

## Supporting Information

**Table S1** Sequences and MRM<sup>HR</sup> transitions of target peptides

| Name                                   | Alias | Probe peptide sequence  | Standard peptide (m/z) |                       | Internal standard (m/z) |                       | CE (V) |
|----------------------------------------|-------|-------------------------|------------------------|-----------------------|-------------------------|-----------------------|--------|
|                                        |       |                         | Q1                     | Fragment              | Q1                      | Fragment              |        |
| Equilibrative nucleoside transporter 1 | ENT1  | WLPSLV <u>L</u> AR      | 527.8                  | 755.3774 - 755.5774   | 531.3                   | 762.3774 - 762.5774   | 30     |
|                                        |       |                         |                        | 658.3246 - 658.5246   |                         | 665.3246 - 665.5246   |        |
|                                        |       |                         |                        | 571.2926 - 571.4926   |                         | 578.2926 - 578.4926   |        |
|                                        |       |                         |                        | 458.2085 - 458.4085   |                         | 465.2085 - 465.4085   |        |
| Equilibrative nucleoside transporter 2 | ENT2  | SLTSYFLWP <u>D</u> EDSR | 858.4                  | 718.2002 - 718.4002   | 861.4                   | 724.2002 - 724.4002   | 32     |
|                                        |       |                         |                        | 904.2795 - 904.4795   |                         | 910.2795 - 910.4795   |        |
|                                        |       |                         |                        | 1164.4320 - 1164.6320 |                         | 1170.4320 - 1170.6320 |        |
|                                        |       |                         |                        | 1017.3636 - 1017.5636 |                         | 1023.3636 - 1023.5636 |        |
| Concentrative nucleoside transporter 1 | CNT1  | AGSSFVFGEAL <u>V</u> K  | 656.4                  | 763.3349 - 763.5349   | 659.9                   | 770.3349 - 770.5349   | 29     |
|                                        |       |                         |                        | 616.2665 - 616.4665   |                         | 623.2665 - 623.4665   |        |
|                                        |       |                         |                        | 862.4033 - 862.6033   |                         | 869.4033 - 869.6033   |        |
|                                        |       |                         |                        | 559.2450 - 559.4450   |                         | 566.2450 - 566.4450   |        |
| Concentrative nucleoside transporter   | CNT2  | LAYPE <u>V</u> EESK     | 582.8                  | 817.2938 - 817.4938   | 585.8                   | 823.2938 - 823.4938   | 31     |
|                                        |       |                         |                        | 980.3571 -            |                         | 986.3571 -            |        |

|                                                     |      |                            |       |                        |  |                        |  |
|-----------------------------------------------------|------|----------------------------|-------|------------------------|--|------------------------|--|
| transporter<br>2                                    |      |                            |       | 980.5571               |  | 986.5571               |  |
|                                                     |      |                            |       | 720.2410 -<br>720.4410 |  | 726.2410 -<br>726.4410 |  |
|                                                     |      |                            |       | 591.1984 -<br>591.3984 |  | 597.1984 -<br>597.3984 |  |
| Concentrati<br>ve<br>nucleoside<br>transporter<br>3 | CNT3 | DHFFA <u>F</u> K           | 456.2 | 659.2552 -<br>659.4552 |  | 669.2552 -<br>669.4552 |  |
|                                                     |      |                            |       | 365.1183 -<br>365.3183 |  | 375.1183 -<br>375.3183 |  |
|                                                     |      |                            |       | 512.1867 -<br>512.3867 |  | 522.1867 -<br>522.3867 |  |
|                                                     |      |                            |       | 765.2355 -<br>765.4355 |  | 775.2355 -<br>775.4355 |  |
| Multidrug<br>resistance-<br>associated<br>protein 1 | MRP1 | TPSGN <u>L</u> VNR         | 479.3 | 759.3108 -<br>759.5108 |  | 766.3108 -<br>766.5108 |  |
|                                                     |      |                            |       | 672.2787 -<br>672.4787 |  | 679.2787 -<br>679.4787 |  |
|                                                     |      |                            |       | 501.2144 -<br>501.4144 |  | 508.2144 -<br>508.4144 |  |
|                                                     |      |                            |       | 615.2573 -<br>615.4573 |  | 622.2573 -<br>622.4573 |  |
| Multidrug<br>resistance-<br>associated<br>protein 2 | MRP2 | QLLNN <u>I</u> <u>L</u> R  | 492.3 | 742.3570 -<br>742.5570 |  | 749.3570 -<br>749.5570 |  |
|                                                     |      |                            |       | 629.2729 -<br>629.4729 |  | 636.2729 -<br>636.4729 |  |
|                                                     |      |                            |       | 515.2300 -<br>515.4300 |  | 522.2300 -<br>522.4300 |  |
|                                                     |      |                            |       | 401.1871 -<br>401.3871 |  | 408.1871 -<br>408.3871 |  |
| Multidrug<br>resistance-<br>associated<br>protein 3 | MRP3 | AEGEISDP <u>F</u> <u>R</u> | 560.8 | 621.1991 -<br>621.3991 |  | 631.1991 -<br>631.3991 |  |
|                                                     |      |                            |       | 734.2832 -<br>734.4832 |  | 744.2832 -<br>744.4832 |  |
|                                                     |      |                            |       | 920.3472 -             |  | 930.3472 -             |  |

