Additional file 4 — Representation of the simulated example.

$n = 50$ or 150 patients

	Low risk patients group $(n/2)$	*High risk patients group* $(n/2)$
Survival time distribution	$S(t) = t$ or $S(t) = [1+t]^{-1}$	$S(t) = te^{-\xi}$ or $S(t) = [1 + t \cdot e^{\xi}]^{-1}$

Genes G		Low risk	High risk
	$g = 1 - 50$	Log-$\mathcal{N}(4, 1.5)$	Log-$\mathcal{N}(0, 1.5)$
	$g = 51 - 100$	Log-$\mathcal{N}(3, 1.5)$	Log-$\mathcal{N}(0, 1.5)$
	$g = 101 - 150$	60% Log-$\mathcal{N}(0, 1.5)$ + 40% Log-$\mathcal{N}(1, 1.5)$	
	$g = 151 - 250$	50% Log-$\mathcal{N}(0, 1.5)$ + 50% Log-$\mathcal{N}(0.5, 1.5)$	
	$g = 251 - 350$	30% Log-$\mathcal{N}(0, 1.5)$ + 70% Log-$\mathcal{N}(0.1, 1.5)$	
	$g = 301 - 1000$	Log-$\mathcal{N}(0, 1.5)$	

To complete this simulation scheme, correlations were added for each group of 10 genes ($\rho = 0.25; 0.5$ or 0.75). A quantile normalization was finally applied.