

# PseudoSeq Update

5/3/11

genome-anno

LH

# Pseudogenes in GENCODE v6

- ENSEMBL / HAVANA transcripts (gt & tt: protein\_coding): 74,226
- ENSEMBL pgenes (gt: pgene): 2,252
- HAVANA pgenes (gt: pgene): 10,343
- HAVANA pgenes (gt: pgene, tt: processed, not transcribed): **7,887**
- HAVANA pgenes (gt: pgene, tt: processed, transcribed): 24
- HAVANA pgenes (gt: pgene, tt: unprocessed, not transcribed): 1,793
- HAVANA pgenes (gt: pgene, tt: unprocessed, transcribed): 20

# Alignment of pseudogenes to the reference genome

- Input: HAVANA pgenes (gt: pgene, tt: processed, not transcribed): **7,887**
- Alignment tool: BLAT
- Reference genome: hg19
- Extract all alignment blocks: at least one of the alignment block has to be longer than 75 nucleotides

# Characterization of pseudogene alignments

- Pgenes with:
  - Zero alignment blocks: 2,670
  - One alignment blocks: 1,538
  - Multiple (2 - 5) alignment blocks: 1,593
  - Too many (> 5) alignment blocks: 2,086

# RNA-Seq data

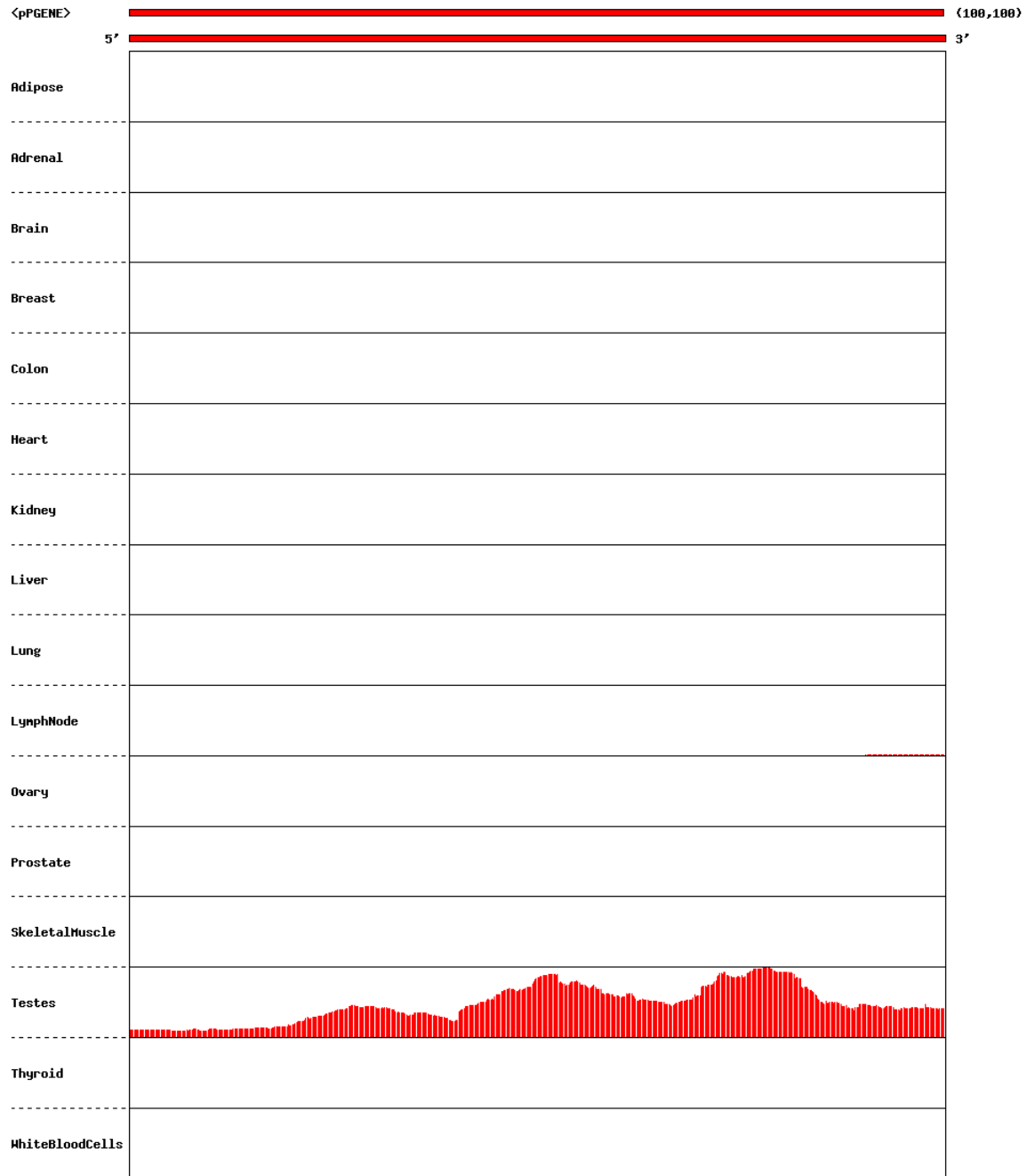
- Human Body Map
  - 16 tissues
  - 75 nucleotide single-end reads
  - HiSeq Illumina platform: 1 lane per tissue
- Alignment tool: bowtie
  - hg19 + gencodeV6 splice junction library (alignment is performed concurrently)
  - Unique mapping
  - 2 mismatches (end-to-end)
- Average number of mapped reads per tissue: ~ 60M

# Results

<b>Category</b>	<b>Total number of pgenes</b>	<b>Number of pgenes with non-zero expression values</b>	<b>Number of pgenes with zero expression values</b>	<b>Number of pgenes with &gt;0.5 expression values</b>
Zero alignment pairs	2670	1530	1140	16
One alignment pair	1538	1165	373	33
2 - 5 alignment pairs	1593	1108	485	61
Too many alignment pairs	2086	N/A	N/A	N/A

