

Supplemental Data

PALS1-dependent modulations of mRNA profiles
in MDCK II cells grown in non-confluent monolayers and
3-dimensional cysts.

by

Klaus Schughart^{1, 2*}, Annika Möller-Kerutt³, Verena Höffken³, Pavel Nedvetsky⁴, Ann-Christin
Groh³, Daniela Anne Braun³, Hermann Pavenstädt³, and Thomas Weide³

¹) Institute of Virology Münster, University of Münster, 48149 Münster, Germany.

²) Department of Microbiology, Immunology and Biochemistry, University of Tennessee
Health Science Center, Memphis, TN 38103, U.S.A.

³) University Hospital of Münster (UKM), Internal Medicine D (MedD), Dept. Molecular
Nephrology, Münster, 48149, Germany

⁴) University Hospital of Münster (UKM), Internal Medicine D (MedD), Dept. Medical Cell
Biology, Münster, 48149, Germany

Corresponding author:

Thomas Weide

University Hospital of Münster (UKM), Internal Medicine D (MedD), Dept. Molecular
Nephrology, Münster, 48149, Germany

Email: weidet@uni-muenster.de

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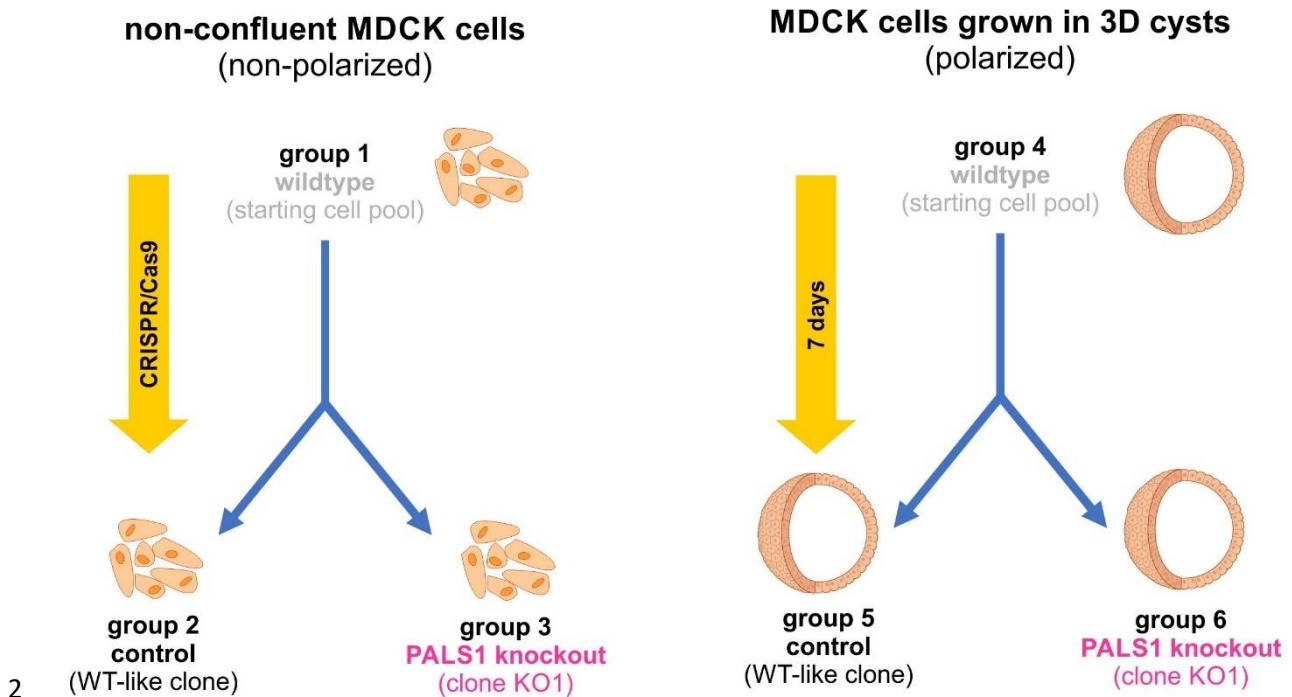
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4

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1 Supplemental Figures



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4 Fig. SF1: Preparation of mRNA samples for transcriptome analyses.

5 A: Scheme of used transcriptomes. Initially the analysis included six groups of transcriptomes samples: The first

6 three groups (1-3) are samples from cells grown under non-confluent conditions (upper panel). *group 1*:

7 transcriptomes derived from the starting pool of non-confluent MDCK II cells (wildtype non-confluent, n=4).

8 *group 2*: Samples derived from a clone that ran through a CRISPR/Cas9 but maintained a wildtype *PALS1* gene

9 (Ctr non-confluent, n=4). *group 3*: samples derived from a *PALS1* knockout clone (KO1 non-confluent, n=4) (Groh

10 et al., 2024). The next are three groups (4-6) are samples derived from cells grown for 7 days in 3D cysts. *group 4*:

11 3D-cyst from the MDCK starting pool (WT-nc, n=4). *group 5*: Samples derived from 3D cysts of the clone that run

12 through a CRISPR/Cas9 but maintained a wildtype *PALS1* gene (Ctr-3D, n=3). *group 6*: Samples derived from 3D

13 cysts of the KO1 clone (KO1 3D, n=3).

