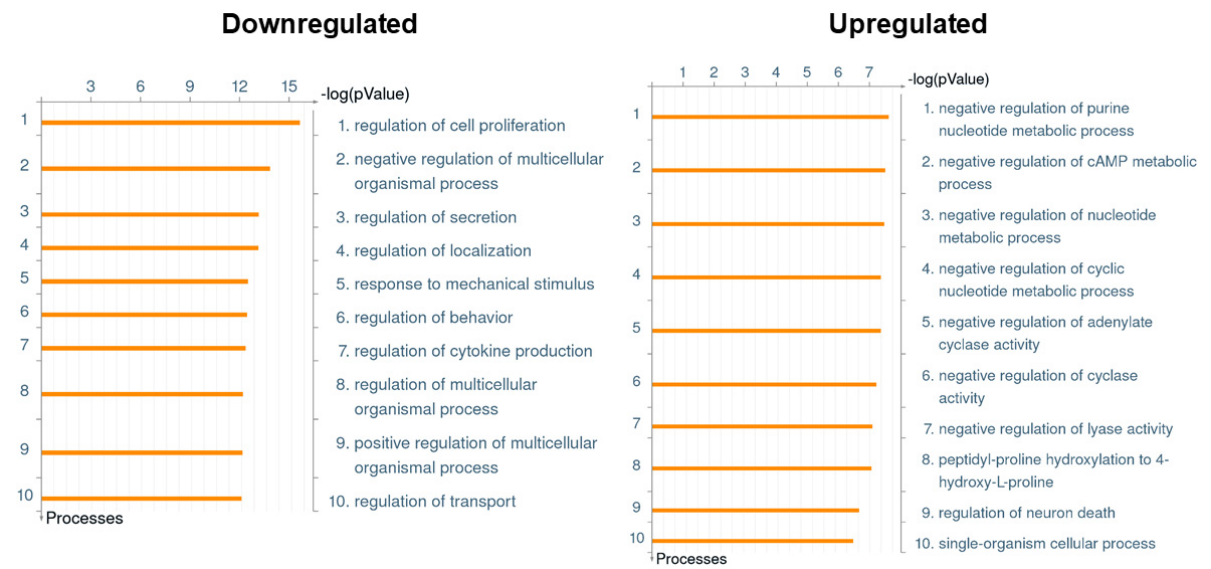


SUPPLEMENTARY MATERIAL

To study the molecular changes observed as a consequence of *TWIST1* silencing compared to control cells, we conducted *in silico* analyses using MetaCore™ software (<http://portal.genego.com/>). This software grouped differentially expressed genes according to gene ontology (Supplementary Figure S1), biological processes (Supplementary Figure S2), and signaling maps (Supplementary Figures S3-S5).

