

Supplementary Figures

Supplementary Figure 1. Correlation scatter plots.

Supplementary Figure 2. Functional analysis of non-detected genes.

Supplementary Tables

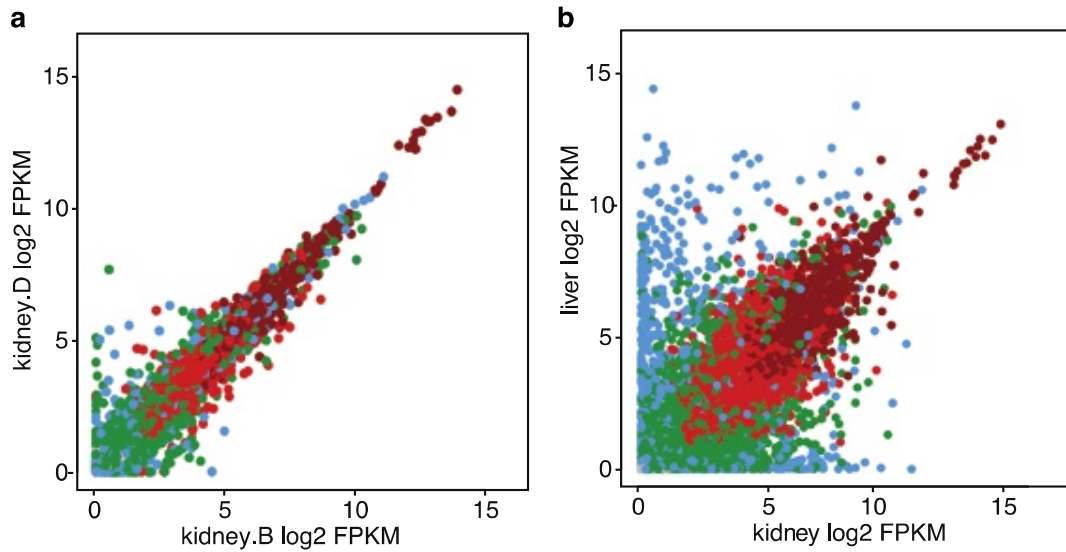
Supplementary Table 1. List of all included tissues and the average Spearman correlation of the gene expression (FPKM) between samples from the same tissue.

Supplementary Table 2. The definition of the gene expression based categories.

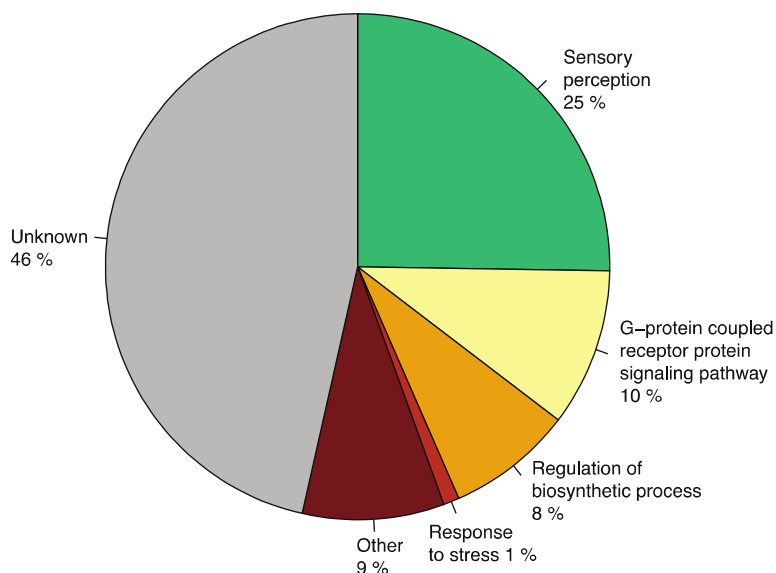
Supplementary Table 3. The number of tissue-specific genes in the analyzed tissues and organs.

Supplementary Table 4. Some examples of identified genes with a tissue-enriched expression pattern.

Supplementary Data set 1. Spreadsheet with the classification of each gene and the average FPKM values for all 27 tissues.



Supplementary Figure 1. Correlation scatter plots. **a)** Scatter plot of FPKM values for all detected genes in two kidney samples from different individuals. The pairwise Spearman correlation coefficient between the samples is 0.98.. Colors represent five categories: not detected (grey), tissue specific, tissue enriched or group enriched (blue), mixed low and high (green), expressed in all low (red), expressed in all high (dark red). **b)** Scatter plot of average FPKM values for all detected genes in four kidney samples (x-axis) and three liver samples (y-axis) from different individuals. The pairwise Spearman correlation coefficient between the two tissues is 0.86 and the colors represent the same categories as in (a).



Supplementary Figure 2. Functional analysis of non-detected genes. Pie chart showing overrepresented biological process Gene Ontology terms for genes that were not detected in any tissue. The category “unknown” refers to genes with no associated terms.

Supplementary Tables

Supplementary Table 1. List of all included tissues and the average Spearman correlation of the gene expression (FPKM) between samples from the same tissue.

Tissue	No of samples	Average correlation coefficient (%)
salivary gland	3	96.4
lung	5	96.5
lymph node	5	96.2
liver	3	96.6
adrenal gland	3	97.7
duodenum	2	97.8
kidney	4	96.9
gallbladder	3	96.2
colon	5	96.2
small intestine	4	97.4
appendix	3	96.6
prostate	4	95.7
testis	7	96.3
cerebral cortex	3	94.9
thyroid gland	4	96.0
heart muscle	4	96.1
esophagus	3	95.8
spleen	4	97.9
stomach	3	94.4
pancreas	2	96.8
placenta	4	96.5
ovary	2	97.6
bone marrow	4	95.8
uterus	3	94.8
urinary bladder	2	95.2
adipose tissue	3	97.2
skin	3	96.1

Supplementary Table 2. The definition of the gene expression based categories.

