

# Supporting Information for

## Guidelines for the Use of Deuterium Oxide (D<sub>2</sub>O) in <sup>1</sup>H NMR Metabolomics

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### Table of Contents:

#### Experimental Section

S1: Superposition of creatinine CH<sub>3</sub> signal with metformin in 2D HSQC and <sup>1</sup>H spectra

S2: Urine spectra from inversion recovery experiment

S3: Determination of T<sub>1</sub> relaxation times for CH<sub>2</sub> and CHD in creatinine

S4: IG <sup>13</sup>C for estimation of CD<sub>2</sub> occurrence under realistic measurement conditions

### Experimental Section

#### Superposition of creatinine CH<sub>3</sub> signal with metformin in 2D HSQC and <sup>1</sup>H spectra

A 2D-HSQC NMR experiment (hsqcetgpsisp2.2) was acquired using a pooled urine sample (QC, based on n=227 samples) from a cohort including patients with various systemic diseases (Gil et al., 2018)<sup>1</sup>. Parameters were used as follows: 4096 x 840 data points were collected using 512 scans per increment, an acquisition time of 0.25 s, and 16 dummy scans. The spectra width was set to 12 and 230 ppm in the <sup>1</sup>H and <sup>13</sup>C dimension. In addition, 7 selected samples with visible overlap of creatinine and metformin were selected from the dataset to illustrate the overlap of creatinine-CH<sub>3</sub> and metformin.

#### T<sub>1</sub> measurements for CH<sub>2</sub> and CHD creatinine peaks

The determination of T<sub>1</sub> was executed using a pooled urine sample via an inversion recovery experiment. The standard experiment (t1ir) containing the excitation sequence was complemented by addition of a solvent suppression array<sup>2</sup> (t1iresgp). Delays were defined to be 0.05, 0.1, 0.2, 0.3, 0.5, 0.8, 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5 and 8 sec. Following parameters were used: ns = 72 and ds = 4 per increment, sw = 16 ppm, aq = 1 sec.

Spectra were imported into Matlab software (R2011b; Mathworks). Integrals were calculated using trapezoidal numerical integration. T<sub>1</sub> relaxation times were calculated via polynomial fitting of peak areas over relaxation delays (τ) and determination of zero-crossing points.

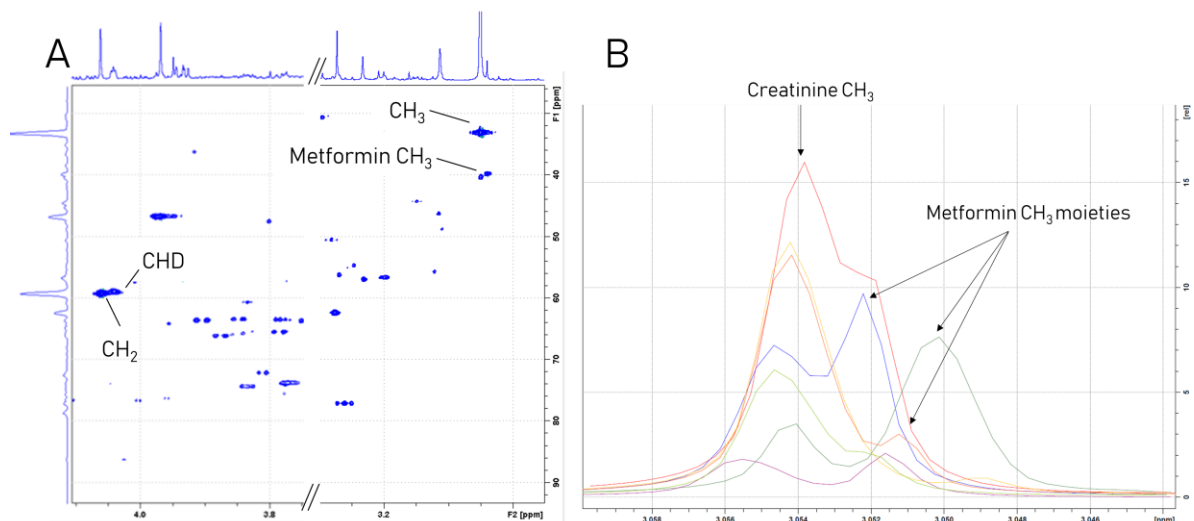


Figure S1: (A) 2D-HSQC from a QC sample highlighting the metformin-overlap of the creatinine-CH<sub>3</sub>, while the creatinine-CH<sub>2</sub> and creatinine-CHD show little to no overlap with other signals. (B) Overlap of selected urine samples from a chronic kidney diseases (CKD) study containing metformin with annotation of creatinine CH<sub>3</sub> and metformin CH<sub>3</sub> moieties.

