BioChain®
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# Data Sheet

**Product Name: CancerSeqPlus Paraffin Tissue Curl**

**Catalog No.: T2235152-SC** **Lot No.: C101115**

**Species: ■Human □ Mouse □ Rat □ Monkey (Rh) □ Guinea Pig □ Porcine**
**□ Bovine □ Hamster □ Dog □ Monkey (Cy) □ Rabbit □ Plant**

**Tissue Type: □ Normal □ Adult □ Fetal ■ Tumor □Disease □ Cell line**

**Tissue Name: Lung**

**Donor Information:**

**Male: 56 year(s) old**
**Female: _____year(s) old**

**Pathological Diagnosis: Adenocarcinoma**

**Tumor Size: diameter 5.5 cm**

**Location: Lung, Right Upper Lobe**

**Components:**
1. **5 curls per package**
2. **Certificate of Analysis**

**FOR IN VITRO RESEARCH USE ONLY** **APPROVED BY:** _____

C101115

For CNV mutations, we utilize stringent criteria to confirm copy number variations -- using normal tissues as controls. We may have samples containing additional CNVs not listed here. Please inquire.

| symbol | type | chromosome | position | reference | mutation | quality | allele type | Depth | variant frequency | transcript_id | consequence | existing variation |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ATM | snp | chr11 | 1.08E+08 | G | A | 484.967 | hom | 17 | 1.00 | NM_00005 | missense_variant | |
| ATM | snp | chr11 | 1.08E+08 | G | A | 441.455 | hom | 16 | 1.00 | NM_00005 | missense_variant | |
| CCND1 | snp | chr11 | 69471017 | G | A | 983.646 | het | 310 | 0.18 | NM_05305 | downstream_gene_va | |
| CDH1 | snp | chr16 | 68771248 | C | T | 815.258 | het | 44 | 0.70 | NM_00436 | 5_prime_U | rs3403377 |
| CDH1 | snp | chr16 | 68771372 | C | T | 1840.14 | hom | 64 | 1.00 | NM_00436 | splice_regi | rs3743674 |
| CDH1 | snp | chr16 | 68846142 | T | A | 763.56 | het | 92 | 0.54 | NM_00436 | missense_variant | |
| CDH1 | snp | chr16 | 68846434 | A | G | 4861.24 | hom | 212 | 1.00 | NM_00436 | intron_variant | |
| CDH1 | snp | chr16 | 68847266 | G | A | 761.824 | het | 41 | 0.73 | NM_00436 | synonymous_variant | |
| CDH1 | del | chr16 | 68849544 | GCCCCCA | GCCCCA | 868.937 | het | 179 | 0.22 | NM_00436 | frameshift_variant&fea | |
| CDH1 | snp | chr16 | 68853202 | A | G | 664.023 | hom | 30 | 1.00 | NM_00436 | missense_variant | |
| CDK4 | snp | chr12 | 58145002 | G | A | 3052.47 | het | 145 | 0.80 | NM_00007 | synonymous_variant | |
| CDKN2A | snp | chr9 | 21968199 | C | G | 12793.2 | hom | 433 | 1.00 | NM_00119 | 3_prime_U | rs11515&C |
| CDKN2A | snp | chr9 | 21974915 | C | T | 5550.26 | hom | 199 | 0.98 | NM_00119 | 5_prime_UTR_variant | |
| DDR2 | snp | chr1 | 1.63E+08 | T | C | 4568.43 | hom | 144 | 1.00 | XM_00524 | intron_vari | rs1780003 |
| DDR2 | snp | chr1 | 1.63E+08 | C | T | 2355.64 | het | 162 | 0.54 | XM_00524 | missense_v | COSM8987 |
| EGFR | snp | chr7 | 55242186 | G | A | 927.534 | hom | 40 | 1.00 | NM_00522 | intron_variant | |
| ERBB3 | snp | chr12 | 56477684 | C | T | 1858.54 | het | 108 | 0.62 | NM_00198 | stop_gained&splice_re | |
| ERBB3 | snp | chr12 | 56477694 | A | T | 2610.35 | hom | 102 | 0.94 | NM_00198 | splice_regi | rs2271194 |
| ESR1 | snp | chr6 | 1.52E+08 | T | C | 1145.97 | het | 67 | 0.63 | XM_00526 | missense_variant | |
| FBXW7 | del,del | chr4 | 1.53E+08 | CAAAAAAA | CAAAAAAA | 708.014 | het | 77 | 0.32 | NM_03363 | splice_region_variant& | |
| FGFR1 | mnp | chr8 | 38282071 | TC | CT | 555.43 | het | 167 | 0.22 | NM_00117 | missense_variant | |
| FGFR2 | snp | chr10 | 1.23E+08 | T | A | 1479.7 | hom | 51 | 1.00 | NM_02297 | missense_variant | |
| FGFR3 | del | chr4 | 1806012 | TGGGGGG | TGGGGGG | 5039.28 | het | 1409 | 0.22 | NM_00116 | intron_variant&feature | |
| FGFR3 | snp | chr4 | 1806016 | G | A | 1140.28 | het | 1738 | 0.12 | NM_00116 | intron_vari | rs3735913 |
