

Each column represents one measured biomarker or variable (fluorescence intensity/ gene or protein expression etc.)

Mandatory: The first row has to name column headers to indicate what variable is being measured.

Each row represents one cell. The entries are the cell-specific measurements that can then be used to classify the cell into phenotypic states

For single cell data, TRANSCOMPP expects at least 100 rows (cells)

	A	B	C
1	Biomarker1	Biomarker2	
2	29.490887	808.332947	
3	22.23123	1187.713989	
4	35.637756	1309.69104	
5	19.153856	1137.568359	
6	69.400398	1383.419189	
7	58.321144	1231.431396	
8	59.841507	1369.00415	
9	155.289993	1191.101196	
10	32.727512	1122.737183	
11	75.286568	1006.394287	
12	17.753311	1184.130005	
13	33.754021	763.834351	
14	126.684006	867.792114	
15	37.046448	1209.918457	
16	39.547493	1330.245728	
17	83.993752	1684.207275	
18	147.600296	1225.605225	
19	41.792988	562.844849	
20	54.851944	1328.26001	
21	63.601379	874.413635	
22	104.350586	1458.538696	
23	135.466644	595.867004	

Mandatory: Each sheet name has to be an integer representing the experimental time-point (units are arbitrary (hours/minutes/days))

**Each file corresponds to one replicate. When more than one replicate is present, multiple files need to be uploaded**