|                                                     |      |                      |       |                        |       |                        |    |
|-----------------------------------------------------|------|----------------------|-------|------------------------|-------|------------------------|----|
|                                                     |      |                      |       | 920.5472               |       | 930.5472               |    |
|                                                     |      |                      |       | 534.1671 -<br>534.3671 |       | 544.1671 -<br>544.3671 |    |
|                                                     |      |                      |       | 584.1827 -<br>584.3827 |       | 584.1827 -<br>584.3827 |    |
| Multidrug<br>resistance-<br>associated<br>protein 4 | MRP4 | APV <u>L</u> FFDR    | 482.8 | 697.2668 -<br>697.4668 | 486.3 | 704.2668 -<br>704.4668 | 30 |
|                                                     |      |                      |       | 796.3352 -<br>796.5352 |       | 803.3352 -<br>803.5352 |    |
|                                                     |      |                      |       | 893.3880 -<br>893.5880 |       | 900.3880 -<br>900.5880 |    |
|                                                     |      |                      |       | 646.2519 -<br>646.4519 |       | 646.2519 -<br>646.4519 |    |
| Multidrug<br>resistance-<br>associated<br>protein 5 | MRP5 | S <u>L</u> SEASVAVDR | 567.3 | 717.2890 -<br>717.4890 | 570.8 | 717.2890 -<br>717.4890 | 28 |
|                                                     |      |                      |       | 933.3636 -<br>933.5636 |       | 933.3636 -<br>933.5636 |    |
|                                                     |      |                      |       | 559.2198 -<br>559.4198 |       | 559.2198 -<br>559.4198 |    |
|                                                     |      |                      |       | 532.2242 -<br>532.4242 |       | 539.2242 -<br>539.4242 |    |
| Multidrug<br>resistance-<br>associated<br>protein 6 | MRP6 | APETEP <u>F</u> LR   | 530.3 | 762.3145 -<br>762.5145 | 533.8 | 769.3145 -<br>769.5145 | 29 |
|                                                     |      |                      |       | 891.3571 -<br>891.5571 |       | 898.3571 -<br>898.5571 |    |
|                                                     |      |                      |       | 661.2668 -<br>661.4668 |       | 668.2668 -<br>668.4668 |    |
|                                                     |      |                      |       | 618.2570 -<br>618.4570 |       | 625.2570 -<br>625.4570 |    |
| Multidrug<br>resistance<br>protein 1                | MDR1 | NTTGAL <u>T</u> TR   | 467.8 | 719.3046 -<br>719.5046 | 471.3 | 726.3046 -<br>726.5046 | 22 |
|                                                     |      |                      |       | 490.1984 -<br>490.3984 |       | 497.1984 -<br>497.3984 |    |
|                                                     |      |                      |       | 561.2355 -             |       | 568.2355 -             |    |