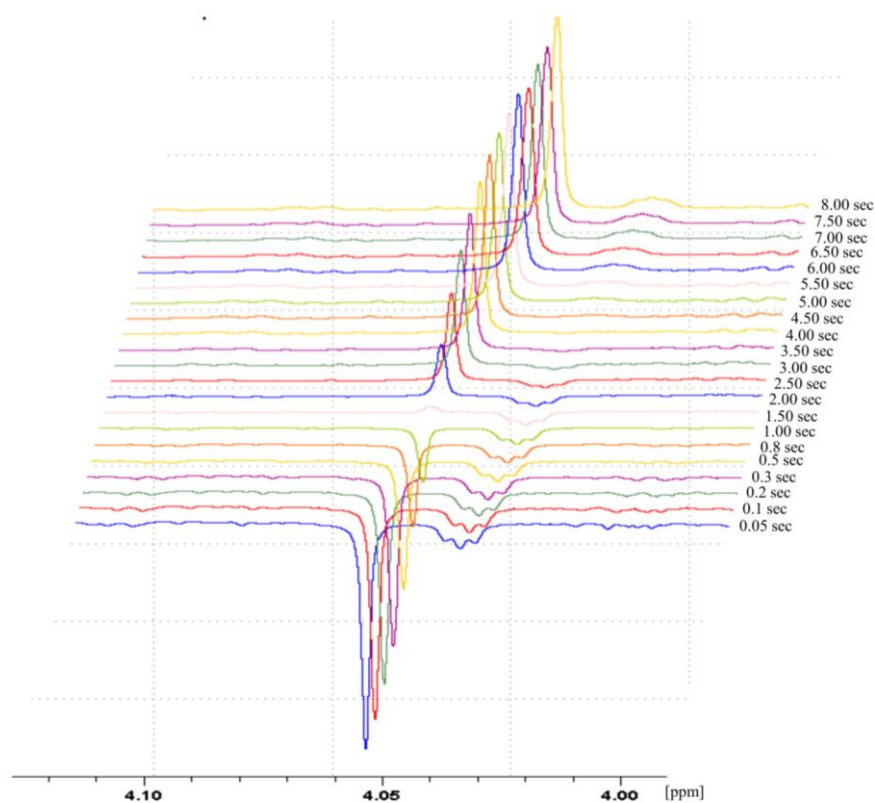


Figure S2: Stacked plot for inversion recovery experiment for urine sample with  $\tau$  ranging from 0.05 sec to 8.5 sec, enlarged in CH<sub>2</sub>/CHD peak area; zero crossing of CH<sub>2</sub> protons at ~ 1.5 sec; CHD protons between 3.5 sec – 4.5 sec

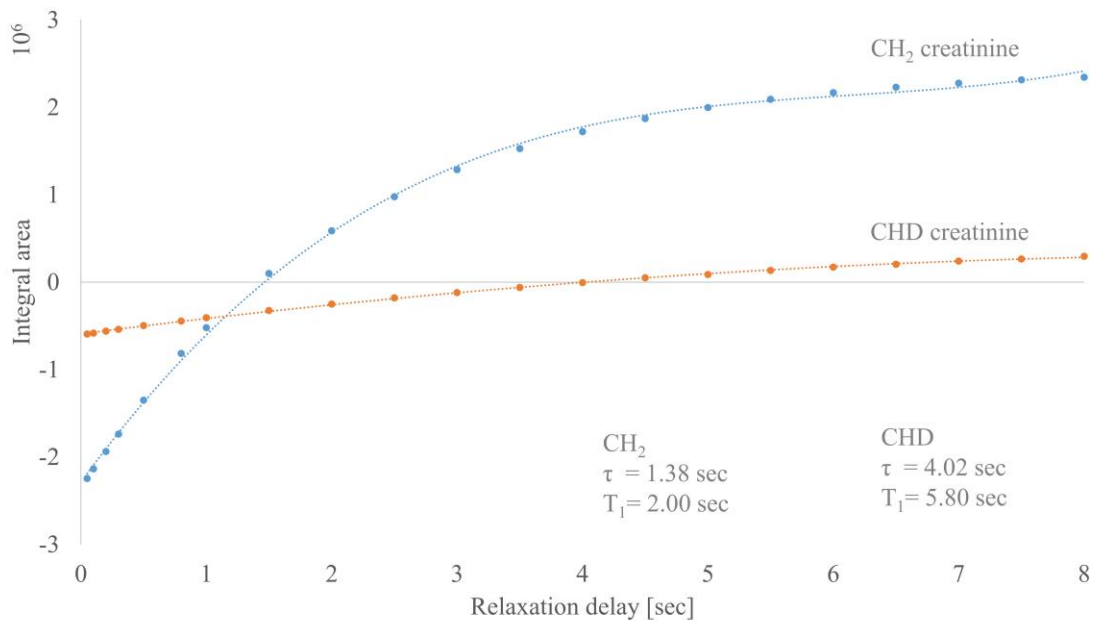


Figure S3: Integral areas over varying relaxation delays ( $\tau$ ) for CH<sub>2</sub> and CHD creatinine peaks