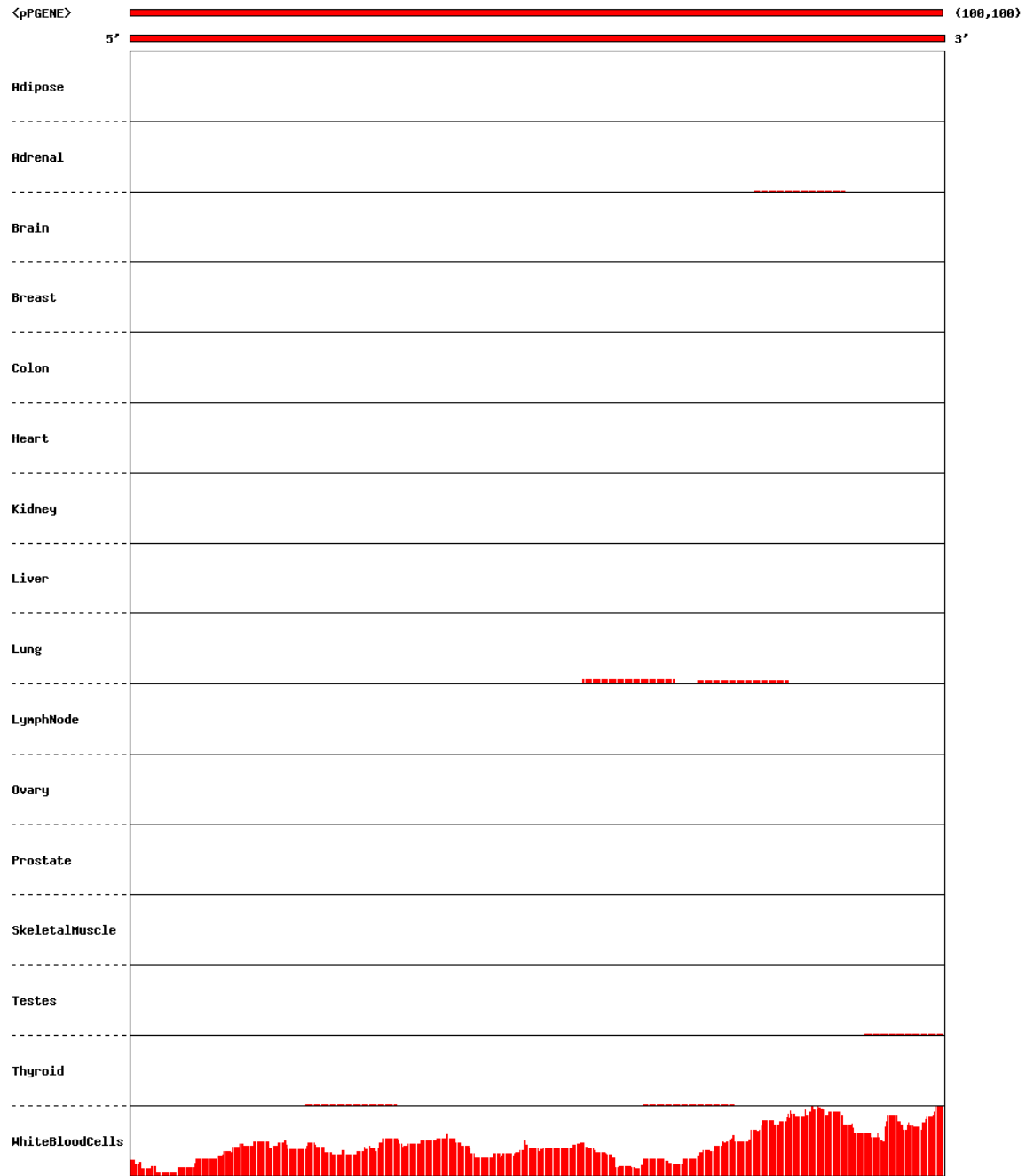
# Examples with zero alignment pairs

Name: ENSG00000102055\_ENST00000378131, Length: 609  
Scale [0,00 5,49], Average: 0,16