|                                           |      |                     |       |            |       |            |    |
|-------------------------------------------|------|---------------------|-------|------------|-------|------------|----|
|                                           |      |                     |       | 561.4355   |       | 568.4355   |    |
|                                           |      |                     |       | 644.2726 - |       | 651.2726 - |    |
|                                           |      |                     |       | 644.4726   |       | 651.4726   |    |
|                                           |      |                     |       | 757.3567 - |       | 764.3567 - |    |
|                                           |      |                     |       | 757.5567   |       | 764.5567   |    |
| Breast<br>cancer<br>resistance<br>protein | BCRP | SSLLDV <u>L</u> AAR | 522.8 |            | 526.3 |            | 23 |
|                                           |      |                     |       | 529.2457 - |       | 536.2457 - |    |
|                                           |      |                     |       | 529.4457   |       | 536.4457   |    |
|                                           |      |                     |       | 430.1772 - |       | 437.1772 - |    |
|                                           |      |                     |       | 430.3772   |       | 437.3772   |    |

Theoretical m/z values of doubly charged ions of intact peptides (Q1) were assumed for precursor ions. Fragment ions from each precursor ion were separated and detected by ToF-MS. Four singly charged fragment ions for each precursor ion were extracted from the ToF-MS spectrum. Underlines indicate amino acid residues labeled with stable isotopes ( $^{13}\text{C}$  and  $^{15}\text{N}$ ).

**Table S2** HPLC-MS parameters for protein analysis

| Parameter                   | Value    |
|-----------------------------|----------|
| Autosampler                 | 4 °C     |
| Column oven                 | 25 °C    |
| Curtain gas                 | 20 p.s.i |
| Ion source gas 1            | 20 p.s.i |
| Ion source gas 2            | 0 p.s.i  |
| Ionspray voltage (positive) | 2300 V   |
| Ion source temperature      | 150 °C   |

Mobile phases A and B consisted of 0.1% formic acid in 98% water and 2% acetonitrile, and 0.1% formic acid in 80% acetonitrile and 20% water, respectively. An aliquot (5  $\mu$ l) of each sample was injected and loaded on a trap column (C18-3  $\mu$ m, 200  $\mu$ m x 0.5 mm, Eksigent) by passing 5  $\mu$ l/min of mobile phase A for 10 min. Elution was done with a 150-min gradient as follows: 2% B at 0 to 1 min after loading, a linear gradient from 2% B to 10% B at 1 to 6 min, 10% B to 50% B at 6 to 120 min, 50% B to 90% B at 120 to 123 min, 90% B at 123 to 129 min, 90% B to 2% B at 129 to 130 min, and 2% B at 130 to 150 min. The flow rate was 200 nl/min. Trapped samples were separated on a nano column (C18-3  $\mu$ m, 75  $\mu$ m x 150 mm, Eksigent). Multiple products derived from single peptide were monitored at specific m/z fragments (Table S1).