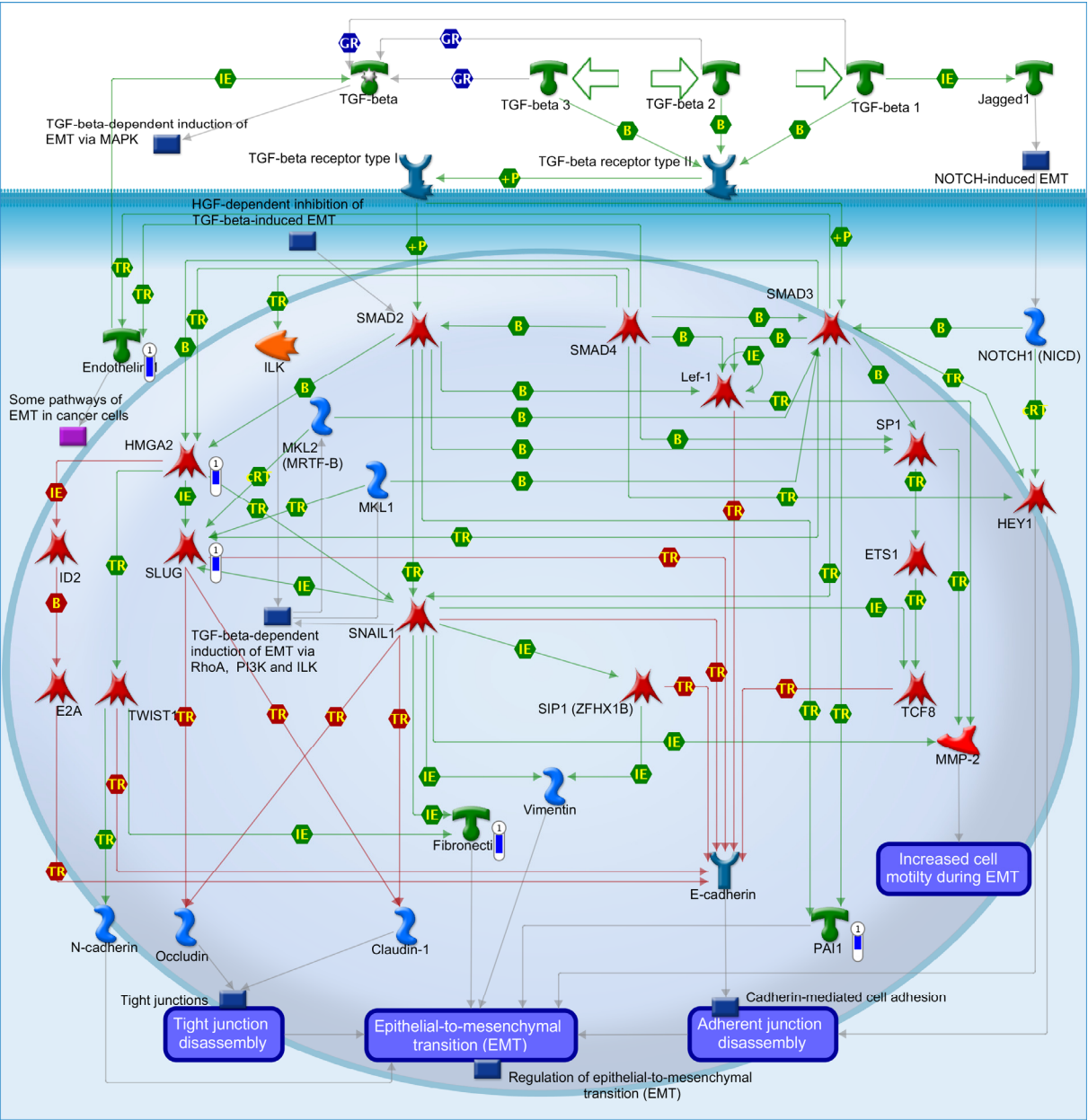


Supplementary Figure S1. Gene ontology of the downregulated and upregulated transcripts as a result of *TWIST1* silencing. The processes are ordered according to the statistical significance of the genes presented in each condition.

