Data in Brief

Expression profiling of wild type and β-catenin gene disrupted human BxPC-3 pancreatic adenocarcinoma cells

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To study the role of WNT/β-catenin signaling in pancreatic adenocarcinoma, human BxPC-3 cell lines deficient of the central canonical WNT signaling protein β-catenin were established by using zinc-finger nuclease mediated targeted genomic disruption of the β-catenin gene (CTNNB1). Comparison of the global transcription levels in wild type cells with two β-catenin gene disrupted clones identified 85 transcripts that were the most differentially regulated. Gene ontology (GO) term enrichment analysis of these transcripts identified “cell adhesion” as the most significantly enriched GO term. Here we describe the data from the transcription profiling analysis published in the article “Implications of Targeted Genomic Disruption of β-Catenin in BxPC-3 Pancreatic Adenocarcinoma Cells” [1]. Data have been deposited to the Gene Expression Omnibus (GEO) database repository with the dataset identifier GSE63072.

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Generation of β-catenin deficient cells

BxPC-3 cells with targeted disruption of the β-catenin gene (CTNNB1) were established using CompoZr custom Zinc Finger Nucleases (ZFNs) (Sigma-Aldrich). Briefly, following transfection of the cells with ZFN mRNA targeting exon 3 of the CTNNB1 gene, monoclonal cell populations were obtained by limiting dilution cloning and analyzed for β-catenin expression. From 150 initial clones five β-catenin gene disrupted clones negative for β-catenin expression were identified and selected for further analysis (clone #4, #31, #79, #93 and #111).

RNA isolation microarray analysis

Total RNA from exponentially growing wild type BxPC-3 cells and β-catenin gene disrupted clones #4 and #111 was isolated using the GenElute Mammalian Total RNA Purification Kit (Sigma-Aldrich). The RNA was subjected to microarray analysis using Illumina HumanHT-12 v4 Expression BeadChips (Illumina, CA, USA) at the Norwegian Genomics Consortium core facility (Oslo University Hospital, Norway). For each sample 6 biological replicates were analyzed. Data extraction and quality control was performed in GenomeStudio (Illumina) and the data analysis was performed using J-Express [2].

