Supporting Online Material
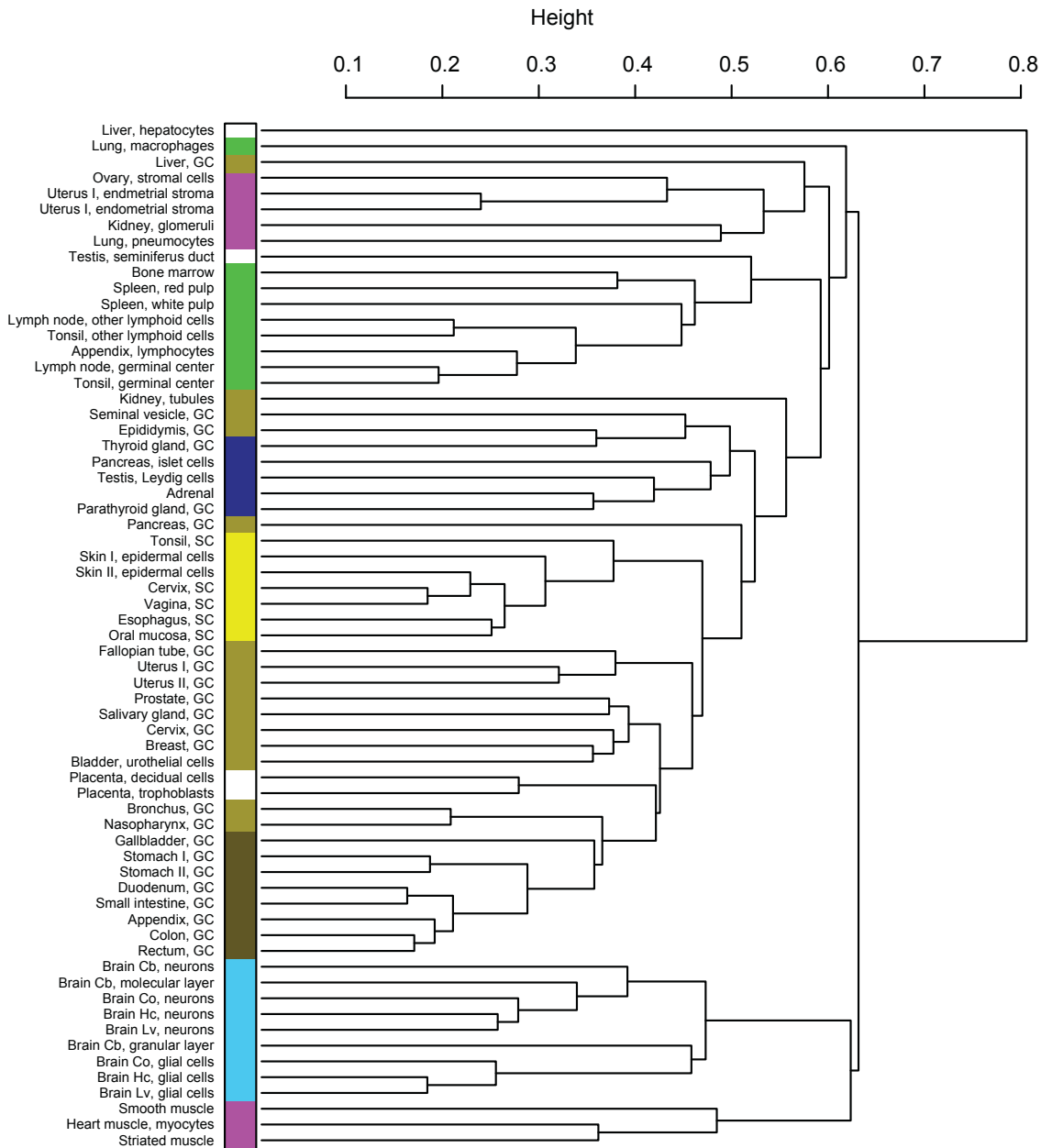
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Supplementary figure 1. Dendrogram of protein expression patterns based on protein-encoded genes from the single human chromosome 9. The dendrogram was generated based on all antibodies (n=215) available for genes encoded on chromosome 9. The colored bar show the tissues with similar functional annotation as described in Figure 1. Light blue represent CNS tissues, green = hematopoetic system, pink = mesenchymal cells, yellow = squamous epithelia, dark blue = endocrine cells and the two shades of brown represent glandular and transitional epithelia. The similarity of the dendrogram generated with a smaller set of antibodies and the dendogram

generated with the complete set of antibodies (Fig. 1) has a cophenetic correlation coefficient of 0.91.
