# Morphology changes of the MT network after DTX treatment in GC cells

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# Cell Lines and Treatment

- **Cell Line 1: TMK1 – responsive (50 cells)**
- **Cell Line 2 : MKN7 – resistant (30 cells)**
- **Cell Line 3 : SNU-1 – varied degree of resistance (30 cells)**
- **Cell Line 4 : AZ521 – varied degree of resistance (30 cells)**
- **Cell Line 5 : MKN45 – varied degree of resistance (30 cells)**

**Imaging MTs before and after treatment with 100nM DTX for each cell line**

**(340 high magnification images in total for MT analysis)**

# Approach

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## A neural network classifier capable of recognizing the patterns of all major subcellular structures in fluorescence microscope images of HeLa cells

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# 9 out of the 13 initial features show differential results and can describe the variety of MT bundling

**Feature Name (features in orange did not show significant differences)**

1) object_size:average - **The average number of above-threshold MT pixels per cell**

2) object_size:variance - **The variance of the number of above-threshold MT pixels per cell**

3) object_size:ratio - **The ratio of the size of the largest object to the smallest**

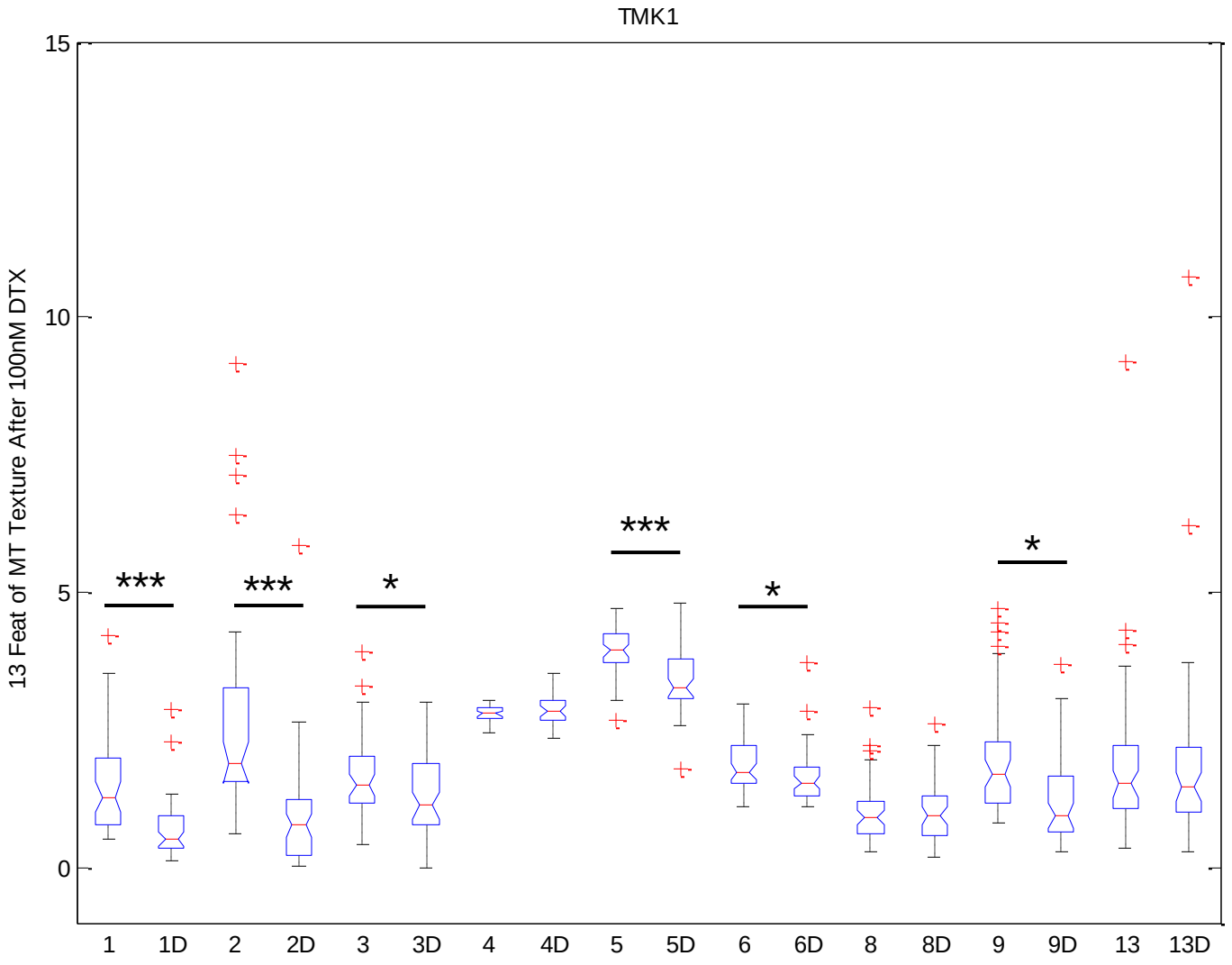
4) edges:area_fraction - **The fraction of the non-zero pixels in a cell that are along an edge**
5) edges:homogeneity - **Measure of edge intensity homogeneity**