**Table S3** Protein concentrations of enzymes in cytosolic fraction of pancreatic cancer cell lines

| Quantified protein                | Protein concentration in cells (fmol / $\mu\text{g}$ cytosolic protein) |                   |                   |                   |                   |
|-----------------------------------|-------------------------------------------------------------------------|-------------------|-------------------|-------------------|-------------------|
|                                   | PK9 <sup>†</sup>                                                        | CFPac-1           | PK1               | SUIT-2            | AsPc-1            |
| Enzymes in <i>salvage</i> pathway |                                                                         |                   |                   |                   |                   |
| dCK                               | 0.477 $\pm$ 0.047                                                       | 0.351 $\pm$ 0.016 | 0.209 $\pm$ 0.006 | 0.188 $\pm$ 0.040 | 0.152 $\pm$ 0.017 |
| UMP-CMP kinase                    | 6.17 $\pm$ 0.23                                                         | 4.46 $\pm$ 0.11   | 4.00 $\pm$ 0.17   | 3.72 $\pm$ 0.18   | 3.73 $\pm$ 0.14   |
| CDA                               | 0.276 $\pm$ 0.018                                                       | 0.390 $\pm$ 0.040 | <0.10             | <0.10             | 1.15 $\pm$ 0.03   |
| DCTD                              | 1.12 $\pm$ 0.04                                                         | 1.39 $\pm$ 0.07   | 1.53 $\pm$ 0.07   | 0.815 $\pm$ 0.055 | 1.38 $\pm$ 0.08   |
| cN-IA                             | <0.05                                                                   | <0.02             | <0.02             | <0.02             | <0.02             |
| cN-IB                             | <0.05                                                                   | <0.02             | <0.02             | <0.02             | <0.02             |
| cN-II                             | 2.38 $\pm$ 0.22                                                         | 2.29 $\pm$ 0.15   | 3.60 $\pm$ 0.15   | 0.871 $\pm$ 0.044 | 1.74 $\pm$ 0.09   |
| cN-III                            | 0.730 $\pm$ 0.083                                                       | 0.730 $\pm$ 0.076 | 1.32 $\pm$ 0.11   | 1.09 $\pm$ 0.06   | 1.42 $\pm$ 0.23   |
| Enzymes in <i>de novo</i> pathway |                                                                         |                   |                   |                   |                   |
| RRM1                              | 1.33 $\pm$ 0.01                                                         | 1.25 $\pm$ 0.04   | 2.46 $\pm$ 0.04   | 0.272 $\pm$ 0.034 | 1.44 $\pm$ 0.12   |
| RRM2                              | <0.10                                                                   | 0.787 $\pm$ 0.103 | 1.34 $\pm$ 0.21   | <0.10             | 1.15 $\pm$ 0.15   |
| CTPS1                             | 2.03 $\pm$ 0.06                                                         | 1.68 $\pm$ 0.05   | 2.78 $\pm$ 0.05   | 1.44 $\pm$ 0.09   | 1.02 $\pm$ 0.06   |
| CTPS2                             | 0.489 $\pm$ 0.019                                                       | 0.376 $\pm$ 0.027 | 0.750 $\pm$ 0.034 | 0.351 $\pm$ 0.069 | 0.374 $\pm$ 0.028 |

<sup>†</sup>Protein concentrations in PK9 cells are cited from Ohmine *et al.*, 2012 (8). Cytosolic fraction from each cell (50  $\mu\text{g}$  protein), spiked with 100 fmol of stable isotope-labeled peptide mixture, was injected into the LC-MS/MS. The protein concentration (fmol/ $\mu\text{g}$  protein) was calculated from the peak area ratio of target and stable isotope-labeled peptide in each MRM transition. The protein concentration of each enzyme was determined as the average from three or four MRM transitions showing signal peaks. The protein concentration of each enzyme in each sample is shown as mean  $\pm$  SEM (n=3-4). If the value was below the limit of quantification, the value of the quantification limit was used.

