	A	Missense_Mutation	91	6.6%	No	Yes	18%	0	36.5%	7.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	HNRNPH1	p.L381F	5	179043934	C	G	Missense_Mutation	92	6.5%	No	Yes	18%	0	36.1%	7.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	POU5F1	p.N214D	6	31133365	T	C	Missense_Mutation	228	0.4%	No	Yes	2%	0	8.5%	0.1%	Subclonal	D	Passenger	N	T	passenger	No	Yes	No	WES
19DCIS	POU5F1	p.N214D	6	31133365	T	C	Missense_Mutation	215	3.7%	No	Yes	9%	0	16.7%	4.1%	Subclonal	D	Passenger	N	T	passenger	No	Yes	No	WES
19IDC	TRERF1	p.Q313E	6	42236392	G	C	Missense_Mutation	279	1.8%	No	No	7%	0	14.8%	2.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	TRERF1	p.Q313E	6	42236392	G	C	Missense_Mutation	288	11.5%	No	No	27%	0	36.9%	19.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	TDRD6	p.T693R	6	46657943	C	G	Missense_Mutation	82	28.0%	No	Yes	76%	0.30632	97.0%	52.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	TDRD6	p.T693R	6	46657943	C	G	Missense_Mutation	85	77.6%	No	Yes	100%	0.95641	100.0%	88.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	KCNQ5	p.A329P	6	73815046	G	C	Missense_Mutation	54	25.9%	No	No	96%	0.59462	100.0%	55.2%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
19DCIS	KCNQ5	p.A329P	6	73815046	G	C	Missense_Mutation	74	33.8%	No	No	81%	0.49028	98.0%	56.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
19IDC	PNISR	p.Q17K	6	99862487	G	T	Missense_Mutation	52	17.3%	No	No	64%	0.20125	96.1%	34.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	PNISR	p.Q17K	6	99862487	G	T	Missense_Mutation	60	40.0%	No	No	96%	0.76917	100.0%	65.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	C6orf203	p.T132S	6	107361343	A	T	Missense_Mutation	92	18.5%	No	No	69%	0.16495	95.4%	43.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	C6orf203	p.T132S	6	107361343	A	T	Missense_Mutation	91	42.9%	No	No	100%	0.85576	100.0%	74.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	GINM1	p.T66A	6	149893658	A	G	Missense_Mutation	54	53.7%	No	Yes	100%	0.93858	100.0%	84.5%	Clonal	D	Passenger	D		passenger	No	No	No	WES
19DCIS	GINM1	p.T66A	6	149893658	A	G	Missense_Mutation	56	89.3%	No	Yes	100%	0.96208	100.0%	92.4%	Clonal	D	Passenger	D		passenger	No	No	No	WES
19IDC	ARID1B	p.V1684Efs*4	6	157527320	TTTTAGTCGAGTAC	T	Frame_Shift_Del	90	21.1%	No	Yes	57%	0.01061	82.5%	37.3%	Subclonal					likely_pathogenic	No	Yes	No	WES
19DCIS	ARID1B	p.V1684Efs*4	6	157527320	TTTTAGTCGAGTAC	T	Frame_Shift_Del	73	63.0%	No	Yes	88%	0.58622	98.3%	70.9%	Clonal					likely_pathogenic	No	Yes	No	WES
19IDC	BBS9	p.A65D	7	33192394	C	A	Missense_Mutation	76	6.6%	No	No	24%	0.00005	53.3%	10.3%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
19IDC	MAGI2	p.M1188K	7	77755015	A	T	Missense_Mutation	92	33.7%	No	No	100%	0.80702	100.0%	77.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19DCIS	MAGI2	p.M1188K	7	77755015	A	T	Missense_Mutation	105	36.2%	No	No	86%	0.616	98.8%	65.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	ZNF655	p.E21K	7	99158243	G	A	Missense_Mutation	117	7.7%	No	Yes	21%	0	37.4%	10.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	KCNH2	p.S1137_L1145del	7	150642497	GAGGGCCCCCAGCTGGCCCGGTAGGG	T	In_Frame_Del	140	11.4%	No	No	42%	0.00007	65.5%	26.1%	Subclonal					passenger	No	No	No	WES
19DCIS	KCNH2	p.S1137_L1145del	7	150642497	GAGGGCCCCCAGCTGGCCCGGTAGGG	T	In_Frame_Del	91	17.6%	No	No	42%	0.00002	63.3%	26.1%	Subclonal					passenger	No	No	No	WES
19IDC	ATG9B	p.Q690Tfs*3	7	150714345	T	TC	Frame_Shift_Ins	134	24.6%	No	No	91%	0.59656	100.0%	65.1%	Clonal					passenger	No	No	No	WES
19DCIS	ATG9B	p.Q690Tfs*3	7	150714345	T	TC	Frame_Shift_Ins	117	35.9%	No	No	86%	0.58317	98.6%	65.5%	Clonal					passenger	No	No	No	WES
19IDC	MNX1	p.M221L	7	156802384	T	G	Missense_Mutation	150	10.7%	No	No	40%	0.00001	61.2%	24.3%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
19IDC	BAI1	p.Q343K	8	143558026	C	A	Missense_Mutation	238	15.5%	No	No	73%	0.11853	94.6%	53.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	BAI1	p.Q343K	8	143558026	C	A	Missense_Mutation	261	18.4%	No	No	81%	0.40947	97.5%	61.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	MAFA	p.H184Q	8	144512025	G	T	Missense_Mutation	396	15.9%	No	No	75%	0.05274	92.4%	59.0%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
19DCIS	MAFA	p.H184Q	8	144512025	G	T	Missense_Mutation	436	10.1%	No	No	44%	0	57.8%	32.9%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
19IDC	EPPK1	p.P2358A	8	144940350	G	C	Missense_Mutation	4243	2.6%	No	No	15%	0	17.2%	11.6%	Subclonal	D	Passenger		T	passenger	Yes	No	No	WES
19DCIS	EPPK1	p.P2358A	8	144940350	G	C	Missense_Mutation	5795	2.8%	No	No	15%	0	17.1%	12.4%	Subclonal	D	Passenger		T	passenger	Yes	No	No	WES

19IDC	EPPK1	p.L599M	8	144945627	G	T	Missense_Mutation	326	14.7%	No	No	84%	0.40615	98.5%	63.6%	Subclonal	N	Passenger		T	passenger	Yes	No	No	WES
19DCIS	EPPK1	p.L599M	8	144945627	G	T	Missense_Mutation	433	17.1%	No	No	92%	0.75086	100.0%	73.2%	Clonal	N	Passenger		T	passenger	Yes	No	No	WES
19IDC	FOXB2	p.A253T	9	79635327	G	A	Missense_Mutation	55	5.5%	No	Yes	15%	0	39.8%	4.9%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
19DCIS	FOXB2	p.A253T	9	79635327	G	A	Missense_Mutation	51	19.6%	No	Yes	27%	0	44.7%	14.9%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
19IDC	NUTM2F	p.P346A	9	97082822	G	C	Missense_Mutation	302	28.5%	No	Yes	77%	0.02746	91.0%	63.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	NUTM2F	p.P346A	9	97082822	G	C	Missense_Mutation	209	74.2%	No	Yes	100%	0.96655	100.0%	91.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	HIATL1	p.R226T	9	97207412	G	C	Missense_Mutation	76	2.6%	No	Yes	7%	0	24.1%	1.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
19DCIS	HIATL1	p.R226T	9	97207412	G	C	Missense_Mutation	48	25.0%	No	Yes	35%	0	53.5%	20.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	OR13D1	p.L71I	9	107456913	C	A	Missense_Mutation	59	8.5%	No	Yes	23%	0.00001	49.3%	9.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	OR1L6	p.L246Rfs*15	9	125512862	CTCACT	C	Frame_Shift_Del	93	1.1%	No	Yes	3%	0	15.2%	0.3%	Subclonal					likely_pathogenic	No	No	No	WES
19DCIS	OR1L6	p.L246Rfs*15	9	125512862	CTCACT	C	Frame_Shift_Del	142	9.2%	No	Yes	13%	0	20.4%	7.1%	Subclonal					likely_pathogenic	No	No	No	WES
19IDC	PRTFDC1	p.A186V	10	25140390	G	A	Missense_Mutation	112	11.6%	No	No	66%	0.19145	95.9%	38.9%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
19DCIS	PRTFDC1	p.A186V	10	25140390	G	A	Missense_Mutation	110	8.2%	No	No	36%	0.00069	64.6%	18.8%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
19IDC	ARHGAP22	p.E371_R377del	10	49659087	CCGCGCGGGGAGGTGGGCCCTT	C	In_Frame_Del	154	5.8%	No	Yes	16%	0	28.6%	8.0%	Subclonal					potentially_pathogen	No	No	No	WES
19DCIS	ARHGAP22	p.E371_R377del	10	49659087	CCGCGCGGGGAGGTGGGCCCTT	C	In_Frame_Del	58	29.3%	No	Yes	41%	0	57.9%	26.1%	Subclonal					potentially_pathogen	No	No	No	WES
19IDC	ERCC6	p.Q254E	10	50732716	G	C	Missense_Mutation	185	5.4%	No	Yes	15%	0	25.7%	7.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	NLRP6	p.E595Q	11	281517	G	C	Missense_Mutation	157	6.4%	No	Yes	17%	0	30.2%	9.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	DCHS1	p.F2738L	11	6644695	A	G	Missense_Mutation	168	4.2%	No	Yes	11%	0	22.1%	5.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	DKK3	p.C147_D150del	11	11990019	CGTCGATGATGCA	C	In_Frame_Del	89	18.0%	No	Yes	49%	0.00103	73.4%	30.4%	Subclonal					potentially_pathogen	No	No	No	WES
19DCIS	DKK3	p.C147_D150del	11	11990019	CGTCGATGATGCA	C	In_Frame_Del	56	50.0%	No	Yes	69%	0.01096	86.6%	51.3%	Subclonal					potentially_pathogen	No	No	No	WES
19IDC	GTF2H1	p.L127V	11	18359687	C	G	Missense_Mutation	40	7.5%	No	Yes	20%	0.00018	53.5%	6.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	LUZP2	p.R199W	11	24998209	A	T	Missense_Mutation	43	27.9%	No	Yes	76%	0.40172	97.9%	44.2%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
19DCIS	LUZP2	p.R199W	11	24998209	A	T	Missense_Mutation	36	75.0%	No	Yes	100%	0.90809	100.0%	77.0%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
19IDC	OR4S1	p.L142V	11	48328198	C	G	Missense_Mutation	157	7.6%	No	No	28%	0	47.3%	16.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	IFLTD1	p.I76N	12	25702343	A	T	Missense_Mutation	59	8.5%	No	No	23%	0.00001	49.3%	9.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	SPATS2	p.K417N	12	49918604	G	C	Missense_Mutation	138	3.6%	No	No	13%	0	29.9%	5.4%	Subclonal	D	Passenger	N		passenger	No	No	No	WES
19IDC	KCNH3	p.T773K	12	49949584	C	A	Missense_Mutation	145	4.1%	No	No	15%	0	31.9%	6.7%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
19IDC	ITGA7	p.W1064C	12	56081758	C	A	Missense_Mutation	168	27.4%	No	No	100%	0.75677	100.0%	74.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19DCIS	ITGA7	p.W1064C	12	56081758	C	A	Missense_Mutation	187	44.4%	No	No	100%	0.91891	100.0%	84.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	ITGA7	p.V481I	12	56091311	C	T	Missense_Mutation	100	24.0%	No	No	89%	0.54804	100.0%	59.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	ITGA7	p.V481I	12	56091311	C	T	Missense_Mutation	91	36.3%	No	No	87%	0.63072	98.8%	63.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	GDF11	p.G215del	12	56142560	GGGC	G	In_Frame_Del	115	30.4%	No	No	100%	0.79662	100.0%	75.5%	Clonal					passenger	No	No	No	WES
19DCIS	GDF11	p.G215del	12	56142560	GGGC	G	In_Frame_Del	52	63.5%	No	No	88%	0.67175	98.7%	68.4%	Clonal					passenger	No	No	No	WES
19IDC	C12orf55	p.E1325K	12	97019582	G	A	Missense_Mutation	71	25.4%	No	No	94%	0.59674	100.0%	58.2%	Clonal	D	Passenger	N		passenger	No	No	No	WES
19DCIS	C12orf55	p.E1325K	12	97019582	G	A	Missense_Mutation	80	45.0%	No	No	100%	0.87501	100.0%	76.2%	Clonal	D	Passenger	N		passenger	No	No	No	WES
19IDC	TMEM132B	p.V283Afs*6	12	125834792	GT	G	Frame_Shift_Del	160	29.4%	No	No	100%	0.81046	100.0%	78.0%	Clonal					passenger	No	No	No	WES
19DCIS	TMEM132B	p.V283Afs*6	12	125834792	GT	G	Frame_Shift_Del	141	41.1%	No	No	98%	0.84755	100.0%	77.1%	Clonal					passenger	No	No	No	WES
19IDC	RFC3	p.T141P	13	34404002	A	C	Missense_Mutation	37	48.6%	No	Yes	100%	0.81854	100.0%	71.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19DCIS	RFC3	p.T141P	13	34404002	A	C	Missense_Mutation	40	67.5%	No	Yes	94%	0.81705	100.0%	70.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19DCIS	SPACA7	p.P107T	13	113053457	C	A	Missense_Mutation	41	9.8%	No	Yes	23%	0.00008	53.5%	9.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	ATP4B	p.S133F	13	114307345	G	A	Missense_Mutation	178	53.4%	No	Yes	100%	0.96456	100.0%	94.5%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
19DCIS	ATP4B	p.S133F	13	114307345	G	A	Missense_Mutation	169	88.2%	No	Yes	100%	0.9577	100.0%	97.2%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
19IDC	CDH24	p.V140L	14	23524346	C	G	Missense_Mutation	249	24.9%	No	No	92%	0.63409	100.0%	72.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	CDH24	p.V140L	14	23524346	C	G	Missense_Mutation	207	41.5%	No	No	99%	0.8777	100.0%	81.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	AKAP6	p.T1669P	14	33292024	A	C	Missense_Mutation	91	28.6%	No	No	100%	0.72985	100.0%	68.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	AKAP6	p.T1669P	14	33292024	A	C	Missense_Mutation	92	39.1%	No	No	93%	0.76541	100.0%	69.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	RALGAPA1	p.S721R	14	36190997	A	C	Missense_Mutation	51	23.5%	No	No	87%	0.50244	98.9%	49.0%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
19DCIS	RALGAPA1	p.S721R	14	36190997	A	C	Missense_Mutation	73	34.2%	No	No	82%	0.52341	98.3%	57.3%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
19IDC	CCDC175	p.A281E	14	60030456	G	T	Missense_Mutation	53	7.5%	No	Yes	20%	0.00001	48.0%	7.8%	Subclonal	N	Passenger	N		passenger	No	No	No	WES
19DCIS	CCDC175	p.A281E	14	60030456	G	T	Missense_Mutation	42	2.4%	No	Yes	3%	0	16.6%	0.4%	Subclonal	N	Passenger	N		passenger	No	No	No	WES
19IDC	ESR2	p.E66K	14	64749508	C	T	Missense_Mutation	54	42.6%	No	Yes	100%	0.8207	100.0%	71.7%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
19DCIS	ESR2	p.E66K	14	64749508	C	T	Missense_Mutation	32	81.3%	No	Yes	100%	0.93027	100.0%	80.5%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
19IDC	PLEKHD1	p.X185_splice	14	69969598	T	C	Splice_Site	116	44.8%	No	Yes	100%	0.88476	100.0%	84.3%	Clonal	D				likely_pathogenic	No	No	No	WES
19DCIS	PLEKHD1	p.X185_splice	14	69969598	T	C	Splice_Site	73	80.8%	No	Yes	100%	0.95443	100.0%	89.1%	Clonal	D				likely_pathogenic	No	No	No	WES
19IDC	CIPC	p.S42C	14	77572176	C	G	Missense_Mutation	91	4.4%	No	Yes	12%	0	28.7%	4.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	KIF26A	p.R1566G	14	104643821	C	G	Missense_Mutation	100	42.0%	No	Yes	100%	0.86897	100.0%	79.7%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
19DCIS	KIF26A	p.R1566G	14	104643821	C	G	Missense_Mutation	66	84.8%	No	Yes	100%	0.91704	100.0%	90.3%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
19IDC	GCNT3	p.N404Y	15	59911647	A	T	Missense_Mutation	73	5.5%	No	Yes	15%	0	35.5%	5.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	GCNT3	p.N404Y	15	59911647	A	T	Missense_Mutation	54	16.7%	No	Yes	23%	0	39.5%	12.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	SNX1	p.Q424P	15	64426912	A	C	Missense_Mutation	144	0.7%	No	Yes	2%	0	9.8%	0.1%	Subclonal	D	Passenger	D		passenger	No	No	No	WES
19DCIS	SNX1	p.Q424P	15	64426912	A	C	Missense_Mutation	86	8.1%	No	Yes	11%	0	21.6%	5.1%	Subclonal	D	Passenger	D		passenger	No	No	No	WES
19IDC	KBTBD13	p.V64G	15	65369344	T	G	Missense_Mutation	111	4.5%	No	Yes	17%	0	37.0%	6.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	IGDCC4	p.V668E	15	65684591	A	T	Missense_Mutation	247	5.7%	No	Yes	21%	0	34.0%	12.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	IGDCC4	p.V668E	15	65684591	A	T	Missense_Mutation	175	0.6%	No	Yes	1%	0	7.0%	0.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	SCAPER	p.L728V	15	76998309	A	C	Missense_Mutation	58	24.1%	No	Yes	90%	0.53347	100.0%	52.4%	Clonal	N	Driver	N	T	likely_pathogenic	No	No	No	WES
19DCIS	SCAPER	p.L728V	15	76998309	A	C	Missense_Mutation	92	46.7%	No	Yes	100%	0.89894	100.0%	80.0%	Clonal	N	Driver	N	T	likely_pathogenic	No	No	No	WES
19IDC	PEAK1	p.R166T	15	77473772	C	G	Missense_Mutation	145	22.8%	No	Yes	84%	0.44533	98.7%	60.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	PEAK1	p.R166T	15	77473772	C	G	Missense_Mutation	133	42.1%	No	Yes	100%	0.86634	100.0%	78.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	PEAK1	p.A157T	15	77473800	C	T	Missense_Mutation	151	22.5%	No	Yes	84%	0.41819	98.5%	60.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	PEAK1	p.A157T	15	77473800	C	T	Missense_Mutation	129	41.1%	No	Yes	98%	0.84146	100.0%	76.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	IL16	p.S13C	15	81517778	C	G	Missense_Mutation	115	6.1%	No	Yes	23%	0	44.2%	10.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	TRAF7	p.E324D	16	2223360	G	C	Missense_Mutation	137	4.4%	No	Yes	16%	0	33.7%	7.1%	Subclonal	D	Passenger	N	T	passenger	No	Yes	No	WES
19IDC	PPL	p.K1638Q	16	4933744	T	G	Missense_Mutation	337	20.8%	No	Yes	98%	0.7422	100.0%	76.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	PPL	p.K1638Q	16	4933744	T	G	Missense_Mutation	351	30.2%	No	Yes	100%	0.90349	100.0%	83.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	ITGAD	p.L1114V	16	31435866	C	G	Missense_Mutation	66	22.7%	No	No	84%	0.47087	98.8%	50.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	ITGAD	p.L1114V	16	31435866	C	G	Missense_Mutation	80	38.8%	No	No	93%	0.7469	100.0%	66.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	N4BP1	p.L381V	16	48595413	A	C	Missense_Mutation	80	1.3%	No	Yes	3%	0	17.7%	0.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	N4BP1	p.L381V	16	48595413	A	C	Missense_Mutation	77	7.8%	No	Yes	11%	0	21.7%	4.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	SNX20	p.T45P	16	50709830	T	G	Missense_Mutation	87	6.9%	No	Yes	19%	0	38.1%	8.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	SNX20	p.T45P	16	50709830	T	G	Missense_Mutation	61	36.1%	No	Yes	50%	0	67.1%	34.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	CBFB	p.G121Afs*14	16	67100662	GTATGGGCTGTCTGGAGTTTGATGAG	T	Frame_Shift_Del	34	5.9%	No	Yes	16%	0.00023	51.4%	4.4%	Subclonal					likely_pathogenic	Yes	Yes	Yes	WES
19IDC	ACD	p.M11I	16	67694349	C	T	Missense_Mutation	155	17.4%	No	Yes	65%	0.03009	88.6%	45.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	ACD	p.M11I	16	67694349	C	T	Missense_Mutation	104	35.6%	No	Yes	100%	0.88899	100.0%	78.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	HYDIN	p.L4515R	16	70867925	A	C	Missense_Mutation	49	8.2%	No	Yes	22%	0.00004	51.6%	8.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
19DCIS	MYBBP1A	p.Q914H	17	4446358	C	A	Missense_Mutation	185	9.7%	No	Yes	23%	0	35.0%	14.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	RABEP1	p.E747Kfs*8	17	5281494	TGAATTAGAAAGAATAAAAGTGGAAA	T	Frame_Shift_Del	58	8.6%	No	Yes	32%	0.00268	68.7%	13.7%	Subclonal					likely_pathogenic	No	Yes	No	WES
19DCIS	RABEP1	p.E747Kfs*8	17	5281494	TGAATTAGAAAGAATAAAAGTGGAAA	T	Frame_Shift_Del	63	6.3%	No	Yes	15%	0	35.9%	5.6%	Subclonal					likely_pathogenic	No	Yes	No	WES
19IDC	SHBG	p.L328V	17	7536199	C	G	Missense_Mutation	104	31.7%	No	Yes	100%	0.80439	100.0%	76.2%	Clonal	N	Passenger		T	passenger	No	No	No	WES
19DCIS	SHBG	p.L328V	17	7536199	C	G	Missense_Mutation	83	37.3%	No	Yes	89%	0.69093	100.0%	64.6%	Clonal	N	Passenger		T	passenger	No	No	No	WES
19IDC	TP53	p.R306*	17	7577022	G	A	Nonsense_Mutation	228	55.3%	No	Yes	100%	0.96628	100.0%	96.0%	Clonal	A				likely_pathogenic	Yes	Yes	Yes	WES
19DCIS	TP53	p.R306*	17	7577022	G	A	Nonsense_Mutation	188	81.9%	No	Yes	100%	0.9838	100.0%	97.1%	Clonal	A				likely_pathogenic	Yes	Yes	Yes	WES
19IDC	DNAH2	p.S2687C	17	7700827	A	T	Missense_Mutation	145	35.2%	No	Yes	100%	0.7963	100.0%	84.7%	Clonal	D	Passenger		T	passenger	No	No	No	WES
19DCIS	DNAH2	p.S2687C	17	7700827	A	T	Missense_Mutation	165	43.6%	No	Yes	100%	0.9038	100.0%	82.4%	Clonal	D	Passenger		T	passenger	No	No	No	WES
19IDC	DNAH2	p.S2687I	17	7700828	G	T	Missense_Mutation	146	34.9%	No	Yes	100%	0.80541	100.0%	84.5%	Clonal	D	Passenger		T	passenger	No	No	No	WES
19DCIS	DNAH2	p.S2687I	17	7700828	G	T	Missense_Mutation	163	43.6%	No	Yes	100%	0.9021	100.0%	82.2%	Clonal	D	Passenger		T	passenger	No	No	No	WES
19IDC	DNAH9	p.Y4175N	17	11840702	T	A	Missense_Mutation	240	4.2%	No	Yes	15%	0	27.3%	8.0%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
19DCIS	DNAH9	p.Y4175N	17	11840702	T	A	Missense_Mutation	194	7.2%	No	Yes	17%	0	27.6%	9.9%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
19IDC	G6PC	p.V308I	17	41063291	G	A	Missense_Mutation	198	5.6%	No	Yes	21%	0	35.4%	11.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	G6PC	p.V308I	17	41063291	G	A	Missense_Mutation	170	1.2%	No	Yes	3%	0	9.5%	0.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	CACNG5	p.D208H	17	64881151	G	C	Missense_Mutation	147	1.4%	No	Yes	5%	0	17.3%	1.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	CACNG5	p.D208H	17	64881151	G	C	Missense_Mutation	136	8.1%	No	Yes	19%	0	32.7%	10.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
19IDC	C17orf77	p.C95G	17	72588468	T	G	Missense_Mutation	176	14.2%	No	Yes	67%	0.07559	92.3%	45.7%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
19DCIS	C17orf77	p.C95G	17	72588468	T	G	Missense_Mutation	245	1.2%	No	Yes	4%	0	11.5%	1.0%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
19IDC	PTPRM	p.S1197C	18	8378389	A	T	Missense_Mutation	103	18.4%	No	No	68%	0.14102	94.8%	44.5%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
19DCIS	PTPRM	p.S1197C	18	8378389	A	T	Missense_Mutation	149	23.5%	No	No	56%	0.00006	73.4%	41.1%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
19IDC	CTIF	p.E273D	18	46284524	G	C	Missense_Mutation	488	14.5%	No	No	98%	0.73341	100.0%	75.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	CTIF	p.E273D	18	46284524	G	C	Missense_Mutation	490	19.4%	No	No	100%	0.90163	100.0%	82.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
19DCIS	DOT1L	p.P1297S	19	2226409	C	T	Missense_Mutation	144	6.9%	No	Yes	10%	0	16.6%	4.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	ATP4A	p.T726K	19	36046217	G	T	Missense_Mutation	259	6.6%	No	No	24%	0	37.6%	14.9%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
19DCIS	ATP4A	p.T726K	19	36046217	G	T	Missense_Mutation	238	0.4%	No	No	1%	0	5.1%	0.1%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
19IDC	RYR1	p.K4699M	19	39063914	A	T	Missense_Mutation	218	26.6%	No	No	99%	0.74578	100.0%	75.6%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
19DCIS	RYR1	p.K4699M	19	39063914	A	T	Missense_Mutation	202	43.6%	No	No	100%	0.9134	100.0%	84.2%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
19IDC	ZNF473	p.H509Nfs*15	19	50549221	AATGCACACTGTCAAAACCCCAT	A	Frame_Shift_Del	133	4.5%	No	No	17%	0	34.7%	7.4%	Subclonal					passenger	No	No	No	WES
19DCIS	ZNF473	p.H509Nfs*15	19	50549221	AATGCACACTGTCAAAACCCCAT	A	Frame_Shift_Del	120	5.0%	No	No	12%	0	24.6%	5.1%	Subclonal					passenger	No	No	No	WES
19IDC	LENG1	p.D259N	19	54659479	C	T	Missense_Mutation	199	7.0%	No	No	26%	0	42.0%	15.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	ADNP	p.Y461C	20	49509869	T	C	Missense_Mutation	90	34.4%	No	Yes	93%	0.69661	100.0%	66.6%	Clonal	D	Driver	D		likely_pathogenic	No	No	Yes	WES
19DCIS	ADNP	p.Y461C	20	49509869	T	C	Missense_Mutation	73	78.1%	No	Yes	100%	0.95303	100.0%	87.3%	Clonal	D	Driver	D		likely_pathogenic	No	No	Yes	WES
19IDC	GRIK1	p.S93L	21	31066223	G	A	Missense_Mutation	37	18.9%	No	Yes	51%	0.07443	89.2%	25.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
19DCIS	GRIK1	p.S93L	21	31066223	G	A	Missense_Mutation	38	78.9%	No	Yes	100%	0.93119	100.0%	81.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19IDC	KRTAP24-1	p.K140Lfs*15	21	31654828	GGCTTT	G	Frame_Shift_Del	102	9.8%	No	Yes	27%	0	45.9%	14.3%	Subclonal					likely_pathogenic	No	No	No	WES
19IDC	TMPRSS3	p.T391K	21	43796672	G	T	Missense_Mutation	255	22.0%	No	No	81%	0.25977	97.3%	63.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	TMPRSS3	p.T391K	21	43796672	G	T	Missense_Mutation	194	43.8%	No	No	100%	0.91449	100.0%	84.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	PCNT	p.Q296E	21	47766822	C	G	Missense_Mutation	178	24.7%	No	No	92%	0.61186	100.0%	68.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	PCNT	p.Q296E	21	47766822	C	G	Missense_Mutation	150	46.0%	No	No	100%	0.92076	100.0%	84.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	PI4KA	p.Y2024C	22	21064999	T	C	Missense_Mutation	333	16.8%	No	No	62%	0.00016	78.2%	48.4%	Subclonal	D	Driver		T	likely_pathogenic	No	No	No	WES
19DCIS	PI4KA	p.Y2024C	22	21064999	T	C	Missense_Mutation	281	18.9%	No	No	45%	0	56.5%	34.6%	Subclonal	D	Driver		T	likely_pathogenic	No	No	No	WES
19IDC	NUP50	p.G75A	22	45571845	G	C	Missense_Mutation	121	23.1%	No	Yes	86%	0.48828	98.9%	59.9%	Subclonal	D	Passenger	D		passenger	No	No	No	WES
19DCIS	NUP50	p.G75A	22	45571845	G	C	Missense_Mutation	143	38.5%	No	Yes	92%	0.74585	100.0%	72.4%	Clonal	D	Passenger	D		passenger	No	No	No	WES
19IDC	SRPX	p.Y68Kfs*29	23	38033544	TGAGGGGCCCTGCAGTA	T	Frame_Shift_Del	103	12.6%	No	No	47%	0.00276	75.2%	27.5%	Subclonal					passenger	No	No	No	WES
19DCIS	SRPX	p.Y68Kfs*29	23	38033544	TGAGGGGCCCTGCAGTA	T	Frame_Shift_Del	139	12.2%	No	No	29%	0	44.3%	18.1%	Subclonal					passenger	No	No	No	WES
19IDC	KLHL4	p.T106I	23	86773213	C	T	Missense_Mutation	73	6.8%	No	Yes	19%	0	40.4%	7.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19DCIS	RBMXL3	p.Q195K	23	114424587	C	A	Missense_Mutation	94	5.3%	No	Yes	7%	0	16.0%	2.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
19IDC	GABRA3	p.L284M	23	151366186	A	T	Missense_Mutation	67	7.5%	No	Yes	20%	0	43.8%	8.4%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
19IDC	FAM3A	p.F179I	23	153735596	A	T	Missense_Mutation	184	30.4%	No	Yes	100%	0.84262	100.0%	81.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
19DCIS	FAM3A	p.F179I	23	153735596	A	T	Missense_Mutation	175	46.3%	No	Yes	100%	0.92912	100.0%	86.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	TTLL10	p.R17W	1	1114644	C	T	Missense_Mutation	115	30.4%	No	No	100%	0.66238	100.0%	82.7%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
21DCIS	TTLL10	p.R17W	1	1114644	C	T	Missense_Mutation	130	26.2%	No	No	68%	0.05195	89.1%	50.2%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
21IDC	TRIM63	p.S256Y	1	26384945	G	T	Missense_Mutation	166	10.2%	No	No	52%	0.0199	80.1%	32.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	TRIM63	p.S256Y	1	26384945	G	T	Missense_Mutation	137	0.7%	No	No	2%	0	9.9%	0.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	YTHDF2	p.S69Lfs*18	1	29068985	AT	A	Frame_Shift_Del	186	16.1%	No	No	82%	0.66872	98.5%	57.9%	Clonal					passenger	No	No	No	WES
21DCIS	YTHDF2	p.S69Lfs*18	1	29068985	AT	A	Frame_Shift_Del	165	8.5%	No	No	22%	0	35.5%	13.0%	Subclonal					passenger	No	No	No	WES
21IDC	TIE1	p.E243*	1	43772899	G	T	Nonsense_Mutation	198	30.8%	No	No	100%	0.96974	100.0%	90.5%	Clonal	D				passenger	No	No	No	WES
21DCIS	TIE1	p.E243*	1	43772899	G	T	Nonsense_Mutation	184	28.8%	No	No	100%	0.85262	100.0%	77.5%	Clonal	D				passenger	No	No	No	WES
21IDC	TIE1	p.S489I	1	43777474	G	T	Missense_Mutation	245	8.6%	No	No	52%	0.00519	77.4%	34.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	TRIM45	p.K461Gfs*96	1	117658281	CTT	C	Frame_Shift_Del	74	25.7%	No	No	100%	0.90617	100.0%	72.9%	Clonal					passenger	No	No	No	WES
21DCIS	TRIM45	p.K461Gfs*96	1	117658281	CTT	C	Frame_Shift_Del	77	26.0%	No	No	94%	0.69756	100.0%	59.9%	Clonal					passenger	No	No	No	WES
21IDC	FLG2	p.E222A	1	152329597	T	G	Missense_Mutation	116	5.2%	No	No	32%	0.00264	65.7%	14.4%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
21DCIS	FLG2	p.E222A	1	152329597	T	G	Missense_Mutation	163	0.6%	No	No	2%	0	11.7%	0.2%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
21IDC	DCST1	p.S691C	1	155023295	C	G	Missense_Mutation	160	33.8%	No	No	100%	0.96962	100.0%	90.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	DCST1	p.S691C	1	155023295	C	G	Missense_Mutation	199	22.1%	No	No	80%	0.34643	97.3%	60.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	FCGR2A	p.P262R	1	161487769	C	G	Missense_Mutation	98	17.3%	No	No	100%	0.78985	100.0%	60.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	FCGR2A	p.P262R	1	161487769	C	G	Missense_Mutation	123	25.2%	No	No	100%	0.84549	100.0%	74.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	F5	p.W152C	1	169529922	C	G	Missense_Mutation	153	19.6%	No	No	100%	0.86962	100.0%	73.9%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21DCIS	F5	p.W152C	1	169529922	C	G	Missense_Mutation	178	1.1%	No	No	5%	0	17.9%	1.1%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21IDC	WDR26	p.G9A	1	224621782	C	G	Missense_Mutation	386	18.7%	No	No	100%	0.78946	100.0%	87.2%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
21DCIS	WDR26	p.G9A	1	224621782	C	G	Missense_Mutation	541	15.3%	No	No	71%	0.00375	85.5%	57.5%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
21DCIS	ZNF672	p.R244Afs*186	1	249142202	GCCACCAGCGCACACACACGGGCGAG	G	Frame_Shift_Del	248	1.6%	No	No	7%	0	18.3%	2.5%	Subclonal					passenger	No	No	No	WES
21IDC	TPO	p.G255R	2	1459998	G	A	Missense_Mutation	214	30.8%	No	No	100%	0.97064	100.0%	91.2%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
21DCIS	TPO	p.G255R	2	1459998	G	A	Missense_Mutation	153	25.5%	No	No	92%	0.71001	100.0%	67.6%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
21IDC	SLC30A3	p.R306W	2	27479356	G	A	Missense_Mutation	165	28.5%	No	No	100%	0.94679	100.0%	87.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	SLC30A3	p.R306W	2	27479356	G	A	Missense_Mutation	149	29.5%	No	No	100%	0.85182	100.0%	76.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	BIRC6	p.T3567I	2	32740188	C	T	Missense_Mutation	77	29.9%	No	No	100%	0.95302	100.0%	78.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	BIRC6	p.T3567I	2	32740188	C	T	Missense_Mutation	77	24.7%	No	No	89%	0.64345	100.0%	56.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	GPR17	p.S44Pfs*31	2	128408354	CT	C	Frame_Shift_Del	65	7.7%	No	No	47%	0.1653	91.8%	20.2%	Subclonal					passenger	No	No	No	WES
21DCIS	GPR17	p.S44Pfs*31	2	128408354	CT	C	Frame_Shift_Del	69	20.3%	No	No	73%	0.38372	97.5%	44.3%	Subclonal					passenger	No	No	No	WES
21IDC	NEB	p.D4229H	2	152463182	C	G	Missense_Mutation	56	55.4%	No	No	100%	0.04245	100.0%	87.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	NEB	p.D4229H	2	152463182	C	G	Missense_Mutation	73	56.2%	No	No	100%	0.96276	100.0%	88.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	EVX2	p.E198K	2	176947013	C	T	Missense_Mutation	135	11.1%	No	No	68%	0.32109	96.1%	41.3%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21DCIS	EVX2	p.E198K	2	176947013	C	T	Missense_Mutation	142	2.1%	No	No	8%	0	21.3%	2.2%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21IDC	TTN	p.D29960H	2	179417749	C	G	Missense_Mutation	53	35.8%	No	No	100%	0.94402	100.0%	77.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	TTN	p.D29960H	2	179417749	C	G	Missense_Mutation	67	20.9%	No	No	76%	0.4292	97.9%	45.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	INO80D	p.G689R	2	206870111	C	T	Missense_Mutation	142	6.3%	No	No	39%	0.00391	70.4%	20.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	INO80D	p.G689R	2	206870111	C	T	Missense_Mutation	147	13.6%	No	No	49%	0.00062	72.2%	32.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	AAMP	p.X41_splice	2	219134258	C	G	Splice_Site	211	3.3%	No	No	20%	0	40.4%	9.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	AAMP	p.X41_splice	2	219134258	C	G	Splice_Site	262	15.6%	No	No	57%	0.00008	73.9%	42.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	IRAK2	p.F210L	3	10254992	C	A	Missense_Mutation	178	7.3%	No	No	52%	0.04294	84.6%	30.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	IRAK2	p.F210L	3	10254992	C	A	Missense_Mutation	162	1.2%	No	No	4%	0	15.3%	0.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	ZNF860	p.E330Q	3	32031559	G	C	Missense_Mutation	658	35.9%	No	No	100%	0.45329	100.0%	97.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	ZNF860	p.E330Q	3	32031559	G	C	Missense_Mutation	521	28.6%	No	No	100%	0.91223	100.0%	86.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	PTPRG	p.E955K	3	62253483	G	A	Missense_Mutation	46	43.5%	No	Yes	100%	0.06248	100.0%	79.1%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
21DCIS	PTPRG	p.E955K	3	62253483	G	A	Missense_Mutation	58	46.6%	No	Yes	100%	0.89535	100.0%	76.2%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
21IDC	CCDC54	p.E161Q	3	107096915	G	C	Missense_Mutation	64	53.1%	No	Yes	100%	0.06625	100.0%	88.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	CCDC54	p.E161Q	3	107096915	G	C	Missense_Mutation	73	46.6%	No	Yes	100%	0.89646	100.0%	84.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	DNAJC13	p.A236V	3	132172311	C	T	Missense_Mutation	59	10.2%	No	Yes	62%	0.38131	96.8%	28.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	DNAJC13	p.A236V	3	132172311	C	T	Missense_Mutation	79	30.4%	No	Yes	100%	0.81206	100.0%	69.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	WDR49	p.L200F	3	167277905	G	A	Missense_Mutation	104	14.4%	No	No	100%	0.80594	100.0%	60.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	WDR49	p.L200F	3	167277905	G	A	Missense_Mutation	154	42.9%	No	No	100%	0.37996	100.0%	93.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	LRRIQ4	p.E406D	3	169548303	G	C	Missense_Mutation	74	1.4%	No	No	11%	0.00466	57.7%	2.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	LRRIQ4	p.E406D	3	169548303	G	C	Missense_Mutation	163	14.7%	No	No	97%	0.72716	100.0%	62.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	GNB4	p.I229N	3	179131213	A	T	Missense_Mutation	51	43.1%	No	No	100%	0.33842	100.0%	82.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	GNB4	p.I229N	3	179131213	A	T	Missense_Mutation	88	55.7%	No	No	100%	0.30711	100.0%	91.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	ABCC5	p.A241P	3	183700666	C	G	Missense_Mutation	278	18.0%	No	No	100%	0.88272	100.0%	82.4%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21DCIS	ABCC5	p.A241P	3	183700666	C	G	Missense_Mutation	236	3.4%	No	No	16%	0	29.7%	7.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21IDC	HTR3C	p.E197Q	3	183776244	G	C	Missense_Mutation	139	31.7%	No	No	100%	0.96812	100.0%	87.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	HTR3C	p.E197Q	3	183776244	G	C	Missense_Mutation	204	31.9%	No	No	100%	0.29956	100.0%	88.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	TP63	p.S153R	3	189526195	C	A	Missense_Mutation	590	16.8%	No	No	100%	0.91464	100.0%	87.5%	Clonal	D	Passenger	N	T	passenger	No	Yes	No	WES
21DCIS	TP63	p.S153R	3	189526195	C	A	Missense_Mutation	661	15.0%	No	No	84%	0.34369	97.4%	69.4%	Subclonal	D	Passenger	N	T	passenger	No	Yes	No	WES
21IDC	XXYLT1	p.E370K	3	194790518	C	T	Missense_Mutation	343	19.8%	No	No	100%	0.81904	100.0%	89.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	XXYLT1	p.E370K	3	194790518	C	T	Missense_Mutation	472	26.7%	No	No	100%	0.90484	100.0%	94.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	TNK2	p.D1038H	3	195594246	C	G	Missense_Mutation	237	8.4%	No	No	68%	0.26976	95.4%	44.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	TNK2	p.D1038H	3	195594246	C	G	Missense_Mutation	365	13.4%	No	No	89%	0.642	100.0%	66.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	NFXL1	p.Q600E	4	47887541	G	C	Missense_Mutation	61	6.6%	No	No	40%	0.10817	88.4%	15.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	NFXL1	p.Q600E	4	47887541	G	C	Missense_Mutation	85	1.2%	No	No	4%	0	22.4%	0.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	FGB	p.Q451*	4	155491677	C	T	Nonsense_Mutation	82	30.5%	No	No	100%	0.95673	100.0%	80.1%	Clonal	D				passenger	No	No	No	WES
21DCIS	FGB	p.Q451*	4	155491677	C	T	Nonsense_Mutation	67	26.9%	No	No	97%	0.71705	100.0%	59.7%	Clonal	D				passenger	No	No	No	WES
21IDC	TLR3	p.P602T	4	187004644	C	A	Missense_Mutation	81	30.9%	No	No	100%	0.95763	100.0%	80.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	TLR3	p.P602T	4	187004644	C	A	Missense_Mutation	99	28.3%	No	No	100%	0.7898	100.0%	68.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	ADAMTS16	p.V781I	5	5239856	G	A	Missense_Mutation	188	5.9%	No	No	36%	0.00021	61.7%	19.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	CTNND2	p.E59K	5	11565168	C	T	Missense_Mutation	56	10.7%	No	No	66%	0.42872	97.3%	29.5%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
21DCIS	CTNND2	p.E59K	5	11565168	C	T	Missense_Mutation	65	1.5%	No	No	6%	0	29.0%	0.9%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
21IDC	ARHGEF28	p.S773F	5	73163945	C	T	Missense_Mutation	125	23.2%	No	No	100%	0.90899	100.0%	73.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	ARHGEF28	p.S773F	5	73163945	C	T	Missense_Mutation	142	31.0%	No	No	100%	0.8703	100.0%	78.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	PAPD4	p.R73*	5	78915896	C	T	Nonsense_Mutation	28	32.1%	No	No	100%	0.83608	100.0%	59.0%	Clonal	A				passenger	No	No	No	WES
21DCIS	PAPD4	p.R73*	5	78915896	C	T	Nonsense_Mutation	33	24.2%	No	No	88%	0.58929	98.8%	42.7%	Clonal	A				passenger	No	No	No	WES
21IDC	PRRC2A	p.G1674V	6	31602615	G	T	Missense_Mutation	157	28.7%	No	No	100%	0.94977	100.0%	87.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	PRRC2A	p.G1674V	6	31602615	G	T	Missense_Mutation	131	31.3%	No	No	100%	0.86781	100.0%	77.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	TREML2	p.A152D	6	41162493	G	T	Missense_Mutation	141	4.3%	No	No	22%	0	45.4%	9.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	NFKBIE	p.R133L	6	44233103	C	A	Missense_Mutation	130	2.3%	No	No	16%	0.00007	46.1%	5.4%	Subclonal	N	Passenger	N	T	passenger	No	Yes	No	WES
21DCIS	NFKBIE	p.R133L	6	44233103	C	A	Missense_Mutation	165	8.5%	No	No	39%	0.00008	63.0%	23.3%	Subclonal	N	Passenger	N	T	passenger	No	Yes	No	WES
21IDC	GPR116	p.T236N	6	46849299	G	T	Missense_Mutation	49	8.2%	No	No	58%	0.38136	96.8%	22.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	GPR116	p.T236N	6	46849299	G	T	Missense_Mutation	64	3.1%	No	No	14%	0.00024	48.8%	3.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	SYNE1	p.H1363Y	6	152762327	G	A	Missense_Mutation	77	23.4%	No	No	100%	0.86883	100.0%	70.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	SYNE1	p.H1363Y	6	152762327	G	A	Missense_Mutation	73	23.3%	No	No	84%	0.57193	98.8%	52.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	NOX3	p.F349L	6	155750026	G	T	Missense_Mutation	178	3.4%	No	No	21%	0	43.2%	9.2%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21DCIS	NOX3	p.F349L	6	155750026	G	T	Missense_Mutation	185	9.7%	No	No	35%	0	53.3%	22.2%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21IDC	ZNF727	p.E337Q	7	63538436	G	C	Missense_Mutation	570	17.2%	No	No	100%	0.90956	100.0%	83.0%	Clonal	N	Passenger		T	passenger	No	No	No	WES
21DCIS	ZNF727	p.E337Q	7	63538436	G	C	Missense_Mutation	490	18.4%	No	No	66%	0.00005	79.3%	54.4%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
21IDC	ZNF107	p.N21K	7	64166745	C	A	Missense_Mutation	323	12.1%	No	No	74%	0.22665	95.0%	54.3%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
21DCIS	ZNF107	p.N21K	7	64166745	C	A	Missense_Mutation	267	3.7%	No	No	14%	0	23.9%	7.0%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
21IDC	LAMB4	p.E554K	7	107732112	C	T	Missense_Mutation	117	20.5%	No	No	100%	0.87545	100.0%	75.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	LAMB4	p.E554K	7	107732112	C	T	Missense_Mutation	113	25.7%	No	No	93%	0.70666	100.0%	64.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	ZNF212	p.S4W	7	148936880	C	G	Missense_Mutation	200	3.0%	No	No	21%	0	44.9%	9.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	ZNF212	p.S4W	7	148936880	C	G	Missense_Mutation	197	24.9%	No	No	90%	0.66984	100.0%	68.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	ACTR3C	p.G30R	7	149990466	C	G	Missense_Mutation	193	34.2%	No	No	100%	0.85099	100.0%	92.4%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
21DCIS	ACTR3C	p.G30R	7	149990466	C	G	Missense_Mutation	213	26.8%	No	No	97%	0.79384	100.0%	74.5%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
21IDC	GBX1	p.R351Q	7	150845716	C	T	Missense_Mutation	147	10.9%	No	No	77%	0.52381	98.2%	47.2%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21DCIS	GBX1	p.R351Q	7	150845716	C	T	Missense_Mutation	118	2.5%	No	No	9%	0	25.5%	2.8%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21IDC	RP1	p.R2005T	8	55542456	G	C	Missense_Mutation	85	30.6%	No	No	100%	0.94941	100.0%	82.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	RP1	p.R2005T	8	55542456	G	C	Missense_Mutation	87	23.0%	No	No	100%	0.77144	100.0%	64.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	CRH	p.V114G	8	67089372	A	C	Missense_Mutation	145	5.5%	No	No	39%	0.00987	74.0%	19.8%	Subclonal	D	Passenger	N		passenger	No	No	No	WES
21IDC	PKHD1L1	p.I3928T	8	110530489	T	C	Missense_Mutation	96	14.6%	No	No	100%	0.83498	100.0%	62.7%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
21DCIS	PKHD1L1	p.I3928T	8	110530489	T	C	Missense_Mutation	83	20.5%	No	No	95%	0.68599	100.0%	57.0%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
21IDC	EXT1	p.W445*	8	118834786	C	T	Nonsense_Mutation	113	69.9%	No	Yes	100%	0.16014	100.0%	95.2%	Clonal	A				likely_pathogenic	No	Yes	No	WES
21DCIS	EXT1	p.W445*	8	118834786	C	T	Nonsense_Mutation	110	66.4%	No	Yes	100%	0.24444	100.0%	94.6%	Clonal	A				likely_pathogenic	No	Yes	No	WES
21IDC	TOP1MT	p.D300H	8	144406231	C	G	Missense_Mutation	194	31.4%	No	No	100%	0.97194	100.0%	90.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	TOP1MT	p.D300H	8	144406231	C	G	Missense_Mutation	189	28.6%	No	No	100%	0.84892	100.0%	77.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	OR1L1	p.S239C	9	125424710	C	G	Missense_Mutation	72	8.3%	No	No	51%	0.18899	92.8%	23.4%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
21DCIS	OR1L1	p.S239C	9	125424710	C	G	Missense_Mutation	67	3.0%	No	No	11%	0	36.5%	2.8%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
21IDC	SKIDA1	p.E767Q	10	21804453	C	G	Missense_Mutation	106	20.8%	No	No	100%	0.85505	100.0%	70.6%	Clonal	D	Passenger	N		passenger	No	No	No	WES
21DCIS	SKIDA1	p.E767Q	10	21804453	C	G	Missense_Mutation	143	31.5%	No	No	100%	0.87594	100.0%	79.2%	Clonal	D	Passenger	N		passenger	No	No	No	WES
21IDC	ADK	p.X91_splice	10	76074505	T	G	Splice_Site	48	8.3%	No	No	51%	0.27962	95.1%	19.8%	Subclonal	D				passenger	No	No	No	WES
21DCIS	ADK	p.X91_splice	10	76074505	T	G	Splice_Site	41	2.4%	No	No	9%	0.00021	45.0%	1.6%	Subclonal	D				passenger	No	No	No	WES
21IDC	TLL2	p.E822Q	10	98133551	C	G	Missense_Mutation	140	34.3%	No	No	100%	0.96623	100.0%	89.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	TLL2	p.E822Q	10	98133551	C	G	Missense_Mutation	118	30.5%	No	No	100%	0.84944	100.0%	75.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	MARVELD1	p.A142E	10	99474058	C	A	Missense_Mutation	97	5.2%	No	No	32%	0.00729	69.6%	13.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	TACC2	p.S959L	10	123844891	C	T	Missense_Mutation	181	3.9%	No	No	24%	0	47.0%	11.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	TACC2	p.S959L	10	123844891	C	T	Missense_Mutation	162	13.6%	No	No	49%	0.00027	70.9%	32.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	NAV2	p.T1862M	11	20104635	C	T	Missense_Mutation	191	2.1%	No	No	27%	0.00767	68.0%	10.6%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21DCIS	NAV2	p.T1862M	11	20104635	C	T	Missense_Mutation	240	7.5%	No	No	57%	0.04036	86.6%	36.1%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21IDC	OR4S2	p.S240C	11	55419098	C	G	Missense_Mutation	53	18.9%	No	No	100%	0.77275	100.0%	53.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	OR4S2	p.S240C	11	55419098	C	G	Missense_Mutation	54	1.9%	No	No	7%	0.00001	34.7%	1.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	RSF1	p.X1188_splice	11	77383276	C	G	Splice_Site	124	8.1%	No	Yes	100%	0.80058	100.0%	54.7%	Clonal	D				likely_pathogenic	No	No	No	WES
21DCIS	RSF1	p.X1188_splice	11	77383276	C	G	Splice_Site	82	28.0%	No	Yes	100%	0.76736	100.0%	65.3%	Clonal	D				likely_pathogenic	No	No	No	WES