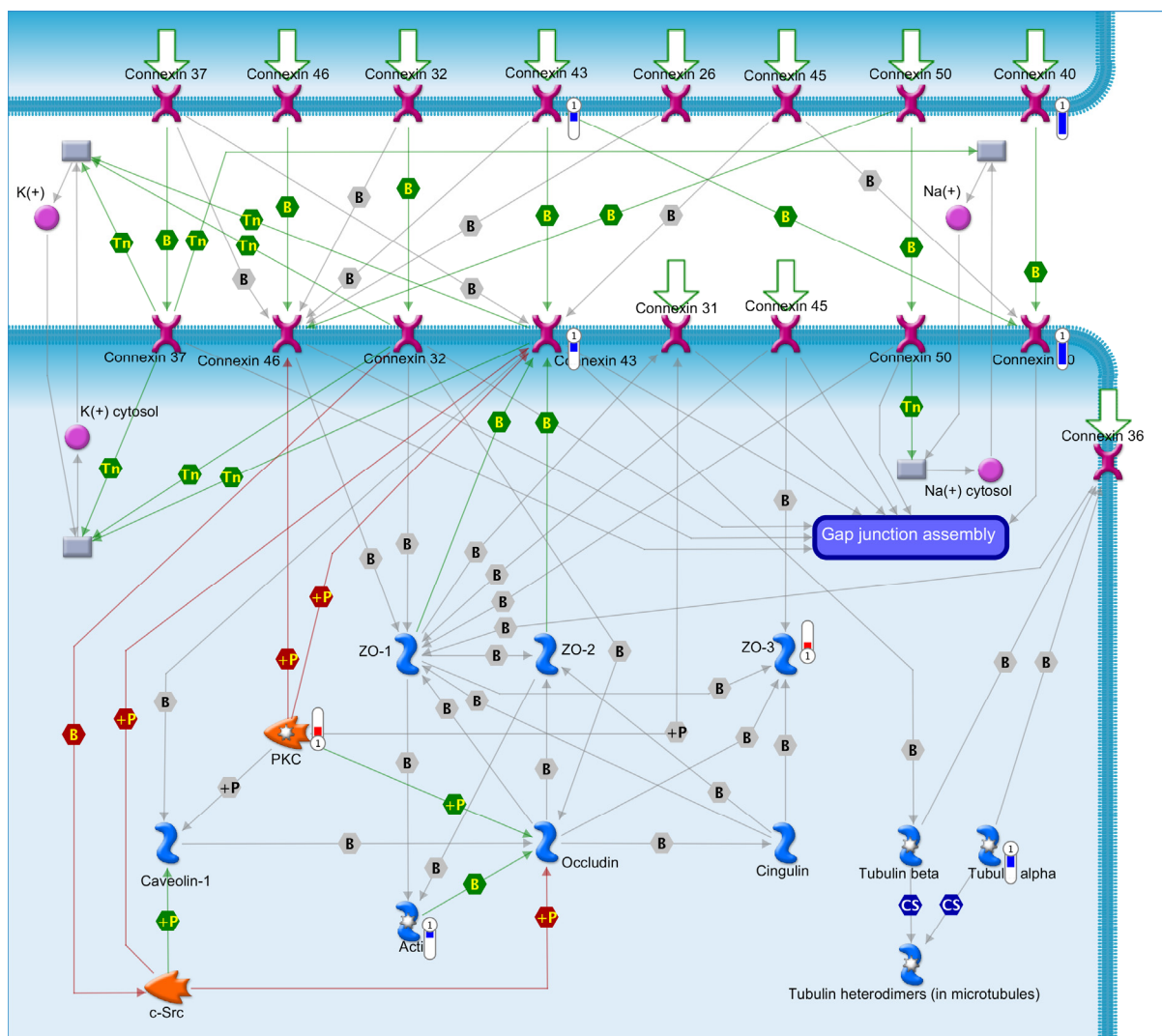


Supplementary Figure S2. Biological processes altered in downregulated and upregulated transcripts as a result of *TWIST1* silencing. The processes are ordered according to the statistical significance of the genes presented in each condition.

