BioChain®
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# Data Sheet

**Product Name: CancerSeqPlus Paraffin Tissue Curl**

**Catalog No.: T2235152-SC** **Lot No.: C101100**

**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: _____ year(s) old**
**Female: 64 year(s) old**

**Pathological Diagnosis: Adenocarcinoma**

**Tumor Size: 4x4x1.5 cm**

**Location: Lung, Left Upper Lobe**

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

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

C101100

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 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ABL1 | snp | chr9 | 1.34E+08 | G | A | 1382.74 | het | 95 | 0.54 | NM_00731 | missense_variant | |
| ABL1 | snp | chr9 | 1.34E+08 | G | A | 765.195 | het | 51 | 0.57 | NM_00731 | missense_variant | |
| ALK | snp | chr2 | 29445458 | G | T | 5649.67 | hom | 189 | 1.00 | NM_00430 | synonymou | rs3795850 |
| APC | snp | chr5 | 1.12E+08 | C | T | 237.291 | hom | 10 | 1.00 | XM_00527 | missense_variant | |
| APC | snp | chr5 | 1.12E+08 | G | A | 4264.71 | hom | 167 | 1.00 | XM_00527 | synonymou | rs465899 |
| APC | snp | chr5 | 1.12E+08 | G | A | 548.183 | hom | 24 | 1.00 | XM_00527 | missense_v | COSM2891 |
| APC | snp | chr5 | 1.12E+08 | C | T | 1695.73 | het | 104 | 0.81 | XM_00527 | missense_variant | |
| APC | snp | chr5 | 1.12E+08 | C | A | 505.881 | het | 48 | 0.54 | XM_00527 | stop_gained | |
| APC | snp | chr5 | 1.12E+08 | C | T | 1138.51 | het | 79 | 0.54 | XM_00527 | missense_variant | |
| ATM | snp | chr11 | 1.08E+08 | G | A | 7017.57 | hom | 288 | 0.95 | NM_00005 | synonymous_variant | |
| ATM | snp | chr11 | 1.08E+08 | G | A | 3074.14 | het | 171 | 0.67 | NM_00005 | synonymous_variant | |
| AURKA | complex | chr20 | 54963136 | CGGAAAGA | ATTACAGA | 507.8 | het | 117 | 0.26 | NM_00360 | intron_variant&feature | |
| AURKA | complex | chr20 | 54963147 | CCC | CAATTTA | 406.286 | het | 119 | 0.23 | NM_00360 | intron_variant&feature | |
| CCNE1 | snp | chr19 | 30303575 | C | T | 1091.86 | het | 82 | 0.54 | NM_00123 | intron_variant | |
| CCNE1 | del,del | chr19 | 30311542 | GTTTTTTTT | GTTTTTTTT | 627.197 | het | 42 | 0.50 | NM_00123 | intron_variant&feature | |
| CDH1 | snp | chr16 | 68771270 | G | T | 10482.7 | het | 472 | 0.74 | NM_00436 | 5_prime_UTR_variant | |
| CDH1 | snp | chr16 | 68771372 | C | T | 17170 | hom | 544 | 0.99 | NM_00436 | splice_regi | rs3743674 |
| CDH1 | snp | chr16 | 68857441 | T | C | 1762.53 | hom | 76 | 1.00 | NM_00436 | synonymou | rs1801552 |
| CDKN2A | snp | chr9 | 21968199 | C | G | 41532 | hom | 1345 | 1.00 | NM_00119 | 3_prime_U | rs11515&C |
| CDKN2A | snp | chr9 | 21968336 | G | A | 4639.83 | hom | 206 | 1.00 | NM_00119 | intron_variant | |
