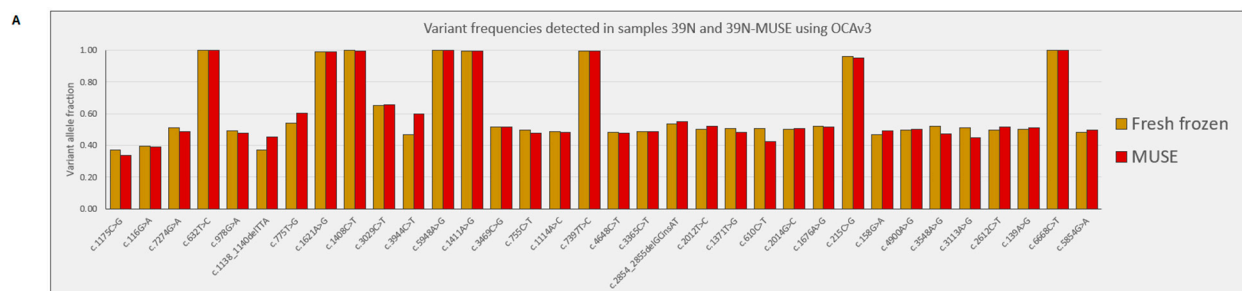


Supplementary Files

Table S1. Normalized RNA read counts across 7 control genes.

| Gene | Amplicon | Sample 39N | | | | Sample 53 | | | |
|---------------|---------------------|------------|----------|--------------|----------|------------|----------|--------------|----------|
| | | MUSE | | Fresh frozen | | MUSE | | Fresh frozen | |
| | | Read Count | RPM | Read Count | RPM | Read Count | RPM | Read Count | RPM |
| <i>ALK</i> | ALK.3p.E22E24 | 33 | 113.1 | 20 | 103.3 | 17 | 49.2 | 55 | 140.2 |
| <i>TBP</i> | TBP.ENCTRL.E3E5 | 62984 | 215837.6 | 13820 | 71349.7 | 107946 | 312475.8 | 133915 | 341469.2 |
| <i>MRPL13</i> | MRPL13.ENCTRL.E1.E3 | 65388 | 224075.8 | 4556 | 23521.6 | 121735 | 352391.3 | 97503 | 248622.4 |
| <i>MYC</i> | MYC.ENCTRL.E2E4 | 17708 | 26121.4 | 21231 | 37164.5 | 56962 | 59510.2 | 61665 | 75666.1 |
| <i>HMBS</i> | HMBS.ENCTRL.E8E10 | 31313 | 46190.4 | 6194 | 10842.5 | 33184 | 34668.5 | 32703 | 40128.3 |
| <i>ITGB7</i> | ITGB7.ENCTRL.E14E16 | 14499 | 21387.7 | 69743 | 122083.9 | 11129 | 11626.9 | 20522 | 25181.5 |
| <i>LRP1</i> | LRP1.ENCTRL.E57E59 | 73023 | 250239.9 | 20936 | 108088.0 | 60399 | 174839.5 | 91739 | 233924.8 |

Note: This table compares RNA read data from samples 39N and 53 (fresh frozen tissue), and 39N-MUSE and 53-MUSE (MUSE treated tissue). RNA sequencing was performed using the Oncomine Comprehensive Assay version 3 (OCAv3). Shown in the table are read counts for each amplicon analyzed and normalized read counts, expressed as Reads Per Million (RPM).