**Table S4** Protein concentrations of transporters in membrane fraction of pancreatic cancer cell lines

| Quantified protein | Protein concentration in cells (fmol / $\mu\text{g}$ membrane protein) |                   |                   |                 |                 |
|--------------------|------------------------------------------------------------------------|-------------------|-------------------|-----------------|-----------------|
|                    | PK9 <sup>†</sup>                                                       | CFPac-1           | PK1               | SUIT-2          | AsPc-1          |
| ENT1               | 1.92 $\pm$ 0.08                                                        | 2.46 $\pm$ 0.25   | 3.84 $\pm$ 0.14   | 4.05 $\pm$ 0.38 | 6.19 $\pm$ 0.71 |
| ENT2               | <2.00                                                                  | <1.00             | <1.00             | <1.00           | <1.00           |
| CNT1               | <0.20                                                                  | <1.00             | <1.00             | <1.00           | <1.00           |
| CNT2               | <0.20                                                                  | <1.00             | <1.00             | <1.00           | <1.00           |
| CNT3               | <0.20                                                                  | <1.00             | <1.00             | <1.00           | <1.00           |
| MRP1               | 1.39 $\pm$ 0.16                                                        | <1.00             | <1.00             | <1.00           | <1.00           |
| MRP2               | 0.504 $\pm$ 0.115                                                      | <0.10             | 0.741 $\pm$ 0.219 | <0.10           | <0.10           |
| MRP3               | <0.20                                                                  | 1.20 $\pm$ 0.14   | 0.690 $\pm$ 0.083 | 1.21 $\pm$ 0.17 | <0.10           |
| MRP4               | 0.508 $\pm$ 0.055                                                      | 0.507 $\pm$ 0.081 | <0.10             | 1.90 $\pm$ 0.15 | 1.84 $\pm$ 0.19 |
| MRP5               | <2.00                                                                  | <1.00             | <1.00             | <1.00           | <1.00           |
| MRP6               | <0.20                                                                  | <0.10             | <0.10             | <0.10           | <0.10           |
| MDR1               | <0.20                                                                  | <1.00             | <1.00             | <1.00           | <1.00           |
| BCRP               | 0.352 $\pm$ 0.040                                                      | <0.20             | 11.1 $\pm$ 0.6    | <0.20           | 2.49 $\pm$ 0.33 |

<sup>†</sup>Protein concentrations in PK9 cells are cited from Ohmine *et al.*, 2012 (8). Membrane fraction from each cell (1  $\mu\text{g}$  protein), spiked with 10 fmol stable isotope-labeled peptide mixture, was injected into the LC-MS/MS. The protein concentration (fmol/ $\mu\text{g}$  protein) was calculated from the peak area ratio of target and stable isotope-labeled peptides in each MRM<sup>HR</sup> transition. The protein concentration of each transporter was determined as the average of three or four MRM<sup>HR</sup> transitions showing signal peaks. The protein concentration of each transporter in each sample is given as mean  $\pm$  SEM (n=3-4). If the value was below the limit of quantification, the value of the quantification limit was used.

**Table S5-1** Protein concentrations of enzymes in cytosolic fraction of samples No. 1-5

| Quantified protein                | Protein concentration in tissues (fmol / $\mu\text{g}$ cytosolic protein) |                   |                   |                   |                   |
|-----------------------------------|---------------------------------------------------------------------------|-------------------|-------------------|-------------------|-------------------|
|                                   | No. 1                                                                     | No. 2             | No. 3             | No. 4             | No. 5             |
| Enzymes in <i>salvage</i> pathway |                                                                           |                   |                   |                   |                   |
| dCK                               | $0.181 \pm 0.021$                                                         | $0.294 \pm 0.016$ | $0.370 \pm 0.026$ | $0.225 \pm 0.031$ | $0.366 \pm 0.039$ |
| UMP-CMP kinase                    | $3.57 \pm 0.11$                                                           | $4.85 \pm 0.13$   | $16.1 \pm 0.6$    | $5.71 \pm 0.16$   | $4.50 \pm 0.17$   |
| CDA                               | $0.279 \pm 0.038$                                                         | $0.542 \pm 0.071$ | $0.495 \pm 0.021$ | $1.45 \pm 0.06$   | $0.372 \pm 0.025$ |
| DCTD                              | $0.648 \pm 0.051$                                                         | $1.44 \pm 0.10$   | $1.72 \pm 0.08$   | $1.18 \pm 0.09$   | $1.10 \pm 0.11$   |
| cN-IA                             | <1.00                                                                     | <1.00             | <1.00             | <1.00             | <1.00             |
| cN-IB                             | <1.00                                                                     | <1.00             | <1.00             | <1.00             | <1.00             |
| cN-II                             | $0.819 \pm 0.036$                                                         | $1.68 \pm 0.08$   | $0.663 \pm 0.061$ | $1.75 \pm 0.10$   | $1.57 \pm 0.17$   |
| cN-III                            | $0.482 \pm 0.073$                                                         | $0.888 \pm 0.261$ | $1.66 \pm 0.53$   | $1.83 \pm 0.29$   | $0.262 \pm 0.053$ |
| Enzymes in <i>de novo</i> pathway |                                                                           |                   |                   |                   |                   |
| RRM1                              | <0.20                                                                     | <0.20             | <0.20             | <0.20             | <0.20             |
| RRM2                              | <0.20                                                                     | <0.20             | <0.20             | <0.20             | <0.20             |
| CTPS1                             | $0.318 \pm 0.03$                                                          | $0.422 \pm 0.012$ | $0.593 \pm 0.090$ | $0.731 \pm 0.033$ | $0.430 \pm 0.026$ |
| CTPS2                             | <0.10                                                                     | <0.10             | $0.847 \pm 0.027$ | $0.385 \pm 0.008$ | $0.207 \pm 0.031$ |