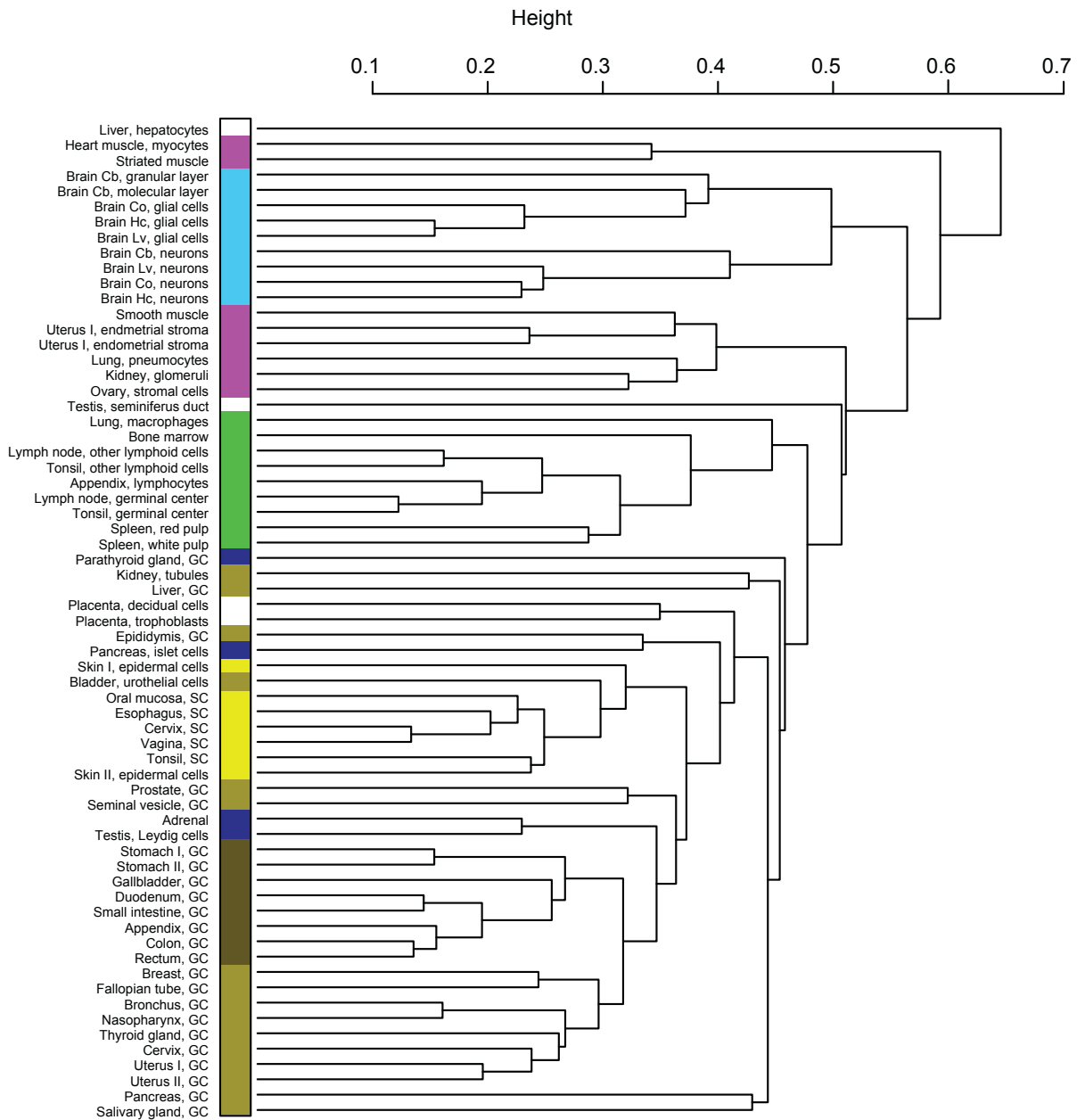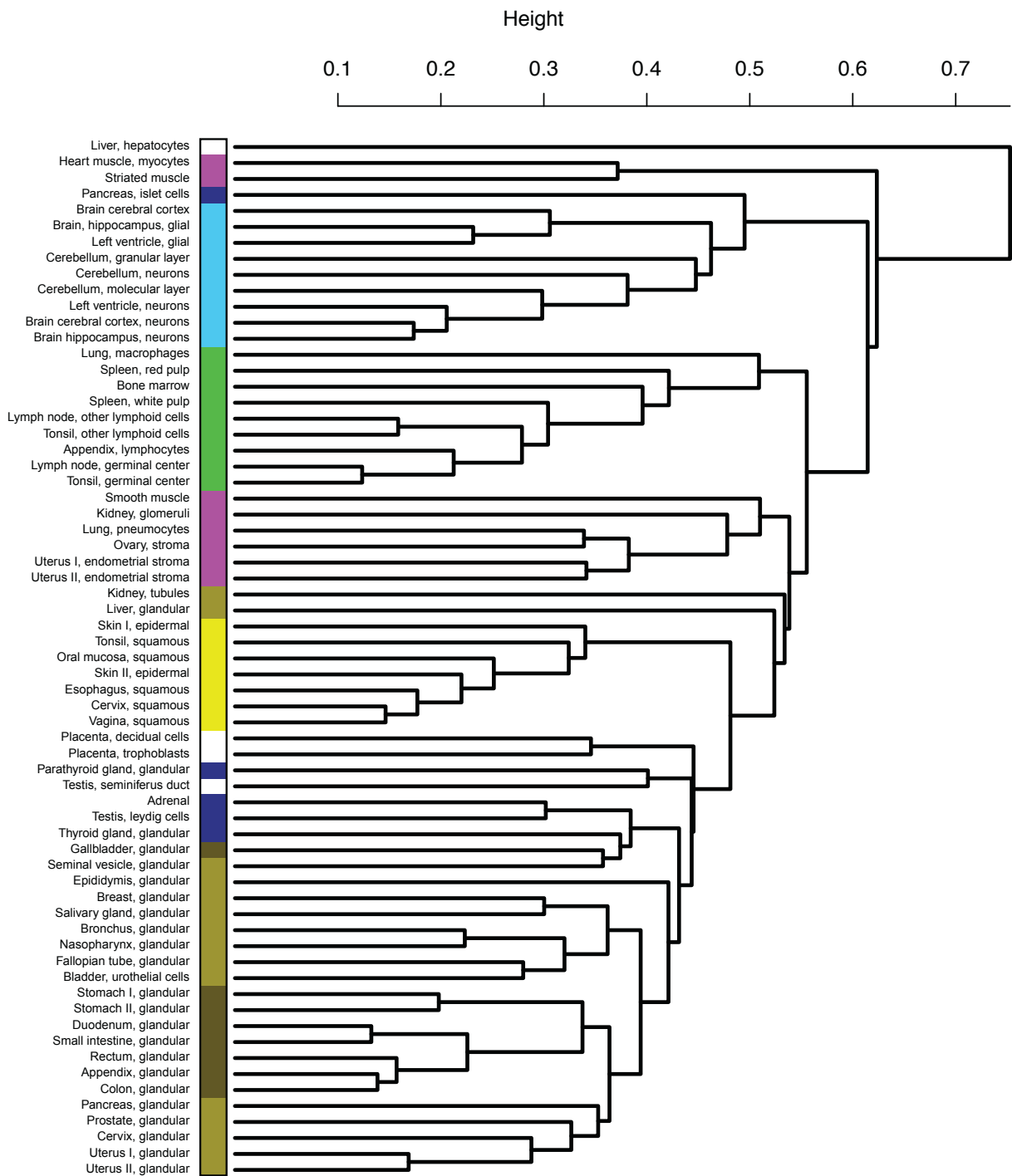
Supplementary figure 2. Dendrogram of protein expression patterns based on protein-encoded genes from the single human chromosome 10. The dendrogram was generated based on all antibodies (n=203) available for genes encoded on chromosome 10. The colored bar indicates the tissues with similar functional annotation as described in figure S1. The similarity of the dendrogram generated with a smaller set of antibodies and the dendogram generated with the