

ERRATUM

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Erratum to: How can functional annotations be derived from profiles of phenotypic annotations?

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Erratum

Upon publication of this article [1], it was brought to our attention that Table 1 was incorrectly presented. The correct Table 1 is shown below and has been updated in the original article.

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Reference

1. Serrano-Solano B, et al. How can functional annotations be derived from profiles of phenotypic annotations? *BMC Bioinformatics*. 2017;18:96. doi:10.1186/s12859-017-1503-5.

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Table 1 Set of 36 phenotypes obtained from the listed siRNA experiments sorted by its CMPO identifier

Experiment	Description	Phenotypes	IDs in CMPO
CellMorph [3]	Genome-wide RNAi screen that examines changes in the morphology of individual HeLa cells within cell populations.	<ul style="list-style-type: none"> - Decreased cell number - Cell with projections - Elongated cell - More lamellipodia cells - Increased number of actin filament - Round cell - Increased cell size - Decreased cell size - Bright nuclei - Metaphase arrested - Increased cell size in population 	<ul style="list-style-type: none"> CMPO:0000052 CMPO:0000071 CMPO:0000077 CMPO:0000083 CMPO:0000105 CMPO:0000118 CMPO:0000128 CMPO:0000129 CMPO:0000154 CMPO:0000305 CMPO:0000340
MitoCheck [2]	Genome-wide RNAi screen for genes required for chromosome segregation in HeLa cells. The screen also reports genes involved in other processes such as cell movement.	<ul style="list-style-type: none"> - Cell death - Increased nucleus size - Graped micronucleus - Abnormal nucleus shape - Mitosis delayed - Binuclear cell - Absence of mitotic chromosome decondensation - Increased cell movement speed - Increased cell movement distance - Proliferating cells - Metaphase delayed - Abnormal chromosome segregation - Prometaphase delayed - Increased variability of nuclear shape in population - Mitotic metaphase plate congression 	<ul style="list-style-type: none"> CMPO:0000030 CMPO:0000140 CMPO:0000156 CMPO:0000157 CMPO:0000202 CMPO:0000213 CMPO:0000216 CMPO:0000236 CMPO:0000237 CMPO:0000241 CMPO:0000307 CMPO:0000326 CMPO:0000344 CMPO:0000345 CMPO:0000348
EMBL secretion [4]	Genome-wide RNAi screen for interference with ER-to-plasma membrane transport of the secretory cargo protein tsO45G in HeLa cells.	<ul style="list-style-type: none"> - Increased rate of protein secretion - Mild decrease in rate of protein secretion - Strong decrease in rate of protein secretion - Decreased rate of intracellular protein transport 	<ul style="list-style-type: none"> CMPO:0000246 CMPO:0000318 CMPO:0000319 CMPO:0000346
GR00053 [10]	Genome-wide RNAi screen for genes involved in DNA damage responses in HeLa cells.	<ul style="list-style-type: none"> - Increased number of site of double-strand break 	<ul style="list-style-type: none"> CMPO:0000182
GR00290 [9]	Genome-wide RNAi screen for genes regulating centriole formation in HeLa cells.	<ul style="list-style-type: none"> - Increased centriole replication - Decreased centriole replication 	<ul style="list-style-type: none"> CMPO:0000361 CMPO:0000362
Copenhagen DNA damage Ubiquitin [8]	RNAi screen of >1300 genes involved in the ubiquitin-proteasome system or encoding zinc-finger proteins looking for modulators of cellular responses to ionizing radiation in HeLa and U2OS cells.	<ul style="list-style-type: none"> - Decreased number of site of double-strand brea 	<ul style="list-style-type: none"> CMPO:0000181
EMBL chromosome condensation [7]	RNAi screen of 100 bioinformatically-selected genes for changes in mitotic prophase duration in HeLa cells.	<ul style="list-style-type: none"> - Increased duration of mitotic prophase - Decreased duration of mitotic prophase 	<ul style="list-style-type: none"> CMPO:0000328 CMPO:0000329