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1 **Supplemental Tables (titles and descriptions)**

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3 Table ST1 MDCK transcriptomes of wildtype, PALS1 knockout and the starting MDCK cell pool.

4 File name: ST01_S1_sample_description_030424.xlsx

5 Description of data: List of samples with sample ID from GEO and their description.

6

7 Table ST2A Differential expressed genes (DEGs) of subset A (WT-3D vs WT-nc)

8 File name: ST02A_sbst7_DESeq2_DEG_Ctr_3D_7d_vs_Ctr_2D_nconf_011223

9 Description of data: see name of table

10

11 Table ST2B DEGs of subset B (KO-3D vs KO-nc)

12 File name: ST02B_sbst7_DESeq2_DEG_KO_3D_7d_vs_KO_2D_nconf_011223

13 Description of data: see name of table

14

15 Table ST2C DEGs of subset C (KO-3D vs WT-3D)

16 File name: ST02C_sbst7_DESeq2_DEG_KO_3D_7d_vs_Ctr_3D_7d_011223

17 Description of data: see name of table

18

19 Table ST2D DEGs of subset D (KO-nc vs WT-nc)

20 File name: ST02D_sbst7_DESeq2_DEG_KO_2D_nconf_vs_Ctr_2D_nconf_140824

21 Description of data: see name of table

22

23 Table ST03 Shared DEGs of subset A and subset B

24 File name: ST03_Shared DEGs of Subset A and B

25 Description of data: Analyses of common and different DEGs of total, up-, and downregulated DEGs of
26 subset A and B, including TOP 20 up- and downregulated DEGS.

27

28 Table ST04 Gene ontology biological processes (GO-BP) enrichment analysis for upregulated DEGs
29 of subset A

30 File name:

31 ST04_UP_EnrichR_GO_Biological_Process_2021_sbst7_Ctr_3D_7d_vs_Ctr_2D_nconf_191223

32 Description of data: see name of table

33

34 Table ST05 GO-BP enrichment analysis for upregulated DEGs of subset B

35 File name:

36 ST05_UP_EnrichR_GO_Biological_Process_2021_sbst7_KO_3D_7d_vs_KO_2D_nconf_191223

37 Description of data: see name of table

38

39 Table ST06 REACTOME analysis for upregulated DEGs of subset A

40 File name: ST06_UP_EnrichR_Reactome_2016_sbst7_Ctr_3D_7d_vs_Ctr_2D_nconf_191223

41 Description of data: see name of table

42

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1
2 Table ST07 REACTOME analysis for upregulated DEGs of subset B
3 File name: ST07_UP_EnrichR_Reactome_2016_sbst7_KO_3D_7d_vs_KO_2D_nconf_191223
4 Description of data: see name of table
5
6 Table ST08 KEGG analysis for upregulated DEGs of subset A
7 ST08_UP_EnrichR_KEGG_2021_Human_sbst7_Ctr_3D_7d_vs_Ctr_2D_nconf_191223
8 Description of data: see name of table
9 Table ST09 KEGG analysis for upregulated DEGs of subset B
10 ST09_UP_EnrichR_KEGG_2021_Human_sbst7_KO_3D_7d_vs_KO_2D_nconf_191223
11 Description of data: see name of table
12
13 Table ST10 GO-BP enrichment analysis for downregulated DEGS of subset A
14 File name:
15 ST10_DN_EnrichR_GO_Biological_Process_2021_sbst7_Ctr_3D_7d_vs_Ctr_2D_nconf_191223
16 Description of data: see name of table
17
18 Table ST11 GO-BP enrichment analysis for downregulated DEGs of subset B
19 File name:
20 ST11_DN_EnrichR_GO_Biological_Process_2021_sbst7_KO_3D_7d_vs_KO_2D_nconf_191223
21 Description of data: see name of table
22
23 Table ST12 REACTOME analysis for downregulated DEGs of subset A
24 File name: ST12_DN_EnrichR_Reactome_2016_sbst7_Ctr_3D_7d_vs_Ctr_2D_nconf_191223
25 Description of data: see name of table
26
27 Table ST13 REACTOME analysis for downregulated DEGs of subset B
28 File name: ST13_DN_EnrichR_Reactome_2016_sbst7_KO_3D_7d_vs_KO_2D_nconf_191223
29 Description of data: see name of table
30
31 Table ST14 KEGG analysis for downregulated DEGs of subset A
32 ST14_DN_EnrichR_KEGG_2021_Human_sbst7_Ctr_3D_7d_vs_Ctr_nconf_191223
33 Description of data: see name of table
34
35 Table ST15 KEGG analysis for downregulated DEGs of subset B
36 File name: ST15_DN_EnrichR_KEGG_2021_Human_sbst7_KO_3D_7d_vs_KO_2D_nconf_191223
37 ST15_DN_EnrichR_KEGG_2021_Human_sbst7_KO_3D_7d_vs_KO_2D_nconf_191223
38 Description of data: see name of table
39
40 Table ST16 Shared DEGs of subset C and subset D
41 File name: ST16_Shared_DEGs_of_subset_C_and_D
42 Description of data: Analyses of common and different DEGs of total, up-, and downregulated DEGs of
43 subset C and D, including TOP 20 up- and downregulated DEGS.
44

