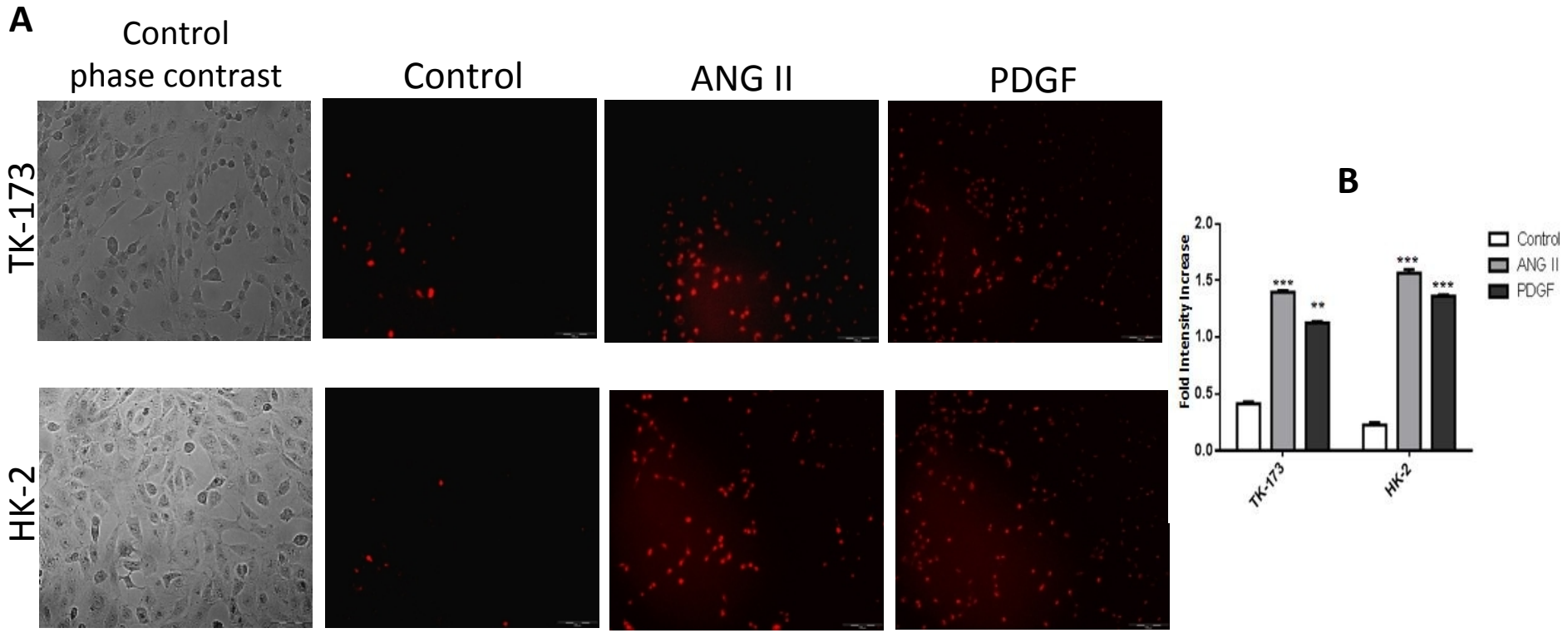
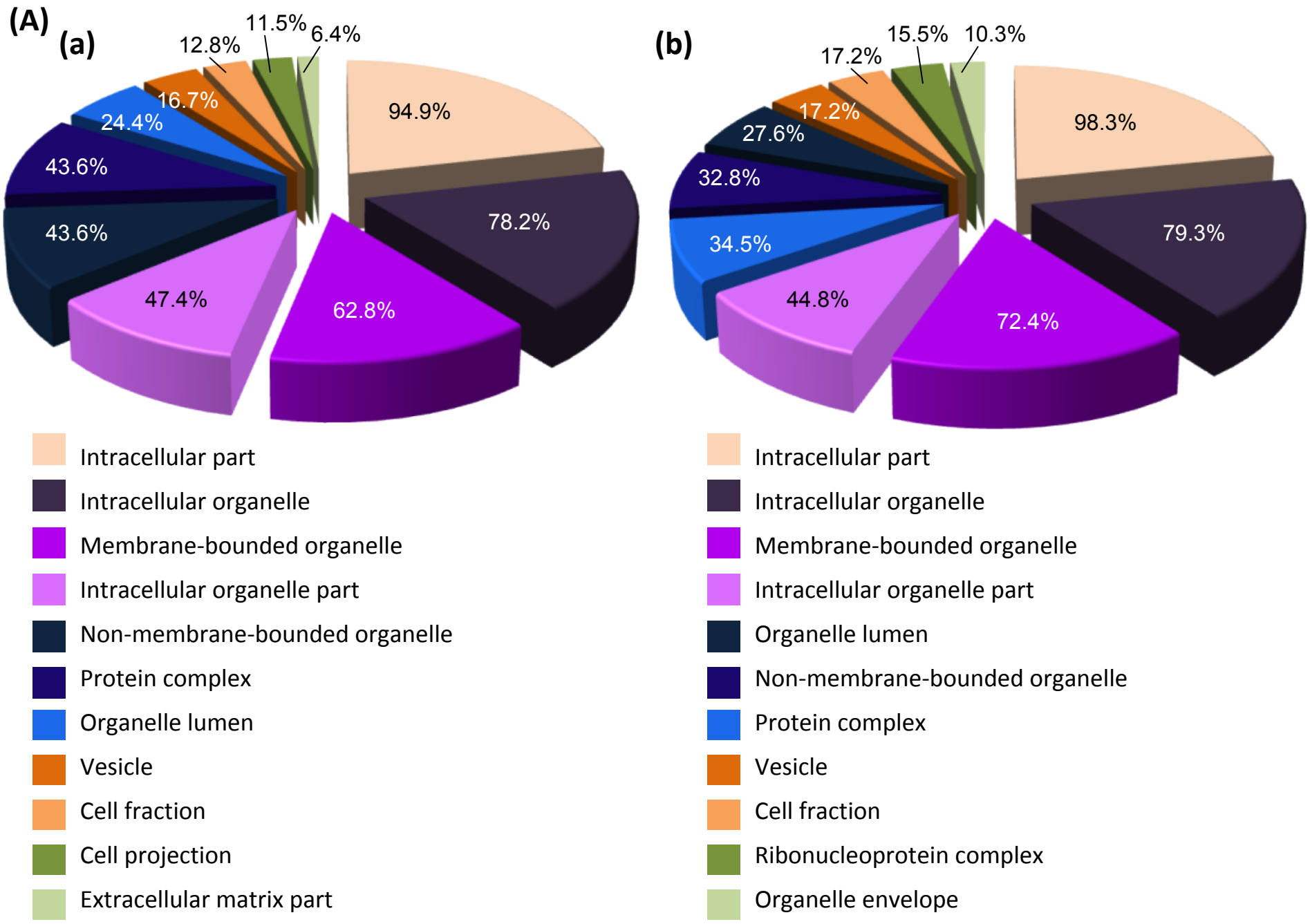
Electronic Supplementary Material (ESI) for Molecular BioSystems.