21IDC	MMP1	p.I253T	11	102666206	A	G	Missense_Mutation	60	23.3%	No	No	100%	0.86495	100.0%	61.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	MMP1	p.I253T	11	102666206	A	G	Missense_Mutation	91	29.7%	No	No	100%	0.81277	100.0%	70.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	TBCEL	p.Q39E	11	120916514	C	G	Missense_Mutation	57	5.3%	No	No	27%	0.02407	72.3%	9.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	TBCEL	p.Q39E	11	120916514	C	G	Missense_Mutation	71	22.5%	No	No	82%	0.52921	98.5%	50.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	LRRC23	p.S99F	12	7015632	C	T	Missense_Mutation	193	5.2%	No	No	42%	0.00864	74.6%	22.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	ART4	p.S38C	12	14995935	G	C	Missense_Mutation	162	10.5%	No	No	64%	0.19087	93.6%	40.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	ART4	p.S38C	12	14995935	G	C	Missense_Mutation	150	30.7%	No	No	100%	0.8704	100.0%	78.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	MAP3K12	p.G566A	12	53876890	C	G	Missense_Mutation	183	10.9%	No	No	67%	0.21326	94.3%	43.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES

21DCIS	MAP3K12	p.G566A	12	53876890	C	G	Missense_Mutation	176	1.7%	No	No	6%	0	17.1%	1.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	GPR84	p.Y198C	12	54757043	T	C	Missense_Mutation	108	30.6%	No	No	100%	0.96148	100.0%	84.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	GPR84	p.Y198C	12	54757043	T	C	Missense_Mutation	116	24.1%	No	No	87%	0.61967	99.0%	60.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	OR6C75	p.E109G	12	55759220	A	G	Missense_Mutation	65	6.2%	No	No	38%	0.07529	85.5%	14.8%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
21IDC	NOS1	p.L830F	12	117696243	C	G	Missense_Mutation	100	20.0%	No	No	100%	0.8433	100.0%	68.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	NOS1	p.L830F	12	117696243	C	G	Missense_Mutation	104	23.1%	No	No	84%	0.54712	98.6%	56.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	NUFIP1	p.E254K	13	45540046	C	T	Missense_Mutation	39	12.8%	No	Yes	66%	0.54558	97.5%	27.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	NUFIP1	p.E254K	13	45540046	C	T	Missense_Mutation	49	26.5%	No	Yes	96%	0.68198	100.0%	53.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	RB1	p.C489*	13	48954346	C	A	Nonsense_Mutation	45	6.7%	No	Yes	34%	0.11547	85.5%	11.8%	Subclonal	A				likely_pathogenic	Yes	Yes	Yes	WES
21IDC	MYO16	p.S462L	13	109535432	C	T	Missense_Mutation	152	32.2%	No	No	100%	0.97013	100.0%	89.0%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
21DCIS	MYO16	p.S462L	13	109535432	C	T	Missense_Mutation	146	17.8%	No	No	64%	0.0469	88.7%	44.6%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
21IDC	OXA1L	p.R394W	14	23240287	C	T	Missense_Mutation	103	7.8%	No	No	47%	0.06898	86.3%	24.1%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
21IDC	PPM1A	p.D111G	14	60749534	A	G	Missense_Mutation	198	9.1%	No	Yes	46%	0.00129	70.7%	29.4%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
21DCIS	PPM1A	p.D111G	14	60749534	A	G	Missense_Mutation	211	0.5%	No	Yes	2%	0	9.0%	0.1%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
21IDC	FAM181A	p.V270I	14	94395253	G	A	Missense_Mutation	184	53.8%	No	Yes	100%	0	100.0%	95.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	FAM181A	p.V270I	14	94395253	G	A	Missense_Mutation	188	58.0%	No	Yes	100%	0.96942	100.0%	95.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	KLC1	p.E401Q	14	104139708	G	C	Missense_Mutation	63	54.0%	No	Yes	100%	0	100.0%	87.9%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
21DCIS	KLC1	p.E401Q	14	104139708	G	C	Missense_Mutation	75	38.7%	No	Yes	100%	0.82048	100.0%	79.2%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
21IDC	AHNAK2	p.V4568I	14	105408086	C	T	Missense_Mutation	1037	47.4%	No	Yes	100%	0	100.0%	98.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	AHNAK2	p.V4568I	14	105408086	C	T	Missense_Mutation	987	47.8%	No	Yes	100%	0.00157	100.0%	98.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	ATP10A	p.S186F	15	26026263	G	A	Missense_Mutation	163	36.8%	No	No	100%	0.94692	100.0%	91.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	ATP10A	p.S186F	15	26026263	G	A	Missense_Mutation	161	24.2%	No	No	88%	0.61927	99.0%	64.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	HERC2	p.R2762L	15	28437273	C	A	Missense_Mutation	95	2.1%	No	No	13%	0.0001	44.3%	3.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	HERC2	p.R2762L	15	28437273	C	A	Missense_Mutation	113	20.4%	No	No	74%	0.2914	96.5%	49.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	HERC2	p.L2333F	15	28456220	G	A	Missense_Mutation	100	1.0%	No	No	6%	0	32.5%	1.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	HERC2	p.L2333F	15	28456220	G	A	Missense_Mutation	94	5.3%	No	No	19%	0	42.4%	8.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	FMN1	p.M968I	15	33192261	C	G	Missense_Mutation	68	10.3%	No	No	63%	0.37	96.7%	30.3%	Subclonal		Passenger		T	passenger	No	No	No	WES
21DCIS	FMN1	p.M968I	15	33192261	C	G	Missense_Mutation	70	1.4%	No	No	5%	0	27.0%	0.8%	Subclonal		Passenger		T	passenger	No	No	No	WES
21IDC	SLC12A6	p.L233F	15	34548476	C	G	Missense_Mutation	40	22.5%	No	No	100%	0.82314	100.0%	55.1%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21DCIS	SLC12A6	p.L233F	15	34548476	C	G	Missense_Mutation	29	10.3%	No	No	37%	0.08772	88.2%	13.0%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21IDC	RTF1	p.R195C	15	41749995	C	T	Missense_Mutation	98	18.4%	No	No	100%	0.81463	100.0%	63.5%	Clonal	D	Passenger	D		passenger	No	No	No	WES
21DCIS	RTF1	p.R195C	15	41749995	C	T	Missense_Mutation	114	25.4%	No	No	92%	0.69597	100.0%	64.0%	Clonal	D	Passenger	D		passenger	No	No	No	WES
21IDC	CCNDBP1	p.G128A	15	43482304	G	C	Missense_Mutation	123	6.5%	No	No	40%	0.01057	74.6%	20.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	DUOX1	p.D135H	15	45427397	G	C	Missense_Mutation	291	36.4%	No	No	100%	0.94711	100.0%	95.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	DUOX1	p.D135H	15	45427397	G	C	Missense_Mutation	289	29.8%	No	No	100%	0.90134	100.0%	84.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	SQRDL	p.I85M	15	45954173	C	G	Missense_Mutation	95	26.3%	No	No	100%	0.91715	100.0%	78.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	SQRDL	p.I85M	15	45954173	C	G	Missense_Mutation	110	23.6%	No	No	86%	0.58575	98.8%	58.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	MESP2	p.T266A	15	90320384	A	G	Missense_Mutation	209	33.0%	No	No	100%	0.97431	100.0%	92.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	MESP2	p.T266A	15	90320384	A	G	Missense_Mutation	183	38.8%	No	No	100%	0.3357	100.0%	89.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	CHD2	p.E133A	15	93472276	A	C	Missense_Mutation	87	9.2%	No	No	56%	0.21663	93.8%	28.6%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
21DCIS	CHD2	p.E133A	15	93472276	A	C	Missense_Mutation	98	1.0%	No	No	4%	0	19.4%	0.4%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
21IDC	MCTP2	p.K329R	15	94888374	A	G	Missense_Mutation	62	24.2%	No	No	100%	0.87637	100.0%	67.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	MCTP2	p.K329R	15	94888374	A	G	Missense_Mutation	75	24.0%	No	No	87%	0.6099	98.9%	54.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	ZP2	p.E361Q	16	21214464	C	G	Missense_Mutation	91	4.4%	No	No	16%	0	38.4%	6.0%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
21IDC	HS3ST4	p.Y47C	16	25703878	A	G	Missense_Mutation	134	4.5%	No	No	27%	0.0003	57.1%	12.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	HS3ST4	p.Y47C	16	25703878	A	G	Missense_Mutation	202	17.8%	No	No	64%	0.01317	85.1%	47.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	APOBR	p.G364W	16	28507452	G	T	Missense_Mutation	272	0.4%	No	No	2%	0	11.9%	0.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	APOBR	p.G364W	16	28507452	G	T	Missense_Mutation	316	11.7%	No	No	42%	0	56.4%	30.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	MVP	p.E412K	16	29852959	G	A	Missense_Mutation	153	26.8%	No	No	100%	0.90904	100.0%	85.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	MVP	p.E412K	16	29852959	G	A	Missense_Mutation	167	26.3%	No	No	95%	0.76026	100.0%	70.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	KAT8	p.R140C	16	31131791	C	T	Missense_Mutation	168	26.8%	No	No	100%	0.90175	100.0%	86.1%	Clonal	D	Passenger		T	passenger	No	No	No	WES
21DCIS	KAT8	p.R140C	16	31131791	C	T	Missense_Mutation	187	23.0%	No	No	83%	0.47668	98.3%	62.7%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
21IDC	TP53	p.G266V	17	7577141	C	A	Missense_Mutation	99	40.4%	Yes	Yes	100%	0.00106	100.0%	87.7%	Subclonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
21DCIS	TP53	p.G266V	17	7577141	C	A	Missense_Mutation	118	40.7%	Yes	Yes	100%	0.90139	100.0%	78.7%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
21IDC	MED24	p.P432L	17	38185193	G	A	Missense_Mutation	2094	9.7%	No	Yes	100%	0.40207	100.0%	97.3%	Clonal	D	Passenger		T	passenger	No	No	No	WES
21DCIS	MED24	p.P432L	17	38185193	G	A	Missense_Mutation	1662	10.3%	No	Yes	100%	0.94203	100.0%	95.7%	Clonal	D	Passenger		T	passenger	No	No	No	WES
21IDC	KRT31	p.A305G	17	39551283	G	C	Missense_Mutation	516	10.9%	No	Yes	56%	0	70.3%	42.7%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21DCIS	KRT31	p.A305G	17	39551283	G	C	Missense_Mutation	434	1.4%	No	Yes	5%	0	10.3%	1.8%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
21IDC	ANKRD12	p.R904T	18	9255976	G	C	Missense_Mutation	133	15.8%	No	No	97%	0.75825	100.0%	60.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	ANKRD12	p.R904T	18	9255976	G	C	Missense_Mutation	165	1.8%	No	No	7%	0	18.3%	1.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	KCTD1	p.D35N	18	24081097	C	T	Missense_Mutation	239	40.2%	No	No	100%	0.67835	100.0%	94.8%	Clonal	D	Passenger		T	passenger	No	No	No	WES
21DCIS	KCTD1	p.D35N	18	24081097	C	T	Missense_Mutation	234	28.6%	No	No	100%	0.86559	100.0%	79.7%	Clonal	D	Passenger		T	passenger	No	No	No	WES
21IDC	RTTN	p.D1512H	18	67742618	C	G	Missense_Mutation	43	4.7%	No	Yes	24%	0.04771	76.5%	6.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	RTTN	p.D1512H	18	67742618	C	G	Missense_Mutation	45	24.4%	No	Yes	64%	0.25228	94.5%	36.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	DIRAS1	p.E134K	19	2717405	C	T	Missense_Mutation	261	4.6%	No	No	28%	0	47.6%	15.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	CASP14	p.R121Q	19	15164728	G	A	Missense_Mutation	149	2.0%	No	No	12%	0	34.6%	4.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	CASP14	p.R121Q	19	15164728	G	A	Missense_Mutation	129	24.8%	No	No	90%	0.66383	100.0%	63.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	C19orf44	p.V562M	19	16623869	G	A	Missense_Mutation	141	19.9%	No	No	100%	0.86636	100.0%	73.2%	Clonal	D	Passenger	N		passenger	No	No	No	WES
21DCIS	C19orf44	p.V562M	19	16623869	G	A	Missense_Mutation	161	25.5%	No	No	92%	0.71015	100.0%	68.1%	Clonal	D	Passenger	N		passenger	No	No	No	WES
21IDC	JAK3	p.S826*	19	17943612	G	C	Nonsense_Mutation	155	34.2%	No	No	100%	0.9679	100.0%	90.1%	Clonal	A				likely_pathogenic	No	Yes	No	WES
21DCIS	JAK3	p.S826*	19	17943612	G	C	Nonsense_Mutation	150	34.0%	No	No	100%	0.8836	100.0%	83.2%	Clonal	A				likely_pathogenic	No	Yes	No	WES
21IDC	ZNF99	p.E808D	19	22940287	C	G	Missense_Mutation	521	20.2%	No	No	100%	0.87675	100.0%	89.1%	Clonal	N	Passenger		T	passenger	No	No	No	WES
21DCIS	ZNF99	p.E808D	19	22940287	C	G	Missense_Mutation	416	22.4%	No	No	81%	0.14871	95.0%	66.8%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
21IDC	KLK5	p.S39C	19	51453330	G	C	Missense_Mutation	169	29.0%	No	No	100%	0.95388	100.0%	88.0%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
21DCIS	KLK5	p.S39C	19	51453330	G	C	Missense_Mutation	173	24.9%	No	No	90%	0.66924	100.0%	67.3%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
21IDC	LILRA4	p.D261N	19	54848842	C	T	Missense_Mutation	423	25.3%	No	No	100%	0.19031	100.0%	92.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	LILRA4	p.D261N	19	54848842	C	T	Missense_Mutation	394	24.6%	No	No	89%	0.59738	98.9%	73.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	ZSCAN5B	p.D397N	19	56701495	C	T	Missense_Mutation	316	24.7%	No	No	100%	0.32107	100.0%	90.2%	Clonal	N	Passenger		T	passenger	No	No	No	WES
21DCIS	ZSCAN5B	p.D397N	19	56701495	C	T	Missense_Mutation	241	25.3%	No	No	92%	0.70578	100.0%	71.9%	Clonal	N	Passenger		T	passenger	No	No	No	WES
21IDC	MZF1	p.E125K	19	59082384	C	T	Missense_Mutation	185	31.4%	No	No	100%	0.97111	100.0%	90.2%	Clonal	N	Passenger		T	passenger	No	No	No	WES
21DCIS	MZF1	p.E125K	19	59082384	C	T	Missense_Mutation	158	22.8%	No	No	82%	0.4788	98.3%	60.4%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
21IDC	PCNA	p.E25Q	20	5100372	C	G	Missense_Mutation	95	32.6%	No	No	100%	0.96276	100.0%	84.0%	Clonal	D	Passenger	N		passenger	No	No	No	WES
21DCIS	PCNA	p.E25Q	20	5100372	C	G	Missense_Mutation	107	24.3%	No	No	88%	0.63026	100.0%	60.3%	Clonal	D	Passenger	N		passenger	No	No	No	WES
21IDC	ASXL1	p.S989C	20	31023481	C	G	Missense_Mutation	204	6.4%	No	No	45%	0.00619	74.8%	26.4%	Subclonal	N	Passenger		T	passenger	Yes	Yes	Yes	WES
21DCIS	ASXL1	p.S989C	20	31023481	C	G	Missense_Mutation	142	0.7%	No	No	3%	0	13.4%	0.2%	Subclonal	N	Passenger		T	passenger	Yes	Yes	Yes	WES
21IDC	COL9A3	p.L15_L16del	20	61448442	CGCTCCT	C	In_Frame_Del	73	1.4%	No	No	10%	0.00161	51.4%	1.9%	Subclonal					passenger	No	No	No	WES
21DCIS	COL9A3	p.L15_L16del	20	61448442	CGCTCCT	C	In_Frame_Del	88	5.7%	No	No	21%	0	45.2%	8.6%	Subclonal					passenger	No	No	No	WES
21IDC	PRDM15	p.A90V	21	43298948	G	A	Missense_Mutation	16	37.5%	No	No	100%	0.88771	100.0%	52.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	PRDM15	p.A90V	21	43298948	G	A	Missense_Mutation	17	23.5%	No	No	85%	0.53911	98.6%	30.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
21IDC	CLTCL1	p.D999G	22	19203690	T	C	Missense_Mutation	71	11.3%	No	No	69%	0.44662	97.5%	34.5%	Subclonal	D	Passenger		T	passenger	No	Yes	No	WES
21IDC	LIMK2	p.I508M	22	31669466	C	G	Missense_Mutation	104	13.5%	No	No	82%	0.60415	98.7%	48.1%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
21DCIS	LIMK2	p.I508M	22	31669466	C	G	Missense_Mutation	96	18.8%	No	No	68%	0.19584	94.7%	43.6%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
21IDC	HMGXB4	p.E450Q	22	35682040	G	C	Missense_Mutation	47	4.3%	No	No	26%	0.05793	81.9%	7.5%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
21DCIS	HMGXB4	p.E450Q	22	35682040	G	C	Missense_Mutation	40	10.0%	No	No	36%	0.03409	81.3%	14.2%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
21IDC	MEI1	p.T40I	22	42095661	C	T	Missense_Mutation	202	15.3%	No	No	94%	0.75934	100.0%	64.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21DCIS	MEI1	p.T40I	22	42095661	C	T	Missense_Mutation	227	28.6%	No	No	100%	0.86355	100.0%	79.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
21IDC	UBQLN2	p.S193R	23	56590885	C	A	Missense_Mutation	150	4.0%	No	No	24%	0.00004	51.2%	11.0%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
21DCIS	UBQLN2	p.S193R	23	56590885	C	A	Missense_Mutation	115	0.9%	No	No	3%	0	16.6%	0.3%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
21IDC	KIF4A	p.S507F	23	69573503	C	T	Missense_Mutation	140	29.3%	No	No	100%	0.95664	100.0%	86.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	KIF4A	p.S507F	23	69573503	C	T	Missense_Mutation	140	32.9%	No	No	100%	0.88311	100.0%	81.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	OGT	p.E1017Q	23	70793552	G	C	Missense_Mutation	77	5.2%	No	No	32%	0.02188	75.7%	12.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
21DCIS	OGT	p.E1017Q	23	70793552	G	C	Missense_Mutation	96	31.3%	No	No	100%	0.84219	100.0%	73.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
21IDC	ZNF275	p.T50N	23	152612292	C	A	Missense_Mutation	182	7.7%	No	No	47%	0.00677	75.9%	28.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
21DCIS	ZNF275	p.T50N	23	152612292	C	A	Missense_Mutation	172	29.1%	No	No	100%	0.85355	100.0%	77.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
22DCIS	SKI	p.R282W	1	2161049	C	T	Missense_Mutation	106	8.5%	No	No	32%	0.00004	56.7%	16.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
22IDC	PEX14	p.G110S	1	10678418	G	A	Missense_Mutation	50	24.0%	No	No	98%	0.56312	100.0%	52.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	PEX14	p.G110S	1	10678418	G	A	Missense_Mutation	45	53.3%	No	No	100%	0.85434	100.0%	78.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	THRAP3	p.N110D	1	36752159	A	G	Missense_Mutation	185	31.4%	No	No	96%	0.75318	100.0%	74.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	THRAP3	p.N110D	1	36752159	A	G	Missense_Mutation	132	44.7%	No	No	100%	0.93608	100.0%	85.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	ZNHIT6	p.N333K	1	86167860	A	T	Missense_Mutation	95	29.5%	No	No	100%	0.77126	100.0%	74.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
22DCIS	ZNHIT6	p.N333K	1	86167860	A	T	Missense_Mutation	80	51.3%	No	No	100%	0.96653	100.0%	88.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
22IDC	PSMA5	p.S117C	1	109954748	G	C	Missense_Mutation	102	6.9%	No	No	28%	0.00002	54.4%	13.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	PSMA5	p.S117C	1	109954748	G	C	Missense_Mutation	117	11.1%	No	No	41%	0.00049	66.9%	24.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	ATXN7L2	p.X453_splice	1	110033012	GAAGT	G	Splice_Site	152	18.4%	No	No	75%	0.19685	96.6%	52.5%	Subclonal					passenger	No	No	No	WES
22DCIS	ATXN7L2	p.X453_splice	1	110033012	GAAGT	G	Splice_Site	171	31.0%	No	No	100%	0.91282	100.0%	81.5%	Clonal					passenger	No	No	No	WES
22IDC	MOV10	p.E867del	1	113242317	TAGA	T	In_Frame_Del	186	17.2%	No	No	70%	0.06879	92.7%	50.2%	Subclonal					passenger	No	No	No	WES
22DCIS	MOV10	p.E867del	1	113242317	TAGA	T	In_Frame_Del	208	29.8%	No	No	100%	0.91496	100.0%	81.8%	Clonal					passenger	No	No	No	WES
22IDC	FLG	p.E990K	1	152284394	C	T	Missense_Mutation	698	14.6%	No	Yes	74%	0.00462	87.8%	61.3%	Subclonal	N	Passenger	N	T	passenger	No	No	Yes	WES
22DCIS	FLG	p.E990K	1	152284394	C	T	Missense_Mutation	841	30.2%	No	Yes	100%	0	100.0%	96.3%	Clonal	N	Passenger	N	T	passenger	No	No	Yes	WES
22IDC	DUSP27	p.G697E	1	167096458	G	A	Missense_Mutation	168	19.6%	No	Yes	80%	0.29938	97.8%	57.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
22DCIS	DUSP27	p.G697E	1	167096458	G	A	Missense_Mutation	224	28.1%	No	Yes	100%	0.81037	100.0%	86.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
22IDC	ASPM	p.S222T	1	197112718	A	T	Missense_Mutation	164	7.9%	No	Yes	32%	0	52.8%	18.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
22DCIS	ASPM	p.S222T	1	197112718	A	T	Missense_Mutation	149	18.8%	No	Yes	70%	0.17476	93.4%	49.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
22IDC	GALNT2	p.H123_D124del	1	230339028	GCATGAC	G	In_Frame_Del	187	13.4%	No	No	68%	0.08363	93.1%	46.3%	Subclonal					passenger	No	No	No	WES
22DCIS	GALNT2	p.H123_D124del	1	230339028	GCATGAC	G	In_Frame_Del	221	28.1%	No	No	100%	0.82069	100.0%	86.4%	Clonal					passenger	No	No	No	WES
22IDC	OR2B11	p.A48T	1	247615143	C	T	Missense_Mutation	164	10.4%	No	No	53%	0.00658	80.3%	32.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
22DCIS	OR2B11	p.A48T	1	247615143	C	T	Missense_Mutation	142	14.8%	No	No	70%	0.28203	95.4%	46.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
22IDC	ST6GAL2	p.D191N	2	107459863	C	T	Missense_Mutation	119	16.8%	No	Yes	68%	0.12364	94.7%	44.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
22DCIS	ST6GAL2	p.D191N	2	107459863	C	T	Missense_Mutation	159	14.5%	No	Yes	54%	0.00294	76.8%	36.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
22IDC	PTMA	p.R90W	2	232577206	C	T	Missense_Mutation	164	23.2%	No	Yes	94%	0.62559	100.0%	68.2%	Clonal	D	Passenger	D		passenger	No	No	No	WES
22DCIS	PTMA	p.R90W	2	232577206	C	T	Missense_Mutation	154	47.4%	No	Yes	100%	0.9275	100.0%	92.3%	Clonal	D	Passenger	D		passenger	No	No	No	WES
22IDC	ARPP21	p.P791T	3	35835379	C	A	Missense_Mutation	85	16.5%	No	No	51%	0.006	78.6%	30.5%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
22DCIS	ARPP21	p.P791T	3	35835379	C	A	Missense_Mutation	76	27.6%	No	No	75%	0.48307	97.0%	50.5%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
22IDC	ARPP21	p.P791L	3	35835380	C	T	Missense_Mutation	86	16.3%	No	No	50%	0.00489	77.7%	30.1%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
22DCIS	ARPP21	p.P791L	3	35835380	C	T	Missense_Mutation	73	26.0%	No	No	71%	0.3602	95.5%	46.6%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
22IDC	FYCO1	p.E734Q	3	46008626	C	G	Missense_Mutation	116	10.3%	No	No	32%	0	52.4%	18.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
22DCIS	FYCO1	p.E734Q	3	46008626	C	G	Missense_Mutation	130	22.3%	No	No	61%	0.00943	81.7%	43.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
22IDC	KIAA1524	p.N67S	3	108303962	T	C	Missense_Mutation	79	17.7%	No	No	72%	0.25232	97.3%	43.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	KIAA1524	p.N67S	3	108303962	T	C	Missense_Mutation	112	41.1%	No	No	100%	0.59642	100.0%	86.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	DPPA2	p.C96R	3	109028073	A	G	Missense_Mutation	142	23.9%	No	No	97%	0.65992	100.0%	68.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
22DCIS	DPPA2	p.C96R	3	109028073	A	G	Missense_Mutation	150	42.7%	No	No	100%	0.52827	100.0%	90.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
22IDC	PARP14	p.L223F	3	122414341	C	T	Missense_Mutation	55	21.8%	No	No	89%	0.49055	99.0%	49.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	PARP14	p.L223F	3	122414341	C	T	Missense_Mutation	64	32.8%	No	No	100%	0.86384	100.0%	70.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	HEG1	p.S722Y	3	124732258	G	T	Missense_Mutation	156	21.8%	No	No	89%	0.51952	100.0%	63.6%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
22DCIS	HEG1	p.S722Y	3	124732258	G	T	Missense_Mutation	171	36.8%	No	No	100%	0.64838	100.0%	87.9%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
22IDC	TFDP2	p.Q261K	3	141682757	G	T	Missense_Mutation	134	4.5%	No	No	18%	0	37.8%	8.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	TFDP2	p.Q261K	3	141682757	G	T	Missense_Mutation	144	0.7%	No	No	3%	0	13.6%	0.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	MED12L	p.A1237S	3	151090504	G	T	Missense_Mutation	82	8.5%	No	No	26%	0	50.5%	12.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	MED12L	p.A1237S	3	151090504	G	T	Missense_Mutation	67	22.4%	No	No	61%	0.13098	89.8%	37.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	SI	p.T279I	3	164781301	G	A	Missense_Mutation	29	34.5%	No	No	100%	0.70827	100.0%	59.2%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
22DCIS	SI	p.T279I	3	164781301	G	A	Missense_Mutation	40	27.5%	No	No	100%	0.75962	100.0%	53.1%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
22IDC	GUF1	p.P457S	4	44692767	C	T	Missense_Mutation	60	23.3%	No	Yes	72%	0.2862	96.9%	43.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
22DCIS	GUF1	p.P457S	4	44692767	C	T	Missense_Mutation	54	51.9%	No	Yes	100%	0.86533	100.0%	80.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
22IDC	WDFY3	p.E928*	4	85722843	C	A	Nonsense_Mutation	102	23.5%	No	Yes	72%	0.18591	95.4%	49.6%	Subclonal	A				likely_pathogenic	No	No	No	WES
22DCIS	WDFY3	p.E928*	4	85722843	C	A	Nonsense_Mutation	107	60.7%	No	Yes	100%	0.00056	100.0%	91.8%	Clonal	A				likely_pathogenic	No	No	No	WES
22IDC	AGGF1	p.V202L	5	76332468	G	T	Missense_Mutation	128	6.3%	No	No	19%	0	35.9%	9.4%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
22DCIS	AGGF1	p.V202L	5	76332468	G	T	Missense_Mutation	79	2.5%	No	No	NA	0	100.0%	0.0%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
22IDC	MSH3	p.P63A	5	79950733	C	G	Missense_Mutation	37	18.9%	No	No	58%	0.1688	94.4%	28.6%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
22IDC	SNCAIP	p.D257N	5	121759201	G	A	Missense_Mutation	91	7.7%	No	No	24%	0	45.7%	11.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	SNCAIP	p.D257N	5	121759201	G	A	Missense_Mutation	57	26.3%	No	No	NA	0	100.0%	0.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	RAPGEF6	p.F742Y	5	130808294	A	T	Missense_Mutation	84	26.2%	No	No	80%	0.42301	98.2%	54.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	RAPGEF6	p.F742Y	5	130808294	A	T	Missense_Mutation	67	61.2%	No	No	NA	0	100.0%	0.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	RNF145	p.M183V	5	158603804	T	C	Missense_Mutation	77	14.3%	No	Yes	44%	0.00199	72.6%	24.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	RNF145	p.M183V	5	158603804	T	C	Missense_Mutation	59	10.2%	No	Yes	NA	0	100.0%	0.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	NKAPL	p.R321K	6	28228111	G	A	Missense_Mutation	223	12.1%	No	No	61%	0.01408	85.6%	42.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
22DCIS	NKAPL	p.R321K	6	28228111	G	A	Missense_Mutation	296	16.2%	No	No	93%	0.77552	100.0%	69.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
22IDC	TFAP2D	p.X179_splice	6	50683327	G	A	Splice_Site	146	7.5%	No	No	38%	0.00029	65.4%	21.2%	Subclonal	D				passenger	No	No	No	WES
22DCIS	TFAP2D	p.X179_splice	6	50683327	G	A	Splice_Site	191	10.5%	No	No	60%	0.06496	87.9%	39.0%	Subclonal	D				passenger	No	No	No	WES
22IDC	KHDRBS2	p.P202S	6	62611156	G	A	Missense_Mutation	84	27.4%	No	No	100%	0.7191	100.0%	68.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	KHDRBS2	p.P202S	6	62611156	G	A	Missense_Mutation	89	60.7%	No	No	100%	0.43616	100.0%	92.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	SYNCRIP	p.N285Tfs*22	6	86332353	GT	G	Frame_Shift_Del	116	22.4%	No	No	91%	0.5577	100.0%	61.8%	Clonal					passenger	No	No	No	WES
22DCIS	SYNCRIP	p.N285Tfs*22	6	86332353	GT	G	Frame_Shift_Del	146	36.3%	No	No	100%	0.9197	100.0%	88.9%	Clonal					passenger	No	No	No	WES
22IDC	ABRACL	p.R35H	6	139363898	G	A	Missense_Mutation	107	10.3%	No	No	42%	0.00111	70.6%	23.4%	Subclonal	D	Passenger	N		passenger	No	No	No	WES
22DCIS	ABRACL	p.R35H	6	139363898	G	A	Missense_Mutation	173	31.2%	No	No	100%	0.54432	100.0%	87.0%	Clonal	D	Passenger	N		passenger	No	No	No	WES
22IDC	OPRM1	p.A19V	6	154360351	C	T	Missense_Mutation	221	10.0%	No	No	40%	0	59.0%	26.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	OPRM1	p.A19V	6	154360351	C	T	Missense_Mutation	254	13.8%	No	No	65%	0.03352	86.9%	47.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	SP8	p.D237N	7	20824727	C	T	Missense_Mutation	129	11.6%	No	No	47%	0.00147	74.0%	28.8%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
22DCIS	SP8	p.D237N	7	20824727	C	T	Missense_Mutation	157	19.7%	No	No	73%	0.2625	95.3%	52.6%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
22IDC	KCTD7	p.N334D	7	66270306	A	G	Missense_Mutation	231	3.0%	No	No	15%	0	30.5%	7.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	KCTD7	p.N334D	7	66270306	A	G	Missense_Mutation	250	0.8%	No	No	4%	0	12.9%	0.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	CLIP2	p.R448H	7	73778608	G	A	Missense_Mutation	123	13.8%	No	No	84%	0.43846	98.8%	51.5%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
22DCIS	CLIP2	p.R448H	7	73778608	G	A	Missense_Mutation	130	16.2%	No	No	100%	0.82328	100.0%	64.8%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
22IDC	KPNA7	p.T51M	7	98800778	G	A	Missense_Mutation	225	17.8%	No	No	100%	0.7547	100.0%	74.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
22DCIS	KPNA7	p.T51M	7	98800778	G	A	Missense_Mutation	195	31.8%	No	No	100%	0.95652	100.0%	90.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
22IDC	TRIM4	p.G465R	7	99489896	C	T	Missense_Mutation	226	18.1%	No	No	92%	0.58622	100.0%	67.3%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
22DCIS	TRIM4	p.G465R	7	99489896	C	T	Missense_Mutation	205	33.7%	No	No	100%	0.6214	100.0%	90.3%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
22IDC	WEE2	p.R546P	7	141429432	G	C	Missense_Mutation	235	26.0%	No	No	100%	0.59454	100.0%	88.7%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
22DCIS	WEE2	p.R546P	7	141429432	G	C	Missense_Mutation	228	25.0%	No	No	100%	0.63022	100.0%	86.6%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
22IDC	OR2A14	p.R219H	7	143826861	G	A	Missense_Mutation	226	11.9%	No	No	37%	0	51.1%	25.1%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
22DCIS	OR2A14	p.R219H	7	143826861	G	A	Missense_Mutation	196	24.5%	No	No	67%	0.00721	83.8%	51.2%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
22IDC	ADRA1A	p.P327L	8	26628087	G	A	Missense_Mutation	113	15.0%	No	No	46%	0.00024	69.5%	29.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
22DCIS	ADRA1A	p.P327L	8	26628087	G	A	Missense_Mutation	94	29.8%	No	No	81%	0.61213	98.1%	57.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
22IDC	WRN	p.F763Lfs*14	8	30973882	AT	A	Frame_Shift_Del	84	11.9%	No	No	37%	0.00012	62.6%	19.9%	Subclonal					likely_pathogenic	No	Yes	No	WES
22DCIS	WRN	p.F763Lfs*14	8	30973882	AT	A	Frame_Shift_Del	84	22.6%	No	No	62%	0.07826	87.8%	40.3%	Subclonal					likely_pathogenic	No	Yes	No	WES
22DCIS	TEX10	p.H728N	9	103082567	G	T	Missense_Mutation	131	11.5%	No	No	31%	0	48.6%	18.8%	Subclonal	D	Passenger	N		passenger	No	No	No	WES
22IDC	SLC46A2	p.P273Lfs*31	9	115652143	AG	A	Frame_Shift_Del	180	21.1%	No	No	86%	0.45007	98.8%	63.1%	Subclonal					passenger	No	No	No	WES
22DCIS	SLC46A2	p.P273Lfs*31	9	115652143	AG	A	Frame_Shift_Del	165	39.4%	No	No	100%	0.93863	100.0%	82.1%	Clonal					passenger	No	No	No	WES
22IDC	NUP188	p.S1126Cfs*9	9	131760452	ACT	A	Frame_Shift_Del	64	21.9%	No	No	89%	0.50061	100.0%	51.9%	Clonal					passenger	No	No	No	WES
22DCIS	NUP188	p.S1126Cfs*9	9	131760452	ACT	A	Frame_Shift_Del	61	31.1%	No	No	85%	0.71982	98.8%	55.3%	Clonal					passenger	No	No	No	WES
22IDC	PRPF18	p.E309K	10	13658530	G	A	Missense_Mutation	122	1.6%	No	No	7%	0	22.9%	1.5%	Subclonal	D	Passenger	D		passenger	No	No	No	WES
22DCIS	PRPF18	p.E309K	10	13658530	G	A	Missense_Mutation	135	13.3%	No	No	63%	0.13957	91.8%	40.2%	Subclonal	D	Passenger	D		passenger	No	No	No	WES
22IDC	KIAA1462	p.Q182R	10	30318532	T	C	Missense_Mutation	198	4.5%	No	No	18%	0	33.7%	9.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
22DCIS	KIAA1462	p.Q182R	10	30318532	T	C	Missense_Mutation	263	16.3%	No	No	77%	0.32394	96.3%	57.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
22IDC	TMEM26	p.D253N	10	63170430	C	T	Missense_Mutation	584	2.1%	No	Yes	23%	0	38.9%	12.6%	Subclonal	D	Passenger	D		passenger	No	No	No	WES
22DCIS	TMEM26	p.D253N	10	63170430	C	T	Missense_Mutation	1051	2.8%	No	Yes	43%	0	61.4%	29.9%	Subclonal	D	Passenger	D		passenger	No	No	No	WES
22IDC	PCGF6	p.Y340*	10	105063694	CA	C	Frame_Shift_Del	51	31.4%	No	No	96%	0.66009	100.0%	58.1%	Clonal					passenger	No	No	No	WES
22DCIS	PCGF6	p.Y340*	10	105063694	CA	C	Frame_Shift_Del	50	60.0%	No	No	NA	0	100.0%	0.0%	Subclonal					passenger	No	No	No	WES
22IDC	SORCS3	p.R794Q	10	106974205	G	A	Missense_Mutation	92	27.2%	No	No	83%	0.4841	98.6%	57.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
22DCIS	SORCS3	p.R794Q	10	106974205	G	A	Missense_Mutation	46	73.9%	No	No	NA	0	100.0%	0.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
22IDC	GRK5	p.R190Q	10	121189922	G	A	Missense_Mutation	71	15.5%	No	No	48%	0.00748	78.2%	26.9%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
22DCIS	GRK5	p.R190Q	10	121189922	G	A	Missense_Mutation	58	31.0%	No	No	NA	0	100.0%	0.0%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
22DCIS	TACC2	p.V2378I	10	123971072	G	A	Missense_Mutation	122	13.9%	No	Yes	NA	0	100.0%	0.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
22IDC	CRY2	p.D381H	11	45891252	G	C	Missense_Mutation	192	9.9%	No	No	60%	0.03713	88.8%	38.6%	Subclonal	D	Passenger	D		passenger	No	No	No	WES
22DCIS	CRY2	p.D381H	11	45891252	G	C	Missense_Mutation	320	7.5%	No	No	58%	0.02296	83.6%	38.9%	Subclonal	D	Passenger	D		passenger	No	No	No	WES
22IDC	NR1H3	p.V218I	11	47282944	G	A	Missense_Mutation	128	19.5%	No	No	79%	0.32761	98.0%	54.4%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
22DCIS	NR1H3	p.V218I	11	47282944	G	A	Missense_Mutation	117	19.7%	No	No	54%	0.00156	75.2%	36.2%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
22IDC	CAPN1	p.E4del	11	64950177	CGGA	C	In_Frame_Del	105	9.5%	No	No	39%	0.00055	67.3%	21.0%	Subclonal					passenger	No	No	No	WES
22DCIS	CAPN1	p.E4del	11	64950177	CGGA	C	In_Frame_Del	140	13.6%	No	No	51%	0.00238	74.8%	32.6%	Subclonal					passenger	No	No	No	WES
22IDC	NUMA1	p.E1334del	11	71724546	TCTC	T	In_Frame_Del	157	16.6%	No	No	67%	0.06343	92.0%	46.5%	Subclonal					potentially_pathogen	No	Yes	No	WES
22DCIS	NUMA1	p.E1334del	11	71724546	TCTC	T	In_Frame_Del	184	30.4%	No	No	100%	0.91347	100.0%	81.5%	Clonal					potentially_pathogen	No	Yes	No	WES
22IDC	KIAA1731	p.P1682Qfs*5	11	93433116	GC	G	Frame_Shift_Del	119	25.2%	No	No	100%	0.69773	100.0%	69.2%	Clonal					passenger	No	No	No	WES
22DCIS	KIAA1731	p.P1682Qfs*5	11	93433116	GC	G	Frame_Shift_Del	138	46.4%	No	No	100%	0.90346	100.0%	91.1%	Clonal					passenger	No	No	No	WES
22IDC	KLRB1	p.L12V	12	9760402	A	C	Missense_Mutation	71	22.5%	No	No	92%	0.53673	100.0%	55.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
22DCIS	KLRB1	p.L12V	12	9760402	A	C	Missense_Mutation	78	43.6%	No	No	100%	0.86951	100.0%	84.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
22IDC	ARID2	p.R1068H	12	46245109	G	A	Missense_Mutation	211	17.1%	No	No	69%	0.04405	91.1%	50.7%	Subclonal	D	Passenger	N	T	passenger	No	Yes	Yes	WES
22DCIS	ARID2	p.R1068H	12	46245109	G	A	Missense_Mutation	179	35.8%	No	No	100%	0.77253	100.0%	87.5%	Clonal	D	Passenger	N	T	passenger	No	Yes	Yes	WES
22IDC	SCYL2	p.L395I	12	100709423	C	A	Missense_Mutation	90	5.6%	No	No	23%	0.00001	49.8%	9.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	UTP20	p.X1014_splice	12	101715409	T	C	Splice_Site	129	20.9%	No	No	85%	0.45016	98.8%	58.8%	Subclonal	D				passenger	No	No	No	WES
22DCIS	UTP20	p.X1014_splice	12	101715409	T	C	Splice_Site	135	40.7%	No	No	100%	0.93897	100.0%	81.8%	Clonal	D				passenger	No	No	No	WES
22IDC	CCDC60	p.E209K	12	119937950	G	A	Missense_Mutation	54	22.2%	No	No	90%	0.50601	100.0%	50.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	CCDC60	p.E209K	12	119937950	G	A	Missense_Mutation	50	38.0%	No	No	100%	0.86441	100.0%	72.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	RSRC2	p.R253Q	12	122995703	C	T	Missense_Mutation	68	33.8%	No	No	100%	0.76352	100.0%	74.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	RSRC2	p.R253Q	12	122995703	C	T	Missense_Mutation	100	44.0%	No	No	100%	0.84468	100.0%	87.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	SETDB2	p.K563*	13	50062498	CTAAAT	C	Frame_Shift_Del	85	25.9%	No	No	79%	0.39942	98.0%	53.5%	Subclonal					passenger	No	No	No	WES
22DCIS	SETDB2	p.K563*	13	50062498	CTAAAT	C	Frame_Shift_Del	60	35.0%	No	No	NA	0	100.0%	0.0%	Subclonal					passenger	No	No	No	WES
22IDC	IGF1R	p.E1037K	15	99478205	G	A	Missense_Mutation	123	9.8%	No	No	30%	0	49.5%	17.0%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
22DCIS	IGF1R	p.E1037K	15	99478205	G	A	Missense_Mutation	106	19.8%	No	No	54%	0.00364	76.9%	35.9%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
22DCIS	SYNGR3	p.P137T	16	2042708	C	A	Missense_Mutation	142	4.2%	No	Yes	12%	0	23.8%	4.9%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
22IDC	ADAMTS18	p.Y799C	16	77353882	T	C	Missense_Mutation	276	12.3%	No	No	62%	0.00731	84.2%	44.9%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
22DCIS	ADAMTS18	p.Y799C	16	77353882	T	C	Missense_Mutation	303	10.9%	No	No	62%	0.01999	84.6%	44.5%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
22IDC	SLC7A5	p.L349H	16	87871545	A	T	Missense_Mutation	110	17.3%	No	No	100%	0.64817	100.0%	62.1%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
22DCIS	SLC7A5	p.L349H	16	87871545	A	T	Missense_Mutation	133	15.8%	No	No	100%	0.81491	100.0%	64.0%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
22IDC	TP53	p.Q192*	17	7578275	G	A	Nonsense_Mutation	108	29.6%	No	No	100%	0.78716	100.0%	76.2%	Clonal	A				likely_pathogenic	Yes	Yes	Yes	WES
22DCIS	TP53	p.Q192*	17	7578275	G	A	Nonsense_Mutation	94	70.2%	No	No	100%	0	100.0%	93.1%	Clonal	A				likely_pathogenic	Yes	Yes	Yes	WES
22IDC	VPS4B	p.S248Kfs*2	18	61067328	C	CT	Frame_Shift_Ins	144	21.5%	No	No	88%	0.49751	99.0%	61.9%	Subclonal					passenger	No	No	No	WES
22DCIS	VPS4B	p.S248Kfs*2	18	61067328	C	CT	Frame_Shift_Ins	146	44.5%	No	No	100%	0.93691	100.0%	86.5%	Clonal					passenger	No	No	No	WES
22IDC	MUC16	p.V3336F	19	9077440	C	A	Missense_Mutation	125	12.0%	No	No	73%	0.26732	97.5%	44.1%	Subclonal		Passenger	N	T	passenger	No	No	No	WES
22DCIS	MUC16	p.V3336F	19	9077440	C	A	Missense_Mutation	186	11.8%	No	No	80%	0.55021	98.3%	52.3%	Clonal		Passenger	N	T	passenger	No	No	No	WES
22IDC	ZNF653	p.P409L	19	11597919	G	A	Missense_Mutation	134	13.4%	No	No	55%	0.00786	81.7%	34.8%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
22DCIS	ZNF653	p.P409L	19	11597919	G	A	Missense_Mutation	159	40.3%	No	No	100%	0.96858	100.0%	91.4%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
22IDC	SLC7A9	p.P248H	19	33351518	G	T	Missense_Mutation	172	21.5%	No	No	100%	0.74791	100.0%	82.3%	Clonal	D	Passenger		D	likely_pathogenic	No	No	No	WES
22DCIS	SLC7A9	p.P248H	19	33351518	G	T	Missense_Mutation	300	34.0%	No	No	100%	0.26498	100.0%	95.5%	Clonal	D	Passenger		D	likely_pathogenic	No	No	No	WES
22IDC	SLC7A9	p.E244K	19	33351531	C	T	Missense_Mutation	170	18.2%	No	No	100%	0.7762	100.0%	76.2%	Clonal	D	Passenger		D	likely_pathogenic	No	No	No	WES
22DCIS	SLC7A9	p.E244K	19	33351531	C	T	Missense_Mutation	285	34.4%	No	No	100%	0.28748	100.0%	95.4%	Clonal	D	Passenger		D	likely_pathogenic	No	No	No	WES
22IDC	PLEKHG2	p.E264K	19	39908240	G	A	Missense_Mutation	192	4.2%	No	No	17%	0	32.1%	8.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
22DCIS	PLEKHG2	p.E264K	19	39908240	G	A	Missense_Mutation	264	9.8%	No	No	37%	0	51.8%	24.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
22IDC	DACT3	p.R286H	19	47152772	C	T	Missense_Mutation	53	13.2%	No	No	54%	0.09435	92.7%	26.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
22DCIS	DACT3	p.R286H	19	47152772	C	T	Missense_Mutation	58	25.9%	No	No	96%	0.75345	100.0%	56.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
22IDC	SIGLEC5	p.A464P	19	52129359	C	G	Missense_Mutation	64	15.6%	No	No	64%	0.16413	95.6%	34.9%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
22DCIS	SIGLEC5	p.A464P	19	52129359	C	G	Missense_Mutation	72	36.1%	No	No	100%	0.93216	100.0%	80.2%	Clonal	N	Passenger		T	passenger	No	No	No	WES
22IDC	USP29	p.N188K	19	57640607	C	A	Missense_Mutation	162	13.0%	No	No	66%	0.08177	92.9%	43.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
22DCIS	USP29	p.N188K	19	57640607	C	A	Missense_Mutation	174	15.5%	No	No	73%	0.31904	96.1%	50.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
22IDC	ZIM3	p.K389N	19	57646538	C	A	Missense_Mutation	135	17.8%	No	No	90%	0.53547	100.0%	59.6%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
22DCIS	ZIM3	p.K389N	19	57646538	C	A	Missense_Mutation	185	30.3%	No	No	100%	0.60151	100.0%	86.9%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
22IDC	AP5S1	p.Q82*	20	3804585	C	T	Nonsense_Mutation	151	20.5%	No	Yes	84%	0.40439	98.6%	59.3%	Subclonal	D				likely_pathogenic	No	No	No	WES
22DCIS	AP5S1	p.Q82*	20	3804585	C	T	Nonsense_Mutation	208	34.6%	No	Yes	100%	0.83228	100.0%	87.9%	Clonal	D				likely_pathogenic	No	No	No	WES
22IDC	MKKS	p.Y474F	20	10386187	T	A	Missense_Mutation	200	4.5%	No	Yes	23%	0	41.7%	11.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	MKKS	p.Y474F	20	10386187	T	A	Missense_Mutation	287	8.4%	No	Yes	48%	0.0002	69.0%	32.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	ZNF341	p.Q105K	20	32333079	C	A	Missense_Mutation	167	10.8%	No	No	55%	0.00978	82.4%	34.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	ZNF341	p.Q105K	20	32333079	C	A	Missense_Mutation	202	15.3%	No	No	72%	0.24677	95.0%	51.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	IL17RA	p.V127L	22	17579733	G	C	Missense_Mutation	110	12.7%	No	No	65%	0.13185	94.8%	38.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES

22DCIS	IL17RA	p.V127L	22	17579733	G	C	Missense_Mutation	95	27.4%	No	No	100%	0.87402	100.0%	74.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	USP9X	p.A479T	23	41007637	G	A	Missense_Mutation	159	11.9%	No	No	44%	0.00009	66.2%	28.5%	Subclonal	D	Passenger	D	T	passenger	Yes	No	No	WES
22IDC	AKAP4	p.G454A	23	49958003	C	G	Missense_Mutation	125	8.8%	No	No	36%	0.00005	60.9%	19.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22DCIS	AKAP4	p.G454A	23	49958003	C	G	Missense_Mutation	130	20.0%	No	No	74%	0.35175	96.5%	51.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
22IDC	RRAGB	p.Q194*	23	55757999	C	T	Nonsense_Mutation	74	9.5%	No	No	38%	0.00437	73.7%	18.7%	Subclonal	A				passenger	No	No	No	WES
22DCIS	RRAGB	p.Q194*	23	55757999	C	T	Nonsense_Mutation	89	22.5%	No	No	84%	0.62994	98.7%	54.4%	Clonal	A				passenger	No	No	No	WES
22IDC	KIAA2022	p.D319N	23	73963437	C	T	Missense_Mutation	95	2.1%	No	No	9%	0	29.3%	2.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
22DCIS	KIAA2022	p.D319N	23	73963437	C	T	Missense_Mutation	99	22.2%	No	No	83%	0.60875	98.6%	55.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
22IDC	ATRX	p.R1401W	23	76912063	G	A	Missense_Mutation	91	12.1%	No	No	49%	0.01306	81.9%	27.7%	Subclonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	No	WES
22DCIS	ATRX	p.R1401W	23	76912063	G	A	Missense_Mutation	82	11.0%	No	No	41%	0.0051	72.3%	21.6%	Subclonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	No	WES
22IDC	ATRX	p.L1276I	23	76920251	G	T	Missense_Mutation	105	8.6%	No	No	35%	0.00018	62.6%	18.3%	Subclonal	D	Passenger	N	D	likely_pathogenic	Yes	Yes	No	WES
22DCIS	ATRX	p.L1276I	23	76920251	G	T	Missense_Mutation	141	18.4%	No	No	69%	0.15898	92.9%	47.5%	Subclonal	D	Passenger	N	D	likely_pathogenic	Yes	Yes	No	WES
22IDC	LUZP4	p.R5W	23	114524338	C	T	Missense_Mutation	47	10.6%	No	No	43%	0.04433	87.4%	18.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
22DCIS	LUZP4	p.R5W	23	114524338	C	T	Missense_Mutation	63	17.5%	No	No	65%	0.31003	95.7%	36.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
22IDC	ZBTB33	p.S297*	23	119388160	C	A	Nonsense_Mutation	193	33.2%	No	No	100%	0.63211	100.0%	87.5%	Clonal	D				passenger	No	No	No	WES
22DCIS	ZBTB33	p.S297*	23	119388160	C	A	Nonsense_Mutation	171	57.3%	No	No	100%	0.96789	100.0%	95.1%	Clonal	D				passenger	No	No	No	WES
22IDC	MAMLD1	p.W303C	23	149638829	G	C	Missense_Mutation	180	8.3%	No	No	34%	0	53.6%	20.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
22DCIS	MAMLD1	p.W303C	23	149638829	G	C	Missense_Mutation	183	19.7%	No	No	73%	0.20169	94.3%	53.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
22IDC	FLNA	p.K1621E	23	153585886	T	C	Missense_Mutation	115	7.0%	No	No	28%	0.00001	52.9%	14.2%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
22DCIS	FLNA	p.K1621E	23	153585886	T	C	Missense_Mutation	110	22.7%	No	No	85%	0.63952	98.8%	57.7%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
22IDC	FLNA	p.I1620F	23	153585889	T	A	Missense_Mutation	112	6.3%	No	No	25%	0	49.7%	12.1%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
22DCIS	FLNA	p.I1620F	23	153585889	T	A	Missense_Mutation	117	22.2%	No	No	83%	0.59756	98.5%	57.1%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