complete set of antibodies (Fig. 1) has a cophenetic correlation coefficient of 0.89.

Supplementary figure 3. Dendrogram of protein expression patterns based on protein-encoded genes from the single human chromosome 22. The dendrogram was generated based on all antibodies (n=206) available for genes encoded on chromosome 22. The colored bar indicates the tissues with similar functional annotation as described in figure S1. The similarity of the dendrogram generated with a smaller set of antibodies and the dendogram generated with the complete set of antibodies (Fig. 1) has a cophenetic correlation coefficient of 0.92.
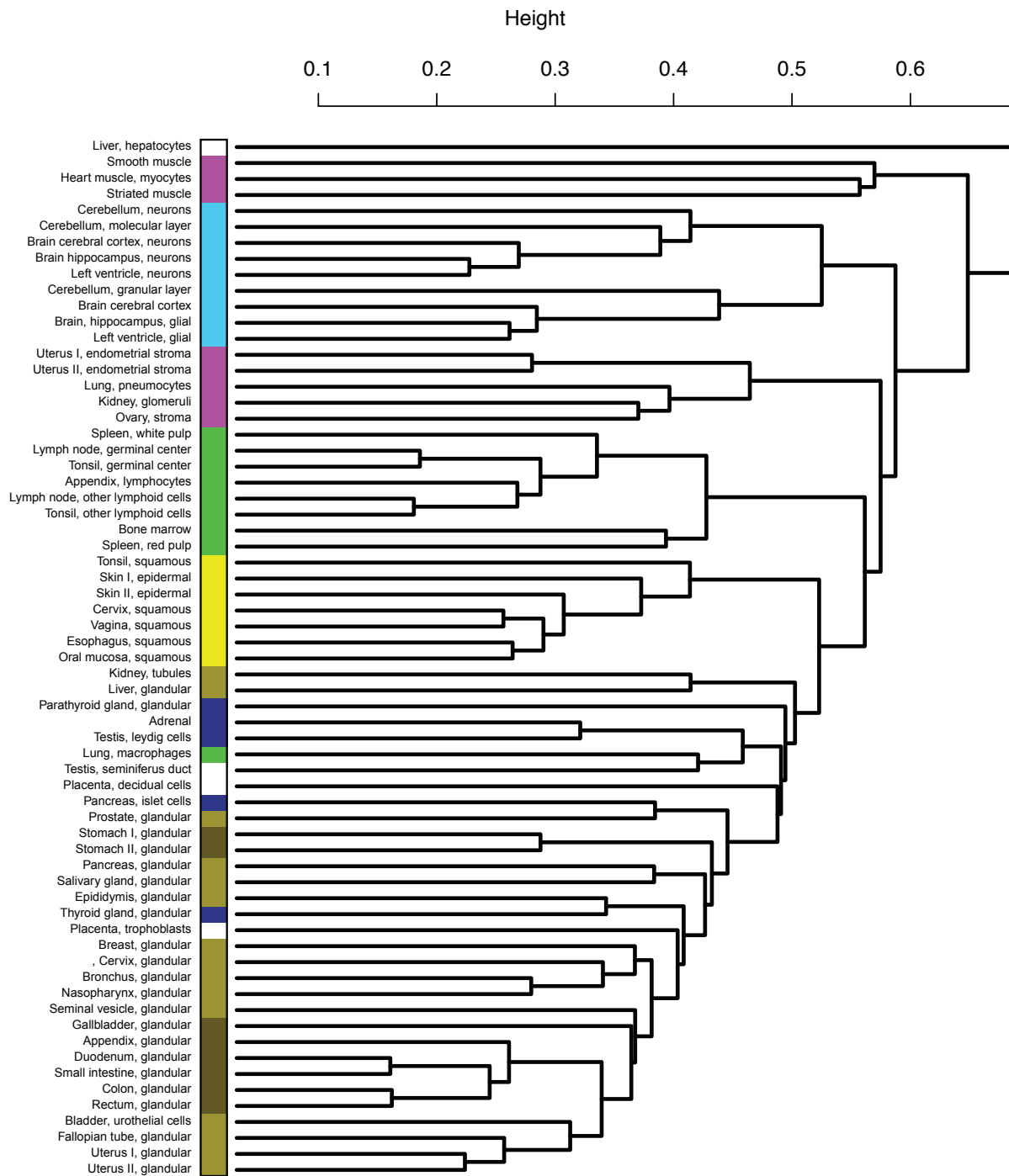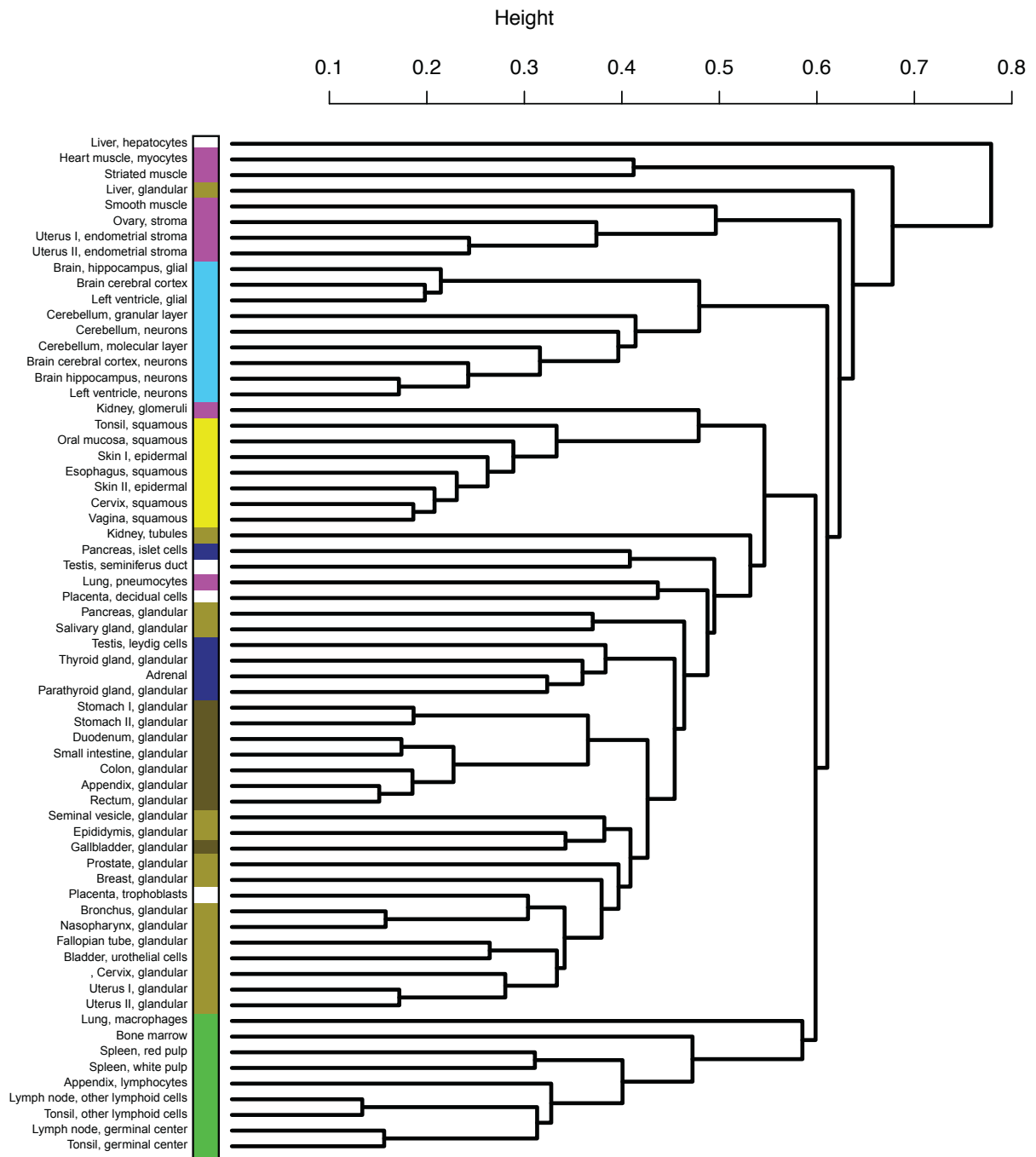
Supplementary figure 4. One of 3000 dendrograms of protein expression patterns based on protein-encoded genes from 200 randomly chosen antibodies. The colored bar indicates the tissues with similar functional annotation as described in figure S1. The mean cophenetic correlation similarity of 3000 generated dendrograms, using a set of 200 antibodies was 0.90.