**Supplemental Figure 1**

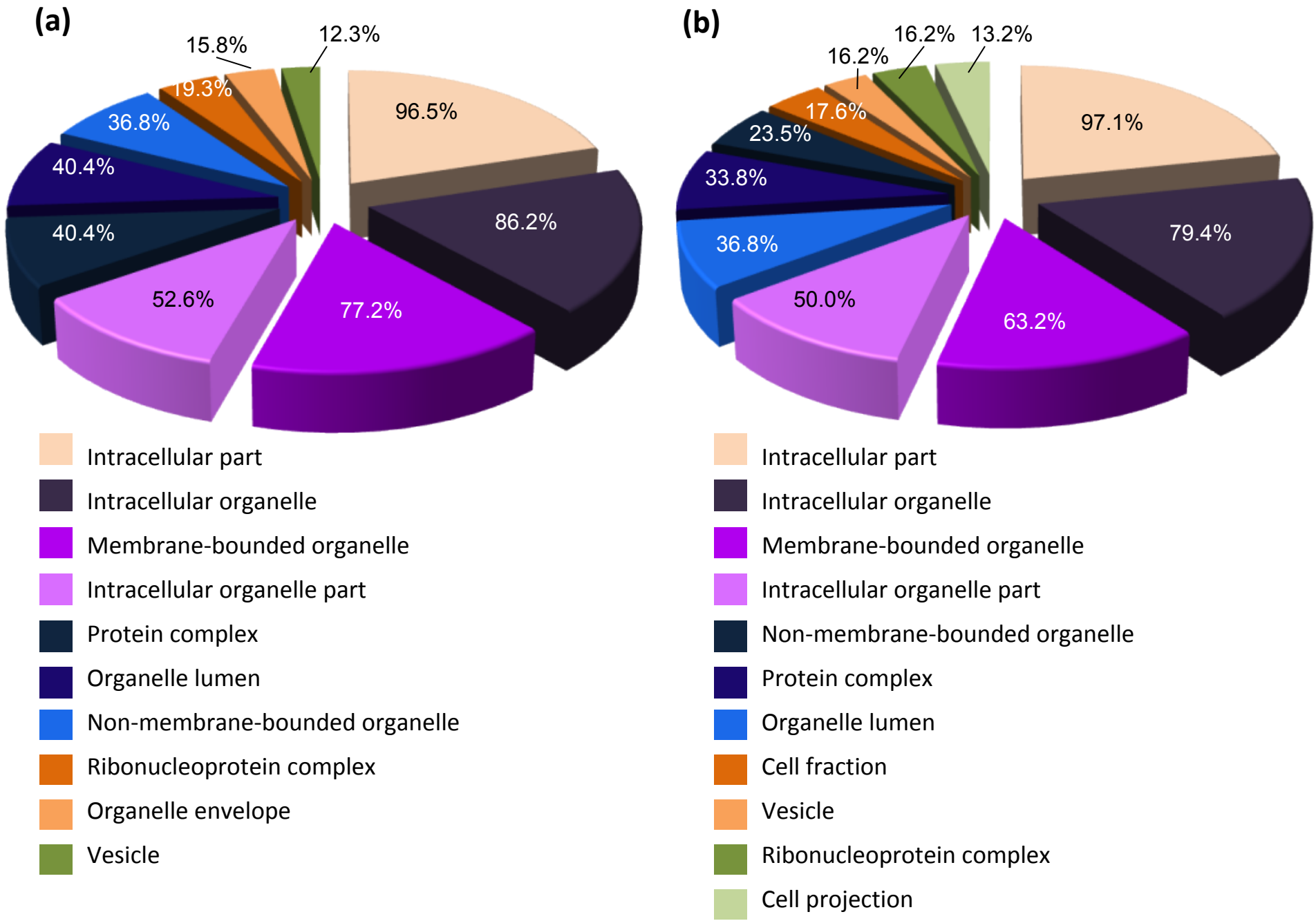



Supplemental Figure 1 (A): Fluorescence microscopy comparing DHR-123 stained control and treated (ANG II and PDGF) TK173 and HK-2 cells. Cells were stained with DHR-123 for 30 min and visualized using specific filter sets for phase contrast and rhodamine. The obtained images were merged to observe cell morphology. Scale bar = 100 µm. (B) The fluorescence expression quantification is presented as grouped bar chart under each experimental condition. Results are given as the means ±SD. **P < 0.01, ***P < 0.001 with respect to their corresponding control.

