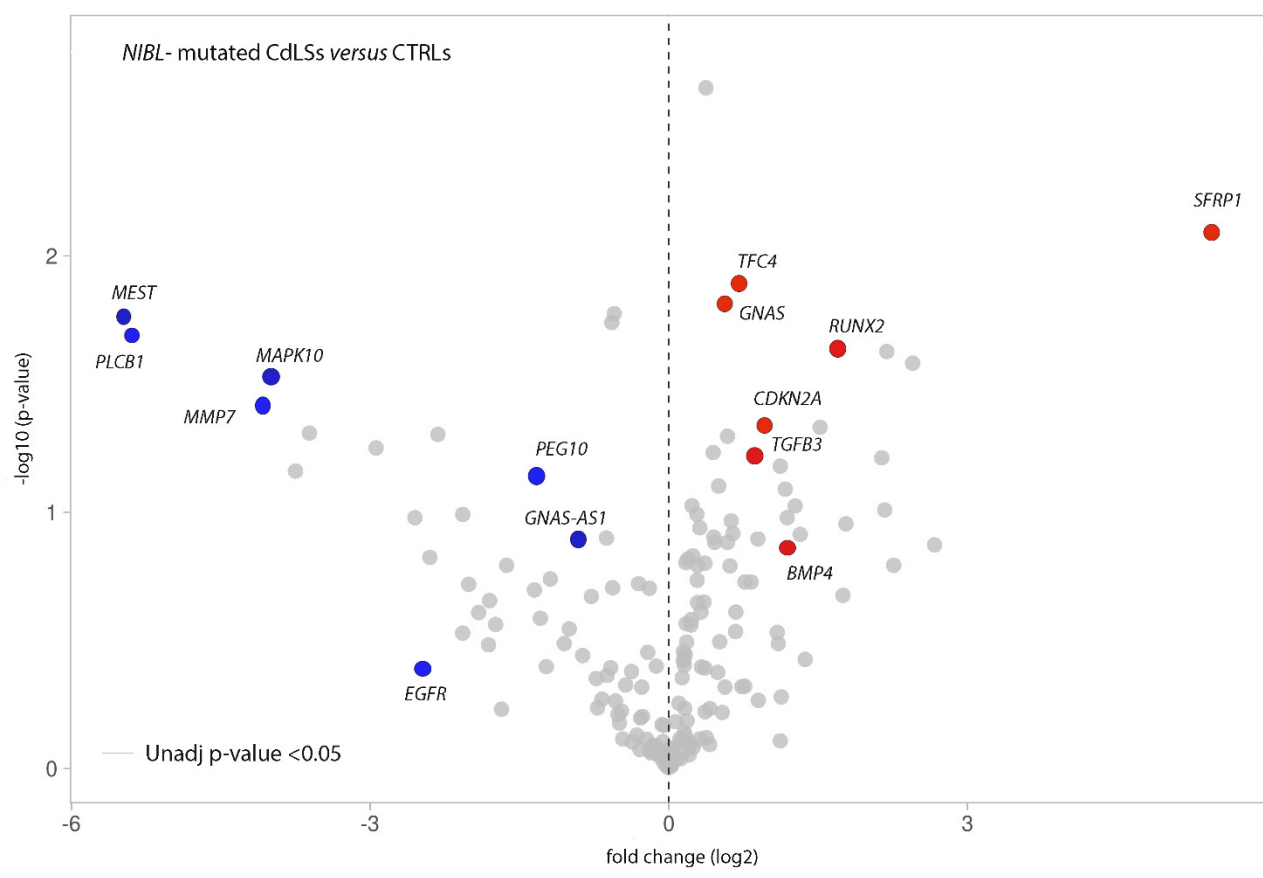
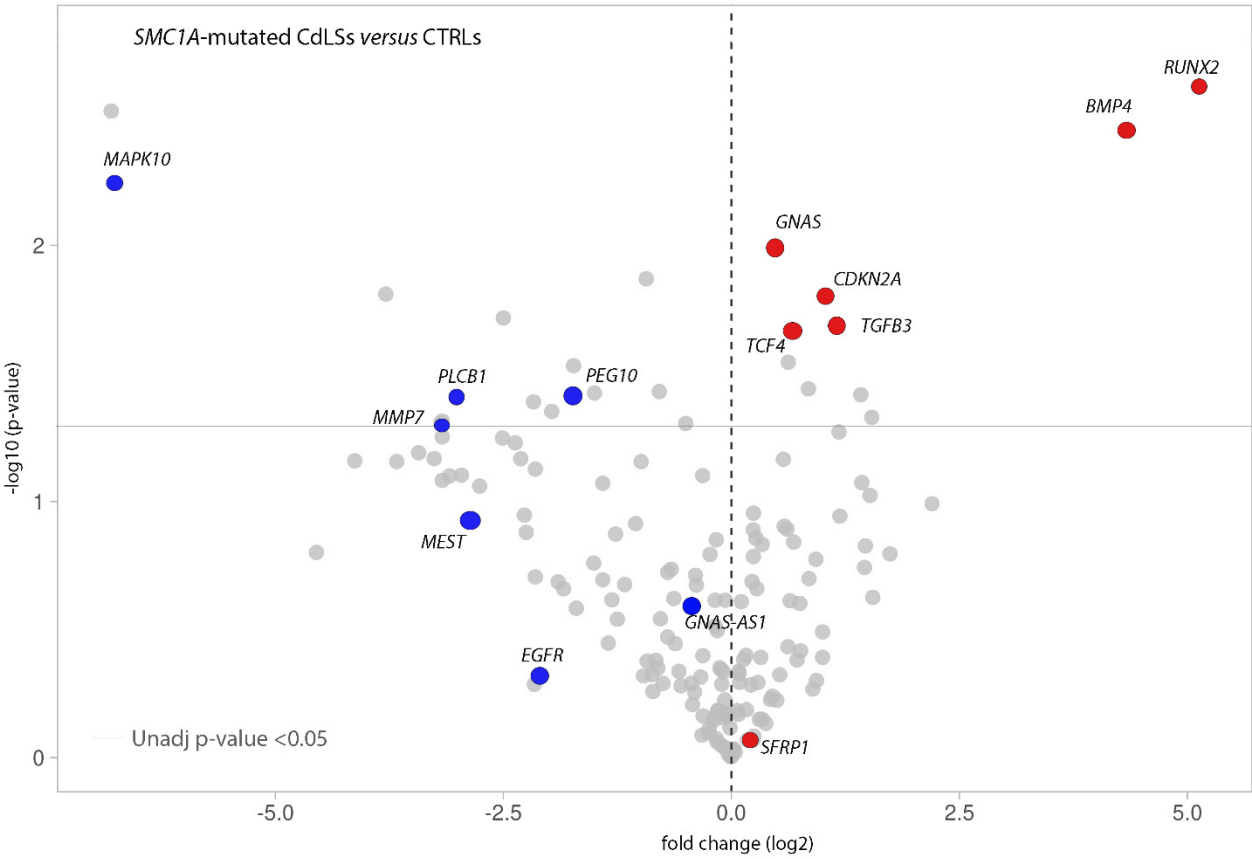


a



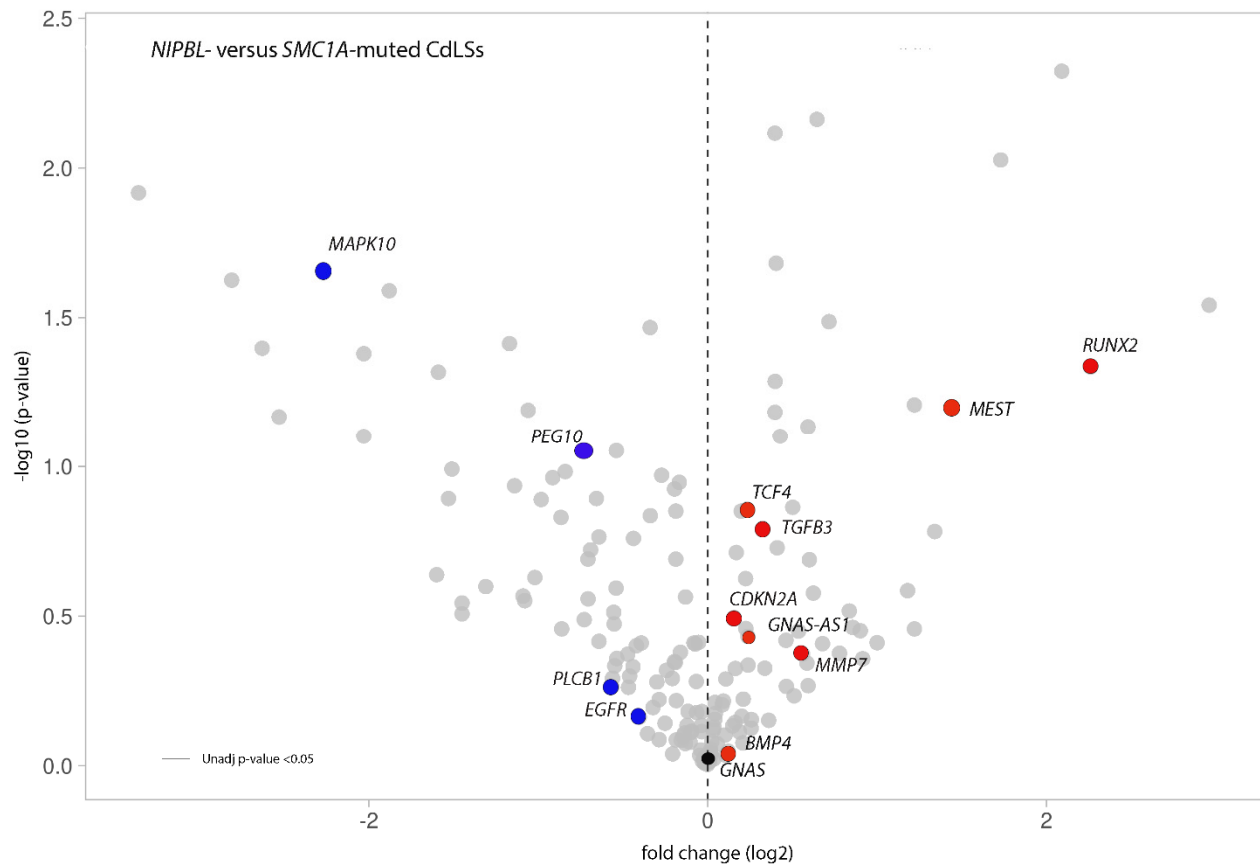
| GENE    | Accession   | Log2 fold change | P-value | BH p-value | Pathway annotation  |
|---------|-------------|------------------|---------|------------|---|
| CUL1    | NM_003592.2 | 0.373            | 0.00221 | 0.375      | KEGG WNT Annotation   |
| SFRP1   | NM_003012.3 | 5.45             | 0.00807 | 0.402      | Canonical Wnt Pathway, KEGG WNT Annotation, WNT Signaling Negative Regulation                             |
| TCF4    | NM_003199.1 | 0.712            | 0.0128  | 0.402      | Transcription Factors   |
| GNAS    | NM_080425.1 | 0.573            | 0.0153  | 0.402      |   |
| BIRC5   | NM_001168.2 | -0.548           | 0.0168  | 0.402      | Cell Cycle  |
| MEST    | NM_177525.1 | -5.47            | 0.0172  | 0.402      |   |
| TBL1XR1 | NM_024665.4 | -0.573           | 0.0182  | 0.402      | KEGG WNT Annotation   |
| PLCB1   | NM_182734.1 | -5.4             | 0.0204  | 0.402      | KEGG WNT Annotation   |
| RUNX2   | NM_004348.3 | 1.69             | 0.0231  | 0.402      | Development & Differentiation, Transcription Factors  |
| TLE1    | NM_005077.3 | 2.19             | 0.0236  | 0.402      | WNT Signaling Negative Regulation   |
| AXIN2   | NM_004655.3 | 2.45             | 0.0262  | 0.405      | Canonical Wnt Pathway, KEGG WNT Annotation, WNT Signaling Negative Regulation, WNT Signaling Target Genes |
| MAPK10  | NM_002753.2 | -4               | 0.0295  | 0.418      | KEGG WNT Annotation   |
