

Table S2: Summary of RepeatMasker information.

```
=====
file name: testis_peaks-20.bed.fk0.fa
sequences: 40808
total length: 1256671 bp (1256671 bp excl N/X-runs)
GC level: 40.63 %
bases masked: 306549 bp ( 24.39 %)
=====
```

	number of elements*	length occupied	percentage of sequence

SINEs:	670	19162 bp	1.52 %
Alu/B1	7	250 bp	0.02 %
B2-B4	651	18539 bp	1.48 %
IDs	0	0 bp	0.00 %
MIRs	6	220 bp	0.02 %
LINEs:	1385	41872 bp	3.33 %
LINE1	1383	41809 bp	3.33 %
LINE2	2	63 bp	0.01 %
L3/CR1	0	0 bp	0.00 %
LTR elements:	7610	240187 bp	19.11 %
ERVL	465	14644 bp	1.17 %
ERVL-MaLRs	148	4724 bp	0.38 %
ERV_classI	422	13089 bp	1.04 %
ERV_classII	6575	207730 bp	16.53 %
DNA elements:	16	542bp	0.04 %
hAT-Charlie	16	542 bp	0.04 %
TcMar-Tigger	0	0 bp	0.00 %
Unclassified:	1	45 bp	0.00 %
Total interspersed repeats:		301808 bp	24.02 %
Small RNA:	140	4205 bp	0.33 %
Satellites:	0	0 bp	0.00 %
Simple repeats:	18	536 bp	0.04 %
Low complexity:	0	0 bp	0.00 %
=====			

* most repeats fragmented by insertions or deletions
have been counted as one element

The query species was assumed to be mus musculus
RepeatMasker version open-4.0.6 , default mode

run with rmblastn version 2.2.27+
RepBase Update 20150807, RM database version 20150807

Table S2: Summary of RepeatMasker information.

```
=====
file name: cortex_peaks-20.bed.fk0.fa
sequences:      1963
total length:   48057 bp (48057 bp excl N/X-runs)
GC level:       46.70 %
bases masked:   2978 bp ( 6.20 %)
=====
```

	number of elements*	length occupied	percentage of sequence
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SINEs:	10	294 bp	0.61 %
Alu/B1	4	132 bp	0.27 %
B2-B4	0	0 bp	0.00 %
IDs	0	0 bp	0.00 %
MIRs	0	0 bp	0.00 %

LINEs:	0	0 bp	0.00 %
LINE1	0	0 bp	0.00 %
LINE2	0	0 bp	0.00 %
L3/CR1	0	0 bp	0.00 %

LTR elements:	0	0 bp	0.00 %
ERV	0	0 bp	0.00 %
ERV-MaLRs	0	0 bp	0.00 %
ERV_classI	0	0 bp	0.00 %
ERV_classII	0	0 bp	0.00 %

DNA elements:	0	0 bp	0.00 %
hAT-Charlie	0	0 bp	0.00 %
TcMar-Tigger	0	0 bp	0.00 %

Unclassified:	0	0 bp	0.00 %
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Total interspersed repeats: 294 bp 0.61 %

Small RNA:	76	2561 bp	5.33 %
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Satellites:	0	0 bp	0.00 %
Simple repeats:	4	123 bp	0.26 %
Low complexity:	0	0 bp	0.00 %

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=====
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```

The query species was assumed to be mus musculus
RepeatMasker version open-4.0.6 , default mode

run with rmbblastn version 2.2.27+
RepBase Update 20150807, RM database version 20150807

Table S2: Summary of RepeatMasker information.

```
=====
file name: hippocampus_peaks-20.bed.fk0.fa
sequences:      5494
total length:   146098 bp (146098 bp excl N/X-runs)
GC level:       44.09 %
bases masked:   8026 bp ( 5.49 %)
=====
```