**Supplemental Figure 2**

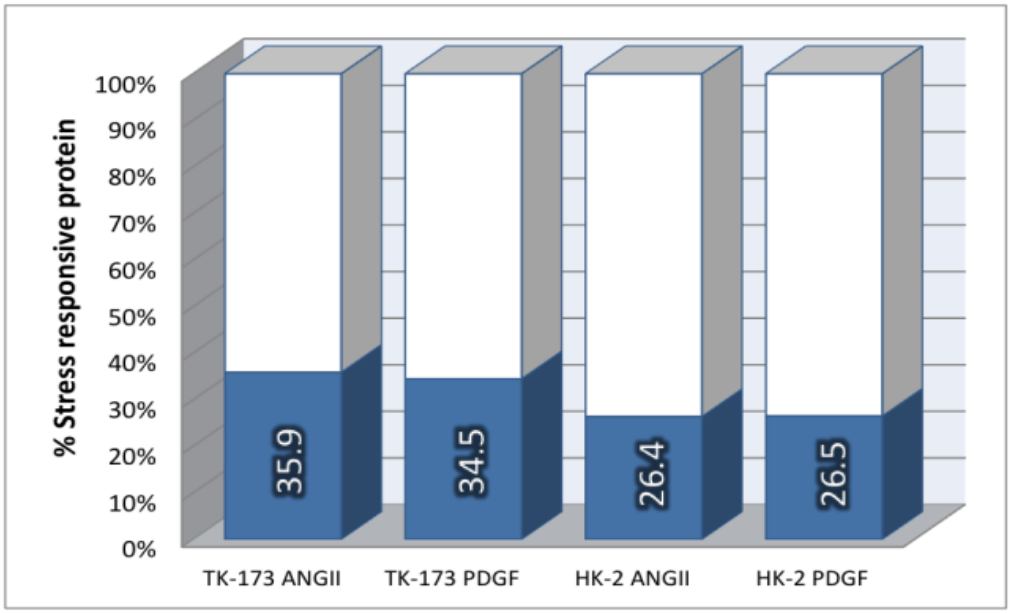


(B)


(a)
96.5%
86.2%
77.2%
52.6%
40.4%
40.4%
36.8%
19.3%
15.8%
12.3%
Intracellular part
Intracellular organelle
Membrane-bounded organelle
Intracellular organelle part
Protein complex
Organelle lumen
Non-membrane-bounded organelle
Ribonucleoprotein complex
Organelle envelope
Vesicle
(b)
97.1%
79.4%
63.2%
50.0%
36.8%
33.8%
23.5%
17.6%
16.2%
16.2%
13.2%
Intracellular part
Intracellular organelle
Membrane-bounded organelle
Intracellular organelle part
Non-membrane-bounded organelle
Protein complex
Organelle lumen
Cell fraction
Vesicle
Ribonucleoprotein complex
Cell projection

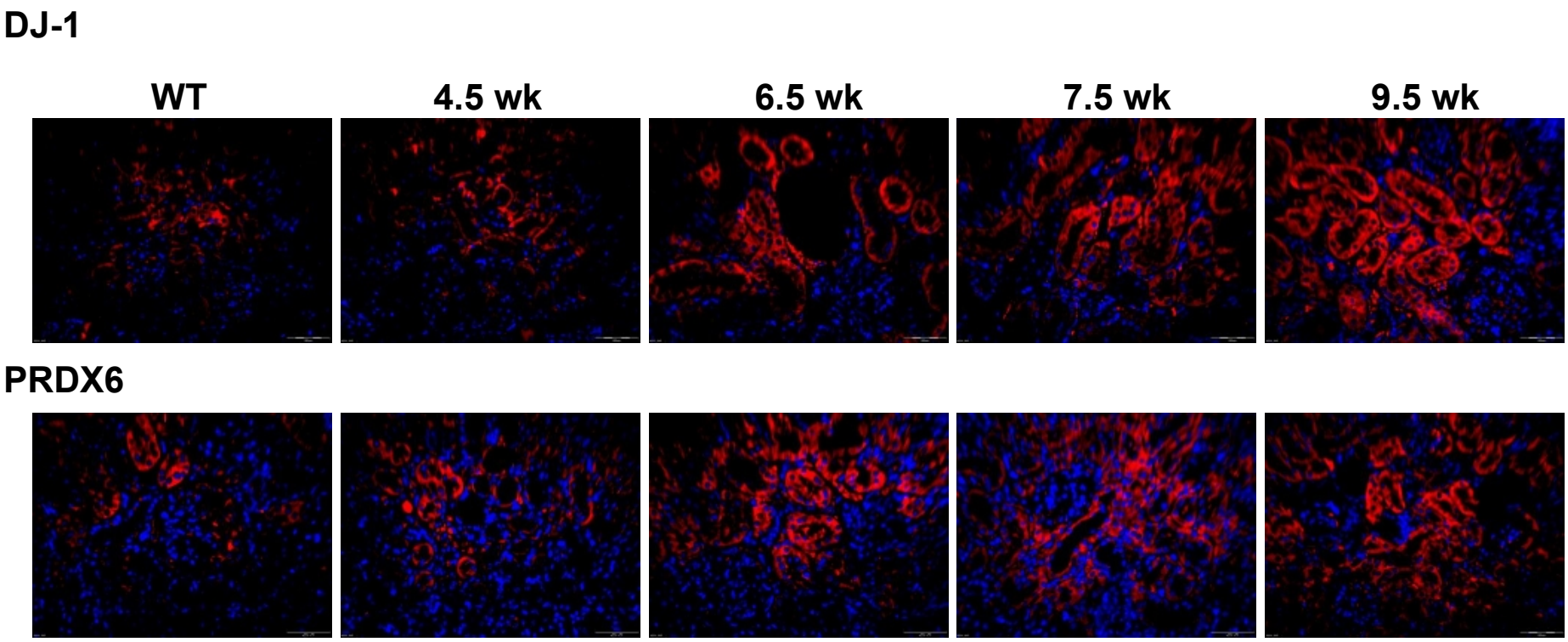
**Supplemental Figure 2 (A): Gene Ontology (GO) classification by DAVID Bioinformatics for the differentially regulated proteins in TK-173 (a) ANGII and (b) PDGF treated cells.** The list of genes to be analyzed was uploaded into Gene list Manager window and *Homo sapiens* was chosen as background. The gene list was then submitted for DAVID conversion tool. Based on the corresponding DAVID gene IDs and thresholds adjustment (Max-Prob.≤0.1 and Min Count≥2) in Chart Option section, functional annotations associated with each gene was displayed in a chart. GO analysis of subcellular location are represented as pie charts showing the different categories. **(B)**: **Gene Ontology (GO) classification by DAVID Bioinformatics for the differentially regulated proteins in HK-2 (a) ANGII and (b) PDGF treated cells.** The list of genes to be analyzed was uploaded into Gene list Manager window and *Homo sapiens* was chosen as background. The gene list was then submitted for DAVID conversion tool. Based on the corresponding DAVID gene IDs and thresholds adjustment (Max-Prob.≤0.1 and Min Count≥2) in Chart Option section, functional annotations associated with each gene was displayed in a chart. GO analysis of subcellular location are represented as pie charts showing the different categories.

