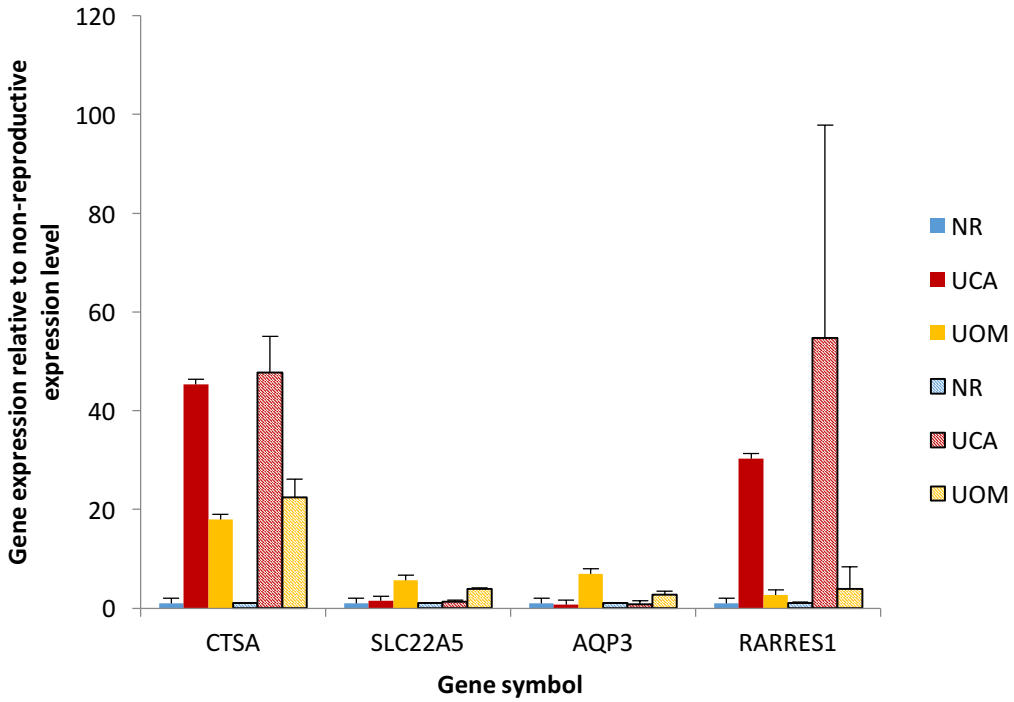
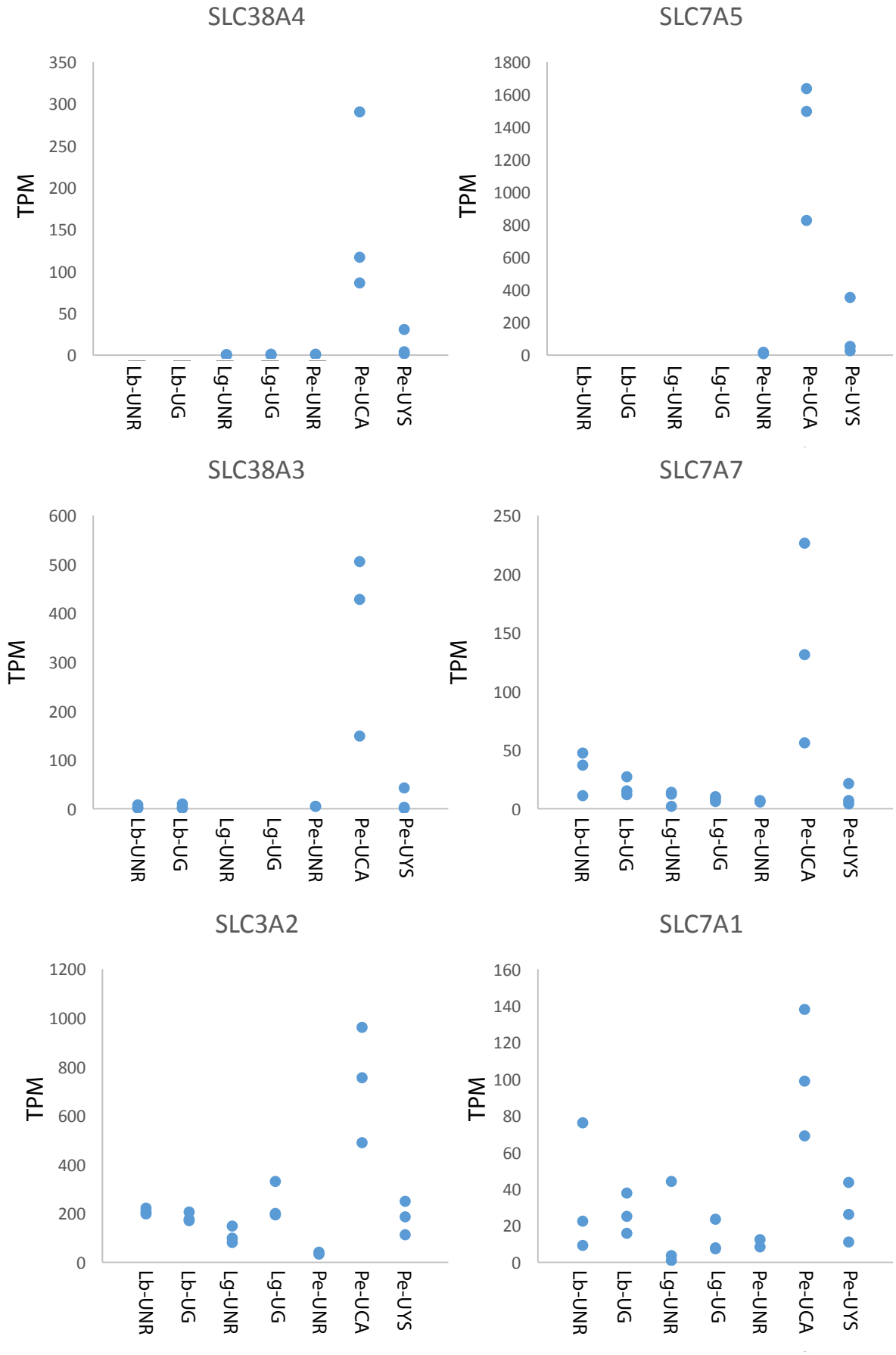
Supplementary methods

Quantitative PCR

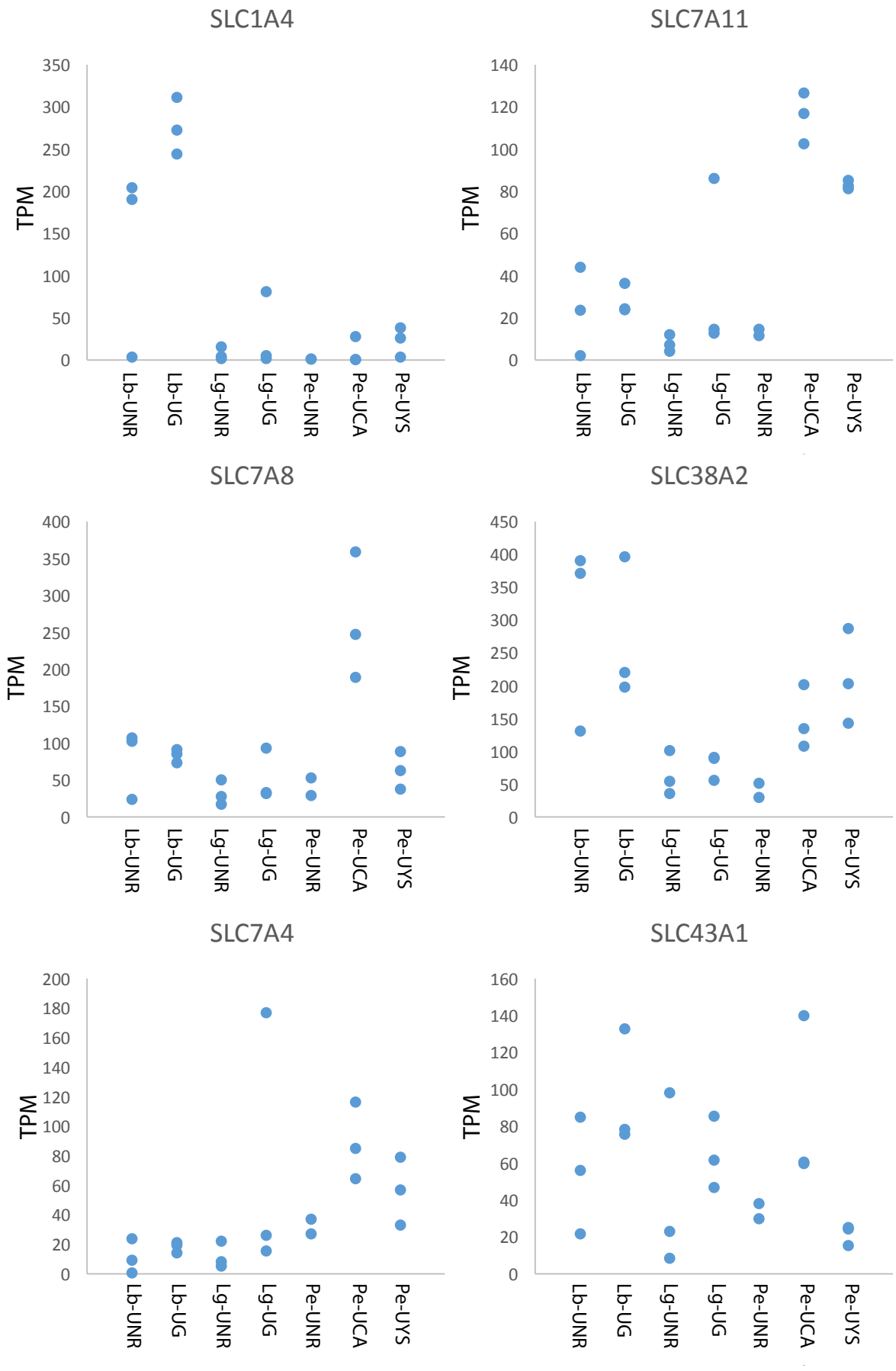
RNA was extracted from the uterus of non-pregnant (n=4), and the uterine component of the chorioallantoic (n=7) and yolk sac placenta (n=7) of pregnant individuals as above. cDNA was reverse transcribed using the QuantiTect Reverse Transcription Kit (QIAGEN) with 461ng of input RNA for all samples. Realtime-PCR analysis was conducted with the QuantiFast SYBR Green PCR protocol (QIAGEN) in 15uL reaction volumes with a cDNA equivalence of 6 ng of RNA. All samples were run in triplicate, non-template controls were run in triplicate in every run. Reactions were set-up manually. The specificity of the PCR reaction was assured by confirming a single PCR product was observed in every reaction by melt curve analysis (50^{o}C - 99^{o}C) and