	number of elements*	length occupied	percentage of sequence

SINEs:	69	2226 bp	1.52 %
Alu/B1	8	244 bp	0.17 %
B2-B4	53	1780 bp	1.22 %
IDs	0	0 bp	0.00 %
MIRs	0	0 bp	0.00 %
 LINEs:	66	2176 bp	1.49 %
LINE1	66	2176 bp	1.49 %
LINE2	0	0 bp	0.00 %
L3/CR1	0	0 bp	0.00 %
 LTR elements:	56	1798 bp	1.23 %
ERV1	1	33 bp	0.02 %
ERV1-MaLRs	28	893 bp	0.61 %
ERV_classI	7	230 bp	0.16 %
ERV_classII	20	642 bp	0.44 %
 DNA elements:	0	0bp	0.00 %
hAT-Charlie	0	0 bp	0.00 %
TcMar-Tigger	0	0 bp	0.00 %
 Unclassified:	0	0 bp	0.00 %
 Total interspersed repeats:		6200 bp	4.24 %

Small RNA: 40 1326 bp 0.91 %

Satellites: 18 478 bp 0.33 %
Simple repeats: 1 22 bp 0.02 %
Low complexity: 0 0 bp 0.00 %

```
=====
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```

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run with rmbblastn version 2.2.27+
RepBase Update 20150807, RM database version 20150807

Table S2: Summary of RepeatMasker information.

```
=====
file name: kidney_peaks-20.bed.fk0.fa
sequences:      580
total length:   13735 bp (13735 bp excl N/X-runs)
GC level:      48.45 %
bases masked:   1410 bp ( 10.27 %)
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```

	number of elements*	length occupied	percentage of sequence

SINEs:	5	131 bp	0.95 %
Alu/B1	0	0 bp	0.00 %
B2-B4	0	0 bp	0.00 %
IDs	0	0 bp	0.00 %
MIRs	0	0 bp	0.00 %
LINEs:	0	0 bp	0.00 %
LINE1	0	0 bp	0.00 %
LINE2	0	0 bp	0.00 %
L3/CR1	0	0 bp	0.00 %
LTR elements:	0	0 bp	0.00 %
ERV	0	0 bp	0.00 %
ERV-MaLRs	0	0 bp	0.00 %
ERV_classI	0	0 bp	0.00 %
ERV_classII	0	0 bp	0.00 %
DNA elements:	0	0bp	0.00 %
hAT-Charlie	0	0 bp	0.00 %
TcMar-Tigger	0	0 bp	0.00 %
Unclassified:	0	0 bp	0.00 %
Total interspersed repeats:		131 bp	0.95 %
Small RNA:	43	1279 bp	9.31 %
Satellites:	0	0 bp	0.00 %
Simple repeats:	0	0 bp	0.00 %
Low complexity:	0	0 bp	0.00 %

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The query species was assumed to be mus musculus
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RepBase Update 20150807, RM database version 20150807

Table S2: Summary of RepeatMasker information.

```
=====
file name: liver_peaks-20.bed.fk0.fa
sequences:      406
total length:   9547 bp (9547 bp excl N/X-runs)
GC level:       46.32 %
bases masked:   207 bp ( 2.17 %)
=====
```

	number of elements*	length occupied	percentage of sequence

SINEs:	1	36 bp	0.38 %
Alu/B1	0	0 bp	0.00 %
B2-B4	1	36 bp	0.38 %
IDs	0	0 bp	0.00 %
MIRs	0	0 bp	0.00 %
LINEs:	0	0 bp	0.00 %
LINE1	0	0 bp	0.00 %
LINE2	0	0 bp	0.00 %
L3/CR1	0	0 bp	0.00 %
LTR elements:	0	0 bp	0.00 %
ERV	0	0 bp	0.00 %
ERV-MaLRs	0	0 bp	0.00 %
ERV_classI	0	0 bp	0.00 %
ERV_classII	0	0 bp	0.00 %
DNA elements:	0	0 bp	0.00 %
hAT-Charlie	0	0 bp	0.00 %
TcMar-Tigger	0	0 bp	0.00 %
Unclassified:	0	0 bp	0.00 %
Total interspersed repeats:		36 bp	0.38 %
Small RNA:	6	171 bp	1.79 %
Satellites:	0	0 bp	0.00 %
Simple repeats:	0	0 bp	0.00 %
Low complexity:	0	0 bp	0.00 %
=====			

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The query species was assumed to be mus musculus
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