Supplementary figure 5. One of 3000 dendrograms of protein expression patterns based on protein-encoded genes from 200 randomly chosen antibodies. The colored bar indicates the tissues with similar functional annotation as described in figure S1. The mean cophenetic correlation similarity of 3000 generated dendrograms, using a set of 200 antibodies was 0.90.

Supplementary figure 6. One of 3000 dendrograms of protein expression patterns based on protein-encoded genes from 200 randomly chosen antibodies. The colored bar indicates the tissues with similar functional annotation as described in figure S1. The mean cophenetic correlation similarity of 3000 generated dendrograms, using a set of 200 antibodies, was 0.90.
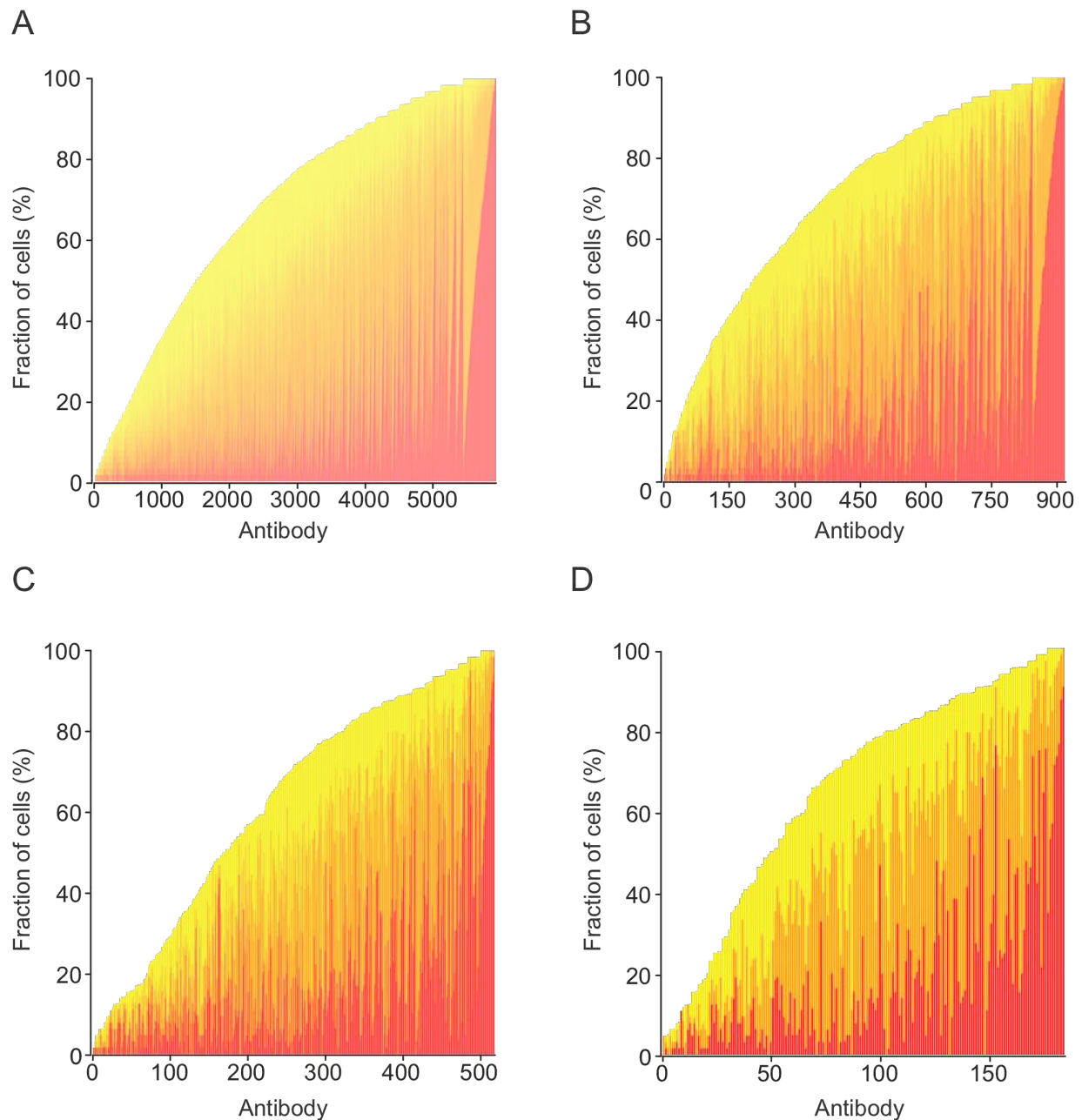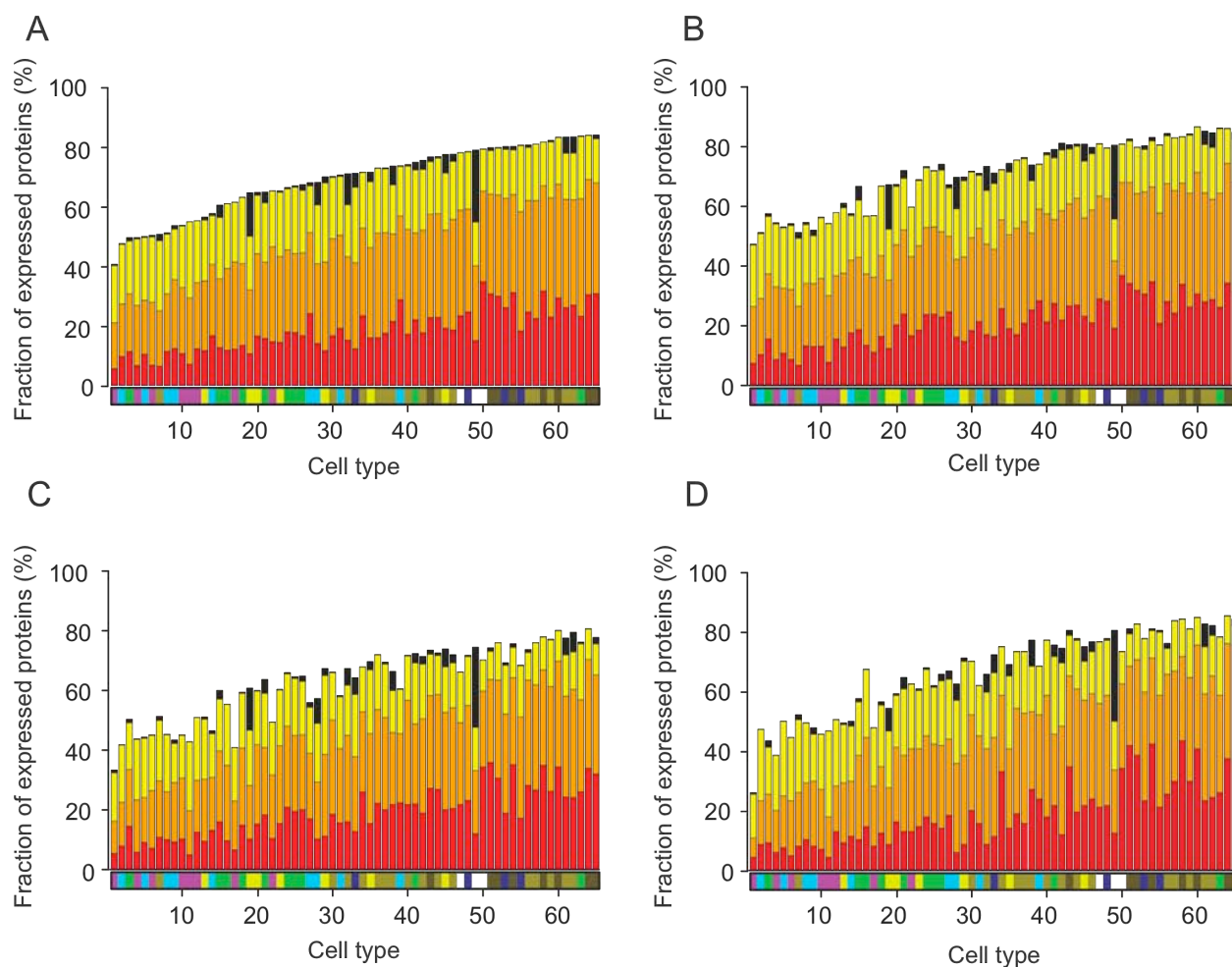
Supplementary figure 7. Comparison of expression levels for 65 cell types with various sub-fractions of antibodies. The fraction (%) of cells in which a particular protein was detected, including the fraction of cells with the relative expression levels strong (red), moderate (orange) and weak (yellow). Antibodies are arranged according to abundance of the corresponding protein target with cell type-specific proteins to the left and "house-keeping proteins to the right. (**A**) Data from all antibodies (n = 5,936) used in this study. (**B**) Data from antibodies with a supportive western blot (n = 920). (**C**) Data from paired antibodies generated to different parts of the same protein and with a correlation coefficient

≥ 0.5 (n = 518). (**D**) Data from paired antibodies generated internally and corresponding to different parts of the same protein and with a correlation coefficient ≥ 0.5 (n = 184). The difference in intensity distribution of the antibodies between the three subsets and the full set was found to be non-significant using a chi square test statistic.