| MMP7    | NM_002423.3 | -4.08            | 0.0382  | 0.474      | Calcium Binding and Signaling, KEGG WNT Annotation, Proteolysis, WNT Signaling Target Genes               |
| CDKN2A  | NM_000077.3 | 0.96             | 0.0455  | 0.474      | Cell Cycle, Development & Differentiation, Transcription Factors  |
| IRS1    | NM_005544.2 | 1.52             | 0.0466  | 0.474      | Migration   |
| FZD5    | NM_003468.2 | -3.61            | 0.0491  | 0.474      | Canonical Wnt Pathway, KEGG WNT Annotation  |
| PTGS2   | NM_000963.1 | -2.32            | 0.0497  | 0.474      | Calcium Binding and Signaling, Cell Cycle   |

b



| GENE    | Accession      | Log2 fold change | P-value | BH p-value | Pathway annotation   |
|---------|----------------|------------------|---------|------------|--|
| RUNX2   | NM_004348.3    | 5.12             | 0.0024  | 0.209      | Development & Differentiation, Transcription Factors   |
| PTGS2   | NM_000963.1    | -6.8             | 0.00299 | 0.209      | Calcium Binding and Signaling, Cell Cycle  |
| BMP4    | NM_001202.3    | 4.33             | 0.00356 | 0.209      | Development & Differentiation  |
| MAPK10  | NM_002753.2    | -6.75            | 0.00571 | 0.251      | KEGG WNT Annotation  |
| GNAS    | NM_080425.1    | 0.476            | 0.0102  | 0.342      |  |
| PLAUR   | NM_001005376.1 | -0.934           | 0.0135  | 0.342      | Proteolysis  |
| KREMEN1 | NM_001039570.1 | -3.79            | 0.0155  | 0.342      | WNT Signaling Negative Regulation  |
| CDKN2A  | NM_000077.3    | 1.03             | 0.0158  | 0.342      | Cell Cycle, Development & Differentiation, Transcription Factors   |