A

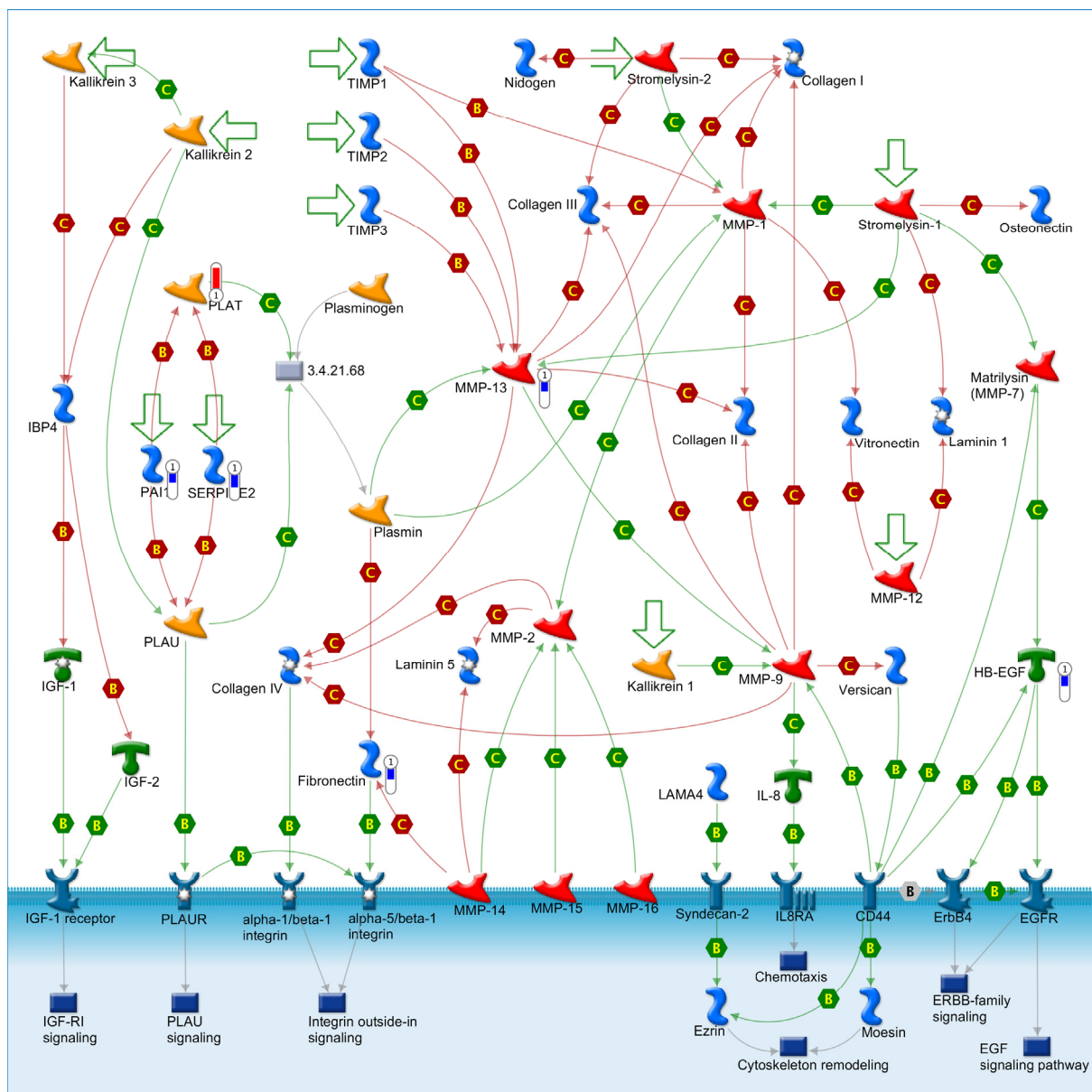


B

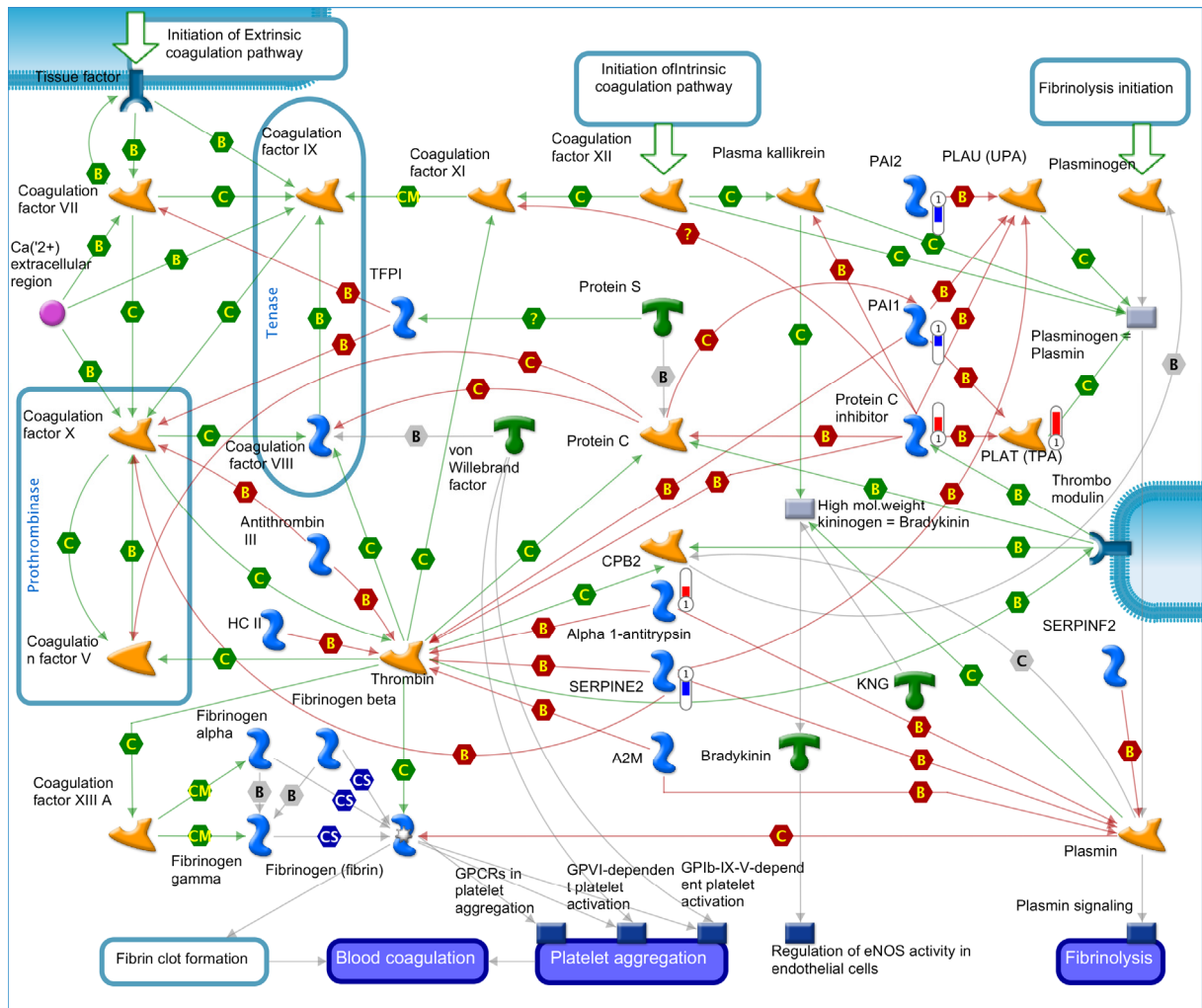


Supplementary Figure S3. “Regulation of Epithelial-Mesenchymal Transition” (A) and “Cell adhesion” (B) were the top scored maps altered as the result of *TWIST1*-silencing based on the enrichment distribution of genes presented in the analyses. The relative gene expression data are visualized on the map by thermometer-like figures in blue (for downregulation) or red (for upregulation).