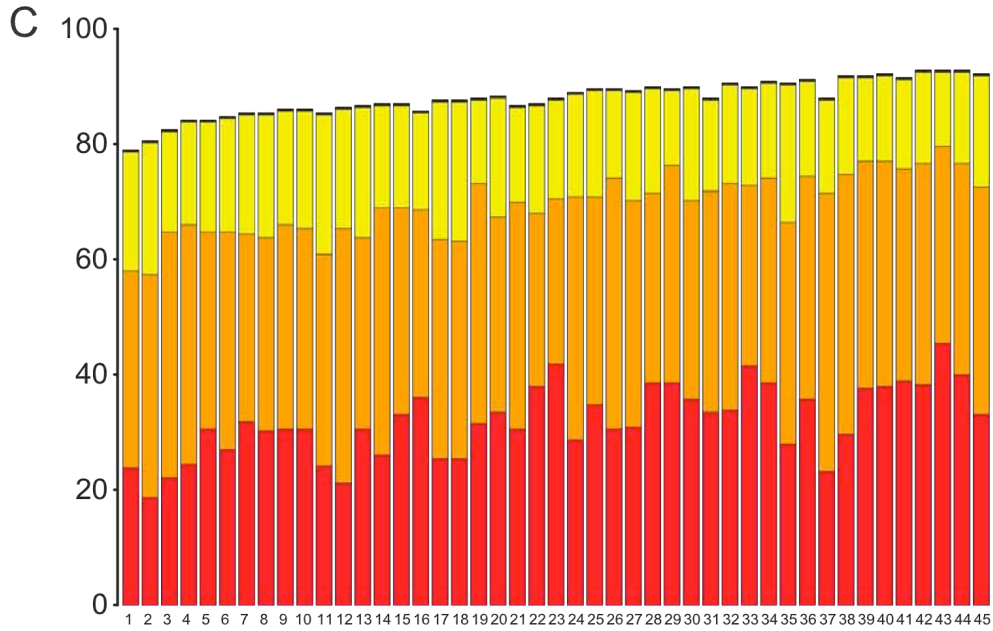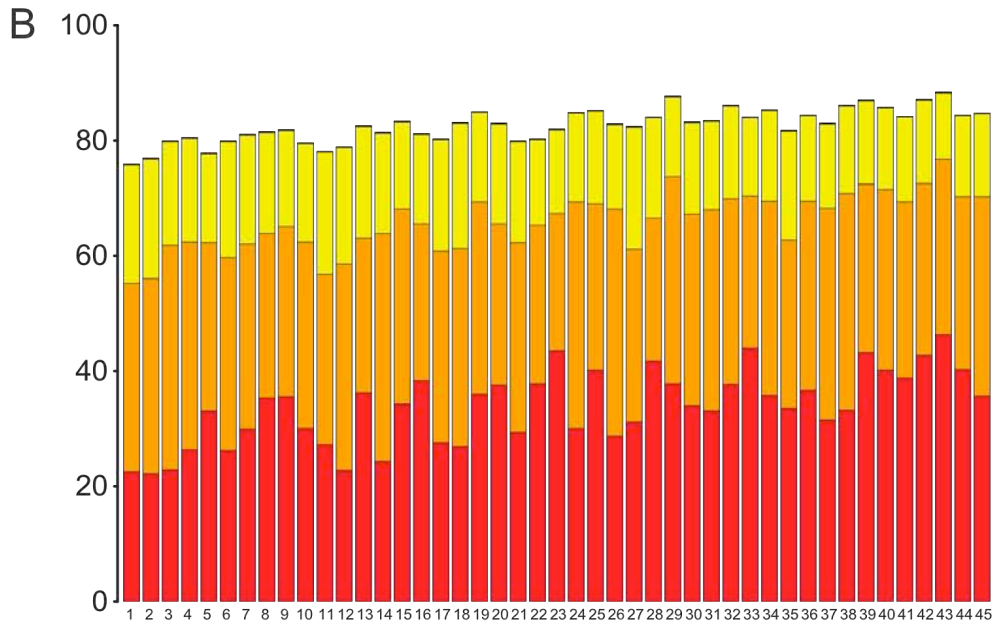**Supplementary figure 8.** Comparison of expression levels for 65 cell types with various sub-fractions of antibodies. Cells are arranged according to the fraction of proteins detected in normal tissues including the fractions of proteins with the relative expression levels strong (red), moderate (orange) and weak (yellow). The black (top) part of the bar represents antibodies with missing data for the particular cell type. A bar displaying the different color codes representing the six major categories of normal cell types (defined in Figure 1) is shown for each cell type. The name of each cell type is shown in table S2 and the results for the various sub-fractions of antibodies are presented in figure S3. (**A**) Data from all antibodies used in this study (n = 5,936). (**B**) Data from antibodies with a supportive western blot (n = 920). (**C**) Data from paired antibodies generated to different parts of the same protein and with a correlation coefficient ≥ 0.5 (n = 518). (**D**) Data from paired antibodies generated internally and corresponding to different parts of the same protein and with a correlation coefficient ≥ 0.8 (n = 184). The difference in intensity distribution of the antibodies between the three subsets and the full set was found to be non-significant using a multiple test corrected chi square test statistic for all tissues.