23IDC	RAVER2	p.V277F	1	65247105	G	T	Missense_Mutation	147	20.4%	No	No	100%	0.73951	100.0%	68.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	RAVER2	p.V277F	1	65247105	G	T	Missense_Mutation	114	18.4%	No	No	100%	0.78871	100.0%	66.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	ZNF687	p.S1123Pfs*43	1	151263335	CAG	C	Frame_Shift_Del	167	10.2%	No	No	51%	0.00575	78.8%	32.2%	Subclonal					passenger	No	No	No	WES
23DCIS	ZNF687	p.S1123Pfs*43	1	151263335	CAG	C	Frame_Shift_Del	139	15.1%	No	No	94%	0.67583	100.0%	59.2%	Clonal					passenger	No	No	No	WES
23IDC	ATF6	p.H660D	1	161928409	C	G	Missense_Mutation	161	23.6%	No	No	100%	0.82792	100.0%	77.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	ATF6	p.H660D	1	161928409	C	G	Missense_Mutation	113	27.4%	No	No	100%	0.9091	100.0%	82.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	BRINP2	p.L393V	1	177247863	C	G	Missense_Mutation	122	13.9%	No	No	87%	0.58651	98.9%	52.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	PTGS2	p.L131I	1	186647459	G	T	Missense_Mutation	119	21.8%	No	No	100%	0.76333	100.0%	69.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	PTGS2	p.L131I	1	186647459	G	T	Missense_Mutation	105	20.0%	No	No	100%	0.8096	100.0%	69.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	CR1	p.P1791T	1	207758062	C	A	Missense_Mutation	374	6.4%	No	No	32%	0	46.9%	21.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	CR1	p.P1791T	1	207758062	C	A	Missense_Mutation	244	2.9%	No	No	18%	0	35.5%	8.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	CENPF	p.F522V	1	214811326	T	G	Missense_Mutation	82	8.5%	No	No	53%	0.1472	92.9%	25.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	EPRS	p.R1209T	1	220153512	C	G	Missense_Mutation	104	5.8%	No	No	29%	0.00039	60.3%	13.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	EPRS	p.R1209T	1	220153512	C	G	Missense_Mutation	80	7.5%	No	No	47%	0.08844	89.5%	21.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	2-Mar	p.V335L	1	220955238	G	T	Missense_Mutation	132	10.6%	No	No	54%	0.02468	84.8%	32.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	2-Mar	p.V335L	1	220955238	G	T	Missense_Mutation	112	14.3%	No	No	89%	0.60954	100.0%	52.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	BIRC6	p.A3738T	2	32740700	G	A	Missense_Mutation	149	1.3%	No	No	7%	0	23.5%	1.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	BIRC6	p.A3738T	2	32740700	G	A	Missense_Mutation	110	14.5%	No	No	90%	0.62589	100.0%	53.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	BIRC6	p.A3738E	2	32740701	C	A	Missense_Mutation	151	1.3%	No	No	7%	0	23.1%	1.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	BIRC6	p.A3738E	2	32740701	C	A	Missense_Mutation	111	14.4%	No	No	89%	0.61782	100.0%	53.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	DHX57	p.Y749H	2	39070327	A	G	Missense_Mutation	81	9.9%	No	No	61%	0.25599	95.9%	31.0%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
23IDC	TET3	p.R469*	2	74274854	C	T	Nonsense_Mutation	188	13.8%	No	No	70%	0.13783	94.5%	48.1%	Subclonal	A				passenger	No	No	No	WES
23DCIS	TET3	p.R469*	2	74274854	C	T	Nonsense_Mutation	175	20.0%	No	No	100%	0.85038	100.0%	77.2%	Clonal	A				passenger	No	No	No	WES
23IDC	SH2D6	p.A3V	2	85662086	C	T	Missense_Mutation	110	12.7%	No	No	64%	0.15656	94.7%	38.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	SH2D6	p.A3V	2	85662086	C	T	Missense_Mutation	116	16.4%	No	No	100%	0.72578	100.0%	60.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	RGPD3	p.L812R	2	107049425	A	C	Missense_Mutation	245	1.6%	No	No	8%	0	20.3%	2.8%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
23DCIS	RGPD3	p.L812R	2	107049425	A	C	Missense_Mutation	213	4.2%	No	No	22%	0	40.3%	11.3%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
23IDC	PRPF40A	p.D811E	2	153515680	A	C	Missense_Mutation	173	0.6%	No	No	4%	0	18.7%	0.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	PRPF40A	p.D811E	2	153515680	A	C	Missense_Mutation	139	9.4%	No	No	58%	0.09919	91.2%	34.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	ITGA6	p.R536K	2	173349567	G	A	Missense_Mutation	109	6.4%	No	No	39%	0.00888	75.9%	18.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	ITGA6	p.R536K	2	173349567	G	A	Missense_Mutation	71	1.4%	No	No	9%	0.00037	46.0%	1.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	OBSL1	p.G1883S	2	220416287	C	T	Missense_Mutation	99	7.1%	No	No	43%	0.02418	82.3%	20.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	OBSL1	p.G1883S	2	220416287	C	T	Missense_Mutation	67	1.5%	No	No	9%	0.00067	48.7%	1.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	SLC16A14	p.G196V	2	230911255	C	A	Missense_Mutation	182	7.1%	No	No	43%	0.00142	71.2%	25.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	SLC16A14	p.G196V	2	230911255	C	A	Missense_Mutation	111	2.7%	No	No	17%	0.00006	46.9%	5.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	DIS3L2	p.T731N	2	233199112	C	A	Missense_Mutation	106	34.9%	No	No	100%	0.9154	100.0%	85.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	DIS3L2	p.T731N	2	233199112	C	A	Missense_Mutation	109	31.2%	No	No	100%	0.94404	100.0%	84.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	CBLB	p.D427N	3	105439019	C	T	Missense_Mutation	142	9.2%	No	No	55%	0.0504	88.5%	32.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	Yes	No	WES
23DCIS	CBLB	p.D427N	3	105439019	C	T	Missense_Mutation	80	20.0%	No	No	100%	0.82443	100.0%	67.6%	Clonal	D	Passenger	D	D	likely_pathogenic	No	Yes	No	WES
23IDC	STXBP5L	p.K223*	3	120840549	A	T	Nonsense_Mutation	91	14.3%	No	No	87%	0.52133	98.9%	48.9%	Clonal	A				passenger	No	No	No	WES
23DCIS	STXBP5L	p.K223*	3	120840549	A	T	Nonsense_Mutation	77	13.0%	No	No	81%	0.51207	98.5%	42.5%	Clonal	A				passenger	No	No	No	WES
23IDC	PIK3CA	p.N1068Kfs*5	3	178952146	G	GA	Frame_Shift_Ins	292	66.4%	No	No	100%	0.18767	100.0%	98.0%	Clonal					likely_pathogenic	Yes	Yes	Yes	WES
23DCIS	PIK3CA	p.N1068Kfs*5	3	178952146	G	GA	Frame_Shift_Ins	300	75.3%	No	No	100%	0.19726	100.0%	98.1%	Clonal					likely_pathogenic	Yes	Yes	Yes	WES
23IDC	MUC4	p.S3159Y	3	195508975	G	T	Missense_Mutation	618	2.3%	No	Yes	9%	0	14.8%	5.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	MUC4	p.S3159Y	3	195508975	G	T	Missense_Mutation	810	0.2%	No	Yes	1%	0	4.2%	0.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	NCBP2	p.Y89F	3	196664514	T	A	Missense_Mutation	71	8.5%	No	Yes	44%	0.05593	86.2%	20.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	DOK7	p.G16R	4	3465148	G	C	Missense_Mutation	72	27.8%	No	Yes	100%	0.80011	100.0%	66.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	DOK7	p.G16R	4	3465148	G	C	Missense_Mutation	103	25.2%	No	Yes	100%	0.83345	100.0%	74.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	ADRA2C	p.S213Y	4	3768971	C	A	Missense_Mutation	126	4.8%	No	No	25%	0.00003	51.6%	11.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	CC2D2A	p.V1229L	4	15575863	G	C	Missense_Mutation	85	10.6%	No	No	54%	0.07912	90.7%	28.3%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
23DCIS	CC2D2A	p.V1229L	4	15575863	G	C	Missense_Mutation	81	8.6%	No	No	45%	0.04402	84.9%	21.9%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
23IDC	GPR125	p.S1280Y	4	22389455	G	T	Missense_Mutation	127	16.5%	No	No	84%	0.4852	98.7%	54.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	GPR125	p.S1280Y	4	22389455	G	T	Missense_Mutation	77	32.5%	No	No	100%	0.90549	100.0%	79.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	KIAA1239	p.R621W	4	37445471	A	T	Missense_Mutation	107	14.0%	No	No	71%	0.26966	96.9%	43.2%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
23DCIS	KIAA1239	p.R621W	4	37445471	A	T	Missense_Mutation	90	20.0%	No	No	100%	0.73762	100.0%	61.3%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
23DCIS	PDGFRA	p.T489N	4	55139805	C	A	Missense_Mutation	80	6.3%	No	No	39%	0.03846	82.9%	16.6%	Subclonal	D	Passenger	N	T	passenger	Yes	Yes	No	WES
23IDC	FAM47E-STBD1	p.W305C	4	77199266	G	T	Missense_Mutation	223	18.4%	No	No	93%	0.6558	100.0%	67.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	FAM47E-STBD1	p.W305C	4	77199266	G	T	Missense_Mutation	170	27.1%	No	No	100%	0.73853	100.0%	84.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	CCNG2	p.E240D	4	78085441	G	C	Missense_Mutation	78	6.4%	No	No	32%	0.00503	70.9%	13.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	CCNG2	p.E240D	4	78085441	G	C	Missense_Mutation	64	1.6%	No	No	8%	0.00014	42.6%	1.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	DKK2	p.S79I	4	107847093	C	A	Missense_Mutation	148	18.2%	No	No	92%	0.6241	100.0%	62.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	DKK2	p.S79I	4	107847093	C	A	Missense_Mutation	75	33.3%	No	No	100%	0.91721	100.0%	79.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	PAM	p.H362D	5	102295757	C	G	Missense_Mutation	42	16.7%	No	Yes	68%	0.37438	97.4%	32.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	PAM	p.H362D	5	102295757	C	G	Missense_Mutation	35	25.7%	No	Yes	100%	0.68975	100.0%	50.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	PRR16	p.N141D	5	120021979	A	G	Missense_Mutation	121	27.3%	No	Yes	100%	0.83995	100.0%	73.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	PRR16	p.N141D	5	120021979	A	G	Missense_Mutation	64	40.6%	No	Yes	100%	0.91053	100.0%	80.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	ADAMTS19	p.E1145D	5	129070765	G	C	Missense_Mutation	84	10.7%	No	Yes	43%	0.01026	77.0%	23.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	ADAMTS19	p.E1145D	5	129070765	G	C	Missense_Mutation	59	5.1%	No	Yes	21%	0.00098	58.1%	7.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	FCHSD1	p.L130H	5	141028862	A	T	Missense_Mutation	159	15.1%	No	Yes	61%	0.02898	86.3%	41.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	FCHSD1	p.L130H	5	141028862	A	T	Missense_Mutation	138	25.4%	No	Yes	100%	0.81996	100.0%	72.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	UIMC1	p.H398Y	5	176395564	G	A	Missense_Mutation	153	9.8%	No	Yes	40%	0.00005	62.6%	24.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	UIMC1	p.H398Y	5	176395564	G	A	Missense_Mutation	134	4.5%	No	Yes	28%	0.00029	58.0%	12.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	GPR111	p.N362H	6	47649379	A	C	Missense_Mutation	131	9.2%	No	No	56%	0.06183	89.6%	31.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	GPR111	p.N362H	6	47649379	A	C	Missense_Mutation	69	10.1%	No	No	63%	0.30431	96.7%	30.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	SENP6	p.N375H	6	76376556	A	C	Missense_Mutation	118	14.4%	No	No	87%	0.53834	99.0%	53.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	SENP6	p.N375H	6	76376556	A	C	Missense_Mutation	118	25.4%	No	No	100%	0.93302	100.0%	82.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	BACH2	p.L27I	6	90718485	G	T	Missense_Mutation	164	11.0%	No	No	79%	0.47174	98.3%	49.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	UFL1	p.H92Q	6	96973196	T	G	Missense_Mutation	98	17.3%	No	No	100%	0.68489	100.0%	60.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	UFL1	p.H92Q	6	96973196	T	G	Missense_Mutation	78	14.1%	No	No	100%	0.67034	100.0%	51.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	ASCC3	p.K1556N	6	101073185	T	A	Missense_Mutation	154	14.3%	No	No	87%	0.53307	98.9%	56.3%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
23DCIS	ASCC3	p.K1556N	6	101073185	T	A	Missense_Mutation	124	21.8%	No	No	100%	0.86315	100.0%	78.3%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
23IDC	PTPRK	p.D444H	6	128410970	C	G	Missense_Mutation	177	0.6%	No	No	3%	0	18.3%	0.4%	Subclonal	D	Passenger	N	T	passenger	No	Yes	No	WES
23DCIS	PTPRK	p.D444H	6	128410970	C	G	Missense_Mutation	134	19.4%	No	No	100%	0.83042	100.0%	75.4%	Clonal	D	Passenger	N	T	passenger	No	Yes	No	WES
23DCIS	AHI1	p.T253N	6	135784436	G	T	Missense_Mutation	92	5.4%	No	No	39%	0.04373	83.9%	16.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	IFNGR1	p.P328A	6	137519656	G	C	Missense_Mutation	98	19.4%	No	No	100%	0.74633	100.0%	65.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	IFNGR1	p.P328A	6	137519656	G	C	Missense_Mutation	73	12.3%	No	No	100%	0.64758	100.0%	47.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	IFNGR1	p.S306L	6	137519721	G	A	Missense_Mutation	99	17.2%	No	No	100%	0.67927	100.0%	60.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	IFNGR1	p.S306L	6	137519721	G	A	Missense_Mutation	72	13.9%	No	No	100%	0.70614	100.0%	52.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	TMEM181	p.G598Afs*13	6	159052873	GGC	G	Frame_Shift_Del	152	11.2%	No	No	68%	0.18859	95.6%	42.5%	Subclonal					passenger	No	No	No	WES
23DCIS	TMEM181	p.G598Afs*13	6	159052873	GGC	G	Frame_Shift_Del	155	2.6%	No	No	19%	0.00002	45.9%	7.1%	Subclonal					passenger	No	No	No	WES
23IDC	POM121	p.S647G	7	72413266	A	G	Missense_Mutation	301	9.6%	No	No	49%	0.00002	67.8%	33.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	POM121	p.S647G	7	72413266	A	G	Missense_Mutation	305	15.1%	No	No	94%	0.71885	100.0%	69.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	KRIT1	p.L557Q	7	91843985	A	T	Missense_Mutation	87	13.8%	No	No	84%	0.48699	98.7%	46.4%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
23DCIS	KRIT1	p.L557Q	7	91843985	A	T	Missense_Mutation	69	21.7%	No	No	100%	0.80097	100.0%	65.2%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
23IDC	GRM8	p.T349A	7	126542707	T	C	Missense_Mutation	79	13.9%	No	No	84%	0.49375	98.8%	45.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
23DCIS	GRM8	p.T349A	7	126542707	T	C	Missense_Mutation	75	21.3%	No	No	100%	0.80068	100.0%	66.0%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
23IDC	WDR91	p.E403del	7	134880930	ACTC	A	In_Frame_Del	140	11.4%	No	No	69%	0.23039	96.4%	42.7%	Subclonal					passenger	No	No	No	WES
23DCIS	WDR91	p.E403del	7	134880930	ACTC	A	In_Frame_Del	134	20.9%	No	No	100%	0.83576	100.0%	75.1%	Clonal					passenger	No	No	No	WES
23DCIS	KDM7A	p.L739M	7	139796514	G	T	Missense_Mutation	88	5.7%	No	No	35%	0.0172	77.0%	15.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	GBX1	p.E190del	7	150846197	TCTC	T	In_Frame_Del	126	12.7%	No	No	77%	0.38177	98.1%	47.1%	Subclonal					passenger	No	No	No	WES
23DCIS	GBX1	p.E190del	7	150846197	TCTC	T	In_Frame_Del	88	18.2%	No	No	100%	0.75601	100.0%	61.6%	Clonal					passenger	No	No	No	WES
23DCIS	RNF32	p.C70*	7	156437387	C	A	Nonsense_Mutation	97	5.2%	No	No	32%	0.00647	70.7%	13.6%	Subclonal	A				passenger	No	No	No	WES
23IDC	HMBOX1	p.X8_splice	8	28827558	A	T	Splice_Site	32	12.5%	No	Yes	51%	0.21534	94.7%	19.9%	Subclonal	D				likely_pathogenic	No	No	No	WES
23IDC	WRN	p.Y413*	8	30938782	T	G	Nonsense_Mutation	115	9.6%	No	Yes	39%	0.00045	65.8%	21.6%	Subclonal	A				likely_pathogenic	No	Yes	No	WES
23DCIS	WRN	p.Y413*	8	30938782	T	G	Nonsense_Mutation	90	6.7%	No	Yes	28%	0.00019	57.6%	12.7%	Subclonal	A				likely_pathogenic	No	Yes	No	WES
23IDC	FNTA	p.Y100C	8	42919256	A	G	Missense_Mutation	173	15.6%	No	No	100%	0.89745	100.0%	79.2%	Clonal	D	Passenger	D		passenger	No	No	No	WES
23DCIS	FNTA	p.Y100C	8	42919256	A	G	Missense_Mutation	197	9.6%	No	No	100%	0.90978	100.0%	74.4%	Clonal	D	Passenger	D		passenger	No	No	No	WES
23IDC	RP1	p.N1453S	8	55540800	A	G	Missense_Mutation	179	6.1%	No	No	37%	0.00027	64.2%	20.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	RP1	p.N1453S	8	55540800	A	G	Missense_Mutation	120	3.3%	No	No	21%	0.00009	50.7%	7.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	KIAA2026	p.T1058P	9	5922824	T	G	Missense_Mutation	116	25.0%	No	Yes	100%	0.78331	100.0%	68.2%	Clonal	N	Passenger	N		passenger	No	No	No	WES
23DCIS	KIAA2026	p.T1058P	9	5922824	T	G	Missense_Mutation	72	36.1%	No	Yes	100%	0.82464	100.0%	78.7%	Clonal	N	Passenger	N		passenger	No	No	No	WES
23IDC	TPD52L3	p.K78E	9	6328827	A	G	Missense_Mutation	132	16.7%	No	Yes	68%	0.14771	93.6%	45.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	TPD52L3	p.K78E	9	6328827	A	G	Missense_Mutation	74	6.8%	No	Yes	28%	0.001	62.1%	12.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	DDX58	p.T260Nfs*19	9	32489360	TTG	T	Frame_Shift_Del	54	20.4%	No	Yes	83%	0.55012	98.7%	45.5%	Clonal					likely_pathogenic	No	No	No	WES
23DCIS	DDX58	p.T260Nfs*19	9	32489360	TTG	T	Frame_Shift_Del	44	27.3%	No	Yes	100%	0.74178	100.0%	57.8%	Clonal					likely_pathogenic	No	No	No	WES
23IDC	AKNA	p.N355D	9	117139024	T	C	Missense_Mutation	171	1.2%	No	No	6%	0	20.4%	1.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	AKNA	p.N355D	9	117139024	T	C	Missense_Mutation	136	11.0%	No	No	68%	0.272	96.3%	41.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	TNC	p.Q1198H	9	117826241	C	A	Missense_Mutation	89	18.0%	No	No	100%	0.75186	100.0%	61.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	GTF3C5	p.R467C	9	135932280	C	T	Missense_Mutation	53	13.2%	No	No	67%	0.30336	97.3%	32.1%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
23DCIS	GTF3C5	p.R467C	9	135932280	C	T	Missense_Mutation	46	39.1%	No	No	100%	0.87184	100.0%	77.6%	Clonal	D	Passenger		T	passenger	No	No	No	WES
23DCIS	DPH7	p.P249T	9	140459376	G	T	Missense_Mutation	79	6.3%	No	No	32%	0.00436	70.0%	13.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	ARRDC1	p.X74_splice	9	140507447	TGGCAGACAAGGGTAA	T	Splice_Site	77	18.2%	No	No	92%	0.58002	100.0%	52.6%	Clonal					passenger	No	No	No	WES
23DCIS	ARRDC1	p.X74_splice	9	140507447	TGGCAGACAAGGGTAA	T	Splice_Site	54	16.7%	No	No	100%	0.66206	100.0%	48.3%	Clonal					passenger	No	No	No	WES
23IDC	ITGA8	p.T380A	10	15688914	T	C	Missense_Mutation	92	21.7%	No	No	100%	0.73117	100.0%	65.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	ITGA8	p.T380A	10	15688914	T	C	Missense_Mutation	60	13.3%	No	No	83%	0.52964	98.6%	39.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	DKK1	p.D88H	10	54074701	G	C	Missense_Mutation	142	6.3%	No	No	32%	0.00006	58.2%	16.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	DKK1	p.D88H	10	54074701	G	C	Missense_Mutation	89	4.5%	No	No	23%	0.00048	56.7%	9.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	C10orf76	p.Q649H	10	103609563	C	A	Missense_Mutation	82	18.3%	No	No	93%	0.58982	100.0%	54.0%	Clonal	D	Passenger	N		passenger	No	No	No	WES
23DCIS	C10orf76	p.Q649H	10	103609563	C	A	Missense_Mutation	64	15.6%	No	No	81%	0.52059	98.6%	43.1%	Clonal	D	Passenger	N		passenger	No	No	No	WES
23IDC	B4GALNT4	p.C24*	11	369875	C	A	Nonsense_Mutation	24	12.5%	No	No	51%	0.26403	95.7%	17.3%	Subclonal	A				passenger	No	No	No	WES
23IDC	ART5	p.X20_splice	11	3661603	T	G	Splice_Site	105	7.6%	No	Yes	31%	0.00008	57.7%	15.5%	Subclonal	D				likely_pathogenic	No	No	No	WES
23DCIS	ART5	p.X20_splice	11	3661603	T	G	Splice_Site	81	19.8%	No	Yes	100%	0.71942	100.0%	58.9%	Clonal	D				likely_pathogenic	No	No	No	WES
23IDC	OR51I2	p.R305H	11	5475632	G	A	Missense_Mutation	71	11.3%	No	No	57%	0.14419	94.0%	29.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	OR51I2	p.R305H	11	5475632	G	A	Missense_Mutation	45	4.4%	No	No	23%	0.02042	75.0%	6.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	OR52L1	p.G111R	11	6007830	C	T	Missense_Mutation	81	7.4%	No	No	37%	0.01017	76.1%	17.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	OR52L1	p.G111R	11	6007830	C	T	Missense_Mutation	50	20.0%	No	No	100%	0.67857	100.0%	50.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	LRRC55	p.D105Y	11	56949680	G	T	Missense_Mutation	177	7.3%	No	No	45%	0.00233	73.2%	26.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	LRRC55	p.D105Y	11	56949680	G	T	Missense_Mutation	189	1.6%	No	No	11%	0	32.3%	3.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	OR4D10	p.I135V	11	59245305	A	G	Missense_Mutation	89	14.6%	No	No	76%	0.43926	98.1%	44.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	AMOTL1	p.D766H	11	94599141	G	C	Missense_Mutation	153	17.6%	No	No	89%	0.58026	100.0%	60.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	AMOTL1	p.D766H	11	94599141	G	C	Missense_Mutation	81	17.3%	No	No	90%	0.61825	100.0%	51.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	KDM5A	p.F298L	12	463379	A	G	Missense_Mutation	128	14.1%	No	No	71%	0.24188	96.6%	45.3%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	Yes	No	WES
23DCIS	KDM5A	p.F298L	12	463379	A	G	Missense_Mutation	93	11.8%	No	No	85%	0.55984	98.8%	45.6%	Clonal	D	Passenger	N	D	likely_pathogenic	No	Yes	No	WES
23IDC	GPR162	p.V337M	12	6934790	G	A	Missense_Mutation	106	15.1%	No	No	91%	0.58109	100.0%	54.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	GPR162	p.V337M	12	6934790	G	A	Missense_Mutation	87	9.2%	No	No	66%	0.33856	97.1%	33.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	ACSM4	p.A277T	12	7470686	G	A	Missense_Mutation	177	10.2%	No	No	62%	0.07176	91.0%	39.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	ACSM4	p.A277T	12	7470686	G	A	Missense_Mutation	158	16.5%	No	No	100%	0.81704	100.0%	71.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	GUCY2C	p.D623G	12	14796570	T	C	Missense_Mutation	102	15.7%	No	No	95%	0.61297	100.0%	55.6%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
23DCIS	GUCY2C	p.D623G	12	14796570	T	C	Missense_Mutation	79	15.2%	No	No	100%	0.71145	100.0%	55.1%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
23IDC	HDAC7	p.A299T	12	48189700	C	T	Missense_Mutation	75	22.7%	No	No	100%	0.72955	100.0%	63.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	HDAC7	p.A299T	12	48189700	C	T	Missense_Mutation	67	3.0%	No	No	22%	0.01475	72.0%	6.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	CNOT2	p.T362S	12	70732508	A	T	Missense_Mutation	108	9.3%	No	No	47%	0.01546	81.0%	25.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	IGF1	p.X134_splice	12	102813286	C	A	Splice_Site	121	17.4%	No	No	88%	0.55201	100.0%	56.7%	Clonal	D				likely_pathogenic	No	No	No	WES
23DCIS	IGF1	p.X134_splice	12	102813286	C	A	Splice_Site	59	23.7%	No	No	100%	0.77406	100.0%	62.2%	Clonal	D				likely_pathogenic	No	No	No	WES
23DCIS	RNF17	p.X1483_splice	13	25444878	G	C	Splice_Site	66	6.1%	No	No	32%	0.01397	74.7%	12.3%	Subclonal	D				passenger	No	No	No	WES
23IDC	ZC3H13	p.S224G	13	46584559	T	C	Missense_Mutation	127	11.0%	No	No	56%	0.03987	87.5%	33.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	ZC3H13	p.S224G	13	46584559	T	C	Missense_Mutation	69	1.4%	No	No	8%	0.00006	39.6%	1.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	RCBTB1	p.D431_T432del	13	50115838	ACTGTGT	A	In_Frame_Del	79	7.6%	No	No	40%	0.02255	79.8%	18.2%	Subclonal					passenger	No	No	No	WES
23IDC	NALCN	p.I1679V	13	101707829	T	C	Missense_Mutation	107	10.3%	No	No	52%	0.03695	86.4%	29.2%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
23DCIS	NALCN	p.I1679V	13	101707829	T	C	Missense_Mutation	81	6.2%	No	No	32%	0.00594	70.4%	13.7%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
23IDC	GRK1	p.S5F	13	114321715	C	T	Missense_Mutation	63	15.9%	No	No	64%	0.26303	95.9%	35.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	GRK1	p.S5F	13	114321715	C	T	Missense_Mutation	69	20.3%	No	No	100%	0.71914	100.0%	57.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	METTL3	p.R536Q	14	21967193	C	T	Missense_Mutation	88	9.1%	No	No	46%	0.02796	83.8%	23.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	METTL3	p.R536Q	14	21967193	C	T	Missense_Mutation	54	1.9%	No	No	10%	0.00084	50.1%	1.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	DNAAF2	p.E694*	14	50092694	C	A	Nonsense_Mutation	97	10.3%	No	No	54%	0.08141	89.7%	29.3%	Subclonal	D				passenger	No	No	No	WES
23IDC	PYGL	p.M351I	14	51383399	C	T	Missense_Mutation	87	13.8%	No	No	70%	0.28273	97.1%	40.0%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
23DCIS	PYGL	p.M351I	14	51383399	C	T	Missense_Mutation	71	29.6%	No	No	100%	0.85558	100.0%	74.7%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
23IDC	MAP3K9	p.A142P	14	71267780	C	G	Missense_Mutation	101	9.9%	No	Yes	40%	0.00173	69.7%	21.8%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
23DCIS	MAP3K9	p.A142P	14	71267780	C	G	Missense_Mutation	76	1.3%	No	Yes	7%	0.00002	36.1%	1.2%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
23IDC	ZFYVE1	p.E166V	14	73465010	T	A	Missense_Mutation	89	19.1%	No	Yes	78%	0.44957	98.0%	48.7%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
23DCIS	ZFYVE1	p.E166V	14	73465010	T	A	Missense_Mutation	75	25.3%	No	Yes	100%	0.81447	100.0%	69.5%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
23DCIS	NUMB	p.P437T	14	73743933	G	T	Missense_Mutation	85	11.8%	No	No	61%	0.2051	94.9%	33.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	PGBD4	p.N332K	15	34395728	C	G	Missense_Mutation	199	14.6%	No	Yes	74%	0.20457	96.1%	51.7%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
23DCIS	PGBD4	p.N332K	15	34395728	C	G	Missense_Mutation	97	9.3%	No	Yes	48%	0.0404	85.0%	25.5%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
23DCIS	TLN2	p.L739M	15	63000743	C	A	Missense_Mutation	97	5.2%	No	Yes	27%	0.00059	59.4%	11.4%	Subclonal	D	Driver	N	D	likely_pathogenic	No	No	No	WES
23DCIS	KBTBD13	p.D234E	15	65369855	C	G	Missense_Mutation	89	14.6%	No	Yes	76%	0.43926	98.1%	44.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	ZNF174	p.E351Q	16	3458746	G	C	Missense_Mutation	176	5.1%	No	No	21%	0	37.8%	10.6%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
23DCIS	ZNF174	p.E351Q	16	3458746	G	C	Missense_Mutation	121	1.7%	No	No	9%	0	29.7%	2.1%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
23IDC	SLX4	p.D1218A	16	3639986	T	G	Missense_Mutation	121	22.3%	No	No	91%	0.6701	100.0%	61.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	SLX4	p.D1218A	16	3639986	T	G	Missense_Mutation	98	24.5%	No	No	100%	0.82754	100.0%	72.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	PPL	p.E1247Afs*19	16	4934916	TCC	T	Frame_Shift_Del	162	21.6%	No	No	88%	0.62258	99.0%	63.3%	Clonal					passenger	No	No	No	WES
23DCIS	PPL	p.E1247Afs*19	16	4934916	TCC	T	Frame_Shift_Del	120	25.0%	No	No	100%	0.84129	100.0%	76.7%	Clonal					passenger	No	No	No	WES
23IDC	WWP2	p.G314*	16	69942689	G	T	Nonsense_Mutation	142	35.2%	No	Yes	100%	0.62677	100.0%	86.1%	Clonal	A				likely_pathogenic	No	No	No	WES
23DCIS	WWP2	p.G314*	16	69942689	G	T	Nonsense_Mutation	102	62.7%	No	Yes	100%	0.28228	100.0%	93.6%	Clonal	A				likely_pathogenic	No	No	No	WES
23IDC	TP53	p.C238G	17	7577569	A	C	Missense_Mutation	52	32.7%	Yes	Yes	100%	0.81585	100.0%	68.6%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
23DCIS	TP53	p.C238G	17	7577569	A	C	Missense_Mutation	48	37.5%	Yes	Yes	100%	0.92794	100.0%	75.8%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
23IDC	SYNRG	p.E273Q	17	35937484	C	G	Missense_Mutation	90	21.1%	No	No	100%	0.71073	100.0%	63.2%	Clonal	N	Passenger		T	passenger	No	No	No	WES
23DCIS	SYNRG	p.E273Q	17	35937484	C	G	Missense_Mutation	68	1.5%	No	No	9%	0.00058	48.0%	1.7%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
23IDC	CWC25	p.K184R	17	36966796	T	C	Missense_Mutation	50	8.0%	No	No	40%	0.06544	88.4%	15.9%	Subclonal	D	Passenger			passenger	No	No	No	WES
23DCIS	CWC25	p.K184R	17	36966796	T	C	Missense_Mutation	54	7.4%	No	No	46%	0.15699	93.0%	18.0%	Subclonal	D	Passenger			passenger	No	No	No	WES
23IDC	RUNDC1	p.F56C	17	41132760	T	G	Missense_Mutation	79	17.7%	No	No	90%	0.55819	100.0%	51.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	RUNDC1	p.F56C	17	41132760	T	G	Missense_Mutation	119	21.8%	No	No	100%	0.81228	100.0%	70.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	CDC27	p.R266*	17	45234325	G	A	Nonsense_Mutation	91	2.2%	No	No	11%	0	38.1%	2.9%	Subclonal	A				likely_pathogenic	No	No	Yes	WES
23DCIS	CDC27	p.R266*	17	45234325	G	A	Nonsense_Mutation	89	4.5%	No	No	23%	0.00048	56.7%	9.0%	Subclonal	A				likely_pathogenic	No	No	Yes	WES
23DCIS	ST6GALNAC2	p.H119Pfs*54	17	74570452	TGA	T	Frame_Shift_Del	105	12.4%	No	No	64%	0.21064	95.1%	37.9%	Subclonal					passenger	No	No	No	WES
23IDC	BAIAP2	p.R476Q	17	79080634	G	A	Missense_Mutation	79	22.8%	No	No	100%	0.73822	100.0%	64.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
23DCIS	BAIAP2	p.R476Q	17	79080634	G	A	Missense_Mutation	86	23.3%	No	No	100%	0.80354	100.0%	68.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
23IDC	SERPINB4	p.Q211H	18	61306554	C	G	Missense_Mutation	125	6.4%	No	No	32%	0.00021	60.8%	16.3%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
23DCIS	SERPINB4	p.Q211H	18	61306554	C	G	Missense_Mutation	79	2.5%	No	No	13%	0.00008	45.0%	3.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
23IDC	PTBP1	p.G332S	19	806431	G	A	Missense_Mutation	76	14.5%	No	Yes	59%	0.13266	92.4%	33.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	PTBP1	p.G332S	19	806431	G	A	Missense_Mutation	79	27.8%	No	Yes	100%	0.83302	100.0%	74.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	MUC16	p.E11386D	19	9047473	T	G	Missense_Mutation	50	10.0%	No	Yes	41%	0.04523	84.0%	17.5%	Subclonal		Passenger	N	T	passenger	No	No	No	WES
23DCIS	MUC16	p.E11386D	19	9047473	T	G	Missense_Mutation	64	34.4%	No	Yes	100%	0.85501	100.0%	80.7%	Clonal		Passenger	N	T	passenger	No	No	No	WES
23IDC	ZNF443	p.E216V	19	12542339	T	A	Missense_Mutation	374	13.4%	No	Yes	54%	0	69.3%	41.3%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
23DCIS	ZNF443	p.E216V	19	12542339	T	A	Missense_Mutation	395	3.0%	No	Yes	19%	0	32.0%	10.4%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
23IDC	MAST1	p.M476L	19	12975682	A	T	Missense_Mutation	91	13.2%	No	Yes	54%	0.0445	86.2%	30.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	MAST1	p.M476L	19	12975682	A	T	Missense_Mutation	124	25.0%	No	Yes	100%	0.84279	100.0%	77.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	WTIP	p.R397C	19	34991070	C	T	Missense_Mutation	126	15.9%	No	No	80%	0.42454	98.4%	52.0%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
23DCIS	WTIP	p.R397C	19	34991070	C	T	Missense_Mutation	145	29.7%	No	No	100%	0.73002	100.0%	85.1%	Clonal	D	Passenger		T	passenger	No	No	No	WES
23IDC	ZNF573	p.H8Q	19	38264346	G	C	Missense_Mutation	70	15.7%	No	No	79%	0.43894	98.5%	43.6%	Subclonal		Passenger			passenger	No	No	No	WES
23DCIS	ZNF573	p.H8Q	19	38264346	G	C	Missense_Mutation	54	1.9%	No	No	12%	0.00428	59.5%	2.3%	Subclonal		Passenger			passenger	No	No	No	WES
23IDC	CIC	p.R201Q	19	42791716	G	A	Missense_Mutation	161	24.8%	No	No	100%	0.8332	100.0%	79.8%	Clonal	D	Passenger			passenger	No	Yes	No	WES
23DCIS	CIC	p.R201Q	19	42791716	G	A	Missense_Mutation	117	17.1%	No	No	89%	0.62388	100.0%	56.6%	Clonal	D	Passenger			passenger	No	Yes	No	WES
23IDC	SIGLEC5	p.S294C	19	52131203	G	C	Missense_Mutation	173	25.4%	No	No	100%	0.83026	100.0%	81.7%	Clonal	N	Passenger		T	passenger	No	No	No	WES
23DCIS	SIGLEC5	p.S294C	19	52131203	G	C	Missense_Mutation	158	21.5%	No	No	100%	0.83214	100.0%	73.8%	Clonal	N	Passenger		T	passenger	No	No	No	WES
23IDC	ZNF835	p.D310E	19	57175637	G	T	Missense_Mutation	307	0.3%	No	No	2%	0	8.7%	0.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	ZNF835	p.D310E	19	57175637	G	T	Missense_Mutation	279	5.0%	No	No	26%	0	42.5%	15.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	CCM2L	p.P38S	20	30602788	C	T	Missense_Mutation	108	25.0%	No	No	100%	0.80416	100.0%	74.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	CCM2L	p.P38S	20	30602788	C	T	Missense_Mutation	164	21.3%	No	No	100%	0.82115	100.0%	81.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	MYH7B	p.S214C	20	33568851	C	G	Missense_Mutation	64	1.6%	No	Yes	6%	0	33.1%	1.1%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
23DCIS	MYH7B	p.S214C	20	33568851	C	G	Missense_Mutation	103	6.8%	No	Yes	42%	0.02667	81.4%	20.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
23IDC	L3MBTL1	p.K680T	20	42164916	A	C	Missense_Mutation	72	22.2%	No	No	100%	0.71457	100.0%	61.9%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
23DCIS	L3MBTL1	p.K680T	20	42164916	A	C	Missense_Mutation	91	20.9%	No	No	100%	0.84719	100.0%	71.7%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
23IDC	SLC12A5	p.H618D	20	44675071	C	G	Missense_Mutation	68	14.7%	No	No	74%	0.37522	98.0%	40.0%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
23DCIS	SLC12A5	p.H618D	20	44675071	C	G	Missense_Mutation	70	47.1%	No	No	100%	0.26413	100.0%	87.8%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
23IDC	PFKL	p.D364Y	21	45739261	G	T	Missense_Mutation	56	12.5%	No	No	63%	0.25537	96.7%	30.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23DCIS	PFKL	p.D364Y	21	45739261	G	T	Missense_Mutation	53	11.3%	No	No	70%	0.41317	97.9%	31.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
23IDC	APOL6	p.P37L	22	36054721	C	T	Missense_Mutation	126	6.3%	No	No	26%	0	48.4%	12.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23DCIS	APOL6	p.P37L	22	36054721	C	T	Missense_Mutation	82	4.9%	No	No	25%	0.0014	61.3%	9.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
23IDC	KLHDC7B	p.C414*	22	50987837	C	A	Nonsense_Mutation	149	11.4%	No	No	46%	0.00064	70.6%	29.0%	Subclonal	D				passenger	No	No	No	WES
23DCIS	KLHDC7B	p.C414*	22	50987837	C	A	Nonsense_Mutation	93	2.2%	No	No	11%	0.00001	38.4%	3.0%	Subclonal	D				passenger	No	No	No	WES
23DCIS	RPL10	p.K170del	23	153629053	CAAA	C	In_Frame_Del	72	30.6%	No	Yes	100%	0.82648	100.0%	72.1%	Clonal					potentially_pathoger	No	Yes	No	WES
24IDC	PDPN	p.W93*	1	13910579	G	A	Nonsense_Mutation	71	28.2%	No	No	100%	0.8222	100.0%	65.3%	Clonal	D				passenger	No	No	No	WES
24IDC	KIF17	p.R770H	1	21009300	C	T	Missense_Mutation	119	39.5%	No	No	100%	0.56618	100.0%	86.6%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
24IDC	TIE1	p.R113H	1	43770801	G	A	Missense_Mutation	208	0.5%	No	No	2%	0	9.7%	0.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
24DCIS	TIE1	p.R113H	1	43770801	G	A	Missense_Mutation	218	4.6%	No	No	13%	0	22.3%	6.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
24IDC	SZT2	p.Y1229*	1	43893728	C	A	Nonsense_Mutation	85	28.2%	No	No	100%	0.83809	100.0%	68.2%	Clonal	A				passenger	No	No	No	WES
24IDC	SZT2	p.R2269G	1	43905374	C	G	Missense_Mutation	163	26.4%	No	No	100%	0.84748	100.0%	73.3%	Clonal	N	Passenger	N		passenger	No	No	No	WES
24IDC	KANK4	p.P483T	1	62739329	G	T	Missense_Mutation	94	5.3%	No	No	20%	0	44.9%	8.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
24DCIS	ANKRD13C	p.K532M	1	70728431	T	A	Missense_Mutation	88	39.8%	No	No	100%	0.84701	100.0%	75.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
24IDC	TSPAN2	p.X172_splice	1	115600157	C	A	Splice_Site	30	30.0%	No	No	100%	0.77091	100.0%	52.4%	Clonal	D				passenger	No	No	No	WES
24DCIS	CFHR4	p.S223T	1	196876499	T	A	Missense_Mutation	134	32.1%	No	No	89%	0.62135	100.0%	67.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
24IDC	CDK5R2	p.G116D	2	219824889	G	A	Missense_Mutation	82	30.5%	No	No	100%	0.8629	100.0%	71.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
24DCIS	KLHL18	p.D392N	3	47382114	G	A	Missense_Mutation	108	35.2%	No	No	97%	0.76899	100.0%	71.2%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
24DCIS	C3orf62	p.I266L	3	49308621	T	G	Missense_Mutation	62	33.9%	No	No	94%	0.68911	100.0%	61.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
24IDC	PARP15	p.N108S	3	122329357	A	G	Missense_Mutation	81	21.0%	No	No	80%	0.56628	98.4%	50.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
24IDC	DCHS2	p.A444T	4	155411178	C	T	Missense_Mutation	110	33.6%	No	No	100%	0.88291	100.0%	80.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
24IDC	AGGF1	p.V202L	5	76332468	G	T	Missense_Mutation	67	7.5%	No	Yes	21%	0	45.7%	8.8%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
24DCIS	AGGF1	p.V202L	5	76332468	G	T	Missense_Mutation	102	2.9%	No	Yes	8%	0	22.4%	2.4%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES

24IDC	CMYA5	p.D3870N	5	79084846	G	A	Missense_Mutation	64	34.4%	No	No	100%	0.86355	100.0%	73.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
24IDC	PCDHA11	p.A369V	5	140249794	C	T	Missense_Mutation	171	19.9%	No	Yes	56%	0.0003	74.5%	40.8%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
24DCIS	BTNL8	p.S117I	5	180335886	G	T	Missense_Mutation	123	34.1%	No	No	94%	0.73747	100.0%	70.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
24IDC	HLA-F	p.P3L	6	29691248	C	T	Missense_Mutation	180	28.9%	No	No	100%	0.89977	100.0%	79.6%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
24DCIS	NOTCH4	p.R1317Q	6	32169083	C	T	Missense_Mutation	87	31.0%	No	No	86%	0.56791	98.8%	60.2%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
24DCIS	HIVEP2	p.C1832Y	6	143085959	C	T	Missense_Mutation	57	43.9%	No	No	100%	0.84373	100.0%	74.5%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
24DCIS	IGF2BP3	p.E95G	7	23458396	T	C	Missense_Mutation	50	34.0%	No	No	94%	0.67889	100.0%	58.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
24IDC	CCDC71L	p.P152Q	7	106300888	G	T	Missense_Mutation	19	15.8%	No	Yes	45%	0.2598	92.9%	15.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
24IDC	BCAP29	p.W114Lfs*25	7	107234539	A	AT	Frame_Shift_Ins	84	33.3%	No	Yes	94%	0.82685	100.0%	65.6%	Clonal					likely_pathogenic	No	No	No	WES
24IDC	OXR1	p.D538V	8	107719359	A	T	Missense_Mutation	125	4.8%	No	No	18%	0	38.1%	8.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
24IDC	TTLL11	p.A79del	9	124855459	ACCG	A	In_Frame_Del	23	21.7%	No	No	83%	0.59618	98.6%	33.3%	Clonal					passenger	No	No	No	WES
24DCIS	TTLL11	p.A79del	9	124855459	ACCG	A	In_Frame_Del	54	11.1%	No	No	31%	0.00031	61.0%	14.1%	Subclonal					passenger	No	No	No	WES
24IDC	TOR1B	p.M286I	9	132571709	G	A	Missense_Mutation	118	28.0%	No	No	100%	0.85881	100.0%	72.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
24IDC	GATA3	p.R330Sfs*20	10	8111502	AGGAAT	A	Frame_Shift_Del	109	27.5%	No	No	100%	0.84501	100.0%	70.5%	Clonal					likely_pathogenic	Yes	Yes	Yes	WES
24DCIS	LCOR	p.A225E	10	98715051	C	A	Missense_Mutation	92	5.4%	No	No	15%	0	32.9%	6.1%	Subclonal	N	Passenger	N		passenger	No	No	No	WES
24DCIS	CARS	p.M601Ifs*90	11	3038445	GCCCGC	G	Frame_Shift_Del	108	17.6%	No	No	66%	0.13878	93.4%	43.0%	Subclonal					likely_pathogenic	No	Yes	No	WES
24IDC	MRPL16	p.R192S	11	59574002	G	T	Missense_Mutation	85	5.9%	No	Yes	17%	0	36.4%	6.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
24IDC	C11orf80	p.P115L	11	66523851	C	T	Missense_Mutation	101	8.9%	No	No	34%	0.00021	61.1%	17.9%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
24DCIS	SHANK2	p.A1385V	11	70332247	G	A	Missense_Mutation	440	8.4%	No	No	99%	0.75178	100.0%	68.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
24IDC	XRRA1	p.D692Y	11	74554950	C	A	Missense_Mutation	140	49.3%	No	Yes	100%	0.37832	100.0%	90.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
24IDC	BCL9L	p.A77V	11	118779161	G	A	Missense_Mutation	123	45.5%	No	Yes	100%	0.89134	100.0%	86.5%	Clonal	D	Passenger	N	T	passenger	No	Yes	No	WES
24DCIS	PRMT8	p.A219E	12	3678674	C	A	Missense_Mutation	59	8.5%	No	No	23%	0.00001	50.3%	9.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
24IDC	IFLTD1	p.A269V	12	25673002	G	A	Missense_Mutation	42	23.8%	No	No	91%	0.68162	100.0%	47.5%	Clonal	N	Passenger	D	D	passenger	No	No	No	WES
24DCIS	NOS1	p.A188V	12	117768312	G	A	Missense_Mutation	101	45.5%	No	No	100%	0.86705	100.0%	83.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
24IDC	GJA3	p.E108K	13	20717106	C	T	Missense_Mutation	65	41.5%	No	Yes	100%	0.8753	100.0%	80.4%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
24IDC	GJA3	p.Q81H	13	20717185	C	A	Missense_Mutation	67	32.8%	No	Yes	100%	0.86304	100.0%	71.9%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
24DCIS	C14orf93	p.C287Y	14	23465215	C	T	Missense_Mutation	96	28.1%	No	No	78%	0.33878	97.3%	54.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
24IDC	AHNAK2	p.P50S	14	105423812	G	A	Missense_Mutation	84	47.6%	No	Yes	100%	0.95556	100.0%	87.3%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
24IDC	RASGRF1	p.T971P	15	79290541	T	G	Missense_Mutation	59	18.6%	No	No	71%	0.43883	97.4%	40.1%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
24DCIS	ZFAND6	p.S97Hfs*99	15	80415065	TATCAGAATCTGTA	T	Frame_Shift_Del	42	19.0%	No	No	53%	0.07346	89.0%	27.2%	Subclonal					passenger	No	No	No	WES
24IDC	LRRK1	p.E369K	15	101550770	G	A	Missense_Mutation	73	11.0%	No	No	42%	0.01337	76.5%	21.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
24IDC	NUBP2	p.V184E	16	1838003	T	A	Missense_Mutation	99	34.3%	No	No	100%	0.87443	100.0%	79.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
24IDC	ZNF597	p.S261R	16	3486916	G	T	Missense_Mutation	100	1.0%	No	No	4%	0	20.2%	0.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
24DCIS	ZNF597	p.S261R	16	3486916	G	T	Missense_Mutation	136	31.6%	No	No	100%	0.87136	100.0%	80.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
24IDC	NPIPB15	p.H44Q	16	74415479	C	G	Missense_Mutation	135	4.4%	No	No	17%	0	35.3%	7.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
24DCIS	NPIPB15	p.H44Q	16	74415479	C	G	Missense_Mutation	152	2.0%	No	No	4%	0	9.5%	0.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
24DCIS	C16orf3	p.I52T	16	90095596	A	G	Missense_Mutation	136	52.9%	No	Yes	93%	0.79613	100.0%	77.5%	Clonal	N	Passenger		T	passenger	No	No	No	WES
24DCIS	C16orf3	p.I52V	16	90095597	T	C	Missense_Mutation	139	54.0%	No	Yes	95%	0.83698	100.0%	79.2%	Clonal	P	Passenger		T	passenger	No	No	No	WES
24IDC	TP53	p.Y236dup	17	7577572	T	TGTA	In_Frame_Ins	82	39.0%	No	Yes	100%	0.90884	100.0%	74.7%	Clonal					potentially_pathogen	Yes	Yes	Yes	WES
24DCIS	MAP2K4	p.R287G	17	12028656	C	G	Missense_Mutation	41	53.7%	No	Yes	95%	0.78429	100.0%	65.6%	Clonal	D	Driver	D	T	likely_pathogenic	Yes	Yes	Yes	WES
24DCIS	MAP2K4	p.S292N	17	12028672	G	A	Missense_Mutation	45	55.6%	No	Yes	98%	0.82423	100.0%	69.2%	Clonal	D	Driver	D	T	likely_pathogenic	Yes	Yes	Yes	WES
24IDC	ZNF287	p.W204*	17	16467029	C	T	Nonsense_Mutation	57	24.6%	No	Yes	69%	0.40183	96.1%	42.4%	Subclonal	A				likely_pathogenic	No	No	No	WES
24IDC	ZNF287	p.E182K	17	16467097	C	T	Missense_Mutation	67	28.4%	No	Yes	80%	0.62601	98.3%	52.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
24IDC	PIPOX	p.X323_splice	17	27382830	G	C	Splice_Site	73	6.8%	No	Yes	47%	0.16412	91.8%	20.1%	Subclonal	D				likely_pathogenic	No	No	No	WES
24IDC	GIP	p.Q80E	17	47041691	G	C	Missense_Mutation	131	36.6%	No	No	100%	0.81468	100.0%	90.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
24IDC	CLTC	p.D1126A	17	57759135	A	C	Missense_Mutation	79	5.1%	No	No	19%	0.00002	46.6%	7.4%	Subclonal	D	Passenger		T	passenger	No	Yes	No	WES
24IDC	CA4	p.R69C	17	58234013	C	T	Missense_Mutation	134	52.2%	No	No	100%	0.45517	100.0%	93.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
24DCIS	MUC16	p.R130S	19	9091425	C	A	Missense_Mutation	69	42.0%	No	No	100%	0.83745	100.0%	81.4%	Clonal		Passenger	N	T	passenger	No	No	No	WES
24IDC	RDH8	p.E66K	19	10127765	G	A	Missense_Mutation	116	48.3%	No	Yes	100%	0.72409	100.0%	87.7%	Clonal	N	Passenger		D	passenger	No	No	No	WES
24IDC	UQCRFS1	p.P208L	19	29698657	G	A	Missense_Mutation	62	11.3%	No	No	32%	0.00034	60.5%	15.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
24DCIS	KCNN4	p.K402Gfs*8	19	44271779	C	CGCCA	Frame_Shift_Ins	122	27.9%	No	No	77%	0.25552	96.3%	56.6%	Subclonal					passenger	No	No	No	WES