Class	Category	Definition
Expressed in all	Expressed in all high	Detected in 27 tissues and all tissues >10 FPKM
	Expressed in all low	Detected in 27 tissues and at least one tissue < 10 FPKM
Mixed	Mixed high	Detected in 1-26 tissues and all detected tissues > 10 FPKM
	Mixed low	Detected in 1-26 tissues and at least one tissue < 10 FPKM
	Highly tissue enriched	50-fold higher FPKM level in one tissue compared to all other tissues
Tissue specific	Moderately tissue enriched	5-fold higher FPKM level in one tissue compared to all other tissues
	Group enriched	5-fold higher average FPKM level in a group of 2-7 tissues compared to all other tissues
Not detected	Not detected	< 1 FPKM in all 27 tissues

Supplementary table 3. The number of genes in each tissue specific category and total number of tissue specific genes for each tissue.

Tissue	Highly tissue enriched	Moderately tissue enriched	Group enriched	Total tissue specific
testis	364	760	254	1378
cerebral cortex	20	316	253	589
liver	69	110	164	343
skin	34	72	149	255
esophagus	18	43	172	233
kidney	20	44	156	220
small intestine	2	2	193	197
duodenum	0	7	190	197
heart muscle	17	84	80	181
placenta	26	59	76	161
bone marrow	20	68	57	145
adrenal	5	35	94	134
colon	1	12	118	131
lung	6	14	96	116
prostate	6	16	85	107
salivary gland	24	23	58	105
stomach	5	22	76	103
pancreas	27	20	45	92
adipose tissue	3	29	57	89
thyroid	2	25	52	79
gallbladder	0	7	63	70
spleen	0	6	58	64
uterus	1	11	49	61
appendix	0	2	56	58
urinary bladder	0	2	48	50
lymph node	0	5	44	49
ovary	0	10	33	43
Total	670	1802	1027	3499

Supplementary Table 3. Examples of tissue-specific proteins. The tissue-specific score (TS-score) is the ratio of the FPKM value in the given tissue and the maximal FPKM value in any of all the other tissues analyzed in this study.

Gene	Description	Tissue	TS-score	FPKM
CTRB2	chymotrypsinogen	pancreas	658	51 697
AMY2A	amylase	pancreas	534	55 124
INS	insulin	pancreas	123	2 178
PNLIP	lipase	pancreas	116	31 024
OPALIN	oligodendrocytic myelin protein	cerebral cortex	525	53
GFAP	glial fibrillary acidic protein	cerebral cortex	394	1 409
OLIG2	oligodendrocyte transcription factor	cerebral cortex	262	38
TUSC5	tumor suppressor candidate 5	adipose tissue	64	152
ADIPOQ	adiponectin, collagen domain containing	adipose tissue	57	840
LEP	leptin	adipose tissue	52	268
MYBPC3	myosin binding protein C, cardiac	heart muscle	815	615
TNNI3	troponin I type 3 (cardiac)	heart muscle	334	2 105
TNNT2	troponin T type 2 (cardiac)	heart muscle	102	2 768
UMOD	uromodulin	kidney	648	1 421
SLC22A8	organic anion transporter	kidney	633	269
F2	coagulation factor II (thrombin)	liver	2 205	556
APOA2	apolipoprotein A-II	liver	1 523	5 762
CYP2A6	cytochrome P450, family	liver	545	674
ADH1A	alcohol dehydrogenase 1A	liver	119	748
HP	haptoglobin	liver	106	26 593
SFTPA1	surfactant protein A1	lung	1 206	4 866
SFTPB	surfactant protein B	lung	726	2 744
PSG2	pregnancy specific beta-1-glycoprotein 2	placenta	1 533	268
CSHL1	chorionic somatomammotropin hormone-like	placenta	973	303
PSG11	pregnancy specific beta-1-glycoprotein 11	placenta	800	80
XAGE2	X antigen family, member 2	placenta	72	90
KLK3	Prostate specific antigen	prostate	816	4 701
TGM4	transglutaminase 4 (prostate)	prostate	86	859
ACPP	acid phosphatase, prostate	prostate	52	1 942
C4orf40	chromosome 4 open reading frame 40	salivary gland	960	1 439
CST5	cystatin D	salivary gland	814	1 109
MUC7	mucin 7, secreted	salivary gland	713	6 786
C1orf68	chromosome 1 open reading frame 68	skin	3 858	386
LCE2B	late cornified envelope 2B	skin	3 717	387
KRT2	keratin 2	skin	1 060	1 193
PGA3	pepsinogen A	stomach	1 578	37 916
GIF	gastric intrinsic factor	stomach	791	822
BOD1L2	biorientation of chromosomes in cell division	testis	4 049	405
PRM2	protamine 2	testis	2 520	2 447
SPATA8	spermatogenesis associated 8	testis	1 288	250
IQCF1	IQ motif containing F1	testis	481	48
139D8.6	No name (RP1-139D8.6)	testis	343	35
C17orf74	Chromosome 17 open reading frame 74	testis	342	34
TG	thyroglobulin	thyroid	497	3 256
TSHR	thyroid stimulating hormone receptor	thyroid	158	323
CRNN	cornulin	esophagus	627	2139
MC2R	melanocortin 2 receptor	adrenal	74	36
DEFA4	defensin, alpha 4, corticostatin	bone marrow	405	1 599
ELANE	elastase, neutrophil expressed	bone marrow	311	1 282