Electronic Supplementary Information

for

One sample fits all: a microfluidic-assisted methodology for label-free isolation of CTCs with downstream methylation analysis of cfDNA in lung cancer

Ângela Carvalho[a,b,c,], Catarina Guimarães-Teixeira[c,d], Vera Constâncio[c,d], Mariana Fernandes[a,b], Catarina Macedo-Silva[c,d], Rui Henrique[c,d,e,f], Fernando Jorge Monteiro[a,b,c,g], Carmen Jerónimo[c,d,f]*

Affiliations

- [a] *i3S-Instituto de Investigação e Inovação em Saúde, Universidade do Porto, Rua Alfredo Allen 208, 4200-135 Porto, Portugal*
- [b] *INEB-Instituto de Engenharia Biomédica, Universidade do Porto, Rua Alfredo Allen 208, 4200-135 Porto, Portugal*
- [c] *Porto Comprehensive Cancer Centre (P.CCC), R. Dr. António Bernardino de Almeida, 4200-072 Porto, Portugal*
- [d] *Cancer Biology and Epigenetics Group, IPO Porto Research Center (GEBC CI-IPOP), Portuguese Oncology Institute of Porto (IPO Porto), R. Dr. António Bernardino de Almeida, 4200-072 Porto, Portugal*
- [e] *Department of Pathology, Portuguese Oncology Institute of Porto (IPO Porto), R. Dr. António Bernardino de Almeida, 4200-072 Porto, Portugal*
- [f] *Department of Pathology and Molecular Immunology, School of Medicine and Biomedical Sciences, University of Porto (ICBAS-UP), Rua Jorge Viterbo Ferreira 228, 4050-513 Porto, Portugal*
- [g] *Faculdade de Engenharia, Departamento de Engenharia Metalúrgica e Materiais, Universidade do Porto, Rua Dr Roberto Frias, s/n, 4200-465 Porto, Portugal*

Corresponding author

* Ângela Carvalho (angela.carvalho@ineb.up.pt)

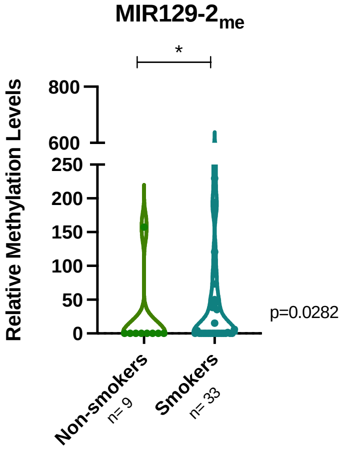

Figure S1 - Distribution of MIR129-2me relative methylation levels according with smoking habits. Mann Whitney U Test, n.s. $p > 0.05$, *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$, ****$p < 0.0001$.