| CXCR4   | NM_003467.2    | -2.5             | 0.0192  | 0.342      | EMTMetastasis  |
| TGFB3   | NM_003239.2    | 1.16             | 0.0205  | 0.342      | Development & Differentiation  |
| TCF4    | NM_003199.1    | 0.683            | 0.0218  | 0.342      | Transcription Factors  |
| NLK     | NM_016231.2    | 0.624            | 0.0286  | 0.342      | KEGG WNT Annotation, WNT Signaling Negative Regulation   |
| H19     | NR_002196.1    | -1.73            | 0.0295  | 0.342      |  |
| FZD3    | NM_017412.2    | 0.845            | 0.0363  | 0.342      | Canonical Wnt Pathway, KEGG WNT Annotation   |
| MAPK8   | NM_002750.2    | -0.79            | 0.0372  | 0.342      | KEGG WNT Annotation, Planar Cell Polarity (PCP)  |
| TIMP1   | NM_003254.2    | -1.5             | 0.0377  | 0.342      | EMTMetastasis  |
| FRAT1   | NM_005479.3    | 1.42             | 0.0383  | 0.342      | Canonical Wnt Pathway, KEGG WNT Annotation   |
| PEG10   | NM_001040152.1 | -1.73            | 0.0384  | 0.342      |  |
| PLCB1   | NM_182734.1    | -3.02            | 0.0392  | 0.342      | KEGG WNT Annotation  |
| FZD6    | NM_003506.2    | -2.17            | 0.0408  | 0.342      | Canonical Wnt Pathway, KEGG WNT Annotation   |
| SOX9    | NM_000346.2    | -1.97            | 0.0445  | 0.342      | Adhesion, Development & Differentiation, Transcription Factors   |
| WNT8B   | NM_003393.2    | 1.54             | 0.0469  | 0.342      | KEGG WNT Annotation  |
| MMP7    | NM_002423.3    | -3.17            | 0.0485  | 0.342      | Calcium Binding and Signaling, KEGG WNT Annotation, Proteolysis, WNT Signaling Target Genes                      |