24IDC	ATP9A	p.V112M	20	50329607	C	T	Missense_Mutation	142	4.2%	No	Yes	25%	0.00004	51.4%	11.1%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
24DCIS	CASS4	p.T778M	20	55033775	C	T	Missense_Mutation	73	6.8%	No	No	19%	0	41.1%	7.9%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
24IDC	SYNJ1	p.E1043K	21	34022521	C	T	Missense_Mutation	91	20.9%	No	No	80%	0.54998	98.3%	51.6%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
24IDC	MAPK1	p.R172H	22	22153395	C	T	Missense_Mutation	64	26.6%	No	No	100%	0.78299	100.0%	60.4%	Clonal	D	Passenger	D	T	passenger	No	Yes	No	WES
24DCIS	CHEK2	p.R145W	22	29121242	G	A	Missense_Mutation	87	33.3%	No	No	92%	0.68689	100.0%	65.0%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	No	WES
24DCIS	TRIOBP	p.A1636D	22	38131250	C	A	Missense_Mutation	85	41.2%	No	No	100%	0.85867	100.0%	77.2%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
24IDC	WNT7B	p.G132S	22	46327154	C	T	Missense_Mutation	152	28.9%	No	No	100%	0.79371	100.0%	83.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
24IDC	RPGR	p.G598*	23	38146460	C	A	Nonsense_Mutation	310	12.9%	No	No	49%	0	65.0%	36.3%	Subclonal	N				passenger	No	No	No	WES
24DCIS	CACNA1F	p.A910G	23	49075378	G	C	Missense_Mutation	52	15.4%	No	No	43%	0.00687	75.6%	21.8%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
24IDC	ATP2B3	p.A900V	23	152825260	C	T	Missense_Mutation	214	55.6%	No	No	100%	0.39135	100.0%	96.4%	Clonal	D	Passenger	D	D	likely_pathogenic	No	Yes	No	WES
25IDC	PRAMEF22	p.R237C	1	13036637	C	T	Missense_Mutation	166	31.3%	No	No	100%	0.98116	100.0%	89.5%	Clonal	N	Passenger		T	passenger	No	No	No	WES
25DCIS	PRAMEF22	p.R237C	1	13036637	C	T	Missense_Mutation	194	23.2%	No	No	100%	0.91057	100.0%	85.5%	Clonal	N	Passenger		T	passenger	No	No	No	WES
25IDC	THRAP3	p.S171C	1	36752343	C	G	Missense_Mutation	215	19.5%	No	No	100%	0.91245	100.0%	79.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	THRAP3	p.S171C	1	36752343	C	G	Missense_Mutation	188	12.2%	No	No	96%	0.85488	100.0%	61.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	WDR65	p.A566T	1	43672544	G	A	Missense_Mutation	170	13.5%	No	No	86%	0.73871	98.9%	56.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	WDR65	p.A566T	1	43672544	G	A	Missense_Mutation	204	11.3%	No	No	89%	0.80564	100.0%	57.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	ELOVL1	p.*280Sext*6	1	43829588	C	G	Nonstop_Mutation	162	33.3%	No	No	100%	0.97767	100.0%	90.3%	Clonal	N				passenger	No	No	No	WES
25DCIS	ELOVL1	p.*280Sext*6	1	43829588	C	G	Nonstop_Mutation	161	22.4%	No	No	100%	0.96739	100.0%	83.9%	Clonal	N				passenger	No	No	No	WES
25IDC	SLC5A9	p.Y187H	1	48695111	T	C	Missense_Mutation	72	12.5%	No	Yes	42%	0.01012	74.1%	22.4%	Subclonal	D	Driver	D	D	likely_pathogenic	No	No	No	WES
25IDC	CDKN2C	p.G162A	1	51439920	G	C	Missense_Mutation	63	52.4%	No	Yes	100%	0.97011	100.0%	85.2%	Clonal	N	Passenger	N	T	passenger	Yes	Yes	No	WES
25DCIS	CDKN2C	p.G162A	1	51439920	G	C	Missense_Mutation	68	41.2%	No	Yes	100%	0.92469	100.0%	80.9%	Clonal	N	Passenger	N	T	passenger	Yes	Yes	No	WES
25IDC	CELSR2	p.L17P	1	109792751	T	C	Missense_Mutation	101	4.0%	No	Yes	13%	0	32.4%	4.9%	Subclonal	P	Passenger	N	T	passenger	No	No	No	WES
25DCIS	CELSR2	p.L17P	1	109792751	T	C	Missense_Mutation	145	0.7%	No	Yes	3%	0	14.0%	0.3%	Subclonal	P	Passenger	N	T	passenger	No	No	No	WES
25DCIS	STRIP1	p.E767K	1	110596319	G	A	Missense_Mutation	135	23.7%	No	Yes	92%	0.84558	100.0%	64.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	UBAP2L	p.S454F	1	154223664	C	T	Missense_Mutation	307	23.8%	No	No	100%	0.53285	100.0%	89.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	UBAP2L	p.S454F	1	154223664	C	T	Missense_Mutation	333	18.6%	No	No	100%	0.9098	100.0%	84.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	IQGAP3	p.V291D	1	156532384	A	T	Missense_Mutation	101	5.0%	No	No	32%	0.0113	69.9%	13.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	PEAR1	p.S915R	1	156883673	A	C	Missense_Mutation	227	55.5%	No	No	100%	0.18392	100.0%	96.5%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25DCIS	PEAR1	p.S915R	1	156883673	A	C	Missense_Mutation	258	44.2%	No	No	100%	0.73415	100.0%	96.0%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25IDC	NHLH1	p.H60Y	1	160340699	C	T	Missense_Mutation	324	57.1%	No	No	100%	0.15776	100.0%	97.5%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25DCIS	NHLH1	p.H60Y	1	160340699	C	T	Missense_Mutation	390	49.7%	No	No	100%	0.16778	100.0%	97.6%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25IDC	ALDH9A1	p.N493Rfs*20	1	165632366	TTC	T	Frame_Shift_Del	56	41.1%	No	No	100%	0.9666	100.0%	81.1%	Clonal					passenger	No	No	No	WES
25DCIS	ALDH9A1	p.N493Rfs*20	1	165632366	TTC	T	Frame_Shift_Del	69	23.2%	No	No	100%	0.90935	100.0%	66.8%	Clonal					passenger	No	No	No	WES
25IDC	ZBTB37	p.R185T	1	173839917	G	C	Missense_Mutation	209	1.0%	No	No	5%	0	17.8%	1.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	ZBTB37	p.R185T	1	173839917	G	C	Missense_Mutation	181	14.4%	No	No	84%	0.75624	98.7%	57.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	ZBTB37	p.E191Q	1	173839934	G	C	Missense_Mutation	206	0.5%	No	No	3%	0	13.9%	0.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	ZBTB37	p.E191Q	1	173839934	G	C	Missense_Mutation	192	13.5%	No	No	79%	0.66638	98.1%	54.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	TNN	p.S567C	1	175066664	C	G	Missense_Mutation	365	0.3%	No	No	2%	0	7.7%	0.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	TNN	p.S567C	1	175066664	C	G	Missense_Mutation	454	13.7%	No	No	80%	0.48935	96.7%	62.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	SUSD4	p.C274Y	1	223402634	C	T	Missense_Mutation	259	25.1%	No	No	100%	0.85694	100.0%	89.4%	Clonal	D	Driver	D	D	likely_pathogenic	No	No	No	WES
25DCIS	SUSD4	p.C274Y	1	223402634	C	T	Missense_Mutation	258	20.9%	No	No	100%	0.73578	100.0%	85.8%	Clonal	D	Driver	D	D	likely_pathogenic	No	No	No	WES
25IDC	OR2B11	p.R175P	1	247614761	C	G	Missense_Mutation	278	32.0%	No	No	100%	0.60661	100.0%	94.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	OR2B11	p.R175P	1	247614761	C	G	Missense_Mutation	278	26.3%	No	No	100%	0.94571	100.0%	92.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	MYT1L	p.S568I	2	1915792	C	A	Missense_Mutation	124	11.3%	No	No	66%	0.44071	95.7%	39.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	GRHL1	p.T143Dfs*35	2	10101322	TAC	T	Frame_Shift_Del	117	41.9%	No	No	100%	0.96627	100.0%	90.1%	Clonal					passenger	No	No	No	WES
25DCIS	GRHL1	p.T143Dfs*35	2	10101322	TAC	T	Frame_Shift_Del	90	30.0%	No	No	100%	0.96696	100.0%	80.6%	Clonal					passenger	No	No	No	WES
25IDC	C2orf44	p.S438*	2	24261052	G	C	Nonsense_Mutation	67	16.4%	No	No	88%	0.74113	98.9%	47.2%	Clonal	A				likely_pathogenic	No	Yes	No	WES
25DCIS	C2orf44	p.S438*	2	24261052	G	C	Nonsense_Mutation	72	20.8%	No	No	100%	0.89302	100.0%	62.8%	Clonal	A				likely_pathogenic	No	Yes	No	WES
25IDC	MEMO1	p.S164*	2	32117150	G	C	Nonsense_Mutation	79	36.7%	No	No	100%	0.9764	100.0%	83.2%	Clonal	D				passenger	No	No	No	WES
25DCIS	MEMO1	p.S164*	2	32117150	G	C	Nonsense_Mutation	77	33.8%	No	No	100%	0.97382	100.0%	81.5%	Clonal	D				passenger	No	No	No	WES
25IDC	RASGRP3	p.L343V	2	33752423	C	G	Missense_Mutation	105	38.1%	No	No	100%	0.97898	100.0%	87.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	RASGRP3	p.L343V	2	33752423	C	G	Missense_Mutation	93	28.0%	No	No	100%	0.95114	100.0%	79.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	FSHR	p.Y626S	2	49190083	T	G	Missense_Mutation	132	28.8%	No	No	100%	0.88917	100.0%	83.5%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25DCIS	FSHR	p.Y626S	2	49190083	T	G	Missense_Mutation	120	30.8%	No	No	100%	0.97254	100.0%	85.2%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25IDC	GPR75-ASB3	p.Q194*	2	53956597	G	A	Nonsense_Mutation	50	32.0%	No	No	100%	0.95831	100.0%	71.7%	Clonal	A				passenger	No	No	No	WES
25DCIS	GPR75-ASB3	p.Q194*	2	53956597	G	A	Nonsense_Mutation	57	31.6%	No	No	100%	0.96716	100.0%	74.7%	Clonal	A				passenger	No	No	No	WES
25IDC	CCT4	p.S173*	2	62106008	G	C	Nonsense_Mutation	48	31.3%	No	No	100%	0.95271	100.0%	70.1%	Clonal	A				passenger	No	No	No	WES
25DCIS	CCT4	p.S173*	2	62106008	G	C	Nonsense_Mutation	52	28.8%	No	No	100%	0.95471	100.0%	69.9%	Clonal	A				passenger	No	No	No	WES
25IDC	MRPL19	p.P29L	2	75874019	C	T	Missense_Mutation	135	1.5%	No	No	8%	0	27.5%	2.0%	Subclonal	N	Passenger	N		passenger	No	No	No	WES
25DCIS	MRPL19	p.P29L	2	75874019	C	T	Missense_Mutation	133	12.8%	No	No	75%	0.62195	97.7%	46.7%	Clonal	N	Passenger	N		passenger	No	No	No	WES
25IDC	CNNM4	p.E526D	2	97463281	G	C	Missense_Mutation	177	34.5%	No	No	100%	0.97926	100.0%	90.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	CNNM4	p.E526D	2	97463281	G	C	Missense_Mutation	186	30.1%	No	No	100%	0.96782	100.0%	89.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	C2ORF15	p.Q45E	2	99767052	C	G	Missense_Mutation	43	39.5%	No	No	100%	0.9666	100.0%	75.7%	Clonal	D	Passenger	N		passenger	No	No	No	WES
25DCIS	C2ORF15	p.Q45E	2	99767052	C	G	Missense_Mutation	55	23.6%	No	No	100%	0.90941	100.0%	63.1%	Clonal	D	Passenger	N		passenger	No	No	No	WES
25IDC	TMEM37	p.G83R	2	120194690	G	A	Missense_Mutation	133	43.6%	No	No	100%	0.94312	100.0%	91.7%	Clonal	D	Passenger	D		passenger	No	No	No	WES
25DCIS	TMEM37	p.G83R	2	120194690	G	A	Missense_Mutation	161	33.5%	No	No	100%	0.98152	100.0%	89.9%	Clonal	D	Passenger	D		passenger	No	No	No	WES
25IDC	TUBA3E	p.E433*	2	130949460	C	A	Nonsense_Mutation	456	0.7%	No	No	4%	0	9.8%	0.7%	Subclonal	D				passenger	No	No	No	WES
25DCIS	TUBA3E	p.E433*	2	130949460	C	A	Nonsense_Mutation	403	11.7%	No	No	68%	0.06537	88.2%	51.6%	Subclonal	D				passenger	No	No	No	WES
25IDC	MYO3B	p.N149S	2	171071258	A	G	Missense_Mutation	52	34.6%	No	No	100%	0.96858	100.0%	75.1%	Clonal	N	Driver	N	T	likely_pathogenic	No	No	No	WES
25DCIS	MYO3B	p.N149S	2	171071258	A	G	Missense_Mutation	45	31.1%	No	No	100%	0.9614	100.0%	69.7%	Clonal	N	Driver	N	T	likely_pathogenic	No	No	No	WES
25IDC	RAPGEF4	p.E40Q	2	173659805	G	C	Missense_Mutation	52	38.5%	No	No	100%	0.97051	100.0%	78.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	RAPGEF4	p.E40Q	2	173659805	G	C	Missense_Mutation	69	46.4%	No	No	100%	0.83171	100.0%	86.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	HOXD13	p.Y243*	2	176958347	C	G	Nonsense_Mutation	83	27.7%	No	No	100%	0.91434	100.0%	75.5%	Clonal	D				likely_pathogenic	No	Yes	No	WES
25DCIS	HOXD13	p.Y243*	2	176958347	C	G	Nonsense_Mutation	102	29.4%	No	No	100%	0.96371	100.0%	81.8%	Clonal	D				likely_pathogenic	No	Yes	No	WES
25IDC	HSPD1	p.E347D	2	198353900	C	G	Missense_Mutation	80	37.5%	No	No	100%	0.9765	100.0%	83.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	HSPD1	p.E347D	2	198353900	C	G	Missense_Mutation	92	31.5%	No	No	100%	0.97294	100.0%	82.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	MAP2	p.Q318*	2	210557846	C	T	Nonsense_Mutation	91	36.3%	No	No	100%	0.97773	100.0%	84.8%	Clonal	A				passenger	No	No	No	WES
25DCIS	MAP2	p.Q318*	2	210557846	C	T	Nonsense_Mutation	113	26.5%	No	No	100%	0.92417	100.0%	80.2%	Clonal	A				passenger	No	No	No	WES
25IDC	PRKAG3	p.L58F	2	219695524	C	G	Missense_Mutation	182	4.4%	No	No	24%	0	44.9%	11.7%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
25IDC	COL4A3	p.R1390T	2	228169716	G	C	Missense_Mutation	50	30.0%	No	No	100%	0.94349	100.0%	69.3%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25DCIS	COL4A3	p.R1390T	2	228169716	G	C	Missense_Mutation	53	30.2%	No	No	100%	0.96168	100.0%	71.9%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25IDC	PER2	p.L826F	2	239162186	C	G	Missense_Mutation	160	36.3%	No	No	100%	0.98284	100.0%	90.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	PER2	p.L826F	2	239162186	C	G	Missense_Mutation	187	34.8%	No	No	100%	0.98259	100.0%	91.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	PER2	p.G520S	2	239168679	C	T	Missense_Mutation	43	30.2%	No	No	100%	0.94173	100.0%	66.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	PER2	p.G520S	2	239168679	C	T	Missense_Mutation	27	40.7%	No	No	100%	0.94531	100.0%	68.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	PER2	p.D224N	2	239180055	C	T	Missense_Mutation	82	32.9%	No	No	100%	0.9689	100.0%	80.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	PER2	p.D224N	2	239180055	C	T	Missense_Mutation	105	38.1%	No	No	100%	0.96723	100.0%	88.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	HDAC4	p.E1076Q	2	239974822	C	G	Missense_Mutation	156	32.7%	No	No	100%	0.96778	100.0%	88.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	HDAC4	p.E1076Q	2	239974822	C	G	Missense_Mutation	168	29.2%	No	No	100%	0.95699	100.0%	87.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	WDR48	p.P197S	3	39111152	C	T	Missense_Mutation	50	62.0%	No	Yes	100%	0.98042	100.0%	86.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	WDR48	p.P197S	3	39111152	C	T	Missense_Mutation	47	46.8%	No	Yes	100%	0.97157	100.0%	79.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	SLC25A38	p.I144M	3	39433087	C	G	Missense_Mutation	117	30.8%	No	Yes	100%	0.89734	100.0%	72.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	SLC25A38	p.I144M	3	39433087	C	G	Missense_Mutation	135	31.9%	No	Yes	100%	0.93402	100.0%	81.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	KLHL18	p.P509H	3	47385232	C	A	Missense_Mutation	152	4.6%	No	Yes	18%	0	35.0%	8.3%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
25IDC	RNF123	p.P1023A	3	49753064	C	G	Missense_Mutation	118	0.8%	No	Yes	3%	0	15.0%	0.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	RNF123	p.P1023A	3	49753064	C	G	Missense_Mutation	114	30.7%	No	Yes	100%	0.93257	100.0%	77.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	DUSP7	p.S15L	3	52090339	G	A	Missense_Mutation	35	5.7%	No	Yes	19%	0.00658	62.4%	5.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	DUSP7	p.S15L	3	52090339	G	A	Missense_Mutation	67	23.9%	No	Yes	92%	0.82871	100.0%	55.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	CRYBG3	p.K187N	3	97596443	G	C	Missense_Mutation	150	24.0%	No	No	100%	0.97593	100.0%	85.3%	Clonal	D	Passenger		T	passenger	No	No	No	WES
25DCIS	CRYBG3	p.K187N	3	97596443	G	C	Missense_Mutation	173	13.3%	No	No	100%	0.90503	100.0%	68.5%	Clonal	D	Passenger		T	passenger	No	No	No	WES
25IDC	ABI3BP	p.L445P	3	100568930	A	G	Missense_Mutation	80	8.8%	No	No	73%	0.60944	98.1%	34.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	ABI3BP	p.L445P	3	100568930	A	G	Missense_Mutation	99	1.0%	No	No	9%	0.00157	47.7%	1.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	KIAA1524	p.D655N	3	108278654	C	T	Missense_Mutation	57	21.1%	No	No	100%	0.94902	100.0%	65.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	KIAA1524	p.D655N	3	108278654	C	T	Missense_Mutation	80	17.5%	No	No	100%	0.93538	100.0%	66.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	KIAA1407	p.E148Q	3	113755607	C	G	Missense_Mutation	123	8.1%	No	No	68%	0.50704	97.2%	36.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	KIAA1407	p.E148Q	3	113755607	C	G	Missense_Mutation	117	13.7%	No	No	100%	0.89162	100.0%	63.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	STXBP5L	p.Q560H	3	120976028	G	C	Missense_Mutation	81	1.2%	No	No	10%	0.00439	54.7%	2.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	STXBP5L	p.Q560H	3	120976028	G	C	Missense_Mutation	99	8.1%	No	No	72%	0.64315	97.9%	35.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	STXBP5L	p.D750H	3	121037387	G	C	Missense_Mutation	61	68.9%	No	No	100%	0.31356	100.0%	91.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	STXBP5L	p.D750H	3	121037387	G	C	Missense_Mutation	91	67.0%	No	No	100%	0.30952	100.0%	93.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	PODXL2	p.G579C	3	127391240	G	T	Missense_Mutation	124	7.3%	No	No	61%	0.37609	95.5%	31.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	PODXL2	p.G579C	3	127391240	G	T	Missense_Mutation	157	9.6%	No	No	85%	0.7638	98.8%	49.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	GATA2	p.P63A	3	128205688	G	C	Missense_Mutation	165	66.1%	No	No	100%	0.25271	100.0%	96.3%	Clonal	D	Passenger	N	D	likely_pathogenic	No	Yes	No	WES
25DCIS	GATA2	p.P63A	3	128205688	G	C	Missense_Mutation	240	61.3%	No	No	100%	0.19856	100.0%	97.2%	Clonal	D	Passenger	N	D	likely_pathogenic	No	Yes	No	WES
25IDC	CPNE4	p.P528_V531del	3	131254120	AACTTGGTTTGGG	A	In_Frame_Del	58	24.1%	No	No	100%	0.87928	100.0%	63.3%	Clonal					passenger	No	No	No	WES
25DCIS	CPNE4	p.P528_V531del	3	131254120	AACTTGGTTTGGG	A	In_Frame_Del	60	26.7%	No	No	100%	0.94006	100.0%	69.7%	Clonal					passenger	No	No	No	WES
25IDC	TF	p.D652G	3	133495975	A	G	Missense_Mutation	113	33.6%	No	No	100%	0.97371	100.0%	85.7%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
25DCIS	TF	p.D652G	3	133495975	A	G	Missense_Mutation	84	26.2%	No	No	100%	0.93309	100.0%	75.1%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
25IDC	RYK	p.S102R	3	133941304	A	T	Missense_Mutation	99	38.4%	No	No	100%	0.9781	100.0%	87.0%	Clonal	D	Passenger		T	passenger	No	No	No	WES
25DCIS	RYK	p.S102R	3	133941304	A	T	Missense_Mutation	91	27.5%	No	No	100%	0.94609	100.0%	78.1%	Clonal	D	Passenger		T	passenger	No	No	No	WES
25IDC	USP13	p.I690M	3	179479021	C	G	Missense_Mutation	197	38.1%	No	No	100%	0.9843	100.0%	92.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	USP13	p.I690M	3	179479021	C	G	Missense_Mutation	165	35.2%	No	No	100%	0.98105	100.0%	90.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	ABCC5	p.P671S	3	183682993	G	A	Missense_Mutation	143	39.2%	No	No	100%	0.97994	100.0%	90.8%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25DCIS	ABCC5	p.P671S	3	183682993	G	A	Missense_Mutation	157	28.0%	No	No	100%	0.93645	100.0%	86.0%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25IDC	ADIPOQ	p.E220Q	3	186572416	G	C	Missense_Mutation	179	39.1%	No	No	100%	0.98163	100.0%	92.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	ADIPOQ	p.E220Q	3	186572416	G	C	Missense_Mutation	163	45.4%	No	No	100%	0.59888	100.0%	93.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	DLG1	p.M745I	3	196792643	C	T	Missense_Mutation	56	17.9%	No	No	100%	0.84153	100.0%	50.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	PIGG	p.E238D	4	501337	G	C	Missense_Mutation	98	54.1%	No	Yes	100%	0.9775	100.0%	90.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	PIGG	p.E238D	4	501337	G	C	Missense_Mutation	102	40.2%	No	Yes	100%	0.82355	100.0%	85.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	CC2D2A	p.L377R	4	15518360	T	G	Missense_Mutation	74	28.4%	No	Yes	96%	0.83036	100.0%	61.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	CC2D2A	p.L377R	4	15518360	T	G	Missense_Mutation	67	22.4%	No	Yes	86%	0.78636	98.9%	51.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	AP1AR	p.E105Q	4	113184174	G	C	Missense_Mutation	78	32.1%	No	No	100%	0.96402	100.0%	79.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	AP1AR	p.E105Q	4	113184174	G	C	Missense_Mutation	68	29.4%	No	No	100%	0.96181	100.0%	75.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	TLR2	p.D419H	4	154625314	G	C	Missense_Mutation	55	18.2%	No	Yes	61%	0.31362	94.3%	33.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	TLL1	p.D947E	4	167020613	C	A	Missense_Mutation	90	5.6%	No	Yes	21%	0.00002	47.2%	9.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	WDR17	p.W529C	4	177063206	G	C	Missense_Mutation	33	51.5%	No	Yes	100%	0.96519	100.0%	75.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	WDR17	p.W529C	4	177063206	G	C	Missense_Mutation	37	45.9%	No	Yes	100%	0.96691	100.0%	74.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	TRIP13	p.A122Lfs*7	5	896882	GCAGCAAAT	G	Frame_Shift_Del	124	32.3%	No	No	100%	0.97763	100.0%	87.2%	Clonal					passenger	No	No	No	WES
25DCIS	TRIP13	p.A122Lfs*7	5	896882	GCAGCAAAT	G	Frame_Shift_Del	122	28.7%	No	No	100%	0.95571	100.0%	83.5%	Clonal					passenger	No	No	No	WES
25IDC	SOWAHA	p.A392P	5	132150487	G	C	Missense_Mutation	129	0.8%	No	Yes	3%	0	13.8%	0.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	SOWAHA	p.A392P	5	132150487	G	C	Missense_Mutation	155	21.9%	No	Yes	85%	0.75277	98.7%	61.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	PKD2L2	p.L528P	5	137260760	T	C	Missense_Mutation	38	13.2%	No	Yes	71%	0.59663	97.9%	29.1%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
25IDC	FAT2	p.V2178F	5	150924156	C	A	Missense_Mutation	67	31.3%	No	Yes	100%	0.95851	100.0%	76.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	FAT2	p.V2178F	5	150924156	C	A	Missense_Mutation	71	29.6%	No	Yes	100%	0.9631	100.0%	76.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	WWC1	p.X667_splice	5	167855793	G	C	Splice_Site	101	65.3%	No	Yes	100%	0.97223	100.0%	93.2%	Clonal	D				likely_pathogenic	No	No	No	WES
25DCIS	WWC1	p.X667_splice	5	167855793	G	C	Splice_Site	105	47.6%	No	Yes	100%	0.97805	100.0%	89.5%	Clonal	D				likely_pathogenic	No	No	No	WES
25IDC	FGFR4	p.E94D	5	176517581	G	C	Missense_Mutation	103	62.1%	No	Yes	100%	0.98471	100.0%	92.8%	Clonal	D	Passenger	N	D	likely_pathogenic	No	Yes	No	WES
25DCIS	FGFR4	p.E94D	5	176517581	G	C	Missense_Mutation	119	53.8%	No	Yes	100%	0.98422	100.0%	92.4%	Clonal	D	Passenger	N	D	likely_pathogenic	No	Yes	No	WES
25IDC	HIST1H2BA	p.E115Q	6	25727479	G	C	Missense_Mutation	181	19.3%	No	No	100%	0.9087	100.0%	76.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	HIST1H2BA	p.E115Q	6	25727479	G	C	Missense_Mutation	207	24.2%	No	No	100%	0.93996	100.0%	87.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	BTN3A1	p.Y396Sfs*6	6	26413564	TA	T	Frame_Shift_Del	323	44.0%	No	No	100%	0.65976	100.0%	96.6%	Clonal					passenger	No	No	No	WES
25DCIS	BTN3A1	p.Y396Sfs*6	6	26413564	TA	T	Frame_Shift_Del	292	44.2%	No	No	100%	0.74579	100.0%	96.3%	Clonal					passenger	No	No	No	WES
25IDC	GPANK1	p.D227H	6	31630435	C	G	Missense_Mutation	137	32.1%	No	No	100%	0.96304	100.0%	86.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	GPANK1	p.D227H	6	31630435	C	G	Missense_Mutation	148	31.1%	No	No	100%	0.97475	100.0%	87.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	ITPR3	p.R1682W	6	33652240	C	T	Missense_Mutation	86	1.2%	No	No	6%	0.00001	33.1%	1.1%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25DCIS	ITPR3	p.R1682W	6	33652240	C	T	Missense_Mutation	94	18.1%	No	No	100%	0.87514	100.0%	60.7%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25DCIS	ENPP4	p.L349V	6	46111060	C	G	Missense_Mutation	60	15.0%	No	No	88%	0.77551	98.9%	43.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	MLIP	p.K14N	6	53883868	G	C	Missense_Mutation	60	30.0%	No	No	100%	0.94632	100.0%	72.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	MLIP	p.K14N	6	53883868	G	C	Missense_Mutation	71	33.8%	No	No	100%	0.97278	100.0%	80.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	GJA10	p.D132H	6	90604581	G	C	Missense_Mutation	102	41.2%	No	No	100%	0.97041	100.0%	88.6%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25DCIS	GJA10	p.D132H	6	90604581	G	C	Missense_Mutation	86	31.4%	No	No	100%	0.97195	100.0%	81.2%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25IDC	QRSL1	p.Y285S	6	107102609	A	C	Missense_Mutation	51	45.1%	No	No	100%	0.94513	100.0%	81.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	QRSL1	p.Y285S	6	107102609	A	C	Missense_Mutation	43	27.9%	No	No	100%	0.94394	100.0%	64.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	ZBTB24	p.L607Ffs*16	6	109787328	AG	A	Frame_Shift_Del	151	0.7%	No	No	4%	0	18.9%	0.4%	Subclonal					passenger	No	No	No	WES
25DCIS	ZBTB24	p.L607Ffs*16	6	109787328	AG	A	Frame_Shift_Del	149	14.8%	No	No	87%	0.78702	98.9%	56.4%	Clonal					passenger	No	No	No	WES
25IDC	AK9	p.D421H	6	109940433	C	G	Missense_Mutation	83	24.1%	No	No	100%	0.89058	100.0%	69.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	AK9	p.D421H	6	109940433	C	G	Missense_Mutation	96	13.5%	No	No	79%	0.71257	98.4%	45.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	SAMD3	p.Q241K	6	130497087	G	T	Missense_Mutation	67	1.5%	No	No	8%	0.00025	42.1%	1.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	SAMD3	p.Q241K	6	130497087	G	T	Missense_Mutation	72	6.9%	No	No	41%	0.12668	85.4%	17.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	TCP1	p.R310T	6	160202011	C	G	Missense_Mutation	103	11.7%	No	No	68%	0.53412	96.8%	39.1%	Clonal	D	Driver	D	D	likely_pathogenic	No	No	No	WES
25IDC	SLC22A1	p.S552*	6	160579604	C	A	Nonsense_Mutation	100	41.0%	No	No	100%	0.97116	100.0%	88.3%	Clonal	N				passenger	No	No	No	WES
25DCIS	SLC22A1	p.S552*	6	160579604	C	A	Nonsense_Mutation	114	24.6%	No	No	100%	0.90351	100.0%	77.7%	Clonal	N				passenger	No	No	No	WES
25IDC	TNRC18	p.G2530V	7	5352933	C	A	Missense_Mutation	251	4.0%	No	No	29%	0.00001	52.5%	15.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	RNF216	p.D220H	7	5780990	C	G	Missense_Mutation	216	10.2%	No	No	75%	0.52922	97.5%	49.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	GRID2IP	p.E208K	7	6566363	C	T	Missense_Mutation	107	36.4%	No	No	100%	0.8332	100.0%	88.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	GRID2IP	p.E208K	7	6566363	C	T	Missense_Mutation	151	35.8%	No	No	100%	0.9064	100.0%	91.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	SP4	p.R665P	7	21521628	G	C	Missense_Mutation	56	19.6%	No	No	100%	0.90238	100.0%	60.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	SP4	p.R665P	7	21521628	G	C	Missense_Mutation	71	23.9%	No	No	100%	0.95123	100.0%	71.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	HOXA13	p.G54R	7	27239537	C	T	Missense_Mutation	55	52.7%	No	No	100%	0.791	100.0%	86.1%	Clonal	N	Passenger	N	D	passenger	No	Yes	No	WES
25DCIS	HOXA13	p.G54R	7	27239537	C	T	Missense_Mutation	87	46.0%	No	No	100%	0.79905	100.0%	89.1%	Clonal	N	Passenger	N	D	passenger	No	Yes	No	WES
25IDC	NT5C3A	p.D322G	7	33054388	T	C	Missense_Mutation	45	11.1%	Yes	No	60%	0.46456	96.6%	25.3%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25DCIS	NT5C3A	p.D322G	7	33054388	T	C	Missense_Mutation	41	7.3%	Yes	No	43%	0.34212	93.4%	14.8%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25IDC	CAMK2B	p.C657S	7	44259692	C	G	Missense_Mutation	122	22.1%	No	No	100%	0.899	100.0%	72.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	CAMK2B	p.C657S	7	44259692	C	G	Missense_Mutation	154	13.6%	No	No	80%	0.69765	98.3%	52.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	CCDC146	p.X329_splice	7	76891437	G	C	Splice_Site	43	44.2%	No	No	100%	0.9519	100.0%	78.8%	Clonal	D				passenger	No	No	No	WES
25DCIS	CCDC146	p.X329_splice	7	76891437	G	C	Splice_Site	49	59.2%	No	No	100%	0.51875	100.0%	86.9%	Clonal	D				passenger	No	No	No	WES
25IDC	MUC17	p.A666T	7	100676693	G	A	Missense_Mutation	701	17.1%	No	No	92%	0.8211	100.0%	77.1%	Clonal	N	Passenger	N	T	passenger	No	No	Yes	WES
25DCIS	MUC17	p.A666T	7	100676693	G	A	Missense_Mutation	636	11.5%	No	No	44%	0	54.3%	35.1%	Subclonal	N	Passenger	N	T	passenger	No	No	Yes	WES
25DCIS	CUX1	p.M621I	7	101840521	G	C	Missense_Mutation	184	14.1%	No	No	83%	0.73465	98.6%	56.3%	Clonal	D	Passenger	D	T	passenger	No	Yes	Yes	WES
25IDC	CTTNBP2	p.E200Q	7	117432652	C	G	Missense_Mutation	138	13.0%	No	No	70%	0.42118	96.3%	44.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	CTTNBP2	p.E200Q	7	117432652	C	G	Missense_Mutation	142	11.3%	No	No	66%	0.39344	95.0%	40.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	PRRT4	p.D277V	7	127998782	T	A	Missense_Mutation	79	6.3%	No	No	37%	0.06433	80.0%	15.9%	Subclonal	D	Passenger	D		passenger	No	No	No	WES
25IDC	TMEM209	p.G100*	7	129842405	C	A	Nonsense_Mutation	79	49.4%	No	No	100%	0.82271	100.0%	89.0%	Clonal	A				passenger	No	No	No	WES
25DCIS	TMEM209	p.G100*	7	129842405	C	A	Nonsense_Mutation	100	47.0%	No	No	100%	0.72448	100.0%	90.7%	Clonal	A				passenger	No	No	No	WES
25IDC	OR2A12	p.R234K	7	143792901	G	A	Missense_Mutation	255	45.5%	No	No	100%	0.98888	100.0%	95.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	OR2A12	p.R234K	7	143792901	G	A	Missense_Mutation	238	37.0%	No	No	100%	0.97035	100.0%	93.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	EZH2	p.V626L	7	148508788	C	G	Missense_Mutation	72	13.9%	No	No	61%	0.31816	94.5%	33.3%	Subclonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
25DCIS	EZH2	p.V626L	7	148508788	C	G	Missense_Mutation	78	16.7%	No	No	81%	0.73123	98.6%	46.8%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
25IDC	LONRF1	p.D555Y	8	12589270	C	A	Missense_Mutation	33	12.1%	No	Yes	41%	0.1345	87.4%	16.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	LONRF1	p.D555Y	8	12589270	C	A	Missense_Mutation	53	26.4%	No	Yes	100%	0.86221	100.0%	57.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	CHRNA2	p.P319L	8	27321004	G	A	Missense_Mutation	290	60.7%	No	Yes	100%	0.99119	100.0%	97.1%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25DCIS	CHRNA2	p.P319L	8	27321004	G	A	Missense_Mutation	378	48.9%	No	Yes	100%	0.98495	100.0%	96.9%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25IDC	RGS22	p.A398V	8	101075803	G	A	Missense_Mutation	191	22.0%	No	Yes	100%	0.97617	100.0%	87.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	RGS22	p.A398V	8	101075803	G	A	Missense_Mutation	223	15.7%	No	Yes	100%	0.92082	100.0%	81.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	CSMD3	p.N1892H	8	113418888	T	G	Missense_Mutation	66	24.2%	No	Yes	100%	0.95414	100.0%	74.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	CSMD3	p.N1892H	8	113418888	T	G	Missense_Mutation	66	31.8%	No	Yes	100%	0.74884	100.0%	81.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	ZFAT	p.E1168Q	8	135490955	C	G	Missense_Mutation	285	3.9%	No	Yes	36%	0.00059	63.1%	20.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	TEK	p.S164*	9	27169490	C	A	Nonsense_Mutation	114	16.7%	No	No	90%	0.77132	100.0%	56.1%	Clonal	A				passenger	No	No	No	WES
25DCIS	TEK	p.S164*	9	27169490	C	A	Nonsense_Mutation	97	13.4%	No	No	79%	0.7027	98.4%	45.3%	Clonal	A				passenger	No	No	No	WES
25IDC	GALNT12	p.V209L	9	101589117	G	C	Missense_Mutation	194	22.2%	No	No	100%	0.91972	100.0%	79.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	GALNT12	p.V209L	9	101589117	G	C	Missense_Mutation	253	16.6%	No	No	97%	0.88901	100.0%	70.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	BSPRY	p.E4*	9	116111869	G	T	Nonsense_Mutation	82	19.5%	No	No	100%	0.88679	100.0%	62.1%	Clonal	A				passenger	No	No	No	WES
25DCIS	OR1L4	p.K81N	9	125486511	G	C	Missense_Mutation	178	11.8%	No	No	69%	0.40462	95.3%	45.4%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
25IDC	SLC2A6	p.A346P	9	136339102	C	G	Missense_Mutation	67	11.9%	No	No	64%	0.46176	96.6%	32.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	SLC2A6	p.A346P	9	136339102	C	G	Missense_Mutation	96	20.8%	No	No	100%	0.90552	100.0%	68.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	PPP1R26	p.R1047T	9	138379496	G	C	Missense_Mutation	135	54.8%	No	Yes	100%	0.98062	100.0%	93.0%	Clonal	N	Passenger		T	passenger	No	No	No	WES
25DCIS	PPP1R26	p.R1047T	9	138379496	G	C	Missense_Mutation	172	46.5%	No	Yes	100%	0.96914	100.0%	93.0%	Clonal	N	Passenger		T	passenger	No	No	No	WES
25IDC	GDI2	p.M66I	10	5838781	C	T	Missense_Mutation	29	37.9%	No	No	100%	0.95929	100.0%	66.5%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25DCIS	GDI2	p.M66I	10	5838781	C	T	Missense_Mutation	31	29.0%	No	No	100%	0.9402	100.0%	59.1%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25IDC	MALRD1	p.A651V	10	19636823	C	T	Missense_Mutation	99	30.3%	No	No	100%	0.94591	100.0%	81.2%	Clonal	D	Passenger		T	passenger	No	No	No	WES

25DCIS	MALRD1	p.A651V	10	19636823	C	T	Missense_Mutation	98	26.5%	No	No	100%	0.93188	100.0%	78.1%	Clonal	D	Passenger		T	passenger	No	No	No	WES
25IDC	MAP3K8	p.Q276E	10	30740626	C	G	Missense_Mutation	30	16.7%	No	No	90%	0.71569	98.7%	34.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	MAP3K8	p.Q276E	10	30740626	C	G	Missense_Mutation	52	25.0%	No	No	100%	0.92201	100.0%	64.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	ATOH7	p.P130A	10	69991047	G	C	Missense_Mutation	175	38.3%	No	No	100%	0.98315	100.0%	92.1%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
25DCIS	ATOH7	p.P130A	10	69991047	G	C	Missense_Mutation	220	35.0%	No	No	100%	0.98356	100.0%	92.9%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
25IDC	DLG5	p.K1577N	10	79567619	C	A	Missense_Mutation	77	39.0%	No	Yes	93%	0.89492	100.0%	66.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	DLG5	p.K1577N	10	79567619	C	A	Missense_Mutation	110	30.9%	No	Yes	88%	0.87891	100.0%	64.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	PTEN	p.D326H	10	89720825	G	C	Missense_Mutation	35	25.7%	No	Yes	61%	0.41808	93.8%	33.1%	Subclonal	D	Driver	D	D	likely_pathogenic	Yes	Yes	Yes	WES
25IDC	TAF5	p.Q618E	10	105146954	C	G	Missense_Mutation	75	22.7%	No	No	99%	0.82818	100.0%	59.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	TAF5	p.Q618E	10	105146954	C	G	Missense_Mutation	81	12.3%	No	No	60%	0.35999	94.2%	32.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	SMTNL1	p.V507L	11	57317565	G	C	Missense_Mutation	146	34.2%	No	No	100%	0.97751	100.0%	88.8%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25DCIS	SMTNL1	p.V507L	11	57317565	G	C	Missense_Mutation	189	27.0%	No	No	100%	0.87335	100.0%	87.1%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25IDC	SCGB1A1	p.A85G	11	62190541	C	G	Missense_Mutation	105	15.2%	No	No	82%	0.6872	98.6%	49.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	PHOX2A	p.A161_A163del	11	71951158	TGGCGCCCGC	T	In_Frame_Del	107	15.0%	No	No	88%	0.79189	99.0%	52.5%	Clonal					passenger	No	No	No	WES
25DCIS	OR2AT4	p.T80K	11	74800520	G	T	Missense_Mutation	69	7.2%	No	Yes	28%	0.0018	60.8%	11.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	SLC2A14	p.T340A	12	7973837	T	C	Missense_Mutation	81	55.6%	No	Yes	100%	0.98176	100.0%	89.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	SLC2A14	p.T340A	12	7973837	T	C	Missense_Mutation	100	43.0%	No	Yes	100%	0.93097	100.0%	87.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	PRH2	p.P103A	12	11083467	C	G	Missense_Mutation	317	15.5%	No	Yes	52%	0	66.6%	39.7%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
25DCIS	PRH2	p.P103A	12	11083467	C	G	Missense_Mutation	330	14.5%	No	Yes	56%	0.00003	71.9%	42.6%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
25IDC	LRRK2	p.E2503K	12	40761490	G	A	Missense_Mutation	40	42.5%	No	No	100%	0.95882	100.0%	76.5%	Clonal	D	Passenger	N	T	passenger	Yes	No	No	WES
25DCIS	LRRK2	p.E2503K	12	40761490	G	A	Missense_Mutation	75	28.0%	No	No	100%	0.96963	100.0%	77.5%	Clonal	D	Passenger	N	T	passenger	Yes	No	No	WES
25IDC	TROAP	p.P359Gfs*14	12	49722995	CACCCATGCCATCAACCCCCAGAGTTCA	A	Frame_Shift_Del	76	5.3%	No	Yes	18%	0	42.6%	6.7%	Subclonal					likely_pathogenic	No	No	No	WES
25DCIS	TROAP	p.P359Gfs*14	12	49722995	CACCCATGCCATCAACCCCCAGAGTTCA	A	Frame_Shift_Del	113	3.5%	No	Yes	17%	0.00001	42.0%	6.5%	Subclonal					likely_pathogenic	No	No	No	WES
25IDC	ASIC1	p.R514Q	12	50475068	G	A	Missense_Mutation	62	56.5%	No	Yes	100%	0.98169	100.0%	86.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	ASIC1	p.R514Q	12	50475068	G	A	Missense_Mutation	157	48.4%	No	Yes	100%	0.91868	100.0%	93.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	ZFC3H1	p.E1975K	12	72004255	C	T	Missense_Mutation	76	43.4%	No	Yes	100%	0.97541	100.0%	85.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	HIP1R	p.S913Gfs*27	12	123345301	CAGCACGGCCCAGCT	C	Frame_Shift_Del	26	19.2%	No	Yes	65%	0.5281	97.2%	27.6%	Clonal					likely_pathogenic	No	No	No	WES
25DCIS	HIP1R	p.S913Gfs*27	12	123345301	CAGCACGGCCCAGCT	C	Frame_Shift_Del	63	19.0%	No	Yes	93%	0.81336	100.0%	50.5%	Clonal					likely_pathogenic	No	No	No	WES
25IDC	SLITRK6	p.H794D	13	86368264	G	C	Missense_Mutation	59	32.2%	No	Yes	100%	0.87404	100.0%	65.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	SLITRK6	p.H794D	13	86368264	G	C	Missense_Mutation	76	14.5%	No	Yes	56%	0.18607	89.8%	31.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	MYH6	p.E380K	14	23871676	C	T	Missense_Mutation	379	43.3%	No	No	100%	0.56846	100.0%	97.1%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25DCIS	MYH6	p.E380K	14	23871676	C	T	Missense_Mutation	420	34.8%	No	No	100%	0.98804	100.0%	96.0%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25IDC	KIAA0391	p.I251M	14	35593204	C	G	Missense_Mutation	88	34.1%	No	No	100%	0.96982	100.0%	84.2%	Clonal	D	Passenger		T	passenger	No	No	No	WES
25DCIS	KIAA0391	p.I251M	14	35593204	C	G	Missense_Mutation	108	28.7%	No	No	100%	0.95732	100.0%	81.9%	Clonal	D	Passenger		T	passenger	No	No	No	WES
25IDC	SYNE2	p.E4535_F4537del	14	64593087	TTGTTTGAAC	T	In_Frame_Del	47	57.4%	No	Yes	100%	0.98047	100.0%	83.7%	Clonal					potentially_pathogen	No	No	No	WES
25DCIS	SYNE2	p.E4535_F4537del	14	64593087	TTGTTTGAAC	T	In_Frame_Del	56	42.9%	No	Yes	100%	0.95184	100.0%	79.3%	Clonal					potentially_pathogen	No	No	No	WES
25IDC	COX16	p.R8L	14	70826282	C	A	Missense_Mutation	61	60.7%	No	Yes	100%	0.98302	100.0%	88.0%	Clonal	N	Passenger	N		passenger	No	No	No	WES
25DCIS	COX16	p.R8L	14	70826282	C	A	Missense_Mutation	68	44.1%	No	Yes	100%	0.95918	100.0%	83.0%	Clonal	N	Passenger	N		passenger	No	No	No	WES
25IDC	BTBD7	p.G971R	14	93709107	C	T	Missense_Mutation	194	37.1%	No	No	100%	0.92723	100.0%	93.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	BTBD7	p.G971R	14	93709107	C	T	Missense_Mutation	189	47.1%	No	No	100%	0.60819	100.0%	95.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	SERPINA4	p.D330H	14	95034530	G	C	Missense_Mutation	146	30.8%	No	No	100%	0.97984	100.0%	88.0%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
25DCIS	SERPINA4	p.D330H	14	95034530	G	C	Missense_Mutation	140	27.1%	No	No	100%	0.97524	100.0%	85.5%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
25IDC	CYP46A1	p.S307Y	14	100184403	C	A	Missense_Mutation	87	31.0%	No	No	100%	0.97424	100.0%	81.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	CYP46A1	p.S307Y	14	100184403	C	A	Missense_Mutation	110	29.1%	No	No	100%	0.9752	100.0%	84.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	DPH6	p.D148Y	15	35742949	C	A	Missense_Mutation	57	10.5%	No	No	46%	0.13483	88.1%	21.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	DPH6	p.D148Y	15	35742949	C	A	Missense_Mutation	76	13.2%	No	No	77%	0.69469	98.3%	41.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	BUB1B	p.R597T	15	40498440	G	C	Missense_Mutation	56	19.6%	No	No	86%	0.72716	98.8%	46.7%	Clonal	D	Passenger	N	T	passenger	No	Yes	No	WES
25DCIS	BUB1B	p.R597T	15	40498440	G	C	Missense_Mutation	71	21.1%	No	No	100%	0.8626	100.0%	57.9%	Clonal	D	Passenger	N	T	passenger	No	Yes	No	WES
25IDC	MYO5C	p.E448Q	15	52548889	C	G	Missense_Mutation	59	20.3%	No	No	89%	0.75266	99.0%	49.3%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25DCIS	MYO5C	p.E448Q	15	52548889	C	G	Missense_Mutation	76	9.2%	No	No	45%	0.09807	84.3%	21.8%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25DCIS	RFX7	p.M1281I	15	56386083	C	T	Missense_Mutation	95	16.8%	No	No	82%	0.73732	98.6%	50.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	CGNL1	p.E71K	15	57730408	G	A	Missense_Mutation	62	43.5%	No	No	100%	0.97674	100.0%	82.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	CGNL1	p.E71K	15	57730408	G	A	Missense_Mutation	56	35.7%	No	No	100%	0.96375	100.0%	76.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	ZNF609	p.L995M	15	64968036	C	A	Missense_Mutation	254	20.9%	No	No	91%	0.81418	100.0%	69.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	ZNF609	p.L995M	15	64968036	C	A	Missense_Mutation	275	19.6%	No	No	95%	0.888	100.0%	72.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	ACAN	p.P2064H	15	89402007	C	A	Missense_Mutation	121	19.0%	No	Yes	83%	0.69474	98.6%	55.6%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
25DCIS	ACAN	p.P2064H	15	89402007	C	A	Missense_Mutation	119	20.2%	No	Yes	98%	0.87114	100.0%	63.5%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
25IDC	PDIA2	p.L223F	16	335004	C	T	Missense_Mutation	203	43.8%	No	No	100%	0.65833	100.0%	94.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	PDIA2	p.L223F	16	335004	C	T	Missense_Mutation	255	37.6%	No	No	100%	0.54785	100.0%	94.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	COQ7	p.R28T	16	19083259	G	C	Missense_Mutation	161	15.5%	No	No	99%	0.84369	100.0%	64.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	COQ7	p.R28T	16	19083259	G	C	Missense_Mutation	139	12.9%	No	No	89%	0.80276	100.0%	54.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	DNAH3	p.S1099L	16	21080821	G	A	Missense_Mutation	99	30.3%	No	No	100%	0.97539	100.0%	83.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	DNAH3	p.S1099L	16	21080821	G	A	Missense_Mutation	91	34.1%	No	No	100%	0.95407	100.0%	85.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	KIAA0556	p.K465Rfs*3	16	27720026	GACAA	G	Frame_Shift_Del	88	42.0%	No	No	100%	0.83609	100.0%	88.2%	Clonal					passenger	No	No	No	WES
25DCIS	KIAA0556	p.K465Rfs*3	16	27720026	GACAA	G	Frame_Shift_Del	90	54.4%	No	No	100%	0.42278	100.0%	91.8%	Clonal					passenger	No	No	No	WES
25IDC	DOC2A	p.R264W	16	30018194	G	A	Missense_Mutation	293	44.4%	No	No	100%	0.69158	100.0%	96.3%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
25DCIS	DOC2A	p.R264W	16	30018194	G	A	Missense_Mutation	302	35.4%	No	No	100%	0.79486	100.0%	95.2%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
25IDC	ITGAL	p.R1020S	16	30529142	C	A	Missense_Mutation	170	0.6%	No	No	4%	0	20.0%	0.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	ITGAL	p.R1020S	16	30529142	C	A	Missense_Mutation	215	14.4%	No	No	99%	0.88251	100.0%	66.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	ZFPM1	p.S552Rfs*242	16	88600018	ACAGCCGGCTGCAG	A	Frame_Shift_Del	158	31.6%	No	No	100%	0.98059	100.0%	89.3%	Clonal					passenger	No	No	No	WES
25DCIS	ZFPM1	p.S552Rfs*242	16	88600018	ACAGCCGGCTGCAG	A	Frame_Shift_Del	207	27.1%	No	No	100%	0.97776	100.0%	89.5%	Clonal					passenger	No	No	No	WES
25IDC	TP53	p.R175H	17	7578406	C	T	Missense_Mutation	154	63.0%	Yes	Yes	100%	0.98357	100.0%	95.1%	Clonal	A	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
25DCIS	TP53	p.R175H	17	7578406	C	T	Missense_Mutation	168	45.8%	Yes	Yes	100%	0.96091	100.0%	92.6%	Clonal	A	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
25IDC	BRCA1	p.L1154Mfs*4	17	41244081	TCATCTAA	T	Frame_Shift_Del	49	40.8%	No	Yes	100%	0.96859	100.0%	77.0%	Clonal					likely_pathogenic	Yes	Yes	Yes	WES
25DCIS	BRCA1	p.L1154Mfs*4	17	41244081	TCATCTAA	T	Frame_Shift_Del	66	43.9%	No	Yes	100%	0.97303	100.0%	84.3%	Clonal					likely_pathogenic	Yes	Yes	Yes	WES
25IDC	ARL4D	p.A104V	17	41477411	C	T	Missense_Mutation	249	4.0%	No	Yes	18%	0	31.2%	9.2%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
25IDC	CDC27	p.K261Q	17	45234340	T	G	Missense_Mutation	44	2.3%	No	Yes	10%	0.00185	51.0%	1.9%	Subclonal	D	Driver	N	T	likely_pathogenic	No	No	Yes	WES
25DCIS	CDC27	p.K261Q	17	45234340	T	G	Missense_Mutation	66	7.6%	No	Yes	37%	0.05441	78.9%	15.8%	Subclonal	D	Driver	N	T	likely_pathogenic	No	No	Yes	WES