| CSF1R | snp | chr5 | 1.49E+08 | C | T | 1897.56 | het | 105 | 0.68 | NM_00521 | missense_variant | |
| CTNNB1 | snp | chr3 | 41265971 | G | A | 7422.49 | het | 512 | 0.55 | XM_00526 | intron_variant | |
| DDR2 | snp | chr1 | 1.63E+08 | T | C | 13268.3 | hom | 417 | 1.00 | XM_00524 | intron_vari | rs1780003 |
| DDR2 | snp | chr1 | 1.63E+08 | G | T | 2161.51 | hom | 87 | 1.00 | XM_00524 | intron_vari | rs1355287 |
| ERBB3 | complex | chr12 | 56477694 | AGCC | TGC | 754.434 | het | 45 | 0.73 | NM_00198 | splice_region_variant& | |
| ERBB3 | snp | chr12 | 56477694 | AGCC | TGCC | 9135.25 | hom | 360 | 0.88 | NM_00198 | splice_region_variant& | |
| EZH2 | snp | chr7 | 1.49E+08 | A | G | 4429.79 | hom | 157 | 1.00 | XM_00524 | intron_vari | rs2072407 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| FBXW7 | snp | chr4 | 1.53E+08 | C | T | 708.74 | het | 39 | 0.87 | NM_03363 | intron_variant | |
| FBXW7 | snp | chr4 | 1.53E+08 | A | G | 3448.31 | hom | 124 | 1.00 | NM_03363 | intron_vari | rs1003601 |
| FBXW7 | snp | chr4 | 1.53E+08 | G | A | 631.51 | hom | 23 | 1.00 | NM_03363 | splice_region_variant& | |
| FBXW7 | del,del | chr4 | 1.53E+08 | CAAAAAAA | CAAAAAAA | 1780.98 | het | 298 | 0.26 | NM_03363 | splice_region_variant& | |
| FGFR1 | snp | chr8 | 38272160 | C | T | 18566.7 | het | 951 | 0.69 | NM_00117 | intron_variant | |
| FGFR3 | del | chr4 | 1806012 | TGGGGGG | TGGGGGG | 6237.2 | het | 1862 | 0.18 | NM_00116 | intron_variant&feature | |
| FGFR3 | snp | chr4 | 1807894 | G | A | 15759.4 | hom | 512 | 0.99 | NM_00116 | synonymou | rs7688609 |
| FGFR3 | complex | chr4 | 1808889 | GCCAGGA | TCCTGGC | 878.058 | het | 40 | 0.88 | NM_00116 | missense_variant | |
| FGFR3 | complex | chr4 | 1808900 | CCC | CGGGG | 758.496 | hom | 31 | 0.94 | NM_00116 | frameshift_variant&fea | |
| FLT3 | snp | chr13 | 28609991 | T | C | 440.212 | hom | 20 | 1.00 | NM_00411 | intron_vari | rs2491229 |
| FLT3 | snp | chr13 | 28609997 | T | C | 478.272 | hom | 21 | 1.00 | NM_00411 | intron_vari | rs2491230 |
| FLT3 | snp | chr13 | 28610183 | A | G | 5406.16 | hom | 188 | 1.00 | NM_00411 | splice_regi | rs2491231 |
| FOXL2 | ins | chr3 | 1.39E+08 | GC | GCAGCCC | 1283.98 | hom | 49 | 1.00 | NM_02306 | frameshift_variant&fea | |
| FOXL2 | complex | chr3 | 1.39E+08 | GGGC | GCCATGA | 1216.26 | hom | 50 | 0.90 | NM_02306 | inframe_insertion | |
| FOXL2 | snp | chr3 | 1.39E+08 | G | A | 327.139 | hom | 14 | 1.00 | NM_02306 | synonymous_variant | |
| GNA11 | snp | chr19 | 3118991 | C | T | 8247.72 | het | 378 | 0.87 | NM_00206 | synonymous_variant | |
| GNA11 | snp | chr19 | 3119085 | G | A | 341.086 | hom | 17 | 1.00 | NM_00206 | intron_variant | |