6) edges:direction_maxmin_ratio **- Measure of edge direction homogeneity**

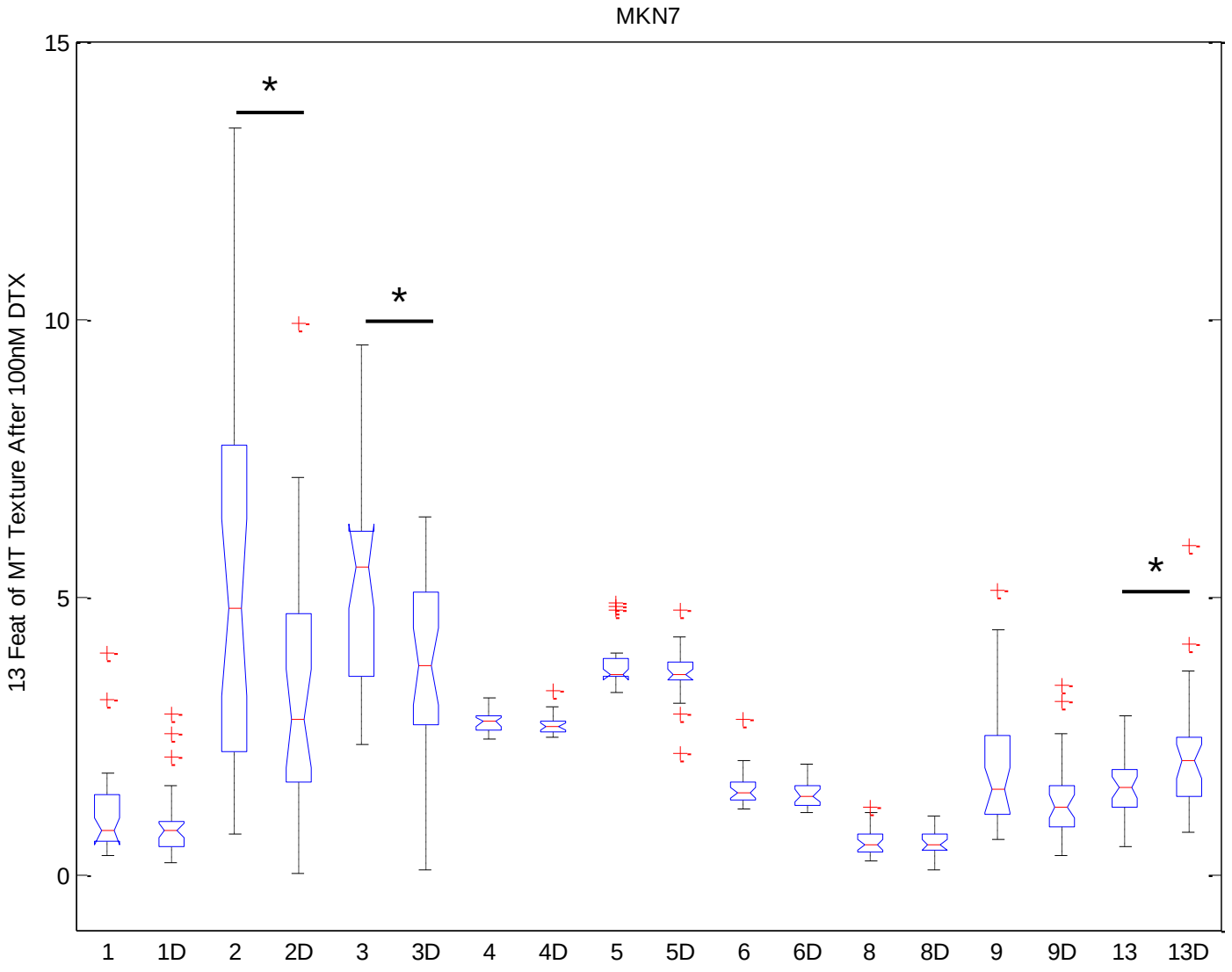
7) edges:direction_maxnextmax_ratio
8) edges:direction_difference **- Measure of edge direction difference**