**Supplemental Figure 3**



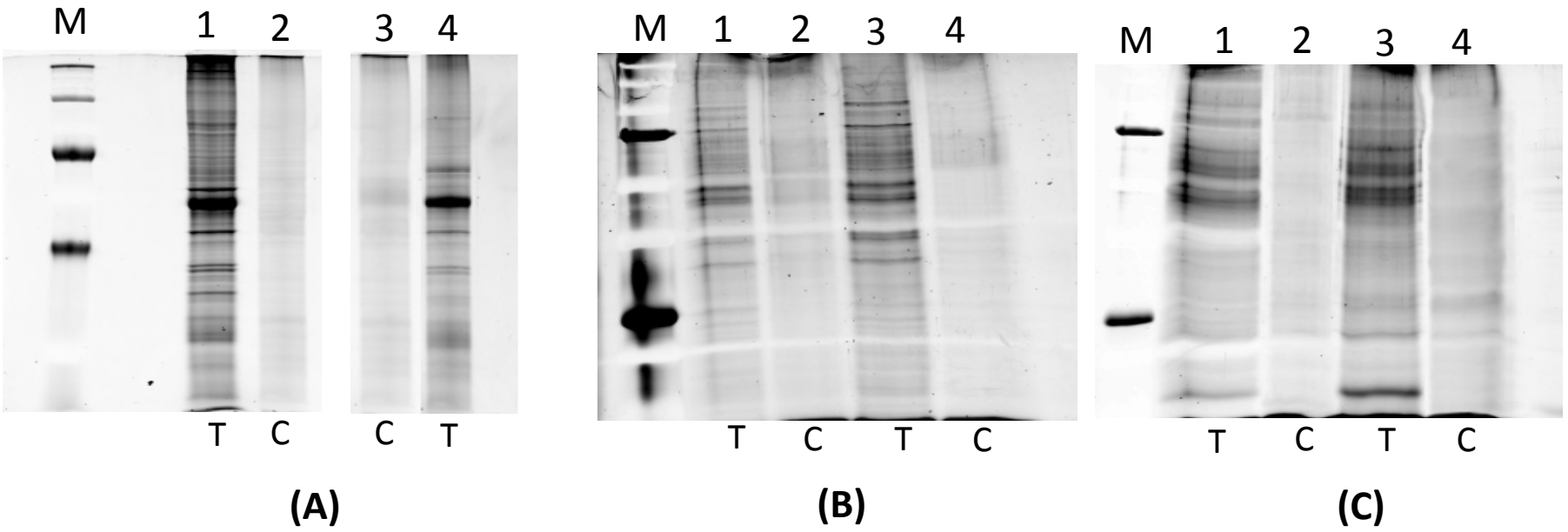

**Supplemental Figure 3: Percentage of the stress responsive proteins under different treatments.** Assignment of identified proteins into groups using DAVID Bioinformatic database resource. The list of genes to be analyzed was uploaded into Gene list Manager window and *Homo sapiens* was chosen as background. The gene list was then submitted for DAVID conversion tool. Based on the corresponding DAVID gene IDs and thresholds adjustment (Max-Prob.≤0.1 and Min Count≥2) in Chart Option section, functional annotations associated with each gene was displayed in a chart. GO analysis of molecular function was chosen. Percent stress responsive proteins under each treatment is represented as bar charts.