| GNAQ | snp | chr9 | 80409345 | A | G | 198.465 | het | 13 | 0.85 | NM_00207 | intron_vari | rs1328529 |
| HRAS | snp | chr11 | 534242 | A | G | 5768.45 | hom | 197 | 1.00 | NM_00534 | synonymou | rs12628&C |
| HRAS | snp | chr11 | 534329 | T | C | 456.514 | het | 40 | 0.45 | NM_00534 | 5_prime_UTR_variant | |
| HRAS | snp | chr11 | 534337 | C | T | 225.667 | het | 40 | 0.28 | NM_00534 | 5_prime_UTR_variant | |
| HRAS | snp | chr11 | 534380 | C | T | 301.488 | het | 44 | 0.30 | NM_00534 | splice_region_variant& | |
| HRAS | del | chr11 | 534403 | GCCCAGGC | GC | 7470.92 | hom | 295 | 0.95 | NM_00534 | intron_variant&feature | |
| HRAS | snp | chr11 | 534413 | A | C | 199.818 | het | 66 | 0.21 | NM_00534 | intron_variant | |
| HRAS | snp | chr11 | 534415 | C | G | 547.113 | het | 56 | 0.38 | NM_00534 | intron_vari | rs61877782 |
| IDH1 | del | chr2 | 2.09E+08 | GAAAAAAA | GAAAAAAA | 3281.43 | het | 573 | 0.25 | XM_00524 | intron_variant&feature | |
| JAK2 | snp | chr9 | 5081894 | A | G | 1935.3 | het | 102 | 0.68 | NM_00497 | intron_variant | |
| JAK3 | snp | chr19 | 17945686 | G | A | 4439.28 | het | 295 | 0.53 | XM_00525 | missense_variant | |
| JAK3 | snp | chr19 | 17947916 | TGGGTGGC | TGAGTGGG | 1054.82 | het | 1391 | 0.18 | XM_00525 | intron_variant | |
| JAK3 | del | chr19 | 17954140 | GCC | GC | 115.038 | het | 326 | 0.12 | XM_00525 | intron_variant&feature | |
| KDR | snp | chr4 | 55961159 | T | C | 7295.51 | hom | 240 | 1.00 | NM_00225 | intron_vari | rs2219471 |
| KDR | complex | chr4 | 55961185 | AACCTTTA | TACATTTTA | 583.879 | hom | 24 | 0.88 | NM_00225 | intron_variant | |
| KDR | snp | chr4 | 55962453 | G | A | 2540.97 | hom | 101 | 0.94 | NM_00225 | missense_variant | |
| KDR | snp | chr4 | 55972974 | T | A | 2483.16 | hom | 90 | 0.99 | NM_00225 | missense_v | rs1870377 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| KDR | snp | chr4 | 55979558 | C | A | 738.282 | het | 30 | 0.93 | NM_00225 | missense_v | rs2305948 |
| KIT | snp | chr4 | 55595573 | C | T | 1552.81 | het | 78 | 0.79 | XM_00526 | missense_variant | |
| KRAS | snp | chr12 | 25398373 | C | T | 2909.86 | het | 164 | 0.66 | NM_03336 | intron_variant | |
| MAP2K1 | snp | chr15 | 66727597 | G | C | 8813.38 | het | 489 | 0.58 | NM_00275 | intron_vari | rs1694992 |
| MAP2K1 | snp | chr15 | 66729141 | G | A | 525.385 | het | 36 | 0.72 | NM_00275 | missense_variant | |
| MDM2 | snp | chr12 | 69218230 | C | T | 1803.86 | het | 122 | 0.85 | NM_00239 | intron_vari | rs1437588 |
| MET | snp | chr7 | 1.16E+08 | C | T | 3139.27 | het | 190 | 0.59 | XM_00525 | synonymou | rs3577572 |
| MET | snp | chr7 | 1.16E+08 | G | T | 3160.4 | hom | 114 | 0.99 | XM_00525 | missense_variant | |