B

| | | | | Sample 39N | | | |
|----------------|--------|-----------------------|--------------|--------------|----------|------|----------|
| | | | | Fresh frozen | | MUSE | |
| Transcript ID | Gene | Variant (DNA) | Protein | VAF | Coverage | VAF | Coverage |
| NM_001033082.2 | MYCL | c.1175C>G | p.Thr392Ser | 0.37 | 3040 | 0.34 | 3625 |
| NM_000179.2 | MSH6 | c.116G>A | p.Gly39Glu | 0.40 | 2051 | 0.39 | 2143 |
| NM_001184.3 | ATR | c.7274G>A | p.Arg2425Gln | 0.51 | 6993 | 0.49 | 5491 |
| NM_001184.3 | ATR | c.632T>C | p.Met211Thr | 1.00 | 7266 | 1.00 | 6590 |
| NM_181523.2 | PIK3R1 | c.978G>A | p.Met326Ile | 0.49 | 4007 | 0.48 | 3317 |
| NM_181523.2 | PIK3R1 | c.1138_1140delTTA | p.Leu380del | 0.37 | 3480 | 0.45 | 3509 |
| NM_001760.4 | CCND3 | c.775T>G | p.Ser259Ala | 0.54 | 6003 | 0.60 | 4394 |
| NM_000535.6 | PMS2 | c.1621A>G | p.Lys541Glu | 0.99 | 3744 | 0.99 | 3832 |
| NM_000535.6 | PMS2 | c.1408C>T | p.Pro470Ser | 1.00 | 13382 | 1.00 | 12500 |
| NM_001127500.2 | MET | c.3029C>T | p.Thr1010Ile | 0.65 | 2609 | 0.65 | 2438 |
| NM_000264.3 | PTCH1 | c.3944C>T | p.Pro1315Leu | 0.47 | 2009 | 0.60 | 1745 |
| NM_000051.3 | ATM | c.5948A>G | p.Asn1983Ser | 1.00 | 4560 | 1.00 | 3059 |
| NM_001274.5 | CHEK1 | c.1411A>G | p.Ile471Val | 1.00 | 3667 | 1.00 | 2773 |
| NM_006231.3 | POLE | c.3469C>G | p.Pro1157Ala | 0.52 | 3086 | 0.52 | 3041 |
| NM_006231.3 | POLE | c.755C>T | p.Ala252Val | 0.50 | 3953 | 0.48 | 3785 |
| NM_000059.3 | BRCA2 | c.1114A>C | p.Asn372His | 0.49 | 4459 | 0.48 | 3080 |
| NM_000059.3 | BRCA2 | c.7397T>C | p.Val2466Ala | 1.00 | 3521 | 1.00 | 2743 |
| NM_032444.3 | SLX4 | c.4648C>T | p.Arg1550Trp | 0.48 | 5738 | 0.48 | 4802 |
| NM_032444.3 | SLX4 | c.3365C>T | p.Pro1122Leu | 0.49 | 7752 | 0.49 | 6140 |
| NM_032444.3 | SLX4 | c.2854_2855delGCinsAT | p.Ala952Met | 0.54 | 2461 | 0.55 | 2428 |
| NM_032444.3 | SLX4 | c.2012T>C | p.Leu671Ser | 0.50 | 3658 | 0.52 | 3515 |
| NM_032444.3 | SLX4 | c.1371T>G | p.Asn457Lys | 0.51 | 6073 | 0.48 | 3305 |
| NM_032444.3 | SLX4 | c.610C>T | p.Arg204Cys | 0.51 | 4008 | 0.42 | 2502 |
| NM_024675.3 | PALB2 | c.2014G>C | p.Glu672Gln | 0.50 | 2661 | 0.51 | 2745 |
| NM_024675.3 | PALB2 | c.1676A>G | p.Gln559Arg | 0.52 | 3362 | 0.52 | 2432 |
| NM_000546.5 | TP53 | c.215C>G | p.Pro72Arg | 0.96 | 6646 | 0.95 | 4589 |
| NM_133629.2 | RAD51D | c.158G>A | p.Arg53Gln | 0.47 | 5214 | 0.49 | 5229 |
| NM_007300.3 | BRCA1 | c.4900A>G | p.Ser1634Gly | 0.50 | 5817 | 0.50 | 5216 |
| NM_007300.3 | BRCA1 | c.3548A>G | p.Lys1183Arg | 0.52 | 6988 | 0.47 | 4640 |
| NM_007300.3 | BRCA1 | c.3113A>G | p.Glu1038Gly | 0.51 | 5569 | 0.45 | 5109 |
| NM_007300.3 | BRCA1 | c.2612C>T | p.Pro871Leu | 0.50 | 4937 | 0.52 | 633 |
| NM_017763.5 | RNF43 | c.139A>G | p.Ile47Val | 0.50 | 1570 | 0.51 | 969 |
| NM_000435.2 | NOTCH3 | c.6668C>T | p.Ala2223Val | 1.00 | 6432 | 1.00 | 6506 |
| NM_000435.2 | NOTCH3 | c.5854G>A | p.Val1952Met | 0.48 | 2392 | 0.50 | 2845 |

Figure S1. Comparison of variants identified in samples 39N and 39N-MUSE using amplicon-based OCAv3. Note: This file compares the variants identified in paired fresh frozen (39N) and MUSE-treated (39N-MUSE) samples. Variants were identified using the OncoPrint Comprehensive Assay version 3 (OCAv3). **A**, Histogram showing the variant allele frequencies (VAF) for each variant in both tissues. **B**, Table listing each variant. Variants are described using Human Genome Variation Society (HGVS) nomenclature, including the RefSeq transcript identifier. Coverage represents total read coverage.