Differential expression quantification and classification

To identify the most differentially expressed genes between wild type BxPC-3 cells and the β-catenin gene disrupted clones #4 and #111 (average) Significance Analysis of Microarrays (SAM) analysis was carried out [3]. From the SAM analysis a threshold of fold change...
| Probe_Id | Symbol | ILMN_GENE | d-Score | Fold change | q-Value |
|----------|--------|-----------|---------|-------------|---------|
| ILMN_1686664 | MT2A | MT2A | 22.155 | 2.45 | 0 |
| ILMN_1659888 | LGLA53BP | LGLA53BP | 15.656 | 2.358 | 0 |
| ILMN_2042771 | DPPS2L | DPPS2L | 12.37 | 2.368 | 0 |
| ILMN_2183409 | SCARB1 | SCARB1 | 12.283 | 2.43 | 0 |
| ILMN_1673356 | FAM83C | FAM83C | 11.125 | 2.327 | 0 |
| ILMN_3240795 | LOC7281188 | LOC7281188 | 10.777 | 2.446 | 0 |
| ILMN_1713147 | MCK1 | MCK1 | 10.705 | 2.178 | 0 |
| ILMN_1655347 | SGBE1A1 | SGBE1A1 | 10.414 | 2.055 | 0 |
| ILMN_2320250 | NOU6 | NOU6 | 10.404 | 2.087 | 0 |
| ILMN_1799098 | LOC520546 | LOC520546 | 10.398 | 2.289 | 0 |
| ILMN_1750324 | IGBP5 | IGBP5 | 9.748 | 2.076 | 0 |
| ILMN_1737356 | COL12A1 | COL12A1 | 9.342 | 2.264 | 0 |
| ILMN_2145516 | TMEM173 | TMEM173 | 9.246 | 2.264 | 0 |
| ILMN_1811972 | MYCBP2 | MYCBP2 | 9.226 | 2.024 | 0 |
| ILMN_1678707 | TAF15 | TAF15 | 9.141 | 2.081 | 0 |
| ILMN_1756541 | SEMA3A | SEMA3A | 9.018 | 2.024 | 0 |
| ILMN_1753196 | PTTC1 | PTTC1 | 8.995 | 2.523 | 0 |
| ILMN_1670323 | EN000 | EN000 | 8.897 | 2.068 | 0 |
| ILMN_1765701 | LOC599942 | LOC599942 | 8.74 | 2.077 | 0 |
| ILMN_2400759 | CPVL | CPVL | 8.644 | 2.023 | 0 |
| ILMN_1661366 | PGAM1 | PGAM1 | 8.606 | 2.736 | 0 |
| ILMN_1740233 | UGT1A10 | UGT1A10 | 8.476 | 2.096 | 0 |
| ILMN_1676358 | RAEB | RAEB | 8.265 | 2.493 | 0 |
| ILMN_2321153 | MUC4 | MUC4 | 8.15 | 2.477 | 0 |
| ILMN_3247578 | FAT1 | FAT1 | 8.034 | 2.08 | 0 |
| ILMN_2419115 | ATG4B | ATG4B | 7.981 | 2.191 | 0 |
| ILMN_1754795 | FAT1 | FAT1 | 7.879 | 3.311 | 0 |
| ILMN_1678757 | B2RN1 | B2RN1 | 7.775 | 3.991 | 0 |
| ILMN_1695917 | C5orf15 | C5orf15 | 7.679 | 2.148 | 0 |
| ILMN_2395389 | PSMC4 | PSMC4 | 7.197 | 2.627 | 0 |
| ILMN_212982 | IGBP5 | IGBP5 | 7.174 | 4.242 | 0 |
| ILMN_1676763 | PIP5L | PIP5L | 7.021 | 2.131 | 0 |
| ILMN_2109708 | EGF1 | EGF1 | 6.793 | 2.086 | 0 |
| ILMN_1795778 | P4HA2 | P4HA2 | 6.646 | 2.211 | 0 |
| ILMN_2055610 | ANXA8 | ANXA8 | 6.489 | 2.124 | 0 |
| ILMN_1691563 | GAGE12I | GAGE12I | 6.241 | 2.119 | 0 |
| ILMN_1704342 | UBE3C | UBE3C | 6.183 | 2.136 | 0 |
| ILMN_1779353 | PI5T | PI5T | 6.17 | 2.483 | 0 |
| ILMN_2326717 | PPIE | PPIE | 6.061 | 2.363 | 0 |
| ILMN_1800131 | LOC652826 | LOC652826 | 6.011 | 2.061 | 0 |
| ILMN_1778180 | TXND5C | TXND5C | 5.947 | 2 | 0 |
| ILMN_2332105 | WRN1P1 | WRN1P1 | 5.922 | 2.222 | 0 |
| ILMN_1687887 | PSMC4 | PSMC4 | 5.851 | 2.251 | 0 |
| ILMN_1685798 | MAGEA6 | MAGEA6 | 5.832 | 2.07 | 0 |
| ILMN_1744765 | KRT4 | KRT4 | 5.788 | 3.158 | 0 |
| ILMN_3308295 | MIR205 | MIR205 | 5.548 | 2.083 | 0 |
| ILMN_3204734 | LOC100134648 | LOC100134648 | 5.337 | 2.551 | 0 |
| ILMN_1766762 | DYNLRB1 | DYNLRB1 | 5.207 | 2.955 | 0 |
| ILMN_1732074 | LOC482120 | LOC482120 | 5.099 | 2.925 | 0 |
| ILMN_2261076 | NEDD9 | NEDD9 | 5.097 | 2.074 | 0 |
| ILMN_1681301 | AIM2 | AIM2 | 5.083 | 2.042 | 0 |
| ILMN_2371169 | ZFY | ZFY | 5.063 | 2.451 | 0 |
| ILMN_2174127 | DCBLD2 | DCBLD2 | 5.038 | 2.605 | 0 |
| ILMN_1696187 | PYGL | PYGL | 5.02 | 2.216 | 0 |
| ILMN_1690259 | RAE1 | RAE1 | 4.98 | 2.121 | 0 |
| ILMN_1680246 | MAT2B | MAT2B | 4.961 | 3.137 | 0 |
| ILMN_1798454 | MAD2L1BP | MAD2L1BP | 4.925 | 2.136 | 0 |
| ILMN_1717102 | CLEC2D | CLEC2D | 4.921 | 2.116 | 0 |
| ILMN_1753449 | CST1 | CST1 | 4.802 | 2.783 | 0 |
| ILMN_1746465 | FJX1 | FJX1 | 4.758 | 2.225 | 0 |
| ILMN_1715175 | MET | MET | 4.688 | 2.751 | 0 |
| ILMN_1795542 | MLPH | MLPH | 4.626 | 2.108 | 0 |
| ILMN_1703108 | UBE2G6 | UBE2G6 | 4.598 | 2.721 | 0 |
| ILMN_2129572 | F3 | F3 | 4.593 | 2.65 | 0 |
| ILMN_1660345 | NGRN | NGRN | 4.578 | 2.387 | 0 |
| ILMN_1658053 | DYNLRB1 | DYNLRB1 | 4.504 | 3.005 | 0 |
| ILMN_2150856 | SERPINB2 | SERPINB2 | 4.471 | 2.41 | 0 |
| ILMN_1664543 | ITIH3 | ITIH3 | 4.47 | 2.218 | 0 |
| ILMN_1766500 | FOXA1 | FOXA1 | 4.469 | 2.072 | 0 |
| ILMN_1829845 | HS5.53301 | HS5.53301 | 4.408 | 3.363 | 0 |
| ILMN_3231944 | LOC100130516 | LOC100130516 | 4.399 | 6.137 | 0 |