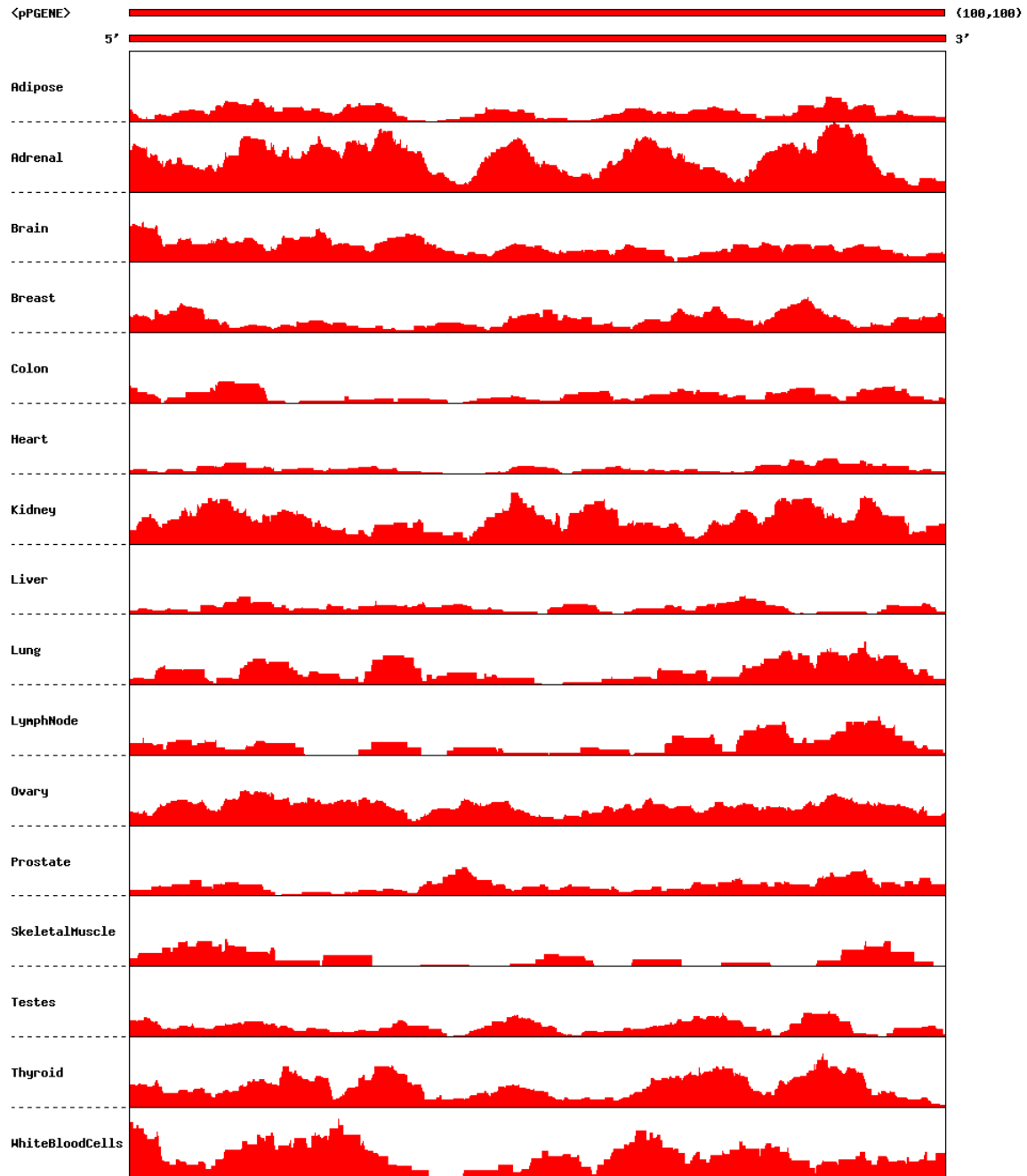




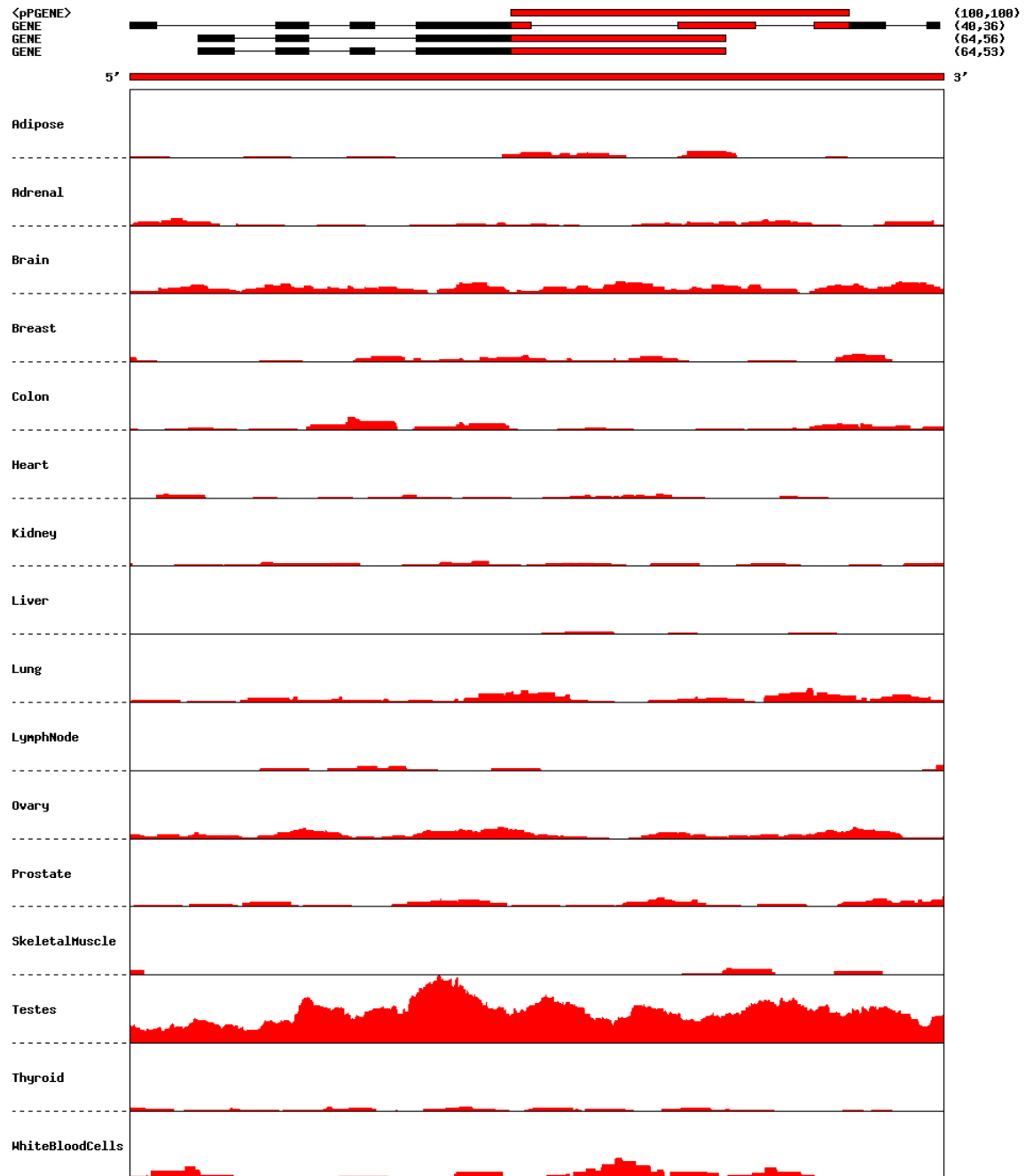
Name: ENSG00000213876\_ENST00000483947, Length: 663  
Scale [0.00 1.99], Average: 0.06



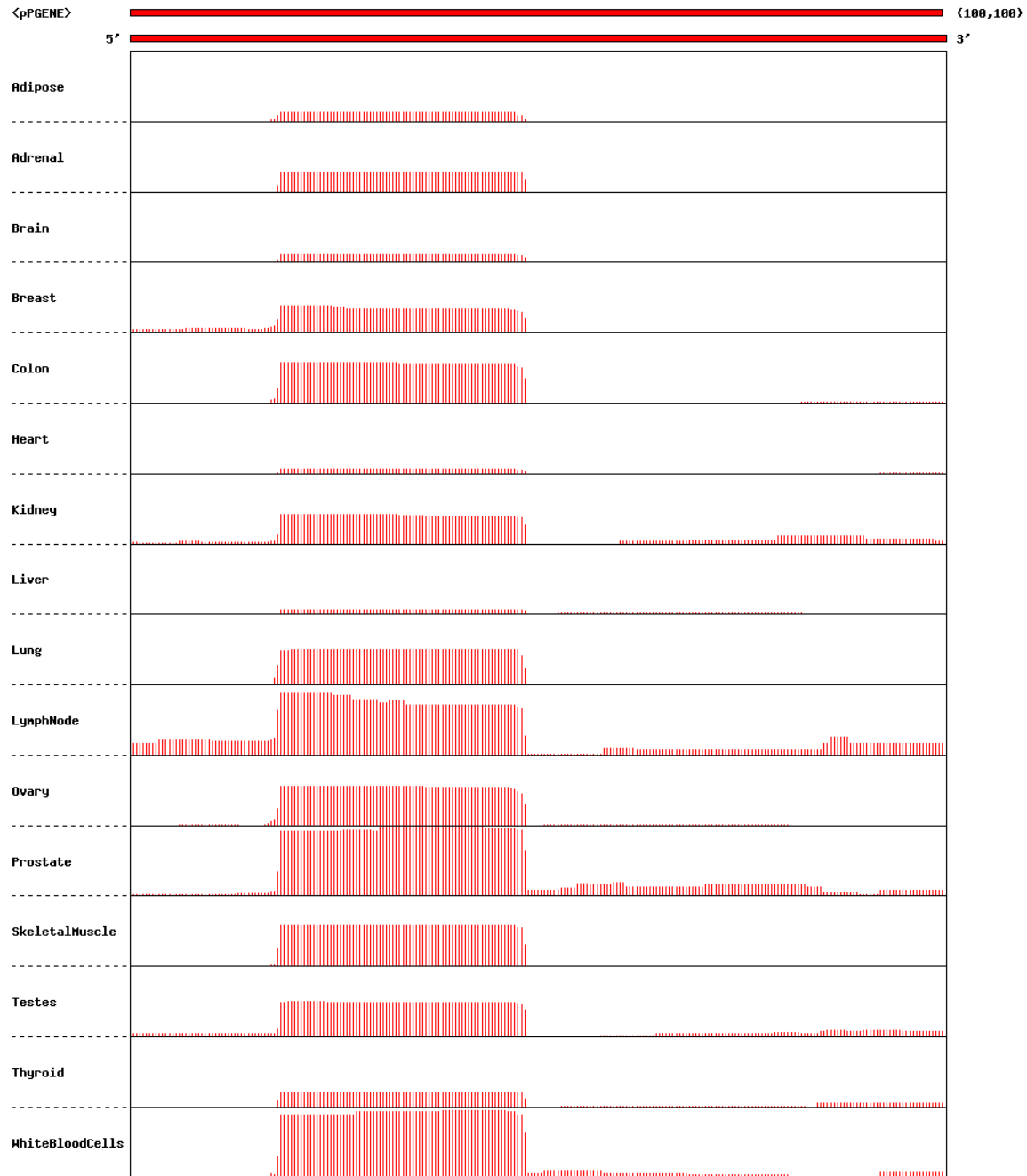
Name: ENSG00000235859\_ENST00000496846, Length: 1234  
Scale [0,00 1,52], Average: 0,32