1 Table ST17 GO-BP enrichment analysis for upregulated DEGs of subset C
2 File name: ST17_UP_EnrichR_GO_Biological_Process_2021_sbst7_KO_3D_7d_vs_Ctr_3D_7d_191223
3 Description of data: see name of table
4
5 Table ST18 GO-BP enrichment analysis for downregulated DEGs of subset C
6 File name: ST18_DN_EnrichR_GO_Biological_Process_2021_sbst7_KO_3D_7d_vs_Ctr_3D_7d_191223
7 Description of data: see name of table
8
9 Table ST19 GO-BP enrichment analysis for upregulated DEGs of subset D
10 File name:
11 ST19_UP_EnrichR_GO_Biological_Process_2021_sbst7_KO_2D_nconf_vs_Ctr_2D_nconf_140824.txt
12 Description of data: see name of table
13
14 Table ST20 GO-BP enrichment analysis for downregulated DEGs of subset D
15 File name:
16 ST20_DN_EnrichR_GO_Biological_Process_2021_sbst7_KO_2D_nconf_vs_Ctr_2D_nconf_140824.txt
17 Description of data: see name of table
18
19 Table ST21 REACTOME analysis for upregulated DEGs of subset C
20 File name: ST21_UP_EnrichR_Reactome_2016_sbst7_KO_3D_7d_vs_Ctr_3D_7d_191223
21 Description of data: see name of table
22
23 Table ST22 REACTOME analysis for downregulated DEGs of subset C
24 File name: ST22_DN_EnrichR_Reactome_2016_sbst7_KO_3D_7d_vs_Ctr_3D_7d_191223
25 Description of data: see name of table
26
27 Table ST23 REACTOME analysis for upregulated DEGs of subset D
28 File name: ST23_UP_EnrichR_Reactome_2016_sbst7_KO_2D_nconf_vs_Ctr_2D_nconf_140824.txt
29 Description of data: see name of table
30
31 Table ST24 REACTOME analysis for downregulated DEGs of subset D
32 File name: ST24_DN_EnrichR_Reactome_2016_sbst7_KO_2D_nconf_vs_Ctr_2D_nconf_140824.txt
33 Description of data: see name of table
34
35 Table ST25 KEGG analysis for upregulated DEGs of subset C
36 File name: ST25_UP_EnrichR_KEGG_2021_Human_sbst7_KO_3D_7d_vs_Ctr_3D_7d_191223
37 Description of data: see name of table
38
39 Table ST26 KEGG analysis for upregulated DEGs of subset C
40 File name: ST26_DN_EnrichR_KEGG_2021_Human_sbst7_KO_3D_7d_vs_Ctr_3D_7d_191223
41 Description of data: see name of table
42
43 Table ST27 KEGG analysis for upregulated DEGs of subset D
44 File name:
45 ST27_UP_EnrichR_KEGG_2021_Human_sbst7_KO_2D_nconf_vs_Ctr_2D_nconf_140824.txt
46 Description of data: see name of table

1 Table ST28 KEGG analysis for upregulated DEGs of subset D
2 File name:
3 ST27_UP_EnrichR_KEGG_2021_Human_sbst7_KO_2D_nconf_vs_Ctr_2D_nconf_140824.txt
4 Description of data: see name of table
5
6 Table ST29 Gene lists: cell junction, cell polarity, and cell-ECM interaction
7 File name:
8 ST27_UP_EnrichR_KEGG_2021_Human_sbst7_KO_2D_nconf_vs_Ctr_2D_nconf_140824.txt
9 Description of data: Basis for the three gene lists are gene included by known GO-terms.
10 For the gene list cell junctions, we used the following GO terms: GO:0043296 (apical junction complex,
11 Cellular Component), GO:0070160 (tight junction, Cellular Component), and GO:0005912 (adherens
12 junction, Cellular Component). The gene list of cell polarity genes based on the GO-term GO:0007163
13 (establishment or maintenance of cell polarity, Biological Process). For cell substrate interactions, cell
14 adhesion or cell adhesion we used GO terms GO:0031589 (cell-substrate adhesion, Biological Process),
15 GO:0007160 (cell-matrix adhesion, Biological Process) and the GO:0033627 (cell adhesion mediated
16 by integrin, Biological Process).
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