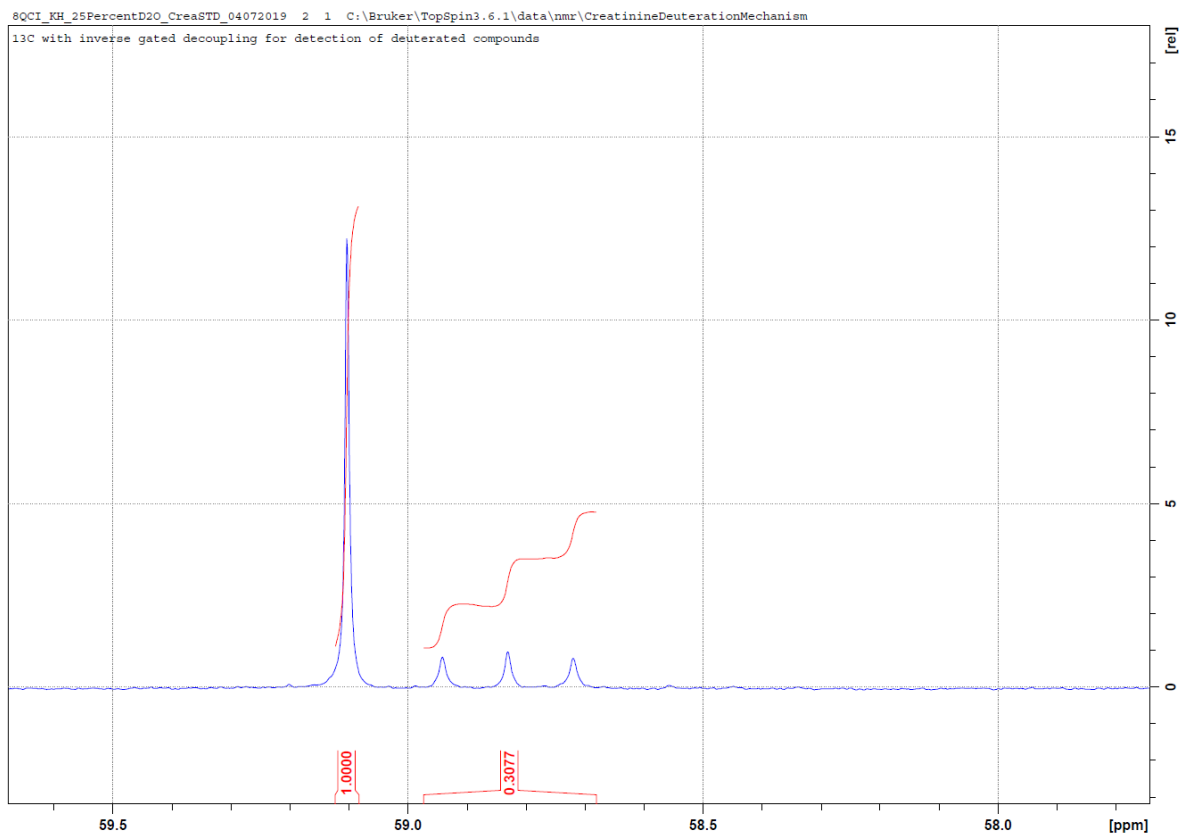


Figure S4: IG <sup>13</sup>C for estimation of CD<sub>2</sub> occurrence under realistic measurement conditions: A urine sample containing 25% D<sub>2</sub>O was analyzed after a dwell time of 24 h. The singlet of creatinine-CH<sub>2</sub> and the triplet of CHD are clearly visible, the quintet of creatinine-CD<sub>2</sub> is below S/N. Peak area integration was performed in TopSpin 3.6.1.

## REFERENCES

- (1) Gil, Ryan B., et al. "Increased urinary osmolyte excretion indicates chronic kidney disease severity and progression rate." *Nephrology Dialysis Transplantation* 33.12 (2018): 2156-2164.
- (2) Hwang, T.-L. & Shaka, A.J. "Water suppression that works. Excitation sculpting using arbitrary wave-forms and pulsed-field gradients." *Journal of Magnetic Resonance, Series A* 112.2 (1995): 275-279.