| PPARD   | NM_006238.3    | -0.502           | 0.0496  | 0.342      | Development & Differentiation, KEGG WNT Annotation, Migration, Transcription Factors, WNT Signaling Target Genes |
| GDNF    | NM_000514.2    | -3.19            | 0.0496  | 0.342      | Development & Differentiation, Migration   |

c



| GENE    | Accession   | Log2 fold change | P-value | BH p-value | Pathway annotation  |
|---------|-------------|------------------|---------|------------|---|
| FZD5    | NM_003468.2 | 2.09             | 0.00475 | 0.416      | Canonical Wnt Pathway, KEGG WNT Annotation                                |
| NFATC1  | NM_172389.1 | 0.645            | 0.00688 | 0.416      | Calcium Binding and Signaling, KEGG WNT Annotation                        |
| TBL1XR1 | NM_024665.4 | 0.397            | 0.00765 | 0.416      | KEGG WNT Annotation   |
| PRKCA   | NM_002737.2 | 1.73             | 0.0094  | 0.416      | KEGG WNT Annotation   |
| NRCAM   | NM_005010.4 | -3.36            | 0.0121  | 0.427      | Adhesion, Development & Differentiation, Migration                        |
| EP300   | NM_001429.2 | 0.404            | 0.0208  | 0.493      | Canonical Wnt Pathway, KEGG WNT Annotation                                |
| MAPK10  | NM_002753.2 | -2.27            | 0.0221  | 0.493      | KEGG WNT Annotation   |
| T       | NM_003181.2 | -2.81            | 0.0237  | 0.493      | Development & Differentiation, Transcription Factors                      |