| MPL | complex | chr1 | 43814886 | GGGGCTC | CAGACTT | 436.75 | hom | 19 | 1.00 | NM_00537 | intron_variant | |
| MPL | mnp | chr1 | 43814899 | GGGT | ACCC | 392.549 | hom | 18 | 1.00 | NM_00537 | intron_variant | |
| MYCN | snp | chr2 | 16080112 | C | T | 462.929 | het | 34 | 0.53 | NM_00537 | upstream_gene_variar | |
| MYCN | snp | chr2 | 16080157 | C | G | 1533.22 | hom | 50 | 1.00 | NM_00537 | upstream_ | rs1188606 |
| MYCN | snp | chr2 | 16085891 | C | T | 400.875 | hom | 17 | 1.00 | NM_00537 | missense_variant | |
| MYCN | snp | chr2 | 16089615 | T | C | 2332.61 | hom | 86 | 0.98 | NM_00537 | downstrea | rs4669018 |
| MYCN | snp | chr2 | 16090003 | C | T | 247.024 | hom | 11 | 1.00 | NM_00537 | downstream_gene_va | |
| NOTCH1 | snp | chr9 | 1.39E+08 | G | A | 3561.82 | hom | 156 | 1.00 | NM_01761 | synonymou | rs2229974 |
| NOTCH1 | snp | chr9 | 1.39E+08 | G | A | 644.718 | hom | 23 | 1.00 | NM_01761 | synonymou | rs10521&C |
| NOTCH1 | complex | chr9 | 1.39E+08 | CTT | CG | 961.999 | hom | 39 | 0.95 | NM_01761 | frameshift_variant&fea | |
| NOTCH1 | ins | chr9 | 1.39E+08 | GG | GACG | 805.815 | hom | 34 | 0.94 | NM_01761 | frameshift_variant&fea | |
| NOTCH1 | complex | chr9 | 1.39E+08 | AGCA | TGCT | 967.594 | hom | 40 | 0.95 | NM_01761 | missense_variant | |
| NOTCH1 | del | chr9 | 1.39E+08 | CGTC | CC | 900.144 | hom | 37 | 0.95 | NM_01761 | frameshift_variant&fea | |
| NOTCH1 | mnp | chr9 | 1.39E+08 | CG | AA | 846.401 | hom | 33 | 0.97 | NM_01761 | missense_variant | |
| NOTCH1 | snp | chr9 | 1.39E+08 | T | A | 276.763 | hom | 12 | 1.00 | NM_01761 | intron_variant | |
| NPM1 | del | chr5 | 1.71E+08 | CTTTTTTTT | CTTTTTTTT | 230.736 | het | 32 | 0.34 | NM_00252 | splice_region_variant& | |
| PDGFRA | snp | chr4 | 55141055 | A | G | 11253.9 | hom | 388 | 1.00 | NM_00620 | synonymou | rs1873778 |
| PDGFRA | snp | chr4 | 55161254 | C | T | 5330.2 | hom | 178 | 1.00 | NM_00620 | intron_vari | rs3733540 |
| PDGFRA | snp | chr4 | 55161517 | A | G | 2533.86 | hom | 85 | 1.00 | NM_00620 | 3_prime_U | rs7680422 |
| PIK3CA | del | chr3 | 1.79E+08 | ATTTTTTTT | ATTTTTTTT | 918.604 | het | 328 | 0.17 | NM_00621 | intron_variant&feature | |
| PIK3CA | snp | chr3 | 1.79E+08 | C | A | 741.368 | hom | 33 | 1.00 | NM_00621 | intron_variant | |
| PIK3R1 | snp | chr5 | 67589406 | C | T | 470.982 | hom | 20 | 1.00 | NM_18152 | intron_variant | |
| PTEN | del | chr10 | 89711855 | CTTTTTTTT | CTTTTTTTC | 95.4432 | het | 321 | 0.12 | NM_00031 | intron_variant&feature | |
| PTEN | snp | chr10 | 89720574 | C | A | 1436.85 | het | 74 | 0.73 | NM_00031 | intron_variant | |
| PTEN | snp | chr10 | 89720581 | A | T | 1326.21 | het | 71 | 0.70 | NM_00031 | intron_variant | |
