Additional files 2-13 Table legends Fernandez et al.

- Additional_Table_S1

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Table S1. *Patient ID, sample information and relevant clinicopathological features obtained from TCGA consortium, Guintinalvo et al. (2013) and Bormann et al., (2016) datasets.*

Table S2. *Annotation and statistical significance of CpG probes differentially methylated in aging and cancer (dmCpGs). Effect size column reflects the mean- sva-corrected- M-value difference between compared groups. Methylstat column indicates the direction of the methylation change (hyper – hypermethylated in OLD compared to YOUNG individuals or hypermethylated in Primary tumors compared to Solid tissue normal; hypo – hypomethylated in OLD in comparison to YOUNG individuals or hypomethylated in Primary Tumor with respect to Solid Tissue Normal). It also includes dmCpGs obtained from additional analyses of lung and blood datasets, related to Additional file 1: Figure S5a.*

Table S3. *Statistical results obtained from Wilcoxon rank-sum non-parametric tests comparing M-value distributions of significant cancer versus aging dmCpGs, related to Fig. 1c.*

Table S4. *Statistical results obtained from Wilcoxon rank-sum non-parametric tests comparing CpG density distributions of significant dmCpGs in aging or cancer versus their corresponding background array distribution, related to Fig. 2a.*

Table S5. *Statistical results obtained from two-tailed Fisher's exact tests calculating CpG and gene location enrichments of significant dmCpGs in aging and cancer compared with their respective background array distribution, related to Figs. 2b and 2c.*

Table S6. *List of common cancer or age related dmCpGs across breast, kidney, thyroid, skin and glia tissues. Common cancer dmCpGs were obtained from the overlap between the five tissues used in our study, while common age related dmCpGs represent the intersection of significant dmCpGs in at least three out of five tissues.*

Table S7. *Statistical results obtained from two-tailed Fisher's exact tests calculating probe-sets overlaps and Jaccard Indices, related to Fig. 3d.*

Table S8. *Histone mark enrichment analysis of dmCpGs in cancer and aging. Enrichments were calculated between the dmCpGs in each of the analyses and the full collection of Roadmap epigenomics hg19 regions integrated in LOLA extended software. Corresponding array backgrounds were used for the different comparisons. Related to Fig. 4. It also includes histone enrichments obtained from additional analyses of lung and blood datasets, related to Additional file 1: Figure S5b.*

Table S9. *Patient ID, sample information and relevant clinicopathological features of LUNG and BLOOD obtained from TCGA consortium and Hannum et al. (2013) datasets, related to Additional file 1: Figure S5a.*

Table S10. *Chromatin state enrichment analysis of dmCpGs in cancer and aging. Enrichments were calculated between the dmCpGs from the different analyses and the hg19 chromatin segmentation regions (ChromHMM, 18 states) obtained from Roadmap and ENCODE consortia. A custom LOLA database including information related to the chromatin states in the different tissues/cell lines and corresponding array backgrounds were used for the correct enrichment calculation. Related to Fig 5a and Additional file 1: Figure S7.*

Table S11. *Transcription factor binding site enrichment analysis of dmCpGs in cancer and aging. Enrichments were calculated between the dmCpGs in each of the comparisons and the collection of transcription factor binding datasets from ENCODE (hg19) integrated in LOLA core software. Related to Fig. 5b and Additional file 1: Figure S8.*

Table S12. *Gene ontology and KEGG enrichment analysis of dmCpGs in cancer and aging. Enrichments were calculated between the dmCpGs obtained from the different datasets and the KEGG and GO databases (*http://www.kegg.jp/kegg/rest/keggapi.html *for KEGG ontology and the R/Bioconductor package GO.db. for GO ontology)*

Table S13. *Patient ID, sample information and relevant clinicopathological features of KIRC data collected from TCGA consortium, related to Fig 7. Table includes statistical results obtained from differential gene expression analyses performed for aging (age_groups 1 & 2 versus 5) or cancer (Primary Tumor versus Solid Tissue Normal) comparisons.*

Table S14. *List of pairwise correlations (Spearman correlation >0.9 or <-0.9) observed between either aging or cancer related dmCpGs and genes expressed in normal KIRC datasets obtained from the TCGA consortium. Correlation analyses were performed with those samples corresponding to normal conditions (Solid Tissue Normal) and which presented both methylation and gene expression data for a given case. Related to Fig. 7e.*