| FGF7    | NM_002009.3 | -1.88            | 0.0257  | 0.493      | Migration   |
| WNT7B   | NM_058238.1 | 2.96             | 0.0287  | 0.493      | Calcium Binding and Signaling, Canonical Wnt Pathway, KEGG WNT Annotation |
| POU5F1  | NM_002701.4 | 0.716            | 0.0326  | 0.493      | Development & Differentiation, Transcription Factors                      |
| FAM50B  | NM_012135.1 | -0.34            | 0.0341  | 0.493      |   |
| FZD6    | NM_003506.2 | -1.17            | 0.0386  | 0.493      | Canonical Wnt Pathway, KEGG WNT Annotation                                |
| IGF1R   | NM_000875.4 | -2.63            | 0.04    | 0.493      |   |

|       |             |       |        |       |   |
|-------|-------------|-------|--------|-------|---|
| WNT7A | NM_004625.3 | -2.03 | 0.0417 | 0.493 | Calcium Binding and Signaling, Canonical Wnt Pathway, KEGG WNT Annotation |
| RUNX2 | NM_004348.3 | 2.26  | 0.0462 | 0.501 | Development & Differentiation, Transcription Factors                      |
| CDH11 | NM_001797.2 | -1.59 | 0.0481 | 0.501 | EMTMetastasis   |

Figure S2. Three different expression profiles of CdLS samples split by *NIPBL* and *SMC1A* variations evaluated by nCounter Nanostring technology. A) *NIPBL*-mutated CdLSs versus CTRLs. B) *SMC1A*-mutated CdLSs versus CTRLs. C) *NIPBL*-mutated versus *SMC1A* -mutated CdLSs. Volcano plots (Top) and panels (Bottom) of significant DEGs. Upregulated and downregulated genes shared with the main cohort (CdLSs compared to CTRLs) are highlighted by red and blue dots, respectively. Unadjusted p-value <0.05 is indicated by horizontal line.