**Table S5-2** Protein concentrations of enzymes in cytosolic fraction of samples No. 6-10

| Quantified protein                | Protein concentration in tissues (fmol / $\mu\text{g}$ cytosolic protein) |                   |                   |                   |                   |
|-----------------------------------|---------------------------------------------------------------------------|-------------------|-------------------|-------------------|-------------------|
|                                   | No. 6                                                                     | No. 7             | No. 8             | No. 9             | No. 10            |
| Enzymes in <i>salvage</i> pathway |                                                                           |                   |                   |                   |                   |
| dCK                               | $0.479 \pm 0.067$                                                         | $0.556 \pm 0.055$ | $0.693 \pm 0.046$ | $0.544 \pm 0.035$ | $0.794 \pm 0.032$ |
| UMP-CMP kinase                    | $33.0 \pm 1.5$                                                            | $14.5 \pm 0.8$    | $3.64 \pm 0.1$    | $10.0 \pm 0.2$    | $19.5 \pm 0.3$    |
| CDA                               | $2.48 \pm 0.03$                                                           | $0.448 \pm 0.076$ | $0.233 \pm 0.020$ | <0.20             | <0.20             |
| DCTD                              | $1.49 \pm 0.21$                                                           | $1.52 \pm 0.07$   | $0.804 \pm 0.097$ | $1.15 \pm 0.08$   | $1.80 \pm 0.21$   |
| cN-IA                             | <1.00                                                                     | <1.00             | <1.00             | <1.00             | <1.00             |
| cN-IB                             | <1.00                                                                     | <1.00             | <1.00             | <1.00             | <1.00             |
| cN-II                             | $2.31 \pm 0.27$                                                           | $0.563 \pm 0.049$ | $0.778 \pm 0.082$ | $2.14 \pm 0.03$   | $2.23 \pm 0.04$   |
| cN-III                            | $1.97 \pm 0.29$                                                           | $1.49 \pm 0.10$   | $0.554 \pm 0.053$ | $1.25 \pm 0.15$   | $1.43 \pm 0.21$   |
| Enzymes in <i>de novo</i> pathway |                                                                           |                   |                   |                   |                   |
| RRM1                              | <0.20                                                                     | <0.20             | <0.20             | <0.20             | <0.20             |
| RRM2                              | <0.20                                                                     | <0.20             | <0.20             | <0.20             | <0.20             |
| CTPS1                             | $1.28 \pm 0.03$                                                           | $0.400 \pm 0.051$ | $0.565 \pm 0.024$ | $0.831 \pm 0.063$ | $1.34 \pm 0.09$   |
| CTPS2                             | $0.828 \pm 0.005$                                                         | $1.00 \pm 0.02$   | $0.248 \pm 0.034$ | $0.993 \pm 0.047$ | $0.720 \pm 0.026$ |

Average, SEM and CV were calculated, excluding samples under the detection limit. Cytosolic fraction from 10 pancreatic cancer tissues (50  $\mu\text{g}$  protein), spiked with 100 fmol of stable isotope-labeled peptide mixture, was injected into the LC-MS/MS. The protein concentration (fmol/ $\mu\text{g}$  protein) was calculated from the peak area ratio of target and stable isotope-labeled peptide in each MRM transition. The protein concentration of each enzyme was determined as the average from three or four MRM transitions showing signal peaks. The protein concentration of each enzyme in each sample is shown as mean  $\pm$  SEM (n=3-4). If the value was below the limit of quantification, the value of the quantification limit was used.