Name: ENSG00000188812\_ENST00000434057, Length: 1234  
Scale [0,00 2.76], Average: 0.18



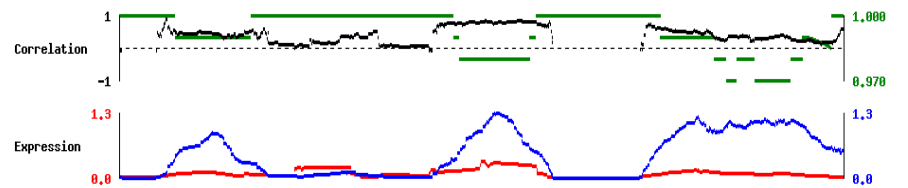
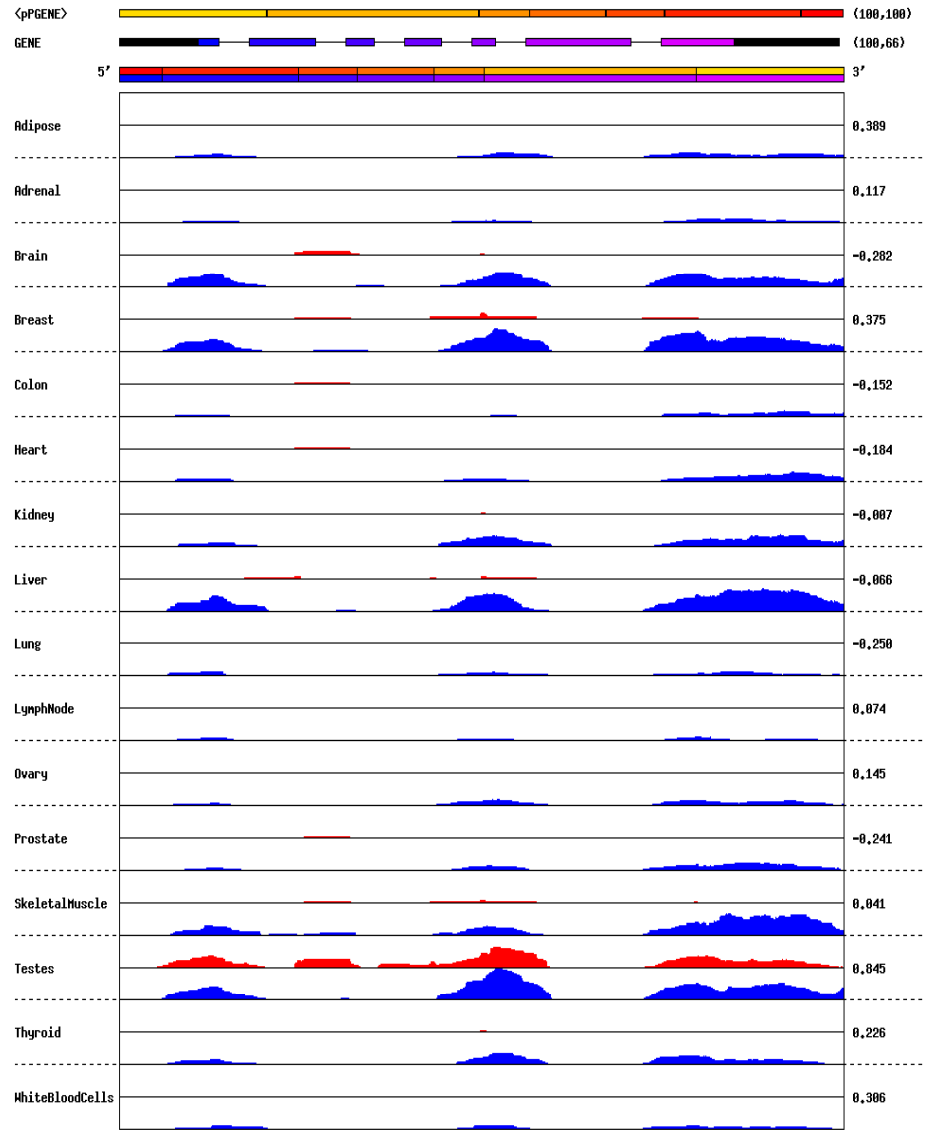
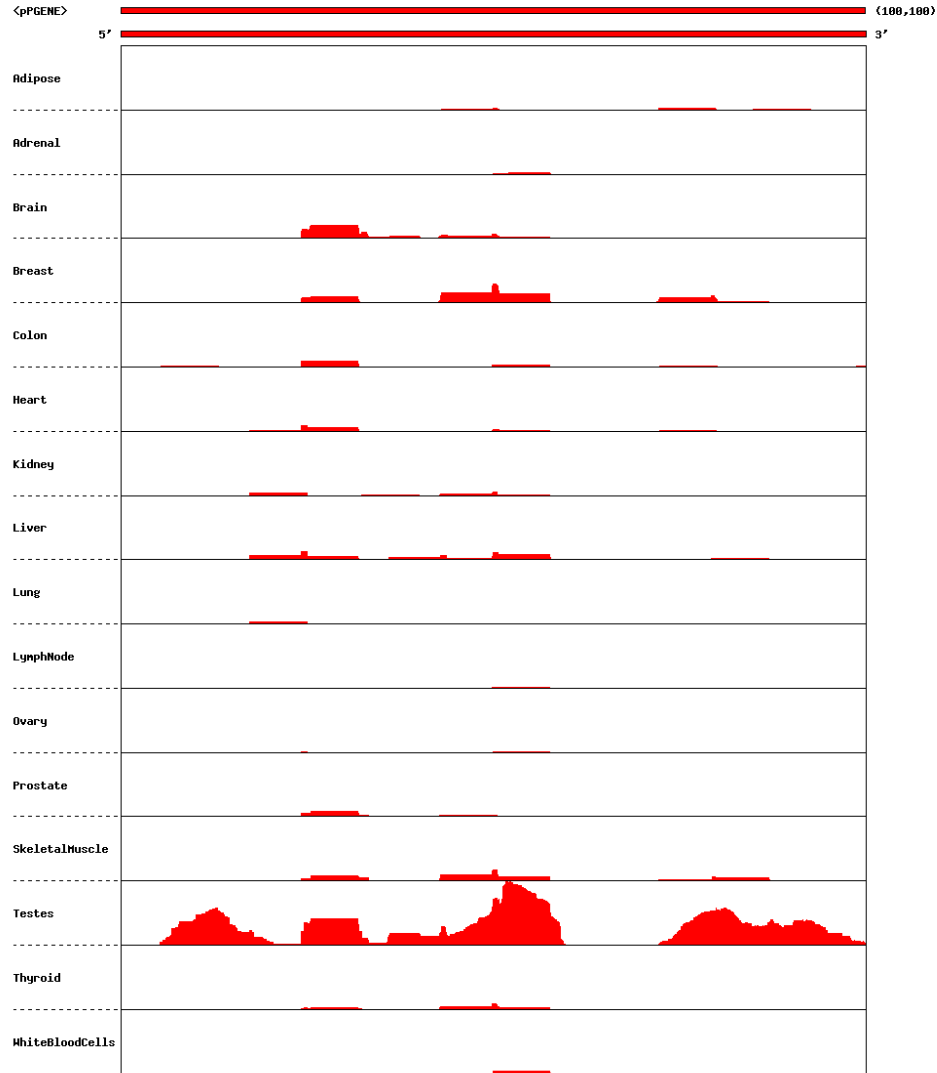
Name: ENSG00000242358\_ENST00000487122, Length: 248  
Scale [0.00 1.61], Average: 0.25