25IDC	SKAP1	p.E179Q	17	46262117	C	G	Missense_Mutation	92	22.8%	No	Yes	100%	0.91168	100.0%	73.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	SKAP1	p.E179Q	17	46262117	C	G	Missense_Mutation	111	21.6%	No	Yes	100%	0.91343	100.0%	72.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	AMZ2	p.L97V	17	66246940	C	G	Missense_Mutation	61	9.8%	No	Yes	63%	0.48645	96.9%	28.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	AMZ2	p.L97V	17	66246940	C	G	Missense_Mutation	85	11.8%	No	Yes	69%	0.57885	97.3%	37.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	ST6GALNAC1	p.Q232E	17	74625231	G	C	Missense_Mutation	251	1.2%	No	Yes	8%	0	21.5%	2.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	ST6GALNAC1	p.Q232E	17	74625231	G	C	Missense_Mutation	242	14.9%	No	Yes	87%	0.79291	99.0%	62.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	ST6GALNAC1	p.E110*	17	74625597	C	A	Nonsense_Mutation	309	0.3%	No	Yes	2%	0	10.9%	0.2%	Subclonal	N				likely_pathogenic	No	No	No	WES
25DCIS	ST6GALNAC1	p.E110*	17	74625597	C	A	Nonsense_Mutation	335	11.9%	No	Yes	70%	0.16979	91.5%	51.6%	Subclonal	N				likely_pathogenic	No	No	No	WES
25IDC	GPS1	p.S12*	17	80010217	C	A	Nonsense_Mutation	216	12.0%	No	Yes	77%	0.53981	97.6%	52.5%	Clonal	A				likely_pathogenic	No	No	No	WES
25DCIS	GPS1	p.S12*	17	80010217	C	A	Nonsense_Mutation	221	14.9%	No	Yes	88%	0.79832	99.0%	61.9%	Clonal	A				likely_pathogenic	No	No	No	WES
25DCIS	CEP192	p.K1870Q	18	13073176	A	C	Missense_Mutation	90	6.7%	No	No	46%	0.18481	88.8%	21.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	SERPINB12	p.D316E	18	61233974	C	G	Missense_Mutation	188	14.9%	No	No	100%	0.91638	100.0%	77.1%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
25IDC	BSG	p.G18E	19	572687	G	A	Missense_Mutation	166	39.8%	No	No	100%	0.97907	100.0%	92.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	BSG	p.G18E	19	572687	G	A	Missense_Mutation	224	28.1%	No	No	100%	0.91277	100.0%	89.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	REXO1	p.D609E	19	1826961	G	C	Missense_Mutation	159	1.3%	No	No	7%	0	23.4%	1.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	REXO1	p.D609E	19	1826961	G	C	Missense_Mutation	202	16.3%	No	No	96%	0.87102	100.0%	66.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	CREB3L3	p.D182N	19	4159747	G	A	Missense_Mutation	53	34.0%	No	No	100%	0.96735	100.0%	74.8%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25DCIS	CREB3L3	p.D182N	19	4159747	G	A	Missense_Mutation	66	30.3%	No	No	100%	0.96552	100.0%	76.0%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25IDC	ARHGEF18	p.S477F	19	7518491	C	T	Missense_Mutation	181	37.0%	No	No	100%	0.98423	100.0%	91.9%	Clonal	D	Passenger		T	passenger	No	No	No	WES
25DCIS	ARHGEF18	p.S477F	19	7518491	C	T	Missense_Mutation	199	33.2%	No	No	100%	0.9829	100.0%	91.4%	Clonal	D	Passenger		T	passenger	No	No	No	WES
25IDC	MUC16	p.Q9401E	19	9059245	G	C	Missense_Mutation	262	34.0%	No	No	100%	0.97701	100.0%	93.9%	Clonal		Passenger	N	T	passenger	No	No	No	WES
25DCIS	MUC16	p.Q9401E	19	9059245	G	C	Missense_Mutation	199	24.1%	No	No	100%	0.80098	100.0%	84.5%	Clonal		Passenger	N	T	passenger	No	No	No	WES
25IDC	ATG4D	p.E205G	19	10657635	A	G	Missense_Mutation	253	0.8%	No	No	4%	0	14.7%	0.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	ATG4D	p.E205G	19	10657635	A	G	Missense_Mutation	293	11.9%	No	No	70%	0.22823	92.7%	50.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	CACNA1A	p.M1583I	19	13365915	C	G	Missense_Mutation	147	0.7%	No	No	4%	0	19.5%	0.4%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25DCIS	CACNA1A	p.M1583I	19	13365915	C	G	Missense_Mutation	129	18.6%	No	No	100%	0.90023	100.0%	67.3%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25IDC	APLP1	p.P439S	19	36365742	C	T	Missense_Mutation	316	25.0%	No	No	100%	0.97872	100.0%	92.1%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
25DCIS	APLP1	p.P439S	19	36365742	C	T	Missense_Mutation	446	30.3%	No	No	100%	0.46706	100.0%	96.2%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
25IDC	ZNF566	p.E4*	19	36964360	C	A	Nonsense_Mutation	132	26.5%	No	No	100%	0.97646	100.0%	84.9%	Clonal	A				passenger	No	No	No	WES
25DCIS	ZNF566	p.E4*	19	36964360	C	A	Nonsense_Mutation	158	23.4%	No	No	100%	0.93372	100.0%	83.2%	Clonal	A				passenger	No	No	No	WES
25IDC	WDR87	p.L2562V	19	38376510	A	C	Missense_Mutation	244	27.5%	No	No	100%	0.98242	100.0%	91.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	WDR87	p.L2562V	19	38376510	A	C	Missense_Mutation	196	24.0%	No	No	100%	0.97736	100.0%	87.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	RYR1	p.N918S	19	38954457	A	G	Missense_Mutation	176	31.3%	No	No	100%	0.9566	100.0%	90.8%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25DCIS	RYR1	p.N918S	19	38954457	A	G	Missense_Mutation	217	24.4%	No	No	100%	0.9794	100.0%	89.1%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25IDC	SPTBN4	p.R2368W	19	41076417	C	T	Missense_Mutation	162	27.2%	No	No	100%	0.97877	100.0%	87.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	SPTBN4	p.R2368W	19	41076417	C	T	Missense_Mutation	169	23.1%	No	No	100%	0.97241	100.0%	85.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	CEACAM5	p.S658P	19	42225042	T	C	Missense_Mutation	153	23.5%	No	No	100%	0.96571	100.0%	83.9%	Clonal	N	Passenger		T	passenger	No	No	No	WES
25DCIS	CEACAM5	p.S658P	19	42225042	T	C	Missense_Mutation	142	26.8%	No	No	100%	0.97386	100.0%	86.4%	Clonal	N	Passenger		T	passenger	No	No	No	WES
25IDC	CADM4	p.G362S	19	44127565	C	T	Missense_Mutation	123	26.0%	No	No	100%	0.97515	100.0%	83.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	CADM4	p.G362S	19	44127565	C	T	Missense_Mutation	135	20.0%	No	No	100%	0.90937	100.0%	75.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	KCNJ14	p.D418H	19	48967975	G	C	Missense_Mutation	123	36.6%	No	Yes	100%	0.98085	100.0%	88.3%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25DCIS	KCNJ14	p.D418H	19	48967975	G	C	Missense_Mutation	131	32.1%	No	Yes	100%	0.97744	100.0%	87.0%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25IDC	SIGLEC7	p.N105Ifs*4	19	51645933	AC	A	Frame_Shift_Del	325	68.0%	No	Yes	100%	0.18579	100.0%	98.1%	Clonal					likely_pathogenic	No	No	No	WES
25DCIS	SIGLEC7	p.N105Ifs*4	19	51645933	AC	A	Frame_Shift_Del	327	59.3%	No	Yes	100%	0.55251	100.0%	97.8%	Clonal					likely_pathogenic	No	No	No	WES
25IDC	PRKCG	p.E135D	19	54393147	G	C	Missense_Mutation	201	48.8%	No	Yes	100%	0.71387	100.0%	95.4%	Clonal	N	Passenger		T	passenger	No	No	No	WES
25DCIS	PRKCG	p.E135D	19	54393147	G	C	Missense_Mutation	251	40.6%	No	Yes	100%	0.8654	100.0%	95.1%	Clonal	N	Passenger		T	passenger	No	No	No	WES
25DCIS	NLRP7	p.Q959E	19	55439079	G	C	Missense_Mutation	129	15.5%	No	Yes	91%	0.82168	100.0%	57.3%	Clonal	N	Passenger		T	passenger	No	No	No	WES
25IDC	NLRP5	p.R456H	19	56538966	G	A	Missense_Mutation	222	41.0%	No	Yes	100%	0.53926	100.0%	94.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	NLRP5	p.R456H	19	56538966	G	A	Missense_Mutation	234	35.0%	No	Yes	100%	0.98395	100.0%	93.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	MCM8	p.Q528E	20	5963660	C	G	Missense_Mutation	52	42.3%	No	No	100%	0.96164	100.0%	80.7%	Clonal	D	Passenger		T	passenger	No	No	No	WES
25DCIS	MCM8	p.Q528E	20	5963660	C	G	Missense_Mutation	80	25.0%	No	No	100%	0.92257	100.0%	72.5%	Clonal	D	Passenger		T	passenger	No	No	No	WES
25IDC	BPIFA2	p.W5*	20	31756966	G	A	Nonsense_Mutation	74	14.9%	No	No	80%	0.66937	98.5%	43.8%	Clonal	A				passenger	No	No	No	WES
25DCIS	BPIFA2	p.W5*	20	31756966	G	A	Nonsense_Mutation	96	13.5%	No	No	79%	0.71257	98.4%	45.7%	Clonal	A				passenger	No	No	No	WES
25IDC	NNAT	p.I13T	20	36149771	T	C	Missense_Mutation	209	37.8%	No	No	100%	0.98501	100.0%	93.1%	Clonal	D	Passenger	D		passenger	No	No	No	WES
25DCIS	NNAT	p.I13T	20	36149771	T	C	Missense_Mutation	240	34.6%	No	No	100%	0.98469	100.0%	93.3%	Clonal	D	Passenger	D		passenger	No	No	No	WES
25IDC	SERINC3	p.T38S	20	43142608	G	C	Missense_Mutation	85	57.6%	No	Yes	100%	0.98514	100.0%	90.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	SERINC3	p.T38S	20	43142608	G	C	Missense_Mutation	93	48.4%	No	Yes	100%	0.9799	100.0%	88.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25IDC	PPP1R3D	p.G45R	20	58514854	C	T	Missense_Mutation	105	44.8%	No	Yes	100%	0.71122	100.0%	90.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	PPP1R3D	p.G45R	20	58514854	C	T	Missense_Mutation	153	34.0%	No	Yes	100%	0.95061	100.0%	90.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	B3GALT5	p.R73C	21	41032703	C	T	Missense_Mutation	129	58.1%	No	Yes	100%	0.98803	100.0%	93.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25DCIS	B3GALT5	p.R73C	21	41032703	C	T	Missense_Mutation	124	49.2%	No	Yes	100%	0.98332	100.0%	91.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	EIF4ENIF1	p.V260L	22	31858927	C	G	Missense_Mutation	201	0.5%	No	No	3%	0	16.9%	0.3%	Subclonal	D	Passenger	N		passenger	No	No	No	WES
25DCIS	EIF4ENIF1	p.V260L	22	31858927	C	G	Missense_Mutation	204	11.8%	No	No	81%	0.70361	98.4%	54.0%	Clonal	D	Passenger	N		passenger	No	No	No	WES
25IDC	APOL5	p.R199K	22	36122711	G	A	Missense_Mutation	215	40.0%	No	No	100%	0.65678	100.0%	94.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	APOL5	p.R199K	22	36122711	G	A	Missense_Mutation	213	39.0%	No	No	100%	0.58718	100.0%	94.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	ACO2	p.E677Q	22	41923367	G	C	Missense_Mutation	282	14.5%	No	No	100%	0.89824	100.0%	70.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	PHF21B	p.G368S	22	45283938	C	T	Missense_Mutation	267	48.7%	No	No	100%	0.73656	100.0%	96.4%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25DCIS	PHF21B	p.G368S	22	45283938	C	T	Missense_Mutation	319	47.3%	No	No	100%	0.57119	100.0%	97.0%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25IDC	BRD1	p.H342L	22	50216941	T	A	Missense_Mutation	256	6.3%	No	No	40%	0.00011	62.7%	24.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
25IDC	PIGA	p.G335E	23	15342971	C	T	Missense_Mutation	53	17.0%	No	No	74%	0.60816	98.0%	38.8%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25DCIS	PIGA	p.G335E	23	15342971	C	T	Missense_Mutation	49	20.4%	No	No	99%	0.82918	100.0%	49.6%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25IDC	DMD	p.Q2569*	23	31697659	G	A	Nonsense_Mutation	69	13.0%	No	No	57%	0.25607	93.0%	30.3%	Subclonal	A				passenger	No	No	No	WES
25DCIS	DMD	p.Q2569*	23	31697659	G	A	Nonsense_Mutation	70	20.0%	No	No	97%	0.84086	100.0%	54.8%	Clonal	A				passenger	No	No	No	WES
25IDC	FAM47C	p.R247H	23	37027223	G	A	Missense_Mutation	863	3.9%	No	No	17%	0	23.4%	11.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	FAM47C	p.R247H	23	37027223	G	A	Missense_Mutation	906	0.3%	No	No	2%	0	4.2%	0.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	MSN	p.R408Q	23	64957172	G	A	Missense_Mutation	165	23.6%	No	No	100%	0.89355	100.0%	72.9%	Clonal	N	Passenger	N	D	passenger	No	Yes	No	WES
25DCIS	MSN	p.R408Q	23	64957172	G	A	Missense_Mutation	165	15.2%	No	No	74%	0.49921	96.5%	50.3%	Subclonal	N	Passenger	N	D	passenger	No	Yes	No	WES
25IDC	DGAT2L6	p.E289K	23	69424807	G	A	Missense_Mutation	76	27.6%	No	No	100%	0.89043	100.0%	69.4%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25DCIS	DGAT2L6	p.E289K	23	69424807	G	A	Missense_Mutation	92	37.0%	No	No	100%	0.97193	100.0%	84.5%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
25IDC	XKRX	p.K342Q	23	100169653	T	G	Missense_Mutation	169	40.8%	No	No	100%	0.97041	100.0%	91.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	XKRX	p.K342Q	23	100169653	T	G	Missense_Mutation	141	34.8%	No	No	100%	0.94763	100.0%	87.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
25DCIS	BHLHB9	p.Q431K	23	102005214	C	A	Missense_Mutation	80	7.5%	No	No	36%	0.02349	74.2%	16.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
25IDC	GLRA4	p.L13F	23	102983095	G	A	Missense_Mutation	80	16.3%	No	Yes	71%	0.5113	97.2%	41.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	GLRA4	p.L13F	23	102983095	G	A	Missense_Mutation	101	19.8%	No	Yes	96%	0.85462	100.0%	60.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
25DCIS	RNF128	p.P315T	23	106033471	C	A	Missense_Mutation	40	10.0%	No	No	49%	0.3688	94.0%	19.0%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
25DCIS	THOC2	p.S1230*	23	122756705	G	C	Nonsense_Mutation	52	19.2%	No	No	93%	0.80859	100.0%	47.7%	Clonal	A				passenger	No	No	No	WES
28DCIS	MTOR	p.L219F	1	11316099	G	A	Missense_Mutation	123	8.9%	No	Yes	82%	0.6354	98.6%	43.9%	Clonal	D	Passenger	D	T	passenger	Yes	Yes	Yes	WES
28DCIS	KIAA0754	p.E623D	1	39878214	G	C	Missense_Mutation	166	5.4%	No	No	77%	0.57538	98.3%	38.7%	Clonal	N	Passenger		D	passenger	No	No	No	WES
28IDC	USP24	p.S581N	1	55619862	C	T	Missense_Mutation	130	43.1%	No	Yes	100%	0.97317	100.0%	90.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
28DCIS	USP24	p.S581N	1	55619862	C	T	Missense_Mutation	139	18.7%	No	Yes	100%	0.95537	100.0%	80.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
28DCIS	HMGCS2	p.L402M	1	120295993	G	T	Missense_Mutation	53	9.4%	No	Yes	86%	0.64563	98.6%	32.9%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
28IDC	ATR	p.T1798A	3	142217605	T	C	Missense_Mutation	125	30.4%	No	No	100%	0.95432	100.0%	87.0%	Clonal	D	Passenger	N	T	passenger	Yes	Yes	No	WES
28DCIS	ATR	p.T1798A	3	142217605	T	C	Missense_Mutation	97	11.3%	No	No	100%	0.82405	100.0%	56.4%	Clonal	D	Passenger	N	T	passenger	Yes	Yes	No	WES
28IDC	CCNL1	p.P5T	3	156877871	G	T	Missense_Mutation	263	0.4%	No	No	3%	0	17.0%	0.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
28DCIS	CCNL1	p.P5T	3	156877871	G	T	Missense_Mutation	134	4.5%	No	No	59%	0.37284	96.3%	26.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
28IDC	PIK3CA	p.H1047R	3	178952085	A	G	Missense_Mutation	132	49.2%	Yes	No	100%	0.39157	100.0%	93.7%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
28DCIS	PIK3CA	p.H1047R	3	178952085	A	G	Missense_Mutation	119	37.8%	Yes	No	100%	0.33846	100.0%	91.2%	Clonal	D	Driver	N	T	likely_pathogenic	Yes	Yes	Yes	WES
28IDC	LRBA	p.P185A	4	151842442	G	C	Missense_Mutation	42	35.7%	No	Yes	100%	0.90426	100.0%	69.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
28DCIS	LRBA	p.P185A	4	151842442	G	C	Missense_Mutation	32	9.4%	No	Yes	86%	0.62864	98.5%	24.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
28IDC	ABCA13	p.S3457R	7	48390406	C	A	Missense_Mutation	175	0.6%	No	No	4%	0	19.3%	0.4%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
28DCIS	ABCA13	p.S3457R	7	48390406	C	A	Missense_Mutation	98	5.1%	No	No	62%	0.44406	97.1%	25.8%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
28IDC	PTPRZ1	p.M710I	7	121651230	G	T	Missense_Mutation	127	25.2%	No	No	100%	0.91348	100.0%	81.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
28DCIS	PTPRZ1	p.M710I	7	121651230	G	T	Missense_Mutation	106	30.2%	No	No	100%	0.40603	100.0%	86.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
28IDC	DGKI	p.A31del	7	137531515	TGGC	T	In_Frame_Del	59	8.5%	No	No	54%	0.29197	95.2%	22.9%	Subclonal					passenger	No	No	No	WES
28DCIS	KCNH2	p.Y827H	7	150646057	A	G	Missense_Mutation	83	4.8%	No	No	49%	0.28973	94.7%	19.0%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
28IDC	SPATA31E1	p.P288T	9	90500264	C	A	Missense_Mutation	255	0.4%	No	No	3%	0	13.2%	0.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
28DCIS	SPATA31E1	p.P288T	9	90500264	C	A	Missense_Mutation	124	5.6%	No	No	63%	0.4148	96.8%	30.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
28DCIS	BRINP1	p.D701E	9	121929545	G	T	Missense_Mutation	120	5.0%	No	No	56%	0.31939	95.4%	25.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
28DCIS	GSTO1	p.R147S	10	106022809	C	A	Missense_Mutation	42	7.1%	No	No	80%	0.59847	98.3%	23.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
28IDC	EDRF1	p.E521K	10	127424276	G	A	Missense_Mutation	76	28.9%	No	No	100%	0.95751	100.0%	77.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
28DCIS	EDRF1	p.E521K	10	127424276	G	A	Missense_Mutation	102	20.6%	No	No	100%	0.93147	100.0%	78.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
28IDC	ERBB3	p.D297Y	12	56482341	G	T	Missense_Mutation	76	42.1%	Yes	No	100%	0.79946	100.0%	86.5%	Clonal	D	Passenger	D	D	likely_pathogenic	No	Yes	Yes	WES
28DCIS	ERBB3	p.D297Y	12	56482341	G	T	Missense_Mutation	51	33.3%	Yes	No	100%	0.43693	100.0%	78.4%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	Yes	Yes	WES
28IDC	SLC17A8	p.N435H	12	100811812	A	C	Missense_Mutation	113	37.2%	No	No	100%	0.9309	100.0%	88.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
28DCIS	SLC17A8	p.N435H	12	100811812	A	C	Missense_Mutation	77	18.2%	No	No	100%	0.93609	100.0%	69.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
28DCIS	ALDH1L2	p.A848E	12	105420496	G	T	Missense_Mutation	133	4.5%	No	No	50%	0.21648	92.9%	23.0%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
28IDC	TBX3	p.F133V	12	115118944	A	C	Missense_Mutation	134	32.1%	No	No	100%	0.97084	100.0%	87.9%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
28DCIS	TBX3	p.F133V	12	115118944	A	C	Missense_Mutation	149	28.2%	No	No	100%	0.43421	100.0%	89.4%	Subclonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
28IDC	TPTE2	p.G451S	13	20000609	C	T	Missense_Mutation	112	4.5%	No	No	24%	0.00013	53.0%	10.0%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
28DCIS	TPTE2	p.G451S	13	20000609	C	T	Missense_Mutation	110	3.6%	No	No	37%	0.08764	85.5%	14.4%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
28IDC	SACS	p.S3505*	13	23907501	G	T	Nonsense_Mutation	36	25.0%	No	No	100%	0.82588	100.0%	54.9%	Clonal	D				passenger	No	No	No	WES
28DCIS	SACS	p.S3505*	13	23907501	G	T	Nonsense_Mutation	76	21.1%	No	No	100%	0.8893	100.0%	74.7%	Clonal	D				passenger	No	No	No	WES
28IDC	WASF3	p.P324R	13	27255445	C	G	Missense_Mutation	140	52.1%	No	Yes	100%	0.94519	100.0%	93.4%	Clonal	D	Passenger	D	T	passenger	No	No	Yes	WES
28DCIS	WASF3	p.P324R	13	27255445	C	G	Missense_Mutation	81	32.1%	No	Yes	100%	0.63286	100.0%	83.9%	Clonal	D	Passenger	D	T	passenger	No	No	Yes	WES
28DCIS	PIBF1	p.T757N	13	73590053	C	A	Missense_Mutation	47	8.5%	No	Yes	78%	0.5951	98.3%	27.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
28IDC	TUBGCP3	p.E884K	13	113140381	C	T	Missense_Mutation	57	3.5%	No	Yes	15%	0.00056	51.1%	4.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
28DCIS	TUBGCP3	p.E884K	13	113140381	C	T	Missense_Mutation	49	16.3%	No	Yes	100%	0.85498	100.0%	53.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
28DCIS	PLA2G4E	p.H392Q	15	42287629	G	T	Missense_Mutation	85	5.9%	No	Yes	54%	0.32388	95.4%	22.8%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
28IDC	LCMT1	p.S34A	16	25123304	T	G	Missense_Mutation	86	31.4%	No	No	100%	0.96437	100.0%	82.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
28DCIS	LCMT1	p.S34A	16	25123304	T	G	Missense_Mutation	45	33.3%	No	No	100%	0.47308	100.0%	76.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
28IDC	CES1	p.T291M	16	55853481	G	A	Missense_Mutation	89	4.5%	No	No	28%	0.00858	68.9%	11.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
28DCIS	CES1	p.T291M	16	55853481	G	A	Missense_Mutation	66	4.5%	No	No	51%	0.37016	96.1%	17.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
28IDC	OGFOD1	p.P193L	16	56500800	C	T	Missense_Mutation	60	25.0%	No	No	100%	0.91199	100.0%	68.5%	Clonal	D	Driver	D		likely_pathogenic	No	No	No	WES
28DCIS	OGFOD1	p.P193L	16	56500800	C	T	Missense_Mutation	59	10.2%	No	No	100%	0.75096	100.0%	41.6%	Clonal	D	Driver	D		likely_pathogenic	No	No	No	WES
28IDC	TP53	p.R249T	17	7577535	C	G	Missense_Mutation	89	43.8%	Yes	Yes	100%	0.9721	100.0%	87.1%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
28DCIS	TP53	p.R249T	17	7577535	C	G	Missense_Mutation	52	23.1%	Yes	Yes	100%	0.77838	100.0%	66.1%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
28IDC	MYH1	p.Y353C	17	10415814	T	C	Missense_Mutation	109	52.3%	No	Yes	100%	0.94828	100.0%	91.8%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
28DCIS	MYH1	p.Y353C	17	10415814	T	C	Missense_Mutation	103	40.8%	No	Yes	100%	0	100.0%	90.0%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
28IDC	CDC27	p.N486H	17	45219332	T	G	Missense_Mutation	38	7.9%	No	Yes	34%	0.08022	85.1%	11.9%	Subclonal	D	Driver	N	T	likely_pathogenic	No	No	Yes	WES
28DCIS	CDC27	p.N486H	17	45219332	T	G	Missense_Mutation	44	4.5%	No	Yes	37%	0.33098	93.5%	10.5%	Subclonal	D	Driver	N	T	likely_pathogenic	No	No	Yes	WES
28IDC	CDC27	p.A274S	17	45234301	C	A	Missense_Mutation	43	4.7%	No	Yes	20%	0.00928	66.2%	5.7%	Subclonal	D	Passenger	N	T	passenger	No	No	Yes	WES
28DCIS	BRIP1	p.I504M	17	59861747	G	C	Missense_Mutation	144	5.6%	No	No	100%	0.73783	100.0%	45.5%	Clonal	N	Passenger	N	T	passenger	No	Yes	No	WES
28IDC	GH1	p.I147F	17	61995137	T	A	Missense_Mutation	652	23.9%	No	No	100%	0.98376	100.0%	96.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
28DCIS	GH1	p.I147F	17	61995137	T	A	Missense_Mutation	338	17.8%	No	No	100%	0.92445	100.0%	91.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
28IDC	TBC1D16	p.E214*	17	77984098	C	A	Nonsense_Mutation	588	40.5%	No	Yes	100%	0.34438	100.0%	98.1%	Clonal	D				likely_pathogenic	No	No	No	WES
28DCIS	TBC1D16	p.E214*	17	77984098	C	A	Nonsense_Mutation	213	28.2%	No	Yes	100%	0.30404	100.0%	93.4%	Clonal	D				likely_pathogenic	No	No	No	WES
28IDC	TBC1D16	p.D210Y	17	77984110	C	A	Missense_Mutation	614	40.4%	No	Yes	100%	0.34907	100.0%	98.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
28DCIS	TBC1D16	p.D210Y	17	77984110	C	A	Missense_Mutation	224	29.0%	No	Yes	100%	0.30109	100.0%	94.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
28DCIS	RTTN	p.A546D	18	67836143	G	T	Missense_Mutation	100	5.0%	No	No	56%	0.35602	96.0%	23.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
28IDC	ZC3H12B	p.E316K	23	64719076	G	A	Missense_Mutation	102	31.4%	No	No	100%	0.96719	100.0%	84.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
28DCIS	ZC3H12B	p.E316K	23	64719076	G	A	Missense_Mutation	81	24.7%	No	No	100%	0.8318	100.0%	79.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
28IDC	ZMYM3	p.Y1064*	23	70464233	CATATGAA	C	Frame_Shift_Del	295	12.2%	No	No	77%	0.40043	97.1%	56.1%	Subclonal					passenger	No	No	No	WES
28DCIS	ZMYM3	p.Y1064*	23	70464233	CATATGAA	C	Frame_Shift_Del	148	12.2%	No	No	100%	0.86782	100.0%	67.6%	Clonal					passenger	No	No	No	WES
30IDC	C1orf170	p.S112Y	1	915793	G	T	Missense_Mutation	230	15.7%	No	No	99%	0.79001	100.0%	68.9%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
30DCIS	C1orf170	p.S112Y	1	915793	G	T	Missense_Mutation	208	0.5%	No	No	2%	0	11.9%	0.2%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
30IDC	C1orf170	p.S107Y	1	915808	G	T	Missense_Mutation	224	16.5%	No	No	100%	0.82732	100.0%	71.6%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
30IDC	PHF13	p.D4N	1	6674136	G	A	Missense_Mutation	184	1.1%	No	No	8%	0	27.6%	2.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	PHF13	p.D4N	1	6674136	G	A	Missense_Mutation	205	9.8%	No	No	55%	0.01109	82.0%	35.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	SPEN	p.D2528Y	1	16260317	G	T	Missense_Mutation	138	21.0%	No	No	100%	0.85651	100.0%	76.1%	Clonal	D	Passenger	D	T	passenger	No	Yes	Yes	WES
30DCIS	SPEN	p.D2528Y	1	16260317	G	T	Missense_Mutation	189	1.6%	No	No	7%	0	20.7%	2.2%	Subclonal	D	Passenger	D	T	passenger	No	Yes	Yes	WES
30IDC	SPEN	p.E2632*	1	16260629	G	T	Nonsense_Mutation	188	18.1%	No	No	100%	0.85611	100.0%	74.0%	Clonal	A				likely_pathogenic	No	Yes	Yes	WES
30DCIS	SPEN	p.E2632*	1	16260629	G	T	Nonsense_Mutation	145	1.4%	No	No	6%	0	22.2%	1.4%	Subclonal	A				likely_pathogenic	No	Yes	Yes	WES
30IDC	IGSF21	p.D51H	1	18554472	G	C	Missense_Mutation	93	7.5%	No	No	47%	0.0854	88.3%	23.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	IPO13	p.P762T	1	44426874	C	A	Missense_Mutation	136	14.7%	No	No	93%	0.69951	100.0%	58.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	IPO13	p.P762T	1	44426874	C	A	Missense_Mutation	140	19.3%	No	No	90%	0.61213	100.0%	61.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	SLC1A7	p.M64I	1	53600045	C	T	Missense_Mutation	73	17.8%	No	No	83%	0.50372	98.7%	47.8%	Clonal	N	Passenger		T	passenger	No	No	No	WES
30DCIS	DHCR24	p.E372K	1	55319814	C	T	Missense_Mutation	142	22.5%	No	No	100%	0.77575	100.0%	70.7%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30IDC	DNASE2B	p.S219*	1	84878140	C	G	Nonsense_Mutation	136	1.5%	No	No	9%	0	32.1%	2.3%	Subclonal	A				passenger	No	No	No	WES
30DCIS	DNASE2B	p.S219*	1	84878140	C	G	Nonsense_Mutation	169	24.9%	No	No	100%	0.84437	100.0%	78.2%	Clonal	A				passenger	No	No	No	WES
30DCIS	COL11A1	p.G1096R	1	103405981	C	G	Missense_Mutation	43	18.6%	No	No	87%	0.52645	98.8%	41.8%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	NOTCH2	p.D1151N	1	120479976	C	T	Missense_Mutation	110	17.3%	No	No	81%	0.45318	98.4%	51.6%	Subclonal	D	Passenger	N	T	passenger	No	Yes	No	WES
30DCIS	GABPB2	p.G127R	1	151065770	G	A	Missense_Mutation	72	9.7%	No	No	55%	0.1557	94.0%	26.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	INTS3	p.E977Q	1	153745435	G	C	Missense_Mutation	186	0.5%	No	No	4%	0	21.0%	0.5%	Subclonal	N	Passenger	N		passenger	No	No	No	WES
30DCIS	INTS3	p.E977Q	1	153745435	G	C	Missense_Mutation	204	17.2%	No	No	97%	0.71697	100.0%	68.0%	Clonal	N	Passenger	N		passenger	No	No	No	WES
30IDC	INTS3	p.E1019*	1	153745672	G	T	Nonsense_Mutation	158	0.6%	No	No	5%	0	24.8%	0.7%	Subclonal	D				passenger	No	No	No	WES
30DCIS	INTS3	p.E1019*	1	153745672	G	T	Nonsense_Mutation	155	19.4%	No	No	100%	0.78711	100.0%	71.0%	Clonal	D				passenger	No	No	No	WES
30IDC	MEX3A	p.A86E	1	156051533	G	T	Missense_Mutation	26	15.4%	No	No	100%	0.65074	99.0%	33.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	MEX3A	p.A86E	1	156051533	G	T	Missense_Mutation	19	15.8%	No	No	89%	0.48479	98.6%	25.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	HDGF	p.E195*	1	156713625	C	A	Nonsense_Mutation	144	20.8%	No	No	100%	0.81343	100.0%	73.6%	Clonal	A				passenger	No	No	No	WES
30IDC	OR6N2	p.E173K	1	158746909	C	T	Missense_Mutation	100	17.0%	No	No	100%	0.81332	100.0%	65.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	OR6N2	p.E173K	1	158746909	C	T	Missense_Mutation	100	13.0%	No	No	74%	0.36277	97.8%	42.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	PVRL4	p.E389K	1	161043578	C	T	Missense_Mutation	111	9.0%	No	No	66%	0.33606	96.7%	35.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	GPA33	p.S101F	1	167038272	G	A	Missense_Mutation	89	9.0%	No	No	66%	0.36869	97.0%	32.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	GPA33	p.S101F	1	167038272	G	A	Missense_Mutation	99	20.2%	No	No	100%	0.76077	100.0%	66.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	POU2F1	p.S164F	1	167343433	C	T	Missense_Mutation	218	6.4%	No	No	47%	0.00652	76.0%	27.9%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
30IDC	CCDC181	p.H281D	1	169390828	G	C	Missense_Mutation	86	17.4%	No	No	100%	0.80762	100.0%	63.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	CCDC181	p.H281D	1	169390828	G	C	Missense_Mutation	107	0.9%	No	No	5%	0	28.1%	0.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	SELP	p.C642G	1	169565340	A	C	Missense_Mutation	74	12.2%	No	No	69%	0.32653	97.4%	36.0%	Subclonal	N	Passenger	D	D	passenger	No	No	Yes	WES
30DCIS	SEC16B	p.D78N	1	177936885	C	T	Missense_Mutation	259	4.2%	No	No	24%	0	41.7%	13.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	LAMC1	p.Q176*	1	183072570	C	T	Nonsense_Mutation	135	14.1%	No	No	100%	0.76167	100.0%	61.0%	Clonal	A				passenger	No	No	No	WES
30DCIS	LAMC1	p.Q176*	1	183072570	C	T	Nonsense_Mutation	154	0.6%	No	No	4%	0	19.6%	0.4%	Subclonal	A				passenger	No	No	No	WES
30DCIS	LAMC1	p.K802N	1	183093770	G	C	Missense_Mutation	85	16.5%	No	No	93%	0.61017	100.0%	53.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	HMCN1	p.A39G	1	185704027	C	G	Missense_Mutation	95	24.2%	No	No	100%	0.89332	100.0%	77.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES

30DCIS	HMCN1	p.A39G	1	185704027	C	G	Missense_Mutation	114	34.2%	No	No	100%	0.9073	100.0%	86.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	HMCN1	p.T2183N	1	186017942	C	A	Missense_Mutation	39	10.3%	No	No	75%	0.50323	98.2%	27.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	TPR	p.Q1052*	1	186314771	G	A	Nonsense_Mutation	57	15.8%	No	No	100%	0.73346	100.0%	50.8%	Clonal	A				likely_pathogenic	No	Yes	No	WES
30DCIS	TPR	p.E808Q	1	186321155	C	G	Missense_Mutation	97	15.5%	No	No	88%	0.55989	99.0%	51.6%	Clonal	D	Passenger	N	T	passenger	No	Yes	No	WES
30IDC	RGS21	p.E49V	1	192321234	A	T	Missense_Mutation	43	7.0%	No	No	51%	0.30615	96.1%	17.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	RGS21	p.E49V	1	192321234	A	T	Missense_Mutation	48	12.5%	No	No	71%	0.38218	97.9%	31.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	CDC73	p.R156H	1	193107258	G	A	Missense_Mutation	81	2.5%	No	No	18%	0.00439	61.6%	5.1%	Subclonal	D	Driver	D	D	likely_pathogenic	No	Yes	No	WES
30DCIS	CDC73	p.R156H	1	193107258	G	A	Missense_Mutation	75	16.0%	No	No	91%	0.57771	100.0%	49.4%	Clonal	D	Driver	D	D	likely_pathogenic	No	Yes	No	WES
30DCIS	CAMK1G	p.Q193H	1	209781222	G	C	Missense_Mutation	140	13.6%	No	No	77%	0.38197	97.9%	49.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	KCNH1	p.D631N	1	210970874	C	T	Missense_Mutation	147	4.8%	No	No	35%	0.00376	68.8%	16.7%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	INTS7	p.Q53E	1	212194492	G	C	Missense_Mutation	56	14.3%	No	No	81%	0.47648	98.6%	39.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	COG2	p.R442C	1	230820926	C	T	Missense_Mutation	129	0.8%	No	No	6%	0	30.3%	0.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	COG2	p.R442C	1	230820926	C	T	Missense_Mutation	107	5.6%	No	No	32%	0.00167	65.7%	14.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	FMN2	p.G941A	1	240370934	G	C	Missense_Mutation	628	28.0%	No	No	100%	0.95993	100.0%	96.5%	Clonal	P	Passenger	N	T	passenger	No	No	No	WES
30DCIS	FMN2	p.G941A	1	240370934	G	C	Missense_Mutation	675	24.4%	No	No	100%	0.00751	100.0%	94.1%	Clonal	P	Passenger	N	T	passenger	No	No	No	WES
30IDC	ZBTB18	p.D14N	1	244217116	G	A	Missense_Mutation	116	12.1%	No	No	88%	0.63765	99.0%	50.5%	Clonal	D	Passenger		T	passenger	No	No	No	WES
30DCIS	OR2M4	p.S148F	1	248402673	C	T	Missense_Mutation	82	7.3%	No	No	41%	0.03113	83.0%	19.1%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
30DCIS	DNMT3A	p.F752L	2	25463237	G	C	Missense_Mutation	201	14.4%	No	No	67%	0.06913	91.3%	47.3%	Subclonal	D	Driver	D	D	likely_pathogenic	Yes	Yes	Yes	WES
30DCIS	THADA	p.Q569E	2	43801499	G	C	Missense_Mutation	51	13.7%	No	No	64%	0.28077	96.8%	31.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	POLR1A	p.E1615Q	2	86255771	C	G	Missense_Mutation	114	6.1%	No	No	39%	0.01288	75.6%	18.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	BUB1	p.G549A	2	111414665	C	G	Missense_Mutation	54	16.7%	No	No	78%	0.44253	98.3%	40.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	TANC1	p.S816F	2	160035611	C	T	Missense_Mutation	162	1.2%	No	No	8%	0	27.0%	1.9%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	TANC1	p.S816F	2	160035611	C	T	Missense_Mutation	191	24.1%	No	No	100%	0.84293	100.0%	78.2%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	SCN3A	p.E46K	2	166032769	C	T	Missense_Mutation	102	19.6%	No	No	91%	0.61871	100.0%	58.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	SCN2A	p.E206Q	2	166165685	G	C	Missense_Mutation	81	19.8%	No	No	100%	0.81084	100.0%	64.4%	Clonal	D	Passenger		D	likely_pathogenic	No	No	No	WES
30DCIS	SCN2A	p.E206Q	2	166165685	G	C	Missense_Mutation	68	4.4%	No	No	21%	0.0006	56.3%	7.0%	Subclonal	D	Passenger		D	likely_pathogenic	No	No	No	WES
30IDC	SCN1A	p.E526Q	2	166901639	C	G	Missense_Mutation	100	19.0%	No	No	100%	0.81809	100.0%	66.4%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	LRP2	p.N3893K	2	170022521	G	T	Missense_Mutation	88	5.7%	No	No	27%	0.00036	58.4%	11.2%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	TTN	p.E24502Q	2	179437355	C	G	Missense_Mutation	94	16.0%	No	No	90%	0.58896	100.0%	52.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	TTN	p.E9992Q	2	179569123	C	G	Missense_Mutation	86	14.0%	No	No	100%	0.71588	100.0%	52.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	TTN	p.E9992Q	2	179569123	C	G	Missense_Mutation	77	1.3%	No	No	7%	0.00004	38.8%	1.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	TTN	p.L7572F	2	179586674	C	G	Missense_Mutation	56	8.9%	No	No	51%	0.15464	93.8%	21.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	NCKAP1	p.E966Q	2	183795498	C	G	Missense_Mutation	58	19.0%	No	No	100%	0.76587	100.0%	56.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	NCKAP1	p.E966Q	2	183795498	C	G	Missense_Mutation	49	26.5%	No	No	100%	0.7409	100.0%	61.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	FAM171B	p.S716*	2	187627216	C	G	Nonsense_Mutation	93	12.9%	No	No	81%	0.56263	98.6%	45.4%	Clonal	D				passenger	No	No	No	WES
30DCIS	FAM171B	p.S716*	2	187627216	C	G	Nonsense_Mutation	78	19.2%	No	No	90%	0.58425	100.0%	52.9%	Clonal	D				passenger	No	No	No	WES
30IDC	CYP20A1	p.M173I	2	204131323	G	T	Missense_Mutation	59	8.5%	No	Yes	53%	0.25029	95.1%	22.8%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
30DCIS	CYP20A1	p.M173I	2	204131323	G	T	Missense_Mutation	65	1.5%	No	Yes	7%	0.00002	37.6%	1.3%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
30IDC	CHPF	p.E296K	2	220406340	C	T	Missense_Mutation	94	14.9%	No	Yes	94%	0.68593	100.0%	53.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	USP40	p.D227N	2	234463076	C	T	Missense_Mutation	61	1.6%	No	No	10%	0.00219	54.0%	2.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	USP40	p.D227N	2	234463076	C	T	Missense_Mutation	74	8.1%	No	No	38%	0.01141	76.4%	17.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	IQCA1	p.I168M	2	237396787	G	C	Missense_Mutation	64	14.1%	No	Yes	89%	0.62146	98.9%	43.8%	Clonal	D	Passenger		D	likely_pathogenic	No	No	No	WES
30DCIS	IQCA1	p.I168M	2	237396787	G	C	Missense_Mutation	55	1.8%	No	Yes	8%	0.00017	44.1%	1.6%	Subclonal	D	Passenger		D	likely_pathogenic	No	No	No	WES
30DCIS	LRRFIP1	p.Q180*	2	238662006	C	T	Nonsense_Mutation	60	18.3%	No	No	86%	0.52853	98.8%	46.4%	Clonal	A				passenger	No	No	No	WES
30IDC	HES6	p.E106K	2	239147827	C	T	Missense_Mutation	106	0.9%	No	No	6%	0	31.7%	1.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	HES6	p.E106K	2	239147827	C	T	Missense_Mutation	134	19.4%	No	No	91%	0.6189	100.0%	61.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	MTMR14	p.F392L	3	9729516	C	G	Missense_Mutation	100	14.0%	No	No	88%	0.63987	99.0%	50.7%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	MTMR14	p.F392L	3	9729516	C	G	Missense_Mutation	96	16.7%	No	No	78%	0.41259	98.2%	47.9%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30IDC	SH3BP5	p.D152H	3	15311261	C	G	Missense_Mutation	177	14.7%	No	No	93%	0.71292	100.0%	61.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	SH3BP5	p.D152H	3	15311261	C	G	Missense_Mutation	180	2.8%	No	No	13%	0	29.0%	5.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	NKIRAS1	p.E142K	3	23934741	C	T	Missense_Mutation	108	0.9%	No	No	6%	0	31.1%	1.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	NKIRAS1	p.E142K	3	23934741	C	T	Missense_Mutation	91	24.2%	No	No	100%	0.77098	100.0%	67.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	EPM2AIP1	p.S562*	3	37032884	G	C	Nonsense_Mutation	55	12.7%	No	No	59%	0.21197	95.6%	28.9%	Subclonal	D				passenger	No	No	No	WES
30DCIS	DLEC1	p.R81C	3	38080957	C	T	Missense_Mutation	256	19.5%	No	No	91%	0.64628	100.0%	69.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	CCDC13	p.E515K	3	42774431	C	T	Missense_Mutation	116	23.3%	No	No	100%	0.83664	100.0%	77.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	CCDC13	p.E466K	3	42775077	C	T	Missense_Mutation	151	14.6%	No	No	92%	0.69645	100.0%	59.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	IP6K2	p.E151Q	3	48728893	C	G	Missense_Mutation	74	16.2%	No	No	76%	0.39972	98.0%	43.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	DALRD3	p.S113L	3	49055579	G	A	Missense_Mutation	193	7.8%	No	No	49%	0.00843	77.7%	29.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	CCDC36	p.E133K	3	49281838	G	A	Missense_Mutation	32	25.0%	No	No	100%	0.80562	100.0%	54.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	CCDC36	p.E133K	3	49281838	G	A	Missense_Mutation	34	32.4%	No	No	100%	0.77693	100.0%	62.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	GNL3	p.E198Q	3	52724658	G	C	Missense_Mutation	63	4.8%	No	No	22%	0.00147	60.5%	7.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	CADPS	p.R732T	3	62518642	C	G	Missense_Mutation	89	1.1%	No	No	7%	0.00004	37.6%	1.2%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
30DCIS	CADPS	p.R732T	3	62518642	C	G	Missense_Mutation	87	14.9%	No	No	70%	0.28336	96.9%	41.0%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
30IDC	C3orf52	p.L15R	3	111805298	T	G	Missense_Mutation	122	1.6%	No	No	10%	0	35.8%	2.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	C3orf52	p.L15R	3	111805298	T	G	Missense_Mutation	128	25.0%	No	No	100%	0.8212	100.0%	74.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	ARHGAP31	p.R323*	3	119112399	A	T	Nonsense_Mutation	94	11.7%	No	No	74%	0.46073	97.9%	40.7%	Subclonal	A				passenger	No	No	No	WES
30DCIS	ARHGAP31	p.R323*	3	119112399	A	T	Nonsense_Mutation	50	26.0%	No	No	100%	0.73517	100.0%	60.5%	Clonal	A				passenger	No	No	No	WES
30IDC	ARHGAP31	p.R323K	3	119112400	G	A	Missense_Mutation	94	10.6%	No	No	67%	0.3562	96.9%	36.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ARHGAP31	p.R323K	3	119112400	G	A	Missense_Mutation	51	25.5%	No	No	100%	0.72916	100.0%	60.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	CD86	p.M214I	3	121825286	G	A	Missense_Mutation	51	19.6%	No	No	91%	0.57469	100.0%	47.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	PARP9	p.K298N	3	122274229	C	G	Missense_Mutation	107	14.0%	No	No	88%	0.64386	99.0%	51.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	PARP9	p.K298N	3	122274229	C	G	Missense_Mutation	119	26.9%	No	No	100%	0.83203	100.0%	76.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ROPN1B	p.E42Q	3	125694413	G	C	Missense_Mutation	112	17.9%	No	No	83%	0.50118	98.7%	53.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	IFT122	p.P983A	3	129226513	C	G	Missense_Mutation	58	15.5%	No	No	98%	0.67415	100.0%	46.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	PLXND1	p.E501D	3	129305548	C	G	Missense_Mutation	175	0.6%	No	No	4%	0	19.2%	0.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	PLXND1	p.E501D	3	129305548	C	G	Missense_Mutation	188	19.7%	No	No	92%	0.65201	100.0%	66.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	DNAJC13	p.D2195N	3	132249899	G	A	Missense_Mutation	58	17.2%	No	No	80%	0.47223	98.5%	42.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	ESYT3	p.L163I	3	138174153	C	A	Missense_Mutation	91	5.5%	No	No	35%	0.01734	75.9%	14.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ESYT3	p.L163I	3	138174153	C	A	Missense_Mutation	99	1.0%	No	No	5%	0	24.9%	0.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	ATR	p.H2203D	3	142186856	G	C	Missense_Mutation	63	11.1%	No	No	70%	0.44334	97.8%	33.2%	Subclonal	N	Passenger	N	T	passenger	Yes	Yes	No	WES
30DCIS	ATR	p.H2203D	3	142186856	G	C	Missense_Mutation	58	22.4%	No	No	100%	0.67771	100.0%	56.1%	Clonal	N	Passenger	N	T	passenger	Yes	Yes	No	WES
30DCIS	DHX36	p.D400N	3	154021137	C	T	Missense_Mutation	41	24.4%	No	No	100%	0.6835	100.0%	53.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	ABCF3	p.Y69*	3	183904428	C	G	Nonsense_Mutation	253	9.1%	No	No	57%	0.01694	83.0%	38.2%	Subclonal	D				passenger	No	No	No	WES
30DCIS	ABCF3	p.Y69*	3	183904428	C	G	Nonsense_Mutation	349	0.3%	No	No	1%	0	6.9%	0.1%	Subclonal	D				passenger	No	No	No	WES
30IDC	GRK4	p.D368N	4	3030969	G	A	Missense_Mutation	54	1.9%	No	No	12%	0.00574	60.4%	2.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	GRK4	p.D368N	4	3030969	G	A	Missense_Mutation	59	11.9%	No	No	55%	0.15232	93.9%	27.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	KIAA0232	p.Q632E	4	6864003	C	G	Missense_Mutation	76	6.6%	No	No	31%	0.00266	67.1%	13.1%	Subclonal	D	Passenger	N		passenger	No	No	No	WES
30DCIS	KIAA0232	p.S646C	4	6864046	C	G	Missense_Mutation	72	5.6%	No	No	26%	0.00135	62.1%	10.1%	Subclonal	D	Passenger	N		passenger	No	No	No	WES
30IDC	TADA2B	p.I29M	4	7045393	C	G	Missense_Mutation	166	13.9%	No	No	87%	0.64369	99.0%	57.3%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	TADA2B	p.I29M	4	7045393	C	G	Missense_Mutation	151	21.2%	No	No	99%	0.72961	100.0%	68.0%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30IDC	PSAPL1	p.M298I	4	7435713	C	T	Missense_Mutation	231	16.5%	No	No	100%	0.82716	100.0%	71.8%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
30IDC	SH3TC1	p.E618K	4	8229273	G	A	Missense_Mutation	191	0.5%	No	No	3%	0	17.6%	0.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	SH3TC1	p.E618K	4	8229273	G	A	Missense_Mutation	190	19.5%	No	No	71%	0.09585	92.5%	52.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	WDR19	p.E1262K	4	39278707	G	A	Missense_Mutation	82	14.6%	No	No	92%	0.66396	100.0%	49.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	WDR19	p.E1262K	4	39278707	G	A	Missense_Mutation	78	25.6%	No	No	100%	0.77973	100.0%	68.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	CENPC	p.S346L	4	68380199	G	A	Missense_Mutation	99	12.1%	No	No	69%	0.28356	96.9%	39.3%	Subclonal	N	Passenger	D		passenger	No	No	No	WES
30IDC	TMPRSS11D	p.Q314E	4	68692991	G	C	Missense_Mutation	114	18.4%	No	No	100%	0.83994	100.0%	70.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	TMPRSS11D	p.Q314E	4	68692991	G	C	Missense_Mutation	105	17.1%	No	No	97%	0.66076	100.0%	58.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	SOWAHB	p.S293F	4	77818125	G	A	Missense_Mutation	189	20.6%	No	Yes	96%	0.71805	100.0%	69.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	ADH1B	p.D361H	4	100231944	C	G	Missense_Mutation	155	16.8%	No	Yes	89%	0.71091	100.0%	60.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	ADH1B	p.D361H	4	100231944	C	G	Missense_Mutation	108	27.8%	No	Yes	100%	0.78538	100.0%	69.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	TET2	p.E219Q	4	106155754	G	C	Missense_Mutation	79	13.9%	No	Yes	74%	0.50755	97.9%	41.0%	Clonal	D	Passenger	N	T	passenger	Yes	Yes	Yes	WES
30IDC	PDE5A	p.E837K	4	120419875	C	T	Missense_Mutation	73	20.5%	No	Yes	100%	0.80287	100.0%	59.7%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	PDE5A	p.E837K	4	120419875	C	T	Missense_Mutation	54	24.1%	No	Yes	88%	0.60689	99.0%	50.7%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30IDC	TRPC3	p.E214K	4	122853773	C	T	Missense_Mutation	263	16.0%	No	Yes	85%	0.61583	98.6%	62.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	TRPC3	p.E214K	4	122853773	C	T	Missense_Mutation	262	0.8%	No	Yes	3%	0	9.5%	0.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	KIAA1109	p.A4245D	4	123267778	C	A	Missense_Mutation	48	4.2%	No	Yes	15%	0.00031	50.7%	4.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	C5orf38	p.R30L	5	2752467	G	T	Missense_Mutation	180	15.6%	No	No	73%	0.19112	95.6%	50.7%	Subclonal	N	Passenger	D		passenger	No	No	No	WES