the product was confirmed to be the right size by running PCR products from each primer combination on an agarose gel (3% TBE agarose, 110V, 20min) and comparing to the DNA standard HyperLadder IV (Bioline). Standard curves were generated using serial 1:4 dilutions of a composite sample containing equal parts of 17 uterine cDNA samples. All dilutions were run in triplicate. Standard curves had an R^2 ≥0.99 and contained at least four dilutions from the dilution series with a linear dynamic range of at least three orders of magnitude and had PCR efficiencies between 0.9 and 1.05. All Cq values for unknowns fall within the linear quantifiable range of the appropriate standard curves. The calculated relative concentrations were normalized by dividing by the geometric mean of 18S rRNA and β-actin expression, which have been confirmed as good reference genes in these tissues of this species (Griffith, et al. 2013a). Normalized relative gene expression was compared between uterus of the chorioallantoic and yolk sac placenta with a paired-student's t-test, whilst gene expression in non-reproductive tissue was compared with the reproductive tissue of each placenta individually. Relative expression levels are reported in Supplementary Figure 1.



Supplementary figure 1. Gene expression levels, in the uterus of non-reproductive females (NR, blue), and the uterus of the chorioallantoic (UCA, red) and yolk sack (UOM, yellow) placenta. Expression levels from the transcriptome sequencing analysis are reported in the solid bars, and by qPCR in the thatched bars. Quantitative-PCR expression levels of each gene were normalized by dividing by the geometric mean of 18S rRNA and B-actin gene expression. Expression is reported relative to the mean expression in non-reproductive tissue.