9) obj_skel_len - **The average length of the morphological skeleton of objects**

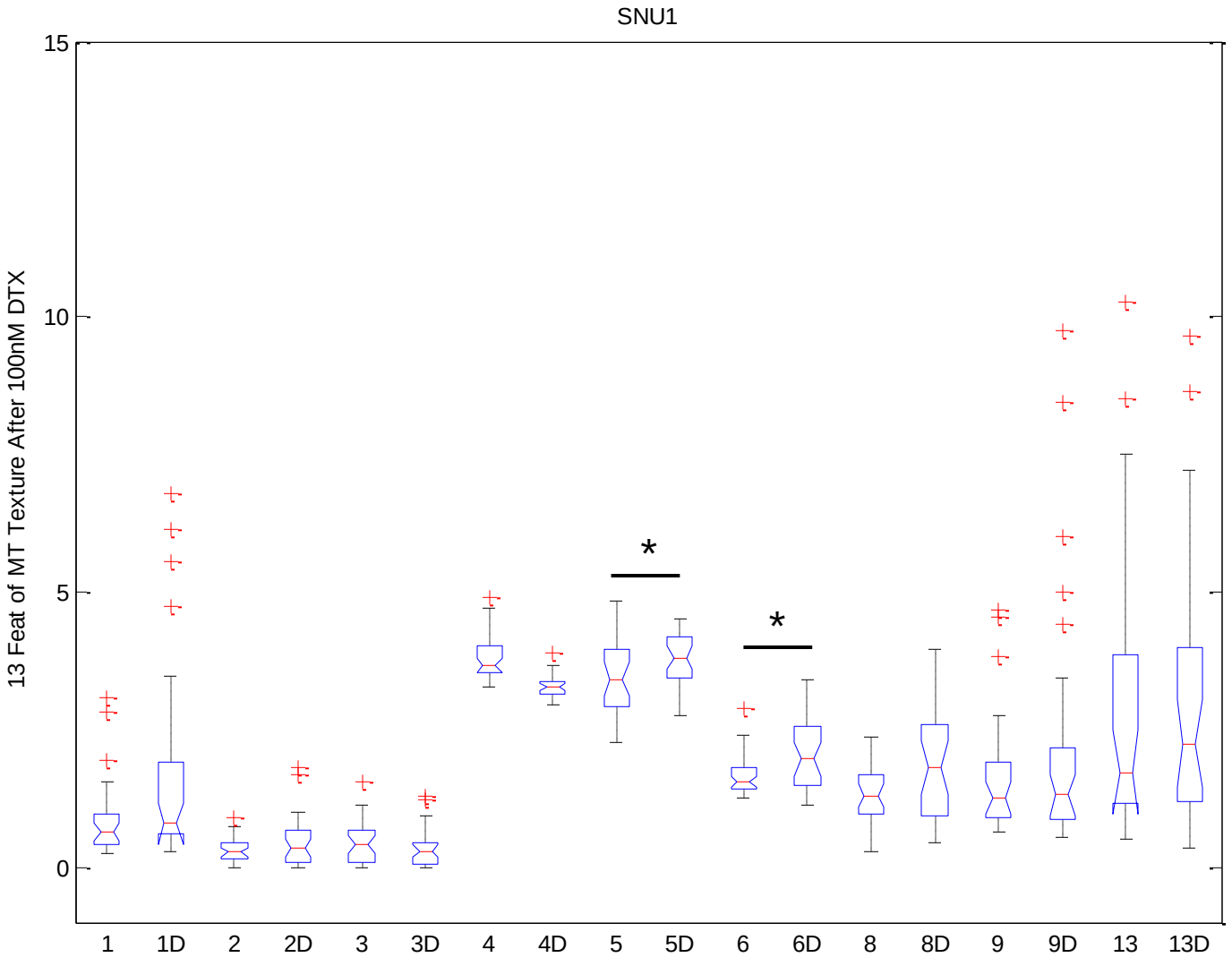
10) obj_skel_hull_area_ratio
11) obj_skel_obj_area_ratio
12) obj_skel_obj_fluor_ratio
13) obj_skel_branch_per_len - **The ratio of the number of branch points in skeleton to length of skeleton, averaged over all objects**: A point was defined as a branch point if 3 or more of its neighbors were contained within the skeleton.