30DCIS	PRLR	p.D346Y	5	35066024	C	A	Missense_Mutation	127	21.3%	No	No	99%	0.71742	100.0%	65.8%	Clonal	D	Passenger		T	passenger	No	No	No	WES
30IDC	C5orf42	p.L1593P	5	37183505	A	G	Missense_Mutation	61	13.1%	No	No	83%	0.5713	98.6%	39.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	C5orf42	p.L1593P	5	37183505	A	G	Missense_Mutation	60	23.3%	No	No	100%	0.70492	100.0%	58.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	FAM169A	p.E496Q	5	74077812	C	G	Missense_Mutation	63	12.7%	No	No	80%	0.5483	98.5%	38.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	MAN2A1	p.S21L	5	109026180	C	T	Missense_Mutation	163	12.9%	No	No	81%	0.54348	98.5%	52.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	MAN2A1	p.S21L	5	109026180	C	T	Missense_Mutation	118	18.6%	No	No	87%	0.56162	99.0%	57.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	APC	p.E658D	5	112173265	G	C	Missense_Mutation	41	12.2%	No	No	57%	0.23106	95.9%	24.3%	Subclonal	D	Passenger	N	T	passenger	Yes	Yes	Yes	WES
30DCIS	KCNN2	p.D363N	5	113798831	G	A	Missense_Mutation	42	19.0%	No	No	89%	0.54151	98.9%	42.5%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
30DCIS	PCDHA1	p.S379*	5	140167011	C	G	Nonsense_Mutation	409	7.1%	No	No	33%	0	46.2%	22.8%	Subclonal	D				passenger	No	No	No	WES
30IDC	PCDHA6	p.P130Q	5	140208065	C	A	Missense_Mutation	623	17.7%	No	No	100%	0.92308	100.0%	86.3%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
30DCIS	PCDHA6	p.P130Q	5	140208065	C	A	Missense_Mutation	632	21.8%	No	No	100%	0.87059	100.0%	84.7%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
30IDC	PCDHGA12	p.E61K	5	140810507	G	A	Missense_Mutation	396	16.9%	No	No	100%	0.88245	100.0%	79.8%	Clonal	N	Passenger		T	passenger	No	No	No	WES
30DCIS	PCDHGA12	p.E61K	5	140810507	G	A	Missense_Mutation	435	22.5%	No	No	100%	0.87152	100.0%	83.4%	Clonal	N	Passenger		T	passenger	No	No	No	WES
30IDC	FBXW11	p.Q88E	5	171337687	G	C	Missense_Mutation	54	11.1%	No	No	70%	0.45301	97.8%	31.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	FBXW11	p.Q88E	5	171337687	G	C	Missense_Mutation	60	1.7%	No	No	8%	0.00006	40.6%	1.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	STK10	p.Q573H	5	171510055	C	G	Missense_Mutation	91	6.6%	No	No	42%	0.04568	83.5%	19.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	LRRC16A	p.E1221K	6	25606315	G	A	Missense_Mutation	78	5.1%	No	No	24%	0.00048	57.6%	9.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	OR12D3	p.Q314E	6	29342125	G	C	Missense_Mutation	65	21.5%	No	No	100%	0.81642	100.0%	64.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	OR12D3	p.Q314E	6	29342125	G	C	Missense_Mutation	51	23.5%	No	No	100%	0.69079	100.0%	56.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	PPP1R10	p.R846C	6	30569890	G	A	Missense_Mutation	428	14.5%	No	No	91%	0.72084	100.0%	70.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	PPP1R10	p.R846C	6	30569890	G	A	Missense_Mutation	495	25.1%	No	No	100%	0.90004	100.0%	89.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	DPCR1	p.E390*	6	30917409	G	T	Nonsense_Mutation	2274	13.7%	No	No	86%	0.08489	94.9%	77.2%	Subclonal	N				passenger	No	No	No	WES
30DCIS	DPCR1	p.E390*	6	30917409	G	T	Nonsense_Mutation	1994	18.1%	No	No	84%	0.00453	91.9%	76.1%	Subclonal	N				passenger	No	No	No	WES
30IDC	EHMT2	p.E204Q	6	31860660	C	G	Missense_Mutation	105	18.1%	No	No	100%	0.80541	100.0%	64.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	GRM4	p.D442H	6	34008370	C	G	Missense_Mutation	138	21.7%	No	No	100%	0.74481	100.0%	68.3%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30IDC	RAB44	p.L378F	6	36689361	C	T	Missense_Mutation	245	16.3%	No	No	100%	0.82677	100.0%	72.1%	Clonal		Passenger			passenger	No	No	No	WES
30DCIS	RAB44	p.L378F	6	36689361	C	T	Missense_Mutation	239	24.3%	No	No	100%	0.86446	100.0%	81.2%	Clonal		Passenger			passenger	No	No	No	WES
30IDC	PEX6	p.H322Nfs*10	6	42942687	TTCGATGTG	T	Frame_Shift_Del	64	9.4%	No	No	59%	0.3059	96.1%	27.0%	Subclonal					passenger	No	No	No	WES
30IDC	PTK7	p.F127L	6	43096992	C	G	Missense_Mutation	169	8.3%	No	No	52%	0.02952	83.5%	31.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	FAM135A	p.S543*	6	71234415	C	G	Nonsense_Mutation	68	5.9%	No	No	37%	0.06177	84.8%	14.5%	Subclonal	D				passenger	No	No	No	WES
30DCIS	KCNQ5	p.R427K	6	73839548	G	A	Missense_Mutation	59	22.0%	No	No	100%	0.66889	100.0%	55.5%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30IDC	DDX43	p.R375K	6	74117769	G	A	Missense_Mutation	128	5.5%	No	No	34%	0.00298	67.9%	16.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	SOBP	p.R869T	6	107956654	G	C	Missense_Mutation	224	4.0%	No	No	19%	0	34.3%	9.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	ROS1	p.L17F	6	117746771	G	A	Missense_Mutation	81	1.2%	No	No	8%	0.00012	41.2%	1.4%	Subclonal	D	Passenger	N	T	passenger	No	Yes	No	WES
30DCIS	ROS1	p.L17F	6	117746771	G	A	Missense_Mutation	44	15.9%	No	No	74%	0.4099	98.1%	35.2%	Subclonal	D	Passenger	N	T	passenger	No	Yes	No	WES
30IDC	GJA1	p.R374T	6	121769114	G	C	Missense_Mutation	64	6.3%	No	No	39%	0.08854	87.7%	15.5%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	GJA1	p.R374T	6	121769114	G	C	Missense_Mutation	63	1.6%	No	No	7%	0.00003	38.7%	1.3%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	CTGF	p.E114Q	6	132271633	C	G	Missense_Mutation	231	6.9%	No	No	32%	0	50.6%	19.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	SLC18B1	p.Q190*	6	133105162	G	A	Nonsense_Mutation	99	14.1%	No	No	66%	0.19499	95.4%	39.6%	Subclonal	A				passenger	No	No	No	WES
30IDC	IFNGR1	p.E323K	6	137519671	C	T	Missense_Mutation	62	9.7%	No	No	61%	0.33525	96.6%	27.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	IFNGR1	p.E323K	6	137519671	C	T	Missense_Mutation	51	19.6%	No	No	91%	0.57469	100.0%	47.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	RPS6KA2	p.R191T	6	166918012	C	G	Missense_Mutation	85	21.2%	No	No	99%	0.67716	100.0%	59.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	SDK1	p.E1518Q	7	4189022	G	C	Missense_Mutation	290	10.3%	No	No	90%	0.60579	100.0%	61.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	SLC29A4	p.M212V	7	5336581	A	G	Missense_Mutation	378	4.8%	No	Yes	73%	0.38911	97.4%	45.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	SLC29A4	p.M212V	7	5336581	A	G	Missense_Mutation	640	4.1%	No	Yes	80%	0.4193	98.3%	53.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	TNRC18	p.S2677F	7	5352492	G	A	Missense_Mutation	534	3.2%	No	Yes	49%	0.00607	76.5%	30.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	TNRC18	p.S2677F	7	5352492	G	A	Missense_Mutation	926	3.3%	No	Yes	66%	0.062	90.8%	46.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	SP8	p.S85W	7	20825182	G	C	Missense_Mutation	133	24.8%	No	Yes	91%	0.67493	100.0%	64.9%	Clonal	D	Passenger		T	passenger	No	No	No	WES
30IDC	CPVL	p.M461I	7	29035436	C	T	Missense_Mutation	49	4.1%	No	No	26%	0.04903	81.4%	7.4%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	CPVL	p.M461I	7	29035436	C	T	Missense_Mutation	73	19.2%	No	No	100%	0.78279	100.0%	65.2%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30IDC	LSM5	p.E90K	7	32526881	C	T	Missense_Mutation	78	9.0%	No	No	57%	0.2333	94.8%	27.4%	Subclonal	D	Passenger	D		passenger	No	No	No	WES
30DCIS	DNAJC30	p.R146W	7	73097318	G	A	Missense_Mutation	188	17.0%	No	No	79%	0.36256	97.8%	56.7%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
30IDC	GTF2IRD1	p.E632K	7	73961498	G	A	Missense_Mutation	141	8.5%	No	No	54%	0.06585	87.7%	30.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	PCLO	p.P836S	7	82764360	G	A	Missense_Mutation	127	0.8%	No	No	5%	0	26.5%	0.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	PCLO	p.P836S	7	82764360	G	A	Missense_Mutation	114	17.5%	No	No	82%	0.47433	98.5%	53.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	DMTF1	p.D710Y	7	86824099	G	T	Missense_Mutation	59	13.6%	No	No	85%	0.59316	98.8%	40.8%	Clonal	D	Driver	N	T	likely_pathogenic	No	No	No	WES
30DCIS	ZSCAN25	p.E26Q	7	99217305	G	C	Missense_Mutation	254	22.0%	No	No	100%	0.81194	100.0%	76.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ZSCAN25	p.E26V	7	99217306	A	T	Missense_Mutation	258	21.7%	No	No	100%	0.7988	100.0%	76.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	ZNF3	p.E161*	7	99669626	C	A	Nonsense_Mutation	84	15.5%	No	No	72%	0.33113	97.4%	42.3%	Subclonal	D				passenger	No	No	No	WES
30IDC	RINT1	p.L397V	7	105190789	C	G	Missense_Mutation	105	13.3%	No	No	84%	0.59535	98.8%	48.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	RINT1	p.L397V	7	105190789	C	G	Missense_Mutation	90	15.6%	No	No	73%	0.32798	97.4%	43.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	RINT1	p.H400Y	7	105190798	C	T	Missense_Mutation	103	13.6%	No	No	86%	0.61383	98.9%	49.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	RINT1	p.H400Y	7	105190798	C	T	Missense_Mutation	86	15.1%	No	No	71%	0.29911	97.1%	41.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	CDHR3	p.R479Q	7	105658301	G	A	Missense_Mutation	55	14.5%	No	No	68%	0.31953	97.3%	34.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ST7	p.*500Sext*48	7	116869910	G	C	Nonstop_Mutation	76	25.0%	No	No	100%	0.76656	100.0%	66.4%	Clonal	N				likely_pathogenic	No	No	No	WES
30IDC	SLC37A3	p.E242K	7	140051231	C	T	Missense_Mutation	73	11.0%	No	No	69%	0.41894	97.5%	34.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	SLC37A3	p.E242K	7	140051231	C	T	Missense_Mutation	48	10.4%	No	No	49%	0.12259	92.4%	20.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ATG9B	p.E273K	7	150720136	C	T	Missense_Mutation	171	4.7%	No	No	22%	0	41.3%	10.8%	Subclonal		Passenger			passenger	No	No	No	WES
30IDC	SHH	p.E259K	7	155596208	C	T	Missense_Mutation	190	0.5%	No	No	3%	0	17.7%	0.4%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	SHH	p.E259K	7	155596208	C	T	Missense_Mutation	176	17.0%	No	No	80%	0.37691	97.9%	56.1%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	SGK223	p.Q933*	8	8185495	G	A	Nonsense_Mutation	288	20.5%	No	No	96%	0.73498	100.0%	73.5%	Clonal	A				passenger	No	No	No	WES
30IDC	ZNF703	p.S285L	8	37555273	C	T	Missense_Mutation	163	4.3%	No	No	27%	0.00005	53.7%	12.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	IMPA1	p.E221K	8	82583256	C	T	Missense_Mutation	29	20.7%	No	No	100%	0.73081	100.0%	45.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	IMPA1	p.E221K	8	82583256	C	T	Missense_Mutation	32	25.0%	No	No	100%	0.6664	100.0%	49.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	KIAA1429	p.Q1703*	8	95503839	G	A	Nonsense_Mutation	91	14.3%	No	No	90%	0.65214	100.0%	50.3%	Clonal	D				passenger	No	No	No	WES
30DCIS	KIAA1429	p.Q1703*	8	95503839	G	A	Nonsense_Mutation	79	1.3%	No	No	6%	0	31.1%	1.0%	Subclonal	D				passenger	No	No	No	WES
30IDC	KIAA1429	p.P1677L	8	95503916	G	A	Missense_Mutation	112	10.7%	No	No	68%	0.33329	96.6%	38.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	KIAA1429	p.P1677L	8	95503916	G	A	Missense_Mutation	96	1.0%	No	No	5%	0	25.7%	0.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	BAI1	p.N246K	8	143546297	C	A	Missense_Mutation	220	6.8%	No	No	43%	0.0007	68.5%	25.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	ZFP41	p.E38D	8	144332127	G	C	Missense_Mutation	335	8.1%	No	No	51%	0.00037	71.8%	34.9%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
30IDC	ZFP41	p.E55Q	8	144332176	G	C	Missense_Mutation	298	7.7%	No	No	49%	0.00043	70.9%	32.3%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
30DCIS	OPLAH	p.D1241H	8	145106373	C	G	Missense_Mutation	88	15.9%	No	No	74%	0.35975	97.7%	44.3%	Subclonal	D	Passenger			passenger	No	No	No	WES
30DCIS	CNTLN	p.L653F	9	17366687	G	C	Missense_Mutation	46	15.2%	No	No	71%	0.37302	97.8%	33.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	IFNW1	p.R190K	9	21141001	C	T	Missense_Mutation	47	14.9%	No	No	94%	0.63562	99.0%	41.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ACO1	p.E327K	9	32423325	G	A	Missense_Mutation	40	20.0%	No	No	93%	0.57019	99.0%	43.9%	Clonal	D	Passenger		T	passenger	No	No	Yes	WES
30DCIS	CCDC107	p.E209Q	9	35660957	G	C	Missense_Mutation	154	12.3%	No	No	58%	0.0229	85.2%	37.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	TPM2	p.E187K	9	35685270	C	T	Missense_Mutation	208	1.0%	No	No	6%	0	21.0%	1.3%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	TPM2	p.E187K	9	35685270	C	T	Missense_Mutation	207	19.3%	No	No	90%	0.6237	100.0%	66.1%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	TPM2	p.D159H	9	35685448	C	G	Missense_Mutation	265	20.0%	No	No	93%	0.69133	100.0%	71.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	HINT2	p.E125*	9	35813290	C	A	Nonsense_Mutation	92	6.5%	No	No	30%	0.00071	62.5%	13.9%	Subclonal	D				passenger	No	No	No	WES
30DCIS	TRPM6	p.E270K	9	77442727	C	T	Missense_Mutation	126	14.3%	No	No	67%	0.15484	94.4%	42.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	RALGPS1	p.N136Y	9	129815141	A	T	Missense_Mutation	53	15.1%	No	No	95%	0.65179	100.0%	43.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	RALGPS1	p.N136Y	9	129815141	A	T	Missense_Mutation	39	28.2%	No	No	100%	0.73898	100.0%	59.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	ENG	p.G603R	9	130578267	C	T	Missense_Mutation	232	14.2%	No	No	90%	0.68386	100.0%	63.1%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
30DCIS	ENG	p.G603R	9	130578267	C	T	Missense_Mutation	228	1.3%	No	No	6%	0	17.1%	1.7%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
30IDC	CRAT	p.E333K	9	131862233	C	T	Missense_Mutation	102	9.8%	No	No	62%	0.25308	95.3%	33.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	NOTCH1	p.S1365C	9	139400254	G	C	Missense_Mutation	154	14.9%	No	No	100%	0.8055	100.0%	66.2%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
30DCIS	NOTCH1	p.S1365C	9	139400254	G	C	Missense_Mutation	153	26.1%	No	No	100%	0.84777	100.0%	79.2%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
30IDC	ANAPC2	p.S567F	9	140074823	G	A	Missense_Mutation	169	10.7%	No	No	78%	0.48986	98.2%	48.8%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	ANAPC2	p.S567F	9	140074823	G	A	Missense_Mutation	144	0.7%	No	No	3%	0	17.2%	0.4%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30IDC	FAM208B	p.Q701*	10	5782234	C	T	Nonsense_Mutation	171	7.0%	No	No	44%	0.00523	74.2%	25.2%	Subclonal	A				passenger	No	No	No	WES
30IDC	ITIH5	p.F319L	10	7628015	G	C	Missense_Mutation	106	16.0%	No	No	100%	0.74562	100.0%	58.9%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30IDC	CELF2	p.D449E	10	11367851	C	A	Missense_Mutation	54	1.9%	No	Yes	10%	0.00146	51.0%	1.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	CELF2	p.D449E	10	11367851	C	A	Missense_Mutation	49	8.2%	No	Yes	30%	0.006	69.8%	11.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	FRMD4A	p.D617H	10	13702365	C	G	Missense_Mutation	64	26.6%	No	Yes	100%	0.84721	100.0%	69.0%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	FRMD4A	p.D617H	10	13702365	C	G	Missense_Mutation	68	38.2%	No	Yes	100%	0.82223	100.0%	77.5%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	MALRD1	p.A392V	10	19569144	C	T	Missense_Mutation	28	28.6%	No	Yes	100%	0.67103	100.0%	47.8%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30IDC	ZNF37A	p.R548T	10	38407722	G	C	Missense_Mutation	88	20.5%	No	No	100%	0.82675	100.0%	67.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ZNF37A	p.R548T	10	38407722	G	C	Missense_Mutation	92	22.8%	No	No	100%	0.79525	100.0%	70.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ALOX5	p.E505Q	10	45938925	G	C	Missense_Mutation	263	9.5%	No	No	44%	0	63.2%	30.0%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30IDC	ARHGAP22	p.S314*	10	49661442	G	C	Nonsense_Mutation	135	11.9%	No	No	75%	0.4378	97.7%	45.8%	Subclonal	A				passenger	No	No	No	WES
30DCIS	ARHGAP22	p.S314*	10	49661442	G	C	Nonsense_Mutation	141	2.8%	No	No	13%	0	32.4%	4.9%	Subclonal	A				passenger	No	No	No	WES
30IDC	PCDH15	p.L1447V	10	55587181	G	C	Missense_Mutation	221	12.7%	No	No	80%	0.48517	98.1%	55.3%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
30DCIS	PCDH15	p.L1447V	10	55587181	G	C	Missense_Mutation	196	1.0%	No	No	5%	0	16.4%	1.0%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
30IDC	TET1	p.E1973K	10	70451077	G	A	Missense_Mutation	171	13.5%	No	No	85%	0.60436	98.8%	55.9%	Clonal	N	Passenger	N	T	passenger	No	Yes	No	WES
30DCIS	TET1	p.E1973K	10	70451077	G	A	Missense_Mutation	174	17.2%	No	No	80%	0.4029	98.1%	56.7%	Subclonal	N	Passenger	N	T	passenger	No	Yes	No	WES
30IDC	CCAR1	p.Q62*	10	70496743	C	T	Nonsense_Mutation	87	17.2%	No	No	100%	0.76627	100.0%	59.2%	Clonal	A				passenger	No	No	No	WES
30DCIS	CCAR1	p.Q62*	10	70496743	C	T	Nonsense_Mutation	95	1.1%	No	No	5%	0	26.0%	0.7%	Subclonal	A				passenger	No	No	No	WES
30IDC	BTAF1	p.D1738H	10	93786485	G	C	Missense_Mutation	68	7.4%	No	No	46%	0.13922	91.4%	19.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	CRTAC1	p.E521K	10	99644034	C	T	Missense_Mutation	172	18.6%	No	No	100%	0.85788	100.0%	74.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	CRTAC1	p.E521K	10	99644034	C	T	Missense_Mutation	169	20.1%	No	No	94%	0.67844	100.0%	66.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	CWF19L1	p.V375M	10	101997910	C	T	Missense_Mutation	126	19.0%	No	No	100%	0.83906	100.0%	70.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	CWF19L1	p.V375M	10	101997910	C	T	Missense_Mutation	107	0.9%	No	No	4%	0	23.1%	0.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	FGF8	p.R244L	10	103530090	C	A	Missense_Mutation	146	6.2%	No	No	29%	0	52.2%	14.9%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
30IDC	RIC8A	p.E438K	11	212920	G	A	Missense_Mutation	190	16.8%	No	No	100%	0.82531	100.0%	70.4%	Clonal	D	Passenger	N		passenger	No	No	No	WES
30DCIS	RIC8A	p.E438K	11	212920	G	A	Missense_Mutation	225	0.4%	No	No	2%	0	10.9%	0.2%	Subclonal	D	Passenger	N		passenger	No	No	No	WES
30DCIS	RNH1	p.S155L	11	499165	G	A	Missense_Mutation	154	22.1%	No	No	100%	0.76804	100.0%	70.7%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
30IDC	MUC5B	p.S48L	11	1247450	C	T	Missense_Mutation	160	1.3%	No	No	9%	0	31.8%	2.3%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
30DCIS	MUC5B	p.S48L	11	1247450	C	T	Missense_Mutation	145	25.5%	No	No	100%	0.839	100.0%	77.4%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
30IDC	WEE1	p.E446K	11	9606852	G	A	Missense_Mutation	70	18.6%	No	No	100%	0.7763	100.0%	58.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	WEE1	p.E446K	11	9606852	G	A	Missense_Mutation	61	19.7%	No	No	92%	0.58962	100.0%	50.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	ABCC8	p.E746K	11	17438496	C	T	Missense_Mutation	178	5.6%	No	No	35%	0.00036	62.8%	19.1%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30IDC	PAMR1	p.K538E	11	35456125	T	C	Missense_Mutation	123	9.8%	No	No	62%	0.20354	94.2%	35.3%	Subclonal	D	Passenger		D	likely_pathogenic	No	No	No	WES
30DCIS	PAMR1	p.K538E	11	35456125	T	C	Missense_Mutation	149	21.5%	No	No	100%	0.74113	100.0%	68.6%	Clonal	D	Passenger		D	likely_pathogenic	No	No	No	WES
30IDC	ALX4	p.R126Q	11	44331236	C	T	Missense_Mutation	277	13.7%	No	No	86%	0.62322	98.9%	62.7%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	ALX4	p.R126Q	11	44331236	C	T	Missense_Mutation	234	1.7%	No	No	8%	0	19.6%	2.7%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30IDC	NR1H3	p.P193S	11	47282869	C	T	Missense_Mutation	245	14.3%	No	No	90%	0.69103	100.0%	64.0%	Clonal	N	Passenger		T	passenger	No	No	No	WES
30DCIS	NR1H3	p.P193S	11	47282869	C	T	Missense_Mutation	216	1.9%	No	No	9%	0	21.2%	3.0%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
30IDC	OR4C16	p.F166L	11	55340101	C	A	Missense_Mutation	59	18.6%	No	No	100%	0.76107	100.0%	55.6%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
30DCIS	OR4C16	p.F166L	11	55340101	C	A	Missense_Mutation	65	1.5%	No	No	7%	0.00002	37.6%	1.3%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
30IDC	AHNAK	p.R593T	11	62300111	C	G	Missense_Mutation	118	18.6%	No	No	100%	0.82695	100.0%	68.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	AHNAK	p.R593T	11	62300111	C	G	Missense_Mutation	127	20.5%	No	No	96%	0.68002	100.0%	63.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	HNRNPUL2	p.D536H	11	62488772	C	G	Missense_Mutation	57	8.8%	No	No	41%	0.04304	85.0%	17.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	RASGRP2	p.P302L	11	64504415	G	A	Missense_Mutation	227	15.9%	No	No	100%	0.7998	100.0%	69.5%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	RASGRP2	p.P302L	11	64504415	G	A	Missense_Mutation	226	0.9%	No	No	4%	0	14.2%	0.7%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	CCND1	p.S111C	11	69457932	C	G	Missense_Mutation	192	6.3%	No	No	29%	0	49.0%	16.4%	Subclonal	D	Passenger	D	T	passenger	Yes	Yes	Yes	WES
30IDC	PPFIA1	p.E106K	11	70170559	G	A	Missense_Mutation	69	18.8%	No	No	100%	0.78026	100.0%	59.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	TRIM64B	p.D372Y	11	89604025	C	A	Missense_Mutation	241	12.4%	No	No	78%	0.43437	97.8%	55.1%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
30DCIS	TRIM64B	p.D372Y	11	89604025	C	A	Missense_Mutation	226	13.3%	No	No	62%	0.01349	84.8%	43.7%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
30IDC	CCDC67	p.E236K	11	93104363	G	A	Missense_Mutation	63	11.1%	No	No	70%	0.44334	97.8%	33.2%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
30DCIS	CCDC67	p.E236K	11	93104363	G	A	Missense_Mutation	60	1.7%	No	No	8%	0.00006	40.6%	1.4%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
30DCIS	ARHGAP42	p.E213Q	11	100803926	G	C	Missense_Mutation	59	25.4%	No	No	100%	0.74492	100.0%	62.6%	Clonal	D	Driver	N	T	likely_pathogenic	No	No	No	WES
30DCIS	ACAT1	p.D288N	11	108013199	G	A	Missense_Mutation	78	6.4%	No	No	30%	0.00193	65.5%	12.7%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	C11orf53	p.S21*	11	111154855	C	G	Nonsense_Mutation	141	18.4%	No	No	86%	0.54461	98.9%	58.6%	Clonal	A				passenger	No	No	No	WES
30IDC	NLRX1	p.S293C	11	119045190	C	G	Missense_Mutation	117	17.1%	No	No	100%	0.79031	100.0%	63.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	NLRX1	p.S293C	11	119045190	C	G	Missense_Mutation	139	0.7%	No	No	3%	0	17.8%	0.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	RPUSD4	p.D291H	11	126074149	C	G	Missense_Mutation	35	22.9%	No	No	100%	0.63344	100.0%	47.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	DYRK4	p.L32F	12	4677178	G	C	Missense_Mutation	87	11.5%	No	No	72%	0.44849	97.8%	38.9%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
30DCIS	CD69	p.S75*	12	9907821	G	C	Nonsense_Mutation	46	15.2%	No	No	71%	0.37302	97.8%	33.9%	Subclonal	A				passenger	No	No	No	WES
30IDC	KLRC1	p.D158N	12	10601853	C	T	Missense_Mutation	117	16.2%	No	No	100%	0.76198	100.0%	61.1%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
30DCIS	KLRC1	p.D158N	12	10601853	C	T	Missense_Mutation	124	2.4%	No	No	11%	0	31.5%	3.6%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
30IDC	BHLHE41	p.A409_A411del	12	26275242	GGCGGCTGCC	G	In_Frame_Del	96	6.3%	No	No	39%	0.02867	80.1%	18.1%	Subclonal					passenger	No	No	No	WES
30IDC	C12orf40	p.M33I	12	40037616	G	A	Missense_Mutation	40	2.5%	No	No	16%	0.03477	76.6%	3.3%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES

30DCIS	C12orf40	p.M33I	12	40037616	G	A	Missense_Mutation	39	25.6%	No	No	100%	0.7005	100.0%	55.0%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
30IDC	LRRK2	p.T1048S	12	40692090	A	T	Missense_Mutation	78	15.4%	No	No	97%	0.69359	100.0%	51.5%	Clonal	N	Passenger	N	T	passenger	Yes	No	No	WES
30DCIS	LRRK2	p.T1048S	12	40692090	A	T	Missense_Mutation	51	19.6%	No	No	91%	0.57469	100.0%	47.1%	Clonal	N	Passenger	N	T	passenger	Yes	No	No	WES
30IDC	SENP1	p.E419K	12	48458868	C	T	Missense_Mutation	79	19.0%	No	No	100%	0.79599	100.0%	62.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	KMT2D	p.E107K	12	49448392	C	T	Missense_Mutation	183	13.7%	No	No	86%	0.62537	98.9%	57.7%	Clonal	N	Passenger	N	T	passenger	Yes	Yes	Yes	WES
30DCIS	DIP2B	p.R1473Q	12	51135262	G	A	Missense_Mutation	126	15.9%	No	No	74%	0.30263	97.2%	48.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	MAP3K12	p.E85K	12	53880923	C	T	Missense_Mutation	191	27.2%	No	No	100%	0.85066	100.0%	83.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	CCDC38	p.D379H	12	96273429	C	G	Missense_Mutation	50	16.0%	No	No	100%	0.67738	100.0%	45.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	CCDC38	p.E340Q	12	96273546	C	G	Missense_Mutation	66	12.1%	No	No	76%	0.51177	98.3%	37.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	AMDHD1	p.X398_splice	12	96361533	G	A	Splice_Site	55	23.6%	No	No	100%	0.7019	100.0%	57.8%	Clonal	D				passenger	No	No	No	WES
30IDC	C12orf55	p.S10F	12	96883416	C	T	Missense_Mutation	163	17.8%	No	No	100%	0.83826	100.0%	71.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	C12orf55	p.S10F	12	96883416	C	T	Missense_Mutation	189	1.6%	No	No	7%	0	20.7%	2.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	C12orf55	p.Q48*	12	96883529	C	T	Nonsense_Mutation	218	11.0%	No	No	69%	0.21251	94.8%	46.8%	Subclonal	N				passenger	No	No	No	WES
30DCIS	C12orf55	p.Q48*	12	96883529	C	T	Nonsense_Mutation	247	1.6%	No	No	8%	0	18.6%	2.5%	Subclonal	N				passenger	No	No	No	WES
30DCIS	NEDD1	p.S143F	12	97313821	C	T	Missense_Mutation	42	21.4%	No	No	100%	0.61687	100.0%	48.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	POLR3B	p.L664V	12	106838275	C	G	Missense_Mutation	84	14.3%	No	No	90%	0.64772	100.0%	49.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	POLR3B	p.L664V	12	106838275	C	G	Missense_Mutation	53	1.9%	No	No	9%	0.00025	45.6%	1.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	ACACB	p.S106F	12	109577527	C	T	Missense_Mutation	312	14.4%	No	No	91%	0.70987	100.0%	67.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ACACB	p.S106F	12	109577527	C	T	Missense_Mutation	291	2.1%	No	No	10%	0	20.1%	4.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	CUX2	p.E1016Q	12	111772364	G	C	Missense_Mutation	252	19.4%	No	No	100%	0.88825	100.0%	81.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	CUX2	p.E1016Q	12	111772364	G	C	Missense_Mutation	235	20.9%	No	No	97%	0.74656	100.0%	72.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	HECTD4	p.G1490A	12	112681208	C	G	Missense_Mutation	200	14.5%	No	No	91%	0.70417	100.0%	62.4%	Clonal	D	Passenger		T	passenger	No	No	No	WES
30DCIS	HECTD4	p.G1490A	12	112681208	C	G	Missense_Mutation	179	2.2%	No	No	10%	0	25.6%	3.7%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
30IDC	KSR2	p.Q825H	12	117914376	C	G	Missense_Mutation	152	13.8%	No	No	87%	0.63893	99.0%	56.0%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
30DCIS	KSR2	p.Q825H	12	117914376	C	G	Missense_Mutation	145	1.4%	No	No	6%	0	22.2%	1.4%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
30IDC	KDM2B	p.M151I	12	121987488	C	T	Missense_Mutation	263	14.8%	No	No	93%	0.74292	100.0%	67.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	KDM2B	p.M151I	12	121987488	C	T	Missense_Mutation	224	22.8%	No	No	100%	0.82584	100.0%	77.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	SETD1B	p.P212A	12	122246203	C	G	Missense_Mutation	140	15.0%	No	No	95%	0.7188	100.0%	59.5%	Clonal	D	Passenger		D	likely_pathogenic	No	No	No	WES
30DCIS	SETD1B	p.P212A	12	122246203	C	G	Missense_Mutation	144	27.1%	No	No	100%	0.84417	100.0%	79.9%	Clonal	D	Passenger		D	likely_pathogenic	No	No	No	WES
30IDC	RILPL1	p.E48Q	12	124017888	C	G	Missense_Mutation	184	0.5%	No	No	3%	0	18.3%	0.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	RILPL1	p.E48Q	12	124017888	C	G	Missense_Mutation	194	14.4%	No	No	67%	0.07585	91.7%	47.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	UBC	p.R74K	12	125398097	C	T	Missense_Mutation	588	0.2%	No	No	1%	0	5.6%	0.1%	Subclonal	N	Driver	N	T	likely_pathogenic	No	No	No	WES
30DCIS	UBC	p.R74K	12	125398097	C	T	Missense_Mutation	636	10.7%	No	No	50%	0	61.7%	39.3%	Subclonal	N	Driver	N	T	likely_pathogenic	No	No	No	WES
30IDC	NUPL1	p.A576G	13	25914199	C	G	Missense_Mutation	75	13.3%	No	No	84%	0.5891	98.7%	43.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	NUPL1	p.A576G	13	25914199	C	G	Missense_Mutation	56	17.9%	No	No	83%	0.50352	98.7%	44.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	CDK8	p.E12K	13	26828812	G	A	Missense_Mutation	127	12.6%	No	No	79%	0.52695	98.4%	48.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	CDK8	p.E12K	13	26828812	G	A	Missense_Mutation	163	1.2%	No	No	6%	0	19.7%	1.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	FLT3	p.L67F	13	28636171	C	G	Missense_Mutation	94	18.1%	No	No	84%	0.52118	98.8%	52.2%	Clonal	N	Passenger	N	T	passenger	Yes	Yes	Yes	WES
30IDC	TRPC4	p.E649K	13	38225536	C	T	Missense_Mutation	56	14.3%	No	Yes	76%	0.55191	98.2%	37.5%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30IDC	PCDH20	p.Q354E	13	61987172	G	C	Missense_Mutation	75	14.7%	No	Yes	78%	0.56619	98.3%	42.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	PCDH20	p.Q354E	13	61987172	G	C	Missense_Mutation	44	25.0%	No	Yes	92%	0.62809	100.0%	49.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	MYCBP2	p.M4391I	13	77632395	C	G	Missense_Mutation	183	6.0%	No	No	28%	0	48.2%	15.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	NALCN	p.D605N	13	101828677	C	T	Missense_Mutation	67	17.9%	No	No	100%	0.7575	100.0%	56.2%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	NALCN	p.D605N	13	101828677	C	T	Missense_Mutation	79	32.9%	No	No	100%	0.78557	100.0%	78.5%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30IDC	KDELC1	p.E79K	13	103449307	C	T	Missense_Mutation	38	10.5%	No	No	66%	0.43719	97.7%	24.8%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
30DCIS	KDELC1	p.E79K	13	103449307	C	T	Missense_Mutation	47	12.8%	No	No	60%	0.2395	96.1%	27.3%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
30IDC	MYO16	p.E1433K	13	109792923	G	A	Missense_Mutation	174	0.6%	No	No	4%	0	19.4%	0.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	MYO16	p.E1433K	13	109792923	G	A	Missense_Mutation	168	22.6%	No	No	100%	0.79475	100.0%	73.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	PNN	p.E184K	14	39648346	G	A	Missense_Mutation	120	18.3%	No	No	100%	0.8227	100.0%	67.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	PNN	p.E184K	14	39648346	G	A	Missense_Mutation	97	2.1%	No	No	10%	0	33.0%	2.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	PLEKHD1	p.R289P	14	69992782	G	C	Missense_Mutation	163	15.3%	No	No	97%	0.74818	100.0%	63.0%	Clonal	N	Passenger	N		passenger	No	No	No	WES
30DCIS	PLEKHD1	p.R289P	14	69992782	G	C	Missense_Mutation	139	16.5%	No	No	77%	0.35665	97.7%	51.8%	Subclonal	N	Passenger	N		passenger	No	No	No	WES
30IDC	MAP3K9	p.E1078K	14	71197222	C	T	Missense_Mutation	230	6.5%	No	No	41%	0.00026	65.6%	24.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	FAM161B	p.E583D	14	74404656	C	G	Missense_Mutation	97	14.4%	No	No	67%	0.22222	95.9%	40.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	TSHR	p.D18N	14	81422076	G	A	Missense_Mutation	172	12.8%	No	No	60%	0.02374	85.9%	39.7%	Subclonal	N	Passenger	N	T	passenger	No	Yes	No	WES
30IDC	SPATA7	p.R6K	14	88852179	G	A	Missense_Mutation	96	17.7%	No	No	100%	0.78792	100.0%	62.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	SPATA7	p.R6K	14	88852179	G	A	Missense_Mutation	118	19.5%	No	No	91%	0.61929	100.0%	59.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	PPP2R5C	p.E31Q	14	102229305	G	C	Missense_Mutation	90	11.1%	No	No	70%	0.40931	97.5%	37.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	PPP2R5C	p.E31Q	14	102229305	G	C	Missense_Mutation	71	16.9%	No	No	79%	0.44807	98.4%	44.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	CDC42BPB	p.E844K	14	103432666	C	T	Missense_Mutation	75	4.0%	No	No	25%	0.00934	69.1%	8.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	CDC42BPB	p.E844K	14	103432666	C	T	Missense_Mutation	75	28.0%	No	No	100%	0.80009	100.0%	71.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	PPP1R13B	p.Q686H	14	104206695	C	G	Missense_Mutation	302	17.9%	No	No	83%	0.40426	98.2%	64.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	PPP1R13B	p.E664D	14	104206761	C	G	Missense_Mutation	382	0.3%	No	No	2%	0	8.7%	0.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	PPP1R13B	p.E664D	14	104206761	C	G	Missense_Mutation	362	18.0%	No	No	84%	0.38027	98.0%	66.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	PPP1R13B	p.E650Q	14	104206805	C	G	Missense_Mutation	331	0.3%	No	No	2%	0	10.0%	0.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	PPP1R13B	p.E650Q	14	104206805	C	G	Missense_Mutation	333	15.6%	No	No	73%	0.05855	91.8%	56.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	GPR176	p.E443K	15	40093554	C	T	Missense_Mutation	103	16.5%	No	No	100%	0.75989	100.0%	59.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	GPR176	p.E443K	15	40093554	C	T	Missense_Mutation	107	0.9%	No	No	4%	0	23.1%	0.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	NDUFAF1	p.Q235E	15	41687113	G	C	Missense_Mutation	115	20.0%	No	No	93%	0.64772	100.0%	60.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	NDUFAF1	p.S74F	15	41689037	G	A	Missense_Mutation	77	19.5%	No	No	91%	0.59596	100.0%	53.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	MAPKBP1	p.G29R	15	42067558	G	C	Missense_Mutation	74	10.8%	No	No	68%	0.40509	97.4%	34.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	MAPKBP1	p.G29R	15	42067558	G	C	Missense_Mutation	83	16.9%	No	No	79%	0.43846	98.3%	46.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	STARD9	p.D4627Y	15	43010986	G	T	Missense_Mutation	114	1.8%	No	No	11%	0.00001	38.2%	2.9%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	STARD9	p.D4627Y	15	43010986	G	T	Missense_Mutation	108	9.3%	No	No	43%	0.00529	75.0%	23.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30IDC	TUBGCP4	p.L629Sfs*20	15	43696646	TC	T	Frame_Shift_Del	82	19.5%	No	No	100%	0.80829	100.0%	64.0%	Clonal					passenger	No	No	No	WES
30DCIS	TUBGCP4	p.L629Sfs*20	15	43696646	TC	T	Frame_Shift_Del	78	17.9%	No	No	84%	0.51235	98.7%	49.2%	Clonal					passenger	No	No	No	WES
30DCIS	WDR72	p.G403E	15	53997325	C	T	Missense_Mutation	97	26.8%	No	No	100%	0.81478	100.0%	73.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	HERC1	p.D2781N	15	63958332	C	T	Missense_Mutation	84	10.7%	No	No	68%	0.38064	97.2%	35.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	HERC1	p.D2781N	15	63958332	C	T	Missense_Mutation	76	1.3%	No	No	6%	0	32.3%	1.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	ZNF609	p.S959L	15	64967929	C	T	Missense_Mutation	242	4.5%	No	No	29%	0	49.7%	15.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	IQCH	p.S422*	15	67664960	C	G	Nonsense_Mutation	62	12.9%	No	No	81%	0.55994	98.6%	39.4%	Clonal	A				passenger	No	No	No	WES
30DCIS	IQCH	p.S422*	15	67664960	C	G	Nonsense_Mutation	62	29.0%	No	No	100%	0.79108	100.0%	69.6%	Clonal	A				passenger	No	No	No	WES
30DCIS	ISLR2	p.D389N	15	74426260	G	A	Missense_Mutation	296	19.3%	No	No	90%	0.61498	100.0%	69.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	CLK3	p.X453_splice	15	74919879	G	C	Splice_Site	129	14.7%	No	No	93%	0.69775	100.0%	57.3%	Clonal	D				passenger	No	No	No	WES
30DCIS	CLK3	p.X453_splice	15	74919879	G	C	Splice_Site	135	0.7%	No	No	3%	0	18.3%	0.4%	Subclonal	D				passenger	No	No	No	WES
30IDC	RCN2	p.E34K	15	77224282	G	A	Missense_Mutation	101	1.0%	No	No	6%	0.00001	33.2%	1.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	RCN2	p.E34K	15	77224282	G	A	Missense_Mutation	93	23.7%	No	No	100%	0.76193	100.0%	67.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	DNAJA4	p.I217M	15	78566684	C	G	Missense_Mutation	328	15.9%	No	No	100%	0.82563	100.0%	73.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	DNAJA4	p.I217M	15	78566684	C	G	Missense_Mutation	311	1.9%	No	No	9%	0	18.8%	3.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	KIAA1024	p.I620M	15	79750349	C	G	Missense_Mutation	133	10.5%	No	No	66%	0.2741	95.8%	39.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	KIAA1024	p.I620M	15	79750349	C	G	Missense_Mutation	143	2.1%	No	No	10%	0	27.4%	3.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	KIAA1024	p.S684C	15	79750540	C	G	Missense_Mutation	174	13.8%	No	No	87%	0.63839	99.0%	57.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	KIAA1024	p.S684C	15	79750540	C	G	Missense_Mutation	169	0.6%	No	No	3%	0	14.6%	0.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	ZNF592	p.Q292*	15	85326780	C	T	Nonsense_Mutation	160	7.5%	No	No	47%	0.01422	79.0%	27.0%	Subclonal	A				passenger	No	No	No	WES
30IDC	TICRR	p.E139*	15	90119232	G	T	Nonsense_Mutation	250	18.0%	No	No	100%	0.87591	100.0%	77.6%	Clonal	A				passenger	No	No	No	WES
30DCIS	TICRR	p.E139*	15	90119232	G	T	Nonsense_Mutation	250	1.2%	No	No	6%	0	15.6%	1.4%	Subclonal	A				passenger	No	No	No	WES
30DCIS	FURIN	p.Q607*	15	91424542	C	T	Nonsense_Mutation	115	25.2%	No	No	100%	0.81395	100.0%	73.5%	Clonal	D				passenger	No	No	No	WES
30IDC	NOXO1	p.Q166H	16	2030101	C	G	Missense_Mutation	126	10.3%	No	No	65%	0.26148	95.5%	38.1%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
30DCIS	NOXO1	p.Q166H	16	2030101	C	G	Missense_Mutation	141	2.8%	No	No	13%	0	32.4%	4.9%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
30DCIS	PRSS33	p.R141G	16	2835469	G	C	Missense_Mutation	116	19.0%	No	No	88%	0.58421	100.0%	57.8%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
30IDC	PPL	p.E1407Q	16	4934437	C	G	Missense_Mutation	279	13.6%	No	No	86%	0.60899	98.8%	62.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	PPL	p.E1407Q	16	4934437	C	G	Missense_Mutation	254	20.1%	No	No	94%	0.69631	100.0%	70.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	EARS2	p.X99_splice	16	23563469	C	T	Splice_Site	110	5.5%	No	No	34%	0.00689	71.1%	15.7%	Subclonal	D				passenger	No	No	No	WES
30IDC	CACNG3	p.V315I	16	24373179	G	A	Missense_Mutation	181	16.0%	No	No	100%	0.78998	100.0%	67.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	CACNG3	p.V315I	16	24373179	G	A	Missense_Mutation	166	13.9%	No	No	65%	0.0693	90.9%	43.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	APOBR	p.Q112K	16	28506696	C	A	Missense_Mutation	351	17.7%	No	No	100%	0.89247	100.0%	80.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	APOBR	p.Q112K	16	28506696	C	A	Missense_Mutation	328	0.9%	No	No	4%	0	11.8%	1.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	TAOK2	p.G1000E	16	29998592	G	A	Missense_Mutation	185	18.4%	No	No	100%	0.86002	100.0%	74.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	TAOK2	p.G1000E	16	29998592	G	A	Missense_Mutation	188	26.1%	No	No	100%	0.861	100.0%	81.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	SRCAP	p.Q153*	16	30718654	C	T	Nonsense_Mutation	157	16.6%	No	No	100%	0.79951	100.0%	66.8%	Clonal	A				passenger	No	No	No	WES
30DCIS	SRCAP	p.Q153*	16	30718654	C	T	Nonsense_Mutation	153	21.6%	No	No	100%	0.74744	100.0%	69.2%	Clonal	A				passenger	No	No	No	WES
30DCIS	RLTPR	p.E232Q	16	67681208	G	C	Missense_Mutation	134	12.7%	No	No	59%	0.04875	88.6%	37.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	RLTPR	p.M321I	16	67681753	G	A	Missense_Mutation	148	17.6%	No	No	82%	0.45842	98.5%	56.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	SLC12A4	p.E748K	16	67980845	C	T	Missense_Mutation	122	17.2%	No	No	80%	0.43996	98.3%	52.7%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	TERF2IP	p.S80F	16	75682019	C	T	Missense_Mutation	143	18.9%	No	No	88%	0.5816	100.0%	60.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	IRF8	p.P407A	16	85954826	C	G	Missense_Mutation	139	10.8%	No	No	50%	0.0073	78.9%	30.6%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30IDC	CDT1	p.L415V	16	88873579	C	G	Missense_Mutation	233	15.9%	No	No	100%	0.86454	100.0%	75.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	CDT1	p.L415V	16	88873579	C	G	Missense_Mutation	210	21.0%	No	No	98%	0.74415	100.0%	71.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	ANKRD11	p.K793N	16	89350571	C	G	Missense_Mutation	245	17.1%	No	No	100%	0.87791	100.0%	79.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ANKRD11	p.K793N	16	89350571	C	G	Missense_Mutation	174	1.7%	No	No	8%	0	22.5%	2.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	ZNF276	p.S21W	16	89788110	C	G	Missense_Mutation	125	12.0%	No	No	88%	0.63546	99.0%	51.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ZNF276	p.S21W	16	89788110	C	G	Missense_Mutation	153	0.7%	No	No	3%	0	16.2%	0.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	WDR81	p.E433Q	17	1629550	G	C	Missense_Mutation	224	1.3%	No	Yes	7%	0	19.9%	2.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	WDR81	p.E433Q	17	1629550	G	C	Missense_Mutation	234	29.5%	No	Yes	100%	0.88553	100.0%	81.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ZZEF1	p.D1566H	17	3967677	C	G	Missense_Mutation	106	11.3%	No	Yes	41%	0.00068	68.3%	23.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	SUPT6H	p.D522H	17	27008965	G	C	Missense_Mutation	171	1.2%	No	No	14%	0.00058	50.4%	3.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	SUPT6H	p.D522H	17	27008965	G	C	Missense_Mutation	263	4.2%	No	No	70%	0.32414	97.4%	38.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	SSH2	p.H1023Y	17	27959064	G	A	Missense_Mutation	179	4.5%	No	No	55%	0.18988	93.7%	27.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	SSH2	p.H1023Y	17	27959064	G	A	Missense_Mutation	333	6.9%	No	No	94%	0.64425	100.0%	59.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	SSH2	p.P1006S	17	27959115	G	A	Missense_Mutation	172	6.4%	No	No	79%	0.52999	98.4%	42.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	SSH2	p.P1006S	17	27959115	G	A	Missense_Mutation	319	6.3%	No	No	86%	0.53608	98.9%	53.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	SSH2	p.D464N	17	27963777	C	T	Missense_Mutation	129	12.4%	No	No	100%	0.84251	100.0%	67.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	SSH2	p.D464N	17	27963777	C	T	Missense_Mutation	190	5.3%	No	No	72%	0.36677	97.8%	38.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	TMIGD1	p.M26I	17	28659074	C	G	Missense_Mutation	101	5.0%	No	No	61%	0.36514	97.0%	25.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	TMIGD1	p.M26I	17	28659074	C	G	Missense_Mutation	141	7.8%	No	No	100%	0.64849	100.0%	51.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	ARL5C	p.S82F	17	37318974	G	A	Missense_Mutation	352	4.8%	No	Yes	88%	0.63812	100.0%	52.7%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30IDC	FBXL20	p.Q311*	17	37425082	G	A	Nonsense_Mutation	241	5.4%	No	Yes	99%	0.69453	100.0%	52.4%	Clonal	A				likely_pathogenic	No	No	No	WES
