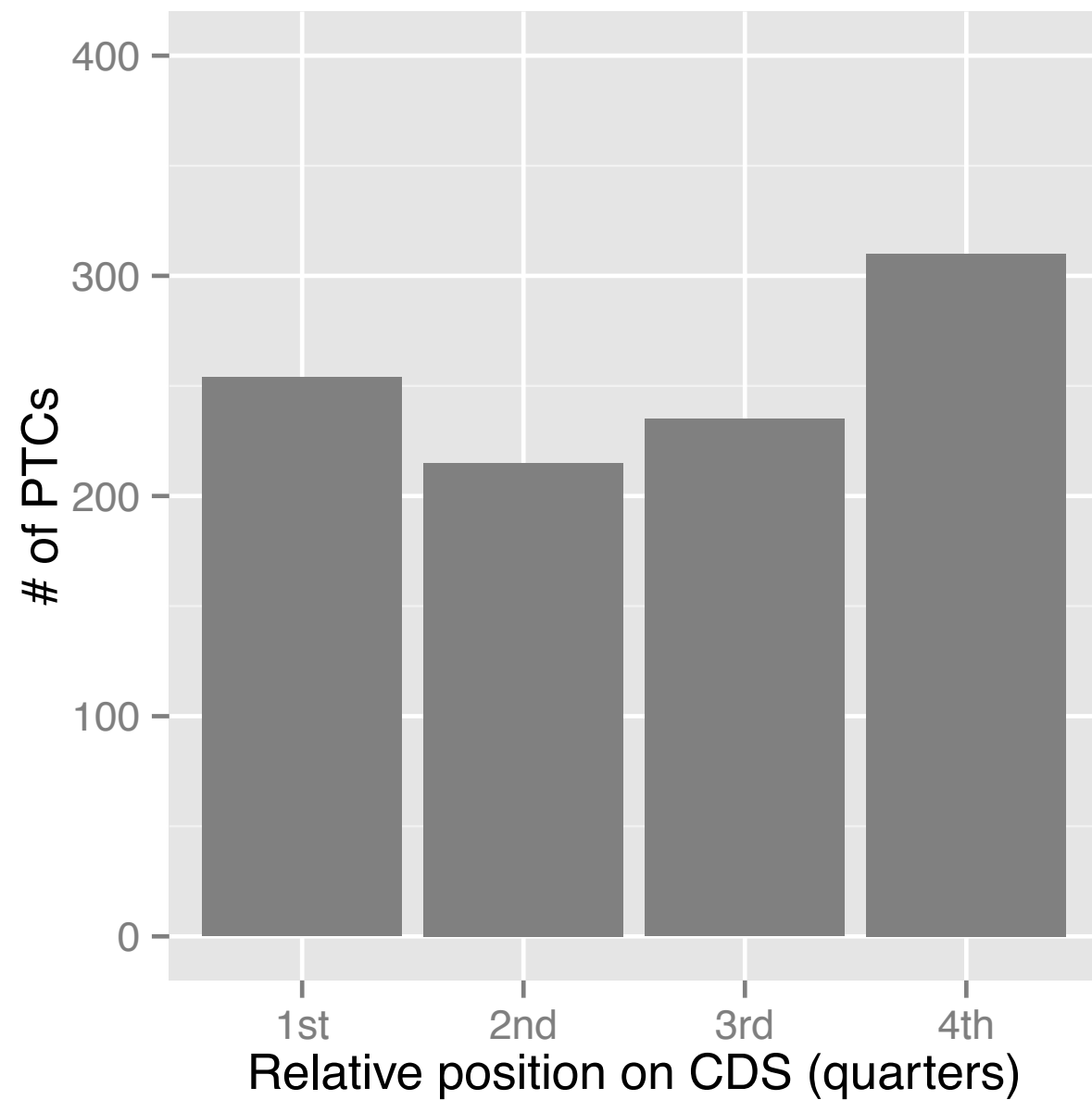