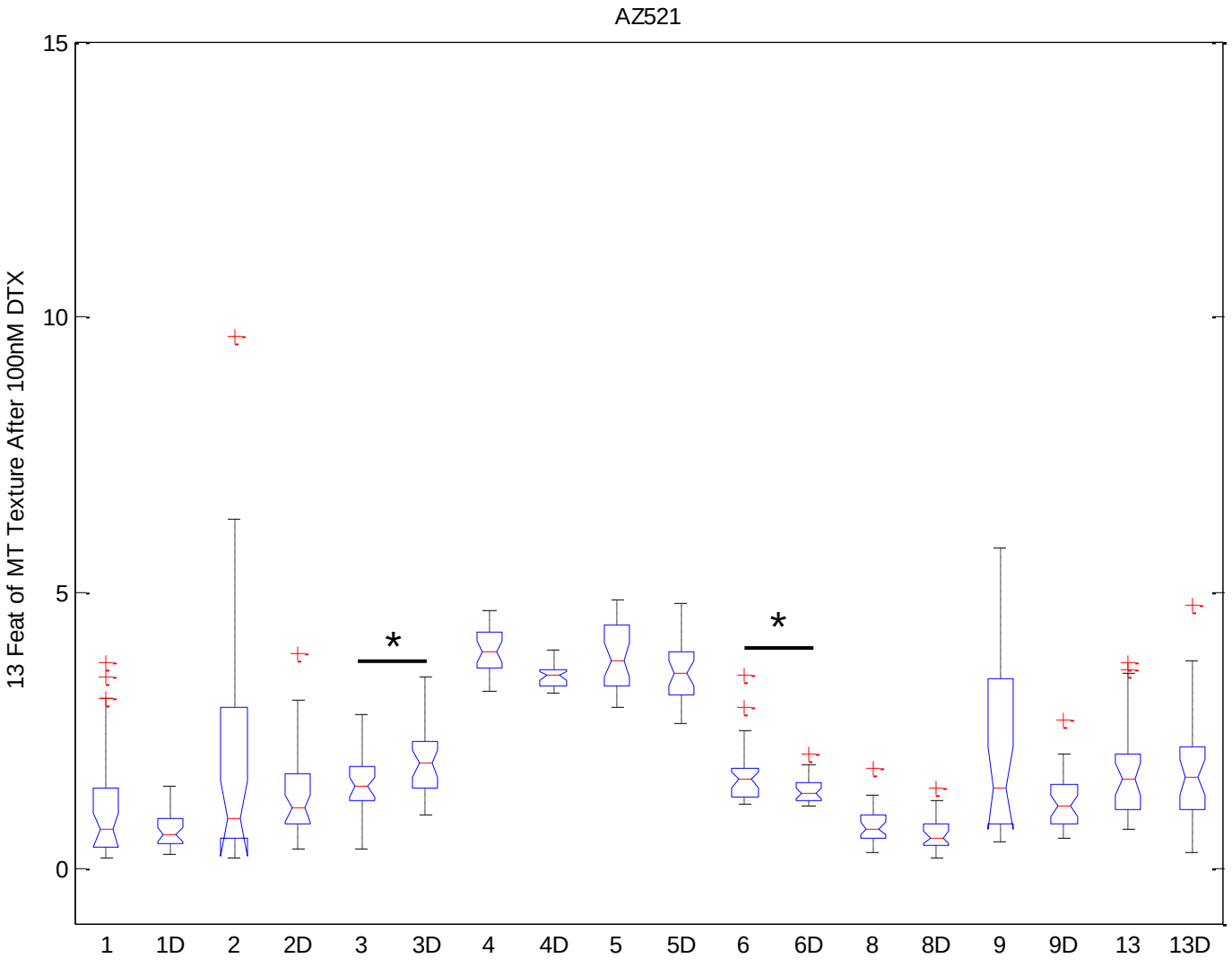

**‘D’ indicates treatment with DTX**
**1 -> 1D compares the changes in Feature 1 after DTX treatment, etc.**
**‘*’ indicated significantly different with p<0.05**
**‘***’ indicated significantly different with p<0.0005**