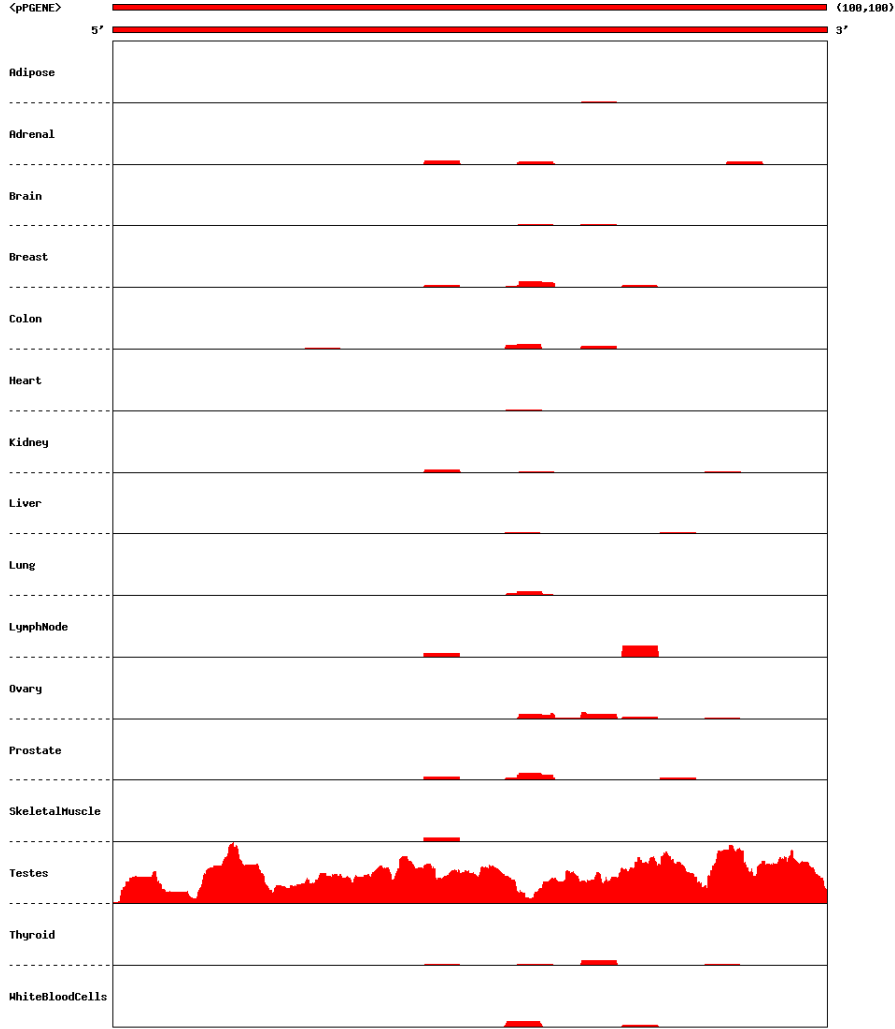
# Examples with one alignment pair

Name: ENSG00000226268\_ENST00000526165\_1, Length: 959, %ID: 99.3, APC: 0.392, APMC: 0.004  
 Scale [0.00 4.34], Average: 0.00  
 Scale [0.00 4.34], Average: 0.43

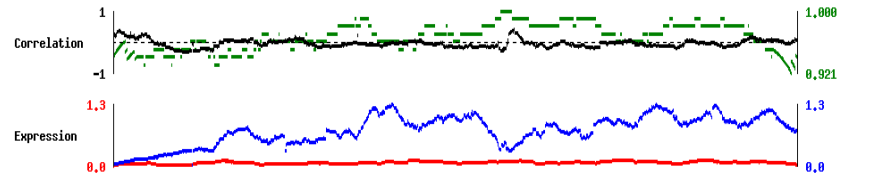
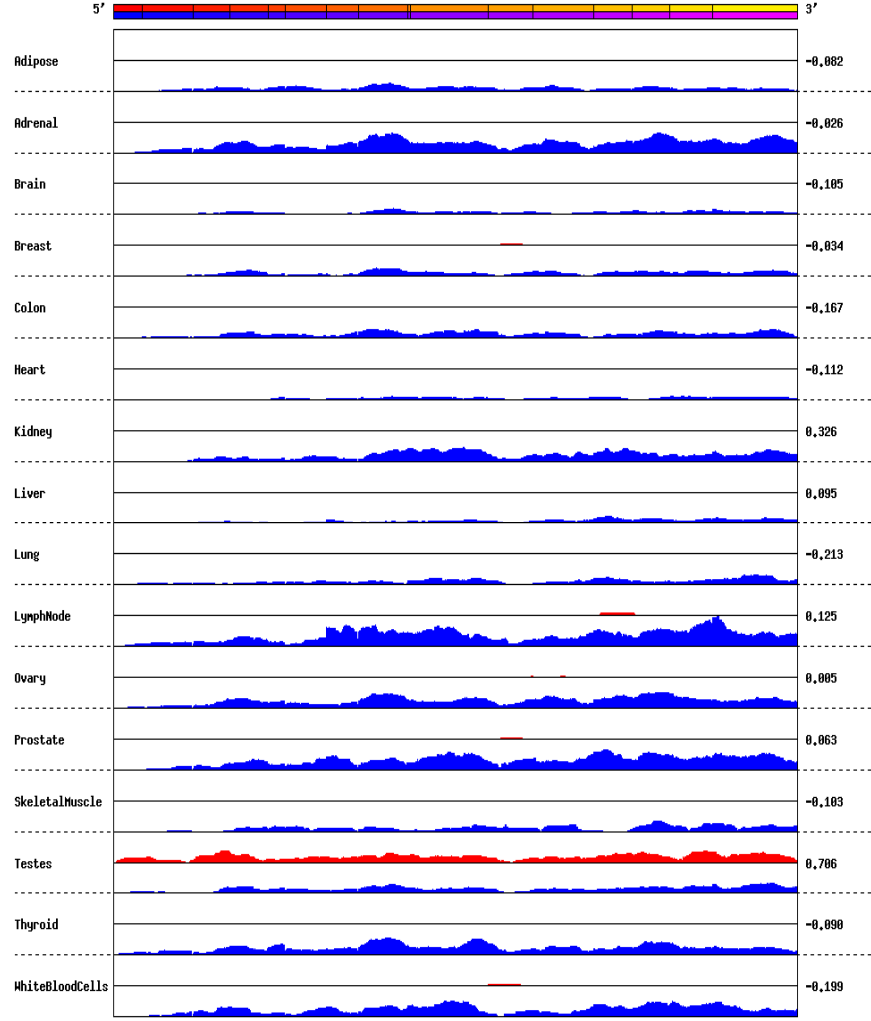
Name: ENSG00000226268\_ENST00000526165, Length: 959  
 Scale [0.00 2.85], Average: 0.08