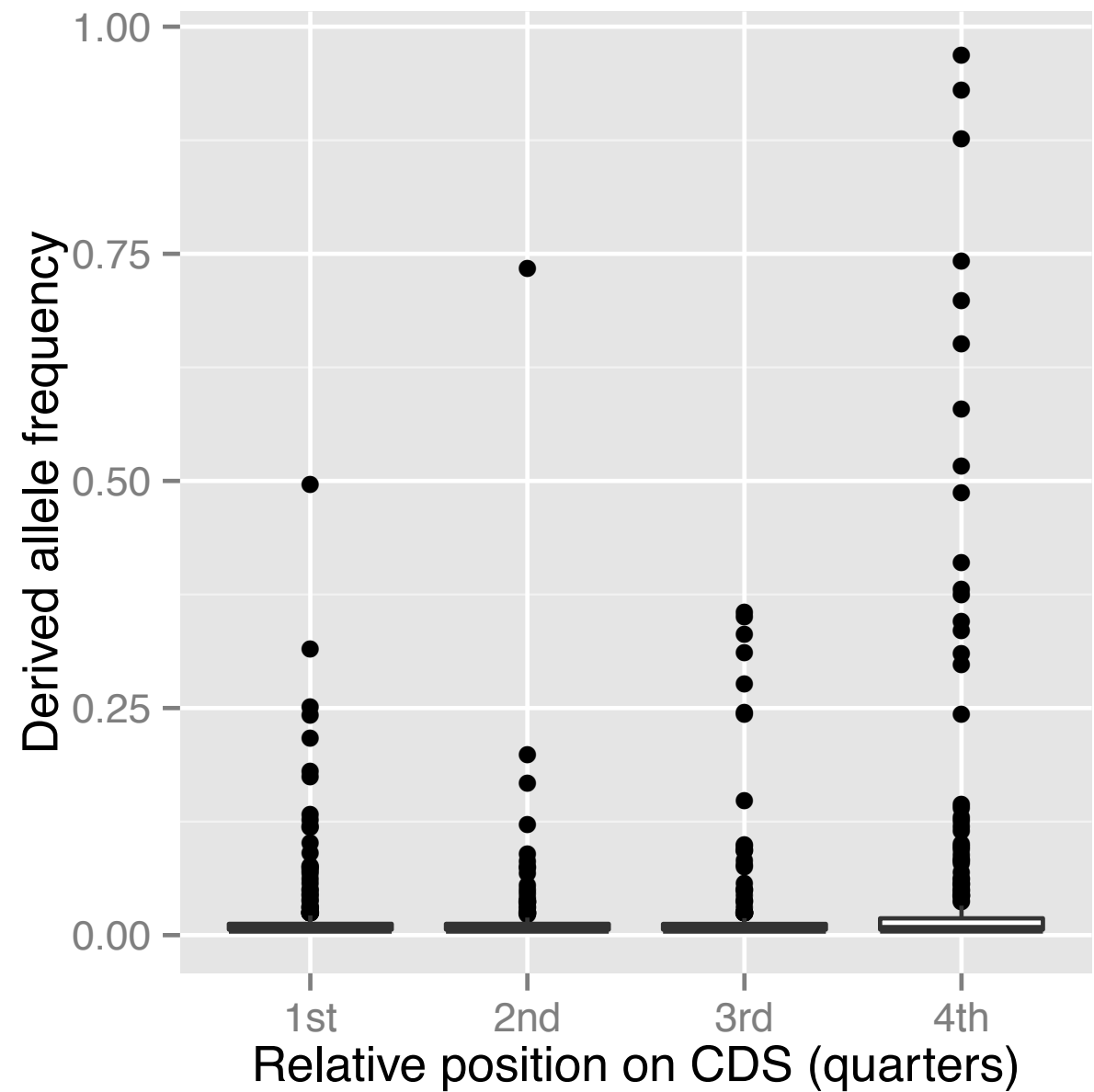


