

SUPPLEMENTARY INFORMATION

Table S1. Overview of the 58 selected candidate genes from phase I regarding the fold change, gender and the TaqMan assay used for performing qRT-PCR.

Table S2. Overview of all genes that were predictive for discriminating survival status based on gene expression differences. Data are presented separately for male (left side) and female (right side) rhesus macaques and ordered starting with untreated, treated, and untreated and treated groups combined. The number of measurements and the mean gene expression values (Ct values) are provided by survival status as well as the fold-change difference (delog of inverse log₂ transformed Ct values). The *P* value of this group comparison originates from a parametric *t* test or a non-parametric Kruskal-Wallis test, where applicable. Data are presented in black for the gender showing significant differences and in gray for the gender where significance was not achieved. Genes are ordered per treatment group starting with genes that were significantly associated with survival in both genders followed by genes with increasing *P* value.

Table S3. Based on the probability function of the receiver operating characteristic (ROC) curves reflecting true positives (surviving), true negatives (not-surviving), false positives (not-surviving identified as surviving) and false negatives (surviving identified as not-surviving) for each measurement, a quantification of the correct/incorrect allocation of gene expression measurements/comparisons was made. The following test characteristics are shown for most predictive genes and gene combinations (*EPX* and *SLC22A*) in males and (*MBOAT4*) in females: sensitivity, 1-specificity, positive predictive value (PPV), negative predictive value (NPV). Rows with bold numbers represent the best prediction per category.

Fig. S1. Network of predicted associations for *MBOAT4* and *SLC22A4* and potential target genes, respective proteins, with additional aggregation of their coding function using their gene ontology data in the table.

Fig. S2. NGS-based fold changes recalculated by only taking reads from the area, covered by the TaqMan assay and the qRT-PCR-based fold changes. Data are shown for four of the most predictive candidate genes (from Table 2) in which differential gene expression values are of comparable magnitude (*MBOAT4*, *LCN2*, *DYSF* and *SLC22A4*). Additionally, the coverage of the TaqMan assay is rated by providing the percentage of

total reads in the assay area for the specific genes. Furthermore, the total exon reads per gene and the exon reads in the probe area are shown, as well as the number of exons per gene.

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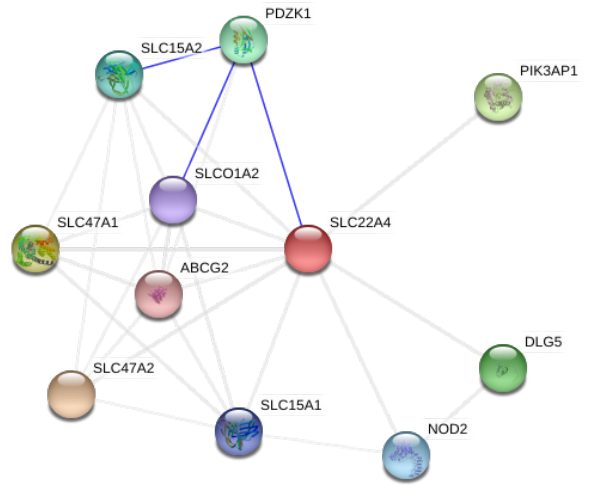
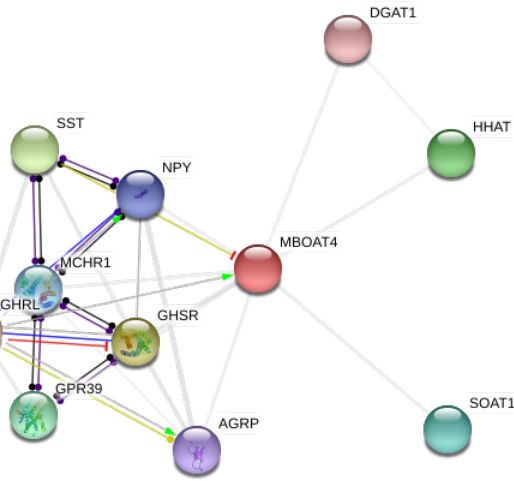
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total reads in the assay area for the specific genes. Furthermore, the total exon reads per gene and the exon reads in the probe area are shown, as well as the number of exons per gene.