**Supplemental Figure 4**




**Supplemental Figure 4: Immunofluorescence staining of DJ-1 and PRDX6 as OS markers.** Representative images of glomerular and tubulointerstitial areas from WT and different stages of Col4a3 knockout mice kidneys stained with DJ-1 (upper panel) and PRDX6 (lower panel). (Magnification x20). Marked increase in the expression of both proteins with the increase of the fibrotic stage was observed.

**Supplemental Figure 5**




Supplemental Figure 5: Protein-protein interaction for (A): WT-DJ-1, (B): mutant E18Q-DJ-1, (C): mutant E18D-DJ-1. Immunoprecipitation (IP) and protein identification in control (empty vector) and transfected TK-173 and HK-2 cells. PARK7 was immunoprecipitated with its interaction partners. The resulting proteins were separated using SDS-PAGE and identified using tryptic digestion and mass spectrometry. Non-specific binding proteins observed in the control groups were skipped from the transfected groups. M= marker, 1 and 2= TK-173 cells, 3 and 4= HK-2 cells. T= transfected, C= control empty vector.

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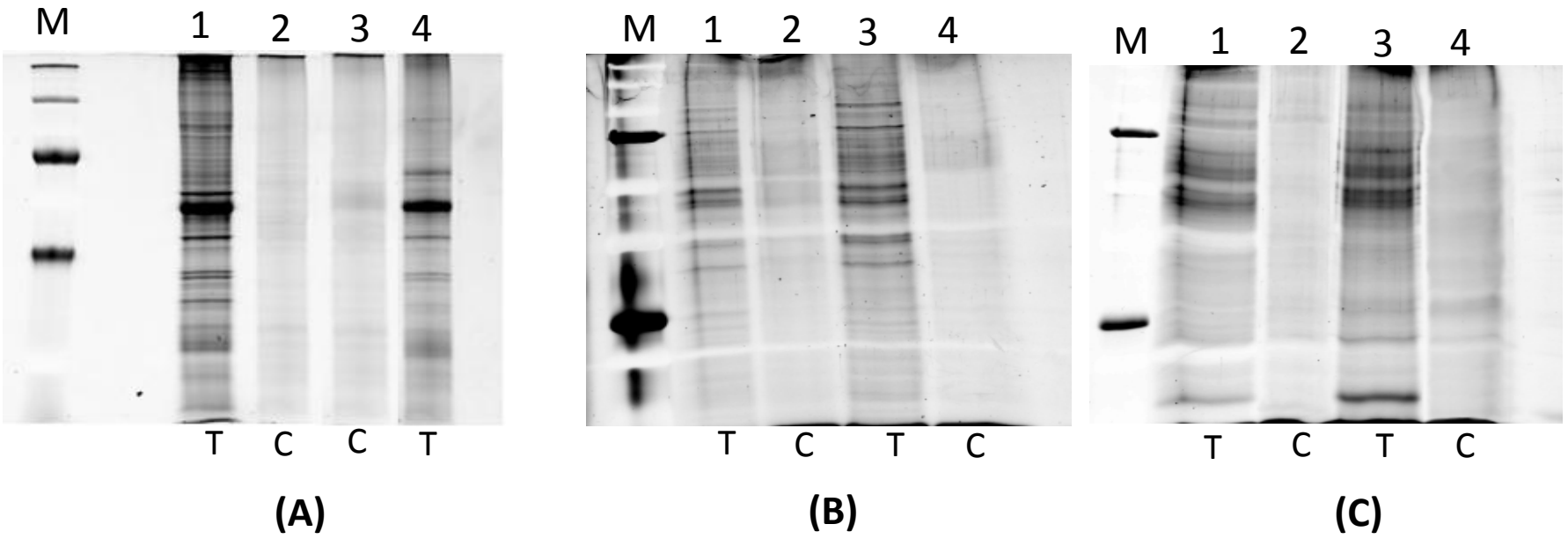


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