| FGFR3 | snp | chr4 | 1808517 | G | A | 701.06 | hom | 30 | 1.00 | NM_00116 | intron_variant | |
| FLT3 | snp | chr13 | 28609846 | A | T | 654.321 | hom | 28 | 1.00 | NM_00411 | intron_vari | rs2491228 |
| FLT3 | snp | chr13 | 28610183 | A | G | 1295.54 | hom | 44 | 1.00 | NM_00411 | splice_regi | rs2491231 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| HNF1A | snp | chr12 | 1.21E+08 | G | C | 636.131 | hom | 29 | 1.00 | XM_00525 | synonymou | rs5634858( |
| HRAS | snp | chr11 | 534242 | A | G | 1075.05 | hom | 36 | 1.00 | NM_00534 | synonymou | rs12628&C |
| KDR | snp | chr4 | 55953874 | C | A | 2086.58 | het | 197 | 0.72 | NM_00225 | stop_gained | |
| KDR | snp | chr4 | 55955058 | G | A | 623.835 | hom | 22 | 1.00 | NM_00225 | missense_variant | |
| KDR | snp | chr4 | 55980073 | G | C | 272.26 | hom | 13 | 0.92 | NM_00225 | intron_variant | |
| KIT | snp | chr4 | 55599129 | T | A | 473.924 | hom | 25 | 1.00 | XM_00526 | intron_vari | rs1193533 |
| MLH1 | complex | chr3 | 37067238 | GGT | AGA | 268.253 | het | 31 | 0.35 | NM_00024 | missense_variant | |
| MPL | snp | chr1 | 43814992 | C | T | 816.634 | hom | 29 | 1.00 | NM_00537 | synonymous_variant | |
| MPL | snp | chr1 | 43815034 | C | T | 765.209 | het | 34 | 0.88 | NM_00537 | splice_region_variant& | |
| MPL | snp | chr1 | 43815059 | C | T | 906.324 | het | 63 | 0.52 | NM_00537 | intron_variant | |
| MYC | snp | chr8 | 1.29E+08 | C | T | 3155.97 | het | 209 | 0.53 | NM_00246 | 5_prime_UTR_variant | |
| NOTCH1 | snp | chr9 | 1.39E+08 | C | T | 884.308 | hom | 39 | 1.00 | NM_01761 | 3_prime_U | rs3124591 |
| NOTCH1 | snp | chr9 | 1.39E+08 | G | A | 1849.7 | het | 132 | 0.52 | NM_01761 | missense_variant | |
| PDGFRA | snp | chr4 | 55141055 | A | G | 17713 | hom | 627 | 0.99 | NM_00620 | synonymou | rs1873788 |
| PDGFRA | snp | chr4 | 55141111 | G | A | 5112.01 | het | 332 | 0.71 | NM_00620 | stop_gained | |
| PDGFRA | snp | chr4 | 55161254 | C | T | 530.425 | het | 42 | 0.48 | NM_00620 | intron_vari | rs3733540 |
| PDGFRA | snp | chr4 | 55161517 | A | G | 795.04 | hom | 27 | 1.00 | NM_00620 | 3_prime_U | rs7680422 |
| PIK3R1 | snp | chr5 | 67586489 | G | A | 2001.6 | hom | 70 | 1.00 | NM_18152 | intron_variant | |
| PTEN | del | chr10 | 89720633 | CTTTTTTTT | CTTTTTTTT | 817.183 | het | 232 | 0.18 | NM_00031 | splice_acceptor_varian | |
| RB1 | snp | chr13 | 48955676 | T | A | 1345.33 | hom | 62 | 0.98 | NM_00032 | intron_vari | rs2804086 |
| RET | snp | chr10 | 43610203 | C | T | 933.544 | hom | 33 | 1.00 | NM_02097 | intron_variant | |
| STK11 | snp | chr19 | 1207238 | G | T | 1348.36 | hom | 51 | 0.96 | XM_00525 | intron_vari | rs3764640 |
| STK11 | snp | chr19 | 1218523 | G | T | 5372.61 | hom | 185 | 1.00 | XM_00525 | intron_vari | rs2075604 |
| STK11 | snp | chr19 | 1220321 | T | C | 3147.99 | hom | 106 | 1.00 | XM_00525 | intron_vari | rs2075606 |
| STK11 | snp | chr19 | 1220645 | G | A | 2220.72 | het | 130 | 0.65 | XM_00525 | synonymous_variant | |
| STK11 | snp | chr19 | 1220666 | G | A | 1118.1 | hom | 48 | 1.00 | XM_00525 | synonymous_variant | |
| TP53 | snp | chr17 | 7576815 | A | G | 1089.93 | hom | 42 | 0.95 | NM_00054 | intron_variant | |
| TP53 | snp | chr17 | 7579472 | G | C | 7179.87 | hom | 234 | 1.00 | NM_00054 | missense_v | rs1042522 |
| TP53 | del | chr17 | 7579643 | CCCCCAGC | CC | 1007.44 | het | 84 | 0.54 | NM_00054 | intron_variant&feature | |
| TP53 | snp | chr17 | 7579801 | G | C | 936.689 | hom | 45 | 0.98 | NM_00054 | intron_vari | rs1642785 |
| TP53 | snp | chr17 | 7590601 | A | C | 178.141 | hom | 10 | 1.00 | NM_00054 | intron_variant | |
| VHL | snp | chr3 | 10183720 | G | A | 4059.71 | het | 274 | 0.54 | NM_00055 | synonymou | CD941803 |
| VHL | snp | chr3 | 10183897 | C | T | 507.022 | het | 26 | 0.77 | NM_00055 | intron_variant | |