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www.biochain.com
Tel: 1-888-762-2568 Fax: 1-510-783-5386 Email: info@biochain.com

# Data Sheet

**Product Name: CancerSeqPlus Paraffin Tissue Curl**

**Catalog No.: T2235248-SC** **Lot No.: B906138**

**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: Stomach**

**Donor Information:**

**Male: 58 year(s) old**
**Female: _____year(s) old**

**Pathological Diagnosis: Adenosquamous carcinoma**

**Tumor Size:**

**Location: stomach**

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

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

B906138

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.

| CNV against colon | Copy Number | STDev of Copy Number | P-value | CNV against **adrenal** | Copy Number | STDev of Copy Number | P-value |
|---|---|---|---|---|---|---|---|
| CCNE1 | 5.33 | 0.38 | 1.64E-03 | CCNE1 | 3.72 | 0.05 | 8.78E-04 |
| ERBB3 | 2.28 | 0.21 | 1.39E-02 | ERBB3 | 3.54 | 0.07 | 3.03E-04 |

| symbol | type | chromosome | position | reference | mutation | quality | allele type | Depth | variant frequency | transcript_id | existing variation | consequence |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ALK | snp | chr2 | 29445458 | G | T | 3079.6 | hom | 98 | 1.00 | NM_004304 | rs3795850 | synonymous_va |
| APC | snp | chr5 | 112177171 | G | A | 467.21 | hom | 18 | 1.00 | XM_005271 | rs465899 | synonymous_va |
| ATM | del | chr11 | 108117897 | ATTTTTTTTT | ATTTTTTTTT | 180.24 | het | 63 | 0.17 | NM_000051.3 | | intron_variant& |
| CCND1 | snp | chr11 | 69465120 | G | A | 413.446 | het | 24 | 0.75 | NM_053056.2 | | intron_variant |
| CDH1 | snp | chr16 | 68771372 | C | T | 6199.84 | hom | 199 | 1.00 | NM_004360 | rs3743674 | splice_region_v |
| CDKN2A | snp | chr9 | 21968199 | C | G | 27078 | hom | 866 | 1.00 | NM_001195 | rs11515&CO | 3_prime_UTR_v |
| CTNNB1 | del | chr3 | 41265953 | CTTTTTTTTT | CTTTTTTTTA | 140.395 | het | 96 | 0.15 | XM_005264887.1 | | intron_variant& |
| DDR2 | snp | chr1 | 162740327 | TGTC | CGTC | 6605.39 | hom | 231 | 0.94 | XM_005245220.1 | | intron_variant |
| DDR2 | complex | chr1 | 162740327 | TGTC | CGTT | 320.881 | hom | 13 | 0.92 | XM_005245220.1 | | intron_variant |
| DDR2 | snp | chr1 | 162743418 | G | T | 1349.86 | hom | 52 | 0.98 | XM_005245 | rs1355287 | intron_variant |
| EGFR | ins | chr7 | 55242248 | CG | CTG | 248.842 | hom | 11 | 1.00 | NM_005228.3 | | intron_variant& |
| EGFR | ins | chr7 | 55242254 | CG | CTG | 260.66 | hom | 11 | 1.00 | NM_005228.3 | | intron_variant& |
| EGFR | complex | chr7 | 55242257 | CACAG | GACG | 268.588 | hom | 12 | 1.00 | NM_005228.3 | | intron_variant& |
| EZH2 | snp | chr7 | 148508833 | A | G | 555.831 | het | 29 | 0.69 | XM_005249 | rs2072407 | intron_variant |
| FBXW7 | del | chr4 | 153247486 | CTTTTTTTTT | CTTTTTTTTT | 300.805 | het | 50 | 0.26 | NM_033632.3 | | intron_variant& |