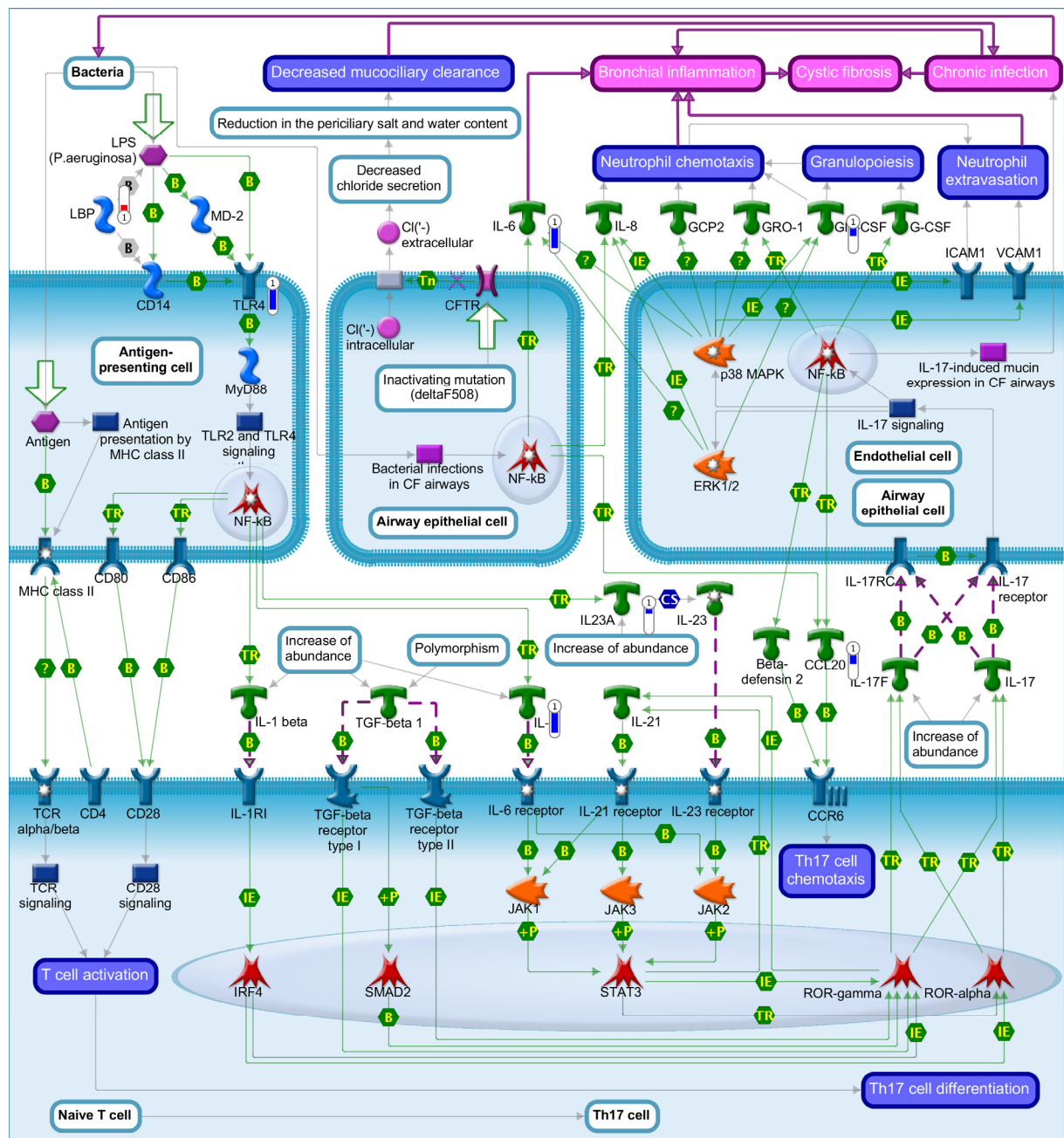
A



B



Supplementary Figure S4. “ECM remodeling” (A) and “Blood coagulation” (B) were the second scored maps altered as the result of *TWIST1* silencing based on the enrichment distribution of genes presented in the analyses. The relative gene expression data are visualized on the map by thermometer-like figures in blue (for downregulation) or red (for upregulation).



Supplementary Figure S5. “Th17-mediated Immune Response” was the third scored map altered as the result of *TWIST1* silencing based on the enrichment distribution of genes presented in the analyses. The relative gene expression data are visualized on the map by thermometer-like figures in blue (for downregulation) or red (for upregulation).

Supplementary Table S1. Primer sequences of the investigated genes.