30DCIS	FBXL20	p.Q311*	17	37425082	G	A	Nonsense_Mutation	277	0.7%	No	Yes	13%	0.00011	45.0%	3.4%	Subclonal	A				likely_pathogenic	No	No	No	WES
30DCIS	MED1	p.L946V	17	37565638	G	C	Missense_Mutation	436	5.7%	No	Yes	100%	0.70333	100.0%	63.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	MED1	p.P381T	17	37576126	G	T	Missense_Mutation	233	0.9%	No	Yes	16%	0.00167	55.3%	4.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	MED1	p.P381T	17	37576126	G	T	Missense_Mutation	336	3.6%	No	Yes	63%	0.19922	95.5%	35.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	NEUROD2	p.L60V	17	37762675	G	C	Missense_Mutation	1818	4.0%	No	No	100%	0.84743	100.0%	85.7%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	NEUROD2	p.L60V	17	37762675	G	C	Missense_Mutation	2888	0.1%	No	No	2%	0	5.5%	0.1%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	DNAJC7	p.E154Q	17	40146908	C	G	Missense_Mutation	57	17.5%	No	Yes	64%	0.24734	95.7%	35.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	HOXB13	p.P37L	17	46805846	G	A	Missense_Mutation	147	15.0%	No	Yes	55%	0.0041	78.8%	36.5%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	RNF43	p.S607L	17	56435317	G	A	Missense_Mutation	222	5.0%	No	Yes	18%	0	31.2%	9.8%	Subclonal	N	Driver	N	T	likely_pathogenic	No	Yes	No	WES
30DCIS	ABCA8	p.E29K	17	66938091	C	T	Missense_Mutation	42	21.4%	No	Yes	79%	0.49286	98.4%	40.9%	Subclonal	N	Passenger	D	D	passenger	No	No	No	WES
30DCIS	RNF213	p.L2020V	17	78317000	C	G	Missense_Mutation	97	5.2%	No	Yes	19%	0	41.7%	7.8%	Subclonal	N	Passenger	N	T	passenger	No	Yes	No	WES
30IDC	LAMA1	p.E2601K	18	6958639	C	T	Missense_Mutation	52	21.2%	No	No	100%	0.79317	100.0%	58.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	LAMA1	p.E2601K	18	6958639	C	T	Missense_Mutation	62	25.8%	No	No	100%	0.75671	100.0%	64.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	RBBP8	p.L588V	18	20573552	C	G	Missense_Mutation	83	18.1%	No	No	84%	0.52027	98.8%	50.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	PTPRS	p.G88R	19	5273570	C	T	Missense_Mutation	188	17.0%	No	No	79%	0.36256	97.8%	56.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	GTF2F1	p.Q488H	19	6380382	C	G	Missense_Mutation	165	11.5%	No	No	73%	0.35929	97.0%	46.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	GTF2F1	p.Q488H	19	6380382	C	G	Missense_Mutation	156	1.3%	No	No	6%	0	20.6%	1.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	STXBP2	p.R463K	19	7711166	G	A	Missense_Mutation	169	17.2%	No	No	100%	0.82516	100.0%	69.8%	Clonal	N	Passenger		T	passenger	No	No	No	WES
30DCIS	STXBP2	p.R463K	19	7711166	G	A	Missense_Mutation	159	1.3%	No	No	6%	0	20.2%	1.3%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
30IDC	MUC16	p.E8316K	19	9062500	C	T	Missense_Mutation	82	11.0%	No	No	80%	0.54976	98.5%	40.6%	Clonal		Passenger	N	T	passenger	No	No	No	WES
30IDC	OLFM2	p.R58G	19	9971362	G	C	Missense_Mutation	176	15.3%	No	No	97%	0.7538	100.0%	64.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	RAVER1	p.D42N	19	10444111	C	T	Missense_Mutation	122	19.7%	No	No	100%	0.84409	100.0%	71.3%	Clonal	N	Passenger		T	passenger	No	No	No	WES
30DCIS	RAVER1	p.D42N	19	10444111	C	T	Missense_Mutation	141	18.4%	No	No	86%	0.54461	98.9%	58.6%	Clonal	N	Passenger		T	passenger	No	No	No	WES
30DCIS	EPOR	p.S407L	19	11488967	G	A	Missense_Mutation	205	18.0%	No	No	84%	0.48389	98.6%	61.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	CRTC1	p.S272F	19	18870919	C	T	Missense_Mutation	206	11.7%	No	No	73%	0.33082	96.7%	49.5%	Subclonal	D	Passenger	D	T	passenger	No	Yes	No	WES
30DCIS	CRTC1	p.S272F	19	18870919	C	T	Missense_Mutation	231	20.3%	No	No	95%	0.71214	100.0%	70.7%	Clonal	D	Passenger	D	T	passenger	No	Yes	No	WES
30IDC	GATAD2A	p.Q446E	19	19612061	C	G	Missense_Mutation	154	10.4%	No	No	65%	0.22058	94.8%	40.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	ZNF681	p.*646Yext*15	19	23926414	C	G	Nonstop_Mutation	77	10.4%	No	No	76%	0.50637	98.2%	37.2%	Clonal	N				passenger	No	No	No	WES
30DCIS	ZNF681	p.*646Yext*15	19	23926414	C	G	Nonstop_Mutation	99	24.2%	No	No	100%	0.80651	100.0%	74.3%	Clonal	N				passenger	No	No	No	WES
30IDC	HPN	p.I332M	19	35556531	C	G	Missense_Mutation	156	15.4%	No	No	97%	0.74754	100.0%	62.5%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30DCIS	HPN	p.I332M	19	35556531	C	G	Missense_Mutation	148	15.5%	No	No	72%	0.23518	96.3%	48.8%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30IDC	FBXO17	p.E172*	19	39437155	C	A	Nonsense_Mutation	197	15.2%	No	No	96%	0.75486	100.0%	65.2%	Clonal					passenger	No	No	No	WES
30DCIS	FBXO17	p.E172*	19	39437155	C	A	Nonsense_Mutation	191	1.6%	No	No	7%	0	20.5%	2.1%	Subclonal					passenger	No	No	No	WES
30IDC	DLL3	p.S536*	19	39998192	C	G	Nonsense_Mutation	234	14.5%	No	No	92%	0.71265	100.0%	64.5%	Clonal	A				passenger	No	No	No	WES
30DCIS	DLL3	p.S536*	19	39998192	C	G	Nonsense_Mutation	214	21.5%	No	No	100%	0.77354	100.0%	73.3%	Clonal	A				passenger	No	No	No	WES
30IDC	BCKDHA	p.E398K	19	41930367	G	A	Missense_Mutation	230	17.4%	No	No	100%	0.85666	100.0%	74.8%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	BCKDHA	p.E398K	19	41930367	G	A	Missense_Mutation	229	21.0%	No	No	98%	0.75114	100.0%	72.5%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30DCIS	GSK3A	p.S468L	19	42734995	G	A	Missense_Mutation	98	13.3%	No	No	62%	0.13467	93.6%	36.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	CIC	p.P1592T	19	42799290	C	A	Missense_Mutation	76	25.0%	No	No	100%	0.85761	100.0%	72.9%	Clonal	N	Passenger			passenger	No	Yes	No	WES
30DCIS	ZNF229	p.S613F	19	44933118	G	A	Missense_Mutation	316	19.0%	No	No	100%	0.84285	100.0%	79.1%	Clonal	N	Passenger			passenger	No	No	No	WES
30DCIS	FUT1	p.L157F	19	49254068	C	G	Missense_Mutation	224	17.9%	No	No	83%	0.44856	98.4%	61.6%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
30IDC	IL4I1	p.D535H	19	50393094	C	G	Missense_Mutation	267	13.1%	No	No	83%	0.53294	98.4%	59.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	IL4I1	p.D535H	19	50393094	C	G	Missense_Mutation	240	17.9%	No	No	84%	0.44774	98.4%	62.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	ZNF880	p.R448T	19	52888176	G	C	Missense_Mutation	223	16.6%	No	No	100%	0.84363	100.0%	80.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ZNF880	p.R448T	19	52888176	G	C	Missense_Mutation	195	3.1%	No	No	17%	0	36.6%	7.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	LENG8	p.F800L	19	54972105	C	G	Missense_Mutation	168	16.1%	No	No	75%	0.26628	96.8%	52.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	SHISA7	p.G459R	19	55944765	C	T	Missense_Mutation	132	15.9%	No	No	100%	0.75923	100.0%	61.9%	Clonal	N	Passenger	N		passenger	No	No	No	WES
30DCIS	SHISA7	p.G459R	19	55944765	C	T	Missense_Mutation	170	0.6%	No	No	3%	0	14.6%	0.3%	Subclonal	N	Passenger	N		passenger	No	No	No	WES
30IDC	ZNF304	p.E588Q	19	57868999	G	C	Missense_Mutation	170	8.8%	No	No	64%	0.21793	94.7%	39.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ZNF304	p.E588Q	19	57868999	G	C	Missense_Mutation	145	17.9%	No	No	100%	0.72794	100.0%	65.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	ZNF584	p.L398F	19	58929077	C	T	Missense_Mutation	144	11.8%	No	No	74%	0.423	97.6%	46.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ZNF584	p.L398F	19	58929077	C	T	Missense_Mutation	134	2.2%	No	No	10%	0	29.2%	3.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	ZCCHC3	p.E56Q	20	278393	G	C	Missense_Mutation	208	17.3%	No	No	100%	0.84654	100.0%	73.2%	Clonal	N	Passenger			passenger	No	No	No	WES
30DCIS	ZCCHC3	p.E56Q	20	278393	G	C	Missense_Mutation	238	1.3%	No	No	6%	0	16.4%	1.6%	Subclonal	N	Passenger			passenger	No	No	No	WES
30IDC	TMC2	p.E741Q	20	2604957	G	C	Missense_Mutation	72	1.4%	No	No	9%	0.00046	46.1%	1.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	TMC2	p.E741Q	20	2604957	G	C	Missense_Mutation	76	10.5%	No	No	49%	0.05287	87.5%	25.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	RRBP1	p.E939*	20	17595462	C	A	Nonsense_Mutation	189	11.1%	No	No	70%	0.26699	95.8%	46.0%	Subclonal	A				passenger	No	No	No	WES
30DCIS	RRBP1	p.E939*	20	17595462	C	A	Nonsense_Mutation	192	1.0%	No	No	5%	0	16.7%	1.0%	Subclonal	A				passenger	No	No	No	WES
30IDC	POLR3F	p.E301D	20	18464154	G	T	Missense_Mutation	42	21.4%	No	No	100%	0.7786	100.0%	54.7%	Clonal	D	Passenger	N		passenger	No	No	No	WES
30DCIS	POLR3F	p.E301D	20	18464154	G	T	Missense_Mutation	37	29.7%	No	No	100%	0.753	100.0%	60.4%	Clonal	D	Passenger	N		passenger	No	No	No	WES
30IDC	FOXA2	p.S169W	20	22563374	G	C	Missense_Mutation	386	13.0%	No	No	82%	0.44183	97.9%	62.1%	Subclonal	D	Passenger		D	likely_pathogenic	Yes	No	No	WES
30DCIS	FOXA2	p.S169W	20	22563374	G	C	Missense_Mutation	406	16.5%	No	No	77%	0.0988	93.9%	61.1%	Subclonal	D	Passenger		D	likely_pathogenic	Yes	No	No	WES
30IDC	MYH7B	p.Q1120*	20	33584527	C	T	Nonsense_Mutation	177	15.3%	No	No	96%	0.74924	100.0%	63.8%	Clonal	A				passenger	No	No	No	WES
30DCIS	MYH7B	p.Q1120*	20	33584527	C	T	Nonsense_Mutation	182	0.5%	No	No	3%	0	13.6%	0.2%	Subclonal	A				passenger	No	No	No	WES
30DCIS	RPN2	p.Q166H	20	35832306	G	C	Missense_Mutation	56	12.5%	No	No	58%	0.19606	95.2%	28.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	OSER1	p.Q105E	20	42826258	G	C	Missense_Mutation	62	14.5%	No	No	92%	0.64011	99.0%	44.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	OSER1	p.Q105E	20	42826258	G	C	Missense_Mutation	46	4.3%	No	No	20%	0.00622	66.9%	5.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	ARFRP1	p.X116_splice	20	62333253	C	G	Splice_Site	129	16.3%	No	No	100%	0.77207	100.0%	62.8%	Clonal	D				passenger	No	No	No	WES
30DCIS	ARFRP1	p.X116_splice	20	62333253	C	G	Splice_Site	134	0.7%	No	No	4%	0	18.5%	0.4%	Subclonal	D				passenger	No	No	No	WES
30IDC	ZBTB46	p.I133M	20	62421712	G	C	Missense_Mutation	274	0.4%	No	No	2%	0	12.2%	0.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ZBTB46	p.I133M	20	62421712	G	C	Missense_Mutation	305	17.4%	No	No	81%	0.31353	97.4%	62.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	GABPA	p.E24Q	21	27113979	G	C	Missense_Mutation	69	7.2%	No	No	34%	0.00793	73.2%	14.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	SCAF4	p.G367E	21	33067262	C	T	Missense_Mutation	69	15.9%	No	No	74%	0.38643	97.9%	41.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	PSMG1	p.E23V	21	40555244	T	A	Missense_Mutation	234	12.4%	No	No	78%	0.43019	97.7%	54.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	PSMG1	p.E23V	21	40555244	T	A	Missense_Mutation	232	19.4%	No	No	90%	0.63183	100.0%	67.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	IGSF5	p.L283F	21	41151145	C	T	Missense_Mutation	137	24.8%	No	No	100%	0.82493	100.0%	75.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	PRDM15	p.E733*	21	43256661	C	A	Nonsense_Mutation	175	9.1%	No	No	43%	0.00016	66.4%	26.2%	Subclonal	A				passenger	No	No	No	WES
30IDC	VPREB1	p.R86C	22	22599567	C	T	Missense_Mutation	221	14.5%	No	No	91%	0.70622	100.0%	63.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	VPREB1	p.R86C	22	22599567	C	T	Missense_Mutation	237	21.1%	No	No	98%	0.76144	100.0%	73.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	PIK3IP1	p.E97K	22	31686969	C	T	Missense_Mutation	191	0.5%	No	No	3%	0	17.6%	0.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	PIK3IP1	p.E97K	22	31686969	C	T	Missense_Mutation	196	21.4%	No	No	100%	0.76299	100.0%	72.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	PRR14L	p.E1960Q	22	32099658	C	G	Missense_Mutation	86	5.8%	No	No	27%	0.00051	59.7%	11.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30IDC	PICK1	p.E69*	22	38461060	G	T	Nonsense_Mutation	148	0.7%	No	No	4%	0	22.7%	0.6%	Subclonal	A	Passenger			passenger	No	No	No	WES
30DCIS	PICK1	p.E69*	22	38461060	G	T	Nonsense_Mutation	159	20.8%	No	No	97%	0.71202	100.0%	67.4%	Clonal	A	Passenger			passenger	No	No	No	WES
30IDC	KCNJ4	p.E384*	22	38822988	C	A	Nonsense_Mutation	238	0.4%	No	No	3%	0	14.1%	0.3%	Subclonal	D				passenger	No	No	No	WES
30DCIS	KCNJ4	p.E384*	22	38822988	C	A	Nonsense_Mutation	231	17.7%	No	No	83%	0.42893	98.3%	61.5%	Subclonal	D				passenger	No	No	No	WES
30IDC	CACNA1I	p.S1008F	22	40058091	C	T	Missense_Mutation	93	12.9%	No	No	81%	0.56263	98.6%	45.4%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
30IDC	CACNA1I	p.Q1193H	22	40059828	G	C	Missense_Mutation	127	11.0%	No	No	69%	0.34581	96.8%	41.4%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
30IDC	TNRC6B	p.D1493N	22	40708550	G	A	Missense_Mutation	91	6.6%	No	No	42%	0.04568	83.5%	19.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
30IDC	MKL1	p.S257L	22	40816962	G	A	Missense_Mutation	271	0.7%	No	No	5%	0	16.1%	1.0%	Subclonal	D	Passenger	D	T	passenger	No	Yes	No	WES
30DCIS	MKL1	p.S257L	22	40816962	G	A	Missense_Mutation	243	16.9%	No	No	79%	0.28747	97.1%	58.5%	Subclonal	D	Passenger	D	T	passenger	No	Yes	No	WES
30IDC	PLXNB2	p.E717*	22	50723034	C	A	Nonsense_Mutation	102	13.7%	No	No	87%	0.62274	98.9%	50.0%	Clonal	A				passenger	No	No	No	WES
30IDC	EGFL6	p.S551C	23	13651201	C	G	Missense_Mutation	73	17.8%	No	No	100%	0.76355	100.0%	57.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	TMEM27	p.E187K	23	15646204	C	T	Missense_Mutation	62	12.9%	No	No	81%	0.55994	98.6%	39.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	TMEM27	p.E187K	23	15646204	C	T	Missense_Mutation	52	3.8%	No	No	18%	0.00212	59.9%	5.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
30DCIS	FAM47B	p.D89N	23	34961213	G	A	Missense_Mutation	472	15.5%	No	No	72%	0.01227	88.1%	57.7%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
30IDC	USP9X	p.E1805K	23	41075233	G	A	Missense_Mutation	126	11.1%	No	No	70%	0.35805	97.0%	41.7%	Subclonal	D	Passenger	D	T	passenger	Yes	No	No	WES
30DCIS	USP9X	p.E1805K	23	41075233	G	A	Missense_Mutation	113	14.2%	No	No	66%	0.16845	94.8%	41.0%	Subclonal	D	Passenger	D	T	passenger	Yes	No	No	WES
30IDC	TSPYL2	p.E80K	23	53111918	G	A	Missense_Mutation	269	9.3%	No	No	59%	0.01768	83.5%	39.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	ITIH6	p.S636L	23	54784600	G	A	Missense_Mutation	161	10.6%	No	No	49%	0.00246	75.4%	30.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	TRO	p.Q324E	23	54949935	C	G	Missense_Mutation	195	0.5%	No	No	3%	0	17.3%	0.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	TRO	p.Q324E	23	54949935	C	G	Missense_Mutation	234	22.2%	No	No	100%	0.81155	100.0%	76.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	PAGE2	p.Q64E	23	55117040	C	G	Missense_Mutation	97	19.6%	No	No	100%	0.82423	100.0%	67.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	PAGE2	p.Q64E	23	55117040	C	G	Missense_Mutation	97	1.0%	No	No	5%	0	25.4%	0.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30IDC	DACH2	p.P297S	23	85950140	C	T	Missense_Mutation	60	8.3%	No	Yes	44%	0.12159	89.2%	19.0%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
30DCIS	KLHL13	p.S648L	23	117032905	G	A	Missense_Mutation	64	20.3%	No	Yes	74%	0.40519	97.8%	43.9%	Subclonal	D	Driver	N	T	likely_pathogenic	No	No	No	WES
30DCIS	NKAP	p.S36C	23	119077462	G	C	Missense_Mutation	166	4.2%	No	Yes	15%	0	30.5%	7.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
30DCIS	RHOXF1	p.Q126E	23	119249397	G	C	Missense_Mutation	94	36.2%	No	Yes	100%	0.85009	100.0%	80.1%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
30IDC	XPNPEP2	p.G397E	23	128888530	G	A	Missense_Mutation	139	19.4%	No	Yes	100%	0.82816	100.0%	67.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
30DCIS	XPNPEP2	p.G397E	23	128888530	G	A	Missense_Mutation	135	25.9%	No	Yes	95%	0.73521	100.0%	67.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	ABCA6	p.L1174Wfs*3	17	67087290	CA	C	Frame_Shift_Del	100	11.0%	No	No	100%	0.88026	100.0%	62.0%	Clonal					passenger	No	No	No	WES
26IDC	ACTR1B	p.P259S	2	98274556	G	A	Missense_Mutation	168	6.5%	No	No	77%	0.50927	98.3%	41.5%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
26IDC	ACTRT3	p.G40V	3	169487190	C	A	Missense_Mutation	120	4.2%	No	Yes	45%	0.12761	90.6%	19.1%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
26DCIS	ACTRT3	p.G40V	3	169487190	C	A	Missense_Mutation	176	10.2%	No	Yes	84%	0.60823	98.8%	52.0%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
26IDC	ADA	p.X121_splice	20	43254326	C	A	Splice_Site	78	19.2%	No	No	100%	0.66144	100.0%	74.8%	Clonal	D				passenger	No	No	No	WES
26IDC	ADAMTS4	p.G773V	1	161161124	C	A	Missense_Mutation	215	3.7%	No	No	62%	0.31938	96.4%	31.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
26DCIS	ADCY4	p.P782L	14	24791912	G	A	Missense_Mutation	88	4.5%	No	No	33%	0.02873	78.1%	12.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	ADCY5	p.L937Q	3	123019057	A	T	Missense_Mutation	141	12.8%	No	Yes	100%	0.84115	100.0%	67.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	ALX4	p.R126Q	11	44331236	C	T	Missense_Mutation	191	6.3%	No	Yes	92%	0.65772	100.0%	49.0%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
26DCIS	AMBRA1	p.X949_splice	11	46439462	C	T	Splice_Site	245	5.3%	No	Yes	49%	0.02038	80.7%	28.4%	Subclonal	D				likely_pathogenic	No	No	No	WES
26IDC	ANKRD13B	p.T556M	17	27940386	C	T	Missense_Mutation	102	10.8%	No	No	100%	0.75636	100.0%	54.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
26IDC	ARAP3	p.G588C	5	141051229	C	A	Missense_Mutation	124	37.9%	No	Yes	100%	0.00093	100.0%	91.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26DCIS	ARAP3	p.G588C	5	141051229	C	A	Missense_Mutation	174	31.0%	No	Yes	100%	0.94222	100.0%	90.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	ARHGEF18	p.P665R	19	7527143	C	G	Missense_Mutation	125	4.0%	No	Yes	43%	0.10227	88.9%	18.3%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
26DCIS	ARHGEF18	p.P665R	19	7527143	C	G	Missense_Mutation	149	16.1%	No	Yes	100%	0.85345	100.0%	72.5%	Clonal	N	Passenger		T	passenger	No	No	No	WES
26DCIS	BMPER	p.H435Y	7	34118693	C	T	Missense_Mutation	253	6.3%	No	No	52%	0.01942	81.5%	31.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	BTC	p.E50K	4	75695283	C	T	Missense_Mutation	75	1.3%	No	Yes	14%	0.0253	72.8%	2.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	BTC	p.E50K	4	75695283	C	T	Missense_Mutation	76	15.8%	No	Yes	100%	0.77043	100.0%	56.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	C1orf68	p.C219Y	1	152692653	G	A	Missense_Mutation	211	5.2%	No	No	58%	0.1858	93.5%	32.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	C5orf60	p.G26S	5	179071946	C	T	Missense_Mutation	144	6.9%	No	Yes	57%	0.17548	93.0%	30.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	CACHD1	p.S521C	1	65120419	C	G	Missense_Mutation	69	18.8%	No	Yes	100%	0.9129	100.0%	67.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
26IDC	CACNA1E	p.E1326Q	1	181724520	G	C	Missense_Mutation	107	8.4%	No	No	100%	0.8166	100.0%	55.0%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
26IDC	CDC42BPA	p.T1421S	1	227216423	G	C	Missense_Mutation	108	2.8%	No	No	52%	0.32413	96.4%	17.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
26DCIS	CDC42BPA	p.T1421S	1	227216423	G	C	Missense_Mutation	123	15.4%	No	No	100%	0.92478	100.0%	73.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES

26DCIS	COL11A1	p.G607S	1	103471420	C	T	Missense_Mutation	154	4.5%	No	Yes	33%	0.00171	64.9%	15.7%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
26IDC	CRLS1	p.H290D	20	6017766	C	G	Missense_Mutation	55	9.1%	No	No	100%	0.66318	99.0%	36.8%	Clonal	D	Passenger	D		passenger	No	No	No	WES
26IDC	CRTC2	p.S516L	1	153921718	G	A	Missense_Mutation	204	4.9%	No	No	82%	0.56359	98.6%	42.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	CSMD1	p.P3272S	8	2815218	G	A	Missense_Mutation	41	29.3%	No	No	100%	0.7972	100.0%	70.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26DCIS	CSMD1	p.P3272S	8	2815218	G	A	Missense_Mutation	56	3.6%	No	No	29%	0.10118	87.6%	8.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	CSPG5	p.A83S	3	47619269	C	A	Missense_Mutation	114	5.3%	No	No	61%	0.35635	96.8%	27.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	CSPG5	p.A83S	3	47619269	C	A	Missense_Mutation	100	16.0%	No	No	100%	0.80014	100.0%	61.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	CUL5	p.Q391H	11	107948962	G	C	Missense_Mutation	38	23.7%	No	Yes	100%	0.88728	100.0%	61.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
26DCIS	CYFIP2	p.E30D	5	156712461	G	C	Missense_Mutation	140	4.3%	No	Yes	31%	0.00206	64.6%	14.1%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
26IDC	CYP3A7	p.S284C	7	99311106	G	C	Missense_Mutation	142	12.0%	No	No	100%	0.82209	100.0%	65.2%	Clonal	N	Passenger		T	passenger	No	No	No	WES
26IDC	DACH1	p.I320S	13	72255938	A	C	Missense_Mutation	44	9.1%	No	No	88%	0.58594	98.6%	29.6%	Clonal	D	Passenger		T	passenger	No	No	No	WES
26DCIS	DACH1	p.I320S	13	72255938	A	C	Missense_Mutation	54	16.7%	No	No	100%	0.76374	100.0%	51.8%	Clonal	D	Passenger		T	passenger	No	No	No	WES
26IDC	DACH1	p.I319K	13	72255941	A	T	Missense_Mutation	44	9.1%	No	No	88%	0.58594	98.6%	29.6%	Clonal	D	Passenger		T	passenger	No	No	No	WES
26DCIS	DACH1	p.I319K	13	72255941	A	T	Missense_Mutation	55	16.4%	No	No	100%	0.75769	100.0%	51.4%	Clonal	D	Passenger		T	passenger	No	No	No	WES
26IDC	DGKB	p.H366Q	7	14712590	A	C	Missense_Mutation	101	12.9%	No	No	100%	0.91035	100.0%	67.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26DCIS	DISP2	p.S119F	15	40656062	C	T	Missense_Mutation	171	5.8%	No	No	42%	0.00789	74.5%	22.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	DNAH11	p.G867V	7	21631128	G	T	Missense_Mutation	193	17.6%	No	No	100%	0.72064	100.0%	86.3%	Clonal	N	Passenger		T	passenger	No	No	No	WES
26IDC	DNAH17-AS1	p.A105T	17	76496381	G	A	Missense_Mutation	79	8.9%	No	Yes	100%	0.67747	100.0%	42.7%	Clonal					passenger	No	No	No	WES
26IDC	EML5	p.S614C	14	89171917	G	C	Missense_Mutation	39	33.3%	No	No	100%	0.42348	100.0%	73.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
26DCIS	EML5	p.S614C	14	89171917	G	C	Missense_Mutation	43	25.6%	No	No	100%	0.91094	100.0%	64.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	FARP2	p.S925R	2	242431082	T	G	Missense_Mutation	94	8.5%	No	No	100%	0.70197	100.0%	46.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	FAT3	p.S64R	11	92085470	C	A	Missense_Mutation	118	9.3%	No	Yes	100%	0.7341	100.0%	52.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	FGFRL1	p.W204C	4	1017783	G	T	Missense_Mutation	101	6.9%	No	No	74%	0.49859	98.1%	34.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	FOXRED2	p.F380C	22	36897365	A	C	Missense_Mutation	130	17.7%	No	No	100%	0.94153	100.0%	78.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	FRG1	p.S26N	4	190864371	G	A	Missense_Mutation	79	7.6%	No	Yes	74%	0.49987	98.1%	32.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	FRG1	p.S26N	4	190864371	G	A	Missense_Mutation	81	1.2%	No	Yes	8%	0.00011	40.5%	1.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	FRMPD3	p.Q1776dup	23	106846429	G	GCAA	In_Frame_Ins	242	16.5%	No	No	100%	0.83227	100.0%	81.9%	Clonal					passenger	No	No	No	WES
26IDC	GLMN	p.Q19E	1	92763071	G	C	Missense_Mutation	54	1.9%	No	Yes	18%	0.07003	83.5%	3.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	GLMN	p.Q19E	1	92763071	G	C	Missense_Mutation	69	7.2%	No	Yes	52%	0.24706	94.7%	22.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	GNAQ	p.Y101*	9	80537095	G	T	Nonsense_Mutation	36	5.6%	No	Yes	59%	0.43111	97.5%	15.3%	Subclonal	D				likely_pathogenic	No	Yes	No	WES
26DCIS	GNAQ	p.Y101*	9	80537095	G	T	Nonsense_Mutation	45	4.4%	No	Yes	32%	0.13739	90.2%	9.2%	Subclonal	D				likely_pathogenic	No	Yes	No	WES
26IDC	GPR113	p.G671R	2	26534585	C	G	Missense_Mutation	156	18.6%	No	No	100%	0.93708	100.0%	82.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
26IDC	HELQ	p.R1023*	4	84338015	G	A	Nonsense_Mutation	67	40.3%	No	Yes	100%	0.03603	100.0%	85.9%	Subclonal	A				likely_pathogenic	No	No	No	WES
26DCIS	HELQ	p.R1023*	4	84338015	G	A	Nonsense_Mutation	79	35.4%	No	Yes	100%	0.8522	100.0%	84.4%	Clonal	A				likely_pathogenic	No	No	No	WES
26IDC	IGSF10	p.V493I	3	151166292	C	T	Missense_Mutation	69	4.3%	No	Yes	46%	0.26139	95.1%	15.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	IGSF10	p.V493I	3	151166292	C	T	Missense_Mutation	116	28.4%	No	Yes	100%	0.9196	100.0%	85.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	IL1RAPL2	p.M556I	23	105011261	G	A	Missense_Mutation	73	2.7%	No	Yes	24%	0.05141	78.2%	6.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
26DCIS	IL1RAPL2	p.M556I	23	105011261	G	A	Missense_Mutation	83	18.1%	No	Yes	100%	0.78892	100.0%	60.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	IMPA1	p.R21M	8	82598089	C	A	Missense_Mutation	140	12.1%	No	No	100%	0.91928	100.0%	71.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	ITIH2	p.D539N	10	7773927	G	A	Missense_Mutation	99	2.0%	No	No	30%	0.10892	88.7%	8.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	ITIH2	p.D539N	10	7773927	G	A	Missense_Mutation	182	11.5%	No	No	100%	0.92878	100.0%	75.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	ITIH2	p.R581S	10	7774396	G	C	Missense_Mutation	122	1.6%	No	No	24%	0.04231	79.7%	6.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
26DCIS	ITIH2	p.R581S	10	7774396	G	C	Missense_Mutation	219	7.3%	No	No	100%	0.77554	100.0%	59.8%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
26IDC	KIAA0232	p.S182F	4	6862654	C	T	Missense_Mutation	94	8.5%	No	Yes	91%	0.63167	98.9%	42.0%	Clonal	D	Passenger	D		passenger	No	No	No	WES
26IDC	KIF14	p.H1508L	1	200523640	T	A	Missense_Mutation	95	48.4%	No	No	100%	0.20896	100.0%	91.9%	Clonal	N	Passenger		T	passenger	No	No	No	WES
26DCIS	KIF14	p.H1508L	1	200523640	T	A	Missense_Mutation	86	38.4%	No	No	100%	0.26255	100.0%	88.1%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
26IDC	KIF1A	p.R1395C	2	241664761	G	A	Missense_Mutation	91	2.2%	No	No	32%	0.1451	91.1%	9.3%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
26DCIS	KIF1A	p.R1395C	2	241664761	G	A	Missense_Mutation	121	16.5%	No	No	100%	0.88335	100.0%	72.3%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
26IDC	KIF1C	p.I549T	17	4918112	T	C	Missense_Mutation	96	1.0%	No	Yes	12%	0.01014	64.2%	2.4%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
26DCIS	KIF1C	p.I549T	17	4918112	T	C	Missense_Mutation	80	5.0%	No	Yes	36%	0.05715	83.7%	14.1%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
26DCIS	KRAS	p.G13D	12	25398281	C	T	Missense_Mutation	147	5.4%	Yes	No	50%	0.11017	89.9%	25.4%	Subclonal	D	Driver	D	T	likely_pathogenic	Yes	Yes	Yes	WES
26IDC	LCMT2	p.R256C	15	43621922	G	A	Missense_Mutation	95	11.6%	No	Yes	100%	0.77947	100.0%	56.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	LLGL1	p.S611R	17	18141016	C	A	Missense_Mutation	90	7.8%	No	No	91%	0.62106	98.9%	39.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
26IDC	LRP6	p.L248S	12	12339958	A	G	Missense_Mutation	103	1.0%	No	No	10%	0.00309	55.3%	2.0%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
26DCIS	LRP6	p.L248S	12	12339958	A	G	Missense_Mutation	138	15.2%	No	No	100%	0.85703	100.0%	71.5%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
26DCIS	LRRC4B	p.E191D	19	51022397	C	G	Missense_Mutation	213	4.2%	No	No	43%	0.02005	78.9%	22.6%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
26IDC	MUC4	p.S3048L	3	195509308	G	A	Missense_Mutation	1354	1.4%	No	Yes	12%	0	18.5%	7.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	MUC4	p.S3048L	3	195509308	G	A	Missense_Mutation	1582	1.2%	No	Yes	11%	0	16.7%	6.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	NBEAL1	p.A1322D	2	204000638	C	A	Missense_Mutation	82	6.1%	No	No	65%	0.42237	97.5%	26.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	NBN	p.A241S	8	90982767	C	A	Missense_Mutation	100	8.0%	No	No	100%	0.72995	100.0%	48.0%	Clonal	D	Passenger	N	T	passenger	No	Yes	No	WES
26IDC	NEUROD6	p.V162I	7	31378399	C	T	Missense_Mutation	186	2.7%	No	No	42%	0.09678	88.7%	18.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
26DCIS	NEUROD6	p.V162I	7	31378399	C	T	Missense_Mutation	169	10.7%	No	No	87%	0.65171	99.0%	53.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
26DCIS	NHSL1	p.R260S	6	138754716	G	T	Missense_Mutation	198	3.5%	No	No	33%	0.00182	65.0%	15.6%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
26IDC	OR2J3	p.V107F	6	29079986	G	T	Missense_Mutation	200	3.0%	No	No	32%	0.00406	67.6%	14.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	OR2J3	p.V107F	6	29079986	G	T	Missense_Mutation	222	1.8%	No	No	15%	0	36.7%	5.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	OR4L1	p.S230*	14	20528892	C	A	Nonsense_Mutation	80	8.8%	No	No	100%	0.67254	100.0%	42.4%	Clonal	D				passenger	No	No	No	WES
26DCIS	PAG1	p.E164G	8	81897396	T	C	Missense_Mutation	305	7.9%	No	No	100%	0.81555	100.0%	66.9%	Clonal	D	Passenger	D		passenger	No	No	No	WES
26IDC	PAK2	p.Q101H	3	196529902	G	C	Missense_Mutation	79	7.6%	No	Yes	81%	0.55816	98.5%	34.4%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
26DCIS	PAK2	p.Q101H	3	196529902	G	C	Missense_Mutation	100	6.0%	No	Yes	55%	0.26307	95.2%	25.2%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
26DCIS	PCDHA2	p.T223M	5	140175217	C	T	Missense_Mutation	104	11.5%	No	Yes	83%	0.59861	98.7%	46.1%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
26IDC	PCDHB12	p.A515S	5	140590022	G	T	Missense_Mutation	739	10.6%	No	Yes	100%	0.86839	100.0%	78.9%	Clonal	D	Passenger		T	passenger	No	No	No	WES
26IDC	PCDHGC3	p.N330K	5	140856673	T	A	Missense_Mutation	128	7.0%	No	Yes	68%	0.40559	97.3%	35.3%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
26DCIS	PCDHGC3	p.N330K	5	140856673	T	A	Missense_Mutation	177	19.2%	No	Yes	100%	0.85067	100.0%	79.2%	Clonal	N	Passenger		T	passenger	No	No	No	WES
26IDC	PDC	p.D244Y	1	186413122	C	A	Missense_Mutation	83	9.6%	No	No	100%	0.81308	100.0%	52.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	PHYH	p.Q42E	10	13340197	G	C	Missense_Mutation	72	2.8%	No	No	41%	0.25875	95.1%	11.5%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
26DCIS	PHYH	p.Q42E	10	13340197	G	C	Missense_Mutation	112	6.3%	No	No	89%	0.61293	98.8%	38.9%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
26IDC	PIK3CA	p.P539R	3	178936074	C	G	Missense_Mutation	51	37.3%	No	Yes	100%	0.15646	100.0%	80.6%	Subclonal	D	Driver	D	D	likely_pathogenic	Yes	Yes	Yes	WES
26DCIS	PIK3CA	p.P539R	3	178936074	C	G	Missense_Mutation	51	29.4%	No	Yes	100%	0.90057	100.0%	73.6%	Clonal	D	Driver	D	D	likely_pathogenic	Yes	Yes	Yes	WES
26IDC	PKD1	p.A21E	16	2185629	G	T	Missense_Mutation	34	11.8%	No	No	100%	0.78988	100.0%	40.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	PKHD1	p.Q430R	6	51923344	T	C	Missense_Mutation	109	2.8%	No	No	32%	0.0657	84.6%	11.1%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
26DCIS	PKHD1	p.Q430R	6	51923344	T	C	Missense_Mutation	140	21.4%	No	No	100%	0.94153	100.0%	81.4%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
26IDC	PKHD1L1	p.T3630A	8	110516615	A	G	Missense_Mutation	90	5.6%	No	No	82%	0.55029	98.5%	31.5%	Clonal	D	Driver	D	D	likely_pathogenic	No	No	No	WES
26IDC	PLEKHM1	p.E308Q	17	43552467	C	G	Missense_Mutation	113	15.9%	No	No	100%	0.93035	100.0%	73.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
26IDC	PPARG	p.M36I	3	12421228	G	T	Missense_Mutation	84	13.1%	No	No	100%	0.84915	100.0%	60.3%	Clonal	D	Passenger	N	T	passenger	No	Yes	No	WES
26IDC	PRPF8	p.R1681Q	17	1562747	C	T	Missense_Mutation	152	16.4%	No	No	100%	0.93437	100.0%	78.3%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
26IDC	PTPRB	p.D2088Y	12	70928374	C	A	Missense_Mutation	151	47.0%	No	Yes	100%	0.04726	100.0%	94.4%	Clonal	D	Driver	D	T	likely_pathogenic	No	Yes	No	WES
26DCIS	PTPRB	p.D2088Y	12	70928374	C	A	Missense_Mutation	148	30.4%	No	Yes	100%	0.94879	100.0%	88.7%	Clonal	D	Driver	D	T	likely_pathogenic	No	Yes	No	WES
26IDC	RBBP8	p.X647_splice	18	20576332	CTAAGATGTATCCTTT	C	Splice_Site	44	11.4%	No	Yes	100%	0.7358	100.0%	40.5%	Clonal					likely_pathogenic	No	No	No	WES
26IDC	RP1	p.K800E	8	55538840	A	G	Missense_Mutation	112	1.8%	No	No	28%	0.08711	86.7%	8.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	RP1	p.K800E	8	55538840	A	G	Missense_Mutation	199	10.1%	No	No	100%	0.88271	100.0%	71.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	SACS	p.S2185T	13	23911461	C	G	Missense_Mutation	56	7.1%	No	No	62%	0.49403	97.3%	23.4%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
26DCIS	SACS	p.S2185T	13	23911461	C	G	Missense_Mutation	104	18.3%	No	No	100%	0.91907	100.0%	73.2%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
26DCIS	SALL3	p.L1020S	18	76755050	T	C	Missense_Mutation	92	6.5%	No	Yes	40%	0.03876	81.8%	18.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
26DCIS	SELE	p.K134Q	1	169701777	T	G	Missense_Mutation	218	5.5%	No	No	56%	0.12041	91.0%	32.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	SELL	p.M381I	1	169660940	C	T	Missense_Mutation	94	4.3%	No	No	71%	0.4774	98.0%	25.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	SELL	p.M381I	1	169660940	C	T	Missense_Mutation	94	9.6%	No	No	98%	0.68039	100.0%	46.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	SFR1	p.K193N	10	105885303	G	T	Missense_Mutation	49	2.0%	No	No	24%	0.1625	91.6%	5.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	SFR1	p.K193N	10	105885303	G	T	Missense_Mutation	85	8.2%	No	No	68%	0.42891	97.5%	32.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	SHANK1	p.G1316S	19	51171271	C	T	Missense_Mutation	69	17.4%	No	No	100%	0.83126	100.0%	69.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	SHKBP1	p.L241P	19	41086720	T	C	Missense_Mutation	160	6.9%	No	No	80%	0.55569	98.5%	43.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	SLC13A3	p.A203V	20	45228610	G	A	Missense_Mutation	102	7.8%	No	No	100%	0.76459	100.0%	50.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
26IDC	SLC22A11	p.V384A	11	64335163	T	C	Missense_Mutation	149	13.4%	No	Yes	100%	0.89077	100.0%	72.6%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
26IDC	SLC22A24	p.G119D	11	62910896	C	T	Missense_Mutation	228	25.0%	No	Yes	100%	0.45974	100.0%	91.7%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
26IDC	SNAP91	p.T434N	6	84311013	G	T	Missense_Mutation	85	5.9%	No	No	63%	0.39632	97.2%	26.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
26IDC	SNTG1	p.E120K	8	51363284	G	A	Missense_Mutation	101	2.0%	No	No	31%	0.12811	90.1%	8.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
26DCIS	SNTG1	p.E120K	8	51363284	G	A	Missense_Mutation	169	7.1%	No	No	100%	0.73925	100.0%	53.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	SOGA1	p.A1656V	20	35414907	G	A	Missense_Mutation	269	7.1%	No	No	100%	0.84134	100.0%	68.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	SOGA3	p.Q80L	6	127837521	T	A	Missense_Mutation	127	18.1%	No	No	100%	0.93297	100.0%	77.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	ST3GAL3	p.R216H	1	44363949	G	A	Missense_Mutation	139	4.3%	No	Yes	40%	0.03794	81.6%	18.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
26IDC	SYNJ1	p.S1074T	21	34018846	C	G	Missense_Mutation	125	4.8%	No	No	51%	0.19438	93.5%	23.4%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
26DCIS	SYNJ1	p.S1074T	21	34018846	C	G	Missense_Mutation	130	19.2%	No	No	100%	0.93925	100.0%	78.6%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
26IDC	SYS1	p.R42Q	20	43992296	G	A	Missense_Mutation	174	4.6%	No	No	77%	0.51436	98.3%	37.1%	Clonal	N	Passenger	N		passenger	No	No	No	WES
26IDC	TAF7L	p.D48N	23	100547892	C	T	Missense_Mutation	152	9.9%	No	No	86%	0.70167	98.9%	50.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	TARBP1	p.X1330_splice	1	234541647	A	G	Splice_Site	152	1.3%	No	No	22%	0.02495	74.8%	6.3%	Subclonal	D				passenger	No	No	No	WES
26DCIS	TARBP1	p.X1330_splice	1	234541647	A	G	Splice_Site	169	7.1%	No	No	80%	0.55311	98.5%	44.1%	Clonal	D				passenger	No	No	No	WES
26IDC	TDRD9	p.R43C	14	104394973	C	T	Missense_Mutation	81	29.6%	No	No	100%	0.42431	100.0%	83.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	TEC	p.R99M	4	48173414	C	A	Missense_Mutation	102	18.6%	No	Yes	100%	0.84636	100.0%	69.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	TFR2	p.G655R	7	100224919	C	T	Missense_Mutation	123	3.3%	No	No	38%	0.08423	87.1%	14.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
26DCIS	TFR2	p.G655R	7	100224919	C	T	Missense_Mutation	160	16.9%	No	No	100%	0.85793	100.0%	75.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
26IDC	TMC6	p.L473M	17	76117212	G	T	Missense_Mutation	186	3.2%	No	Yes	38%	0.02436	78.5%	17.2%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
26DCIS	TMEM255B	p.Y231C	13	114507880	A	G	Missense_Mutation	80	5.0%	No	No	41%	0.12274	89.9%	16.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	TOM1L1	p.T245K	17	53007447	C	A	Missense_Mutation	195	2.1%	No	No	34%	0.04551	82.1%	13.4%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
26DCIS	TOM1L1	p.T245K	17	53007447	C	A	Missense_Mutation	264	8.3%	No	No	100%	0.82372	100.0%	67.3%	Clonal	D	Passenger		T	passenger	No	No	No	WES
26IDC	TP53	p.P177_C182del	17	7578383	AGCAGCGCTCATGGTGGGG	A	In_Frame_Del	135	36.3%	No	No	100%	0.29796	100.0%	91.7%	Clonal					potentially_pathogen	Yes	Yes	Yes	WES
26DCIS	TP53	p.P177_C182del	17	7578383	AGCAGCGCTCATGGTGGGG	A	In_Frame_Del	123	23.6%	No	No	100%	0.95268	100.0%	82.1%	Clonal					potentially_pathogen	Yes	Yes	Yes	WES
26IDC	TTBK2	p.R340Q	15	43075795	C	T	Missense_Mutation	55	10.9%	No	Yes	100%	0.71111	100.0%	42.2%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26DCIS	UBE2L3	p.E112K	22	21965182	G	A	Missense_Mutation	142	4.9%	No	No	45%	0.07179	86.6%	22.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	UGT2B15	p.D222N	4	69535673	C	T	Missense_Mutation	144	4.2%	No	Yes	45%	0.09009	88.2%	20.4%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
26DCIS	UGT2B15	p.D222N	4	69535673	C	T	Missense_Mutation	179	8.4%	No	Yes	60%	0.13782	92.0%	36.7%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
26IDC	UNC5B	p.E718*	10	73053661	TGCCTGGAGGACAC	T	Frame_Shift_Del	170	6.5%	No	No	89%	0.62787	98.9%	46.3%	Clonal					passenger	No	No	No	WES
26IDC	USP28	p.L267I	11	113702676	G	T	Missense_Mutation	88	5.7%	No	Yes	55%	0.29192	95.8%	23.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
26DCIS	USP28	p.L267I	11	113702676	G	T	Missense_Mutation	94	1.1%	No	Yes	9%	0.00058	46.5%	1.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
26IDC	VSIG10	p.G416A	12	118509247	C	G	Missense_Mutation	106	8.5%	No	No	100%	0.75996	100.0%	51.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
26IDC	VSIG10L	p.A73V	19	51845084	G	A	Missense_Mutation	127	17.3%	No	No	100%	0.92717	100.0%	78.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	WDR93	p.E85K	15	90245230	G	A	Missense_Mutation	158	19.6%	No	Yes	100%	0.94577	100.0%	83.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	ZFP92	p.Y22*	23	152684163	C	A	Nonsense_Mutation	94	5.3%	No	Yes	44%	0.11314	89.5%	18.7%	Subclonal					likely_pathogenic	No	No	No	WES
26IDC	ZNF257	p.H108D	19	22270874	C	G	Missense_Mutation	162	10.5%	No	Yes	91%	0.75249	100.0%	54.5%	Clonal	N	Passenger			passenger	No	No	No	WES
26IDC	ZNF317	p.H208Y	19	9270943	C	T	Missense_Mutation	169	30.8%	No	Yes	100%	0.31171	100.0%	91.4%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
26DCIS	ZNF317	p.H208Y	19	9270943	C	T	Missense_Mutation	216	31.5%	No	Yes	100%	0.62754	100.0%	92.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	ZNF335	p.R602C	20	44589143	G	A	Missense_Mutation	163	6.1%	No	No	100%	0.69365	100.0%	48.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
26IDC	ZNF510	p.T52S	9	99525889	G	C	Missense_Mutation	154	3.2%	No	Yes	35%	0.02249	77.2%	14.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
26DCIS	ZNF510	p.T52S	9	99525889	G	C	Missense_Mutation	194	18.0%	No	Yes	100%	0.86905	100.0%	78.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
26IDC	ZNF536	p.I503F	19	30935976	A	T	Missense_Mutation	125	0.8%	No	No	8%	0.00017	41.6%	1.4%	Subclonal	D	Passenger		T	passenger	No	No	No	WES
26DCIS	ZNF536	p.I503F	19	30935976	A	T	Missense_Mutation	150	22.0%	No	No	100%	0.94843	100.0%	83.1%	Clonal	D	Passenger		T	passenger	No	No	No	WES
26IDC	ZNF585A	p.S704P	19	37642526	A	G	Missense_Mutation	198	2.0%	No	No	24%	0.00121	58.7%	9.1%	Subclonal	N	Passenger		T	passenger	No	No	No	WES
26DCIS	ZNF585A	p.S704P	19	37642526	A	G	Missense_Mutation	292	12.7%	No	No	100%	0.86804	100.0%	75.3%	Clonal	N	Passenger		T	passenger	No	No	No	WES
26IDC	ZNF714	p.N513S	19	21301008	A	G	Missense_Mutation	173	3.5%	No	Yes	34%	0.00692	70.5%	15.3%	Subclonal	N	Passenger			passenger	No	No	No	WES
26DCIS	ZNF714	p.N513S	19	21301008	A	G	Missense_Mutation	166	1.2%	No	Yes	7%	0	25.9%	1.8%	Subclonal	N	Passenger			passenger	No	No	No	WES
31DCIS	ZYG11A	p.A650P	1	53351508	G	C	Missense_Mutation	70	7.1%	No	No	33%	0.00696	71.4%	14.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
31DCIS	F13B	p.C486F	1	197021862	C	A	Missense_Mutation	111	18.0%	No	No	100%	0.73399	100.0%	61.6%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
31DCIS	KCNJ11	p.R136P	11	17409232	C	G	Missense_Mutation	79	15.2%	No	No	70%	0.33895	97.1%	40.2%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
31DCIS	AMBRA1	p.N906S	11	46439592	T	C	Missense_Mutation	121	5.0%	No	No	23%	0	47.4%	10.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
31DCIS	SLC43A1	p.R10W	11	57281557	G	A	Missense_Mutation	43	16.3%	No	No	75%	0.46213	98.2%	35.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
31DCIS	GLYAT	p.L18F	11	58491916	C	A	Missense_Mutation	41	12.2%	No	No	56%	0.25354	95.7%	24.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
31DCIS	FGF19	p.P128L	11	69514298	G	A	Missense_Mutation	258	12.8%	No	Yes	100%	0.93018	100.0%	82.0%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
31DCIS	RELT	p.R145W	11	73103321	C	T	Missense_Mutation	91	20.9%	No	No	100%	0.88547	100.0%	72.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
31DCIS	SMCO2	p.X45_splice	12	27623699	G	C	Splice_Site	122	17.2%	No	No	96%	0.70672	100.0%	60.6%	Clonal	N	.	.	.	passenger	No	No	No	WES
31DCIS	COL2A1	p.E232_G234dup	12	48389497	A	ACACCAGGTT	In_Frame_Ins	112	8.9%	No	No	41%	0.00291	71.6%	22.3%	Subclonal	.	.	.	.	potentially_pathogen	No	Yes	No	WES
31DCIS	BAZ2A	p.R1832S	12	56992710	G	T	Missense_Mutation	162	4.3%	No	No	20%	0	39.3%	9.3%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
31DCIS	MYRFL	p.A501D	12	70304610	C	A	Missense_Mutation	478	3.6%	No	Yes	87%	0.57949	99.0%	52.2%	Clonal	D	Driver	D	.	likely_pathogenic	No	No	No	WES
31DCIS	UBE3B	p.D125E	12	109924308	C	A	Missense_Mutation	71	7.0%	No	Yes	25%	0.00013	55.2%	10.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
31DCIS	RPH3A	p.C98*	12	113303282	C	A	Nonsense_Mutation	47	8.5%	No	Yes	31%	0.00762	71.2%	12.0%	Subclonal	A	.	.	.	likely_pathogenic	No	No	No	WES
31DCIS	PCDH8	p.V1017I	13	53418859	C	T	Missense_Mutation	74	8.1%	No	No	45%	0.07449	88.0%	20.9%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
31DCIS	UNC79	p.L1463I	14	94088497	C	A	Missense_Mutation	89	5.6%	No	No	20%	0	44.5%	8.4%	Subclonal	D	Driver	N	T	likely_pathogenic	No	No	No	WES
