## Supplementary Materials: Development and validation of a high-throughput mass spectrometry based urine metabolomic test for colorectal cancer screening

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Table S1. Optimized MS parameters for each compound. MRM pair 1 is used for quantitation and MRM pair 2 is for qualification.

| Compound | Polarity | Q1 | Q3 | DP | CE | CXP |
| :--- | :---: | :---: | :---: | :---: | :---: | :---: |
| Succinic acid 1 | - | 117.0 | 73.0 | -40 | -16 | -1 |
| Succinic acid 2 | - | 117.0 | 55.1 | -40 | -22 | -7 |
| Succinic acid-D4 | - | 121.0 | 77.0 | -40 | -16 | -1 |
| Ascorbic acid 1 | - | 175.0 | 114.9 | -45 | -18 | -7 |
| Ascorbic acid 2 | - | 175.0 | 86.8 | -45 | -28 | -13 |
| Ascorbic acid-13C | - | 176.0 | 116.0 | -45 | -18 | -7 |
| Carnitine 1 | + | 162.1 | 103.1 | 51 | 25 | 6 |
| Carnitine 2 | + | 162.1 | 43.2 | 51 | 47 | 6 |
| Carnitine-D9 | + | 171.0 | 103.0 | 51 | 25 | 6 |

Table S2. Extraction recoveries and accuracies for each metabolite.

| Metabolite | Recovery (\%) | Accuracy (\%) |
| :---: | :---: | :---: |
| Succinic acid | 101.0 | 110.2 |
| Ascorbic acid | 93.8 | 98.7 |
| Carnitine | 93.1 | 102.7 |

a. $\quad \operatorname{Recovery}(\%)=($ Response $($ spiked sample $)) /($ Response $($ post-spiked sample) $) \times 100$
b. Accuracy $(\%)=($ spiked sample-upspiked sample $) /($ spiked amount $) \times 100$

Table S3. CV\% of QC samples for each metabolite within each plate.

|  | Succinic acid |  | Ascorbic acid |  | Carnitine |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Average |  |  |  |  |  |
| concentration |  |  |  |  |  |  |
| $(\mu \mathrm{M})$ | CV\% |  | Average |  |  |  |
| concentration |  |  |  |  |  |  |
| $(\mu \mathrm{M})$ | CV\% |  | Average |  |  |  |
| Kit 1 | 21.1 | $14.7 \%$ | 125.2 | $8.6 \%$ | 45.5 | $9.8 \%$ |
| Kit 2 | 23.0 | $5.9 \%$ | 121.8 | $8.3 \%$ | 49.2 | $10.4 \%$ |
| Kit 3 | 25.7 | $16.7 \%$ | 109.0 | $10.2 \%$ | 46.2 | $8.4 \%$ |
| Kit 4 | 25.3 | $5.3 \%$ | 119.6 | $4.1 \%$ | 49.5 | $5.5 \%$ |
| Kit 5 | 25.8 | $10.3 \%$ | 135.0 | $7.7 \%$ | 47.7 | $4.3 \%$ |
| Kit 6 | 27.7 | $13.6 \%$ | 107.0 | $4.1 \%$ | 46.7 | $6.4 \%$ |
| Kit 7 | 11.4 | $13.1 \%$ | 104.7 | $14.0 \%$ | 25.9 | $10.9 \%$ |
| Kit 8 | 14.0 | $11.7 \%$ | 123.0 | $4.5 \%$ | 35.0 | $6.0 \%$ |
| Kit 9 | 17.4 | $12.5 \%$ | 114.6 | $9.1 \%$ | 40.3 | $11.9 \%$ |
| overall | 21.1 | $10.0 \%$ | 116.7 | $6.8 \%$ | 42.6 | $7.6 \%$ |

coefficient of variation $(\mathrm{CV} \%)=($ standard deviation $) /($ mean value $)$


Figure S1. A representative LCMS of Calibrant 6.

| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| A | Blank | Ca17 | Urine6 | Urine14 | Urine21 | Urine29 | Urine36 | Urine44 | Urine51 | Urine59 | Urine66 | Urine74 |
| B | ISTD | Ca18 | Urine7 | Urine15 | Urine22 | Urine30 | Urine37 | Urine45 | Urine52 | Urine60 | Urine67 | Urine75 |
| C | Cal1 | Urine1 | Urine8 | Urine16 | Urine23 | Urine31 | Urine38 | Urine46 | Urine53 | Urine61 | Urine68 | Urine76 |
| D | Cal2 | Urine2 | Urine9 | Urine17 | Urine24 | Urine32 | Urine39 | Urine47 | Urine54 | Urine62 | Urine69 | Urine77 |
| E Ca13 | Urine3 | Urine10 | Urine18 | Urine25 | Urine33 | Urine40 | Urine48 | Urine55 | Urine63 | Urine70 | Urine78 |  |
| F | Ca14 | Urine4 | Urine11 | Urine19 | Urine26 | Urine34 | Urine41 | Urine49 | Urine56 | Urine64 | Urine71 | Urine79 |
| G | Cal5 | Urine5 | Urine12 | Urine20 | Urine27 | Urine35 | Urine42 | Urine50 | Urine57 | Urine65 | Urine72 | Urine80 |
| H | Cal6 | QC | Urine13 | QC | Urine28 | QC | Urine43 | QC | Urine58 | QC | Urine73 | QC |

Figure S2. A representative plate map. LCMS sequence runs vertically.


Figure S3. Passing and Bablok regression analyses of MS-quantified on NMR-quantified data for Succinic acid, $\mathrm{N}=685$; concentration range $0-362 \mu \mathrm{~mol} / \mathrm{L}$; Pearson correlation coefficient $\mathrm{r}=0.862, \mathrm{P}<0.0001$. (A) Scatter diagram with regression line and confidence bands for regression line. Identity line is dashed. Regression line equation: y=4.17+1.32 x; $95 \%$ CI for intercept 2.72 to 5.33 and for slope 1.26 to 1.38 indicated small constant and small proportional difference. Cusum test for linearity indicates significant deviation from linearity ( $\mathrm{P}<0.01$ ). (B) Residual plot presents distribution of difference around fitted regression line.


Figure S4. Passing and Bablok regression analyses of MS-quantified on NMR-quantified data for Ascorbic acid, $\mathrm{N}=685$; concentration range $0-13368 \mu \mathrm{~mol} / \mathrm{L}$; Pearson correlation coefficient $\mathrm{r}=0.800, \mathrm{P}<0.0001$. (A) Scatter diagram with regression line and confidence bands for regression line. Identity line is dashed. Regression line equation: y $=2.50+$ 1.12 x; 95\% CI for intercept 2.50 to 2.50 and for slope 1.06 to 1.19 indicated small constant and small proportional difference. Cusum test for linearity indicates significant deviation from linearity ( $\mathrm{P}<0.01$ ). (B) Residual plot presents distribution of difference around fitted regression line.


Figure S5. Passing and Bablok regression analyses of MS-quantified on NMR-quantified data for Carnitine, $\mathrm{N}=685$; concentration range $0-948 \mu \mathrm{~mol} / \mathrm{L}$; Pearson correlation coefficient $\mathrm{r}=0.921, \mathrm{P}<0.0001$. (A) Scatter diagram with regression line and confidence bands for regression line. Identity line is dashed. Regression line equation: $\mathrm{y}=1.73+0.99$ x; $95 \%$ CI for intercept 0.77 to 2.50 and for slope 0.96 to 1.02 indicated small constant and small proportional difference. Cusum test for linearity indicates significant deviation from linearity ( $\mathrm{P}=0.04$ ). (B) Residual plot presents distribution of difference around fitted regression line.