Supplemental Figure S1

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Functional enrichments in your network

| Biological Process (GO) | | | |
|-------------------------|--|-------------------|----------------------|
| GO-term | description | count in gene set | false discovery rate |
| GO:0008343 | adult feeding behavior | 4 of 10 | 3.74e-08 |
| GO:0007631 | feeding behavior | 5 of 94 | 4.68e-07 |
| GO:0032100 | positive regulation of appetite | 3 of 4 | 1.07e-06 |
| GO:2000253 | positive regulation of feeding behavior | 3 of 10 | 3.74e-06 |
| GO:0007186 | G protein-coupled receptor signaling pathway | 7 of 1247 | 5.30e-05 |

| Molecular Function (GO) | | | |
|-------------------------|-------------------------------------|-------------------|----------------------|
| GO-term | description | count in gene set | false discovery rate |
| GO:0008374 | O-acyltransferase activity | 4 of 49 | 1.23e-06 |
| GO:0005179 | hormone activity | 4 of 123 | 2.13e-05 |
| GO:0005184 | neuropeptide hormone activity | 2 of 29 | 0.0015 |
| GO:0005102 | signaling receptor binding | 5 of 1513 | 0.0082 |
| GO:0004930 | G protein-coupled receptor activity | 4 of 824 | 0.0082 |

| Cellular Component (GO) | | | |
|-------------------------|----------------------------|-------------------|----------------------|
| GO-term | description | count in gene set | false discovery rate |
| GO:0044432 | endoplasmic reticulum part | 5 of 1294 | 0.0345 |

| Reference publications | | | |
|------------------------|---|-------------------|----------------------|
| publication | (year) title | count in gene set | false discovery rate |
| PMID:21428875 | (2011) Interaction between gastric and upper small intestin... | 8 of 27 | 4.07e-16 |
| PMID:23103610 | (2013) Obesity pharmacotherapy: what is next? | 7 of 32 | 4.35e-13 |
| PMID:22523723 | (2012) Yin and Yang - the Gastric XA-like Cell as Possible D... | 7 of 30 | 4.35e-13 |
| PMID:23621300 | (2013) New advances in models and strategies for developi... | 7 of 37 | 8.09e-13 |
| PMID:23653638 | (2013) Changes in ghrelin-related factors in gastroesophag... | 6 of 12 | 1.23e-12 |

| KEGG Pathways | | | |
|---------------|---|-------------------|----------------------|
| pathway | description | count in gene set | false discovery rate |
| hsa04024 | cAMP signaling pathway | 3 of 195 | 0.0019 |
| hsa04920 | Adipocytokine signaling pathway | 2 of 69 | 0.0042 |
| hsa04080 | Neuroactive ligand-receptor interaction | 2 of 272 | 0.0395 |

| Reactome Pathways | | | |
|-------------------|--------------------------------------|-------------------|----------------------|
| pathway | description | count in gene set | false discovery rate |
| HSA-373076 | Class A/1 (Rhodopsin-like receptors) | 5 of 311 | 1.86e-05 |
| HSA-375276 | Peptide ligand-binding receptors | 4 of 183 | 5.18e-05 |
| HSA-416476 | G alpha (q) signalling events | 3 of 205 | 0.0019 |
| HSA-388396 | GPCR downstream signalling | 5 of 1082 | 0.0019 |
| HSA-418594 | G alpha (i) signalling events | 3 of 387 | 0.0067 |

Functional enrichments in your network

| Biological Process (GO) | | | |
|-------------------------|--------------------------------|-------------------|----------------------|
| GO-term | description | count in gene set | false discovery rate |
| GO:0015893 | drug transport | 5 of 155 | 9.34e-06 |
| GO:0006811 | ion transport | 8 of 1292 | 1.57e-05 |
| GO:0006812 | cation transport | 7 of 866 | 1.98e-05 |
| GO:1902600 | proton transmembrane transport | 4 of 137 | 0.00013 |
| GO:0055085 | transmembrane transport | 7 of 1235 | 0.00013 |

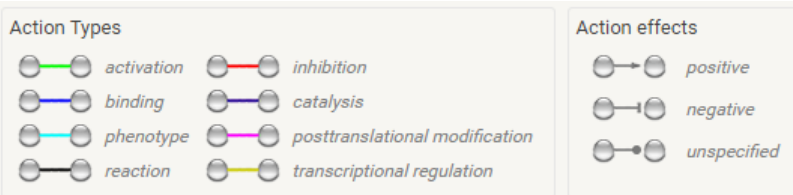
| Molecular Function (GO) | | | |
|-------------------------|---|-------------------|----------------------|
| GO-term | description | count in gene set | false discovery rate |
| GO:0022804 | active transmembrane transporter activity | 7 of 354 | 2.33e-08 |
| GO:0015291 | secondary active transmembrane transporter activity | 6 of 235 | 7.89e-08 |
| GO:0005215 | transporter activity | 8 of 1223 | 1.22e-06 |
| GO:0015078 | proton transmembrane transporter activity | 4 of 120 | 1.08e-05 |
| GO:0015298 | solute:cation antiporter activity | 3 of 33 | 1.71e-05 |