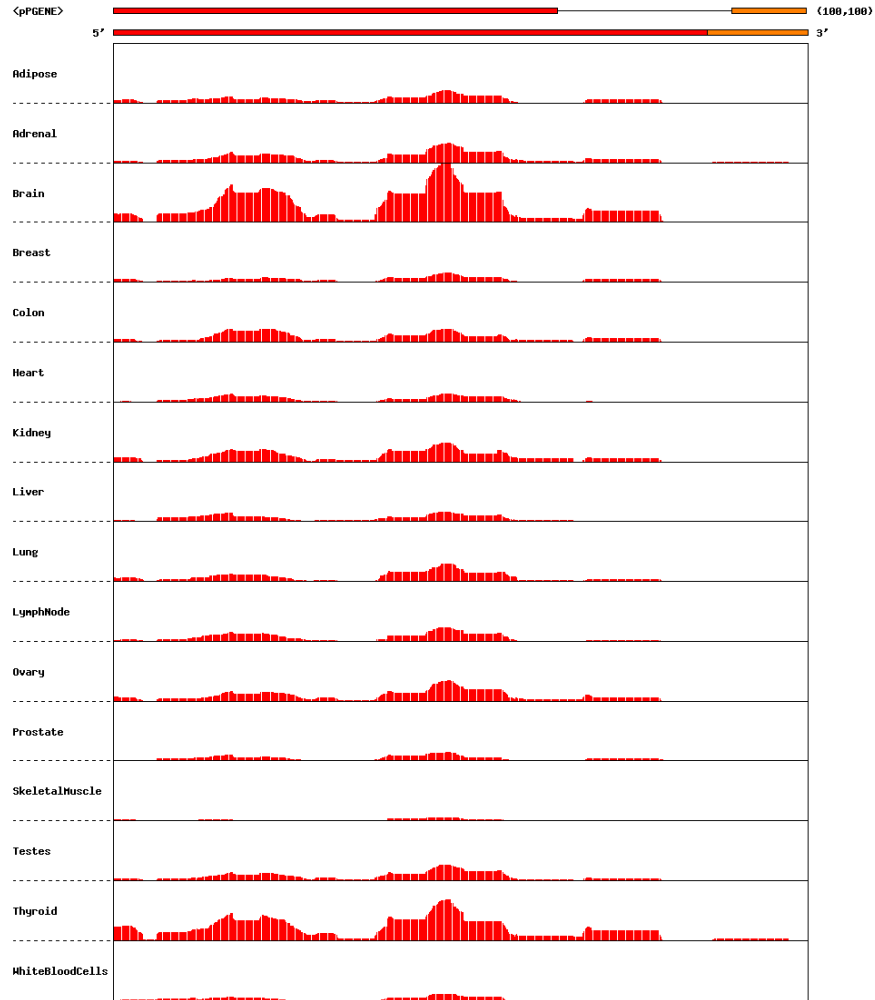
Name: ENSG00000232553\_ENST00000416636, Length: 1476  
 Scale [0,00 1,72], Average: 0,86



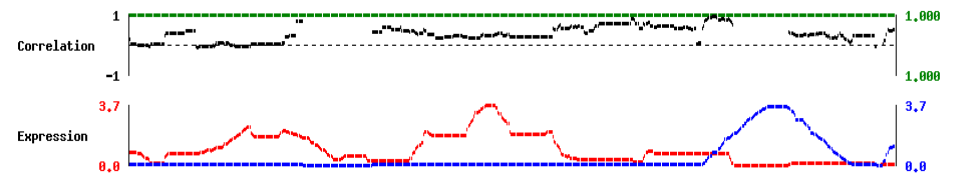
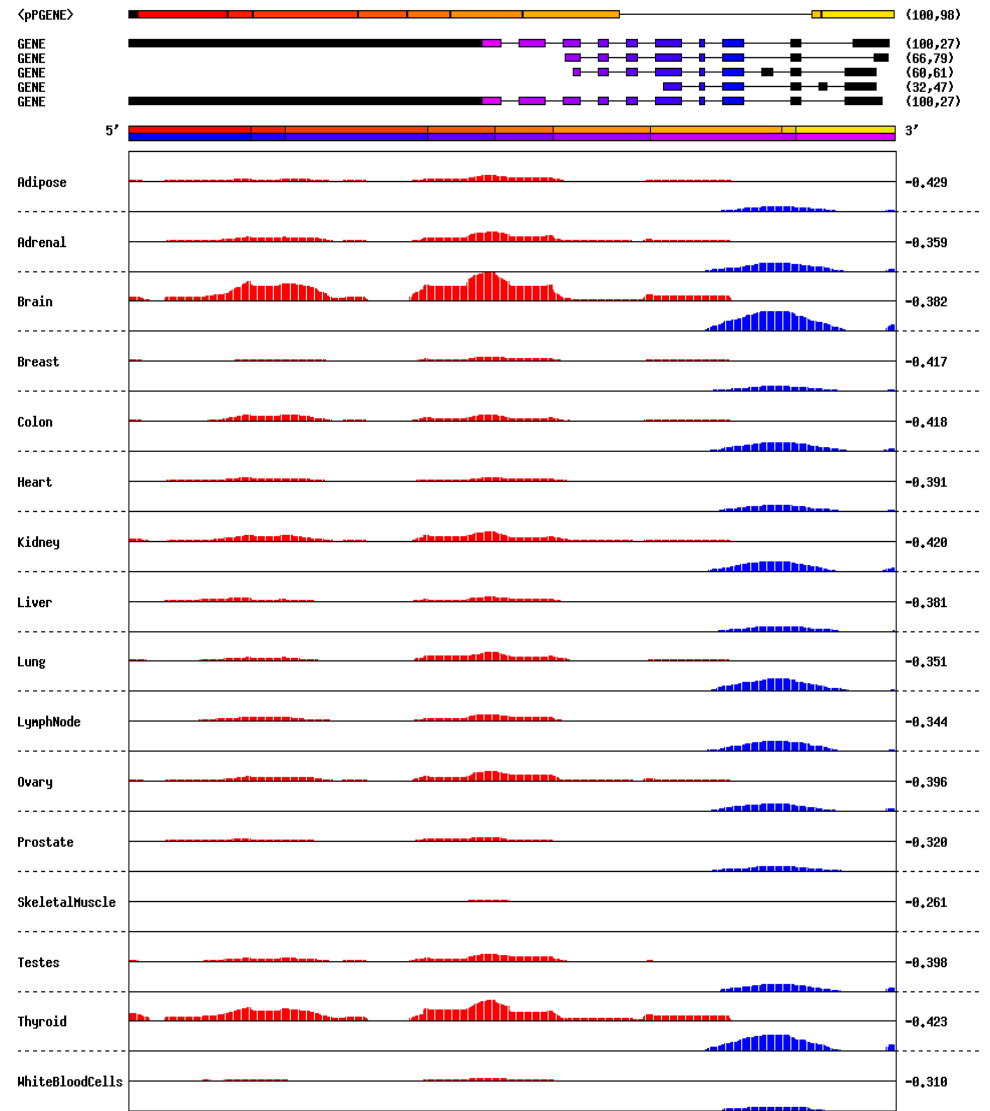
Name: ENSG00000232553\_ENST00000416636\_1, Length: 1461, %ID: 96.6, APC: -0,052, APNC: 0,012  
 Scale [0,00 4,02], Average: 0,96  
 Scale [0,00 4,02], Average: 0,73



