GUDMAP genes - Gadd et al (2012) data

Summary of analysis

Gene lists

For each of the tissues below, gene lists have been retrieved from the GUDMAP Metanephros page at:
http://www.gudmap.org/Organ_Summaries/index.php

Tissues:

- nephrogenic zone (TS21-TS28)
- cap mesenchyme (TS19-TS28)
- pretubular aggregate (TS20-TS28)
- ureteric tip (TS18-TS28)
- stage I / stage II nephron (TS20-TS27)
- renal vesicle (TS20-TS27)
- comma-shaped body (TS20-TS27)
- s-shaped body (TS21-TS27)
- stage III / stage IV nephron (TS22-TS28)
- renal proximal tubule (TS25-TS28)
- loop of Henle (TS25-TS28)
- renal distal tubule (TS25-TS28)
- renal corpuscle (TS21-TS28)
- capillary loop stage nephron (stage III) (TS22-TS28)
- maturing nephron (stage IV) (TS22-TS28)
- collecting duct (TS21-TS28)
- cortical collecting duct (TS22-TS28)
- medullary collecting duct (TS22-TS28)
- renal interstitium (TS20-TS28)
- nephrogenic interstitium (TS20-TS28)
- renal cortical interstitium (TS22-TS28)
- renal medullary interstitium (TS22-TS28)
- pelvis (TS21-TS28)
- perihilar interstitium (TS22-TS28)
- pelvic smooth muscle (TS23-TS28)
- immature loop of Henle (TS22-TS24)
- pelvic urothelial lining (TS22-TS28)
- early distal tubule (TS21-TS27)
- anlage of loop of Henle (TS21-TS27)
- small blood vessels (TS23-TS28)

Methods

For each tissue type, "Anchor" and "Marker" gene information was retrieved, although only the Marker lists are currently used in the analysis below.

Using the Marker list for each tissue, data for these genes was extracted from the Gadd et al (2012) data set (GSE31403: 224 samples).

Per tissue, the following information is presented for the GSE31403 data set:

- an image of the tissue location (taken from GUDMAP)
- a table of Marker genes associated with that tissue. Columns are:
  - mouse gene name,
  - Affymetrix probe IDs associated with human gene (NB - no alias matching performed yet)
  - Affymetrix probe used to represent gene (based on `collapseRows` function from the `WGCNA` package)
- Heatmap of the genes using representative probes:
  - scaled to mean 0, standard deviation 1 per gene (red is high expression, blue low)
  - sorted by increasing metagene value (based on first eigenvector from Singular Value Decomposition).
  - Metagene score is presented above the heatmap as a blue-red bar (ordered).
  - coloured bar above represents tumour subgroups (S1-S5) as defined in the Gadd et al publication (see boxplots for colour legend).
- Boxplots (with overlayed dot plots) of metagene values for each sample across the tumour subgroups.

Results

Based on the outputs presented below, the tissue types with the strongest links to the S1 subgroup are:

- pretubular aggregate (TS20-TS28). Prominent genes: LHX1, CDH4, CCND1
- stage I / stage II nephron (TS20-TS27). Prominent genes: LHX1, CDH4, BMP2, POU3F3, CCND1, JAG1
- renal vesicle (TS20-TS27). Prominent genes: LHX1, CDH4, BMP2, POU3F3, CCND1, JAG1
- comma-shaped body (TS20-TS27). Prominent genes: LHX1, CDH4, BMP2, POU3F3, CCND1, JAG1
- s-shaped body (TS21-TS27). Prominent genes: LHX1, CDH4, BMP2, POU3F3, CCND1, JAG1

In all cases the metagene scores indicated higher levels of expression in the S1 subgroup for many of the tissue-defining genes. It is clear that there is substantial overlap across the gene lists for these tissue types, and that these results are largely being driven by the genes: LHX1, CDH4, BMP2, POU3F3, CCND1, JAG1.
nephrogenic zone (TS21-TS28)

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nephrogenic zone (TS21-TS28)

![Heatmap image](image-url)
### cap mesenchyme (TS19-TS28)

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*cap mesenchyme (TS19-TS28)*

![Gene expression heatmap](chart.png)
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NOT ENOUGH GENES FOR METAGENE
### stage I / stage II nephron (TS20-TS27)

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### renal vesicle (TS20-TS27)

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**Image Description:**
- The image shows a heat map for renal vesicle (TS20-TS27) with genes and probes displayed.
- The heat map colors indicate expression levels with warmer colors representing higher expression.
- Specific genes such as BMP2, CCND1, and CDH4 are highlighted.
- The selected probes for each gene are noted on the right side of the heat map.
<table>
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<tr>
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<th>Probes</th>
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### s-shaped body (TS21-TS27)

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![Heatmap of gene expression patterns for s-shaped body (TS21-TS27)](image-url)
### stage III / stage IV nephron (TS22-TS28)

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stage III / stage IV nephron (TS22-TS28)
### renal proximal tubule (TS25-TS28)

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![Heatmap Image]
## loop of Henle (TS25-TS28)

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NOT ENOUGH GENES FOR METAGENE
renal distal tubule (TS25-TS28)

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NOT ENOUGH GENES FOR METAGENE
renal corpuscle (TS21-TS28)

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renal corpuscle (TS21-TS28)
## capillary loop stage nephron (stage III) (TS22-TS28)

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![Gene expression heatmap](image.png)

Subgroup S1, S2, S3, S4, S5

- **SCNN1B**
- **UPK1B**
- **VLDLR**
- **CAPG**
- **TESC**
- **SOX9**
- **PPPI1R3C**

- **0.092**
- **0.21**
- **0.67**
- **3.2e-05**
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![Gene expression heatmap](image-url)
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immature loop of Henle (TS22-TS24)

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immature loop of Henle (TS22-TS24)
### early distal tubule (TS21-TS27)

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