**Table S6-1** Protein concentrations of transporters in membrane fraction of samples No. 2-5

| Quantified protein | Protein concentration in tissues (fmol / $\mu\text{g}$ membrane protein) |                   |                 |                 |
|--------------------|--------------------------------------------------------------------------|-------------------|-----------------|-----------------|
|                    | No. 2                                                                    | No. 3             | No. 4           | No. 5           |
| ENT1               | $2.76 \pm 0.32$                                                          | $3.38 \pm 0.04$   | $2.61 \pm 0.09$ | $2.55 \pm 0.14$ |
| ENT2               | <1.00                                                                    | <1.00             | <1.00           | <1.00           |
| CNT1               | <1.00                                                                    | <1.00             | <1.00           | <1.00           |
| CNT2               | <1.00                                                                    | <1.00             | <1.00           | <1.00           |
| CNT3               | <1.00                                                                    | <1.00             | <1.00           | <1.00           |
| MRP1               | <1.00                                                                    | <1.00             | <1.00           | <1.00           |
| MRP2               | <0.10                                                                    | <0.10             | <0.10           | <0.10           |
| MRP3               | <0.10                                                                    | <0.10             | <0.10           | <0.10           |
| MRP4               | <0.50                                                                    | <0.50             | <0.50           | <0.50           |
| MRP5               | <1.00                                                                    | <1.00             | <1.00           | <1.00           |
| MRP6               | $0.268 \pm 0.034$                                                        | $0.299 \pm 0.042$ | <0.10           | <0.10           |
| MDR1               | <1.00                                                                    | <1.00             | <1.00           | <1.00           |
| BCRP               | <0.50                                                                    | <0.50             | <0.50           | <0.50           |

**Table S6-2** Protein concentrations of transporters in membrane fraction of samples No. 6-10

| Quantified protein | Protein concentration in tissues (fmol / $\mu$ g membrane protein) |                 |                 |                 |
|--------------------|--------------------------------------------------------------------|-----------------|-----------------|-----------------|
|                    | No. 6                                                              | No. 7           | No. 9           | No. 10          |
| ENT1               | 3.59 $\pm$ 0.16                                                    | 2.60 $\pm$ 0.21 | 3.97 $\pm$ 0.61 | 3.21 $\pm$ 0.17 |
| ENT2               | <1.00                                                              | <1.00           | <1.00           | <1.00           |
| CNT1               | <1.00                                                              | <1.00           | <1.00           | <1.00           |
| CNT2               | <1.00                                                              | <1.00           | <1.00           | <1.00           |
| CNT3               | <1.00                                                              | <1.00           | <1.00           | <1.00           |
| MRP1               | <1.00                                                              | <1.00           | <1.00           | <1.00           |
| MRP2               | <0.10                                                              | <0.10           | <0.10           | <0.10           |
| MRP3               | <0.10                                                              | <0.10           | <0.10           | <0.10           |
| MRP4               | <0.50                                                              | <0.50           | <0.50           | <0.50           |
| MRP5               | <1.00                                                              | <1.00           | <1.00           | <1.00           |
| MRP6               | <0.10                                                              | <0.10           | <0.10           | <0.10           |
| MDR1               | <1.00                                                              | <1.00           | <1.00           | <1.00           |
| BCRP               | <0.50                                                              | <0.50           | <0.50           | <0.50           |

Average, SEM and CV were calculated, excluding samples under the detection limit. Membrane fraction from 8 pancreatic cancer tissues (1  $\mu$ g protein), spiked with 10 fmol stable isotope-labeled peptide mixture, was injected into the LC-MS/MS. The protein concentration (fmol/ $\mu$ g protein) was calculated from the peak area ratio of target and stable isotope-labeled peptides in each MRM<sup>HR</sup> transition. The protein concentration of each transporter was determined as the average of three or four MRM<sup>HR</sup> transitions showing signal peaks. The protein concentration of each transporter in each sample is given as mean  $\pm$  SEM (n=3-4). If the value was below the limit of quantification, the value of the quantification limit was used.