Name: ENSG00000174028\_ENST00000312214, Length: 681  
 Scale [0,00 12,55], Average: 0,89



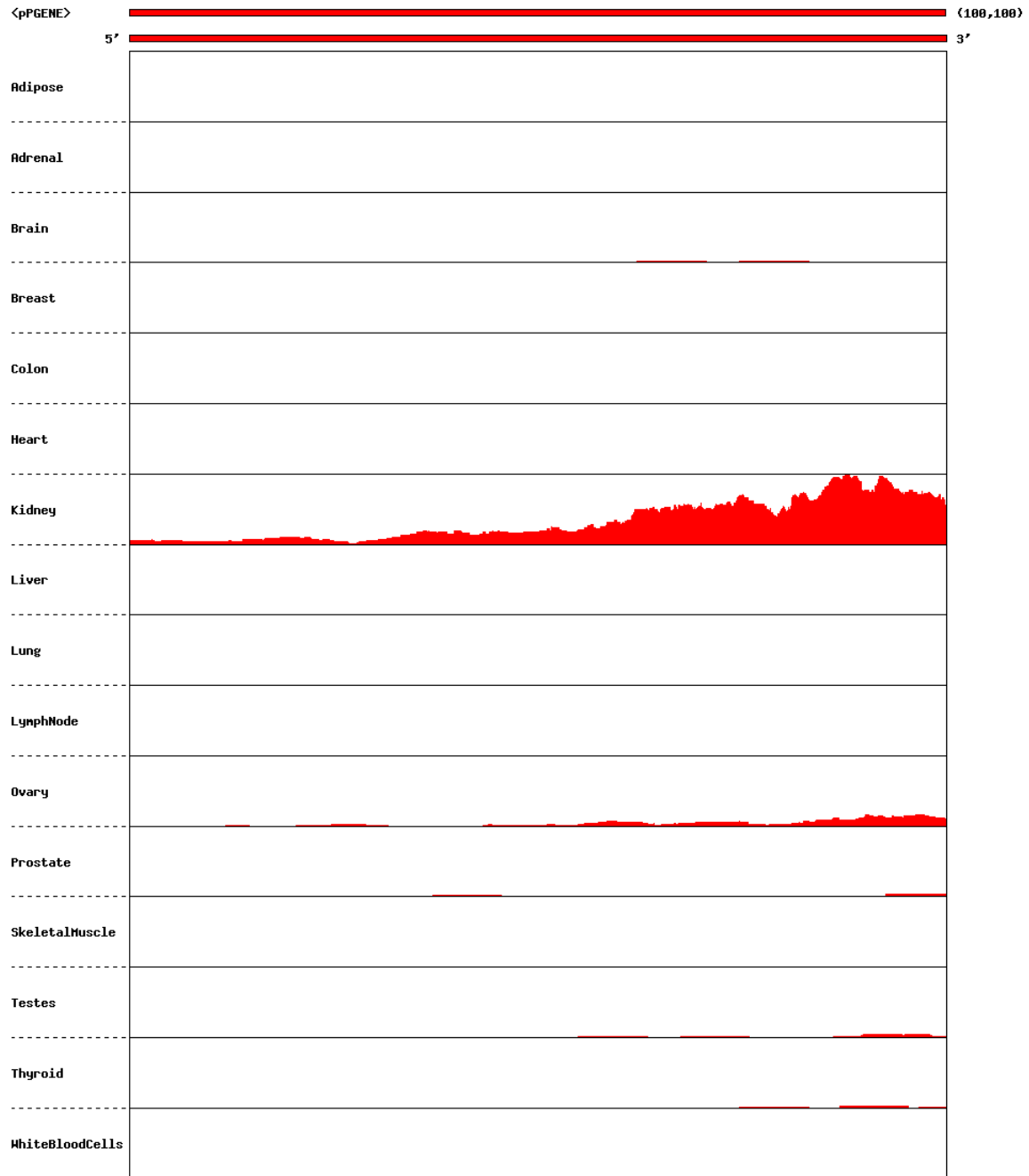
Name: ENSG00000174028\_ENST00000312214\_1, Length: 670, %ID: 100,0, APC: 0,352, APMC: -0,375  
 Scale [0,00 12,55], Average: 0,89  
 Scale [0,00 12,55], Average: 0,42