31DCIS	NTRK3	p.E179Rfs*24	15	88680721	TC	T	Frame_Shift_Del	67	46.3%	No	No	100%	0.9503	100.0%	85.3%	Clonal	.	.	.	.	likely_pathogenic	No	Yes	No	WES
31DCIS	ALOX15	p.G113S	17	4542725	C	T	Missense_Mutation	59	8.5%	No	No	39%	0.03517	82.2%	16.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
31DCIS	UBE2O	p.R1107H	17	74387583	C	T	Missense_Mutation	131	20.6%	No	No	95%	0.7143	100.0%	63.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
31DCIS	DNAH17	p.T3808M	17	76440749	G	A	Missense_Mutation	119	15.1%	No	No	70%	0.25123	95.9%	44.4%	Subclonal	D	Passenger	.	T	passenger	No	No	No	WES
31DCIS	ZNF516	p.C611*	18	74092237	G	T	Nonsense_Mutation	138	4.3%	No	No	24%	0.00002	50.8%	11.0%	Subclonal	A	.	.	.	passenger	No	No	No	WES
31DCIS	ARHGEF18	p.R918W	19	7532406	C	T	Missense_Mutation	74	40.5%	No	No	100%	0.95216	100.0%	83.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
31DCIS	MYO9B	p.E1598D	19	17313070	G	T	Missense_Mutation	63	14.3%	No	No	66%	0.3081	96.7%	34.7%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
31DCIS	ZNF626	p.C464R	19	20807293	A	G	Missense_Mutation	24	16.7%	No	No	77%	0.48124	98.3%	27.8%	Subclonal	N	Passenger	.	.	passenger	No	No	No	WES
31DCIS	ZNF208	p.S1043R	19	22154707	G	T	Missense_Mutation	422	3.3%	No	No	15%	0	24.8%	8.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
31DCIS	ZNF841	p.H709N	19	52569010	G	T	Missense_Mutation	168	6.0%	No	No	27%	0	48.4%	14.6%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
31DCIS	ZNF580	p.P45T	19	56154007	C	A	Missense_Mutation	75	6.7%	No	No	37%	0.02768	80.3%	16.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
31DCIS	COQ10B	p.R189*	2	198338496	C	T	Nonsense_Mutation	82	6.1%	No	No	28%	0.00098	61.6%	11.9%	Subclonal	D	.	.	.	passenger	No	No	No	WES
31DCIS	C20orf26	p.P270T	20	20079407	C	A	Missense_Mutation	129	4.7%	No	No	26%	0.00009	54.3%	11.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
31DCIS	TP53TG5	p.E156Rfs*3	20	44003981	C	CT	Frame_Shift_Ins	557	69.7%	No	Yes	100%	0.22651	100.0%	99.0%	Clonal	.	.	.	.	likely_pathogenic	No	No	No	WES
31DCIS	ZNF512B	p.P622A	20	62594552	G	C	Missense_Mutation	286	5.9%	No	Yes	100%	0.71376	100.0%	58.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
31DCIS	CXADR	p.S168T	21	18931380	T	A	Missense_Mutation	112	7.1%	No	No	40%	0.00819	74.7%	20.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
31DCIS	SLC25A18	p.R90Q	22	18065398	G	A	Missense_Mutation	86	5.8%	No	No	33%	0.00748	71.5%	13.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
31DCIS	TTC38	p.D246Y	22	46679870	G	T	Missense_Mutation	47	23.4%	No	No	100%	0.77718	100.0%	58.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
31DCIS	ZNF717	p.L39V	3	75790830	G	C	Missense_Mutation	13	30.8%	No	No	100%	0.71772	100.0%	38.0%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
31DCIS	KLB	p.V869L	4	39448951	G	T	Missense_Mutation	124	36.3%	No	No	100%	0.96026	100.0%	88.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
31DCIS	SREK1IP1	p.P21S	5	64050142	G	A	Missense_Mutation	99	26.3%	No	No	100%	0.83398	100.0%	72.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
31DCIS	PHIP	p.G243V	6	79735754	C	A	Missense_Mutation	87	40.2%	No	Yes	100%	0.9533	100.0%	85.4%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
31DCIS	PHIP	p.M239I	6	79735765	C	G	Missense_Mutation	84	42.9%	No	Yes	100%	0.95969	100.0%	86.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
31DCIS	PHIP	p.D230H	6	79735794	C	G	Missense_Mutation	92	44.6%	No	Yes	100%	0.96059	100.0%	88.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
31DCIS	PHIP	p.D214N	6	79735842	C	T	Missense_Mutation	77	36.4%	No	Yes	100%	0.91374	100.0%	81.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
31DCIS	ASCC3	p.G1314R	6	101086659	C	T	Missense_Mutation	49	16.3%	No	Yes	42%	0.0088	75.1%	21.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
31DCIS	USP42	p.I3Sfs*2	7	6150769	CCA	C	Frame_Shift_Del	148	16.2%	No	No	91%	0.65955	100.0%	59.9%	Clonal	.	.	.	.	passenger	No	No	No	WES
31DCIS	PCLO	p.R4294I	7	82544421	C	A	Missense_Mutation	116	19.0%	No	No	100%	0.77102	100.0%	65.1%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
31DCIS	EPHA1	p.S344P	7	143096000	A	G	Missense_Mutation	115	20.0%	No	No	100%	0.79764	100.0%	67.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
31DCIS	ANK1	p.P671S	8	41566382	G	A	Missense_Mutation	127	40.2%	No	No	100%	0.93383	100.0%	90.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
32DCIS	HP1BP3	p.A351D	1	21076305	G	T	Missense_Mutation	72	6.9%	No	Yes	18%	0	38.3%	7.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
32DCIS	ASCC1	p.T224K	10	73921335	G	T	Missense_Mutation	146	4.1%	No	No	15%	0	30.2%	6.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
32DCIS	MUC2	p.P1598S	11	1092973	C	T	Missense_Mutation	339	8.6%	No	Yes	22%	0	30.0%	14.8%	Subclonal	N	Passenger	.	T	passenger	No	No	No	WES
32DCIS	UBE4A	p.S132Ifs*2	11	118240228	T	TTGATA	Frame_Shift_Ins	55	40.0%	No	Yes	100%	0.75035	100.0%	66.3%	Clonal	.	.	.	.	likely_pathogenic	No	No	No	WES
32DCIS	UBE4A	p.S132R	11	118240238	C	A	Missense_Mutation	47	61.7%	No	Yes	100%	0.39778	100.0%	83.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
32DCIS	DCP1B	p.Q252H	12	2062350	C	G	Missense_Mutation	212	5.7%	No	No	20%	0	33.6%	11.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
32DCIS	CDH24	p.W599G	14	23518401	A	C	Missense_Mutation	89	21.3%	No	No	97%	0.59565	100.0%	59.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
32DCIS	CEP170B	p.A832E	14	105353071	C	A	Missense_Mutation	87	5.7%	No	Yes	15%	0	31.9%	6.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
32DCIS	IL34	p.R9C	16	70680875	C	T	Missense_Mutation	55	34.5%	No	No	100%	0.73348	100.0%	68.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
32DCIS	ABCA9	p.A1474T	17	66980276	C	T	Missense_Mutation	211	6.6%	No	No	30%	0	48.7%	17.7%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
32DCIS	LYPD3	p.A164V	19	43967331	G	A	Missense_Mutation	186	31.2%	No	No	100%	0.82256	100.0%	81.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
32DCIS	HOXD13	p.N302K	2	176959332	C	A	Missense_Mutation	73	6.8%	No	No	24%	0.00003	52.8%	10.2%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	Yes	No	WES
32DCIS	PHACTR3	p.E122K	20	58330242	G	A	Missense_Mutation	114	15.8%	No	Yes	100%	0.69374	100.0%	64.9%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
32DCIS	COL20A1	p.A1025V	20	61951548	C	T	Missense_Mutation	32	34.4%	No	No	100%	0.66329	100.0%	58.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
32DCIS	DNAH1	p.L3144I	3	52422888	C	A	Missense_Mutation	88	5.7%	No	No	20%	0	44.2%	8.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
32DCIS	SLC51A	p.L114M	3	195954586	C	A	Missense_Mutation	72	6.9%	No	No	25%	0.00004	53.5%	10.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
32DCIS	CEP120	p.D45E	5	122754124	G	T	Missense_Mutation	97	5.2%	No	Yes	13%	0	28.7%	5.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
32DCIS	KIF3A	p.P355Q	5	132051514	G	T	Missense_Mutation	75	8.0%	No	Yes	20%	0	41.1%	9.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
32DCIS	ATXN1	p.R373H	6	16327424	C	T	Missense_Mutation	152	7.2%	No	No	26%	0	43.8%	14.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
32DCIS	AGER	p.Q294H	6	32150106	C	G	Missense_Mutation	205	5.4%	No	No	19%	0	32.6%	10.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
32DCIS	GOT1L1	p.N185K	8	37794540	G	T	Missense_Mutation	170	5.3%	No	Yes	40%	0.00324	72.9%	20.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
32DCIS	TRPM6	p.T87K	9	77457152	G	T	Missense_Mutation	84	25.0%	No	Yes	63%	0.03863	88.4%	42.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
32DCIS	NR5A1	p.T40M	9	127265483	G	A	Missense_Mutation	73	8.2%	No	No	54%	0.12873	94.4%	24.6%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
32DCIS	KIAA1210	p.P649L	23	118223247	G	A	Missense_Mutation	58	15.5%	No	No	55%	0.06503	90.9%	29.3%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
33DCIS	SAMD11	p.E389K	1	878039	G	A	Missense_Mutation	40	10.0%	No	No	30%	0.00259	68.5%	11.7%	Subclonal	D	Passenger	N	.	passenger	No	No	No	WES
33DCIS	C1orf170	p.A647D	1	911932	G	T	Missense_Mutation	81	21.0%	No	No	63%	0.05114	90.7%	40.0%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
33DCIS	FUCA1	p.G23Rfs*145	1	24194710	C	CT	Frame_Shift_Ins	78	34.6%	No	No	100%	0.69995	100.0%	69.3%	Clonal	.	.	.	.	passenger	No	No	No	WES
33DCIS	EXTL1	p.S413C	1	26357954	C	G	Missense_Mutation	32	43.8%	No	No	100%	0.71701	100.0%	66.1%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
33DCIS	ZNF697	p.E324K	1	120165996	C	T	Missense_Mutation	190	4.2%	No	No	13%	0	23.7%	6.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
33DCIS	TOR3A	p.V343L	1	179064186	G	C	Missense_Mutation	127	32.3%	No	No	96%	0.66642	100.0%	71.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	TPR	p.E1633Q	1	186304484	C	G	Missense_Mutation	133	31.6%	No	No	94%	0.63367	100.0%	70.4%	Clonal	D	Passenger	N	T	passenger	No	Yes	No	WES
33DCIS	CUBN	p.F3251S	10	16882958	A	G	Missense_Mutation	114	22.8%	No	No	68%	0.05631	91.8%	47.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	C10orf12	p.E317Q	10	98742096	G	C	Missense_Mutation	123	17.9%	No	No	53%	0.00086	76.1%	35.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
33DCIS	C10orf12	p.Q1225H	10	98744822	G	C	Missense_Mutation	144	16.0%	No	No	48%	0.00002	67.8%	32.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
33DCIS	TENM4	p.R1212Q	11	78433878	C	T	Missense_Mutation	98	24.5%	No	No	73%	0.15974	95.9%	50.3%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
33DCIS	ANGPTL5	p.W224C	11	101765785	C	A	Missense_Mutation	153	35.3%	No	No	100%	0.79182	100.0%	79.0%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
33DCIS	SLC37A2	p.A406V	11	124955004	C	T	Missense_Mutation	45	22.2%	No	No	66%	0.18534	96.2%	36.8%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
33DCIS	CACNA1C	p.E1913K	12	2794921	G	A	Missense_Mutation	57	10.5%	No	No	42%	0.02005	82.5%	19.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
33DCIS	AKAP3	p.C572F	12	4736353	C	A	Missense_Mutation	162	9.9%	No	No	39%	0.00001	61.1%	24.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
33DCIS	HOXC12	p.G117E	12	54349063	G	A	Missense_Mutation	69	40.6%	No	No	100%	0.78282	100.0%	75.8%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
33DCIS	OR6C70	p.Q7K	12	55863904	G	T	Missense_Mutation	50	8.0%	No	No	24%	0.00014	55.9%	9.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	SRGAP1	p.R974*	12	64536114	C	T	Nonsense_Mutation	107	24.3%	No	No	73%	0.13189	95.2%	50.7%	Subclonal	D	.	.	.	passenger	No	No	No	WES
33DCIS	NEDD1	p.P451T	12	97337373	C	A	Missense_Mutation	74	33.8%	No	No	100%	0.67072	100.0%	67.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	HNRNPC	p.F128C	14	21698499	A	C	Missense_Mutation	105	24.8%	No	No	99%	0.64351	100.0%	65.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
33DCIS	MYH7	p.E779K	14	23894579	C	T	Missense_Mutation	125	9.6%	No	No	38%	0.00009	63.5%	21.9%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
33DCIS	GALNT16	p.S388L	14	69806312	C	T	Missense_Mutation	90	13.3%	No	No	53%	0.02422	85.8%	30.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	SERPINA10	p.V191M	14	94756360	C	T	Missense_Mutation	96	21.9%	No	No	87%	0.48417	99.0%	56.9%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
33DCIS	TP53BP1	p.Q31*	15	43784583	G	A	Nonsense_Mutation	132	39.4%	No	No	100%	0.48194	100.0%	88.1%	Subclonal	A	.	.	.	passenger	No	No	No	WES
33DCIS	MAP1A	p.E40K	15	43803304	G	A	Missense_Mutation	100	7.0%	No	No	28%	0.00002	54.4%	13.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	CA12	p.E269K	15	63631087	C	T	Missense_Mutation	176	9.1%	No	No	36%	0	56.4%	22.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	SRRM2	p.R294Q	16	2810349	G	A	Missense_Mutation	131	17.6%	No	No	52%	0.00038	74.2%	35.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
33DCIS	THAP11	p.E277K	16	67877286	G	A	Missense_Mutation	121	33.1%	No	No	99%	0.6957	100.0%	72.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	CLEC3A	p.C87W	16	78064378	C	G	Missense_Mutation	74	37.8%	No	No	100%	0.75993	100.0%	73.4%	Clonal	D	Passenger	.	.	passenger	No	No	No	WES
33DCIS	ATMIN	p.N117S	16	81074974	A	G	Missense_Mutation	103	35.9%	No	No	100%	0.76373	100.0%	75.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	NLRP1	p.A1063S	17	5436251	C	A	Missense_Mutation	52	26.9%	No	No	80%	0.37868	98.4%	48.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
33DCIS	DNAH9	p.D841N	17	11556245	G	A	Missense_Mutation	79	31.6%	No	No	95%	0.60188	100.0%	64.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
33DCIS	GPR179	p.Q1169E	17	36485947	G	C	Missense_Mutation	58	6.9%	No	Yes	14%	0	32.2%	5.1%	Subclonal	N	Passenger	.	T	passenger	No	No	No	WES
33DCIS	MPO	p.D245E	17	56356519	G	T	Missense_Mutation	194	3.6%	No	Yes	36%	0.00365	71.8%	17.3%	Subclonal	D	Passenger	D	T	passenger	No	No	Yes	WES
33DCIS	ACTG1	p.E364K	17	79477754	C	T	Missense_Mutation	178	4.5%	No	Yes	9%	0	16.7%	4.1%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
33DCIS	SLC16A3	p.W176R	17	80195172	T	C	Missense_Mutation	60	20.0%	No	No	60%	0.06617	91.5%	34.9%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
33DCIS	C18orf56	p.R110Q	18	657919	C	T	Missense_Mutation	69	18.8%	No	Yes	37%	0	58.5%	22.1%	Subclonal	D	Passenger	.	T	passenger	No	No	No	WES
33DCIS	SMAD4	p.R496H	18	48604665	G	A	Missense_Mutation	56	42.9%	No	Yes	85%	0.4897	98.7%	60.0%	Subclonal	D	Driver	D	D	likely_pathogenic	Yes	Yes	Yes	WES
33DCIS	CAPS	p.R84W	19	5914740	C	T	Missense_Mutation	60	30.0%	No	No	90%	0.51682	100.0%	56.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
33DCIS	ZSWIM4	p.A910E	19	13941623	C	A	Missense_Mutation	80	37.5%	No	No	100%	0.76396	100.0%	74.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	ZFP82	p.E135K	19	36884839	C	T	Missense_Mutation	105	6.7%	No	No	20%	0	38.8%	9.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
33DCIS	ZNF180	p.Q637*	19	44980789	G	A	Nonsense_Mutation	191	31.9%	No	No	95%	0.67582	100.0%	75.0%	Clonal	N	.	.	.	passenger	No	No	No	WES
33DCIS	GFY	p.D271H	19	49930498	G	C	Missense_Mutation	98	8.2%	No	No	24%	0	45.2%	12.2%	Subclonal	.	Passenger	.	.	passenger	No	No	No	WES
33DCIS	ZNF836	p.L233V	19	52660239	G	C	Missense_Mutation	282	4.3%	No	No	13%	0	21.3%	6.9%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
33DCIS	DNAAF3	p.T50I	19	55677774	G	A	Missense_Mutation	97	42.3%	No	No	100%	0.81058	100.0%	82.2%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	PLEK	p.E206K	2	68613777	G	A	Missense_Mutation	82	13.4%	No	No	40%	0.00024	66.7%	22.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	IMMT	p.Q6*	2	86422490	G	A	Nonsense_Mutation	77	26.0%	No	No	78%	0.29259	97.8%	51.4%	Subclonal	A	.	.	.	passenger	No	No	No	WES
33DCIS	TEKT4	p.A406T	2	95542422	G	A	Missense_Mutation	55	14.5%	No	No	43%	0.00666	77.6%	22.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
33DCIS	10-Sep	p.E288K	2	110322109	C	T	Missense_Mutation	108	7.4%	No	No	22%	0	41.2%	11.0%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
33DCIS	SP3	p.R661Ifs*5	2	174777845	CTT	C	Frame_Shift_Del	128	32.0%	No	No	96%	0.65483	100.0%	70.9%	Clonal	.	.	.	.	passenger	No	No	No	WES
33DCIS	PLCL1	p.R824G	2	198950711	C	G	Missense_Mutation	94	5.3%	No	No	16%	0	34.9%	6.5%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
33DCIS	ERBB4	p.S75C	2	212989487	G	C	Missense_Mutation	76	5.3%	No	No	16%	0	37.7%	5.9%	Subclonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	No	WES
33DCIS	ADAM33	p.P496T	20	3652892	G	T	Missense_Mutation	57	8.8%	No	No	26%	0.00008	56.2%	11.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES

33DCIS	TPTE	p.I302M	21	10934071	G	C	Missense_Mutation	213	10.8%	No	No	32%	0	46.4%	21.3%	Subclonal	N	Passenger	.	D	passenger	No	No	No	WES
33DCIS	BRWD1	p.Y1197Lfs*14	21	40590130	AAGCTACTACAGTACAGT	A	Frame_Shift_Del	131	23.7%	No	No	71%	0.0657	92.7%	50.9%	Subclonal	.	.	.	.	passenger	No	No	No	WES
33DCIS	CACNA1I	p.D1023E	22	40058137	C	A	Missense_Mutation	40	10.0%	No	No	30%	0.00259	68.5%	11.7%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
33DCIS	FAM107A	p.E23Q	3	58555521	C	G	Missense_Mutation	85	24.7%	No	No	74%	0.19926	96.6%	49.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	ADAMTS3	p.V715M	4	73175150	C	T	Missense_Mutation	146	29.5%	No	No	88%	0.48748	99.0%	66.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
33DCIS	SORBS2	p.E1164K	4	186510884	C	T	Missense_Mutation	95	32.6%	No	No	98%	0.65673	100.0%	68.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
33DCIS	MSH3	p.R224W	5	79966006	C	T	Missense_Mutation	152	4.6%	No	No	14%	0	27.0%	6.3%	Subclonal	N	Passenger	D	D	passenger	No	No	No	WES
33DCIS	IL9	p.A17S	5	135231457	C	A	Missense_Mutation	81	35.8%	No	No	100%	0.73317	100.0%	71.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
33DCIS	PCDHGB6	p.R518H	5	140789322	G	A	Missense_Mutation	150	12.0%	No	No	48%	0.00051	72.0%	30.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
33DCIS	SPRY4	p.S47R	5	141694602	G	C	Missense_Mutation	115	14.8%	No	No	44%	0.00005	66.5%	27.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	DBN1	p.P579T	5	176885106	G	T	Missense_Mutation	98	6.1%	No	No	18%	0	37.6%	8.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
33DCIS	LAMA2	p.I115T	6	129380989	T	C	Missense_Mutation	79	6.3%	No	No	19%	0	41.3%	7.9%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
33DCIS	LAMA2	p.R2383Q	6	129785590	G	A	Missense_Mutation	63	9.5%	No	No	28%	0.00006	57.2%	13.0%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
33DCIS	SYNE1	p.V6336G	6	152577866	A	C	Missense_Mutation	141	4.3%	No	No	13%	0	26.3%	5.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
33DCIS	NPC1L1	p.E1138Q	7	44556490	C	G	Missense_Mutation	75	5.3%	No	No	16%	0	38.2%	6.0%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
33DCIS	COL1A2	p.A629V	7	94047058	C	T	Missense_Mutation	116	5.2%	No	No	15%	0	31.9%	6.8%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
33DCIS	GIGYF1	p.E293Q	7	100283874	C	G	Missense_Mutation	81	4.9%	No	No	15%	0	35.4%	5.5%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
33DCIS	EPHB4	p.D836N	7	100403295	C	T	Missense_Mutation	158	6.3%	No	No	19%	0	33.2%	10.0%	Subclonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
33DCIS	PREX2	p.S1293C	8	69046404	A	T	Missense_Mutation	92	32.6%	No	No	97%	0.65294	100.0%	68.0%	Clonal	N	Passenger	N	T	passenger	No	Yes	No	WES
33DCIS	PLEKHF2	p.S108F	8	96166595	C	T	Missense_Mutation	263	11.0%	No	No	44%	0	60.9%	30.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
33DCIS	MATN2	p.D840N	8	99044482	G	A	Missense_Mutation	81	17.3%	No	No	69%	0.19109	96.4%	41.5%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	CDKN2A	p.H83Y	9	21971111	G	A	Missense_Mutation	89	62.9%	Yes	Yes	100%	0.8261	100.0%	88.0%	Clonal	D	Driver	D	T	likely_pathogenic	Yes	Yes	Yes	WES
33DCIS	TLN1	p.E1085D	9	35713290	C	G	Missense_Mutation	50	26.0%	No	No	78%	0.33805	98.2%	46.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
33DCIS	RPL12	p.L125H	9	130210621	A	T	Missense_Mutation	57	36.8%	No	No	100%	0.71062	100.0%	67.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
33DCIS	MAGEB6	p.E171K	23	26212474	G	A	Missense_Mutation	136	14.7%	No	No	44%	0.00001	64.2%	28.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
33DCIS	RPA4	p.G17A	23	96139359	G	C	Missense_Mutation	74	18.9%	No	No	57%	0.02317	86.4%	34.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
33DCIS	TENM1	p.G2350D	23	123517732	C	T	Missense_Mutation	71	7.0%	No	No	21%	0	45.7%	8.8%	Subclonal	D	Passenger	D	D	likely_pathogenic	Yes	No	Yes	WES
33DCIS	GABRE	p.T268M	23	151124314	G	A	Missense_Mutation	59	23.7%	No	No	71%	0.20892	96.7%	43.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
33DCIS	PDZD4	p.E290K	23	153070250	C	T	Missense_Mutation	49	8.2%	No	No	24%	0.00019	57.0%	9.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
33DCIS	TMLHE	p.D304N	23	154736644	C	T	Missense_Mutation	118	23.7%	No	No	71%	0.08552	93.6%	50.2%	Subclonal	N	Passenger	N	D	passenger	No	No	No	WES
34DCIS	PHC2	p.N224T	1	33833022	T	G	Missense_Mutation	59	54.2%	No	Yes	100%	0.01223	100.0%	87.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
34DCIS	RBMXL1	p.L296P	1	89448623	A	G	Missense_Mutation	159	8.2%	No	Yes	54%	0.05224	86.5%	31.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
34DCIS	RBMXL1	p.G265R	1	89448717	C	T	Missense_Mutation	124	6.5%	No	Yes	42%	0.01996	79.0%	21.4%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
34DCIS	TRMT13	p.N325K	1	100613607	C	G	Missense_Mutation	88	4.5%	No	Yes	30%	0.01119	71.8%	11.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
34DCIS	CHIA	p.D319N	1	111861781	G	A	Missense_Mutation	77	10.4%	No	Yes	68%	0.40227	97.4%	34.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
34DCIS	ECM1	p.W172C	1	150483401	G	T	Missense_Mutation	220	11.8%	No	No	100%	0.90244	100.0%	77.2%	Clonal	N	Passenger	D	D	passenger	No	No	No	WES
34DCIS	ZBTB41	p.S57C	1	197169434	G	C	Missense_Mutation	160	10.6%	No	No	100%	0.84748	100.0%	67.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
34DCIS	GATA3	p.P419Rfs*57	10	8115906	A	ACG	Frame_Shift_Ins	202	18.3%	No	No	100%	0.86876	100.0%	82.5%	Clonal	.	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
34DCIS	SMC3	p.T830N	10	112360258	C	A	Missense_Mutation	47	8.5%	No	Yes	56%	0.3205	96.4%	21.5%	Subclonal	D	Passenger	N	T	passenger	Yes	No	Yes	WES
34DCIS	B3GNT6	p.V266M	11	76751391	G	A	Missense_Mutation	37	10.8%	No	Yes	71%	0.47315	98.0%	26.0%	Subclonal	D	Passenger	.	T	passenger	No	No	No	WES
34DCIS	MAP3K9	p.T847A	14	71199589	T	C	Missense_Mutation	77	7.8%	No	Yes	59%	0.30316	96.2%	26.8%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
34DCIS	CHD2	p.D346V	15	93486283	A	T	Missense_Mutation	104	22.1%	No	No	100%	0.94524	100.0%	78.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
34DCIS	SCN4A	p.I753T	17	62034640	A	G	Missense_Mutation	115	12.2%	No	No	100%	0.77227	100.0%	59.2%	Clonal	D	Driver	D	D	likely_pathogenic	No	No	No	WES
34DCIS	ICAM4	p.A181D	19	10398436	C	A	Missense_Mutation	84	6.0%	No	No	51%	0.21471	94.3%	21.7%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
34DCIS	OR1I1	p.A331D	19	15198868	C	A	Missense_Mutation	37	10.8%	No	No	92%	0.59185	98.7%	30.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
34DCIS	RASAL3	p.R39C	19	15575055	G	A	Missense_Mutation	108	5.6%	No	No	48%	0.12319	90.8%	21.8%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
34DCIS	PLEKHA4	p.G41W	19	49368831	C	A	Missense_Mutation	104	37.5%	No	No	100%	0.32277	100.0%	89.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
34DCIS	AUP1	p.S363C	2	74754176	G	C	Missense_Mutation	152	5.9%	No	No	45%	0.02519	80.8%	23.5%	Subclonal	D	Passenger	N	.	passenger	No	No	No	WES
34DCIS	SLC5A7	p.T529K	2	108627160	C	A	Missense_Mutation	95	5.3%	No	No	40%	0.05743	84.8%	17.1%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
34DCIS	FMNL2	p.V582I	2	153476139	G	A	Missense_Mutation	165	4.8%	No	No	37%	0.00353	69.5%	18.4%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
34DCIS	NMUR1	p.V185I	2	232393179	C	T	Missense_Mutation	68	19.1%	No	No	100%	0.84137	100.0%	63.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
34DCIS	BCR	p.R1080C	22	23653939	C	T	Missense_Mutation	79	8.9%	No	No	67%	0.40078	97.4%	31.9%	Subclonal	D	Passenger	D	T	passenger	No	Yes	No	WES
34DCIS	PNPLA5	p.S82N	22	44287123	C	T	Missense_Mutation	48	8.3%	No	No	63%	0.40322	97.4%	23.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
34DCIS	DNAH12	p.R1943C	3	57399609	G	A	Missense_Mutation	78	32.1%	No	No	100%	0.77329	100.0%	83.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
34DCIS	FGFRL1	p.S486T	4	1019076	T	A	Missense_Mutation	120	7.5%	No	No	72%	0.4427	97.8%	36.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
34DCIS	FAT2	p.Q4283K	5	150885329	G	T	Missense_Mutation	42	9.5%	No	No	72%	0.48071	98.1%	26.2%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
34DCIS	ZPBP	p.H178Q	7	50070860	A	T	Missense_Mutation	81	9.9%	No	No	100%	0.68002	100.0%	45.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
34DCIS	NYAP1	p.T137M	7	100084785	C	T	Missense_Mutation	56	16.1%	No	Yes	100%	0.70396	100.0%	48.7%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
34DCIS	ATP6V1F	p.Q69*	7	128505220	C	T	Nonsense_Mutation	247	34.8%	No	Yes	100%	0.29003	100.0%	95.3%	Clonal	D	.	.	.	likely_pathogenic	No	No	No	WES
34DCIS	GJB1	p.I33_M34del	23	70443652	GAATCAT	G	In_Frame_Del	70	35.7%	No	No	100%	0.55989	100.0%	83.7%	Clonal	.	.	.	.	passenger	No	No	No	WES
34DCIS	HTR2C	p.F220L	23	114141259	T	C	Missense_Mutation	93	12.9%	No	No	100%	0.74201	100.0%	55.0%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
35DCIS	CITED4	p.F161L	1	41327317	G	T	Missense_Mutation	43	9.3%	No	No	50%	0.24598	94.9%	19.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
35DCIS	ARHGEF2	p.H919Y	1	155920222	G	A	Missense_Mutation	69	39.1%	No	No	100%	0.95041	100.0%	83.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
35DCIS	SLC19A2	p.Q125H	1	169446825	T	G	Missense_Mutation	205	34.1%	No	No	100%	0.96344	100.0%	91.6%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
35DCIS	RYR2	p.N2365D	1	237802479	A	G	Missense_Mutation	141	39.0%	No	No	100%	0.96239	100.0%	90.7%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
35DCIS	GATA3	p.D335Gfs*17	10	8111513	T	TG	Frame_Shift_Ins	277	36.5%	No	No	100%	0.97639	100.0%	94.3%	Clonal	.	.	.	.	likely_pathogenic	Yes	Yes	Yes	WES
35DCIS	ZIC2	p.G177R	13	100634847	G	A	Missense_Mutation	97	5.2%	No	No	28%	0.00133	61.9%	11.9%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
35DCIS	OR4Q3	p.Q234R	14	20216287	A	G	Missense_Mutation	143	35.7%	No	No	100%	0.96658	100.0%	89.4%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
35DCIS	APOBR	p.E361D	16	28507445	G	C	Missense_Mutation	184	13.6%	No	No	74%	0.32533	96.6%	50.2%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
35DCIS	CYBA	p.G145R	16	88709916	C	T	Missense_Mutation	28	10.7%	No	No	47%	0.32499	94.9%	16.3%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
35DCIS	HEATR6	p.P11S	17	58156245	G	A	Missense_Mutation	271	12.5%	No	No	100%	0.85711	100.0%	77.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
35DCIS	ARHGDIA	p.T132M	17	79827069	G	A	Missense_Mutation	93	5.4%	No	Yes	NA	0	100.0%	0.0%	Subclonal	D	Passenger	D	.	passenger	No	No	No	WES
35DCIS	GNA11	p.A342E	19	3121122	C	A	Missense_Mutation	27	11.1%	No	No	49%	0.35247	95.4%	16.8%	Subclonal	D	Passenger	N	D	likely_pathogenic	No	Yes	No	WES
35DCIS	OR7A10	p.F288L	19	14951826	G	T	Missense_Mutation	208	3.8%	No	No	21%	0	39.7%	10.3%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
35DCIS	DNAAF3	p.L490M	19	55670789	G	T	Missense_Mutation	94	5.3%	No	No	24%	0.0001	52.0%	9.9%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
35DCIS	ZBTB45	p.P483A	19	59025510	G	C	Missense_Mutation	95	43.2%	No	No	100%	0.91497	100.0%	88.7%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
35DCIS	RQCD1	p.S87P	2	219447748	T	C	Missense_Mutation	82	39.0%	Yes	No	100%	0.24799	100.0%	83.5%	Subclonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
35DCIS	COL20A1	p.E924V	20	61950517	A	T	Missense_Mutation	152	82.2%	No	No	100%	0	100.0%	97.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
35DCIS	COL20A1	p.S1021R	20	61951537	C	G	Missense_Mutation	100	78.0%	No	No	100%	0.00032	100.0%	95.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
35DCIS	COL20A1	p.A1063V	20	61952399	C	T	Missense_Mutation	123	80.5%	No	No	100%	0	100.0%	96.2%	Clonal	N	Passenger	D	D	passenger	No	No	No	WES
35DCIS	DNAH1	p.L2839M	3	52419353	C	A	Missense_Mutation	20	15.0%	No	No	66%	0.5403	97.7%	21.5%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
35DCIS	NISCH	p.P962L	3	52522393	C	T	Missense_Mutation	47	10.6%	No	No	47%	0.18815	91.3%	20.3%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
35DCIS	FNDC3B	p.X658_splice	3	172060800	G	A	Splice_Site	44	31.8%	No	No	100%	0.91756	100.0%	69.1%	Clonal	D	.	.	.	passenger	No	No	No	WES
35DCIS	LAMP3	p.V45I	3	182872096	C	T	Missense_Mutation	87	5.7%	No	No	31%	0.00524	68.6%	13.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
35DCIS	NIM1K	p.R372Q	5	43280635	G	A	Missense_Mutation	114	35.1%	No	No	100%	0.96169	100.0%	86.8%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
35DCIS	CDX1	p.A207S	5	149563064	G	T	Missense_Mutation	57	24.6%	No	No	100%	0.82829	100.0%	58.9%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
35DCIS	WWC1	p.A489S	5	167850728	G	T	Missense_Mutation	121	43.8%	No	No	100%	0.88696	100.0%	91.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
35DCIS	DOK3	p.L368M	5	176931373	G	T	Missense_Mutation	61	8.2%	No	No	44%	0.10812	89.5%	19.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
35DCIS	DAAM2	p.P522T	6	39846972	C	A	Missense_Mutation	48	8.3%	No	No	45%	0.16651	92.4%	17.7%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
35DCIS	AIMP2	p.S77Y	7	6054871	C	A	Missense_Mutation	175	5.7%	No	No	31%	0.00002	54.9%	16.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
35DCIS	USP42	p.D1052N	7	6194339	G	A	Missense_Mutation	76	30.3%	No	No	100%	0.91581	100.0%	77.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
35DCIS	TOP1MT	p.A471V	8	144398215	G	A	Missense_Mutation	48	8.3%	No	No	45%	0.16651	92.4%	17.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
35DCIS	DMRT1	p.D99E	9	842135	C	A	Missense_Mutation	48	8.3%	No	No	45%	0.16651	92.4%	17.7%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
35DCIS	DMRT1	p.C102Y	9	842143	G	A	Missense_Mutation	47	8.5%	No	No	46%	0.18107	93.0%	18.1%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
35DCIS	CCIN	p.H484N	9	36170949	C	A	Missense_Mutation	96	5.2%	No	No	28%	0.00153	62.5%	12.0%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
35DCIS	SEC16A	p.S1136*	9	139368661	G	T	Nonsense_Mutation	43	9.3%	No	No	41%	0.13932	88.7%	16.2%	Subclonal	N	.	.	.	passenger	No	No	No	WES
35DCIS	PFKFB1	p.Q145K	23	54985310	G	T	Missense_Mutation	56	10.7%	No	No	58%	0.28809	95.8%	26.6%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
38DCIS	ATAD3A	p.X470_splice	1	1460672	G	A	Splice_Site	207	15.9%	No	No	100%	0.96465	100.0%	82.6%	Clonal	D	.	.	.	passenger	No	No	No	WES
38DCIS	BTBD19	p.X161_splice	1	45278737	G	A	Splice_Site	184	20.1%	No	No	100%	0.96951	100.0%	85.7%	Clonal	D	.	.	.	passenger	No	No	No	WES
38DCIS	COL24A1	p.G1322S	1	86252132	C	T	Missense_Mutation	121	16.5%	No	No	100%	0.95065	100.0%	74.1%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
38DCIS	SYT11	p.E430*	1	155851291	G	T	Nonsense_Mutation	139	15.1%	No	No	100%	0.92971	100.0%	73.4%	Clonal	D	.	.	.	passenger	No	No	No	WES
38DCIS	ATP1A4	p.Y914C	1	160151478	A	G	Missense_Mutation	158	15.8%	No	No	100%	0.94318	100.0%	77.2%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
38DCIS	SEC24C	p.G768E	10	75528789	G	A	Missense_Mutation	222	13.5%	No	No	100%	0.91521	100.0%	78.7%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
38DCIS	OR5B17	p.P127S	11	58126164	G	A	Missense_Mutation	84	33.3%	No	No	100%	0.96809	100.0%	83.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
38DCIS	RAB3IL1	p.F341Tfs*22	11	61666824	TAGGTGAA	T	Frame_Shift_Del	53	13.2%	No	No	83%	0.69985	98.6%	37.9%	Clonal	.	.	.	.	passenger	No	No	No	WES
38DCIS	BRMS1	p.X47_splice	11	66109566	C	T	Splice_Site	133	33.1%	No	No	100%	0.97432	100.0%	88.3%	Clonal	D	.	.	.	passenger	No	No	No	WES
38DCIS	NLRX1	p.R547W	11	119045951	C	T	Missense_Mutation	93	23.7%	No	No	100%	0.9143	100.0%	74.3%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
38DCIS	KRT8	p.S59A	12	53296675	A	C	Missense_Mutation	157	12.7%	No	No	100%	0.85613	100.0%	62.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
38DCIS	NFATC4	p.S136L	14	24838822	C	T	Missense_Mutation	143	4.9%	No	No	41%	0.04192	79.5%	19.6%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
38DCIS	PNN	p.R696L	14	39651000	G	T	Missense_Mutation	119	26.9%	No	No	100%	0.91196	100.0%	85.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
38DCIS	SPTB	p.R416W	14	65263370	G	A	Missense_Mutation	103	11.7%	No	No	85%	0.72468	98.8%	46.8%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
38DCIS	RBFOX1	p.Y350C	16	7726831	A	G	Missense_Mutation	98	10.2%	No	No	100%	0.8311	100.0%	52.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
38DCIS	TP53	p.M246V	17	7577545	T	C	Missense_Mutation	72	72.2%	No	Yes	100%	0	100.0%	92.7%	Clonal	D	Passenger	D	D	likely_pathogenic	Yes	Yes	Yes	WES
38DCIS	ZNF652	p.D168Y	17	47394586	C	A	Missense_Mutation	317	18.3%	No	No	100%	0.97491	100.0%	89.5%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
38DCIS	OR4D1	p.R64Q	17	56232705	G	A	Missense_Mutation	127	18.9%	No	No	100%	0.96472	100.0%	79.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
38DCIS	RPS15	p.Y37C	19	1440038	A	G	Missense_Mutation	62	17.7%	No	No	100%	0.92631	100.0%	62.0%	Clonal	D	Passenger	.	.	passenger	No	No	Yes	WES
38DCIS	MYO9B	p.I1970M	19	17321637	C	G	Missense_Mutation	140	20.0%	No	No	100%	0.96637	100.0%	81.0%	Clonal	N	Passenger	D	D	passenger	No	No	No	WES
38DCIS	FGF21	p.G179R	19	49261382	G	A	Missense_Mutation	98	18.4%	No	No	100%	0.92319	100.0%	70.6%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
38DCIS	KLK14	p.A172T	19	51582706	C	T	Missense_Mutation	59	8.5%	No	No	79%	0.6626	98.4%	31.1%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
38DCIS	EPS8L1	p.A214V	19	55592727	C	T	Missense_Mutation	113	15.9%	No	No	100%	0.95765	100.0%	74.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
38DCIS	ZNF329	p.P105L	19	58640557	G	A	Missense_Mutation	129	10.9%	No	No	100%	0.81571	100.0%	54.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
38DCIS	NRXN1	p.P501H	2	50780102	G	T	Missense_Mutation	78	6.4%	No	No	53%	0.37025	95.1%	22.6%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
38DCIS	TTN	p.T22362I	2	179444929	G	A	Missense_Mutation	89	18.0%	No	No	100%	0.91561	100.0%	68.0%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
38DCIS	SIDT1	p.D397E	3	113321925	C	A	Missense_Mutation	79	6.3%	No	No	40%	0.0934	84.4%	17.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
38DCIS	FTMT	p.A51T	5	121187809	G	A	Missense_Mutation	90	13.3%	No	No	100%	0.83495	100.0%	55.1%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
38DCIS	PCDHGA3	p.R630G	5	140725488	C	G	Missense_Mutation	497	6.6%	No	No	55%	0.00172	75.6%	39.1%	Subclonal	N	Passenger	D	T	passenger	No	No	No	WES
38DCIS	AIM1	p.P373H	6	106967425	C	A	Missense_Mutation	111	5.4%	No	No	34%	0.01058	70.4%	15.5%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
38DCIS	TMEM200A	p.A143D	6	130761995	C	A	Missense_Mutation	56	8.9%	No	Yes	NA	0	100.0%	0.0%	Subclonal	D	Driver	D	.	likely_pathogenic	No	No	No	WES
38DCIS	CAMK2B	p.E82K	7	44298502	C	T	Missense_Mutation	87	18.4%	No	No	100%	0.94413	100.0%	73.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
38DCIS	PDP1	p.C157F	8	94934682	G	T	Missense_Mutation	185	30.3%	No	No	100%	0.37151	100.0%	92.5%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
38DCIS	ABHD17B	p.Y157C	9	74485176	T	C	Missense_Mutation	116	24.1%	No	No	100%	0.96832	100.0%	82.0%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
38DCIS	ZNF510	p.S651G	9	99521161	T	C	Missense_Mutation	121	26.4%	No	No	100%	0.96223	100.0%	84.7%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
38DCIS	ACTL7B	p.V126M	9	111617835	C	T	Missense_Mutation	145	9.7%	No	No	80%	0.67358	98.5%	46.7%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
38DCIS	TNC	p.P1530S	9	117810803	G	A	Missense_Mutation	92	22.8%	No	No	100%	0.96331	100.0%	76.9%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
38DCIS	XKRX	p.Y133*	23	100177987	A	T	Nonsense_Mutation	147	5.4%	No	No	51%	0.17887	90.3%	25.6%	Subclonal	A	.	.	.	passenger	No	No	No	WES
38DCIS	FMR1NB	p.G93V	23	147084721	G	T	Missense_Mutation	114	21.9%	No	No	100%	0.96505	100.0%	80.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
40DCIS	NOL9	p.D61N	1	6614382	C	T	Missense_Mutation	70	32.9%	No	No	80%	0.5145	98.1%	55.4%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
40DCIS	LYPD8	p.G59D	1	248902976	C	T	Missense_Mutation	93	39.8%	No	No	97%	0.82232	100.0%	71.5%	Clonal	.	Passenger	.	.	passenger	No	No	No	WES
40DCIS	MYOF	p.D53Y	10	95211886	C	A	Missense_Mutation	110	39.1%	No	No	96%	0.81245	100.0%	72.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
40DCIS	PIK3AP1	p.A224G	10	98412496	G	C	Missense_Mutation	109	31.2%	No	No	76%	0.26799	95.7%	56.4%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
40DCIS	TNNI2	p.R9S	11	1861644	G	T	Missense_Mutation	81	42.0%	No	No	100%	0.85557	100.0%	73.2%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
40DCIS	FAT3	p.R4027C	11	92600327	C	T	Missense_Mutation	88	36.4%	No	No	89%	0.70124	100.0%	64.8%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
40DCIS	CCDC82	p.S391I	11	96104214	C	A	Missense_Mutation	117	47.0%	No	No	100%	0.91976	100.0%	83.8%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
40DCIS	PIK3C2G	p.S1196C	12	18715756	C	G	Missense_Mutation	94	42.6%	No	No	100%	0.87377	100.0%	75.9%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
40DCIS	ITGA5	p.V410M	12	54798676	C	T	Missense_Mutation	114	6.1%	No	No	27%	0.00004	53.5%	13.1%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
40DCIS	OTOGL	p.H1601Q	12	80730754	T	G	Missense_Mutation	339	21.5%	No	No	100%	0.91724	100.0%	84.5%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
40DCIS	ATP2B1	p.E346K	12	90020324	C	T	Missense_Mutation	438	18.0%	No	No	98%	0.85491	100.0%	77.6%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
40DCIS	NDFIP2	p.V75E	13	80055562	T	A	Missense_Mutation	57	71.9%	No	Yes	100%	0.93166	100.0%	81.3%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
40DCIS	ZFHX2	p.R2179*	14	23992616	G	A	Nonsense_Mutation	155	40.0%	No	No	98%	0.855	100.0%	77.4%	Clonal	A	.	.	.	passenger	No	No	No	WES
40DCIS	ATP10A	p.K207*	15	26026201	T	A	Nonsense_Mutation	99	39.4%	No	No	96%	0.81579	100.0%	71.6%	Clonal	A	.	.	.	passenger	No	No	No	WES
40DCIS	AQR	p.V766G	15	35189853	A	C	Missense_Mutation	149	52.3%	No	No	100%	0.72157	100.0%	90.1%	Clonal	N	Passenger	N	D	passenger	No	No	No	WES
40DCIS	FAM63B	p.E206Q	15	59064210	G	C	Missense_Mutation	313	18.2%	No	No	81%	0.39123	97.2%	63.1%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
40DCIS	DNAH3	p.G1424V	16	21061307	C	A	Missense_Mutation	56	42.9%	No	No	100%	0.84107	100.0%	69.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
40DCIS	ZFHX3	p.S64R	16	72993853	G	T	Missense_Mutation	136	49.3%	No	No	100%	0.91137	100.0%	87.2%	Clonal	D	Passenger	D	T	passenger	No	Yes	Yes	WES
40DCIS	ARRB2	p.G355W	17	4623593	G	T	Missense_Mutation	173	35.8%	No	No	88%	0.62789	98.8%	70.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
40DCIS	SLFN14	p.E407Q	17	33880434	C	G	Missense_Mutation	117	41.0%	No	No	100%	0.86285	100.0%	76.2%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
40DCIS	CDC27	p.G265D	17	45234327	C	T	Missense_Mutation	95	6.3%	No	No	15%	0	31.6%	6.8%	Subclonal	D	Driver	N	T	likely_pathogenic	No	No	Yes	WES
40DCIS	ZNF627	p.R379Q	19	11728454	G	A	Missense_Mutation	646	41.0%	No	No	100%	0.93802	100.0%	89.5%	Clonal	N	Passenger	N	T	passenger	No	No	No	WES
40DCIS	TRIM54	p.L178S	2	27522417	T	C	Missense_Mutation	68	5.9%	No	No	14%	0	34.2%	5.3%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
40DCIS	VIT	p.D68H	2	36970326	G	C	Missense_Mutation	146	37.7%	No	No	92%	0.7657	100.0%	72.6%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
40DCIS	IL36A	p.K88M	2	113764313	A	T	Missense_Mutation	73	39.7%	No	No	97%	0.8065	100.0%	68.4%	Clonal	N	Passenger	D	T	passenger	No	No	No	WES
40DCIS	METAP1D	p.V199E	2	172935690	T	A	Missense_Mutation	157	34.4%	No	No	84%	0.49334	98.0%	66.4%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
40DCIS	UNC80	p.Q1923H	2	210795751	G	C	Missense_Mutation	92	44.6%	No	No	100%	0.89424	100.0%	78.3%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
40DCIS	DIDO1	p.I272Sfs*8	20	61542140	CTGGCGGCAAA	C	Frame_Shift_Del	236	36.9%	No	No	100%	0.63816	100.0%	92.5%	Clonal	.	.	.	.	passenger	No	No	No	WES
40DCIS	THUMPD3	p.N232K	3	9413109	C	G	Missense_Mutation	156	43.6%	No	No	100%	0.91527	100.0%	82.9%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
40DCIS	IFRD2	p.R278L	3	50327016	C	A	Missense_Mutation	60	8.3%	No	Yes	12%	0	25.7%	4.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
40DCIS	MYLK	p.D1734Y	3	123345703	C	A	Missense_Mutation	112	39.3%	No	No	96%	0.81905	100.0%	72.8%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
40DCIS	AHSG	p.V249G	3	186337716	T	G	Missense_Mutation	62	38.7%	No	No	95%	0.77231	100.0%	64.5%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES
40DCIS	RASL11B	p.S182F	4	53731770	C	T	Missense_Mutation	79	39.2%	No	No	96%	0.79947	100.0%	68.6%	Clonal	D	Passenger	D	D	likely_pathogenic	No	No	No	WES
40DCIS	PRKG2	p.Q605K	4	82031729	G	T	Missense_Mutation	130	6.2%	No	No	15%	0	28.1%	7.3%	Subclonal	D	Passenger	N	T	passenger	No	No	No	WES
40DCIS	RICTOR	p.X1467_splice	5	38945827	C	G	Splice_Site	56	58.9%	No	No	100%	0.67979	100.0%	83.8%	Clonal	D	.	.	.	passenger	No	No	No	WES
40DCIS	NSG2	p.P15S	5	173473801	C	T	Missense_Mutation	88	38.6%	No	No	95%	0.78827	100.0%	68.9%	Clonal	D	Passenger	N	.	passenger	No	No	No	WES
40DCIS	NUP153	p.S242L	6	17675263	G	A	Missense_Mutation	188	26.6%	No	No	92%	0.75416	100.0%	70.1%	Clonal	D	Driver	N	T	likely_pathogenic	No	No	No	WES
40DCIS	SLC44A4	p.P486R	6	31833680	G	C	Missense_Mutation	172	22.1%	No	No	76%	0.27932	95.8%	56.5%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
40DCIS	GABRR1	p.A21D	6	89926980	G	T	Missense_Mutation	74	6.8%	No	Yes	10%	0	21.0%	3.8%	Subclonal	N	Passenger	N	T	passenger	No	No	No	WES
40DCIS	FOXO3	p.R312Tfs*43	6	108984968	CACGCACCAATTCT	C	Frame_Shift_Del	55	45.5%	No	Yes	66%	0.00699	84.3%	47.3%	Subclonal	.	.	.	.	likely_pathogenic	No	Yes	No	WES
40DCIS	HIVEP2	p.Y1790C	6	143086085	T	C	Missense_Mutation	72	69.4%	No	Yes	100%	0.92192	100.0%	81.2%	Clonal	D	Driver	D	T	likely_pathogenic	No	No	No	WES
40DCIS	STXBP5	p.R947C	6	147684764	C	T	Missense_Mutation	104	9.6%	No	Yes	14%	0	23.9%	7.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
40DCIS	ARID1B	p.Q1039E	6	157495231	C	G	Missense_Mutation	76	9.2%	No	Yes	13%	0	25.4%	6.1%	Subclonal	D	Passenger	N	T	passenger	No	Yes	No	WES
40DCIS	CLIP2	p.K872Q	7	73803483	A	C	Missense_Mutation	114	42.1%	No	No	100%	0.87958	100.0%	77.5%	Clonal	D	Passenger	N	D	likely_pathogenic	No	No	No	WES
40DCIS	PCLO	p.P4730H	7	82467567	G	T	Missense_Mutation	95	5.3%	No	No	13%	0	28.2%	5.2%	Subclonal	D	Passenger	D	T	passenger	No	No	No	WES
40DCIS	FAM110B	p.C248S	8	59059532	G	C	Missense_Mutation	143	44.1%	No	No	100%	0.91492	100.0%	82.6%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
40DCIS	ODF1	p.P51T	8	103564106	C	A	Missense_Mutation	229	19.2%	No	No	85%	0.61536	98.7%	64.1%	Clonal	D	Passenger	N	T	passenger	No	No	No	WES
40DCIS	ARHGAP39	p.K998N	8	145756242	C	A	Missense_Mutation	209	14.4%	No	No	93%	0.7445	100.0%	63.4%	Clonal	D	Passenger	D	T	passenger	No	No	No	WES