Supplementary figure 2. Expression of differentially expressed amino acid transport proteins in the uterus of *Lerista bougainvillii* (Lb), *Lampropholis guichenotti* (Lg), and *Pseudemoia entrecasteauxii* (Pe). Uterine tissue is from either non-pregnant (UNR) or early pregnant (UG) females, or from the chorioallantoic (UCA) or yolk sac (UYS) placenta of late pregnant females .



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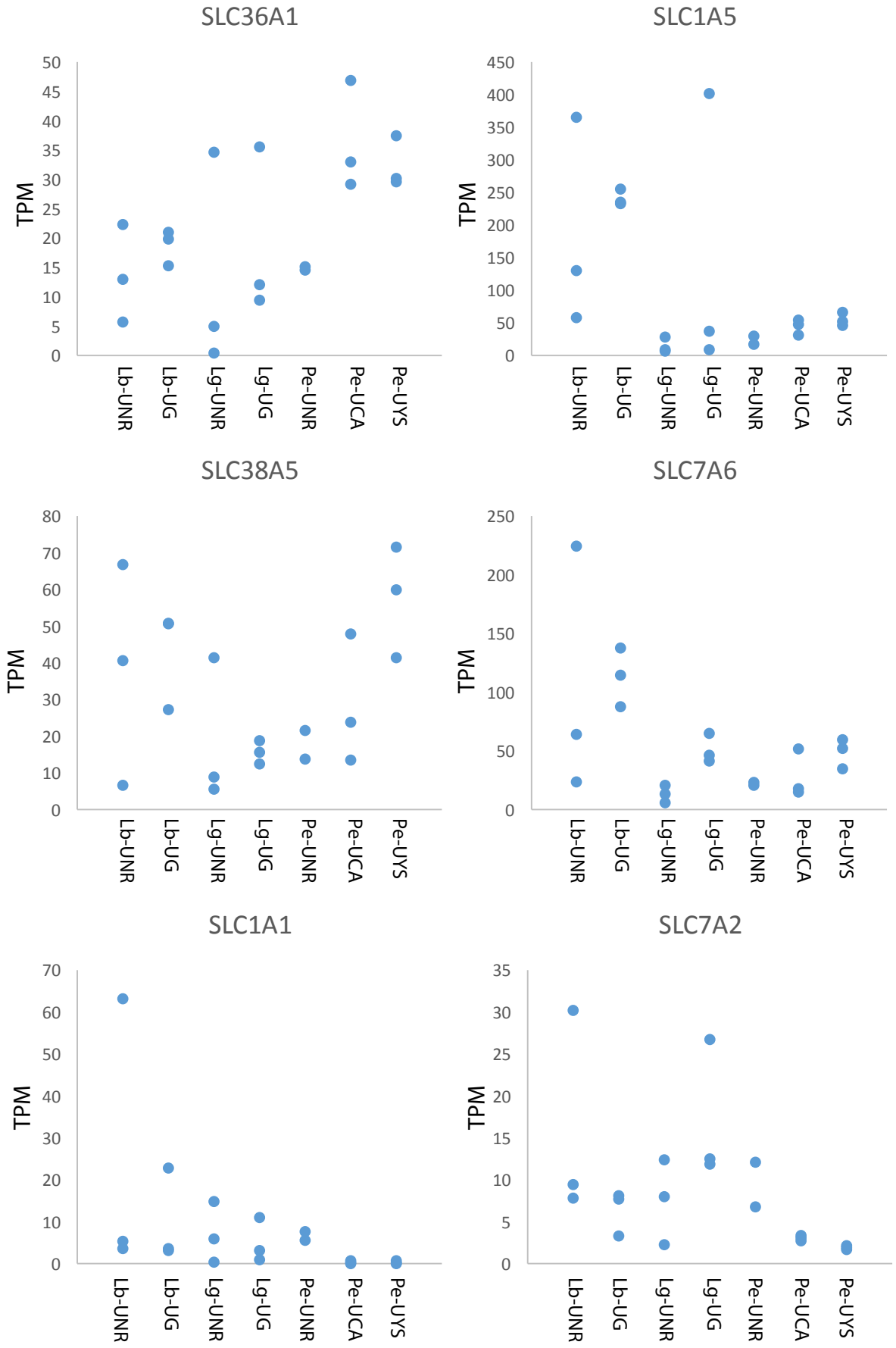

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