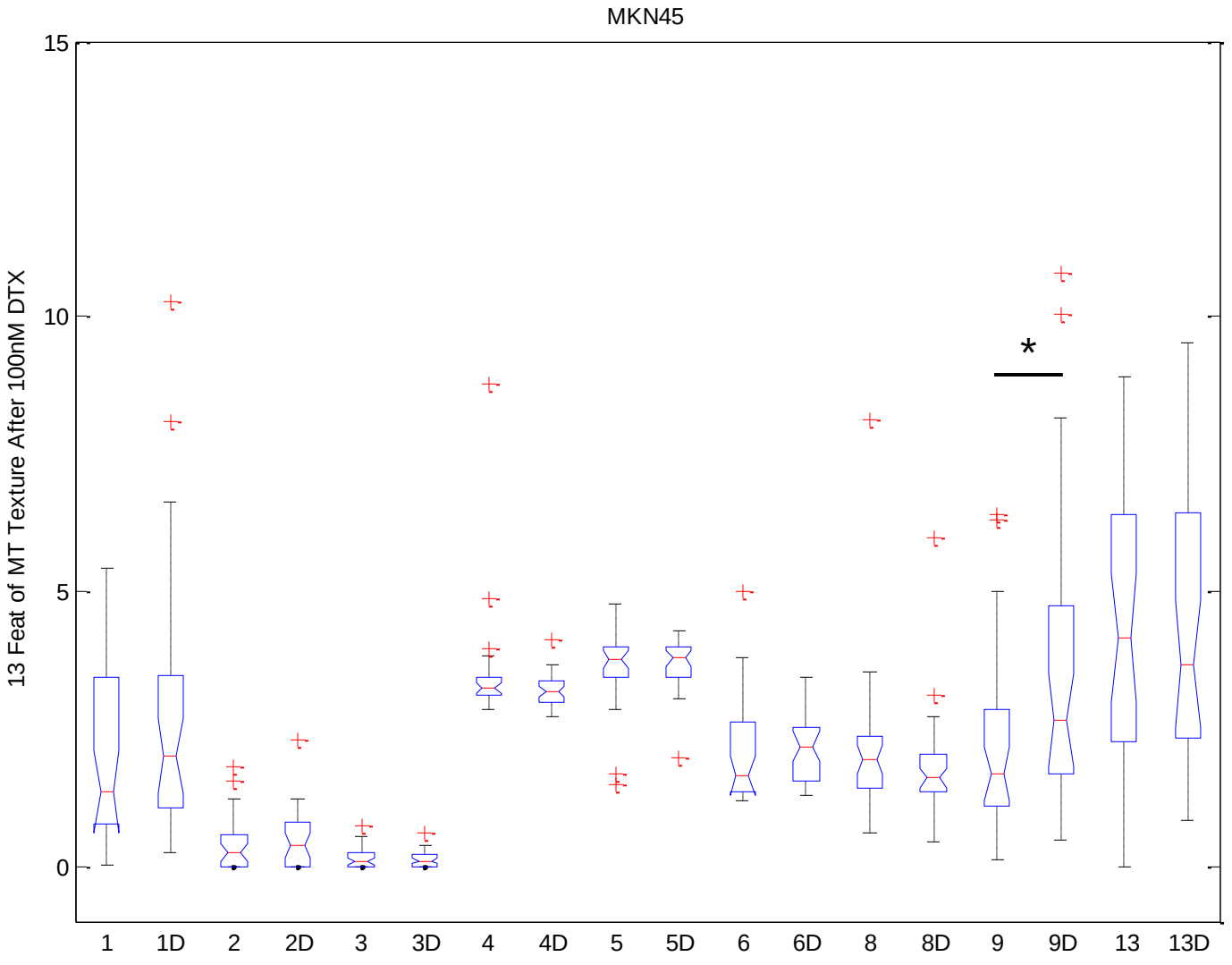

**‘D’ indicates treatment with DTX**
**2 -> 2D compares the changes in Feature 2 after DTX treatment, etc.**
**‘*’ indicated significantly different with p<0.05**




**‘D’ indicates treatment with DTX**
**5 -> 5D compares the changes in Feature 5 after DTX treatment, etc.**
**‘*’ indicated significantly different with p<0.05**
**‘***’ indicated significantly different with p<0.0005**




**‘D’ indicates treatment with DTX**
**3 -> 3D compares the changes in Feature 3 after DTX treatment, etc.**
**‘*’ indicated significantly different with p<0.05**




**‘D’ indicates treatment with DTX**
**9 -> 9D compares the changes in Feature 9 after DTX treatment**
**‘*’ indicated significantly different with p<0.05**