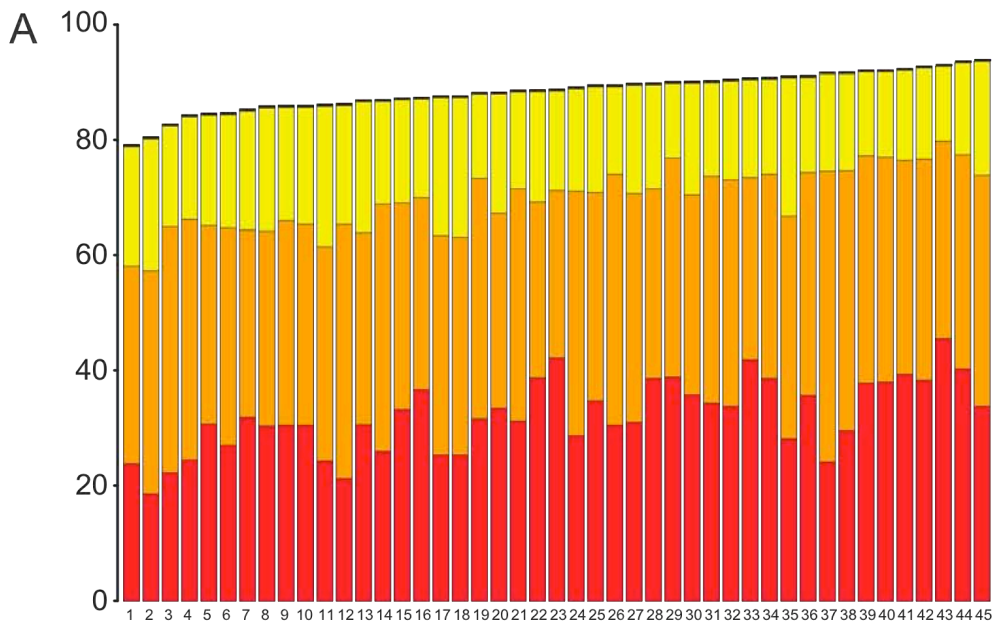**Supplementary figure 9.** Comparison of expression levels for 45 cell lines with various sub-fractions of antibodies. The fraction (%) of proteins detected in a specific cell line, including the fraction of the three different staining categories: strong (red), moderate (orange) and weak (yellow). The black (top) part of the bar represents antibodies with missing data for the particular cell line. The corresponding name and number of each cell line is shown in Supplementary Table S3. Results from three different datasets are shown: **(A)** All antibodies (n = 5,352), ordered according to the fraction of proteins detected. **(B)** Antibodies with supportive results from Western blot analysis (n = 872). **(C)** Paired antibodies generated to the same protein and with a correlation coefficient ≥ 0.5 (n = 310). The correlation coefficients are based on protein expression data which has been normalized using cellular size (*5*).

Supplementary Table S1. The sets of antibodies used in the study.

Antibody group	Study	Fig	No of antibodies	Number of target genes	Comment
All tissues	Tissues	1,2	5,934	4,842	All antibodies in the study for analysis of 65 cell types
Western	Tissues	S4-S5	920	841	All antibodies with a single band of predicted size on Western blot
Correlation > 0.5	Tissues	S4-S5	518	259	Paired antibodies with cell profiling correlation larger than 0.5
Correlation > 0.5, HPA paired	Tissues	S4-S5	184	92	All paired HPA antibodies with cell profiling correlation larger than 0,5
Chromosome 9	Tissues	S1	172	172	Antibodies towards proteins encoded on human chromosome 9
Chromosome 10	Tissues	S2	168	168	Antibodies towards proteins encoded on human chromosome 10
Chromosome 22	Tissues	S3	173	173	Antibodies towards proteins encoded on human chromosome 22
Random selection of antibodies	Tissues	S4	200	Average = 199	Antibodies selected by random sampling of the complete set of antibodies
Random selection of antibodies	Tissues	S5	200	Average = 199	Antibodies selected by random sampling of the complete set of antibodies
Random selection of antibodies	Tissues	S6	200	Average = 199	Antibodies selected by random sampling of the complete set of antibodies
All	Cells	3	5,349	4,349	All antibodies used for analysis of 45 cell lines using IHC
Western	Cells	S6	872	791	Antibodies with a single band of predicted size on Western blot
Correlation > 0.5	Cells	S6	310	155	Paired antibodies with cell profiling corrleation larger than 0.5
Correlation > 0.8	Cells	S6	88	44	Paired antibodies with cell profiling corrleation larger than 0.8
All IF	Cells	4	2,249	2,179	Antibodies used for analysis of 3 cell lines using confocal microscopy

Supplementary Table S2. The total fraction of proteins detected in the 65 human cell types from 48 tissues. The numbers refer to order of cells in Figure 2B. The sub fraction of antibodies is listed in table S1. "All" refers to all 5,936 antibodies used for analysis of 65 cell types, "Western" refers to the 920 antibodies with a single band of predicted size using a standardized Western blot assay, "Paired" refers to the 518 antibodies selected due to the high correlation (≥0.5) of these paired antibodies in the analysis of the cells and "HPA" are the sub fraction of 92 highly correlated (≥0.5) paired antibodies which has been generated "in-house" with distinct and non-overlapping epitopes.

Supplementary Table S3. The total fraction of proteins detected in the 45 human cell lines. The numbers refer to order of cells in Figure 3B. The sub fraction of antibodies is listed in table S1. "All" refers to all 5,352 antibodies used for analysis of 45 cell lines, "Western" refers to the 872 antibodies with a single band of predicted size using a standardized Western blot assay, "Corr. > 0.5" refers to the 310 antibodies selected due to the high correlation (≥ 0.5) of these paired antibodies in the analysis of the cells and "Corr. ≥ 0.8" are the sub fraction of 88 highly correlated (> 0.8) paired antibodies.

Supplementary Table S4. A list of 74 proteins only detected in a single cell type**.** The query was conducted to show proteins with strong binding exclusively in one of the analyzed 65 cell types (see table S2) and not more than five cells with weak staining.