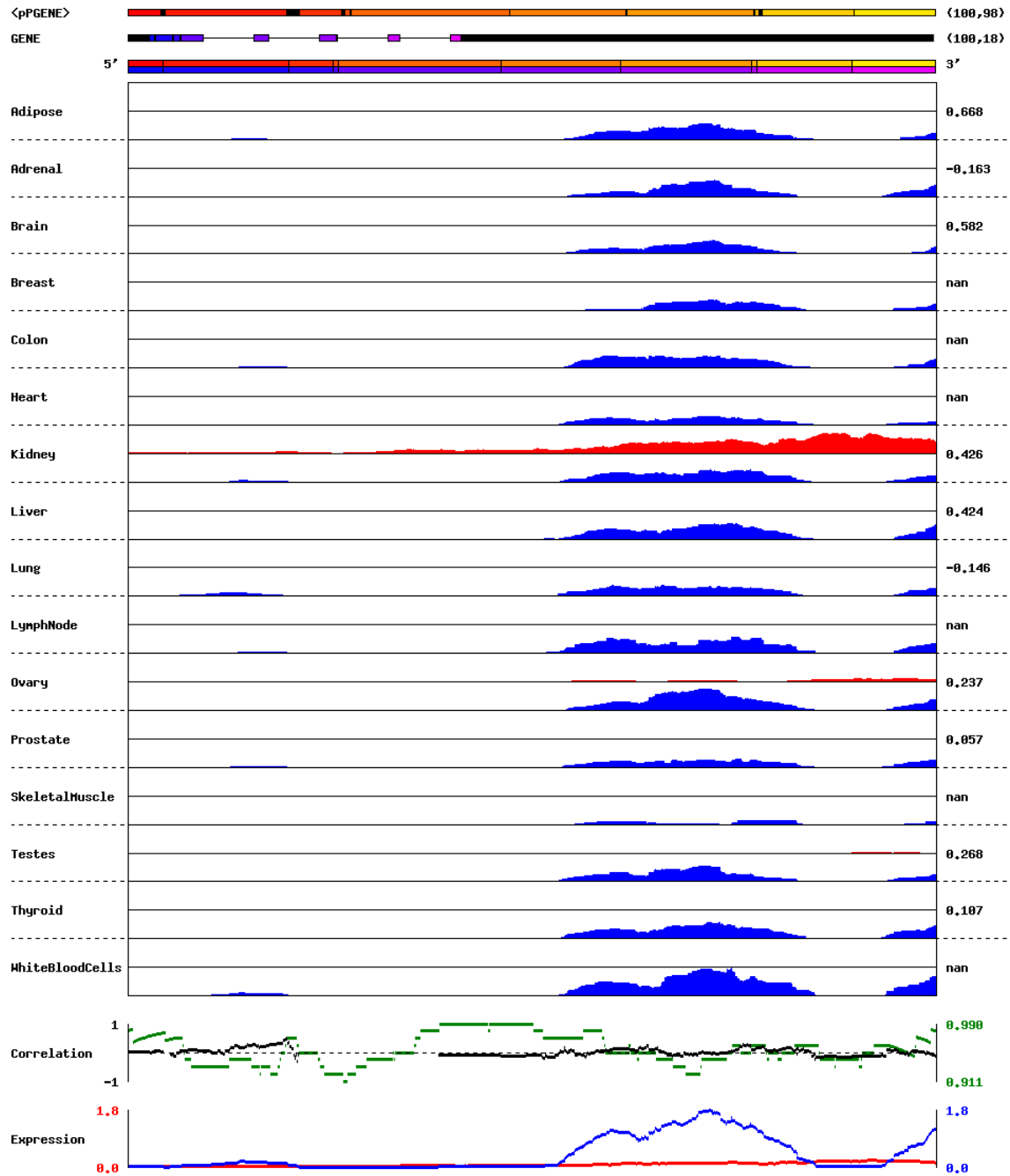


# Example with multiple alignment pairs

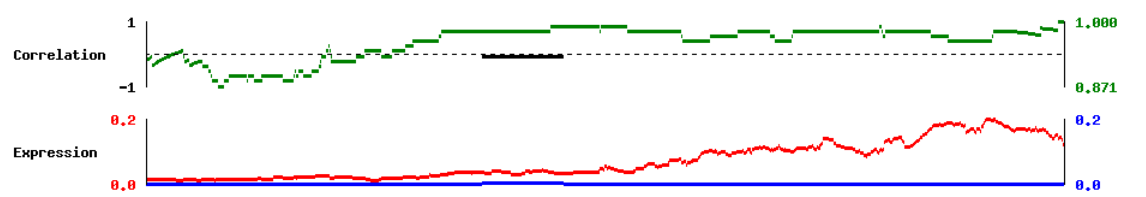
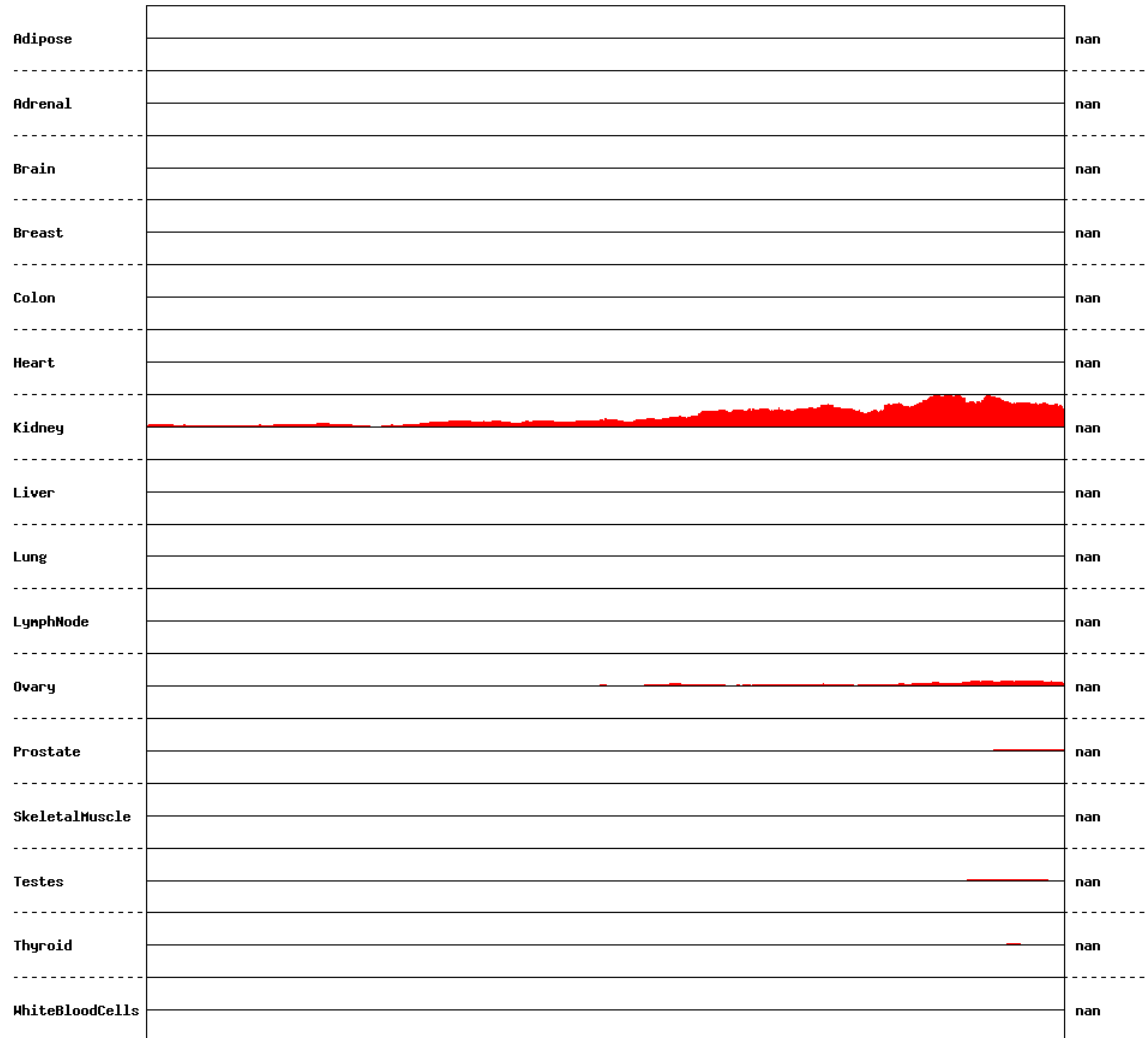
Name: ENSG00000234685\_ENST00000417358, Length: 873  
Scale [0.00 2.78], Average: 0.07



Name: ENSG00000234685\_ENST00000417358\_2, Length: 852, %ID: 95.5, APC: 0.011, APHC: 0.246  
 Scale [0.00 3.79], Average: 0.07  
 Scale [0.00 3.79], Average: 0.39



Name: ENSG00000234685\_ENST00000417358\_1, Length: 844, %ID: 95.9, APC: -0.075, APHC: nan  
 Scale [0.00 2.78], Average: 0.07  
 Scale [0.00 2.78], Average: 0.00



Name: ENSG00000234685\_ENST00000417358\_3, Length: 854, %ID: 95.1, APC: 0.129, APHC: 0.193  
 Scale [0.00 2.78], Average: 0.07  
 Scale [0.00 2.78], Average: 0.05