| PTEN | snp | chr10 | 89720588 | T | G | 1250.78 | het | 72 | 0.65 | NM_00031 | intron_variant | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PTEN | mnp | chr10 | 89720593 | CA | TC | 1228 | het | 68 | 0.71 | NM_00031 | intron_variant | |
| PTEN | del | chr10 | 89720633 | CTTTTTTTT | CTTTTTTTT | 421.228 | het | 150 | 0.20 | NM_00031 | splice_acceptor_varian | |
| PTEN | del | chr10 | 89725293 | CTTTTTTTT | CTTTTTTTT | 315.93 | het | 311 | 0.13 | NM_00031 | 3_prime_UTR_variant& | |
| PTPN11 | snp | chr12 | 1.13E+08 | G | A | 1647.47 | het | 118 | 0.54 | NM_00283 | missense_variant | |
| RB1 | snp | chr13 | 48919358 | T | G | 3388.04 | hom | 126 | 1.00 | NM_00032 | intron_vari | rs198617 |
| RB1 | snp | chr13 | 48919484 | G | T | 179.807 | het | 26 | 0.85 | NM_00032 | intron_variant | |
| RB1 | ins | chr13 | 48953655 | CAAAAAAA | CAAAAAAA | 613.51 | het | 116 | 0.30 | NM_00032 | intron_variant&feature | |
| RET | snp | chr10 | 43613843 | G | T | 8277 | hom | 261 | 1.00 | NM_02097 | synonymou | rs1800861 |
| RET | complex | chr10 | 43615494 | CATGGC | GAGGGT | 231.555 | hom | 10 | 1.00 | NM_02097 | intron_variant | |
| SMO | snp | chr7 | 1.29E+08 | G | C | 12860.3 | hom | 425 | 1.00 | NM_00563 | intron_vari | rs2075777 |
| SMO | snp | chr7 | 1.29E+08 | G | C | 3281.45 | hom | 114 | 1.00 | NM_00563 | synonymou | rs2228617 |
| SRC | snp | chr20 | 36031596 | G | C | 8284.45 | het | 559 | 0.55 | NM_00541 | synonymous_variant | |
| STK11 | snp | chr19 | 1207238 | G | T | 4799.02 | hom | 169 | 0.99 | XM_00525 | intron_vari | rs3764640 |
| STK11 | snp | chr19 | 1218520 | ACCG | ACCT | 7744.64 | het | 764 | 0.35 | XM_00525 | intron_variant | |
| STK11 | complex | chr19 | 1219433 | CCAGGGT | GGGGGGG | 53.7366 | het | 146 | 0.16 | XM_00525 | intron_variant | |
| STK11 | ins | chr19 | 1219443 | GCGGGGG | GCGGGGG | 974.282 | het | 59 | 0.80 | XM_00525 | intron_variant&feature | |
| STK11 | snp | chr19 | 1219553 | G | T | 1359.01 | hom | 58 | 1.00 | XM_00525 | intron_vari | rs1108488 |
| STK11 | snp | chr19 | 1220321 | T | C | 24433.1 | hom | 774 | 0.99 | XM_00525 | intron_vari | rs2075606 |
| STK11 | snp | chr19 | 1222085 | G | A | 1972.85 | hom | 85 | 1.00 | XM_00525 | intron_variant | |
| TERT | snp | chr5 | 1295349 | A | G | 61000.8 | hom | 1907 | 1.00 | NM_19825 | upstream_ | rs2853669 |
| TP53 | complex | chr17 | 7579387 | CTG | ATA | 438.915 | het | 141 | 0.30 | NM_00054 | missense_variant | |
| TP53 | snp | chr17 | 7579387 | CTG | CTA | 2729.39 | het | 266 | 0.46 | NM_00054 | stop_gained | |
| TP53 | del | chr17 | 7579643 | CCCCCAGC | CC | 299.213 | het | 218 | 0.18 | NM_00054 | intron_variant&feature | |