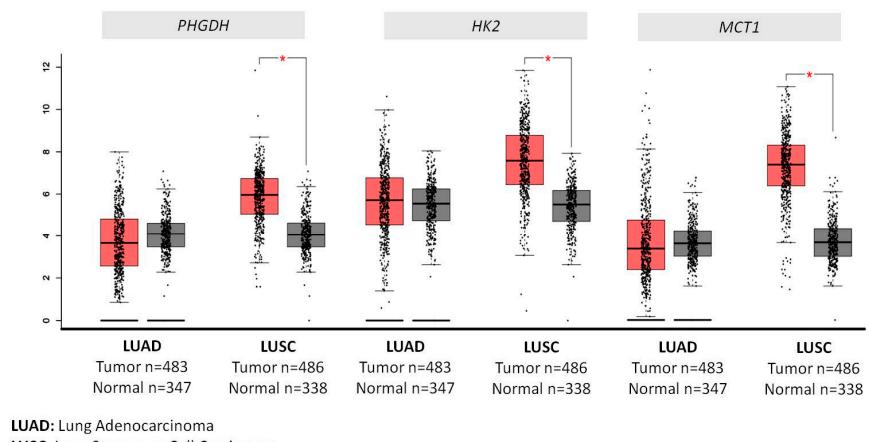
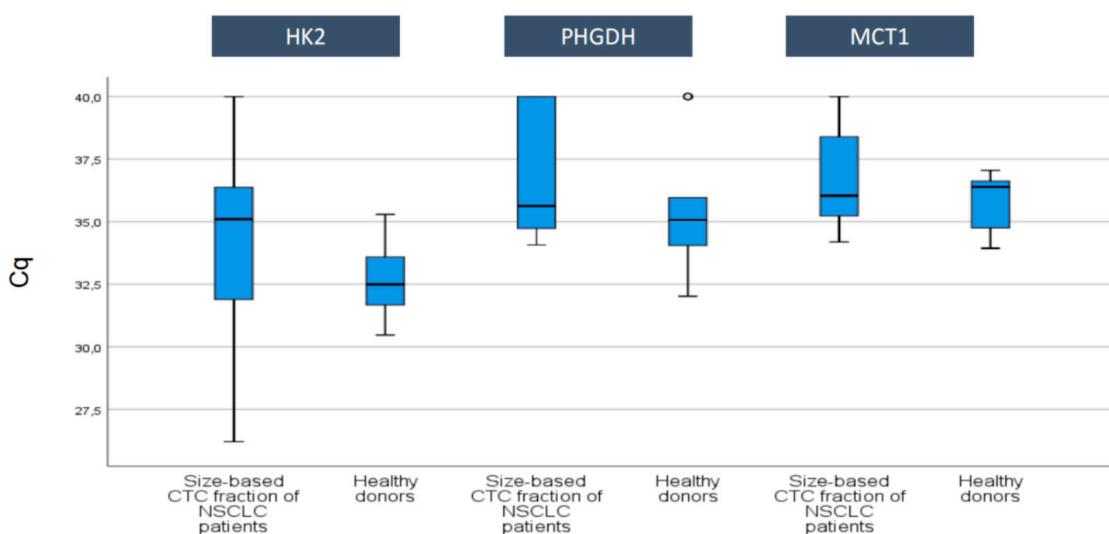


**Table S1. PCR primers and probes sequences.**

<b>HK2</b>	<b>Forward</b>	5'-CCCTCTACAAGCTACATCCTCACTT-3'	60.6
	<b>Reverse</b>	5'-CACGGATCGGGCAGGC-3'	61.8
<b>PHGDH</b>	<b>Forward</b>	5'-GGGAGCGGAAGAAGTTCA-3'	55.4
	<b>Reverse</b>	5'-CTATAGTCTTCATCCCAAAGGAC-3'	54.8
<b>MCT1</b>	<b>Forward</b>	5'-CATGATTGTTGGTGGCTGC-3'	54.9
	<b>Reverse</b>	5'-GAAGGCAAGCCAAGACC-3'	56.5
	<b>TaqMan Probe</b>	5'-FAM-TCAGGCTGTGGCTTGATTGCA-BHQ-3'	59.8



**Figure S1.** A plot of gene expression level between cancerous and normal tissues based on TCGA analysis.



**Figure S2.** Cq values of each tested gene at baseline in the size-based CTC fractions of early stage NSCLC patients and healthy donors.