(continued on next page)
In Table 1 the resulting list of the 85 most differentially regulated probes is shown. To identify relevant shared biological functions associated with the identified 85 most differentially regulated transcripts, Gene Ontology (GO) term enrichment analysis was done using DAVID with the GOTERM_BP_2 annotation (Table 2).

### Discussion

We describe the dataset from the transcriptome analysis comparing wild type and β-catenin deficient BxPC-3 cells. In this analysis 85 transcripts were identified to be the most differentially regulated between the two groups. GO term enrichment analysis of the transcripts identified “cell adhesion” as the GO term that was most significantly enriched for. These results together with the rest the data from the previous published article [1] points towards a central role of β-catenin in enabling cell-cell contacts in BxPC3 cells.

### References

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### Table 2

| Category: GOTERM_BP_2 | Term | Count | % Genes/transcripts | Fold enrichment | Bonferroni |
|------------------------|------|-------|---------------------|-----------------|-----------|
| GO:0007155 - cell adhesion | DCBLD2, LGALS3BP, FAT1, NEDD9, COL12A1, SCARB1, MFG8, ZYX, MUC4 | 9 | 1.4 | 3.26 | 0.46 |
| GO:0008037 - cell recognition | SCARB1, MFG8, SEMA3A | 3 | 0.5 | 13.83 | 0.90 |
| GO:0004008 - regulation of growth | DCBLD2, CDKN1A, NEDD9, SEMA3A, IGBP5 | 5 | 0.8 | 3.72 | 0.99 |
| GO:00065008 - regulation of biological quality | DCBLD2, UGT1A10, CDKN1A, ANXA8, PYGL, TXNDC5, F3, FOXA1, MT2A, SCARB1, SEMA3A | 11 | 1.8 | 1.90 | 1.00 |
| GO:0006950 - response to stress | DCBLD2, UGT1A10, CDKN1A, ANXA8, SEMA173, LGALS3BP, ANXAR, F3, WRNIP1, GAGE12I, SERPIN12, SCARB1, PTG1 | 12 | 1.9 | 1.81 | 1.00 |
| GO:0006905 - response to external stimulus | DCBLD2, UGT1A10, CDKN1A, ANXA8, F3, SERPIN2, SCARB1, SEMA3A | 8 | 1.3 | 2.22 | 1.00 |
| GO:0042445 - hormone metabolic process | UGT1A10, FOXA1, SCARB1 | 3 | 0.5 | 7.18 | 1.00 |
| GO:00022402 - cell cycle process | DCBLD2, CDKN1A, PSMC4, NEDD9, ANLN, PTG1, LOC552826 | 6 | 1.0 | 2.69 | 1.00 |
| GO:0045926 - negative regulation of growth | DCBLD2, CDKN1A, SEMA3A | 3 | 0.5 | 6.91 | 1.00 |
| GO:0032879 - regulation of localization | SCARB1, MFG8, SEMA3A, IGBP5, MYCBP2 | 6 | 1.0 | 2.49 | 1.00 |
| GO:0044419 - interspecies interaction between organisms | SCARB1, MFG8, ZYX | 4 | 0.6 | 3.58 | 1.00 |