PTC tend to be in the last 25%
of the CDS

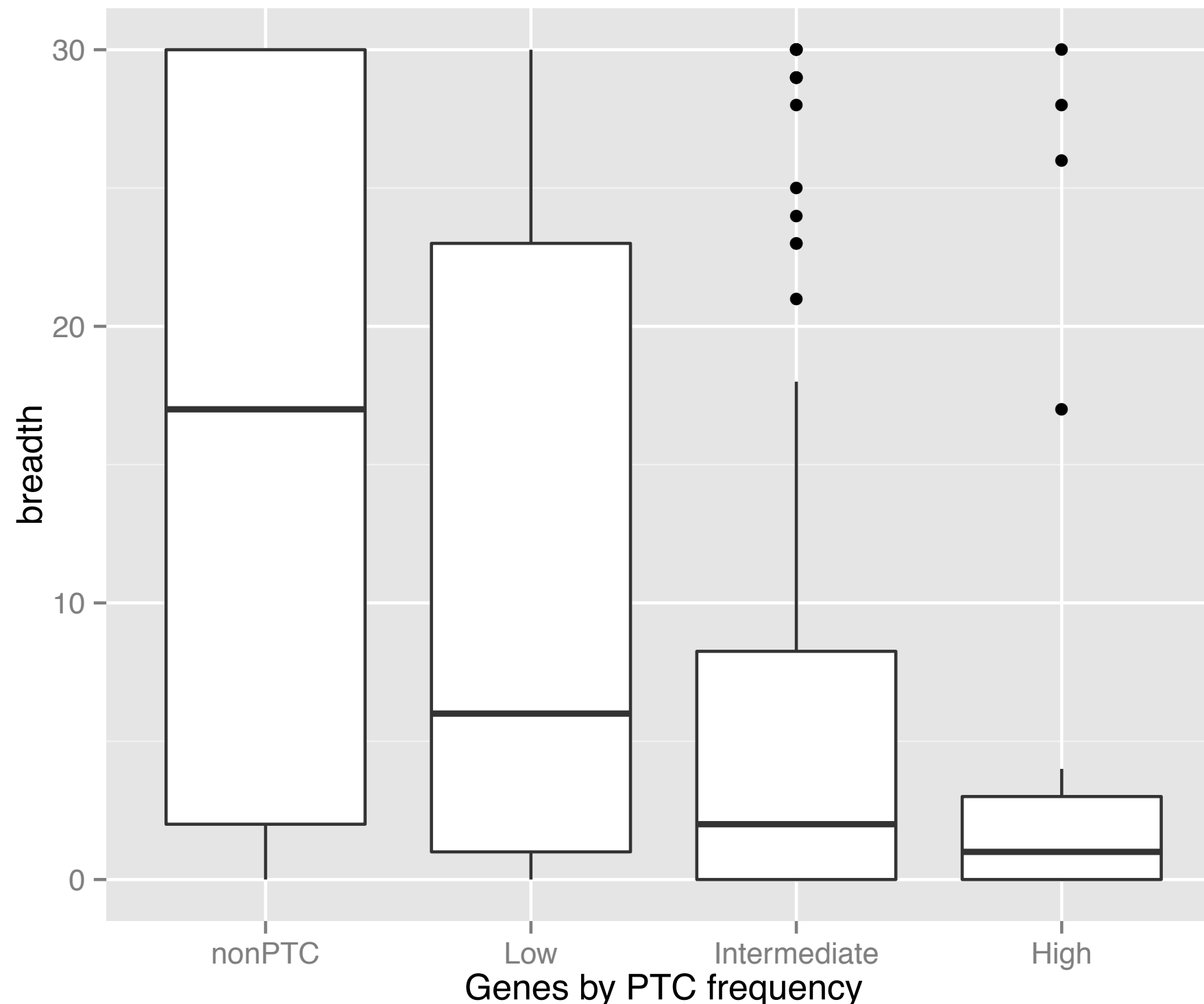


Especially the high derived
allele frequency PTC SNPs



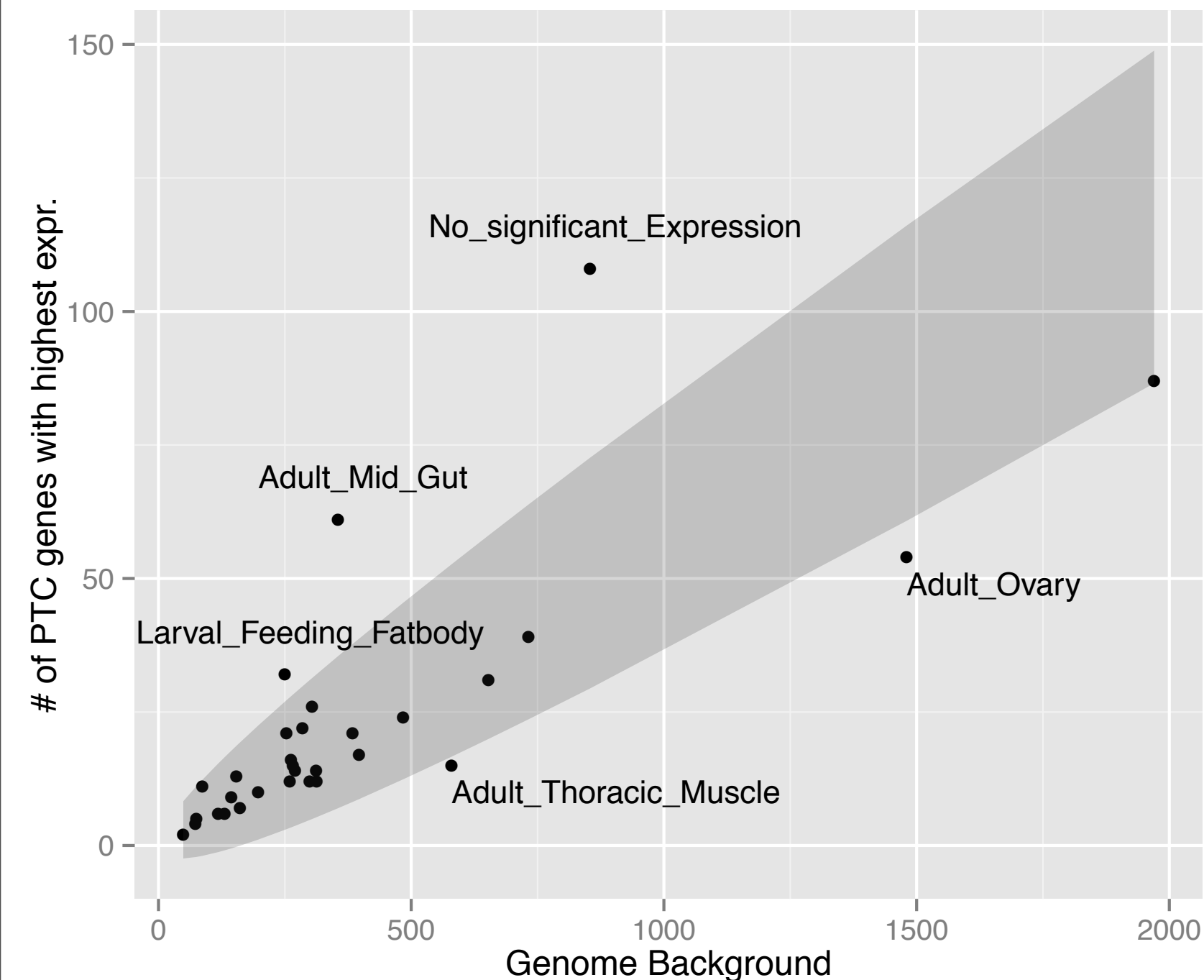
breadth: number of tissues (out of 30) called present for the gene

The higher the DAF, the narrower its expression profile tends to be (check the outliers for the high class?)



I intend to replace Fig 2 with this.

Based on the table to the right. Plotted “Total” ~ Genome Background.
The shaded area indicate 95% prediction interval based on binomial distribution (corrected for multiple testing). It clearly shows mid_gut has more PTC-encoding genes than expected based on genome-wide levels.



Tissue	Genome Background	Total
Adult Accessory gland	484	24
Adult Brain	732	39
Adult Carcass	49	2
Adult Crop	260	12
Adult Eye	299	12
Adult Fat Body	161	7
Adult Female Spermatheca Mated	73	4
Adult Female Spermatheca Virgin	118	6
Adult Head	75	5
Adult Heart	154	13
Adult Hind Gut	131	6
Adult Male Ejaculatory Duct	197	10
Adult Mid Gut	355	61
Adult Ovary	1480	54
Adult Salivary Gland	270	14
Adult Testes	1970	87
Adult Thoracic Muscle	580	15
Adult Thoracoabdominal Ganglion	313	12
Adult Trachea	87	11
Adult Wings	304	26
Larvae Wandering Tubules	384	21
Larval Feeding Carcass	253	21
Larval Feeding Central Nervous System	653	31
Larval Feeding Fat Body	250	32
Larval Feeding Hind Gut	144	9
Larval Feeding Malpighian Tubule	266	15
Larval Feeding Mid Gut	285	22
Larval Feeding Salivary Gland	397	17
Larval Feeding Trachea	312	14
Larval Wandering Fat Body	262	16
No Significant Expression	854	108