| Cellular Component (GO) | | | |
|-------------------------|------------------------|-------------------|----------------------|
| GO-term | description | count in gene set | false discovery rate |
| GO:0005886 | plasma membrane | 11 of 5159 | 3.42e-05 |
| GO:0098590 | plasma membrane region | 5 of 1061 | 0.0026 |
| GO:0044459 | plasma membrane part | 7 of 2651 | 0.0026 |
| GO:0044425 | membrane part | 10 of 6517 | 0.0026 |
| GO:0016324 | apical plasma membrane | 3 of 307 | 0.0067 |

| Reference publications | | | |
|------------------------|---|-------------------|----------------------|
| publication | (year) title | count in gene set | false discovery rate |
| PMID:28375174 | (2017) Protein Kinases C-Mediated Regulations of Drug Tra... | 7 of 41 | 1.27e-12 |
| PMID:26056583 | (2014) Role of solute carriers in response to anticancer dru... | 7 of 38 | 1.27e-12 |
| PMID:27843352 | (2016) Profile of once-daily darunavircostat fixed-dose ... | 6 of 20 | 8.43e-12 |
| PMID:24856391 | (2014) Ocular cytochrome P450s and transporters: roles in ... | 7 of 64 | 9.26e-12 |
| PMID:28401035 | (2017) Development and Application of Human Renal Proxi... | 6 of 25 | 1.62e-11 |

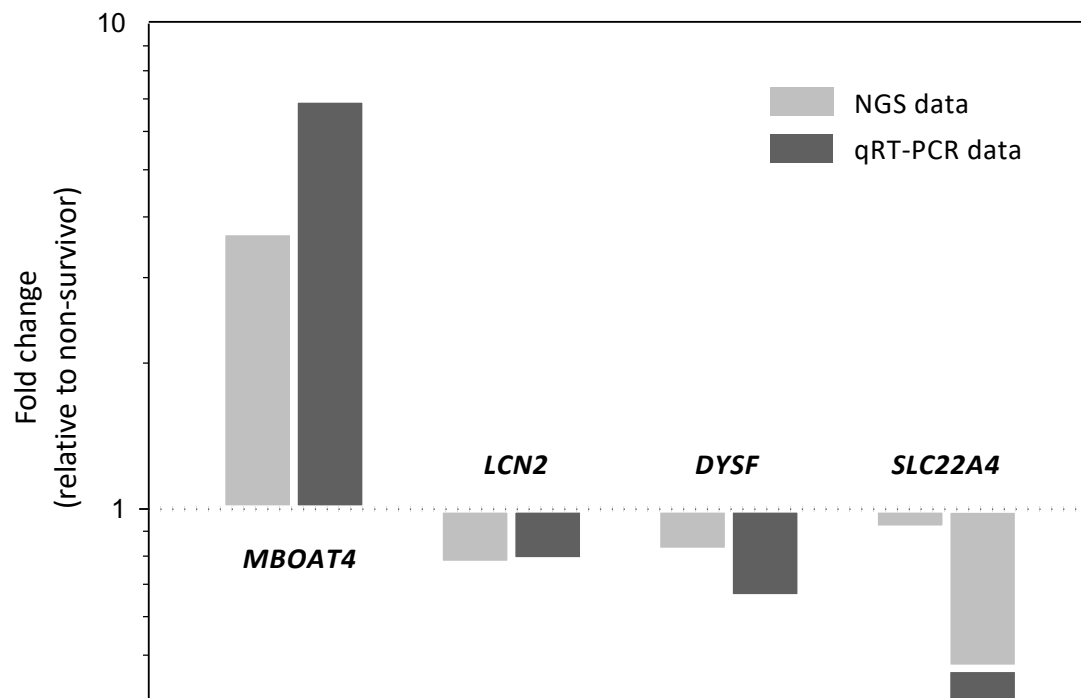
| KEGG Pathways | | | |
|---------------|----------------|-------------------|----------------------|
| pathway | description | count in gene set | false discovery rate |
| hsa04976 | Bile secretion | 2 of 71 | 0.0089 |

| Reactome Pathways | | | |
|-------------------|--|-------------------|----------------------|
| pathway | description | count in gene set | false discovery rate |
| HSA-425407 | SLC-mediated transmembrane transport | 6 of 241 | 1.03e-07 |
| HSA-382551 | Transport of small molecules | 7 of 706 | 7.43e-07 |
| HSA-427975 | Proton/oligopeptide cotransporters | 2 of 4 | 8.89e-05 |
| HSA-425366 | Transport of bile salts and organic acids, metal ions and a... | 3 of 85 | 0.00022 |



Supplemental Figure S2

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| | | | | |
|--|-----|------|------|-----|
| # exons per gene | 3 | 9 | 60 | 15 |
| Total exon reads | 193 | 3362 | 8241 | 188 |
| Exon reads in PPD area | 140 | 690 | 407 | 34 |
| Coverage - % of total reads in PPD area | 73 | 21 | 5 | 18 |