| FBXW7 | snp | chr4 | 153252061 | A | G | 1363.44 | het | 64 | 0.75 | NM_033632 | rs10033601 | intron_variant |
| FBXW7 | snp | chr4 | 153267968 | A | G | 423.054 | hom | 15 | 1.00 | NM_033632 | rs2714803 | intron_variant |
| FBXW7 | del,del | chr4 | 153268227 | CAAAAAAAA | CAAAAAAAA | 1314.02 | het | 140 | 0.35 | NM_033632.3 | | splice_region_v |
| FBXW7 | snp | chr4 | 153271120 | A | G | 330.318 | het | 24 | 0.54 | NM_033632.3 | | intron_variant |
| FGFR3 | del | chr4 | 1806012 | TGGGGGGG | TGGGGGGG | 580.701 | het | 185 | 0.18 | NM_001163213.1 | | intron_variant& |
| FGFR3 | snp | chr4 | 1807894 | G | A | 4040.82 | hom | 136 | 1.00 | NM_001163 | rs7688609 | synonymous_va |
| FLT3 | snp | chr13 | 28610183 | A | G | 3553.29 | hom | 119 | 1.00 | NM_004119 | rs2491231 | splice_region_v |
| FOXL2 | complex | chr3 | 138664790 | TGTACGGCC | CGTAGTGAA | 386.353 | het | 184 | 0.20 | NM_023067.3 | | frameshift_vari |
| FOXL2 | complex | chr3 | 138664804 | GAGGCGGC | AATGGCCTG | 474.463 | het | 180 | 0.20 | NM_023067.3 | | frameshift_vari |
| IDH1 | snp | chr2 | 209116134 | C | T | 5753.86 | het | 349 | 0.52 | XM_005246 | rs111233394 | intron_variant |
| IDH1 | del | chr2 | 209116299 | GAAAAAAAA | GAAAAAAAA | 514.822 | het | 100 | 0.24 | XM_005246521.1 | | intron_variant& |
| JAK2 | del | chr9 | 5073681 | CTTTTTTTTT | CTTTTTTTTT | 296.969 | het | 37 | 0.32 | NM_004972.3 | | splice_region_v |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| JAK3 | del | chr19 | 17947924 | TGGGGGGC | TGGGGGC | 807.518 | het | 323 | 0.19 | XM_005259 | 896.1 | splice_region_v |
| KDR | snp | chr4 | 55961159 | T | C | 1567.03 | hom | 55 | 1.00 | NM_002253 | rs2219471 | intron_variant |
| KDR | ins | chr4 | 55962545 | TGG | TGGG | 105.859 | het | 59 | 0.19 | NM_002253 | .2 | intron_variant& |
| KDR | snp | chr4 | 55972974 | T | A | 406.935 | hom | 14 | 1.00 | NM_002253 | rs1870377& | missense_varia |
| KDR | snp | chr4 | 55980456 | C | T | 2792.1 | het | 158 | 0.58 | NM_002253 | rs2305949 | intron_variant |
| MYCN | snp | chr2 | 16080157 | C | G | 474.886 | hom | 16 | 1.00 | NM_005378 | rs11886063 | upstream_gene |
| MYCN | snp | chr2 | 16089615 | T | C | 1516.46 | hom | 55 | 0.96 | NM_005378 | rs4669018 | downstream_g |
| NOTCH1 | mnp | chr9 | 139391461 | TG | CA | 454.084 | het | 178 | 0.17 | NM_017617 | .3 | missense_varia |
| NOTCH1 | mnp | chr9 | 139391467 | GG | CC | 504.146 | het | 181 | 0.18 | NM_017617 | .3 | missense_varia |
| NOTCH1 | mnp | chr9 | 139391473 | TG | CA | 540.898 | het | 177 | 0.18 | NM_017617 | .3 | missense_varia |
| NOTCH1 | snp | chr9 | 139391636 | G | A | 1748.92 | hom | 72 | 1.00 | NM_017617 | rs2229974 | synonymous_va |
| NOTCH1 | snp | chr9 | 139397707 | G | A | 2290.04 | hom | 79 | 1.00 | NM_017617 | rs10521&CC | synonymous_va |
| NPM1 | del | chr5 | 170837513 | CTTTTTTTTT | CTTTTTTTT | 290.64 | het | 45 | 0.29 | NM_002520 | .6 | splice_region_v |
