

Table 1. Maximal Lysosome-to-Nucleus Distance in Microns for pH 7.4 (Control), pH 6.8, and pH 6.4 in an HMEC Line and Three Breast Cancer Cell Lines Representing Different Stages of Breast Carcinogenesis.

Cell Line	Maximal Lysosome Distance [μm] (Number of Images)		
	pH 7.4 (<i>n</i>)	pH 6.8 (<i>n</i>)	pH 6.4 (<i>n</i>)
MCF-12A	15.8 \pm 1.1 (34)	16.7 \pm 1.0 (23)	16.6 \pm 0.7 (10)
MCF-7	27.1 \pm 2.8 (10)	27.0 \pm 4.3 (4)	26.9 \pm 1.0 (9)
MDA-MB-231	19.2 \pm 1.1 (31)	19.1 \pm 1.9 (27)	19.1 \pm 0.8 (31)
MDA-MB-435	25.1 \pm 2.6 (14)	24.8 \pm 3.0 (5)	25.3 \pm 2.2 (9)

Data were obtained by analyzing *n* images from four different stainings per pH and cell line using our in-house software. Values are mean \pm SE.

Table 1 | Frequency of aneuploidy

Cell division	Method of detection	Incidence of aneuploidy or chromosome mis-segregation rate*	Refs
Mitotic division			
<i>Saccharomyces cerevisiae</i>	Plasmid and YAC loss	0.001–0.01%	19–22
<i>Schizosaccharomyces pombe</i>	Minichromosome loss	0.01%	137
Human tissue culture cells	FISH	~1%	23,24
Mouse keratinocytes	Single-cell sequencing	2.7%	26
Human keratinocytes	Single-cell sequencing	0%	26
Human and mouse brain	Single-cell sequencing	3–5%	26,34
Human and mouse liver	Single-cell sequencing	~5%	26
Human tissue culture cells displaying CIN	FISH	20–100%	23
Cancer	SKY	>85%	6,138
Meiotic division			
<i>Saccharomyces cerevisiae</i>	YAC mis-segregation	~4%	19
<i>Schizosaccharomyces pombe</i>	Minichromosome loss	~4%	139
<i>Drosophila melanogaster</i>	SKY	~0.1%	140–142
Mouse fertilized eggs	SKY	1–2%	143
Human sperm	SKY	1–4%	144,145
	FISH	1–3%	146
Human oocytes	SKY	10–35%	147,148
	FISH	20–70%	147,148
	CGH	30–75%	149,150
Zygotes (human)	FISH and SKY	5–25%	17
Spontaneous abortions (human)	SKY	35%	17,36,37
Stillbirths (human)	SKY	4%	17,36,37
Newborns (human)	SKY	0.3%	17,36,37

CGH, comparative genomic hybridization; CIN, chromosomal instability; FISH, fluorescence in situ hybridization; SKY, spectral karyotyping; YAC, yeast artificial chromosome. *Plasmid, minichromosome and YAC loss measure mis-segregation rates; SKY, FISH, CGH and single-cell sequencing measure incidence of aneuploidy.