Primer	Sequence
<i>ACTB</i> forward	5'-TTC CTT CCT GGG CAT GGA GTC-3'
<i>ACTB</i> reverse	5'-AGA CAG CAC TGT GTT GGC GTA-3'
<i>GAPDH</i> forward	5'-ACC CAC TCC TCC ACC TTT GA-3'
<i>GAPDH</i> reverse	5'-CTG TTG CTG TAG CCA AAT TCG T-3'
<i>NF-κB(RELA)</i> forward	5'-CTA CGA CCT GAA TGC TGT GC-3'
<i>NF-κB(RELA)</i> reverse	5'-CTG CCA GAG TTT CGG TTC AC-3'
<i>TWIST1</i> forward	5'-GGC ACC ATC CTC ACA CCT CT -3'
<i>TWIST1</i> reverse	5'-TGG CTG ATT GGC ACG ACC T-3'
<i>SLUG</i> forward	5'-AAG CAT TTC AAC GCC TCC AAA-3'
<i>SLUG</i> reverse	5'-GGA TCT CTG GTT GTG GTA TGA CA-3'
<i>SIP1(ZEB2)</i> forward	5'-AAA CAA GCC AAT CCC AGG AG-3'
<i>SIP1(ZEB2)</i> reverse	5'-GCA CAC TAG CTG GAC TCG TCT C-3'
<i>HBEGF</i> forward	5'- GCT GTG GTG CTG TCA TCT GT -3'
<i>HBEGF</i> reverse	5'- CAT GCC CAA CTT CAC TTT CTC -3'
<i>IL6</i> forward	5'- GGT ACA TCC TCG ACG GCA TC -3'
<i>IL6</i> reverse	5'- GCC TCT TTG CTG CTT TCA CAC -3'
<i>THBS1</i> forward	5'- AGA CTC CGC ATC GCA AAG G -3'
<i>THBS1</i> reverse	5'- GCA GCC TTT GTT CCT GAG GA -3'
<i>TUBA3C</i> forward	5'- CGC ACC ATC CAG TTT GTA GA -3'
<i>TUBA3C</i> reverse	5'- GTG TTG CTC AGC ATG CAC AC -3'
<i>PAI1</i> forward	5'- CAA GAG CCT CTC CAC GTC G -3'
<i>PAI1</i> reverse	5'- CGG ACC ACA AAG AGG AAG GG -3'
<i>PAI2</i> forward	5'- CTC AGA ACC CCA GGC AGT AG -3'
<i>PAI2</i> reverse	5'- ACA GCA TTC ACC AGG ACC AT -3'
<i>ZO3</i> forward	5'- GAC AGG ACA GCA TGC GAA CC -3'
<i>ZO3</i> reverse	5'- CCC CAG TCA TAG CCG TCT TC -3'
<i>PLAT</i> forward	5'- TCA CCG ACA ACA TGC TGT G -3'
<i>PLAT</i> reverse	5'- AGC TGA TGA TGC CCA CCA AA -3'
<i>SERPINA1</i> forward	5'- AAG GTC TTC AGC AAT GGG GC -3'
<i>SERPINA1</i> reverse	5'- TTC TCG TCG ATG GTC AGC AC -3'
<i>KRT4</i> forward	5'- GAC AGC GTG GAG GAC TTC AA -3'
<i>KRT4</i> reverse	5'- GCC TCC AAC TCC ACC TTG TT -3'
<i>CLDN8</i> forward	5'- CGT GAG GCA GGC TAA CAT CA -3'
<i>CLDN8</i> reverse	5'- AGC AGC ACA CAT CAG TCC TC -3'
<i>IP3R1</i> forward	5'- CTG GCC AGC TGT CGG AAT TA -3'
<i>IP3R1</i> reverse	5'- GCT GGT TGT TGT GGG TTG AC -3'
<i>PKCA</i> forward	5'- AGA GAG CAT GCC TTC TTC CG -3'
<i>PKCA</i> reverse	5'- GGC TGT CCT CGT GTG AAG AA -3'
<i>IL8</i> forward	5'- GTG CAG AGG GTT GTG GAG AAG -3'
<i>IL8</i> reverse	5'- CCC TAC AAC AGA CCC ACA CAA -3'
<i>IL23A</i> forward	5'- AGA AGC TCT GCA CAC TGG C -3'
<i>IL23A</i> reverse	5'- TCA CAG CCA TCT CCA CAC TG -3'
<i>ACT1</i> forward	5'- CAT CCC TGT GCT CTT CCC AA -3'
<i>ACT1</i> reverse	5'- TTC TTG GGC CAG CTG TAG AC -3'

<i>CCL20</i> forward	5'- ACA CAG ACC GTA TTC TTC ATC CT -3'
<i>CCL20</i> reverse	5'- TTG CGC ACA CAG ACA ACT TT -3'
<i>IL17RC</i> forward	5'- CGA TGA CTT GGG AGC GCT AT -3'
<i>IL17RC</i> reverse	5'- AGC GGC AAA GAG TAG GCA G -3'
<i>IL17RA</i> forward	5'- GTA CTG GTT CAT CAC GGG CA -3'
<i>IL17RA</i> reverse	5'- GCA GGC CAT CGG TGT ATT TG -3'
<i>IL17A</i> forward	5'- ACC AAT CCC AAA AGG TCC TC -3'
<i>IL17A</i> reverse	5'- GGG GAC AGA GTT CAT GTG GT -3'
<i>IL17F</i> forward	5'- CCT CCC CCT GGA ATT ACA CT -3'
<i>IL17F</i> reverse	5'- TTC CTT GAG CAT TGA TGC AG -3'
<i>RORC2</i> forward	5'- TGG ACC ACC CCC TGC TGA GAA GG -3'
<i>RORC2</i> reverse	5'- CTT CAA TTT GTG TTC TCA TGA CT -3'