| PDGFRA | snp | chr4 | 55141055 | A | G | 3829.93 | hom | 129 | 1.00 | NM_006206 | rs1873778& | synonymous_va |
| PDGFRA | snp | chr4 | 55152040 | C | T | 5097.76 | het | 227 | 0.87 | NM_006206 | rs2228230& | synonymous_va |
| PDGFRA | snp | chr4 | 55161254 | C | T | 945.942 | het | 60 | 0.55 | NM_006206 | rs3733540 | intron_variant |
| PDGFRA | snp | chr4 | 55161391 | T | C | 302.979 | hom | 11 | 1.00 | NM_006206 | rs7685117 | synonymous_va |
| PDGFRA | snp | chr4 | 55161517 | A | G | 1702.42 | hom | 57 | 0.98 | NM_006206 | rs7680422 | 3_prime_UTR_v |
| PIK3CA | del | chr3 | 178916904 | CTTTTTA | CTTTTA | 326.985 | het | 39 | 0.36 | NM_006218 | .2 | frameshift_vari |
| PIK3R1 | snp | chr5 | 67593337 | G | A | 496.249 | het | 41 | 0.46 | NM_181523 | .2 | missense_varia |
| PTEN | del | chr10 | 89720633 | CTTTTTTTTT | CTTTTTTTT | 136.555 | het | 49 | 0.20 | NM_000314 | .4 | splice_acceptor |
| PTEN | snp | chr10 | 89720907 | T | G | 589.496 | hom | 21 | 1.00 | NM_000314 | rs555895&C | intron_variant |
| PTEN | del | chr10 | 89725293 | CTTTTTTTTT | CTTTTTTTT | 189.993 | het | 64 | 0.19 | NM_000314 | .4 | 3_prime_UTR_v |
| RB1 | snp | chr13 | 48919358 | T | G | 988.937 | hom | 33 | 1.00 | NM_000321 | rs198617 | intron_variant |
| RB1 | ins | chr13 | 49034022 | ATT | ATTT | 271.289 | het | 20 | 0.65 | NM_000321 | .2 | intron_variant& |
| RET | snp | chr10 | 43610189 | G | T | 262.569 | hom | 10 | 1.00 | NM_020975 | .4 | splice_region_v |
| RET | mnp | chr10 | 43610190 | GG | CT | 262.569 | hom | 10 | 1.00 | NM_020975 | .4 | splice_region_v |
| RET | mnp | chr10 | 43610199 | GGG | CCC | 278.039 | hom | 10 | 1.00 | NM_020975 | .4 | intron_variant |
| RET | snp | chr10 | 43613843 | G | T | 1069.84 | hom | 36 | 0.97 | NM_020975 | rs1800861& | synonymous_va |
| SMO | snp | chr7 | 128845277 | G | C | 2689.81 | het | 127 | 0.74 | NM_005631 | rs2075777 | intron_variant |
| STK11 | snp | chr19 | 1207238 | G | T | 5024.53 | hom | 163 | 1.00 | XM_005259 | rs3764640 | intron_variant |
| STK11 | snp | chr19 | 1218523 | G | T | 3260.4 | het | 225 | 0.50 | XM_005259 | rs2075604 | intron_variant |
| STK11 | complex | chr19 | 1218605 | TGGCACAC | GGGAAGAG | 244.376 | het | 20 | 0.60 | XM_005259 | 617.1 | intron_variant |
| STK11 | snp | chr19 | 1220321 | T | C | 2889.16 | hom | 92 | 1.00 | XM_005259 | rs2075606 | intron_variant |
| TP53 | snp | chr17 | 7577407 | A | C | 775.091 | het | 52 | 0.52 | NM_000546 | rs12951053 | intron_variant |
| TP53 | snp | chr17 | 7579472 | G | C | 1062.95 | het | 54 | 0.69 | NM_000546 | rs1042522& | missense_varia |
| TP53 | del | chr17 | 7579643 | CCCCCAGCC | CC | 436.329 | het | 75 | 0.29 | NM_000546 | .5 | intron_variant& |
| TP53 | snp | chr17 | 7579801 | G | C | 459.523 | het | 27 | 0.78 | NM_000546 | rs1642785 | intron_variant |
| TP53 | del | chr17 | 7579863 | TCC | TC | 18295.8 | het | 1481 | 0.40 | NM_000546 | .5 | frameshift_vari |